STATA BAYESIAN ANALYSIS REFERENCE MANUAL
RELEASE 18

A Stata Press Publication
StataCorp LLC
College Station, Texas

Version 18

Published by Stata Press, 4905 Lakeway Drive, College Station, Texas 77845

ISBN-10: 1-59718-372-5
ISBN-13: 978-1-59718-372-7

The suggested citation for this software is

> StataCorp. 2023. *Stata 18*. Statistical software. StataCorp LLC.

The suggested citation for this manual is

> StataCorp. 2023. *Stata 18 Bayesian Analysis Reference Manual*. College Station, TX: Stata Press.

Contents

Cross-referencing the documentation

When reading this manual, you will find references to other Stata manuals, for example, **[U] 27 Overview of Stata estimation commands**; [R] **regress**; and [D] **reshape**. The first example is a reference to chapter 27, *Overview of Stata estimation commands*, in the *User's Guide*; the second is a reference to the `regress` entry in the *Base Reference Manual*; and the third is a reference to the `reshape` entry in the *Data Management Reference Manual*.

All the manuals in the Stata Documentation have a shorthand notation:

[GSM]	*Getting Started with Stata for Mac*
[GSU]	*Getting Started with Stata for Unix*
[GSW]	*Getting Started with Stata for Windows*
[U]	*Stata User's Guide*
[R]	*Stata Base Reference Manual*
[ADAPT]	*Stata Adaptive Designs: Group Sequential Trials Reference Manual*
[BAYES]	*Stata Bayesian Analysis Reference Manual*
[BMA]	*Stata Bayesian Model Averaging Reference Manual*
[CAUSAL]	*Stata Causal Inference and Treatment-Effects Estimation Reference Manual*
[CM]	*Stata Choice Models Reference Manual*
[D]	*Stata Data Management Reference Manual*
[DSGE]	*Stata Dynamic Stochastic General Equilibrium Models Reference Manual*
[ERM]	*Stata Extended Regression Models Reference Manual*
[FMM]	*Stata Finite Mixture Models Reference Manual*
[FN]	*Stata Functions Reference Manual*
[G]	*Stata Graphics Reference Manual*
[IRT]	*Stata Item Response Theory Reference Manual*
[LASSO]	*Stata Lasso Reference Manual*
[XT]	*Stata Longitudinal-Data/Panel-Data Reference Manual*
[META]	*Stata Meta-Analysis Reference Manual*
[ME]	*Stata Multilevel Mixed-Effects Reference Manual*
[MI]	*Stata Multiple-Imputation Reference Manual*
[MV]	*Stata Multivariate Statistics Reference Manual*
[PSS]	*Stata Power, Precision, and Sample-Size Reference Manual*
[P]	*Stata Programming Reference Manual*
[RPT]	*Stata Reporting Reference Manual*
[SP]	*Stata Spatial Autoregressive Models Reference Manual*
[SEM]	*Stata Structural Equation Modeling Reference Manual*
[SVY]	*Stata Survey Data Reference Manual*
[ST]	*Stata Survival Analysis Reference Manual*
[TABLES]	*Stata Customizable Tables and Collected Results Reference Manual*
[TS]	*Stata Time-Series Reference Manual*
[I]	*Stata Index*
[M]	*Mata Reference Manual*

Title

Intro — Introduction to Bayesian analysis

Description Remarks and examples References Also see

Description

This entry provides a software-free introduction to Bayesian analysis. See [BAYES] **Bayesian commands** for an overview of the software for performing Bayesian analysis and for an overview example.

For Bayesian model averaging, which is Bayesian analysis that averages over multiple plausible models, see [BMA] **Intro**.

Remarks and examples

Remarks are presented under the following headings:

The first five sections provide a general introduction to Bayesian analysis. The remaining sections provide a more technical discussion of the concepts of Bayesian analysis.

What is Bayesian analysis?

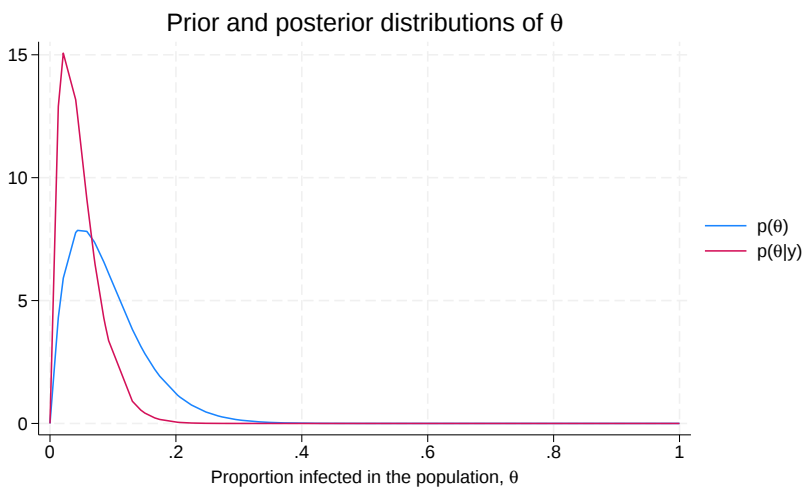
Bayesian analysis is a statistical analysis that answers research questions about unknown parameters of statistical models by using probability statements. Bayesian analysis rests on the assumption that all model parameters are random quantities and thus can incorporate prior knowledge. This assumption is in sharp contrast with the more traditional, also called frequentist, statistical inference where all parameters are considered unknown but fixed quantities. Bayesian analysis follows a simple rule of probability, the Bayes rule, which provides a formalism for combining prior information with evidence from the data at hand. The Bayes rule is used to form the so called posterior distribution of model parameters. The posterior distribution results from updating the prior knowledge about model

parameters with evidence from the observed data. Bayesian analysis uses the posterior distribution to form various summaries for the model parameters including point estimates such as posterior means, medians, percentiles, and interval estimates such as credible intervals. Moreover, all statistical tests about model parameters can be expressed as probability statements based on the estimated posterior distribution.

As a quick introduction to Bayesian analysis, we use an example, described in Hoff (2009, 3), of estimating the prevalence of a rare infectious disease in a small city. A small random sample of 20 subjects from the city will be checked for infection. The parameter of interest $\theta \in [0, 1]$ is the fraction of infected individuals in the city. Outcome y records the number of infected individuals in the sample. A reasonable sampling model for y is a binomial model: $y|\theta \sim \text{Binomial}(20, \theta)$. Based on the studies from other comparable cities, the infection rate ranged between 0.05 and 0.20, with an average prevalence of 0.10. To use this information, we must conduct Bayesian analysis. This information can be incorporated into a Bayesian model with a prior distribution for θ, which assigns a large probability between 0.05 and 0.20, with the expected value of θ close to 0.10. One potential prior that satisfies this condition is a $\text{Beta}(2, 20)$ prior with the expected value of $2/(2+20) = 0.09$. So, let's assume this prior for the infection rate θ, that is, $\theta \sim \text{Beta}(2, 20)$. We sample individuals and observe none who have an infection, that is, $y = 0$. This value is not that uncommon for a small sample and a rare disease. For example, for a true rate $\theta = 0.05$, the probability of observing 0 infections in a sample of 20 individuals is about 36% according to the binomial distribution. So, our Bayesian model can be defined as follows:

$$y|\theta \sim \text{Binomial}(20, \theta)$$
$$\theta \sim \text{Beta}(2, 20)$$

For this Bayesian model, we can actually compute the posterior distribution of $\theta|y$, which is $\theta|y \sim \text{Beta}(2+0, 20+20-0) = \text{Beta}(2, 40)$. The prior and posterior distributions of θ are depicted below.



The posterior density (shown in red) is more peaked and shifted to the left compared with the prior distribution (shown in blue). The posterior distribution combined the prior information about θ with the information from the data, from which $y = 0$ provided evidence for a low value of θ and shifted the prior density to the left to form the posterior density. Based on this posterior distribution, the

posterior mean estimate of θ is $2/(2+40) = 0.048$ and the posterior probability that, for example, $\theta < 0.10$ is about 93%.

If we compute a standard frequentist estimate of a population proportion θ as a fraction of the infected subjects in the sample, $\overline{y} = y/n$, we will obtain 0 with the corresponding 95% confidence interval $(\overline{y} - 1.96\sqrt{\overline{y}(1-\overline{y})/n}, \overline{y} + 1.96\sqrt{\overline{y}(1-\overline{y})/n})$ reducing to 0 as well. It may be difficult to convince a health policy maker that the prevalence of the disease in that city is indeed 0, given the small sample size and the prior information available from comparable cities about a nonzero prevalence of this disease.

We used a beta prior distribution in this example, but we could have chosen another prior distribution that supports our prior knowledge. For the final analysis, it is important to consider a range of different prior distributions and investigate the sensitivity of the results to the chosen priors.

For more details about this example, see Hoff (2009). Also see *Beta-binomial model* in [BAYES] **bayesmh** for how to fit this model using `bayesmh`.

Rabe-Hesketh and Skrondal (2022, chap. 16) and Cameron and Trivedi (2022, chap. 28) provide introductions to Bayesian analysis with Stata-specific examples.

Bayesian versus frequentist analysis, or why Bayesian analysis?

Why use Bayesian analysis? Perhaps a better question is when to use Bayesian analysis and when to use frequentist analysis. The answer to this question mainly lies in your research problem. You should choose an analysis that answers your specific research questions. For example, if you are interested in estimating the probability that the parameter of interest belongs to some prespecified interval, you will need the Bayesian framework, because this probability cannot be estimated within the frequentist framework. If you are interested in a repeated-sampling inference about your parameter, the frequentist framework provides that.

Bayesian and frequentist approaches have very different philosophies about what is considered fixed and, therefore, have very different interpretations of the results. The Bayesian approach assumes that the observed data sample is fixed and that model parameters are random. The posterior distribution of parameters is estimated based on the observed data and the prior distribution of parameters and is used for inference. The frequentist approach assumes that the observed data are a repeatable random sample and that parameters are unknown but fixed and constant across the repeated samples. The inference is based on the sampling distribution of the data or of the data characteristics (statistics). In other words, Bayesian analysis answers questions based on the distribution of parameters conditional on the observed sample, whereas frequentist analysis answers questions based on the distribution of statistics obtained from repeated hypothetical samples, which would be generated by the same process that produced the observed sample given that parameters are unknown but fixed. Frequentist analysis consequently requires that the process that generated the observed data is repeatable. This assumption may not always be feasible. For example, in meta-analysis, where the observed sample represents the collected studies of interest, one may argue that the collection of studies is a one-time experiment.

Frequentist analysis is entirely data-driven and strongly depends on whether or not the data assumptions required by the model are met. On the other hand, Bayesian analysis provides a more robust estimation approach by using not only the data at hand but also some existing information or knowledge about model parameters.

In frequentist statistics, estimators are used to approximate the true values of the unknown parameters, whereas Bayesian statistics provides an entire distribution of the parameters. In our example of a prevalence of an infectious disease from *What is Bayesian analysis?*, frequentist analysis produced one point estimate for the prevalence, whereas Bayesian analysis estimated the entire posterior distribution of the prevalence based on a given sample.

Frequentist inference is based on the sampling distributions of estimators of parameters and provides parameter point estimates and their standard errors as well as confidence intervals. The exact sampling distributions are rarely known and are often approximated by a large-sample normal distribution. Bayesian inference is based on the posterior distribution of the parameters and provides summaries of this distribution including posterior means and their MCMC standard errors (MCSE) as well as credible intervals. Although exact posterior distributions are known only in a number of cases, general posterior distributions can be estimated via, for example, Markov chain Monte Carlo (MCMC) sampling without any large-sample approximation.

Frequentist confidence intervals do not have straightforward probabilistic interpretations as do Bayesian credible intervals. For example, the interpretation of a 95% confidence interval is that if we repeat the same experiment many times and compute confidence intervals for each experiment, then 95% of those intervals will contain the true value of the parameter. For any given confidence interval, the probability that the true value is in that interval is either zero or one, and we do not know which. We may only infer that any given confidence interval provides a plausible range for the true value of the parameter. A 95% Bayesian credible interval, on the other hand, provides a range for a parameter such that the probability that the parameter lies in that range is 95%.

Frequentist hypothesis testing is based on a deterministic decision using a prespecified significance level of whether to accept or reject the null hypothesis based on the observed data, assuming that the null hypothesis is actually true. The decision is based on a p-value computed from the observed data. The interpretation of the p-value is that if we repeat the same experiment and use the same testing procedure many times, then given our null hypothesis is true, we will observe the result (test statistic) as extreme or more extreme than the one observed in the sample $(100 \times p\text{-value})\%$ of the times. The p-value cannot be interpreted as a probability of the null hypothesis, which is a common misinterpretation. In fact, it answers the question of how likely are our data given that the null hypothesis is true, and not how likely is the null hypothesis given our data. The latter question can be answered by Bayesian hypothesis testing, where we can compute the probability of any hypothesis of interest.

How to do Bayesian analysis

Bayesian analysis starts with the specification of a posterior model. The posterior model describes the probability distribution of all model parameters conditional on the observed data and some prior knowledge. The posterior distribution has two components: a likelihood, which includes information about model parameters based on the observed data, and a prior, which includes prior information (before observing the data) about model parameters. The likelihood and prior models are combined using the Bayes rule to produce the posterior distribution:

$$\text{Posterior} \propto \text{Likelihood} \times \text{Prior}$$

If the posterior distribution can be derived in a closed form, we may proceed directly to the inference stage of Bayesian analysis. Unfortunately, except for some special models, the posterior distribution is rarely available explicitly and needs to be estimated via simulations. MCMC sampling can be used to simulate potentially very complex posterior models with an arbitrary level of precision. MCMC methods for simulating Bayesian models are often demanding in terms of specifying an efficient sampling algorithm and verifying the convergence of the algorithm to the desired posterior distribution. See [BAYES] **Bayesian estimation**.

Inference is the next step of Bayesian analysis. If MCMC sampling is used for approximating the posterior distribution, the convergence of MCMC must be established before proceeding to inference (see, for example, [BAYES] **bayesgraph** and [BAYES] **bayesstats grubin**). Point and interval estimators

are either derived from the theoretical posterior distribution or estimated from a sample simulated from the posterior distribution. Many Bayesian estimators, such as posterior mean and posterior standard deviation, involve integration. If the integration cannot be performed analytically to obtain a closed-form solution, sampling techniques such as Monte Carlo integration and MCMC and numerical integration are commonly used. See [BAYES] **Bayesian postestimation** and [BAYES] **bayesstats**.

Another important step of Bayesian analysis is model checking, which is typically performed via posterior predictive checking. The idea behind posterior predictive checking is the comparison of various aspects of the distribution of the observed data with those of the replicated data. Replicated data are simulated from the posterior predictive distribution of the fitted Bayesian model under the same conditions that generated the observed data, such as the same values of covariates, etc. The discrepancy between the distributions of the observed and replicated data is measured by test quantities (functions of the data and model parameters) and is quantified by so-called posterior predictive p-values. See [BAYES] **bayesstats ppvalues** and [BAYES] **bayespredict**.

Bayesian hypothesis testing can take two forms, which we refer to as interval-hypothesis testing and model-hypothesis testing. In an interval-hypothesis testing, the probability that a parameter or a set of parameters belongs to a particular interval or intervals is computed. In model hypothesis testing, the probability of a Bayesian model of interest given the observed data is computed. See [BAYES] **bayestest**.

Model comparison is another common step of Bayesian analysis. The Bayesian framework provides a systematic and consistent approach to model comparison using the notion of posterior odds and related to them Bayes factors. See [BAYES] **bayesstats ic** for details.

Finally, prediction of some future unobserved data may also be of interest in Bayesian analysis. The prediction of a new data point is performed conditional on the observed data using the so-called posterior predictive distribution, which involves integrating out all parameters from the model with respect to their posterior distribution. Again, Monte Carlo integration is often the only feasible option for obtaining predictions. Prediction can also be helpful in estimating the goodness of fit of a model. See [BAYES] **bayespredict**.

Advantages and disadvantages of Bayesian analysis

Bayesian analysis is a powerful analytical tool for statistical modeling, interpretation of results, and prediction of data. It can be used when there are no standard frequentist methods available or the existing frequentist methods fail. However, one should be aware of both the advantages and disadvantages of Bayesian analysis before applying it to a specific problem.

The universality of the Bayesian approach is probably its main methodological advantage to the traditional frequentist approach. Bayesian inference is based on a single rule of probability, the Bayes rule, which is applied to all parametric models. This makes the Bayesian approach universal and greatly facilitates its application and interpretation. The frequentist approach, however, relies on a variety of estimation methods designed for specific statistical problems and models. Often, inferential methods designed for one class of problems cannot be applied to another class of models.

In Bayesian analysis, we can use previous information, either belief or experimental evidence, in a data model to acquire more balanced results for a particular problem. For example, incorporating prior information can mitigate the effect of a small sample size. Importantly, the use of the prior evidence is achieved in a theoretically sound and principled way.

By using the knowledge of the entire posterior distribution of model parameters, Bayesian inference is far more comprehensive and flexible than the traditional inference.

Bayesian inference is exact, in the sense that estimation and prediction are based on the posterior distribution. The latter is either known analytically or can be estimated numerically with an arbitrary

precision. In contrast, many frequentist estimation procedures such as maximum likelihood rely on the assumption of asymptotic normality for inference.

Bayesian inference provides a straightforward and more intuitive interpretation of the results in terms of probabilities. For example, credible intervals are interpreted as intervals to which parameters belong with a certain probability, unlike the less straightforward repeated-sampling interpretation of the confidence intervals.

Bayesian models satisfy the likelihood principle (Berger and Wolpert 1988) that the information in a sample is fully represented by the likelihood function. This principle requires that if the likelihood function of one model is proportional to the likelihood function of another model, then inferences from the two models should give the same results. Some researchers argue that frequentist methods that depend on the experimental design may violate the likelihood principle.

Finally, as we briefly mentioned earlier, the estimation precision in Bayesian analysis is not limited by the sample size—Bayesian simulation methods may provide an arbitrary degree of precision.

Despite the conceptual and methodological advantages of the Bayesian approach, its application in practice is still considered controversial sometimes. There are two main reasons for this—the presumed subjectivity in specifying prior information and the computational challenges in implementing Bayesian methods. Along with the objectivity that comes from the data, the Bayesian approach uses potentially subjective prior distribution. That is, different individuals may specify different prior distributions. Proponents of frequentist statistics argue that for this reason, Bayesian methods lack objectivity and should be avoided. Indeed, there are settings such as clinical trial cases when the researchers want to minimize a potential bias coming from preexisting beliefs and achieve more objective conclusions. Even in such cases, however, a balanced and reliable Bayesian approach is possible. The trend in using noninformative priors in Bayesian models is an attempt to address the issue of subjectivity. On the other hand, some Bayesian proponents argue that the classical methods of statistical inference have built-in subjectivity such as a choice for a sampling procedure, whereas the subjectivity is made explicit in Bayesian analysis.

Building a reliable Bayesian model requires extensive experience from the researchers, which leads to the second difficulty in Bayesian analysis—setting up a Bayesian model and performing analysis is a demanding and involving task. This is true, however, to an extent for any statistical modeling procedure.

Lastly, one of the main disadvantages of Bayesian analysis is the computational cost. As a rule, Bayesian analysis involves intractable integrals that can only be computed using intensive numerical methods. Most of these methods such as MCMC are stochastic by nature and do not comply with the natural expectation from a user of obtaining deterministic results. Using simulation methods does not compromise the discussed advantages of Bayesian approach, but unquestionably adds to the complexity of its application in practice.

For more discussion about advantages and disadvantages of Bayesian analysis, see, for example, Thompson (2012), Bernardo and Smith (2000), and Berger and Wolpert (1988).

Brief background and literature review

The principles of Bayesian analysis date back to the work of Thomas Bayes, who was a Presbyterian minister in Tunbridge Wells and Pierre Laplace, a French mathematician, astronomer, and physicist in the 18th century. Bayesian analysis started as a simple intuitive rule, named after Bayes, for updating beliefs on account of some evidence. For the next 200 years, however, Bayes's rule was just an obscure idea. Along with the rapid development of the standard or frequentist statistics in 20th century, Bayesian methodology was also developing, although with less attention and at a slower pace. One of the obstacles for the progress of Bayesian ideas has been the lasting opinion among mainstream

statisticians of it being subjective. Another more-tangible problem for adopting Bayesian models in practice has been the lack of adequate computational resources. Nowadays, Bayesian statistics is widely accepted by researchers and practitioners as a valuable and feasible alternative.

Bayesian analysis proliferates in diverse areas including industry and government, but its application in sciences and engineering is particularly visible. Bayesian statistical inference is used in econometrics (Poirier [1995]; Chernozhukov and Hong [2003]; Kim, Shephard, and Chib [1998], Zellner [1997]); education (Johnson 1997); epidemiology (Greenland 1998); engineering (Godsill and Rayner 1998); genetics (Iversen, Parmigiani, and Berry 1999); social sciences (Pollard 1986); hydrology (Parent et al. 1998); quality management (Rios Insua 1990); atmospheric sciences (Berliner et al. 1999); and law (DeGroot, Fienberg, and Kadane 1986), to name a few.

The subject of general statistics has been greatly influenced by the development of Bayesian ideas. Bayesian methodologies are now present in biostatistics (Carlin and Louis [2009]; Berry and Stangl [1996]); generalized linear models (Dey, Ghosh, and Mallick 2000); hierarchical modeling (Hobert 2000); statistical design (Chaloner and Verdinelli 1995); classification and discrimination (Neal [1996]; Neal [1999]); graphical models (Pearl 1998); nonparametric estimation (Müller and Vidakovic [1999]; Dey, Müller, and Sinha [1998]); survival analysis (Barlow, Clarotti, and Spizzichino 1993); sequential analysis (Carlin, Kadane, and Gelfand 1998); predictive inference (Aitchison and Dunsmore 1975); spatial statistics (Wolpert and Ickstadt [1998]; Besag and Higdon [1999]); testing and model selection (Kass and Raftery [1995]; Berger and Pericchi [1996]; Berger [2006]); and time series (Pole, West, and Harrison [1994]; West and Harrison [1997]).

Recent advances in computing allowed practitioners to perform Bayesian analysis using simulations. The simulation tools came from outside the statistics field—Metropolis et al. (1953) developed what is now known as a random-walk Metropolis algorithm to solve problems in statistical physics. Another landmark discovery was the Gibbs sampling algorithm (Geman and Geman 1984), initially used in image processing, which showed that exact sampling from a complex and otherwise intractable probability distribution is possible. These ideas were the seeds that led to the development of Markov chain Monte Carlo (MCMC)—a class of iterative simulation methods proved to be indispensable tools for Bayesian computations. Starting from the early 1990s, MCMC-based techniques slowly emerged in the mainstream statistical practice. More powerful and specialized methods appeared, such as perfect sampling (Propp and Wilson 1996), reversible-jump MCMC (Green 1995) for traversing variable dimension state spaces, and particle systems (Gordon, Salmond, and Smith 1993). Consequent widespread application of MCMC was imminent (Berger 2000) and influenced various specialized fields. For example, Gelman and Rubin (1992) investigated MCMC for the purpose of exploring posterior distributions; Geweke (1999) surveyed simulation methods for Bayesian inference in econometrics; Kim, Shephard, and Chib (1998) used MCMC simulations to fit stochastic volatility models; Carlin, Kadane, and Gelfand (1998) implemented Monte Carlo methods for identifying optimal strategies in clinical trials; Chib and Greenberg (1995) provided Bayesian formulation of a number of important econometrics models; and Chernozhukov and Hong (2003) reviewed some econometrics models involving Laplace-type estimators from an MCMC perspective. For more comprehensive exposition of MCMC, see, for example, Robert and Casella (2004); Tanner (1996); Gamerman and Lopes (2006); Chen, Shao, and Ibrahim (2000); and Brooks et al. (2011).

Bayesian statistics

Posterior distribution

To formulate the principles of Bayesian statistics, we start with a simple case when one is concerned with the interaction of two random variables, $\mathbf{A}$ and $\mathbf{B}$. Let $p(\cdot)$ denote either a probability mass function or a density, depending on whether the variables are discrete or continuous. The rule of conditional probability,

$$p(\mathbf{A}|\mathbf{B}) = \frac{p(\mathbf{A},\mathbf{B})}{p(\mathbf{B})}$$

can be used to derive the so-called Bayes's theorem:

$$p(\mathbf{B}|\mathbf{A}) = \frac{p(\mathbf{A}|\mathbf{B})p(\mathbf{B})}{p(\mathbf{A})} \tag{1}$$

This rule also holds in the more general case when $\mathbf{A}$ and $\mathbf{B}$ are random vectors.

In a typical statistical problem, we have a data vector $\mathbf{y}$, which is assumed to be a sample from a probability model with an unknown parameter vector $\boldsymbol{\theta}$. We represent this model using the likelihood function $L(\boldsymbol{\theta};\mathbf{y}) = f(\mathbf{y};\boldsymbol{\theta}) = \prod_{i=1}^{n} f(y_i|\boldsymbol{\theta})$, where $f(y_i|\boldsymbol{\theta})$ denotes the probability density function of y_i given $\boldsymbol{\theta}$. We want to infer some properties of $\boldsymbol{\theta}$ based on the data $\mathbf{y}$. In Bayesian statistics, model parameters $\boldsymbol{\theta}$ is a random vector. We assume that $\boldsymbol{\theta}$ has a probability distribution $p(\boldsymbol{\theta}) = \pi(\boldsymbol{\theta})$, which is referred to as a prior distribution. Because both $\mathbf{y}$ and $\boldsymbol{\theta}$ are random, we can apply Bayes's theorem (1) to derive the posterior distribution of $\boldsymbol{\theta}$ given data $\mathbf{y}$,

$$p(\boldsymbol{\theta}|\mathbf{y}) = \frac{p(\mathbf{y}|\boldsymbol{\theta})p(\boldsymbol{\theta})}{p(\mathbf{y})} = \frac{f(\mathbf{y};\boldsymbol{\theta})\pi(\boldsymbol{\theta})}{m(\mathbf{y})} \tag{2}$$

where $m(\mathbf{y}) \equiv p(\mathbf{y})$, known as the marginal distribution of $\mathbf{y}$, is defined by

$$m(\mathbf{y}) = \int f(\mathbf{y};\boldsymbol{\theta})\pi(\boldsymbol{\theta})d\boldsymbol{\theta} \tag{3}$$

The marginal distribution $m(\mathbf{y})$ in (3) does not depend on the parameter of interest $\boldsymbol{\theta}$, and we can, therefore, reduce (2) to

$$p(\boldsymbol{\theta}|\mathbf{y}) \propto L(\boldsymbol{\theta};\mathbf{y})\pi(\boldsymbol{\theta}) \tag{4}$$

Equation (4) is fundamental in Bayesian analysis and states that the posterior distribution of model parameters is proportional to their likelihood and prior probability distributions. We will often use (4) in the computationally more-convenient log-scale form

$$\ln\{p(\boldsymbol{\theta}|\mathbf{y})\} = l(\boldsymbol{\theta};\mathbf{y}) + \ln\{\pi(\boldsymbol{\theta})\} - c \tag{5}$$

where $l(\cdot;\cdot)$ denotes the log likelihood of the model. Depending on the analytical procedure involving the log-posterior $\ln\{p(\boldsymbol{\theta}|\mathbf{y})\}$, the actual value of the constant $c = \ln\{m(\mathbf{y})\}$ may or may not be relevant. For valid statistical analysis, however, we will always assume that c is finite.

Selecting priors

In Bayesian analysis, we seek a balance between prior information in a form of expert knowledge or belief and evidence from data at hand. Achieving the right balance is one of the difficulties in Bayesian modeling and inference. In general, we should not allow the prior information to overwhelm the evidence from the data, especially when we have a large data sample. A famous theoretical result, the Bernstein–von Mises theorem, states that in large data samples, the posterior distribution is independent of the prior distribution and, therefore, Bayesian and likelihood-based inferences should yield essentially the same results. On the other hand, we need a strong enough prior to support weak evidence that usually comes from insufficient data. It is always good practice to perform sensitivity analysis to check the dependence of the results on the choice of a prior.

The flexibility of choosing the prior freely is one of the main controversial issues associated with Bayesian analysis and the reason why some practitioners view the latter as subjective. It is also the reason why the Bayesian practice, especially in the early days, was dominated by noninformative priors. Noninformative priors, also called flat or vague priors, assign equal probabilities to all possible states of the parameter space with the aim of rectifying the subjectivity problem. One of the disadvantages of flat priors is that they are often improper; that is, they do not specify a legitimate probability distribution. For example, a uniform prior for a continuous parameter over an unbounded domain does not integrate to a finite number. However, this is not necessarily a problem because the corresponding posterior distribution may still be proper. Although Bayesian inference based on improper priors is possible, this is equivalent to discarding the terms $\log\pi(\boldsymbol{\theta})$ and c in (5), which nullifies the benefit of Bayesian analysis because it reduces the latter to an inference based only on the likelihood. This is why there is a strong objection to the practice of noninformative priors. In recent years, an increasing number of researchers have advocated the use of sound informative priors, for example, Thompson (2014). For example, using informative priors is mandatory in areas such as genetics, where prior distributions have a physical basis and reflect scientific knowledge.

Another convenient preference for priors is to use conjugate priors. Their choice is desirable from technical and computational standpoints but may not necessarily provide a realistic representation of the model parameters. Because of the limited arsenal of conjugate priors, an inclination to overuse them severely limits the flexibility of Bayesian modeling.

Point and interval estimation

In Bayesian statistics, inference about parameters $\boldsymbol{\theta}$ is based on the posterior distribution $p(\boldsymbol{\theta}|\mathbf{y})$ and various ways of summarizing this distribution. Point and interval estimates can be used to summarize this distribution.

Commonly used point estimators are the posterior mean,

$$E(\boldsymbol{\theta}|\mathbf{y}) = \int \boldsymbol{\theta} p(\boldsymbol{\theta}|\mathbf{y}) d\boldsymbol{\theta}$$

and the posterior median, $q_{0.5}(\boldsymbol{\theta})$, which is the 0.5 quantile of the posterior; that is,

$$P\{\boldsymbol{\theta} \leq q_{0.5}(\boldsymbol{\theta}|\mathbf{y})\} = 0.5$$

Another point estimator is the posterior mode, which is the value of $\boldsymbol{\theta}$ that maximizes $p(\boldsymbol{\theta}|\mathbf{y})$.

Interval estimation is performed by constructing so-called credible intervals (CrIs). CrIs are special cases of credible regions. Let $1-\alpha \in (0,1)$ be some predefined credible level. Then, an $\{(1-\alpha)\times 100\}\%$ credible set R of θ is such that

$$\Pr(\theta \in R|\mathbf{y}) = \int_R p(\theta|\mathbf{y})d\theta = 1 - \alpha$$

We consider two types of CrIs. The first one is based on quantiles. The second one is the highest posterior density (HPD) interval.

An $\{(1-\alpha)\times 100\}\%$ quantile-based, or also known as an equal-tailed CrI, is defined as $(q_{\alpha/2}, q_{1-\alpha/2})$, where q_a denotes the ath quantile of the posterior distribution. A commonly reported equal-tailed CrI is $(q_{0.025}, q_{0.975})$.

HPD interval is defined as an $\{(1-\alpha)\times 100\}\%$ CrI of the shortest width. As its name implies, this interval corresponds to the region of the posterior density with the highest concentration. For a unimodal posterior distribution, HPD is unique, but for a multimodal distribution it may not be unique. Computational approaches for calculating HPD are described in Chen and Shao (1999) and Eberly and Casella (2003).

Comparing Bayesian models

Model comparison is another important aspect of Bayesian statistics. We are often interested in comparing two or more plausible models for our data.

Let's assume that we have models M_j parameterized by vectors $\boldsymbol{\theta}_j$, $j = 1, \ldots, r$. We may have varying degree of belief in each of these models given by prior probabilities $p(M_j)$, such that $\sum_{j=1}^{r} p(M_j) = 1$. By applying Bayes's theorem, we find the posterior model probabilities

$$p(M_j|\mathbf{y}) = \frac{p(\mathbf{y}|M_j)p(M_j)}{p(\mathbf{y})}$$

where $p(\mathbf{y}|M_j) = m_j(y)$ is the marginal likelihood of M_j with respect to $\mathbf{y}$. Because of the difficulty in calculating $p(\mathbf{y})$, it is a common practice to compare two models, say, M_j and M_k, using the posterior odds ratio

$$\text{PO}_{jk} = \frac{p(M_j|\mathbf{y})}{p(M_k|\mathbf{y})} = \frac{p(\mathbf{y}|M_j)p(M_j)}{p(\mathbf{y}|M_k)p(M_k)}$$

If all models are equally plausible, that is, $p(M_j) = 1/r$, the posterior odds ratio reduces to the so-called Bayes factors (BF) (Jeffreys 1935),

$$\text{BF}_{jk} = \frac{p(\mathbf{y}|M_j)}{p(\mathbf{y}|M_k)} = \frac{m_j(\mathbf{y})}{m_k(\mathbf{y})}$$

which are simply ratios of marginal likelihoods.

Jeffreys (1961) recommended an interpretation of BF_{jk} based on half-units of the log scale. The following table provides some rules of thumb:

$\log_{10}(\text{BF}_{jk})$	BF_{jk}	Evidence against M_k
0 to 1/2	1 to 3.2	Bare mention
1/2 to 1	3.2 to 10	Substantial
1 to 2	10 to 100	Strong
>2	>100	Decisive

The Schwarz criterion BIC (Schwarz 1978) is an approximation of BF in case of arbitrary but proper priors. Kass and Raftery (1995) and Berger (2006) provide a detailed exposition of Bayes factors, their calculation, and their role in model building and testing.

Posterior prediction

Prediction is another essential part of statistical analysis. In Bayesian statistics, prediction is performed using the posterior predictive distribution. The probability of observing some future data $\mathbf{y}^*$ given the observed data $\mathbf{y}$ can be obtained by the marginalization of

$$p(\mathbf{y}^*|\mathbf{y}) = \int p(\mathbf{y}^*|\mathbf{y}, \boldsymbol{\theta})p(\boldsymbol{\theta}|\mathbf{y})d\boldsymbol{\theta}$$

which, assuming that $\mathbf{y}^*$ is independent of $\mathbf{y}$ given $\boldsymbol{\theta}$, can be simplified to

$$p(\mathbf{y}^*|\mathbf{y}) = \int p(\mathbf{y}^*|\boldsymbol{\theta})p(\boldsymbol{\theta}|\mathbf{y})d\boldsymbol{\theta} \tag{6}$$

Equation (6) is called a posterior predictive distribution and is used for Bayesian prediction. See [BAYES] **bayespredict** and [BAYES] **bayesstats ppvalues**.

Bayesian computation

An unavoidable difficulty in performing Bayesian analysis is the need to compute integrals such as those expressing marginal distributions and posterior moments. The integrals involved in Bayesian inference are of the form $E\{g(\boldsymbol{\theta})\} = \int g(\boldsymbol{\theta})p(\boldsymbol{\theta}|\mathbf{y})d\boldsymbol{\theta}$ for some function $g(\cdot)$ of the random vector $\boldsymbol{\theta}$. With the exception of a few cases for which analytical integration is possible, the integration is performed via simulations.

Given a sample from the posterior distribution, we can use Monte Carlo integration to approximate the integrals. Let $\boldsymbol{\theta}_1$, $\boldsymbol{\theta}_2$, ..., $\boldsymbol{\theta}_T$ be an independent sample from $p(\boldsymbol{\theta}|\mathbf{y})$.

The original integral of interest $E\{g(\boldsymbol{\theta})\}$ can be approximated by

$$\widehat{g} = \frac{1}{T}\sum_{t=1}^{T} g(\boldsymbol{\theta}_t)$$

Moreover, if g is a scalar function, under some mild conditions, the central limit theorem holds

$$\widehat{g} \approx N\left[E\{g(\boldsymbol{\theta})\}, \sigma^2/T\right]$$

where $\sigma^2 = \mathrm{Cov}\{g(\boldsymbol{\theta}_i)\}$ can be approximated by the sample variance $\sum_{t=1}^{T}\{g(\boldsymbol{\theta}_t) - \widehat{g}\}^2/T$. If the sample is not independent, then $\widehat{g}$ still approximates $E\{g(\boldsymbol{\theta})\}$ but the variance σ^2 is given by

$$\sigma^2 = \mathrm{Var}\{g(\boldsymbol{\theta}_t)\} + 2\sum_{k=1}^{\infty}\mathrm{Cov}\{g(\boldsymbol{\theta}_t), g(\boldsymbol{\theta}_{t+k})\} \tag{7}$$

and needs to be approximated. Moreover, the conditions needed for the central limit theorem to hold involve the convergence rate of the chain and can be difficult to check in practice (Tierney 1994).

The Monte Carlo integration method solves the problem of Bayesian computation of computing a posterior distribution by sampling from that posterior distribution. The latter has been an important problem in computational statistics and a focus of intense research. Rejection sampling techniques serve as basic tools for generating samples from a general probability distribution (von Neumann 1951). They are based on the idea that samples from the target distribution can be obtained from another, easy-to-sample distribution according to some acceptance–rejection rule for the samples from this distribution. It was soon recognized, however, that the acceptance–rejection methods did not scale well with the increase of dimensions, a problem known as the "curse of dimensionality", essentially reducing the acceptance probability to zero. An alternative solution was to use the Markov chains to generate sequences of correlated sample points from the domain of the target distribution and keeping a reasonable rate of acceptance. It was not long before Markov chain Monte Carlo methods were accepted as effective tools for approximate sampling from general posterior distributions (Tanner and Wong 1987).

Markov chain Monte Carlo methods

Every MCMC method is designed to generate values from a transition kernel such that the draws from that kernel converge to a prespecified target distribution. It simulates a Markov chain with the target distribution as the stationary or equilibrium distribution of the chain. By definition, a Markov chain is any sequence of values or states from the domain of the target distribution, such that each value depends on its immediate predecessor only. For a well-designed MCMC, the longer the chain, the closer the samples to the stationary distribution. MCMC methods differ substantially in their simulation efficiency and computational complexity.

The Metropolis algorithm proposed in Metropolis and Ulam (1949) and Metropolis et al. (1953) appears to be the earliest version of MCMC. The algorithm generates a sequence of states, each obtained from the previous one, according to a Gaussian proposal distribution centered at that state. Hastings (1970) described a more-general version of the algorithm, now known as a Metropolis–Hastings (MH) algorithm, which allows any distribution to be used as a proposal distribution. Below we review the general MH algorithm and some of its special cases.

Metropolis–Hastings algorithm

Here we present the MH algorithm for sampling from a posterior distribution in a general formulation. It requires the specification of a proposal probability distribution $q(\cdot)$ and a starting state $\boldsymbol{\theta}_0$ within the domain of the posterior, that is, $p(\boldsymbol{\theta}_0|\mathbf{y}) > 0$. The algorithm generates a Markov chain $\{\boldsymbol{\theta}_t\}_{t=0}^{T-1}$ such that at each step t 1) a proposal state $\boldsymbol{\theta}_*$ is generated conditional on the current state, and 2) $\boldsymbol{\theta}_*$ is accepted or rejected according to the suitably defined acceptance probability.

For $t = 1, \ldots, T-1$:

1. Generate a proposal state: $\boldsymbol{\theta}_* \sim q(\cdot|\boldsymbol{\theta}_{t-1})$.
2. Calculate the acceptance probability $\alpha(\boldsymbol{\theta}_*|\boldsymbol{\theta}_{t-1}) = \min\{r(\boldsymbol{\theta}_*|\boldsymbol{\theta}_{t-1}), 1\}$, where

$$r(\boldsymbol{\theta}_*|\boldsymbol{\theta}_{t-1}) = \frac{p(\boldsymbol{\theta}_*|\mathbf{y})q(\boldsymbol{\theta}_{t-1}|\boldsymbol{\theta}_*)}{p(\boldsymbol{\theta}_{t-1}|\mathbf{y})q(\boldsymbol{\theta}_*|\boldsymbol{\theta}_{t-1})}$$

3. Draw $u \sim \text{Uniform}(0, 1)$.
4. Set $\boldsymbol{\theta}_t = \boldsymbol{\theta}_*$ if $u < \alpha(\boldsymbol{\theta}_*|\boldsymbol{\theta}_{t-1})$, and $\boldsymbol{\theta}_t = \boldsymbol{\theta}_{t-1}$ otherwise.

We refer to the iteration steps 1 through 4 as an MH update. By design, any Markov chain simulated using this MH algorithm is guaranteed to have $p(\boldsymbol{\theta}|\mathbf{y})$ as its stationary distribution.

Two important criteria measuring the efficiency of MCMC are the acceptance rate of the chain and the degree of autocorrelation in the generated sample. When the acceptance rate is close to 0, then most of the proposals are rejected, which means that the chain failed to explore regions of appreciable posterior probability. The other extreme is when the acceptance probability is close to 1, in which case the chain stays in a small region and fails to explore the whole posterior domain. An efficient MCMC has an acceptance rate that is neither too small nor too large and also has small autocorrelation. Gelman, Gilks, and Roberts (1997) showed that in the case of a multivariate posterior and proposal distributions, an acceptance rate of 0.234 is asymptotically optimal and, in the case of a univariate posterior, the optimal value is 0.45.

A special case of MH employs a Metropolis update with $q(\cdot)$ being a symmetric distribution. Then, the acceptance ratio reduces to a ratio of posterior probabilities,

$$r(\boldsymbol{\theta}_*|\boldsymbol{\theta}_{t-1}) = \frac{p(\boldsymbol{\theta}_*|\mathbf{y})}{p(\boldsymbol{\theta}_{t-1}|\mathbf{y})}$$

The symmetric Gaussian distribution is a common choice for a proposal distribution $q(\cdot)$, and this is the one used in the original Metropolis algorithm.

Another important MCMC method that can be viewed as a special case of MH is Gibbs sampling (Gelfand et al. 1990), where the updates are the full conditional distributions of each parameter given the rest of the parameters. Gibbs updates are always accepted. If $\boldsymbol{\theta} = (\theta^1, \ldots, \theta^d)$ and, for $j = 1 \ldots, d$, q_j is the conditional distribution of θ^j given the rest $\boldsymbol{\theta}^{\{-j\}}$, then the Gibbs algorithm is the following. For $t = 1, \ldots, T-1$ and for $j = 1, \ldots, d$: $\theta_t^j \sim q_j(\cdot|\boldsymbol{\theta}_{t-1}^{\{-j\}})$. This step is referred to as a Gibbs update.

All MCMC methods share some limitations and potential problems. First, any simulated chain is influenced by its starting values, especially for short MCMC runs. It is required that the starting point has a positive posterior probability, but even when this condition is satisfied, if we start somewhere in a remote tail of the target distribution, it may take many iterations to reach a region of appreciable probability. Second, because there is no obvious stopping criterion, it is not easy to decide for how long to run the MCMC algorithm to achieve convergence to the target distribution. Third, the observations in MCMC samples are strongly dependent and this must be taken into account in any subsequent statistical inference. For example, the errors associated with the Monte Carlo integration should be calculated according to (7), which accounts for autocorrelation.

Adaptive random-walk Metropolis–Hastings

The choice of a proposal distribution $q(\cdot)$ in the MH algorithm is crucial for the mixing properties of the resulting Markov chain. The problem of determining an optimal proposal for a particular target posterior distribution is difficult and is still being researched actively. All proposed solutions are based on some form of an adaptation of the proposal distribution as the Markov chain progresses, which is carefully designed to preserve the ergodicity of the chain, that is, its tendency to converge to the target distribution. These methods are known as adaptive MCMC methods (Haario, Saksman, and Tamminen [2001]; Giordani and Kohn [2010]; and Roberts and Rosenthal [2009]).

The majority of adaptive MCMC methods are random-walk MH algorithms with updates of the form: $\boldsymbol{\theta}_* = \boldsymbol{\theta}_{t-1} + Z_t$, where Z_t follows some symmetric distribution. Specifically, we consider a Gaussian random-walk MH algorithm with $Z_t \sim N(0, \rho^2\Sigma)$, where ρ is a scalar controlling the scale of random jumps for generating updates and Σ is a d-dimensional covariance matrix. One of the first important results regarding adaptation is from Gelman, Gilks, and Roberts (1997), where the authors derive the optimal scaling factor $\rho = 2.38/\sqrt{d}$ and note that the optimal Σ is the true covariance matrix of the target distribution.

Haario, Saksman, and Tamminen (2001) proposes Σ to be estimated by the empirical covariance matrix plus a small diagonal matrix $\epsilon \times I_d$ to prevent zero covariance matrices. Alternatively, Roberts and Rosenthal (2009) proposed a mixture of the two covariance matrices,

$$\Sigma_t = \beta\widehat{\Sigma} + (1-\beta)\Sigma_0$$

for some fixed covariance matrix Σ_0 and $\beta \in [0, 1]$.

Because the proposal distribution of an adaptive MH algorithm changes at each step, the ergodicity of the chain is not necessarily preserved. However, under certain assumptions about the adaptation procedure, the ergodicity does hold; see Roberts and Rosenthal (2007), Andrieu and Moulines (2006), Atchadé and Rosenthal (2005), and Giordani and Kohn (2010) for details.

Blocking of parameters

In the original MH algorithm, the update steps of generating proposals and applying the acceptance–rejection rule are performed for all model parameters simultaneously. For high-dimensional models, this may result in a poor mixing—the Markov chain may stay in the tails of the posterior distribution for long periods of time and traverse the posterior domain very slowly. Suboptimal mixing is manifested by either very high or very low acceptance rates. Adaptive MH algorithms are also prone to this problem, especially when model parameters have very different scales. An effective solution to this problem is called *blocking*—model parameters are separated into two or more subsets or blocks and MH updates are applied to each block separately in the order that the blocks are specified.

Let's separate a vector of parameters into B blocks: $\boldsymbol{\theta} = \{\boldsymbol{\theta}^1, \ldots, \boldsymbol{\theta}^B\}$. The version of the Gaussian random-walk MH algorithm with blocking is as follows.

Let T_0 be the number of burn-in iterations, T be the number of MCMC samples, and $\rho_b^2\Sigma^b$, $b = 1, \ldots, B$, be block-specific proposal covariance matrices. Let $\boldsymbol{\theta}_0$ be the starting point within the domain of the posterior, that is, $p(\boldsymbol{\theta}_0|\mathbf{y}) > 0$.

1. At iteration t, let $\boldsymbol{\theta}_t = \boldsymbol{\theta}_{t-1}$.
2. For a block of parameters $\boldsymbol{\theta}_t^b$:
   2.1. Let $\boldsymbol{\theta}_* = \boldsymbol{\theta}_t$. Generate a proposal for the bth block: $\boldsymbol{\theta}_*^b = \boldsymbol{\theta}_{t-1}^b + \epsilon$, where $\epsilon \sim N(0, \rho_b^2\Sigma^b)$.
   2.2. Calculate the acceptance ratio,
   $$r(\boldsymbol{\theta}_*|\boldsymbol{\theta}_t) = \frac{p(\boldsymbol{\theta}_*|\mathbf{y})}{p(\boldsymbol{\theta}_t|\mathbf{y})}$$
   where $\theta_* = (\boldsymbol{\theta}_t^1, \boldsymbol{\theta}_t^2, \ldots, \boldsymbol{\theta}_t^{b-1}, \boldsymbol{\theta}_*^b, \boldsymbol{\theta}_t^{b+1}, \ldots, \boldsymbol{\theta}_t^B)$.
   2.3. Draw $u \sim \text{Uniform}(0, 1)$.
   2.4. Let $\boldsymbol{\theta}_t^b = \boldsymbol{\theta}_*^b$ if $u < \min\{r(\boldsymbol{\theta}_*|\boldsymbol{\theta}_t), 1\}$.
3. Repeat step 2 for $b = 1, \ldots, B$.
4. Repeat steps 1 through 3 for $t = 1, \ldots, T + T_0 - 1$.
5. The final sequence is $\{\boldsymbol{\theta}_t\}_{t=T_0}^{T+T_0-1}$.

Blocking may not always improve efficiency. For example, separating all parameters in individual blocks (the so-called one-at-a-time update regime) can lead to slow mixing when some parameters are highly correlated. A Markov chain may explore the posterior domain very slowly if highly correlated parameters are updated independently. There are no theoretical results about optimal blocking, so

you will need to use your judgment when determining the best set of blocks for your model. As a rule, parameters that are expected to be highly correlated are specified in one block. This will generally improve mixing of the chain unless the proposal correlation matrix does not capture the actual correlation structure of the block. For example, if there are two parameters in the block that have very different scales, adaptive MH algorithms that use the identity matrix for the initial proposal covariance may take a long time to approximate the optimal proposal correlation matrix. The user should, therefore, consider not only the probabilistic relationship between the parameters in the model, but also their scales to determine an optimal set of blocks.

Metropolis–Hastings with Gibbs updates

The original Gibbs sampler updates each model parameter one at a time according to its full conditional distribution. We have already noted that Gibbs is a special case of the MH algorithm. Some of the advantages of Gibbs sampling include its high efficiency, because all proposals are automatically accepted, and that it does not require any additional tuning for proposal distributions in MH algorithms. Unfortunately, for most posterior distributions in practice, the full conditionals are either not available or are very difficult to sample from. It may be the case, however, that for some model parameters or groups of parameters, the full conditionals are available and are easy to generate samples from. This is done in a hybrid MH algorithm, which implements Gibbs updates for only some blocks of parameters. A hybrid MH algorithm combines Gaussian random-walk updates with Gibbs updates to improve the mixing of the chain.

The MH algorithm with blocking allows different samplers to be used for updating different blocks. If there is a group of model parameters with a conjugate prior (or semiconjugate prior), we can place this group of parameters in a separate block and use Gibbs sampling for it. This can greatly improve the overall sampling efficiency of the algorithm.

For example, suppose that the data are normally distributed with a known mean μ and that we specify an inverse-gamma prior for σ^2 with shape α and scale β, which are some fixed constants.

$$y \sim N(\mu, \sigma^2), \quad \sigma^2 \sim \text{InvGamma}(\alpha,\ \beta)$$

The full conditional distribution for σ^2 in this case is also an inverse-gamma distribution, but with different shape and scale parameters,

$$\sigma^2 \sim \text{InvGamma}\left\{\widetilde{\alpha} = \alpha + \frac{n}{2},\ \widetilde{\beta} = \beta + \frac{1}{2}\sum_{i=1}^{n}(y_i - \mu)^2\right\}$$

where n is the data sample size. So, an inverse-gamma prior for the variance is a conjugate prior in this model. We can thus place σ^2 in a separate block and set up a Gibbs sampling for it using the above full conditional distribution.

See *Methods and formulas* in [BAYES] **bayesmh** for details.

Convergence diagnostics of MCMC

Checking convergence of MCMC is an essential step in any MCMC simulation. Bayesian inference based on an MCMC sample is valid only if the Markov chain has converged and the sample is drawn from the desired posterior distribution. It is important that we verify the convergence for all model parameters and not only for a subset of parameters of interest. One difficulty with assessing

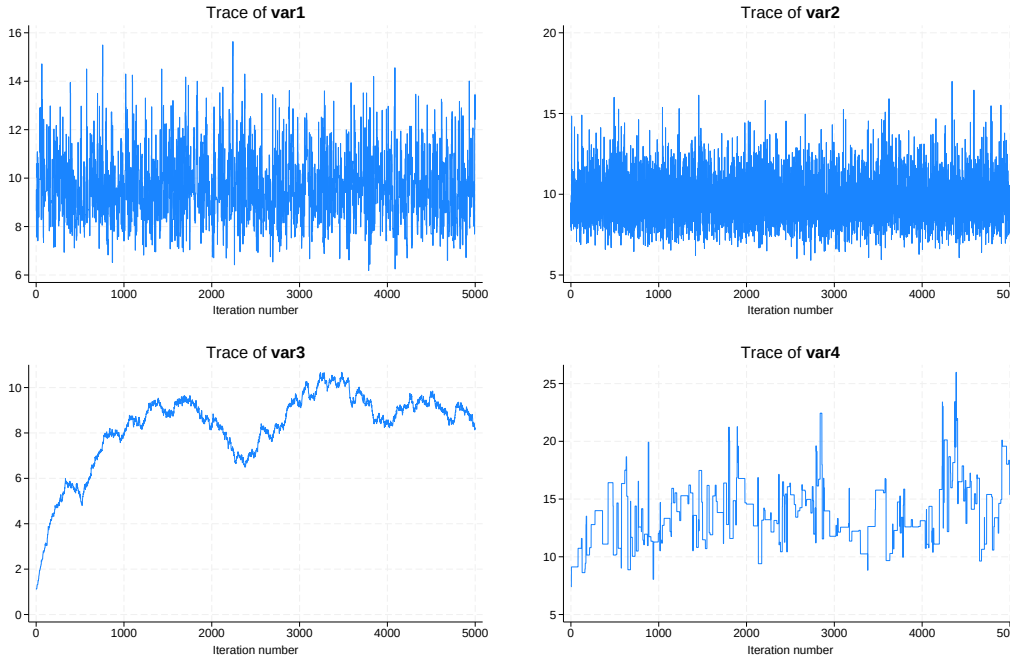
convergence of MCMC is that there is no single conclusive convergence criterion. The diagnostic usually involves checking for several necessary (but not necessarily sufficient) conditions for convergence. In general, the more aspects of the MCMC sample you inspect, the more reliable your results are.

The most extensive review of the methods for assessing convergence is Cowles and Carlin (1996). Other discussions about monitoring convergence can be found in Gelman et al. (2014) and Brooks et al. (2011).

There are at least two general approaches for detecting convergence issues. The first one is to inspect the mixing and time trends within the chains of individual parameters. The second one is to examine the mixing and time trends of multiple chains for each parameter. The lack of convergence in a Markov chain can be especially difficult to detect in a case of pseudoconvergence, which often occurs with multimodal posterior distributions. Pseudoconvergence occurs when the chain appears to have converged but it actually explored only a portion of the domain of a posterior distribution. To check for pseudoconvergence, Gelman and Rubin (1992) recommend running multiple chains from different starting states and comparing them; see [BAYES] **bayesstats grubin**.

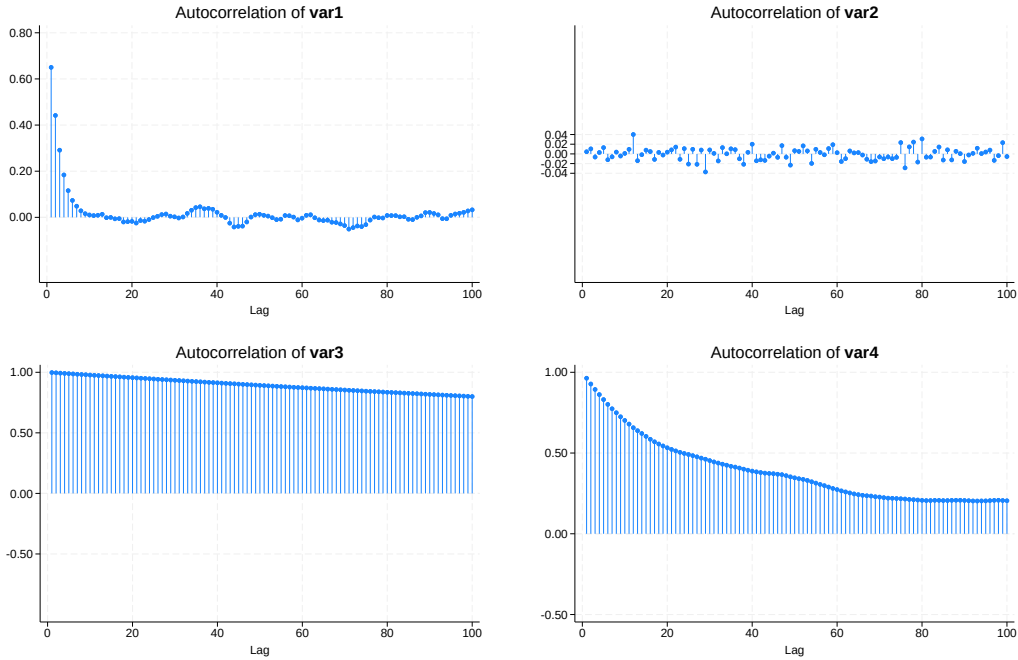
Trace plots are the most accessible convergence diagnostics and are easy to inspect visually. The trace plot of a parameter plots the simulated values for this parameter versus the iteration number. The trace plot of a well-mixing parameter should traverse the posterior domain rapidly and should have nearly constant mean and variance. See [BAYES] **bayesgraph** for details.

In the next figure, we show examples of trace plots for four parameters: `var1`, `var2`, `var3`, and `var4`. The first two parameters, `var1` and `var2`, have well-mixing chains, and the other two have poorly mixing chains. The chain for the parameter `var1` has a moderate acceptance rate, about 35%, and efficiency between 10% and 20%. This is a typical result for a Gaussian random-walk MH algorithm that has achieved convergence. The trace plot of `var2` in the top right panel shows almost perfect mixing—this is a typical example of Gibbs sampling with an acceptance rate close to 1 and efficiency above 95%. Although both chains traverse their marginal posterior domains, the right one does it more rapidly. On the downside, more efficient MCMC algorithms such as Gibbs sampling are usually associated with a higher computational cost.

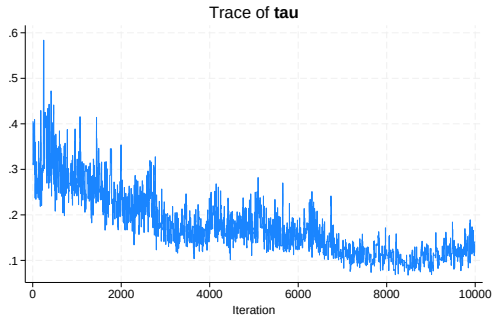


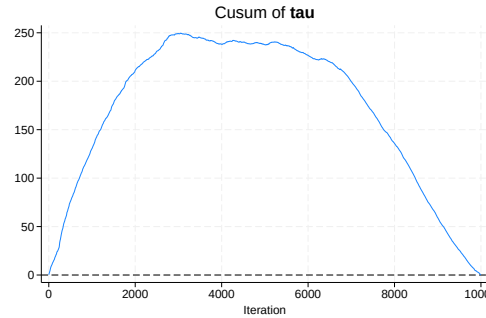
The bottom two trace plots illustrate cases of bad mixing and a lack of convergence. On the left, the chain for `var3` exhibits high acceptance rate but poor coverage of the posterior domain manifested by random drifting in isolated regions. This chain was produced by a Gaussian random-walk MH algorithm with a proposal distribution with a very small variance. On the right, the chain for the parameter `var4` has a very low acceptance rate, below 3%, because the used proposal distribution had a very large variance. In both cases, the chains do not converge; the simulation results do not represent the posterior distribution and should thus be discarded.

As we stated before, samples simulated using MCMC methods are correlated. The smaller the correlation, the more efficient the sampling process. Most of the MH algorithms typically generate highly correlated draws, whereas the Gibbs algorithm typically generates less-correlated draws. Below we show autocorrelation plots for the same four parameters using the same MCMC samples. The autocorrelation of `var1`, the one that comes from a well-mixing MH chain, becomes negligible fairly quickly, after about 10 lags. On the other hand, the autocorrelation of `var2` simulated using Gibbs sampling is essentially negligible for all positive lags. In the case of a poor mixing because of a small proposal variance (parameter `var3`), we observe very high positive correlation for at least 100 lags. The autocorrelation of `var4` is high but is lower than that of `var3`.

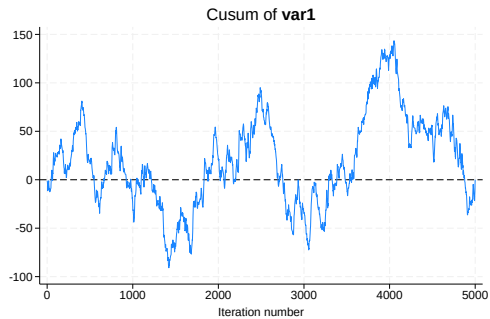


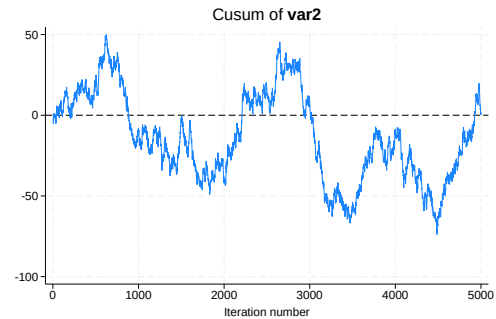
Yu and Mykland (1998) proposed a graphical procedure for assessing the convergence of individual parameters based on cumulative sums, also known as a cusum plot. By definition, any cusum plot starts at 0 and ends at 0. Cusum plots are useful for detecting drifts in the chain. For a chain without trend, the cusum plot should cross the x axis. For example, early drifts may indicate dependence on starting values. If we detect an early drift, we should discard an initial part of the chain and run it longer. Below, we show the trace plot of a poorly mixing parameter `tau` and its corresponding cusum plot on the right. There is an apparent positive drift for approximately the first half of the chain followed by the drift in the negative direction. As a result, the cusum plot has a distinctive mountain-like shape and never crosses the x axis.

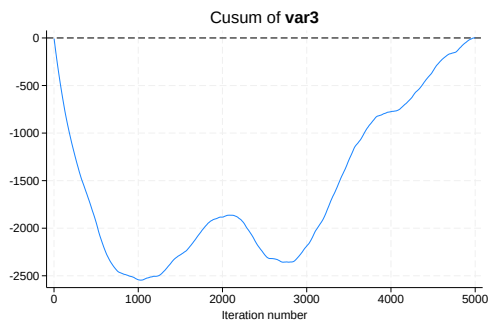


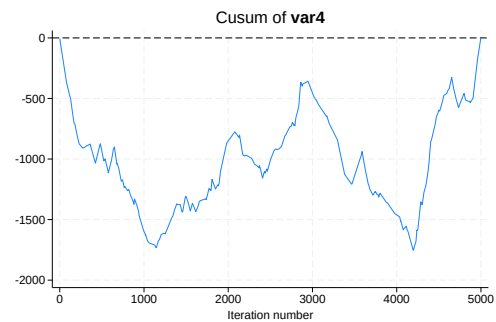


Cusum plots can be also used for assessing how fast the chain is mixing. The slower the mixing of the chain, the smoother the cusum plots. Conversely, the faster the mixing of the chain, the more jagged the cusum plots. Below, we demonstrate the cusum plots for the four variables considered previously. We can clearly see the contrast between the jagged lines of the fast mixing parameters `var1` and `var2` and the very smooth cusum line of the poorly mixing parameter `var3`.









Besides graphical convergence diagnostics, there are some formal convergence tests (Geweke [1992]; Gelman and Rubin [1992]; Heidelberger and Welch [1983]; Raftery and Lewis [1992]; Zellner and Min [1995]). See *Convergence diagnostics using multiple chains* in [BAYES] **bayesmh** and see [BAYES] **bayesstats grubin** for more details.

Summary

Bayesian analysis is a statistical procedure that answers research questions by expressing uncertainty about unknown parameters using probabilities. Bayesian inference is based on the posterior distribution of model parameters conditional on the observed data. The posterior distribution is composed of a likelihood distribution of the data and the prior distribution of the model parameters. The likelihood model is specified in the same way it is specified with any standard likelihood-based analysis. The prior distribution is constructed based on the prior (before observing the data) scientific knowledge and results from previous studies. Sensitivity analysis is typically performed to evaluate the influence of different competing priors on the results.

Many posterior distributions do not have a closed form and must be simulated using MCMC methods such as MH methods or the Gibbs method or sometimes their combination. The convergence of MCMC must be verified before any inference can be made.

Marginal posterior distributions of the parameters are used for inference. These are summarized using point estimators such as posterior mean and median and interval estimators such as equal-tailed credible intervals and highest posterior density intervals. Credible intervals have an intuitive interpretation as fixed ranges to which a parameter is known to belong with a prespecified probability. Hypothesis testing provides a way to assign an actual probability to any hypothesis of interest. A number of criteria are available for comparing models of interest. Predictions and model checking are also available based on the posterior predictive distribution.

Bayesian analysis provides many advantages over the standard frequentist analysis, such as an ability to incorporate prior information in the analysis, higher robustness to sparse data, more-comprehensive inference based on the knowledge of the entire posterior distribution, and more intuitive and direct interpretations of results by using probability statements about parameters.

Video examples

Introduction to Bayesian statistics, part 1: The basic concepts

Introduction to Bayesian statistics, part 2: MCMC and the Metropolis–Hastings algorithm

Thomas Bayes (1701(?)–1761) was a Presbyterian minister with an interest in calculus, geometry, and probability theory. He was born in Hertfordshire, England. The son of a Nonconformist minister, Bayes was banned from English universities and so studied at Edinburgh University before becoming a clergyman himself. Only two works are attributed to Bayes during his lifetime, both published anonymously. He was admitted to the Royal Society in 1742 and never published thereafter.

The paper that gives us "Bayes's Theorem" was published posthumously by Richard Price. The theorem has become an important concept for frequentist and Bayesian statisticians alike. However, the paper indicates that Bayes considered the theorem as relatively unimportant. His main interest appears to have been that probabilities were not fixed but instead followed some distribution. The notion, now foundational to Bayesian statistics, was largely ignored at the time.

Whether Bayes's theorem is appropriately named is the subject of much debate. Price acknowledged that he had written the paper based on information he found in Bayes's notebook, yet he never said how much he added beyond the introduction. Some scholars have also questioned whether Bayes's notes represent original work or are the result of correspondence with other mathematicians of the time.

Andrey Markov (1856–1922) was a Russian mathematician who made many contributions to mathematics and statistics. He was born in Ryazan, Russia. In primary school, he was known as a poor student in all areas except mathematics. Markov attended St. Petersburg University, where he studied under Pafnuty Chebyshev and later joined the physicomathematical faculty. He was a member of the Russian Academy of the Sciences.

Markov's first interest was in calculus. He did not start his work in probability theory until 1883 when Chebyshev left the university and Markov took over his teaching duties. A large and influential body of work followed, including applications of the weak law of large numbers and what are now known as Markov processes and Markov chains. His work on processes and chains would later influence the development of a variety of disciplines such as biology, chemistry, economics, physics, and statistics.

Known in the Russian press as the "militant academician" for his frequent written protests about the czarist government's interference in academic affairs, Markov spent much of his adult life at odds with Russian authorities. In 1908, he resigned from his teaching position in response to a government requirement that professors report on students' efforts to organize protests in the wake of the student riots earlier that year. He did not resume his university teaching duties until 1917, after the Russian Revolution. His trouble with Russian authorities also extended to the Russian Orthodox Church. In 1912, he was excommunicated at his own request in protest over the Church's excommunication of Leo Tolstoy.

Bruno de Finetti (1906–1985) was born in Innsbruck, Austria. He received a degree in applied mathematics from the Polytechnic University of Milan. One of his first publications was in the field of genetics, in which he introduced what is now called the de Finetti diagram. Upon graduation, he began working for the Italian Central Statistical Institute and later moved to Trieste to work as an actuary. He became a professor at the University of Trieste in 1947 and later became a professor of the theory of probability at the University of Rome "La Sapienza", a post he held for 15 years.

De Finetti made many contributions to the fields of probability and statistics. His text *Theory of Probability* helped lay the foundation for Bayesian theory. He also wrote papers on sequences of exchangeable random variables and processes with independent increments. In a paper published in 1955, de Finetti used an extension of the Lorenz–Gini concentration function to prove the Radon–Nikodym theorem. This extension has been employed in Bayesian statistics as a measure of robustness. His publications also include work on nonparametric estimation of a cumulative distribution function and group decision making, among other topics. For his many contributions, he was named a fellow of the Royal Statistical Society and the Institute of Mathematical Statistics.

David Harold Blackwell (1919–2010) was a world-renowned statistician and mathematician. At age 16, he began attending the University of Illinois, where he obtained a master's degree in mathematics and then a PhD in statistics at age 22. Shortly after, he joined Princeton University as a visiting fellow, becoming the university's first African-American faculty member and paving the way for future generations.

Blackwell is best known for developing the Rao–Blackwell theorem, used in statistics, and the Blackwell renewal theorem, used in engineering. In regard to Markov decision processes, he introduced the concepts of Blackwell optimality and positive and negative dynamic programs. His contributions also include pioneering texts, such as *Basic Statistics*, one of the first texts on Bayesian statistics, and *Theory of Games and Statistical Decisions*, which he coauthored with M. A. Girschick. Additionally, in 1949, he coauthored a paper that helped lay the groundwork for Bayesian sequential analysis. He published over 80 papers in many fields, including game theory, probability theory, and mathematical statistics.

Blackwell's contributions are also reflected in the honors bestowed upon him and in his leadership roles in prominent organizations. In 1976, he was elected an honorary fellow of the Royal Statistical Society, and in 1979, he won the John von Neumann Theory Prize. He also held 12 honorary degrees and was the first African-American man elected to the National Academy of Sciences. Additionally, he served as vice president of the American Statistical Association, American Mathematical Society, and the International Statistical Institute.

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Also see

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Glossary**

[BMA] **Intro** — Introduction to Bayesian model averaging

Title

Bayesian commands — Introduction to commands for Bayesian analysis

Description

This entry describes commands to perform Bayesian analysis. Bayesian analysis is a statistical procedure that answers research questions by expressing uncertainty about unknown parameters using probabilities. It is based on the fundamental assumption that not only the outcome of interest but also all the unknown parameters in a statistical model are essentially random and are subject to prior beliefs.

Estimation

`Bayesian estimation`	Bayesian estimation commands
`bayes`	Bayesian regression models using the `bayes` prefix
`bayesmh`	Bayesian models using MH
`bayesmh evaluators`	User-defined Bayesian models using MH

Convergence tests and graphical summaries

`bayesgraph`	Graphical summaries
`bayesstats grubin`	Gelman–Rubin convergence diagnostics

Postestimation statistics

`bayesstats ess`	Effective sample sizes and related statistics
`bayesstats summary`	Bayesian summary statistics
`bayesstats ic`	Bayesian information criteria and Bayes factors
`bayesirf`	Bayesian IRFs and more after VAR and DSGE models

Predictions

`bayespredict`	Bayesian predictions
`bayesstats ppvalues`	Bayesian predictive p-values
`bayesfcast`	Bayesian forecasts after VAR models

Hypothesis testing

`bayestest model`	Hypothesis testing using model posterior probabilities
`bayestest interval`	Interval hypothesis testing

Remarks and examples

This entry describes commands to perform Bayesian analysis. See [BAYES] **Intro** for an introduction to the topic of Bayesian analysis.

Bayesian estimation in Stata can be as easy as prefixing your estimation command with the `bayes` prefix ([BAYES] **bayes**). For example, if your estimation command is a linear regression of `y` on `x`

```
. regress y x
```

then Bayesian estimates for this model can be obtained by typing

```
. bayes: regress y x
```

See [BAYES] **Bayesian estimation** for a list of estimation commands that work with the `bayes` prefix.

In addition to the `bayes` prefix, there is a general-purpose Bayesian estimation command—the `bayesmh` command ([BAYES] **bayesmh**). `bayesmh` fits a variety of Bayesian models including multiple-equation linear and nonlinear models and, like the `bayes` prefix, estimates parameters using an adaptive MH Markov chain Monte Carlo (MCMC) method. You can choose from a variety of supported Bayesian models by specifying the `likelihood()` and `prior()` options. Or you can program your own Bayesian models by supplying a program evaluator for the posterior distributions of model parameters in the `evaluator()` option; see [BAYES] **bayesmh evaluators** for details.

After estimation, you can use `bayesgraph` to check convergence of MCMC visually. If you simulated multiple chains, you can use `bayesstats grubin` to compute Gelman–Rubin convergence diagnostics. You can also use `bayesstats ess` to compute effective sample sizes and related statistics for model parameters and functions of model parameters to assess the efficiency of the sampling algorithm and autocorrelation in the obtained MCMC sample. Once convergence is established, you can use `bayesstats summary` to obtain Bayesian summaries such as posterior means and standard deviations of model parameters and functions of model parameters and `bayesstats ic` to compute Bayesian information criteria and Bayes factors for models. You can use `bayestest model` to test hypotheses by comparing posterior probabilities of models. You can also use `bayestest interval` to test interval hypotheses about parameters and functions of parameters. You can use `bayespredict` and `bayesstats ppvalues` for model diagnostics using posterior predictive checking. You can also use `bayespredict` to predict future observations.

Below we provide an overview example demonstrating the Bayesian suite of commands. In this entry, we mainly concentrate on the general command, `bayesmh`. For examples of using the simpler `bayes` prefix, see example 11 and *Remarks and examples* in [BAYES] **bayes**. Also, for more examples of `bayesmh`, see *Remarks and examples* in [BAYES] **bayesmh**.

Overview example

Consider an example from Kuehl (2000, 551) about the effects of exercise on oxygen uptake. The research objective is to compare the impact of the two exercise programs—12 weeks of step aerobic training and 12 weeks of outdoor running on flat terrain—on maximal oxygen uptake. Twelve healthy men were randomly assigned to one of the two groups, the "aerobic" group or the "running" group. Their changes in maximal ventilation (liters/minute) of oxygen for the 12-week period were recorded.

`oxygen.dta` contains 12 observations of changes in maximal ventilation of oxygen, recorded in variable `change`, from two groups, recorded in variable `group`. Additionally, ages of subjects are recorded in variable `age`, and an interaction between `age` and `group` is stored in variable `interaction`.

```
. use https://www.stata-press.com/data/r18/oxygen
(Oxygen uptake data)
. describe
Contains data from https://www.stata-press.com/data/r18/oxygen.dta
 Observations:            12                  Oxygen uptake data
    Variables:             4                  20 Jan 2022 15:56
                                              (_dta has notes)
```

Variable name	Storage type	Display format	Value label	Variable label
change	float	%9.0g		Change in maximal oxygen uptake (liters/minute)
group	byte	%8.0g	grouplab	Exercise group
age	byte	%8.0g		Age (years)
ageXgr	byte	%9.0g		Interaction between age and group

```
Sorted by:
```

Kuehl (2000) uses analysis of covariance to analyze these data. We use linear regression instead,

$$\texttt{change} = \beta_0 + \beta_{\text{group}}\texttt{group} + \beta_{\text{age}}\texttt{age} + \epsilon$$

where ϵ is a random error with zero mean and variance σ^2. Also see Hoff (2009) for Bayesian analysis of these data.

Examples are presented under the following headings:

▷ Example 1: OLS

Let's fit OLS regression to our data first.

```
. regress change group age
```

Source	SS	df	MS		
				Number of obs	= 12
				F(2, 9)	= 41.42
Model	647.874893	2	323.937446	Prob > F	= 0.0000
Residual	70.388768	9	7.82097423	R-squared	= 0.9020
				Adj R-squared	= 0.8802
Total	718.263661	11	65.2966964	Root MSE	= 2.7966

change	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
group	5.442621	1.796453	3.03	0.014	1.378763	9.506479
age	1.885892	.295335	6.39	0.000	1.217798	2.553986
_cons	-46.4565	6.936531	-6.70	0.000	-62.14803	-30.76498

From the table, both `group` and `age` are significant predictors of the outcome in this model.

For example, we reject the hypothesis of H_0: $\beta_{\text{group}} = 0$ at a 5% level based on the p-value of 0.014. The actual interpretation of the reported p-value is that if we repeat the same experiment and use the same testing procedure many times, then given our null hypothesis of no effect of group, we will observe the result (test statistic) as extreme or more extreme than the one observed in this sample (`t` $= 3.03$) only 1.4% of the times. The p-value cannot be interpreted as a probability of the null hypothesis, which is a common misinterpretation. In fact, it answers the question of how likely our data are, given that the null hypothesis is true, and not how likely the null hypothesis is, given our data. The latter question can be answered using Bayesian hypothesis testing, which we demonstrate in example 9.

Confidence intervals are popular alternatives to p-values that eliminate some of the p-value shortcomings. For example, the 95% confidence interval for the coefficient for `group` is [1.38, 9.51] and does not contain the value of 0, so we consider `group` to be a significant predictor of `change`. The interpretation of a 95% confidence interval is that if we repeat the same experiment many times and compute confidence intervals for each experiment, then 95% of those intervals will contain the true value of the parameter. Thus we cannot conclude that the true coefficient for `group` lies between 1.38 and 9.51 with a probability of 0.95—a common misinterpretation of a confidence interval. This probability is either 0 or 1, and we do not know which for any particular confidence interval. All we know is that [1.38, 9.51] is a plausible range for the true value of the coefficient for `group`. Intervals that can actually be interpreted as probabilistic ranges for a parameter of interest may be constructed within the Bayesian paradigm; see example 9.

◁

▷ Example 2: Bayesian normal linear regression with noninformative prior

In example 1, we stated that frequentist methods cannot provide probabilistic summaries for the parameters of interest. This is because in frequentist statistics, parameters are viewed as unknown but fixed quantities. The only random quantity in a frequentist model is an outcome of interest. Bayesian statistics, on the other hand, in addition to the outcome of interest, also treats all model parameters as random quantities. This is what sets Bayesian statistics apart from frequentist statistics and enables one to make probability statements about the likely values of parameters and to assign probabilities to hypotheses of interest.

Bayesian statistics focuses on the estimation of various aspects of the posterior distribution of a parameter of interest, an initial or a prior distribution that has been updated with information about a parameter contained in the observed data. A posterior distribution is thus described by the prior distribution of a parameter and the likelihood function of the data given the parameter.

Let's now fit a Bayesian linear regression to `oxygen.dta`. To fit a Bayesian parametric model, we need to specify the likelihood function or the distribution of the data and prior distributions for all model parameters. Our Bayesian linear model has four parameters: three regression coefficients and the variance of the data. We assume a normal distribution for our outcome, `change`, and start with a noninformative Jeffreys prior for the parameters. Under the Jeffreys prior, the joint prior distribution of the coefficients and the variance is proportional to the inverse of the variance.

We can write our model as follows,

$$\texttt{change} \sim N(X\boldsymbol{\beta}, \sigma^2)$$
$$(\boldsymbol{\beta}, \sigma^2) \sim \frac{1}{\sigma^2}$$

where X is our design matrix, and $\boldsymbol{\beta} = (\beta_0, \beta_{\text{group}}, \beta_{\text{age}})'$, which is a vector of coefficients.

We use the bayesmh command to fit our Bayesian model. Let's consider the specification of the model first.

```
bayesmh change group age, likelihood(normal({var}))    ///
     prior({change:}, flat) prior({var}, jeffreys)
```

The specification of the regression function in bayesmh is the same as in any other Stata regression command—the name of the dependent variable follows the command, and the covariates of interest are specified next. Likelihood or outcome distribution is specified in the likelihood() option, and prior distributions are specified in the prior() options, which are repeated options.

All model parameters must be specified in curly braces, {}. bayesmh automatically creates parameters associated with the regression function—regression coefficients—but it is your responsibility to define the remaining model parameters. In our example, the only parameter we need to define is the variance parameter, which we define as {var}. The three regression coefficients {change:group}, {change:age}, and {change:_cons} are automatically created by bayesmh.

The last step is to specify the likelihood and the prior distributions. bayesmh provides several different built-in distributions for the likelihood and priors. If a certain distribution is not available or you have a particularly complicated Bayesian model, you may consider writing your own evaluator for the posterior distribution; see [BAYES] **bayesmh evaluators** for details. In our example, we specify distribution normal({var}) in option likelihood() to request the likelihood function of the normal model with the variance parameter {var}. This specification together with the regression specification defines the likelihood model for our outcome change. We assign the flat prior, a prior with a density of 1, to all regression coefficients with prior({change:}, flat), where {change:} is a shortcut for referring to all parameters with equation name change, our regression coefficients. Finally, we specify prior jeffreys for the variance parameter {var} to request the density $1/\sigma^2$.

Let's now run our command. bayesmh uses MCMC sampling, specifically, an adaptive random-walk MH MCMC method, to estimate marginal posterior distributions of parameters. Because bayesmh is using an MCMC method, which is stochastic, we must specify a random-number seed for reproducibility of our results. For consistency and simplicity, we use the same random seed of 14 in all of our examples throughout the manual.

```
. set seed 14
. bayesmh change group age, likelihood(normal({var}))
> prior({change:}, flat) prior({var}, jeffreys)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ normal(xb_change,{var})
Priors:
  {change:group age _cons} ~ 1 (flat)                                    (1)
                     {var} ~ jeffreys
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         12
                                                Acceptance rate  =      .1371
                                                Efficiency:  min =     .02687
                                                             avg =     .03765
Log marginal-likelihood = -24.703776                         max =     .05724
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
change						
group	5.429677	2.007889	.083928	5.533821	1.157584	9.249262
age	1.8873	.3514983	.019534	1.887856	1.184714	2.567883
_cons	-46.49866	8.32077	.450432	-46.8483	-62.48236	-30.22105
var	10.27946	5.541467	.338079	9.023905	3.980325	25.43771

First, `bayesmh` provides a summary for the specified model. It is particularly useful for complicated models with many parameters and hyperparameters. In fact, we recommend that you first specify the `dryrun` option, which provides only the summary of the model without estimation, to verify the specification of your model and then proceed with estimation. You can then use the `nomodelsummary` option during estimation to suppress the model summary, which may be rather long.

Next, `bayesmh` provides a header with various model summaries on the right-hand side. It reports the total number of MCMC iterations, 12,500, including the default 2,500 burn-in iterations, which are discarded from the analysis MCMC sample, and the number of iterations retained in the MCMC sample, or MCMC sample size, which is 10,000 by default. These default values should be viewed as initial estimates and further adjusted for the problem at hand to ensure convergence of the MCMC; see example 5.

An acceptance rate and a summary of the parameter-specific efficiencies are also part of the output header. An acceptance rate specifies the proportion of proposed parameter values that was accepted by the algorithm. An acceptance rate of 0.14 in our example means that 14% out of 10,000 proposal parameter values were accepted by the algorithm. For the MH algorithm, this number rarely exceeds 50% and is typically below 30%. A low acceptance rate (for example, below 10%) may indicate convergence problems. In our example, the acceptance rate is a bit low, so we may need to investigate this further. In general, MH tends to have lower efficiencies compared with other MCMC methods. For example, efficiencies of 10% and higher are considered good. Efficiencies below 1% may be a source of concern. The efficiencies are somewhat low in our example, so we may consider tuning our MCMC sampler; see *Improving efficiency of the MH algorithm—blocking of parameters*.

Finally, `bayesmh` reports a table with a summary of the results. The `Mean` column reports the estimates of posterior means, which are means of the marginal posterior distributions of the parameters. The posterior mean estimates are pretty close to the OLS estimates obtained in example 1. This is expected, provided MCMC converged, because we used a noninformative prior. That is, we did not provide any additional information about parameters beyond that contained in the data.

The next column reports estimates of posterior standard deviations, which are standard deviations of the marginal posterior distribution. These values describe the variability in the posterior distribution of the parameter and are comparable to our OLS standard errors.

The precision of the posterior mean estimates is described by their Monte Carlo standard errors. These numbers should be small, relative to the scales of the parameters. Increasing the MCMC sample size should decrease these numbers.

The `Median` column provides estimates of the median of the posterior distribution and can be used to assess the symmetries of the posterior distribution. At a quick glance, the estimates of posterior means and medians are pretty close for the regression coefficients, so we suspect that their posterior distributions may be symmetric.

The last two columns provide credible intervals for the parameters. Unlike confidence intervals, as discussed in example 1, these intervals have a straightforward probabilistic interpretation. For example, the probability that the coefficient for `group` is between 1.16 and 9.25 is about 0.95. The lower bound of the interval is greater than 0, so we conclude that there is an effect of the exercise program on the change in oxygen uptake. We can also use Bayesian hypothesis testing to test effects of parameters; see example 9.

Before any interpretation of the results, however, it is important to verify the convergence of MCMC; see example 5.

See example 11 for how to fit Bayesian linear regression more easily using the `bayes` prefix.

◁

▷ Example 3: Bayesian linear regression with informative prior

In example 2, we considered a noninformative prior for the model parameters. The strength (as well as the weakness) of Bayesian modeling is specifying an informative prior distribution, which may improve results. The strength is that if we have reliable prior knowledge about the distribution of a parameter, incorporating this in our model will improve results and potentially make certain analysis that would not be possible to perform in the frequentist domain feasible. The weakness is that a strong incorrect prior may lead to results that are not supported by the observed data. As with any modeling task, Bayesian or frequentist, a substantive research of the process generating the data and its parameters will be necessary for you to find appropriate models.

Let's consider an informative conjugate prior distribution for our normal regression model.

$$(\boldsymbol{\beta}|\sigma^2) \sim \text{i.i.d. } N(0, \sigma^2)$$
$$\sigma^2 \sim \text{InvGamma}(2.5, 2.5)$$

Here, for simplicity, all coefficients are assumed to be independently and identically distributed as normal with zero mean and variance σ^2, and the variance parameter is distributed according to the above inverse gamma distribution. In practice, a better prior would be to allow each parameter to have a different variance, at least for parameters with different scales.

Let's fit this model using `bayesmh`. Following the model above, we specify the `normal(0,{var})` prior for the coefficients and the `igamma(2.5,2.5)` prior for the variance.

```
. set seed 14
. bayesmh change group age, likelihood(normal({var}))
> prior({change:}, normal(0, {var}))
> prior({var}, igamma(2.5, 2.5))
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ normal(xb_change,{var})
Priors:
  {change:group age _cons} ~ normal(0,{var})                              (1)
                     {var} ~ igamma(2.5,2.5)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         12
                                                Acceptance rate  =      .1984
                                                Efficiency:  min =     .03732
                                                             avg =     .04997
Log marginal-likelihood = -49.744054                         max =     .06264
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
change						
group	6.510807	2.812828	.129931	6.50829	.9605561	12.23164
age	.2710499	.2167863	.009413	.2657002	-.1556194	.7173697
_cons	-6.838302	4.780343	.191005	-6.683556	-16.53356	2.495631
var	28.83438	10.53573	.545382	26.81462	14.75695	54.1965

The results from this model are substantially different from the results we obtained in example 2. Considering that we used this simple prior for demonstration purposes only and did not use any external information about model parameters based on prior studies, we would be reluctant to trust the results from this model.

◁

▷ Example 4: Bayesian normal linear regression with multivariate prior

Continuing with informative priors, we will consider Zellner's g-prior (Zellner 1986), which is one of the more commonly used priors for the regression coefficients in a normal linear regression. Hoff (2009) provides more details about this example, and he includes the interaction between age and group as in example 8. Here we concentrate on demonstrating how to fit our model using `bayesmh`.

The mathematical formulation of the priors is the following,

$$(\boldsymbol{\beta}|\sigma^2) \sim \text{MVN}(0, g\sigma^2(X'X)^{-1})$$
$$\sigma^2 \sim \text{InvGamma}(\nu_0/2, \nu_0\sigma_0^2/2)$$

where g reflects prior sample size, ν_0 is the prior degrees of freedom for the inverse gamma distribution, and σ_0^2 is the prior variance for the inverse gamma distribution. This prior incorporates dependencies between coefficients. We use values of the parameters similar to those in Hoff (2009): $g = 12$, $\nu_0 = 1$, and $\sigma_0^2 = 8$.

bayesmh provides the zellnersg0() prior to accommodate the above prior. The first argument is the dimension of the distribution, which is 3 in our example, the second argument is the prior degrees of freedom, which is 12 in our example, and the last argument is the variance parameter, which is {var} in our example. The mean is assumed to be a zero vector of the corresponding dimension. (You can use zellnersg() if you want to specify a nonzero mean vector; see [BAYES] **bayesmh**.)

```
. set seed 14
. bayesmh change group age, likelihood(normal({var}))
> prior({change:}, zellnersg0(3,12,{var}))
> prior({var}, igamma(0.5, 4))
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ normal(xb_change,{var})
Priors:
  {change:group age _cons} ~ zellnersg(3,12,0,{var})                    (1)
                     {var} ~ igamma(0.5,4)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         12
                                                Acceptance rate  =     .06169
                                                Efficiency:  min =      .0165
                                                             avg =     .02018
Log marginal-likelihood = -35.356501                         max =     .02159
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
change						
group	4.988881	2.260571	.153837	4.919351	.7793098	9.775568
age	1.713159	.3545698	.024216	1.695671	1.053206	2.458556
_cons	-42.31891	8.239571	.565879	-41.45385	-59.30145	-27.83421
var	12.29575	6.570879	.511475	10.3609	5.636195	30.93576

These results are more in agreement with results from example 2 than with results of example 3, but our acceptance rate and efficiencies are low and require further investigation.

◁

❑ Technical note

We can reproduce what zellnersg0() does above manually. First, we must compute $(X'X)^{-1}$. We can use Stata's matrix functions to do that.

```
. matrix accum xTx = group age
(obs=12)
. matrix S = invsym(xTx)
```

We now specify the desired multivariate normal prior for the coefficients, mvnormal0(3,12*{var}*S). The first argument of mvnormal0() specifies the dimension of the distribution, and the second argument specifies the variance–covariance matrix. A mean of zero is assumed for all dimensions. One interesting feature of this specification is that the variance–covariance matrix is specified as a function of {var}.

```
. set seed 14
. bayesmh change group age, likelihood(normal({var}))
> prior({change:}, mvnormal0(3,12*{var}*S))
> prior({var}, igamma(0.5, 4))
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ normal(xb_change,{var})
Priors:
  {change:group age _cons} ~ mvnormal(3,0,0,0,12*{var}*S)                 (1)
                     {var} ~ igamma(0.5,4)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         12
                                                Acceptance rate  =     .06169
                                                Efficiency:  min =      .0165
                                                             avg =     .02018
Log marginal-likelihood = -35.356501                         max =     .02159
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
change						
group	4.988881	2.260571	.153837	4.919351	.7793098	9.775568
age	1.713159	.3545698	.024216	1.695671	1.053206	2.458556
_cons	-42.31891	8.239571	.565879	-41.45385	-59.30145	-27.83421
var	12.29575	6.570879	.511475	10.3609	5.636195	30.93576

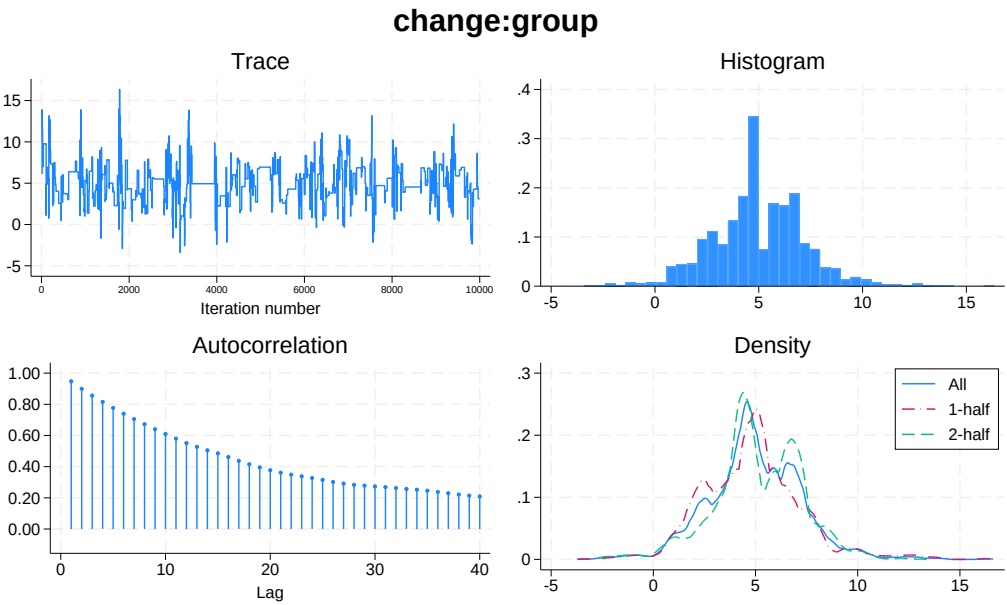
❑

▷ Example 5: Checking convergence

We can use the bayesgraph command to visually check convergence of MCMC of parameter estimates. bayesgraph provides a variety of graphs. For several commonly used visual diagnostics displayed in a compact form, use bayesgraph diagnostics.

For example, we can look at graphical diagnostics for the coefficient for `group`.

```
. bayesgraph diagnostics {change:group}
```



The displayed diagnostics include a trace plot, an autocorrelation plot, a histogram, and a kernel density estimate overlaid with densities estimated using the first and the second halves of the MCMC sample. Both the trace plot and the autocorrelation plot demonstrate high autocorrelation. The shape of the histogram is not unimodal. We definitely have some convergence issues in this example.

Similarly, we can look at diagnostics for other model parameters. To see all graphs at once, type

```
bayesgraph diagnostics _all
```

Other useful summaries are effective sample sizes and statistics related to them. These can be obtained by using the `bayesstats ess` command.

```
. bayesstats ess
Efficiency summaries     MCMC sample size =    10,000
                         Efficiency:  min =     .0165
                                      avg =    .02018
                                      max =    .02159
```

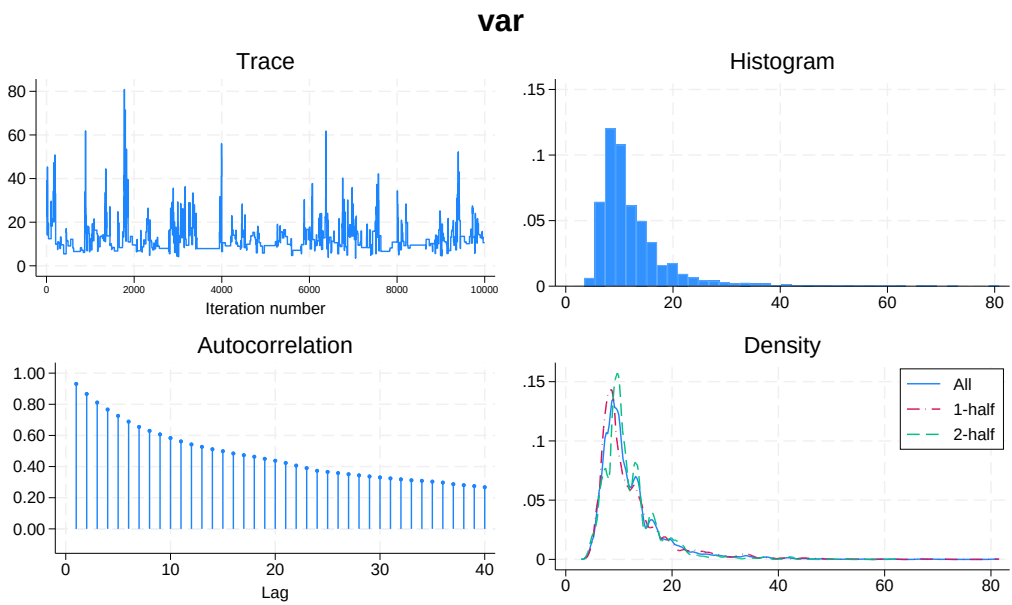
	ESS	Corr. time	Efficiency
change			
group	215.93	46.31	0.0216
age	214.39	46.64	0.0214
_cons	212.01	47.17	0.0212
var	165.04	60.59	0.0165

The closer ESS estimates are to the MCMC sample size, the less correlated the MCMC sample is, and the more precise our estimates of parameters are. Do not expect to see values close to the MCMC sample size with the MH algorithm, but values below 1% of the MCMC sample size are certainly red flags. In our example, ESS for {var} is somewhat low, so we may need to look into improving its sampling efficiency. For example, blocking on {var} should improve the efficiency for the variance; see *Improving efficiency of the MH algorithm—blocking of parameters*. It is usually a good idea to sample regression coefficients and the variance in two separate blocks.

Correlation times may be viewed as estimates of autocorrelation lags in the MCMC samples. For example, correlation times of the coefficients range between 46 and 47, and the correlation time for the variance parameter is higher, 61. Consequently, the efficiency for the variance is lower than for the regression coefficients. More investigation of the MCMC for {var} is needed.

Indeed, the MCMC for the variance has very poor mixing and very high autocorrelation.

```
. bayesgraph diagnostics {var}
```



One remedy is to update the variance parameter separately from the regression coefficients by putting the variance parameter in a separate block; see *Improving efficiency of the MH algorithm—blocking of parameters* for details about this procedure. In `bayesmh`, this can be done by specifying the `block()` option.

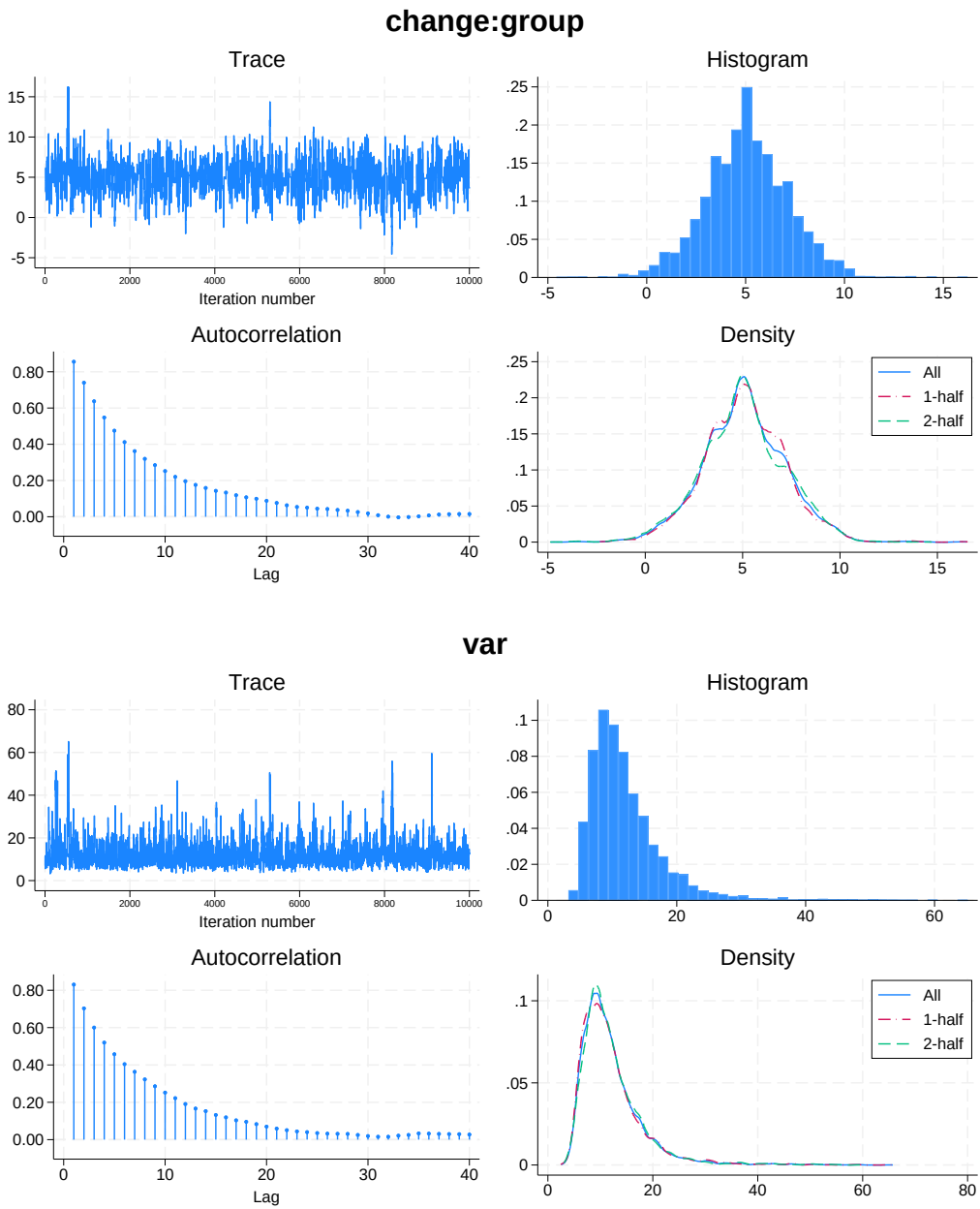
```
. set seed 14
. bayesmh change group age, likelihood(normal({var}))
> prior({change:}, zellnersg0(3,12,{var}))
> prior({var}, igamma(0.5, 4)) block({var})
> saving(agegroup_simdata)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ normal(xb_change,{var})
Priors:
  {change:group age _cons} ~ zellnersg(3,12,0,{var})                    (1)
                     {var} ~ igamma(0.5,4)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         12
                                                Acceptance rate  =      .3232
                                                Efficiency:  min =     .06694
                                                             avg =      .1056
Log marginal-likelihood = -35.460606                         max =      .1443
------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
change       |
       group |   5.080653   2.110911   .080507   5.039834   .8564619   9.399672
         age |   1.748516   .3347172   .008875   1.753897   1.128348   2.400989
       _cons |  -43.12425   7.865979   .207051   -43.2883  -58.64107  -27.79122
-------------+----------------------------------------------------------------
         var |   12.09916   5.971454   .230798   10.67555   5.375774   27.32451
------------------------------------------------------------------------------
file agegroup_simdata.dta saved.
. estimates store agegroup
```

Our acceptance rate and efficiencies are now higher.

In this example, we also used `estimates store agegroup` to store current estimation results as `agegroup` for future use. To use `estimates store` after `bayesmh`, we had to specify the `saving()` option with `bayesmh` to save the `bayesmh` simulation results to a permanent Stata dataset; see *Storing estimation results after Bayesian estimation*.

The MCMC chains are now mixing much better. We may consider increasing the default MCMC sample size to achieve even lower autocorrelation.

```
. bayesgraph diagnostics {change:group} {var}
```



Multiple chains are often used to diagnose the convergence of MCMC; see *Convergence diagnostics using multiple chains* in [BAYES] **bayesmh** and [BAYES] **bayesstats grubin**. Also see *Convergence of MCMC* in [BAYES] **bayesmh** for more information.

◁

▷ Example 6: Postestimation summaries

We can use the `bayesstats summary` command to compute postestimation summaries for model parameters and functions of model parameters. For example, we can compute an estimate of the standardized coefficient for `change`, which is $\widehat{\beta}_{\text{group}} \times \sigma_x/\sigma_y$, where σ_x and σ_y are sample standard deviations of `group` and `change`, respectively.

We use `summarize` (see [R] **summarize**) to compute sample standard deviations and store them in respective scalars.

```
. summarize group
    Variable |        Obs        Mean    Std. dev.       Min        Max
-------------+---------------------------------------------------------
       group |         12          .5     .522233          0          1

. scalar sd_x = r(sd)
. summarize change
    Variable |        Obs        Mean    Std. dev.       Min        Max
-------------+---------------------------------------------------------
      change |         12    2.469167    8.080637     -10.74      17.05

. scalar sd_y = r(sd)
```

The standardized coefficient is an expression of the model parameter `{change:group}`, so we specify it in parentheses.

```
. bayesstats summary (group_std:{change:group}*sd_x/sd_y)
Posterior summary statistics                     MCMC sample size =    10,000
   group_std : {change:group}*sd_x/sd_y

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
   group_std |  .3283509   .1364233   .005203   .3257128   .0553512   .6074792
------------------------------------------------------------------------------
```

The posterior mean estimate of the standardized `group` coefficient is 0.33 with a 95% credible interval of [0.055, 0.61].

◁

▷ Example 7: Bayesian predictions

Bayesian predictions are useful for checking model fit and for predicting future observations.

We can use the `bayespredict` command to generate replication samples for the outcome variable `change` and save them in a new dataset, `change_pred.dta`. Samples are drawn from the posterior predictive distribution of `change`. We specify `{_ysim}` with `bayespredict` to simulate the outcome values and use a random-number seed for reproducibility.

```
. bayespredict {_ysim}, saving(change_pred) rseed(16)
Computing predictions ...
file change_pred.dta saved.
file change_pred.ster saved.
```

change_pred.dta contains an MCMC sample of predicted values for each of the 12 observations. We can use bayesstats summary to calculate posterior summaries for the predicted observations by specifying using with the prediction dataset.

```
. bayesstats summary {_ysim} using change_pred
Posterior summary statistics                        MCMC sample size =    10,000
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
_ysim1_1	-2.954378	3.763301	.060963	-2.930854	-10.39297	4.528522
_ysim1_2	-4.610688	3.771203	.059014	-4.660554	-11.9289	2.948378
_ysim1_3	-4.620784	3.758543	.057517	-4.645584	-12.03851	2.917013
_ysim1_4	.6417156	3.756645	.063162	.6019013	-6.83463	8.330498
_ysim1_5	4.069868	3.972042	.072874	4.065139	-3.780329	12.06363
_ysim1_6	-8.120147	3.832453	.061674	-8.096888	-15.54334	-.3579446
_ysim1_7	16.18539	4.076738	.072385	16.2033	8.105208	24.23569
_ysim1_8	2.156433	3.921	.072344	2.135557	-5.528265	10.00732
_ysim1_9	9.14268	3.780417	.071241	9.154486	1.571643	16.59816
_ysim1_10	10.91948	3.776916	.068083	10.92263	3.445305	18.59981
_ysim1_11	.3919052	3.969695	.079798	.344616	-7.389234	8.386358
_ysim1_12	3.902787	3.809399	.077872	3.884087	-3.530938	11.49579

The first column contains posterior means, MCMC estimates of the expected outcome observations with respect to the posterior predictive distribution. Both posterior means and medians can be used as Bayesian predictors.

One way to assess goodness of fit of the model is by comparing replicated outcome samples with the observed outcome sample. The discrepancy between these two can be measured using the so-called posterior predictive p-values. We can use the bayesstats ppvalues command to compute these p-values. The posterior predictive p-values are typically computed for functions of the data or test statistics. Here, as a quick demonstration, we will compute them for each individual observation.

```
. bayesstats ppvalues {_ysim} using change_pred
Posterior predictive summary   MCMC sample size =    10,000
```

T	Mean	Std. dev.	E(T_obs)	P(T>=T_obs)
_ysim1_1	-2.954378	3.763301	-.87	.2786
_ysim1_2	-4.610688	3.771203	-10.74	.9512
_ysim1_3	-4.620784	3.758543	-3.27	.3479
_ysim1_4	.6417156	3.756645	-1.97	.773
_ysim1_5	4.069868	3.972042	7.5	.1819
_ysim1_6	-8.120147	3.832453	-7.25	.4034
_ysim1_7	16.18539	4.076738	17.05	.4124
_ysim1_8	2.156433	3.921	4.96	.2198
_ysim1_9	9.14268	3.780417	10.4	.3644
_ysim1_10	10.91948	3.776916	11.05	.4858
_ysim1_11	.3919052	3.969695	.26	.5106
_ysim1_12	3.902787	3.809399	2.51	.6498

```
Note: P(T>=T_obs) close to 0 or 1 indicates lack of fit.
```

All estimated posterior predictive p-values are between 0.05 and 0.95 (except for `_ysim1_2`) and thus indicate adequate fit for the individual observations. However, more stringent model checking typically requires that various test quantities be computed using the entire replicated sample to inspect the distribution of replicated outcome values to assess the overall fit of the model. See [BAYES] **bayesstats ppvalues** for examples.

We can also use `bayespredict` to generate out-of-sample predictions. For illustration, let's add two new observations to the dataset: one for age 26 and group `Aerobic` (`group=1`) and another for age 26 and group `Running` (`group=0`).

```
. set obs 14
Number of observations (_N) was 12, now 14.
. replace group = 1 in 13
(1 real change made)
. replace group = 0 in 14
(1 real change made)
. replace age = 26 in 13/14
(2 real changes made)
```

We want to predict the outcome `change` for the new observations. Possible Bayesian predictors are the posterior means of the simulated outcome observations. These can be calculated using the `mean` option and saved in a new variable, say, `pname`.

```
. bayespredict pmean, mean rseed(16)
Computing predictions ...
. list change age group pmean
```

	change	age	group	pmean
1.	-.87	23	Running	-2.914124
2.	-10.74	22	Running	-4.613421
3.	-3.27	22	Running	-4.701283
4.	-1.97	25	Running	.545417
5.	7.5	27	Running	4.060798
6.	-7.25	20	Running	-8.111091
7.	17.05	31	Aerobic	16.15393
8.	4.96	23	Aerobic	2.183771
9.	10.4	27	Aerobic	9.155602
10.	11.05	28	Aerobic	10.87576
11.	.26	22	Aerobic	.4234267
12.	2.51	24	Aerobic	3.937901
13.	.	26	Aerobic	7.380203
14.	.	26	Running	2.405744

The predicted estimates for the out-of-sample observations 13 and 14 are 7.4 and 2.4 for the change in maximal oxygen uptake (liters/minute) for a 26-year old in the aerobic and running groups, respectively.

See [BAYES] **bayespredict** for more examples.

Finally, we drop the two new observations we added and erase the prediction dataset and the auxiliary estimation file created by `bayespredict`.

```
. drop in 13/14
(2 observations deleted)
. erase change_pred.dta
. erase change_pred.ster
```

◁

▷ Example 8: Model comparison

As we can with frequentist analysis, we can use various information criteria to compare different models. There is great flexibility in which model can be compared: you can compare models with different distributions for the outcome, you can compare models with different priors, you can compare models with different forms for the regression function, and more. The only requirement is that the same data are used to fit the models. Comparisons using Bayes factors additionally require that parameters be sampled from the complete posterior distribution, which includes the normalizing constant.

Let's compare our reduced model with the full model including an interaction term. We again use a multivariate Zellner's g-prior for the coefficients and an inverse gamma prior for the variance. We use the same values as in example 4 for prior parameters. (We use the interaction variable in this example for notational simplicity. We could have used the factor-variable notation `c.age#i.group` to include this interaction directly in our model; see [U] **11.4.3 Factor variables**.)

```
. set seed 14
. bayesmh change group age ageXgr, likelihood(normal({var}))
> prior({change:}, zellnersg0(4,12,{var}))
> prior({var}, igamma(0.5, 4)) block({var})
> saving(full_simdata)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ normal(xb_change,{var})
Priors:
  {change:group age ageXgr _cons} ~ zellnersg(4,12,0,{var})              (1)
                          {var} ~ igamma(0.5,4)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         12
                                                Acceptance rate  =      .3113
                                                Efficiency:  min =      .0562
                                                             avg =      .06425
Log marginal-likelihood = -36.738363                         max =      .08478
------------------------------------------------------------------------------
                                                              Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
change       |
       group |   11.94079   16.74992   .706542   12.13983  -22.31056   45.11963
         age |   1.939266   .5802772   .023359   1.938756   .7998007   3.091072
      ageXgr |  -.2838718   .6985226   .028732  -.285647   -1.671354   1.159183
       _cons |  -47.57742    13.4779    .55275  -47.44761  -74.64672  -20.78989
-------------+----------------------------------------------------------------
         var |   11.72886    5.08428   .174612   10.68098   5.302265   24.89543
------------------------------------------------------------------------------
file full_simdata.dta saved.
. estimates store full
```

We can use the `bayesstats ic` command to compare the models. We list the names of the corresponding estimation results following the command name.

```
. bayesstats ic full agegroup
Bayesian information criteria
------------------------------------------------------------------------------
             |        DIC     log(ML)      log(BF)
-------------+----------------------------------------------------------------
        full |   65.03326   -36.73836            .
    agegroup |    63.5884   -35.46061     1.277756
------------------------------------------------------------------------------
Note: Marginal likelihood (ML) is computed
      using Laplace-Metropolis approximation.
```

The smaller that `DIC` is and the larger that `log(ML)` is, the better. The model without interaction, `agegroup`, is preferred according to these statistics. The log Bayes-factor for the `agegroup` model relative to the `full` model is 1.28. Kass and Raftery (1995) provide a table of values for Bayes factors; see, for example, *Bayes factors* in [BAYES] **bayesstats ic**. According to their scale, because $2 \times 1.28 = 2.56$ is greater than 2 (slightly), there is some mild evidence that model `agegroup` is better than model `full`.

◁

Example 9: Hypothesis testing

Continuing with example 8, we can compute the actual probability associated with each of the models. We can use the `bayestest model` command to do this.

Similar to `bayesstats ic`, this command requires the names of estimation results corresponding to the models of interest.

```
. bayestest model full agegroup
Bayesian model tests
```

	log(ML)	P(M)	P(M|y)
full	-36.7384	0.5000	0.2179
agegroup	-35.4606	0.5000	0.7821

```
Note: Marginal likelihood (ML) is computed using
      Laplace-Metropolis approximation.
```

Under the assumption that both models are equally probable a priori, the model without interaction, `agegroup`, has the probability of 0.78, whereas the `full` model has the probability of only 0.22. Despite the drastic disparity in the probabilities, according to the results from example 8, model `agegroup` is only slightly preferable to model `full`. To have stronger evidence against `full`, we would expect to see higher probabilities (above 0.9) for `agegroup`.

We may be interested in testing an interval hypothesis about the parameter of interest. For example, for a model without interaction, let's compute the probability that the coefficient for `group` is between 4 and 8. We use `estimates restore` (see [R] **estimates store**) to load the results of the `agegroup` model back into memory.

```
. estimates restore agegroup
(results agegroup are active now)
. bayestest interval {change:group}, lower(4) upper(8)
Interval tests     MCMC sample size =    10,000
       prob1 : 4 < {change:group} < 8
```

	Mean	Std. dev.	MCSE
prob1	.6159	0.48641	.0155788

The estimated probability or, technically, its posterior mean estimate is 0.62 with a standard deviation of 0.49 and Monte Carlo standard errors of 0.016.

◁

Example 10: Erasing simulation datasets

After you are done with your analysis, remember to erase any simulation datasets that you created using `bayesmh` and no longer need. If you want to save your estimation results to disk for future reference, use `estimates save`; see [R] **estimates save**.

We are done with our analysis, and we do not need the datasets for future reference, so we remove both simulation files we created using `bayesmh`.

```
. erase agegroup_simdata.dta
. erase full_simdata.dta
```

◁

▷ Example 11: Bayesian linear regression using the bayes prefix

Recall our OLS regression from example 1. There is a more convenient way to obtain Bayesian estimates for this regression than using the `bayesmh` command as in previous examples. Because `regress` is one of the estimation commands that supports the `bayes` prefix ([BAYES] **Bayesian estimation**), we can simply type

```
. set seed 14
. bayes: regress change group age
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ regress(xb_change,{sigma2})
Priors:
  {change:group age _cons} ~ normal(0,10000)                              (1)
                  {sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.
Bayesian linear regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         12
                                                Acceptance rate  =       .283
                                                Efficiency:  min =     .02715
                                                             avg =     .05779
Log marginal-likelihood = -45.562124                         max =      .0692
------------------------------------------------------------------------------
                                                              Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
change       |
       group |  5.425311   2.111038   .080252   5.368975   1.104434   9.425197
         age |  1.885651   .3255098   .012472   1.887263   1.244666   2.517292
       _cons | -46.47537   7.632058   .295505  -46.73244  -60.39245   -30.5054
-------------+----------------------------------------------------------------
      sigma2 |  10.28431   7.614468   .462105   8.412747   3.595971   31.47161
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

With the `bayes` prefix command, the likelihood is determined automatically by the specified estimation command—`regress` in our example. The `bayes` prefix also provides the default prior specifications for model parameters, displaying this information as a note at the bottom of the output table; see *Default priors* in [BAYES] **bayes**. Model summary provides details about the used default priors. For linear regression, the regression coefficients are assigned independent normal priors with zero mean and variance of 10,000, and the variance is assigned an inverse-gamma prior with the same shape and scale parameters of 0.01.

The default priors are provided for convenience and are chosen to be fairly uninformative for models with moderately scaled parameters. However, they are not guaranteed to be uninformative for all models and datasets; see *Linear regression: A case of informative default priors* in [BAYES] **bayes**. You should choose priors carefully based on your research and model of interest.

As with bayesmh, the default MCMC method is an adaptive MH, but we can specify the gibbs option to request Gibbs sampling.

```
. set seed 14
. bayes, gibbs: regress change group age
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ normal(xb_change,{sigma2})
Priors:
  {change:group age _cons} ~ normal(0,10000)                              (1)
                {sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.
Bayesian linear regression                      MCMC iterations  =     12,500
Gibbs sampling                                  Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         12
                                                Acceptance rate  =          1
                                                Efficiency:  min =       .556
                                                             avg =       .889
Log marginal-likelihood =  -45.83666                         max =          1
------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
change       |
       group |  5.452439   2.062795   .020628   5.460372   1.360104   9.512987
         age |  1.875606    .330127   .003301   1.877129   1.228647   2.543129
       _cons | -46.21334   7.746862   .077469  -46.18291  -61.82541  -31.09702
-------------+----------------------------------------------------------------
      sigma2 |  9.929756   5.899176   .079113   8.426173   3.731261   24.76194
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

As expected, we obtain higher efficiency when using the Gibbs sampling. However, the gibbs option is available only with bayes: regress and bayes: mvreg and only for certain prior distributions.

We can easily change the default priors by specifying the `prior()` option, as with `bayesmh`. For example, we can reproduce `bayesmh`'s results from example 4 but with the `bayes` prefix.

```
. set seed 14
. bayes, prior({change:}, zellnersg0(3,12,{sigma2}))
> prior({sigma2}, igamma(0.5, 4)): regress change group age
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ regress(xb_change,{sigma2})
Priors:
  {change:group age _cons} ~ zellnersg(3,12,0,{sigma2})                   (1)
                  {sigma2} ~ igamma(0.5,4)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.
Bayesian linear regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         12
                                                Acceptance rate  =      .2838
                                                Efficiency:  min =     .06423
                                                             avg =     .07951
Log marginal-likelihood = -35.448029                         max =     .09277
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
change						
group	4.944955	2.184113	.086181	5.052278	.7065487	9.35098
age	1.747984	.3390581	.011132	1.747477	1.045677	2.416091
_cons	-43.09605	7.904334	.263186	-43.01961	-58.57942	-27.11278
sigma2	12.17932	5.87997	.220888	10.72651	5.511202	28.1211

The results are similar to those from example 4 using `bayesmh` but not identical. By default, `bayes: regress` automatically splits the regression coefficients and the variance into two separate blocks, whereas `bayesmh` treats all parameters as one block; see *Improving efficiency of the MH algorithm—blocking of parameters* in [BAYES] **bayesmh** for details about blocking.

To match the results exactly, you can either specify the `block({var})` option with `bayesmh` in example 4 or specify the `noblocking` option to request no default blocking with the `bayes` prefix.

```
. set seed 14
. bayes, prior({change:}, zellnersg0(3,12,{sigma2}))
> prior({sigma2}, igamma(0.5, 4)) noblocking: regress change group age
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ regress(xb_change,{sigma2})
Priors:
  {change:group age _cons} ~ zellnersg(3,12,0,{sigma2})                   (1)
                {sigma2} ~ igamma(0.5,4)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.
Bayesian linear regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         12
                                                Acceptance rate  =     .06169
                                                Efficiency:  min =      .0165
                                                             avg =     .02018
Log marginal-likelihood = -35.356501                         max =     .02159
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
change						
group	4.988881	2.260571	.153837	4.919351	.7793098	9.775568
age	1.713159	.3545698	.024216	1.695671	1.053206	2.458556
_cons	-42.31891	8.239571	.565879	-41.45385	-59.30145	-27.83421
sigma2	12.29575	6.570879	.511475	10.3609	5.636195	30.93576

See [BAYES] **bayes** for more details.

◁

Acknowledgments

We thank John Thompson (retired) of the Department of Health Sciences at the University of Leicester, UK, and author of *Bayesian Analysis with Stata*, and Matthew J. Baker of Hunter College and the Graduate Center, CUNY for their software and contributions to Bayesian analysis in Stata.

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Also see

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Glossary**

Title

Bayesian estimation — Bayesian estimation commands

Description Video examples Also see

Description

Bayesian estimation in Stata is similar to standard estimation—simply prefix the estimation commands with `bayes:` (see [BAYES] **bayes**). You can also refer to [BAYES] **bayesmh** and [BAYES] **bayesmh evaluators** for fitting more general Bayesian models.

The following estimation commands support the `bayes` prefix.

Command	Entry	Description
Linear regression models		
`regress`	[BAYES] **bayes: regress**	Linear regression
`hetregress`	[BAYES] **bayes: hetregress**	Heteroskedastic linear regression
`tobit`	[BAYES] **bayes: tobit**	Tobit regression
`intreg`	[BAYES] **bayes: intreg**	Interval regression
`truncreg`	[BAYES] **bayes: truncreg**	Truncated regression
`mvreg`	[BAYES] **bayes: mvreg**	Multivariate regression
Binary-response regression models		
`logistic`	[BAYES] **bayes: logistic**	Logistic regression, reporting odds ratios
`logit`	[BAYES] **bayes: logit**	Logistic regression, reporting coefficients
`probit`	[BAYES] **bayes: probit**	Probit regression
`cloglog`	[BAYES] **bayes: cloglog**	Complementary log–log regression
`hetprobit`	[BAYES] **bayes: hetprobit**	Heteroskedastic probit regression
`binreg`	[BAYES] **bayes: binreg**	GLM for the binomial family
`biprobit`	[BAYES] **bayes: biprobit**	Bivariate probit regression
Ordinal-response regression models		
`ologit`	[BAYES] **bayes: ologit**	Ordered logistic regression
`oprobit`	[BAYES] **bayes: oprobit**	Ordered probit regression
`hetoprobit`	[BAYES] **bayes: hetoprobit**	Heteroskedastic ordered probit regression
`ziologit`	[BAYES] **bayes: ziologit**	Zero-inflated ordered logit regression
`zioprobit`	[BAYES] **bayes: zioprobit**	Zero-inflated ordered probit regression
Categorical-response regression models		
`mlogit`	[BAYES] **bayes: mlogit**	Multinomial (polytomous) logistic regression
`mprobit`	[BAYES] **bayes: mprobit**	Multinomial probit regression
`clogit`	[BAYES] **bayes: clogit**	Conditional logistic regression

Count-response regression models

poisson	[BAYES] **bayes: poisson**	Poisson regression
nbreg	[BAYES] **bayes: nbreg**	Negative binomial regression
gnbreg	[BAYES] **bayes: gnbreg**	Generalized negative binomial regression
tpoisson	[BAYES] **bayes: tpoisson**	Truncated Poisson regression
tnbreg	[BAYES] **bayes: tnbreg**	Truncated negative binomial regression
zip	[BAYES] **bayes: zip**	Zero-inflated Poisson regression
zinb	[BAYES] **bayes: zinb**	Zero-inflated negative binomial regression

Generalized linear models

glm	[BAYES] **bayes: glm**	Generalized linear models

Fractional-response regression models

fracreg	[BAYES] **bayes: fracreg**	Fractional response regression
betareg	[BAYES] **bayes: betareg**	Beta regression

Survival regression models

streg	[BAYES] **bayes: streg**	Parametric survival models

Sample-selection regression models

heckman	[BAYES] **bayes: heckman**	Heckman selection model
heckprobit	[BAYES] **bayes: heckprobit**	Probit regression with sample selection
heckoprobit	[BAYES] **bayes: heckoprobit**	Ordered probit model with sample selection

Longitudinal/panel-data regression models

xtreg	[BAYES] **bayes: xtreg**	Random-effects linear regression
xtlogit	[BAYES] **bayes: xtlogit**	Random-effects logit regression
xtprobit	[BAYES] **bayes: xtprobit**	Random-effects probit regression
xtologit	[BAYES] **bayes: xtologit**	Random-effects ordered logit regression
xtoprobit	[BAYES] **bayes: xtoprobit**	Random-effects ordered probit regression
xtmlogit	[BAYES] **bayes: xtmlogit**	Random-effects multinomial logit regression
xtpoisson	[BAYES] **bayes: xtpoisson**	Random-effects Poisson regression
xtnbreg	[BAYES] **bayes: xtnbreg**	Random-effects negative binomial regression

Multilevel regression models

mixed	[BAYES] **bayes: mixed**	Multilevel linear regression
metobit	[BAYES] **bayes: metobit**	Multilevel tobit regression
meintreg	[BAYES] **bayes: meintreg**	Multilevel interval regression
melogit	[BAYES] **bayes: melogit**	Multilevel logistic regression
meprobit	[BAYES] **bayes: meprobit**	Multilevel probit regression
mecloglog	[BAYES] **bayes: mecloglog**	Multilevel complementary log–log regression
meologit	[BAYES] **bayes: meologit**	Multilevel ordered logistic regression
meoprobit	[BAYES] **bayes: meoprobit**	Multilevel ordered probit regression
mepoisson	[BAYES] **bayes: mepoisson**	Multilevel Poisson regression
menbreg	[BAYES] **bayes: menbreg**	Multilevel negative binomial regression
meglm	[BAYES] **bayes: meglm**	Multilevel generalized linear model
mestreg	[BAYES] **bayes: mestreg**	Multilevel parametric survival regression

Time-series models		
`var`	[BAYES] **bayes: var**	Vector autoregression
DSGE models		
`dsge`	[BAYES] **bayes: dsge**	Linear DSGE model
`dsgenl`	[BAYES] **bayes: dsgenl**	Nonlinear DSGE model

Video examples

Introduction to Bayesian statistics, part 1: The basic concepts

Introduction to Bayesian statistics, part 2: MCMC and the Metropolis–Hastings algorithm

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

[BAYES] **bayesmh evaluators** — User-defined evaluators with bayesmh

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes — Bayesian regression models using the bayes prefix

Description

The `bayes` prefix fits Bayesian regression models. It provides Bayesian support for many likelihood-based estimation commands. The `bayes` prefix uses default or user-supplied priors for model parameters and estimates parameters using MCMC by drawing simulation samples from the corresponding posterior model. Also see [BAYES] **bayesmh** and [BAYES] **bayesmh evaluators** for fitting more general Bayesian models.

Quick start

Bayesian linear regression of `y` on `x`, using default normal priors for the regression coefficients and an inverse-gamma prior for the variance

```
bayes: regress y x
```

Same as above, but use a standard deviation of 10 instead of 100 for the default normal priors and shape of 2 and scale of 1 instead of values of 0.01 for the default inverse-gamma prior

```
bayes, normalprior(10) igammaprior(2 1): regress y x
```

Same as above, but simulate four chains

```
bayes, normalprior(10) igammaprior(2 1) nchains(4): regress y x
```

Bayesian logistic regression of `y` on `x1` and `x2`, showing model summary without performing estimation

```
bayes, dryrun: logit y x1 x2
```

Same as above, but estimate model parameters and use uniform priors for all regression coefficients

```
bayes, prior({y: x1 x2 _cons}, uniform(-10,10)): logit y x1 x2
```

Same as above, but use a shortcut notation to refer to all regression coefficients

```
bayes, prior({y:}, uniform(-10,10)): logit y x1 x2
```

Same as above, but report odds ratios and use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
       prior({y:_cons}, normal(0,10)) or: logit y x1 x2
```

Report odds ratios for the logit model on replay

```
bayes, or
```

Bayesian ordered logit regression of `y` on `x1` and `x2`, saving simulation results to `simdata.dta` and using a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): ologit y x1 x2 x3
```

Bayesian multinomial regression of y on x1 and x2, specifying 20,000 MCMC samples, setting length of the burn-in period to 5,000, and requesting that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): mlogit y x1 x2
```

Bayesian Poisson regression of y on x1 and x2, putting regression slopes in separate blocks and showing block summary

```
bayes, block({y:x1}) block({y:x2}) blocksummary: poisson y x1 x2
```

Bayesian multivariate regression of y1 and y2 on x1, x2, and x3, using Gibbs sampling and requesting 90% HPD credible interval instead of the default 95% equal-tailed credible interval

```
bayes, gibbs clevel(90) hpd: mvreg y1 y2 = x1 x2 x3
```

Same as above, but use mvreg's option level() instead of bayes's option clevel()

```
bayes, gibbs hpd: mvreg y1 y2 = x1 x2 x3, level(90)
```

Suppress estimates of the covariance matrix from the output

```
bayes, noshow(Sigma, matrix)
```

Bayesian Weibull regression of stset survival-time outcome on x1 and x2, specifying starting values of 1 for {y:x1} and of 2 for {y:x2}

```
bayes, initial({y:x1} 1 {y:x2} 2): streg x1 x2, distribution(weibull)
```

Bayesian panel-data regression of y on x1 and x2 with random intercepts by id, after xtseting id as the panel variable

```
xtset id
bayes: xtreg y x1 x2
```

Bayesian two-level linear regression of y on x1 and x2 with random intercepts by id

```
bayes: mixed y x1 x2 || id:
```

Menu

Statistics > Bayesian analysis > Regression models > *estimation_command*

Syntax

```
bayes [ , bayesopts ] : estimation_command [ , estopts ]
```

estimation_command is a likelihood-based estimation command, and *estopts* are command-specific estimation options; see [BAYES] **Bayesian estimation** for a list of supported commands, and see the command-specific entries for the supported estimation options, *estopts*.

bayesopts	Description
Priors	
* `gibbs`	specify Gibbs sampling; available only with `regress`, `xtreg`, or `mvreg` for certain prior combinations
* `normalprior(#)`	specify standard deviation of default normal priors for regression coefficients and other real scalar parameters; default is `normalprior(100)`
* `igammaprior(# #)`	specify shape and scale of default inverse-gamma prior for variances; default is `igammaprior(0.01 0.01)`
* `iwishartprior(# [...])`	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
`restubs(`*restub1 restub2* ...`)`	specify stubs for random-effects parameters for all levels; allowed only with multilevel models
Blocking	
* `blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [, *blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
* `noblocking`	do not block parameters by default
Initialization	
`initial(`*initspec*`)`	specify initial values for model parameters with a single chain
`init#(`*initspec*`)`	specify initial values for #th chain; requires `nchains()`
`initall(`*initspec*`)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
* `noisily`	display output from the estimation command during initialization

Adaptation	
`adaptation(`*adaptopts*`)`	control the adaptive MCMC procedure
`scale(#)`	initial multiplier for scale factor; default is `scale(2.38)`
`covariance(`*cov*`)`	initial proposal covariance; default is the identity matrix
Reporting	
`clevel(#)`	set credible interval level; default is `clevel(95)`
`hpd`	display HPD credible intervals instead of the default equal-tailed credible intervals
eform_option	display coefficient table in exponentiated form
`remargl`	compute log marginal-likelihood for random-effects models
`batch(#)`	specify length of block for batch-means calculations; default is `batch(0)`
`saving(`*filename*`[ , replace ])`	save simulation results to *filename*`.dta`
`nomodelsummary`	suppress model summary
`nomesummary`	suppress multilevel-structure summary; allowed only with multilevel models
`chainsdetail`	display detailed simulation summary for each chain
`[no]dots`	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is command-specific
`dots(#[ , every(#) ])`	display dots as simulation is performed
`[no]show(`*paramref*`)`	specify model parameters to be excluded from or included in the output
`showreffects[ (`*reref*`) ]`	specify that all or a subset of random-effects parameters be included in the output; allowed only with panel-data and multilevel commands
`melabel`	display estimation table using the same row labels as *estimation_command*; allowed only with multilevel commands
`nogroup`	suppress table summarizing groups; allowed only with multilevel models
`notable`	suppress estimation table
`noheader`	suppress output header
`title(`*string*`)`	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells
Advanced	
`search(`*search_options*`)`	control the search for feasible initial values
`corrlag(#)`	specify maximum autocorrelation lag; default varies
`corrtol(#)`	specify autocorrelation tolerance; default is `corrtol(0.01)`

*Starred options are specific to the `bayes` prefix; other options are common between `bayes` and `bayesmh`.

The full specification of `iwishartprior()` is `iwishartprior(#[ matname ][ , relevel(levelvar) ])`.

Options `prior()` and `block()` may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Options

Priors

`gibbs` specifies that Gibbs sampling be used to simulate model parameters instead of the default adaptive Metropolis–Hastings sampling. This option is allowed only with the `regress`, `xtreg`, and `mvreg` estimation commands. It is available only with certain prior combinations such as normal prior for regression coefficients and an inverse-gamma prior for the variance. Specifying the `gibbs` option is equivalent to specifying `block()`'s `gibbs` suboption for all default blocks of parameters. If you use the `block()` option to define your own blocks of parameters, the `gibbs` option will have no effect on those blocks, and an MH algorithm will be used to update parameters in those blocks unless you also specify `block()`'s `gibbs` suboption.

With panel-data and multilevel linear models, Gibbs sampling is used by default for regression coefficients and variance components, and Metropolis–Hastings sampling is used for random effects. For panel-data linear models, you can specify option `gibbs` to use Gibbs sampling also for random effects.

`normalprior(#)` specifies the standard deviation of the default normal priors. The default is `normalprior(100)`. The normal priors are used for scalar parameters defined on the whole real line; see *Default priors* for details.

`igammaprior(# #)` specifies the shape and scale parameters of the default inverse-gamma priors. The default is `igammaprior(0.01 0.01)`. The inverse-gamma priors are used for positive scalar parameters such as a variance; see *Default priors* for details. Instead of a number #, you can specify a missing value (`.`) to refer to the default value of 0.01.

`iwishartprior(#` [*matname*] [`, relevel(`*levelvar*`)`]`)` specifies the degrees of freedom and, optionally, the scale matrix *matname* of the default inverse-Wishart priors used for unstructured covariances of random effects with multilevel models. The degrees of freedom # is a positive real scalar with the default value of $d+1$, where d is the number of random-effects terms at the level of hierarchy *levelvar*. Instead of a number #, you can specify a missing value (`.`) to refer to the default value. Matrix name *matname* is the name of a positive-definite Stata matrix with the default of $I(d)$, the identity matrix of dimension d. If `relevel(`*levelvar*`)` is omitted, the specified parameters are used for inverse-Wishart priors for all levels with unstructured random-effects covariances. Otherwise, they are used only for the prior for the specified level *levelvar*. See *Default priors* for details.

`prior(`*priorspec*`)` specifies a prior distribution for model parameters. This option may be repeated. A prior may be specified for any of the model parameters, except the random-effects parameters in multilevel models. Model parameters with the same prior specifications are placed in a separate block. Model parameters that are not included in prior specifications are assigned default priors; see *Default priors* for details. Model parameters may be scalars or matrices, but both types may not be combined in one prior statement. If multiple scalar parameters are assigned a single univariate prior, they are considered independent, and the specified prior is used for each parameter. You may assign a multivariate prior of dimension *d* to *d* scalar parameters. Also see *Referring to model parameters* in [BAYES] **bayesmh**.

All `prior()` distributions are allowed, but they are not guaranteed to correspond to proper posterior distributions for all likelihood models. You need to think carefully about the model you are building and evaluate its convergence thoroughly; see *Convergence of MCMC* in [BAYES] **bayesmh**.

`dryrun` specifies to show the summary of the model that would be fit without actually fitting the model. This option is recommended for checking specifications of the model before fitting the model. The model summary reports the information about the likelihood model and about priors for all model parameters.

Simulation

`nchains(#)` specifies the number of Markov chains to simulate. You must specify at least two chains. By default, only one chain is produced. Simulating multiple chains is useful for convergence diagnostics and to improve precision of parameter estimates. Four chains are often recommended in the literature, but you can specify more or less depending on your objective. The reported estimation results are based on all chains. You can use `bayesstats summary` with option `sepchains` to see the results for each chain. The reported acceptance rate, efficiencies, and log marginal-likelihood are averaged over all chains. You can use option `chainsdetail` to see these simulation summaries for each chain. Also see *Convergence diagnostics using multiple chains* in [BAYES] **bayesmh** and *Gelman–Rubin convergence diagnostic* in [BAYES] **bayesstats grubin**.

`mcmcsize(#)` specifies the target MCMC sample size. The default MCMC sample size is `mcmcsize(10000)`. The total number of iterations for the MH algorithm equals the sum of the burn-in iterations and the MCMC sample size in the absence of thinning. If thinning is present, the total number of MCMC iterations is computed as `burnin()` + (`mcmcsize()` − 1) × `thinning()` + 1. Computation time of the MH algorithm is proportional to the total number of iterations. The MCMC sample size determines the precision of posterior summaries, which may be different for different model parameters and will depend on the efficiency of the Markov chain. With multiple chains, `mcmcsize()` applies to each chain. Also see *Burn-in period and MCMC sample size* in [BAYES] **bayesmh**.

`burnin(#)` specifies the number of iterations for the burn-in period of MCMC. The values of parameters simulated during burn-in are used for adaptation purposes only and are not used for estimation. The default is `burnin(2500)`. Typically, burn-in is chosen to be as long as or longer than the adaptation period. The burn-in period may need to be larger for multilevel models because these models introduce high-dimensional random-effects parameters and thus require longer adaptation periods. With multiple chains, `burnin()` applies to each chain. Also see *Burn-in period and MCMC sample size* in [BAYES] **bayesmh** and *Convergence of MCMC* in [BAYES] **bayesmh**.

`thinning(#)` specifies the thinning interval. Only simulated values from every $(1+k\times\#)$th iteration for $k = 0, 1, 2, \ldots$ are saved in the final MCMC sample; all other simulated values are discarded. The default is `thinning(1)`; that is, all simulation values are saved. Thinning greater than one is typically used for decreasing the autocorrelation of the simulated MCMC sample. With multiple chains, `thinning()` applies to each chain.

`rseed(#)` sets the random-number seed. This option can be used to reproduce results. With one chain, `rseed(#)` is equivalent to typing `set seed #` prior to calling the `bayes` prefix; see [R] **set seed**. With multiple chains, you should use `rseed()` for reproducibility; see *Reproducing results* in [BAYES] **bayesmh**.

`exclude(`*paramref*`)` specifies which model parameters should be excluded from the final MCMC sample. These model parameters will not appear in the estimation table, and postestimation features for these parameters and log marginal-likelihood will not be available. This option is useful for suppressing nuisance model parameters. For example, if you have a factor predictor variable with many levels but you are only interested in the variability of the coefficients associated with its levels, not their actual values, then you may wish to exclude this factor variable from the simulation results. If you simply want to omit some model parameters from the output, see the `noshow()` option. *paramref* can include individual random-effects parameters.

`restubs(`*restub1 restub2* ...`)` specifies the stubs for the names of random-effects parameters. You must specify stubs for all levels—one stub per level. This option overrides the default random-effects stubs. See *Likelihood model* for details about the default names of random-effects parameters.

Blocking

`blocksize(#)` specifies the maximum block size for the model parameters; default is `blocksize(50)`. This option does not apply to random-effects parameters. Each group of random-effects parameters is placed in one block, regardless of the number of random-effects parameters in that group.

`block(`*paramref* [`,` *blockopts*]`)` specifies a group of model parameters for the blocked MH algorithm. By default, model parameters, except the random-effects parameters, are sampled as independent blocks of 50 parameters or of the size specified in option `blocksize()`. Regression coefficients from different equations are placed in separate blocks. Auxiliary parameters such as variances and correlations are sampled as individual separate blocks, whereas the cutpoint parameters of the ordinal-outcome regressions are sampled as one separate block. With multilevel models, each group of random-effects parameters is placed in a separate block, and the `block()` option is not allowed with random-effects parameters. The `block()` option may be repeated to define multiple blocks. Different types of model parameters, such as scalars and matrices, may not be specified in one `block()`. Parameters within one block are updated simultaneously, and each block of parameters is updated in the order it is specified; the first specified block is updated first, the second is updated second, and so on. See *Improving efficiency of the MH algorithm—blocking of parameters* in [BAYES] **bayesmh**.

blockopts include `gibbs`, `split`, `scale()`, `covariance()`, and `adaptation()`.

`gibbs` specifies to use Gibbs sampling to update parameters in the block. This option is allowed only for hyperparameters and only for specific combinations of prior and hyperprior distributions; see *Gibbs sampling for some likelihood-prior and prior-hyperprior configurations* in [BAYES] **bayesmh**. For more information, see *Gibbs and hybrid MH sampling* in [BAYES] **bayesmh**. `gibbs` may not be combined with `scale()`, `covariance()`, or `adaptation()`.

`split` specifies that all parameters in a block are treated as separate blocks. This may be useful for levels of factor variables.

`scale(#)` specifies an initial multiplier for the scale factor corresponding to the specified block. The initial scale factor is computed as $\#/\sqrt{n_p}$ for continuous parameters and as $\#/n_p$ for discrete parameters, where n_p is the number of parameters in the block. The default is `scale(2.38)`. If specified, this option overrides the respective setting from the `scale()` option specified with the command. `scale()` may not be combined with `gibbs`.

`covariance(`*matname*`)` specifies a scale matrix *matname* to be used to compute an initial proposal covariance matrix corresponding to the specified block. The initial proposal covariance is computed as *rho*×*Sigma*, where *rho* is a scale factor and *Sigma* = *matname*. By default, *Sigma* is the identity matrix. If specified, this option overrides the respective setting from the `covariance()` option specified with the command. `covariance()` may not be combined with `gibbs`.

`adaptation(tarate())` and `adaptation(tolerance())` specify block-specific TAR and acceptance tolerance. If specified, they override the respective settings from the `adaptation()` option specified with the command. `adaptation()` may not be combined with `gibbs`.

`blocksummary` displays the summary of the specified blocks. This option is useful when `block()` is specified.

`noblocking` requests that no default blocking is applied to model parameters. By default, model parameters are sampled as independent blocks of 50 parameters or of the size specified in option `blocksize()`. For multilevel models, this option has no effect on random-effects parameters; blocking is always applied to them.

Initialization

`initial(`*initspec*`)` specifies initial values for the model parameters to be used in the simulation. With multiple chains, this option is equivalent to specifying option `init1()`. You can specify a parameter name, its initial value, another parameter name, its initial value, and so on. For example, to initialize a scalar parameter `alpha` to 0.5 and a 2x2 matrix `Sigma` to the identity matrix `I(2)`, you can type

```
bayes, initial({alpha} 0.5 {Sigma,m} I(2)) : ...
```

You can also specify a list of parameters using any of the specifications described in *Referring to model parameters* in [BAYES] **bayesmh**. For example, to initialize all regression coefficients from equations `y1` and `y2` to zero, you can type

```
bayes, initial({y1:} {y2:} 0) : ...
```

The general specification of *initspec* is

paramref initval [*paramref initval* [...]]

where *initval* is a number, a Stata expression that evaluates to a number, or a Stata matrix for initialization of matrix parameters.

Curly braces may be omitted for scalar parameters but must be specified for matrix parameters. Initial values declared using this option override the default initial values or any initial values declared during parameter specification in the `likelihood()` option. See *Initial values* for details.

`init#(`*initspec*`)` specifies initial values for the model parameters for the #th chain. This option requires option `nchains()`. `init1()` overrides the default initial values for the first chain, `init2()` for the second chain, and so on. You specify initial values in `init#()` just like you do in option `initial()`. See *Initial values* for details.

`initall(`*initspec*`)` specifies initial values for the model parameters for all chains. This option requires option `nchains()`. You specify initial values in `initall()` just like you do in option `initial()`. You should avoid specifying fixed initial values in `initall()` because then all chains will use the same initial values. `initall()` is useful to specify random initial values when you define your own priors within `prior()`'s `density()` and `logdensity()` suboptions. See *Initial values* for details.

`nomleinitial` suppresses using maximum likelihood estimates (MLEs) as starting values for model parameters. With multiple chains, this option and discussion below apply only to the first chain. By default, when no initial values are specified, MLE values from *estimation_command* are used as initial values. For multilevel commands, MLE estimates are used only for regression coefficients. Random effects are assigned zero values, and random-effects variances and covariances are initialized with ones and zeros, respectively. If `nomleinitial` is specified and no initial values are provided, the command uses ones for positive scalar parameters, zeros for other scalar parameters, and identity matrices for matrix parameters. `nomleinitial` may be useful for providing an alternative starting state when checking convergence of MCMC. This option cannot be combined with `initrandom`.

`initrandom` specifies that the model parameters be initialized randomly. Random initial values are generated from the prior distributions of the model parameters. If you want to use fixed initial values for some of the parameters, you can specify them in the `initial()` option or during parameter declarations in the `likelihood()` option. Random initial values are not available for parameters with `flat`, `jeffreys`, `density()`, `logdensity()`, and `jeffreys()` priors; you must provide your own initial values for such parameters. This option cannot be combined with `nomleinitial`. See *Specifying initial values* in [BAYES] **bayesmh** for details.

`initsummary` specifies that the initial values used for simulation be displayed.

`noisily` specifies that the output from the estimation command be shown during initialization. The estimation command is executed once to set up the model and calculate initial values for model parameters.

Adaptation

`adaptation(`*adaptopts*`)` controls adaptation of the MCMC procedure. Adaptation takes place every prespecified number of MCMC iterations and consists of tuning the proposal scale factor and proposal covariance for each block of model parameters. Adaptation is used to improve sampling efficiency. Provided defaults are based on theoretical results and may not be sufficient for all applications. See *Adaptation of the MH algorithm* in [BAYES] **bayesmh** for details about adaptation and its parameters.

adaptopts are any of the following options:

`every(#)` specifies that adaptation be attempted every #th iteration. The default is `every(100)`. To determine the adaptation interval, you need to consider the maximum block size specified in your model. The update of a block with k model parameters requires the estimation of a $k \times k$ covariance matrix. If the adaptation interval is not sufficient for estimating the $k(k+1)/2$ elements of this matrix, the adaptation may be insufficient.

`maxiter(#)` specifies the maximum number of adaptive iterations. Adaptation includes tuning of the proposal covariance and of the scale factor for each block of model parameters. Once the TAR is achieved within the specified tolerance, the adaptation stops. However, no more than # adaptation steps will be performed. The default is variable and is computed as $\max\{25, \texttt{floor(burnin()/adaptation(every()))}\}$.

`maxiter()` is usually chosen to be no greater than $(\texttt{mcmcsize()} + \texttt{burnin()})/\texttt{adaptation(every())}$.

`miniter(#)` specifies the minimum number of adaptive iterations to be performed regardless of whether the TAR has been achieved. The default is `miniter(5)`. If the specified `miniter()` is greater than `maxiter()`, then `miniter()` is reset to `maxiter()`. Thus, if you specify `maxiter(0)`, then no adaptation will be performed.

`alpha(#)` specifies a parameter controlling the adaptation of the AR. `alpha()` should be in $[0, 1]$. The default is `alpha(0.75)`.

`beta(#)` specifies a parameter controlling the adaptation of the proposal covariance matrix. `beta()` must be in [0,1]. The closer `beta()` is to zero, the less adaptive the proposal covariance. When `beta()` is zero, the same proposal covariance will be used in all MCMC iterations. The default is `beta(0.8)`.

`gamma(#)` specifies a parameter controlling the adaptation rate of the proposal covariance matrix. `gamma()` must be in [0,1]. The larger the value of `gamma()`, the less adaptive the proposal covariance. The default is `gamma(0)`.

`tarate(#)` specifies the TAR for all blocks of model parameters; this is rarely used. `tarate()` must be in (0,1). The default AR is 0.234 for blocks containing continuous multiple parameters, 0.44 for blocks with one continuous parameter, and 1/*n_maxlev* for blocks with discrete parameters, where *n_maxlev* is the maximum number of levels for a discrete parameter in the block.

`tolerance(#)` specifies the tolerance criterion for adaptation based on the TAR. `tolerance()` should be in (0,1). Adaptation stops whenever the absolute difference between the current AR and TAR is less than `tolerance()`. The default is `tolerance(0.01)`.

`scale(#)` specifies an initial multiplier for the scale factor for all blocks. The initial scale factor is computed as $\#/\sqrt{n_p}$ for continuous parameters and $\#/n_p$ for discrete parameters, where n_p is the number of parameters in the block. The default is `scale(2.38)`.

`covariance(`*cov*`)` specifies a scale matrix *cov* to be used to compute an initial proposal covariance matrix. The initial proposal covariance is computed as $\rho \times \Sigma$, where ρ is a scale factor and $\Sigma =$ *matname*. By default, Σ is the identity matrix. Partial specification of Σ is also allowed. The rows and columns of *cov* should be named after some or all model parameters. According to some theoretical results, the optimal proposal covariance is the posterior covariance matrix of model parameters, which is usually unknown. This option does not apply to the blocks containing random-effects parameters.

Reporting

`clevel(#)` specifies the credible level, as a percentage, for equal-tailed and HPD credible intervals. The default is `clevel(95)` or as set by [BAYES] **set clevel**.

`hpd` displays the HPD credible intervals instead of the default equal-tailed credible intervals.

eform_option causes the coefficient table to be displayed in exponentiated form; see [R] ***eform_option***. The estimation command determines which *eform_option* is allowed (`eform(`*string*`)` and `eform` are always allowed).

`remargl` specifies to compute the log marginal-likelihood for panel-data and multilevel models. It is not reported by default for these models. Bayesian panel-data and multilevel models contain many parameters because, in addition to regression coefficients and variance components, they also estimate individual random effects. The computation of the log marginal-likelihood involves the inverse of the determinant of the sample covariance matrix of all parameters and loses its accuracy as the number of parameters grows. For high-dimensional models such as multilevel models, the computation of the log marginal-likelihood can be time consuming, and its accuracy may become unacceptably low. Because it is difficult to access the levels of accuracy of the computation for all panel-data and multilevel models, the log marginal-likelihood is not reported by default. For models containing a small number of random effects, you can use the `remargl` option to compute and display the log marginal-likelihood.

`batch(#)` specifies the length of the block for calculating batch means and an MCSE using batch means. The default is `batch(0)`, which means no batch calculations. When `batch()` is not specified, the MCSE is computed using effective sample sizes instead of batch means. `batch()` may not be combined with `corrlag()` or `corrtol()`.

`saving(`*filename*`[ , replace ])` saves simulation results in *filename*`.dta`. The `replace` option specifies to overwrite *filename*`.dta` if it exists. If the `saving()` option is not specified, the `bayes` prefix saves simulation results in a temporary file for later access by postestimation commands. This temporary file will be overridden every time the `bayes` prefix is run and will also be erased if the current estimation results are cleared. `saving()` may be specified during estimation or on replay.

The saved dataset has the following structure. Variable `_chain` records chain identifiers. Variable `_index` records iteration numbers. The `bayes` prefix saves only states (sets of parameter values) that are different from one iteration to another and the frequency of each state in variable `_frequency`. (Some states may be repeated for discrete parameters.) As such, `_index` may not necessarily contain consecutive integers. Remember to use `_frequency` as a frequency weight if you need to obtain any summaries of this dataset. Values for each parameter are saved in a separate variable in the dataset. Variables containing values of parameters without equation names are named as `eq0_p#`, following the order in which parameters are declared in the `bayes` prefix. Variables containing values of parameters with equation names are named as `eq#_p#`, again following the

order in which parameters are defined. Parameters with the same equation names will have the same variable prefix eq#. For example,

```
. bayes, saving(mcmc): ...
```

will create a dataset, mcmc.dta, with variable names eq1_p1 for {y:x1}, eq1_p2 for {y:_cons}, and eq0_p1 for {var}. Also see macros e(parnames) and e(varnames) for the correspondence between parameter names and variable names.

In addition, the bayes prefix saves variable _loglikelihood to contain values of the log likelihood from each iteration and variable _logposterior to contain values of the log posterior from each iteration.

nomodelsummary suppresses the detailed summary of the specified model. The model summary is reported by default.

nomesummary suppresses the summary about the multilevel structure of the model. This summary is reported by default for multilevel commands.

chainsdetail specifies that acceptance rates, efficiencies, and log marginal-likelihoods be reported separately for each chain. By default, the header reports these statistics averaged over all chains. This option requires option nchains().

nodots, dots, and dots(#) specify to suppress or display dots during simulation. With multiple chains, these options affect all chains. dots(#) displays a dot every # iterations. During the adaptation period, a symbol a is displayed instead of a dot. If dots(..., every(#)) is specified, then an iteration number is displayed every #th iteration instead of a dot or a. dots(, every(#)) is equivalent to dots(1, every(#)). dots displays dots every 100 iterations and iteration numbers every 1,000 iterations; it is a synonym for dots(100, every(1000)). dots is the default with multilevel commands, and nodots is the default with other commands.

show(*paramref*) or noshow(*paramref*) specifies a list of model parameters to be included in the output or excluded from the output, respectively. By default, all model parameters (except random-effects parameters with multilevel models) are displayed. Do not confuse noshow() with exclude(), which excludes the specified parameters from the MCMC sample. When the noshow() option is specified, for computational efficiency, MCMC summaries of the specified parameters are not computed or stored in e(). *paramref* can include individual random-effects parameters.

showreffects and showreffects(*reref*) are used with panel-data and multilevel commands and specify that all or a list *reref* of random-effects parameters be included in the output in addition to other model parameters. By default, all random-effects parameters are excluded from the output as if you have specified the noshow() option. This option computes, displays, and stores in e() MCMC summaries for the random-effects parameters.

melabel specifies that the bayes prefix use the same row labels as *estimation_command* in the estimation table. This option is allowed only with multilevel commands. It is useful to match the estimation table output of bayes: *mecmd* with that of *mecmd*. This option implies nomesummary and nomodelsummary.

nogroup suppresses the display of group summary information (number of groups, average group size, minimum, and maximum) from the output header. This option is for use with multilevel commands.

notable suppresses the estimation table from the output. By default, a summary table is displayed containing all model parameters except those listed in the exclude() and noshow() options. Regression model parameters are grouped by equation names. The table includes six columns and reports the following statistics using the MCMC simulation results: posterior mean, posterior standard deviation, MCMC standard error or MCSE, posterior median, and credible intervals.

`noheader` suppresses the output header either at estimation or upon replay.

`title(`*string*`)` specifies an optional title for the command that is displayed above the table of the parameter estimates. The default title is specific to the specified likelihood model.

display_options: `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `nofvlabel`, `fvwrap(#)`, `fvwrapon(`*style*`)`, and `nolstretch`; see [R] **Estimation options**.

Advanced

`search(`*search_options*`)` searches for feasible initial values. *search_options* are `on`, `repeat(#)`, and `off`.

`search(on)` is equivalent to `search(repeat(500))`. This is the default.

`search(repeat(`*k*`))`, $k > 0$, specifies the number of random attempts to be made to find a feasible initial-value vector, or initial state. The default is `repeat(500)`. An initial-value vector is feasible if it corresponds to a state with positive posterior probability. If feasible initial values are not found after *k* attempts, an error will be issued. `repeat(0)` (rarely used) specifies that no random attempts be made to find a feasible starting point. In this case, if the specified initial vector does not correspond to a feasible state, an error will be issued.

`search(off)` prevents the command from searching for feasible initial values. We do not recommend specifying this option.

`corrlag(#)` specifies the maximum autocorrelation lag used for calculating effective sample sizes. The default is $\min\{500, \texttt{mcmcsize()}/2\}$. The total autocorrelation is computed as the sum of all lag-k autocorrelation values for k from 0 to either `corrlag()` or the index at which the autocorrelation becomes less than `corrtol()` if the latter is less than `corrlag()`. Options `corrlag()` and `batch()` may not be combined.

`corrtol(#)` specifies the autocorrelation tolerance used for calculating effective sample sizes. The default is `corrtol(0.01)`. For a given model parameter, if the absolute value of the lag-k autocorrelation is less than `corrtol()`, then all autocorrelation lags beyond the kth lag are discarded. Options `corrtol()` and `batch()` may not be combined.

Remarks and examples

Remarks and examples are presented under the following headings:

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using adaptive MH and Gibbs algorithms, see [BAYES] **bayesmh**. See [BAYES] **Bayesian estimation** for a list of supported estimation commands. For a quick overview example of all Bayesian commands, see *Overview example* in [BAYES] **Bayesian commands**.

Using the bayes prefix

The `bayes` prefix provides Bayesian estimation for many likelihood-based regression models. Simply prefix your estimation command with `bayes` to get Bayesian estimates—`bayes:` *estimation_command*; see [BAYES] **Bayesian estimation** for a list of supported commands. Also see [BAYES] **bayesmh** for other Bayesian models.

Similarly to the `bayesmh` command, the `bayes` prefix sets up a Bayesian posterior model, uses MCMC to simulate parameters of this model, and summarizes and reports results. The process of specifying a Bayesian model is similar to that described in *Setting up a posterior model* in [BAYES] **bayesmh**, except the likelihood model is now determined by the specified *estimation_command* and default priors are used for model parameters. The `bayes` prefix and the `bayesmh` command share the same methodology of MCMC simulation and the same summarization and reporting of simulation results; see [BAYES] **bayesmh** for details. In the following sections, we provide information specific to the `bayes` prefix.

Likelihood model

With the `bayes` prefix, the likelihood component of the Bayesian model is determined by the prefixed estimation command, and all posterior model parameters are defined by the likelihood model. For example, the parameters of the model

```
. bayes: streg age smoking, distribution(lognormal)
```

are the regression coefficients and auxiliary parameters you see when you fit

```
. streg age smoking, distribution(lognormal)
```

All estimation commands have regression coefficients as their model parameters. Some commands have additional parameters such as variances and correlation coefficients.

The bayes prefix typically uses the likelihood parameterization and the naming convention of the estimation command to define model parameters, but there are exceptions. For example, the truncreg command uses the standard deviation parameter {sigma} to parameterize the likelihood, whereas bayes: truncreg uses the variance parameter {sigma2}.

Most model parameters are scalar parameters supported on the whole real line such as regression coefficients, log-transformed positive parameters, and atanh-transformed correlation coefficients. For example, positive scalar parameters are the variance parameters in bayes: regress, bayes: tobit, and bayes: truncreg, and matrix parameters are the covariance matrix {Sigma, matrix} in bayes: mvreg and covariances of random effects in multilevel commands such as bayes: meglm.

The names of model parameters are provided in the model summary displayed by the bayes prefix. Knowing these names is useful when specifying the prior distributions, although the bayes prefix does provide default priors; see *Default priors*. You can use the dryrun option with the bayes prefix to see the names of model parameters prior to the estimation. In general, the names of regression coefficients are formed as {*depvar*:*indepvar*}, where *depvar* is the name of the specified dependent variable and *indepvar* is the name of an independent variable. There are exceptions such as bayes: streg, for which *depvar* is replaced with _t. Variance parameters are named {sigma2}, log-standard-deviation parameters are named {lnsigma}, atanh-transformed correlation parameters are named {athrho}, and the covariance matrix of bayes: mvreg is named {Sigma, matrix} (or {Sigma, m} for short).

For panel-data and multilevel models such as bayes: xtreg and bayes: meglm, in addition to regression coefficients and variance components, the bayes prefix also estimates random-effects parameters. This is different from the corresponding frequentist commands, such as xtreg and meglm, in which random effects are integrated out and thus are not among the final model parameters. (They can be predicted after estimation.) As such, the bayes prefix has its own naming convention for model parameters of multilevel commands. Before moving on to Bayesian analysis of multilevel models, you should be familiar with the syntax of the multilevel commands; see, for example, *Syntax* in [ME] **meglm**.

For panel-data models, the regression coefficients are labeled as usual, {*depvar*:*indepvar*}. Random-effects parameters are labeled as {U[*panelvar*]} (or simply {U}), where *panelvar* is the panel variable. For multinomial logistic models, each outcome can have its own random effect, so the random effects are labeled as {U1[*panelvar*]}, {U2[*panelvar*]}, etc. (or simply {U1}, {U2}, etc.), for each outcome level except the baseline outcome. See command-specific entries for the naming convention of additional parameters such as cutpoints with ordinal models. Also see *Different ways of specifying model parameters* for how to refer to individual random effects during postestimation. For examples, see *Panel-data models*.

For multilevel models, the regression coefficients are labeled as usual, {*depvar*:*indepvar*}. Random-effects parameters are labeled as outlined in tables 1 and 2. You can change the default names by specifying the restubs() option. The common syntax of {*rename*} is {*restub#*}, where *restub* is a capital letter, U for the level specified first, or a sequence of capital letters that is unique to each random-effects level, and # refers to the group of random effects at that level: 0 for random intercepts, 1 for random coefficients associated with the variable specified first in the random-effects equation, 2 for random coefficients associated with the variable specified second, and so on. The full syntax of {*rename*}, {*fullrename*}, is {*restub#*[*levelvar*]}, where *levelvar* is the variable identifying the level of hierarchy and is often omitted from the specification for brevity. Random effects at the observation level or crossed effects, specified as _all: R.*varname* with multilevel commands, are labeled as {U0}, {V0}, {W0}, and so on. Random effects at nesting levels, or nested effects, are labeled using a sequence of capital letters starting with the letter corresponding to the top level. For example, the multilevel model

```
. bayes: melogit y x1 x2 || id1: x1 x2 || id2: x1 || id3:
```

will have random-effects parameters {U0}, {U1}, and {U2} to represent, respectively, random intercepts, random coefficients for x1, and random coefficients for x2 at the id1 level; parameters {UU0} and {UU1} for random intercepts and random coefficients for x1 at the id2 level; and random intercepts {UUU0} at the id3 level. See *Multilevel models* for more examples. Also see *Different ways of specifying model parameters* for how to refer to individual random effects during postestimation.

Table 1. Random effects at nesting levels of hierarchy (nested effects)

Hierarchy	Random effects	{*rename*}
lev1	Random intercepts	{U0}
	Random coefficients	{U1}, {U2}, etc.
lev1>*lev2*	Random intercepts	{UU0}
	Random coefficients	{UU1}, {UU2}, etc.
lev1>*lev2*>*lev3*	Random intercepts	{UUU0}
	Random coefficients	{UUU1}, {UUU2}, etc.
...		

Table 2. Random effects at the observation level, _all (crossed effects)

Hierarchy	Random effects	{*rename*}
lev1	Random intercepts	{U0}
lev2	Random intercepts	{V0}
lev3	Random intercepts	{W0}
...		

Variance components for independent random effects are labeled as {*rename*:sigma2}. In the above example, there are six variance components: {U0:sigma2}, {U1:sigma2}, {U2:sigma2}, {UU0:sigma2}, {UU1:sigma2}, and {UUU0:sigma2}.

Covariance matrices of correlated random effects are labeled as {*restub*:Sigma,matrix} (or {*restub*:Sigma,m} for short), where *restub* is the letter stub corresponding to the level at which random effects are defined. For example, if we specify an unstructured covariance for the random effects at the id1 and id2 levels (with cov(un) short for covariance(unstructured))

```
. bayes: melogit y x1 x2 || id1: x1 x2, cov(un) || id2: x1, cov(un) || id3:
```

we will have two covariance matrix parameters, a 3×3 covariance {U:Sigma,m} at the id1 level and a 2×2 covariance {UU:Sigma,m} at the id2 level, and the variance component {UUU0:sigma2} at the id3 level.

For Gaussian multilevel models such as bayes: mixed, the error variance component is labeled as {e.*depvar*:sigma2}.

Also see command-specific entries for the naming convention of additional parameters such as cutpoints with ordinal models or overdispersion parameters with negative binomial models.

Default priors

For convenience, the `bayes` prefix provides default priors for model parameters. The priors are chosen to be general across models and are fairly uninformative for a typical combination of a likelihood model and dataset. However, the default priors may not always be appropriate. You should always inspect their soundness and, if needed, override the prior specification for some or all model parameters using the `prior()` option.

All scalar parameters supported on the whole real line, such as regression coefficients and log-transformed positive parameters, are assigned a normal distribution with zero mean and variance σ^2_{prior}, $N(0, \sigma^2_{\text{prior}})$, where σ_{prior} is given by the `normalprior()` option. The default value for σ_{prior} is 100, and thus the default priors for these parameters are $N(0, 10000)$. These priors are fairly uninformative for parameters of moderate size but may become informative for large-scale parameters. See the *Linear regression: A case of informative default priors* example below.

All positive scalar parameters, such as the variance parameters in `bayes: regress` and `bayes: tobit`, are assigned an inverse-gamma prior with shape parameter α and scale parameter β, InvGamma(α, β). The default values for α and β are 0.01, and thus the default prior for these parameters is InvGamma$(0.01, 0.01)$.

All cutpoint parameters of ordinal-outcome models, such as `bayes: ologit` and `bayes: oprobit` are assigned flat priors, improper uniform priors with a constant density of 1, equivalent to specifying the `flat` prior option. The reason for this choice is that the cutpoint parameters are sensitive to the range of the outcome variables, which is usually unknown a priori.

For panel-data models except `bayes: xtpoisson` and `bayes: xtnbreg`, the random effects are assigned normal priors with zero mean and variance `{var_U}`, and `{var_U}` is assigned an inverse-gamma prior InvGamma$(0.01, 0.01)$. For a Poisson model, the random effects are assigned an exponential gamma prior with a hyperprior parameter `{alpha}` having an inverse-gamma prior InvGamma$(0.01, 0.01)$. For a negative binomial model, the random effects are assigned a beta prior with hyperparameters `{r}` and `{s}`, which are assigned a Pareto-type prior as described in *Methods and formulas* of [BAYES] **bayes: xtnbreg**.

For multilevel models with `independent` and `identity` random-effects covariance structures, variances of random effects are assigned inverse-gamma priors, InvGamma$(0.01, 0.01)$. For `unstructured` random-effects covariances, covariance matrix parameters are assigned fairly uninformative inverse-Wishart priors, InvWishart$(d + 1, I(d))$, where d is the dimension of the random-effects covariance matrix and $I(d)$ is the identity matrix of dimension d. Setting the degrees-of-freedom parameter of the inverse-Wishart prior to $d + 1$ is equivalent to specifying uniform on $(-1, 1)$ distributions for the individual correlation parameters.

The model summary displayed by the `bayes` prefix describes the chosen default priors, which you can see prior to estimation if you specify `bayes`'s `dryrun` option. You can use the `prior()` option repeatedly to override the default prior specifications for some or all model parameters.

Initial values

By default, the `bayes` prefix uses the ML estimates from the prefixed estimation command as initial values for all scalar model parameters.

For example, the specification

```
. bayes: logit y x
```

will use the ML estimates from

```
. logit y x
```

as default initial values for the regression coefficients.

You can override the default initial values by using the initial() option; see *Specifying initial values* in [BAYES] **bayesmh**.

If the nomleinitial option is specified, instead of using the estimates from the prefixed command, all scalar model parameters are initialized with zeros, except for the variance parameters, which are initialized with ones.

The covariance matrix parameter {Sigma, matrix} of bayes: mvreg is always initialized with the identity matrix.

For panel-data and multilevel models, regression coefficients are initialized using the ML estimates from the corresponding model without random effects, variances of random effects are initialized with ones, covariances of random effects are initialized with zeros, and random effects themselves are initialized with zeros.

With multiple chains, the following default initialization takes place. The first chain is initialized as described above. The subsequent chains use random initial values. In general, random initial values are generated from the prior distributions. For some improper priors such as flat and jeffreys, to avoid extremely large values, random initial values are sampled from a normal distribution with the mean centered at the initial values of the first chain and with standard deviations proportional to the magnitudes of the respective initial estimates.

See *Specifying initial values* in [BAYES] **bayesmh** for more information about default initial values and for how to specify your own.

Command-specific options

Not all command-specific options, that is, options specified with the estimation command, are applicable within the Bayesian framework. One example is the group of maximum-likelihood optimization options such as technique() and gradient. For a list of supported options, refer to the entry specific to each command; see [BAYES] **Bayesian estimation** for a list of commands.

Some of the command-specific reporting options, such as *eform_option* and display options, can be specified either with *estimation_command* or with the bayes prefix. For example, to obtain estimates of odds ratios instead of coefficients after the logit model, you can specify the or option with the command

```
. bayes: logit y x, or
```

or with the bayes prefix

```
. bayes, or: logit y x
```

You can also specify this option on replay with the bayes prefix

```
. bayes: logit y x
. bayes, or
```

Introductory example

We start with a simple linear regression model applied to womenwage.dta, which contains income data for a sample of working women.

```
. use https://www.stata-press.com/data/r18/womenwage
(Wages of women)
```

Suppose we want to regress women's yearly income, represented by the wage variable, on their age, represented by the age variable. We can fit this model using the regress command.

```
. regress wage age
```

Source	SS	df	MS	Number of obs	=	488
				F(1, 486)	=	43.53
Model	3939.49247	1	3939.49247	Prob > F	=	0.0000
Residual	43984.4891	486	90.503064	R-squared	=	0.0822
				Adj R-squared	=	0.0803
Total	47923.9816	487	98.406533	Root MSE	=	9.5133

wage	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
age	.399348	.0605289	6.60	0.000	.2804173	.5182787
_cons	6.033077	1.791497	3.37	0.001	2.513041	9.553112

▷ Example 1: Bayesian simple linear regression

We can fit a corresponding Bayesian regression model by simply adding bayes: in front of the regress command. Because the bayes prefix is simulation based, we set a random-number seed to get reproducible results.

```
. set seed 15

. bayes: regress wage age
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  wage ~ regress(xb_wage,{sigma2})

Priors:
  {wage:age _cons} ~ normal(0,10000)                                      (1)
         {sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_wage.

Bayesian linear regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =        488
                                                Acceptance rate  =      .3739
                                                Efficiency:  min =      .1411
                                                             avg =      .1766
Log marginal-likelihood = -1810.1432                         max =      .2271
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
wage						
age	.4008591	.0595579	.001586	.4005088	.2798807	.5183574
_cons	5.969069	1.737247	.043218	5.997571	2.60753	9.396475
sigma2	90.76252	5.891887	.123626	90.43802	79.71145	102.8558

```
Note: Default priors are used for model parameters.
```

The Bayesian model has two regression coefficient parameters, {wage:age} and {wage:_cons}, and a positive scalar parameter, {sigma2}, representing the variance of the error term. The model summary shows the default priors used for the model parameters: normal(0, 10000) for the

regression coefficients and `igamma(0.01, 0.01)` for the variance parameter. The default priors are provided for convenience and should be used with caution. These priors are fairly uninformative in this example, but this may not always be the case; see the example in *Linear regression: A case of informative default priors*.

The first two columns of the `bayes` prefix's estimation table report the posterior means and standard deviations of the model parameters. We observe that for the regression coefficients `{wage:age}` and `{wage:_cons}`, the posterior means and standard deviations are very similar to the least-square estimates and their standard errors as reported by the `regress` command. The posterior mean estimate for `{sigma2}`, 90.76, is close to the residual mean squared estimate, 90.50, listed in the ANOVA table of the `regress` command. The estimation table of the `bayes` prefix also reports Monte Carlo standard errors (MCSEs), medians, and equal-tailed credible intervals.

The Bayesian estimates are stochastic in nature and, by default, are based on an MCMC sample of size 10,000. It is important to verify that the MCMC simulation has converged; otherwise, the Bayesian estimates cannot be trusted. The simulation efficiencies reported in the header of the estimation table can serve as useful initial indicators of convergence problems. The minimum efficiency in our example is about 0.14, and the average efficiency is about 0.17. These numbers are typical for the MH sampling algorithm used by `bayes` and do not indicate convergence problems; see example 1 in [BAYES] **bayesstats grubin** for convergence diagnostics using multiple chains for this example. Also see *Convergence of MCMC* in [BAYES] **bayesmh** for details about convergence diagnostics.

◁

▷ Example 2: Predictions

There are several postestimation commands available after the `bayes` prefix; see [BAYES] **Bayesian postestimation**. Among them is the `bayesstats summary` command, which we can use to compute simple predictions. Suppose that we want to predict the expected wage of a 40-year-old woman conditional on the above fitted posterior model. Based on our model, this expected wage corresponds to the linear combination $\{\texttt{wage}:\texttt{\_cons}\} + \{\texttt{wage}:\texttt{age}\} \times 40$. We name this expression `wage40` and supply it to the `bayesstats summary` command.

```
. bayesstats summary (wage40: {wage:_cons} + {wage:age}*40)
Posterior summary statistics                     MCMC sample size =    10,000
      wage40 : {wage:_cons} + {wage:age}*40
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
wage40	22.00343	.81679	.024045	21.99231	20.39435	23.6718

The posterior mean estimate for the expected wage is about 22 with a 95% credible interval between 20.39 and 23.67.

◁

▷ Example 3: Gibbs sampling

The `bayes` prefix uses adaptive MH as its default sampling algorithm. However, in the special case of linear regression, a more efficient Gibbs sampling is available. We can request Gibbs sampling by specifying the `gibbs` option.

```
. set seed 15
. bayes, gibbs: regress wage age
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  wage ~ normal(xb_wage,{sigma2})
Priors:
  {wage:age _cons} ~ normal(0,10000)                                      (1)
          {sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_wage.
Bayesian linear regression                      MCMC iterations  =     12,500
Gibbs sampling                                  Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =        488
                                                Acceptance rate  =          1
                                                Efficiency:  min =          1
                                                             avg =          1
Log marginal-likelihood =  -1810.087                         max =          1
------------------------------------------------------------------------------
                                                                Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
wage         |
         age |  .3999669   .0611328   .000611   .4005838   .2787908    .518693
       _cons |  6.012074   1.804246   .018042   6.000808   2.488816   9.549921
-------------+----------------------------------------------------------------
      sigma2 |  90.84221   5.939535   .059395   90.54834    79.8132   103.0164
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

The posterior summary results obtained by Gibbs sampling and MH sampling are very close except for the MCSEs. The Gibbs sampler reports substantially lower MCSEs than the default sampler because of its higher efficiency. In fact, in this example, the Gibbs sampler achieves the highest possible efficiency of 1.

◁

Linear regression: A case of informative default priors

Our example in *Introductory example* used the default priors, which were fairly uninformative for those data and that model. This may not always be true. Consider a linear regression model using the familiar `auto.dta`. Let us regress the response variable `price` on the covariate `length` and factor variable `foreign`.

```
. use https://www.stata-press.com/data/r18/auto, clear
(1978 automobile data)
. regress price length i.foreign
```

Source	SS	df	MS	Number of obs	=	74
				F(2, 71)	=	16.35
Model	200288930	2	100144465	Prob > F	=	0.0000
Residual	434776467	71	6123612.21	R-squared	=	0.3154
				Adj R-squared	=	0.2961
Total	635065396	73	8699525.97	Root MSE	=	2474.6

price	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
length	90.21239	15.83368	5.70	0.000	58.64092	121.7839
foreign						
Foreign	2801.143	766.117	3.66	0.000	1273.549	4328.737
_cons	-11621.35	3124.436	-3.72	0.000	-17851.3	-5391.401

▷ Example 4: Default priors

We first fit a Bayesian regression model using the `bayes` prefix with default priors. Because the range of the outcome variable `price` is at least an order of magnitude larger than the range of the predictor variables `length` and `foreign`, we anticipate that some of the model parameters may have large scale, and longer adaptation may be necessary for the MCMC algorithm to reach optimal sampling for these parameters. We allow for longer adaptation by increasing the burn-in period from the default value of 2,500 to 5,000.

```
. set seed 15
. bayes, burnin(5000): regress price length i.foreign
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  price ~ regress(xb_price,{sigma2})
Priors:
  {price:length 1.foreign _cons} ~ normal(0,10000)                      (1)
                        {sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_price.
```

```
Bayesian linear regression                      MCMC iterations  =     15,000
Random-walk Metropolis-Hastings sampling        Burn-in          =      5,000
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .3272
                                                Efficiency:  min =     .05887
                                                             avg =      .1093
Log marginal-likelihood = -699.23257                         max =      .1958
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
price						
length	33.03301	1.80186	.060848	33.07952	29.36325	36.41022
foreign						
Foreign	32.77011	98.97104	4.07922	34.3237	-164.1978	222.0855
_cons	-8.063175	102.9479	3.34161	-9.110308	-205.9497	196.9341
sigma2	7538628	1297955	29334.9	7414320	5379756	1.04e+07

Note: Default priors are used for model parameters.

The posterior mean estimates of the regression coefficients are smaller (in absolute value) than the corresponding estimates from the `regress` command, because the default prior for the coefficients, `normal(0, 10000)`, is informative and has a strong shrinkage effect. For example, the least-square estimate of the constant term from `regress` is about −11,621, and its scale is much larger than the default prior standard deviation of 100. As a result, the default prior shrinks the estimate of the constant toward 0 and, specifically, to −8.06.

You should be aware that the default priors are provided for convenience and are not guaranteed to be uninformative in all cases. They are designed to have little effect on model parameters, the maximum likelihood estimates of which are of moderate size, say, less than 100 in absolute value. For large-scale parameters, as in this example, the default priors can become informative.

◁

▷ Example 5: Flat priors

Continuing with example 4, we can override the default priors using the `prior()` option. We can, for example, apply the completely uninformative `flat` prior, a prior with the density of 1, for the coefficient parameters.

```
. set seed 15
. bayes, prior({price:}, flat) burnin(5000): regress price length i.foreign
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  price ~ regress(xb_price,{sigma2})
Priors:
  {price:length 1.foreign _cons} ~ 1 (flat)                              (1)
                       {sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_price.
```

```
Bayesian linear regression                      MCMC iterations  =     15,000
Random-walk Metropolis-Hastings sampling        Burn-in          =      5,000
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .3404
                                                Efficiency:  min =     .07704
                                                             avg =      .1086
Log marginal-likelihood = -669.62603                         max =      .1898
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
price						
length	89.51576	16.27187	.586237	89.60969	57.96996	122.7961
foreign						
Foreign	2795.683	770.6359	26.0589	2787.139	1305.773	4298.785
_cons	-11478.83	3202.027	113.271	-11504.65	-17845.87	-5244.189
sigma2	6270294	1089331	25002.1	6147758	4504695	8803268

```
Note: Default priors are used for some model parameters.
```

The posterior mean estimates for the coefficient parameters are now close to the least-square estimates from `regress`. For example, the posterior mean estimate for `{price:_cons}` is about −11,479, whereas the least-square estimate is −11,621.

However, the `flat` priors should be used with caution. Flat priors are improper and may result in improper posterior distributions for which Bayesian inference cannot be carried out. You should thus choose the priors carefully, accounting for the properties of the likelihood model.

◁

▷ Example 6: Zellner's g-prior

A type of prior specific to the normal linear regression model is Zellner's g-prior. We can apply it to our example using the `zellnersg0()` prior. For this prior, we need to specify the dimension of the prior, which is the number of regression coefficients (3), a degree of freedom (50) and the variance parameter of the error term in the regression model, `{sigma2}`; the mean parameter is assumed to be 0 by `zellnersg0()`. See example 9 in [BAYES] **bayesmh** for more details about Zellner's g-prior.

```
. set seed 15
. bayes, prior({price:}, zellnersg0(3, 50, {sigma2})) burnin(5000):
> regress price length i.foreign
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  price ~ regress(xb_price,{sigma2})
Priors:
  {price:length 1.foreign _cons} ~ zellnersg(3,50,0,{sigma2})             (1)
                       {sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_price.
```

```
Bayesian linear regression                      MCMC iterations  =     15,000
Random-walk Metropolis-Hastings sampling        Burn-in          =      5,000
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .3019
                                                Efficiency:  min =      .06402
                                                             avg =       .105
Log marginal-likelihood = -697.84862                         max =      .1944
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
price						
length	87.53039	16.24762	.569888	87.72965	55.5177	119.9915
foreign						
Foreign	2759.267	794.043	31.3829	2793.241	1096.567	4202.283
_cons	-11223.95	3211.553	113.34	-11308.39	-17534.25	-4898.139
sigma2	6845242	1159035	26286.9	6716739	4978729	9521252

```
Note: Default priors are used for some model parameters.
```

We see that using this Zellner's g-prior has little effect on the coefficient parameters, and the simulated posterior mean estimates are close to the least-square estimates from `regress`.

◁

Logistic regression with perfect predictors

Let's revisit the example in *Logistic regression model: A case of nonidentifiable parameters* of [BAYES] **bayesmh**. The example uses `heartswitz.dta` to model the binary outcome `disease`, the presence of a heart disease, using the predictor variables `restecg`, `isfbs`, `age`, and `male`. The dataset is a sample from Switzerland.

```
. use https://www.stata-press.com/data/r18/heartswitz, clear
(Subset of Switzerland heart disease data from UCI Machine Learning Repository)
```

▷ Example 7: Perfect prediction

The logistic regression model for these data is

```
. logit disease restecg isfbs age male
  (output omitted)
```

To fit a Bayesian logistic regression, we prefix the `logit` command with `bayes`. We also specify the `noisily` option to show the estimation output of the `logit` command, which is run by the `bayes` prefix to set up the model and compute starting values for the parameters.

```
. set seed 15
. bayes, noisily: logit disease restecg isfbs age male
note: restecg != 0 predicts success perfectly;
      restecg omitted and 17 obs not used.
note: isfbs != 0 predicts success perfectly;
      isfbs omitted and 3 obs not used.
note: male != 1 predicts success perfectly;
      male omitted and 2 obs not used.
Iteration 0:  Log likelihood = -4.2386144
Iteration 1:  Log likelihood = -4.2358116
Iteration 2:  Log likelihood = -4.2358076
Iteration 3:  Log likelihood = -4.2358076
Logistic regression                                     Number of obs =     26
                                                        LR chi2(1)    =   0.01
                                                        Prob > chi2   = 0.9403
Log likelihood = -4.2358076                             Pseudo R2     = 0.0007

------------------------------------------------------------------------------
     disease | Coefficient  Std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
     restecg |          0  (omitted)
       isfbs |          0  (omitted)
         age |  -.0097846   .1313502    -0.07   0.941    -.2672263    .2476572
        male |          0  (omitted)
       _cons |   3.763893   7.423076     0.51   0.612    -10.78507    18.31285
------------------------------------------------------------------------------

Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  disease ~ logit(xb_disease)
Prior:
  {disease:age _cons} ~ normal(0,10000)                                   (1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_disease.

Bayesian logistic regression                    MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         26
                                                Acceptance rate  =      .2337
                                                Efficiency:  min =      .1076
                                                             avg =      .1113
Log marginal-likelihood = -14.795726                         max =       .115

------------------------------------------------------------------------------
                                                              Equal-tailed
     disease |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
     restecg |  (omitted)
       isfbs |  (omitted)
         age |  -.0405907   .1650514   .004868  -.0328198  -.4005246   .2592641
        male |  (omitted)
       _cons |   6.616447   9.516872   .290075   5.491008  -8.852858   28.99392
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

As evident from the output of the `logit` command, the covariates `restecg`, `isfbs`, and `male` are omitted because of perfect prediction. Although these predictors cannot be identified using the likelihood alone, they can be identified, potentially, in a posterior model with an informative prior. The default prior `normal(0, 10000)`, used by the `bayes` prefix for the regression coefficients, is not

informative enough to resolve the perfect prediction, and we must override it with a more informative prior.

◁

▷ Example 8: Informative prior

In the example in *Logistic regression model: A case of nonidentifiable parameters* of [BAYES] **bayesmh**, we use information from another similar dataset, `hearthungary.dta`, to come up with informative priors for the regression coefficients. We use the same priors with the `bayes` prefix. We specify the `asis` option with the `logit` command to prevent dropping the perfect predictors from the model. We also specify the `nomleinitial` option to prevent the `bayes` prefix from trying to obtain ML estimates to use as starting values; reliable ML estimates cannot be provided by the `logit` command when the perfect predictors are retained.

```
. set seed 15
. bayes, prior({disease:restecg age}, normal(0,10))
> prior({disease:isfbs male}, normal(1,10))
> prior({disease:_cons}, normal(-4,10)) nomleinitial:
> logit disease restecg isfbs age male, asis
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  disease ~ logit(xb_disease)
Priors:
  {disease:restecg age} ~ normal(0,10)                                    (1)
   {disease:isfbs male} ~ normal(1,10)                                    (1)
        {disease:_cons} ~ normal(-4,10)                                   (1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_disease.
Bayesian logistic regression                    MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         48
                                                Acceptance rate  =      .2121
                                                Efficiency:  min =     .01885
                                                             avg =     .04328
Log marginal-likelihood = -11.006071                         max =     .06184
------------------------------------------------------------------------------
                                                              Equal-tailed
     disease |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
     restecg |  1.965122   2.315475   .115615   1.655961  -2.029873   6.789415
       isfbs |  1.708631   2.726071   .113734   1.607439  -3.306837   7.334592
         age |  .1258811   .0707431   .003621   .1245266  -.0016807   .2719748
        male |  .2671381   2.237349   .162967   .3318061  -4.106425   4.609955
       _cons | -2.441911   2.750613   .110611  -2.538183  -7.596747   3.185172
------------------------------------------------------------------------------
```

For this posterior model with informative priors, we successfully estimate all regression parameters in the logistic regression model.

The informative prior in this example is based on information from an independent dataset, `hearthungary.dta`, which is a sample of observations on the same heart condition and predictor attributes as `heartswitz.dta` but sampled from Hungary's population. Borrowing information from independent datasets to construct informative priors is justified only when the datasets are compatible with the currently analyzed data.

◁

Multinomial logistic regression

Consider the health insurance dataset, sysdsn1.dta, to model the insurance outcome, insure, which takes the values Indemnity, Prepaid, and Uninsure, using the predictor variables age, male, nonwhite, and site. This model is considered in more detail in example 4 in [R] **mlogit**.

```
. use https://www.stata-press.com/data/r18/sysdsn1, clear
(Health insurance data)
```

First, we use the mlogit command to fit the model

```
. mlogit insure age male nonwhite i.site, nolog
Multinomial logistic regression                 Number of obs =    615
                                                LR chi2(10)   =  42.99
                                                Prob > chi2   = 0.0000
Log likelihood = -534.36165                     Pseudo R2     = 0.0387
```

insure	Coefficient	Std. err.	z	P>|z|	[95% conf.	interval]
Indemnity	(base outcome)					
Prepaid						
age	-.011745	.0061946	-1.90	0.058	-.0238862	.0003962
male	.5616934	.2027465	2.77	0.006	.1643175	.9590693
nonwhite	.9747768	.2363213	4.12	0.000	.5115955	1.437958
site						
2	.1130359	.2101903	0.54	0.591	-.2989296	.5250013
3	-.5879879	.2279351	-2.58	0.010	-1.034733	-.1412433
_cons	.2697127	.3284422	0.82	0.412	-.3740222	.9134476
Uninsure						
age	-.0077961	.0114418	-0.68	0.496	-.0302217	.0146294
male	.4518496	.3674867	1.23	0.219	-.268411	1.17211
nonwhite	.2170589	.4256361	0.51	0.610	-.6171725	1.05129
site						
2	-1.211563	.4705127	-2.57	0.010	-2.133751	-.2893747
3	-.2078123	.3662926	-0.57	0.570	-.9257327	.510108
_cons	-1.286943	.5923219	-2.17	0.030	-2.447872	-.1260134

Next, we use the bayes prefix to perform Bayesian estimation of the same multinomial logistic regression model.

```
. set seed 15
. bayes: mlogit insure age male nonwhite i.site
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  Prepaid Uninsure ~ mlogit(xb_Prepaid,xb_Uninsure)
Priors:
   {Prepaid:age male nonwhite i.site _cons} ~ normal(0,10000)             (1)
  {Uninsure:age male nonwhite i.site _cons} ~ normal(0,10000)             (2)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_Prepaid.
(2) Parameters are elements of the linear form xb_Uninsure.
```

```
Bayesian multinomial logistic regression        MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
Base outcome: Indemnity                         Number of obs    =        615
                                                Acceptance rate  =      .2442
                                                Efficiency:  min =     .01992
                                                             avg =     .03086
Log marginal-likelihood = -614.49286                         max =     .05659
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
Prepaid						
age	-.0125521	.006247	.000396	-.0125871	-.024602	-.0005809
male	.5462718	.2086422	.012818	.5573004	.1263754	.9271802
nonwhite	.9796293	.2275709	.015746	.9737777	.53642	1.401076
site						
2	.098451	.214039	.012887	.0994476	-.3172914	.5260208
3	-.6043961	.2348319	.011596	-.6072807	-1.045069	-.1323191
_cons	.3183984	.3309283	.021325	.3219128	-.3423583	.956505
Uninsure						
age	-.008377	.0118479	.000581	-.0082922	-.0323571	.0140366
male	.4687524	.3537416	.02376	.4748359	-.2495656	1.147333
nonwhite	.1755361	.42708	.022566	.198253	-.7214481	.938098
site						
2	-1.298562	.4746333	.033628	-1.27997	-2.258622	-.4149035
3	-.2057122	.3533365	.020695	-.2009649	-.904768	.4924401
_cons	-1.305083	.5830491	.02451	-1.296332	-2.463954	-.1758435

```
Note: Default priors are used for model parameters.
```

For this model and these data, the default prior specification of the `bayes` prefix is fairly uninformative and, as a result, the posterior mean estimates for the parameters are close to the ML estimates obtained with `mlogit`.

We can report posterior summaries for the relative-risk ratios instead of the regression coefficients. This is equivalent to applying an exponential transformation, $\exp(b)$, to the simulated values of each of the regression coefficients, b, and then summarizing them. We can obtain relative-risk ratio summaries by replaying the `bayes` command with the `rrr` option specified. We use the already available simulation results from the last estimation and do not refit the model. We could have also specified the `rrr` option during the estimation.

```
. bayes, rrr
Model summary
------------------------------------------------------------------------------
Likelihood:
  Prepaid Uninsure ~ mlogit(xb_Prepaid,xb_Uninsure)
Priors:
   {Prepaid:age male nonwhite i.site _cons} ~ normal(0,10000)             (1)
  {Uninsure:age male nonwhite i.site _cons} ~ normal(0,10000)             (2)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_Prepaid.
(2) Parameters are elements of the linear form xb_Uninsure.
```

```
Bayesian multinomial logistic regression        MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
Base outcome: Indemnity                         Number of obs    =        615
                                                Acceptance rate  =      .2442
                                                Efficiency:  min =     .02149
                                                             avg =     .03181
Log marginal-likelihood = -614.49286                         max =     .06007
```

	RRR	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
Prepaid						
age	.9875456	.0061686	.000391	.9874918	.9756982	.9994192
male	1.764212	.3634348	.022268	1.745953	1.134708	2.527372
nonwhite	2.732931	.6240495	.042568	2.647929	1.709875	4.059566
site						
2	1.129077	.2450092	.015242	1.104561	.7281185	1.692189
3	.5617084	.1338774	.00665	.5448304	.3516675	.8760614
_cons	1.451983	.4904589	.029972	1.379764	.7100938	2.60259
Uninsure						
age	.9917276	.0117452	.000575	.991742	.9681608	1.014136
male	1.699605	.6045513	.040763	1.60775	.7791391	3.149782
nonwhite	1.301138	.5448086	.027742	1.219271	.4860479	2.555117
site						
2	.3045686	.1461615	.009698	.2780457	.1044944	.6604046
3	.8663719	.3155926	.01806	.8179411	.4046357	1.636304
_cons	.3203309	.1976203	.008063	.2735332	.0850978	.8387492

```
Note: _cons estimates baseline relative risk for each outcome.
Note: Default priors are used for model parameters.
```

Generalized linear model

Consider the insecticide experiment dataset, `beetle.dta`, to model the number of beetles killed, `r`, on the number of subjected beetles, `n`; the type of beetles, `beetle`; and the log-dose of insecticide, `ldose`. More details can be found in example 2 of [R] **glm**.

```
. use https://www.stata-press.com/data/r18/beetle, clear
```

Consider a generalized linear model with a binomial family and a complementary log–log link function for these data.

```
. glm r i.beetle ldose, family(binomial n) link(cloglog) nolog
Generalized linear models                         Number of obs   =         24
Optimization     : ML                             Residual df     =         20
                                                  Scale parameter =          1
Deviance         =  73.76505595                   (1/df) Deviance =   3.688253
Pearson          =   71.8901173                   (1/df) Pearson  =   3.594506
Variance function: V(u) = u*(1-u/n)               [Binomial]
Link function    : g(u) = ln(-ln(1-u/n))          [Complementary log-log]
                                                  AIC             =    6.74547
Log likelihood   = -76.94564525                   BIC             =   10.20398
```

r	OIM Coefficient	OIM std. err.	z	P>|z|	[95% conf.	interval]
beetle						
Red flour	-.0910396	.1076132	-0.85	0.398	-.3019576	.1198783
Mealworm	-1.836058	.1307125	-14.05	0.000	-2.09225	-1.579867
ldose	19.41558	.9954265	19.50	0.000	17.46458	21.36658
_cons	-34.84602	1.79333	-19.43	0.000	-38.36089	-31.33116

To fit a Bayesian generalized linear model with default priors, we type

```
. set seed 15
. bayes: glm r i.beetle ldose, family(binomial n) link(cloglog)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  r ~ glm(xb_r)
Prior:
  {r:i.beetle ldose _cons} ~ normal(0,10000)                             (1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_r.
Bayesian generalized linear models                MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling          Burn-in          =      2,500
                                                  MCMC sample size =     10,000
Family: binomial n                                Number of obs    =         24
Link:   complementary log-log                     Scale parameter  =          1
                                                  Acceptance rate  =      .2003
                                                  Efficiency:  min =      .03414
                                                               avg =      .05094
Log marginal-likelihood =  -102.9776                          max =      .08012
```

r	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
beetle						
Red flour	-.0903569	.106067	.004527	-.093614	-.2964984	.112506
Mealworm	-1.843952	.130297	.004603	-1.848374	-2.091816	-1.594582
ldose	19.52814	.9997765	.054106	19.52709	17.6146	21.6217
_cons	-35.04832	1.800461	.096777	-35.0574	-38.81427	-31.61378

Note: Default priors are used for model parameters.

The posterior mean estimates of the regression parameters are not that different from the ML estimates obtained with `glm`.

If desired, we can request highest posterior density intervals be reported instead of default equal-tailed credible intervals by specifying the `hpd` option. We can also change the credible-interval level; for example, to request 90% credible intervals, we specify the `clevel(90)` option. We also could specify these options during estimation.

```
. bayes, clevel(90) hpd
Model summary
------------------------------------------------------------------------------
Likelihood:
  r ~ glm(xb_r)
Prior:
  {r:i.beetle ldose _cons} ~ normal(0,10000)                             (1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_r.
Bayesian generalized linear models                  MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling            Burn-in          =      2,500
                                                    MCMC sample size =     10,000
Family: binomial n                                  Number of obs    =         24
Link:   complementary log-log                       Scale parameter  =          1
                                                    Acceptance rate  =      .2003
                                                    Efficiency:  min =     .03414
                                                                 avg =     .05094
Log marginal-likelihood =  -102.9776                             max =     .08012
------------------------------------------------------------------------------
                                                                        HPD
           r |       Mean   Std. dev.      MCSE     Median  [90% cred. interval]
-------------+----------------------------------------------------------------
      beetle |
  Red flour  | -.0903569    .106067   .004527  -.093614  -.2444412   .1020305
   Mealworm  | -1.843952    .130297   .004603 -1.848374   -2.03979  -1.620806
             |
       ldose |  19.52814   .9997765   .054106   19.52709   17.86148   21.16389
       _cons | -35.04832   1.800461   .096777  -35.0574  -37.96057  -32.00411
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

Truncated Poisson regression

The semiconductor manufacturing dataset, `probe.dta`, contains observational data of failure rates, `failure`, of silicon wafers with width, `width`, and depth, `depth`, tested at four different probes, `probe`. A wafer is rejected if more than 10 failures are detected. See example 2 in [R] **tpoisson**.

```
. use https://www.stata-press.com/data/r18/probe, clear
(Silicon wafers)
```

We fit a truncated Poisson regression model with a truncation point of 10. We suppress the constant regression term from the likelihood equation using the `noconstant` option to retain all four probe levels by including `ibn.probe` in the list of covariates, which declares `probe` to be a factor variable with no base level.

```
. tpoisson failures ibn.probe depth width, noconstant ll(10) nolog
Truncated Poisson regression
Limits:  lower =         10                     Number of obs     =         88
         upper =       +inf                     Wald chi2(6)      =   11340.50
Log likelihood = -239.35746                     Prob > chi2       =     0.0000
```

failures	Coefficient	Std. err.	z	P>|z|	[95% conf.	interval]
probe						
1	2.714025	.0752617	36.06	0.000	2.566515	2.861536
2	2.602722	.0692732	37.57	0.000	2.466949	2.738495
3	2.725459	.0721299	37.79	0.000	2.584087	2.866831
4	3.139437	.0377137	83.24	0.000	3.065519	3.213354
depth	-.0005034	.0033375	-0.15	0.880	-.0070447	.006038
width	.0330225	.015573	2.12	0.034	.0025001	.063545

▷ Example 9: Default priors

We first apply the `bayes` prefix with default priors to perform Bayesian estimation of the model. The estimation takes a little longer, so we specify the `dots` option to see the progress.

```
. set seed 15
. bayes, dots: tpoisson failures ibn.probe depth width, noconstant ll(10)
Burn-in 2500 aaaaaaaaa1000.........2000..... done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  failures ~ tpoisson(xb_failures)
Prior:
  {failures:i.probe depth width} ~ normal(0,10000)                        (1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_failures.
Bayesian truncated Poisson regression           MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
Limits: Lower =         10                      Number of obs    =         88
        Upper =       +inf                      Acceptance rate  =      .1383
                                                Efficiency:  min =    .004447
                                                             avg =     .01322
Log marginal-likelihood = -288.22663                         max =     .04082
```

failures	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
probe						
1	2.689072	.0696122	.008596	2.688881	2.557394	2.833737
2	2.581567	.0644141	.00966	2.588534	2.436973	2.701187
3	2.712054	.0695932	.006415	2.717959	2.55837	2.844429
4	3.13308	.0397521	.004592	3.133433	3.055979	3.208954
depth	-.000404	.0033313	.000165	-.000504	-.0067928	.0061168
width	.036127	.0165308	.001821	.0360637	.001239	.067552

```
Note: Default priors are used for model parameters.
Note: There is a high autocorrelation after 500 lags.
```

With the default prior specification, the posterior mean estimates for the regression parameters are similar to the ML estimates obtained with the `tpoisson` command. However, the `bayes` prefix issues a high autocorrelation warning note and reports a minimum efficiency of only 0.004. The posterior model with default priors seems to be somewhat challenging for the MH sampler. We could allow for longer burn-in and increase the MCMC sample size to improve the MCMC convergence and increase the estimation precision. Instead, we will provide an alternative prior specification that will increase the model flexibility and improve its fit to the data.

◁

▷ Example 10: Hyperpriors

We now assume that the four probe coefficients, `{failures:ibn.probe}`, have a normal prior distribution with mean parameter `{probe_mean}` and a variance of 10,000. It is reasonable to assume that all four probes have positive failure rates and that `{probe_mean}` is a positive hyperparameter. We decide to assign `{probe_mean}` a `gamma(2, 1)` hyperprior, which is a distribution with a positive domain and a mean of 2. We use this prior for the purpose of illustration; this prior is not informative for this model and these data. We initialize `{probe_mean}` with 1 to give it a starting value compatible with its hyperprior.

```
. set seed 15
. bayes, prior({failures:ibn.probe}, normal({probe_mean}, 10000))
> prior({probe_mean}, gamma(2, 1)) initial({probe_mean} 1) dots:
> tpoisson failures ibn.probe depth width, noconstant ll(10)
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  failures ~ tpoisson(xb_failures)
Priors:
      {failures:i.probe} ~ normal({probe_mean},10000)                     (1)
  {failures:depth width} ~ normal(0,10000)                                (1)
Hyperprior:
  {probe_mean} ~ gamma(2,1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_failures.
```

```
Bayesian truncated Poisson regression           MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
Limits: Lower =         10                      Number of obs    =         88
        Upper =       +inf                      Acceptance rate  =       .304
                                                Efficiency:  min =     .04208
                                                             avg =     .0775
Log marginal-likelihood = -287.91504                         max =      .127
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
failures						
probe						
1	2.703599	.0770656	.003757	2.704613	2.551404	2.848774
2	2.592738	.0711972	.002796	2.594628	2.446274	2.728821
3	2.716223	.0755001	.003549	2.719622	2.568376	2.863064
4	3.137069	.0388127	.001317	3.136773	3.062074	3.211616
depth	-.000461	.0033562	.000109	-.0004457	-.0067607	.0062698
width	.0337508	.0152654	.000532	.0337798	.003008	.0622191
probe_mean	2.051072	1.462867	.041051	1.71286	.2211973	5.809428

```
Note: Default priors are used for some model parameters.
```

The MCMC simulation achieves an average efficiency of about 8% with no indication of convergence problems. The posterior mean estimates for the regression parameters are similar to the ML estimates; moreover, the MCMC standard errors are much lower than those achieved by the previous model with default priors. By introducing the hyperparameter `{probe_mean}`, we have improved the goodness of fit of the model.

◁

Zero-inflated negative binomial model

In this example, we consider a Bayesian model using zero-inflated negative binomial likelihood. We revisit example 1 in [R] **zinb**, which models the number of fish caught by visitors to a national park. The probability that a particular visitor fished is assumed to depend on the variables `child` and `camper`, which are supplied as covariates to the `inflate()` option of `zinb`.

```
. use https://www.stata-press.com/data/r18/fish, clear
(Fictional fishing data)
. zinb count persons livebait, inflate(child camper) nolog
Zero-inflated negative binomial regression              Number of obs =    250
Inflation model: logit                                  Nonzero obs   =    108
                                                        Zero obs      =    142
                                                        LR chi2(2)    =  82.23
Log likelihood = -401.5478                              Prob > chi2   = 0.0000
```

count	Coefficient	Std. err.	z	P>|z|	[95% conf.	interval]
count						
persons	.9742984	.1034938	9.41	0.000	.7714543	1.177142
livebait	1.557523	.4124424	3.78	0.000	.7491503	2.365895
_cons	-2.730064	.476953	-5.72	0.000	-3.664874	-1.795253
inflate						
child	3.185999	.7468551	4.27	0.000	1.72219	4.649808
camper	-2.020951	.872054	-2.32	0.020	-3.730146	-.3117567
_cons	-2.695385	.8929071	-3.02	0.003	-4.44545	-.9453189
/lnalpha	.5110429	.1816816	2.81	0.005	.1549535	.8671323
alpha	1.667029	.3028685			1.167604	2.380076

Let's fit a Bayesian model with default normal prior distributions.

```
. set seed 15
. bayes, dots: zinb count persons livebait, inflate(child camper)
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  count ~ zinb(xb_count,xb_inflate,{lnalpha})
Priors:
  {count:persons livebait _cons} ~ normal(0,10000)                      (1)
    {inflate:child camper _cons} ~ normal(0,10000)                      (2)
                       {lnalpha} ~ normal(0,10000)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_count.
(2) Parameters are elements of the linear form xb_inflate.
```

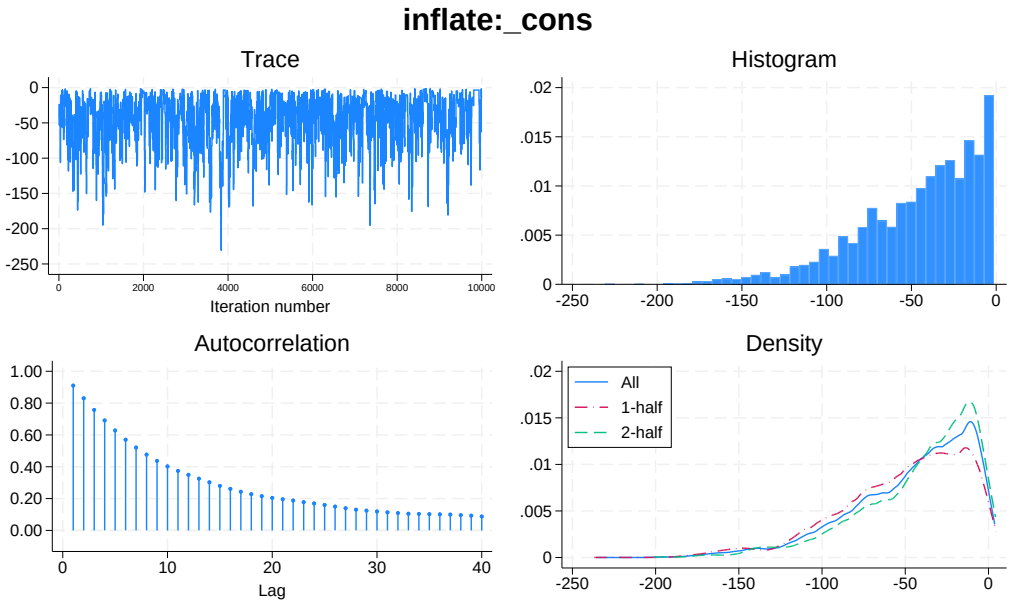
```
Bayesian zero-inflated negative binomial model   MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in         =      2,500
                                                 MCMC sample size =     10,000
Inflation model: logit                           Number of obs   =        250
                                                 Acceptance rate =      .3084
                                                 Efficiency:  min =     .03716
                                                              avg =      .0791
Log marginal-likelihood = -438.47876                          max =      .1613
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
count						
persons	.9851217	.1084239	.003601	.985452	.7641609	1.203561
livebait	1.536074	.4083865	.013509	1.515838	.753823	2.3539
_cons	-2.805915	.4700702	.014974	-2.795244	-3.73847	-1.89491
inflate						
child	46.95902	36.33974	1.87977	38.77997	3.612863	138.3652
camper	-46.123	36.34857	1.88567	-37.66796	-137.4568	-2.544566
_cons	-46.62439	36.36232	1.88355	-38.5171	-137.5522	-3.272469
lnalpha	.7055935	.1591234	.003962	.7048862	.3959316	1.025356

Note: Default priors are used for model parameters.

The posterior mean estimates for the main regression coefficients {count:persons}, {count:livebait}, and {count:_cons} are relatively close to the ML estimates from the zinb command, but the inflation coefficients, {inflate:child}, {inflate:camper}, and {inflate:_cons}, are quite different. For example, zinb estimates {inflate:_cons} are about -2.7, whereas the corresponding posterior mean estimate is about -46.6. To explain this large discrepancy, we draw the diagnostic plot of {inflate:_cons}.

```
. bayesgraph diagnostic {inflate:_cons}
```



The marginal posterior distribution of `{inflate:_cons}` is highly skewed to the left, and it is apparent that its posterior mean is much smaller than its posterior mode. In large samples, under proper noninformative priors, the posterior mode estimator and the ML estimator are equivalent. Therefore, it is not surprising that the posterior mean of `{inflate:_cons}` is much smaller than its ML estimate. We can obtain a rough estimate of the posterior mode in this example.

First, we need to save the simulation results in a dataset, say, `sim_zinb.dta`. You can do this during estimation or on replay by specifying the `saving()` option with the `bayes` prefix.

```
. bayes, saving(sim_zinb)
note: file sim_zinb.dta saved.
```

Next, we load the dataset and identify the variable that represents the parameter {inflate:_cons}.

```
. use sim_zinb, clear
. describe
Contains data from sim_zinb.dta
 Observations:         6,874
    Variables:            12                  23 Mar 2023 14:48
```

Variable name	Storage type	Display format	Value label	Variable label
_chain	int	%8.0g		Chain identifier
_index	int	%8.0g		Iteration number
_loglikelihood	double	%10.0g		Log likelihood
_logposterior	double	%10.0g		Log posterior
eq1_p1	double	%10.0g		{count:persons}
eq1_p2	double	%10.0g		{count:livebait}
eq1_p3	double	%10.0g		{count:_cons}
eq2_p1	double	%10.0g		{inflate:child}
eq2_p2	double	%10.0g		{inflate:camper}
eq2_p3	double	%10.0g		{inflate:_cons}
eq0_p1	double	%10.0g		{lnalpha}
_frequency	int	%8.0g		Frequency weight

```
Sorted by:
```

Variable eq2_p3 with the variable label {inflate:_cons} contains MCMC estimates for the {inflate:_cons} parameter.

We use the egen's mode() function to generate a constant variable, mode, which contains the mode estimate for {inflate:_cons}.

```
. egen mode = mode(eq2_p3)
. display mode[1]
-3.417458
```

The mode estimate for {inflate:_cons} is about −3.42, and it is indeed much closer to the ML estimate of −2.70 than its posterior mean estimate.

The inflation parameter α in the likelihood of the zero-inflated negative binomial model is log-transformed, and it is represented by {lnalpha} in our posterior model. To summarize the simulation result for α directly, we can use the bayesstats summary command to exponentiate {lnalpha}.

```
. bayesstats summary (alpha: exp({lnalpha}))
Posterior summary statistics                     MCMC sample size =    10,000
       alpha : exp({lnalpha})
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
alpha	2.050889	.3292052	.008191	2.023616	1.485768	2.788087

Parametric survival model

Consider example 7 in [ST] **streg**, which analyzes the effect of a hip-protection device, age, and sex on the risk of hip fractures in patients. The survival dataset is hip3.dta with time to event variable time1 and failure variable fracture. The data are already stset.

```
. use https://www.stata-press.com/data/r18/hip3, clear
(Hip-fracture study)
. stset
-> stset time1, id(id) failure(fracture) time0(time0)
Survival-time data settings
          ID variable: id
        Failure event: fracture!=0 & fracture<.
Observed time interval: (time0, time1]
     Exit on or before: failure
------------------------------------------------------------------------------
       206  total observations
         0  exclusions
------------------------------------------------------------------------------
       206  observations remaining, representing
       148  subjects
        37  failures in single-failure-per-subject data
     1,703  total analysis time at risk and under observation
                                              At risk from t =         0
                                   Earliest observed entry t =         0
                                        Last observed exit t =        39
```

It is assumed that the hazard curves for men and women have different shapes. We use the `streg` command to fit a model with Weibull survival distribution and the ancillary variable `male` to account for the difference between men and women.

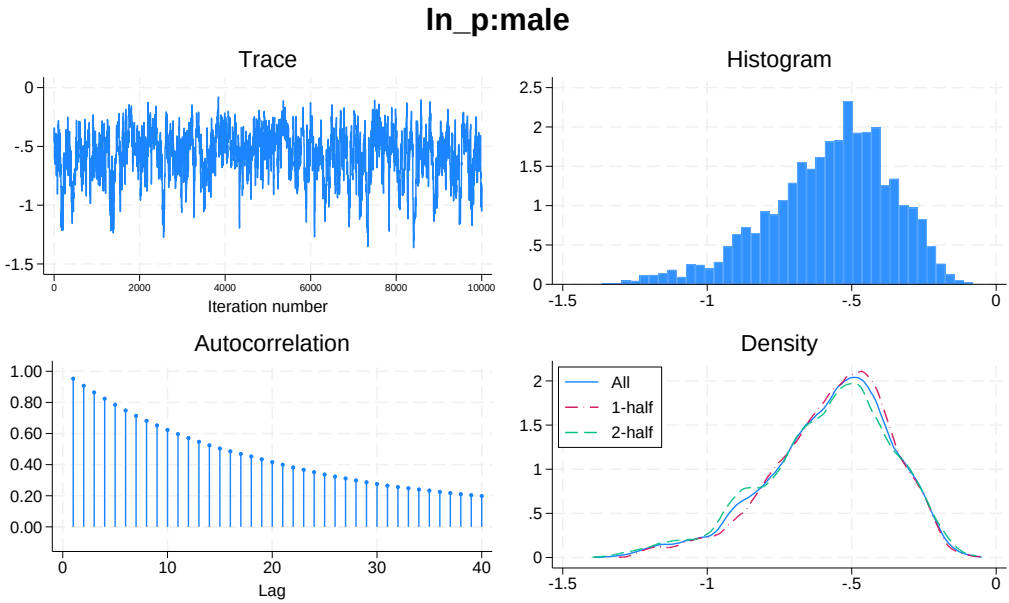
```
. streg protect age, distribution(weibull) ancillary(male) nolog
        Failure _d: fracture
  Analysis time _t: time1
       ID variable: id
Weibull PH regression
No. of subjects =   148                                 Number of obs =    206
No. of failures =    37
Time at risk    = 1,703
                                                        LR chi2(2)    =  39.80
Log likelihood = -69.323532                             Prob > chi2   = 0.0000
------------------------------------------------------------------------------
          _t | Coefficient  Std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
_t           |
     protect |  -2.130058   .3567005    -5.97   0.000    -2.829178   -1.430938
         age |   .0939131   .0341107     2.75   0.006     .0270573    .1607689
       _cons |  -10.17575   2.551821    -3.99   0.000    -15.17722   -5.174269
-------------+----------------------------------------------------------------
ln_p         |
        male |  -.4887189    .185608    -2.63   0.008    -.8525039   -.1249339
       _cons |   .4540139   .1157915     3.92   0.000     .2270667    .6809611
------------------------------------------------------------------------------
```

We then perform Bayesian analysis of the same model using the `bayes` prefix. We apply more conservative normal priors, `normal(0, 100)`, by specifying the `normalprior(10)` option. To allow for longer adaptation of the MCMC sampler, we increase the burn-in period to 5,000, `burnin(5000)`.

```
. set seed 15
. bayes, normalprior(10) burnin(5000) dots:
> streg protect age, distribution(weibull) ancillary(male)
        Failure _d: fracture
  Analysis time _t: time1
       ID variable: id
Burn-in 5000 aaaaaaaaa1000aaaaaaaaa2000aaaaaaaaa3000aaaaaaaaa4000aaaaaaaaa5000
> done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  _t ~ streg_weibull(xb__t,xb_ln_p)
Priors:
  {_t:protect age _cons} ~ normal(0,100)                                  (1)
       {ln_p:male _cons} ~ normal(0,100)                                  (2)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb__t.
(2) Parameters are elements of the linear form xb_ln_p.
Bayesian Weibull PH regression                  MCMC iterations  =     15,000
Random-walk Metropolis-Hastings sampling        Burn-in          =      5,000
                                                MCMC sample size =     10,000
No. of subjects =        148                    Number of obs    =        206
No. of failures =         37
Time at risk    =       1703
                                                Acceptance rate  =      .3418
                                                Efficiency:  min =        .01
                                                             avg =     .03421
Log marginal-likelihood = -91.348814                         max =     .05481
------------------------------------------------------------------------------
             |                                                     Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
_t           |
     protect |  -2.114715   .3486032   .017409  -2.105721  -2.818483   -1.46224
         age |   .0859305   .0328396   .001403   .0862394   .0210016   .1518009
       _cons |  -9.57056    2.457818   .117851  -9.551418  -14.49808   -4.78585
-------------+----------------------------------------------------------------
ln_p         |
        male |  -.5753907   .2139477   .014224  -.5468488   -1.07102   -.2317242
       _cons |   .4290642     .11786   .011786   .4242712    .203933    .6548229
------------------------------------------------------------------------------
```

The posterior mean estimates for the regression parameters `{_t:protect}`, `{_t:age}`, and `{_t:_cons}` are close to the estimates reported by the `streg` command. However, the estimate for `{ln_p:male}` is somewhat different. If we inspect the diagnostic plot for `{ln_p:male}`, we will see that the reason for this is the asymmetrical shape of its marginal posterior distribution.

```
. bayesgraph diagnostic {ln_p:male}
```



As evident from the density plot, the posterior distribution of `{ln_p:male}` is skewed to the left, so the posterior mean estimate, −0.58, is expected to be smaller than the ML estimate, −0.49, given that we used fairly uninformative priors; see *Zero-inflated negative binomial model* for the comparison of posterior mean, posterior mode, and ML estimates for highly skewed posterior distributions.

Heckman selection model

▷ Example 11

A representative example of a Heckman selection model is provided by `wagenwk.dta`, which contains observations on the income of women who choose to work. See example 1 in [R] **heckman**.

```
. use https://www.stata-press.com/data/r18/womenwk, clear
```

The women's income (`wage`) is assumed to depend on their education (`educ`) and their age (`age`). In addition, the selection decision, or the choice of a woman to work, is assumed to depend on their marital status (`married`), number of children (`children`), education, and age. We fit this selection model using the `heckman` command.

```
. heckman wage educ age, select(married children educ age) nolog
Heckman selection model                         Number of obs     =      2,000
(regression model with sample selection)              Selected    =      1,343
                                                      Nonselected =        657

                                                Wald chi2(2)      =     508.44
Log likelihood = -5178.304                      Prob > chi2       =     0.0000
```

wage	Coefficient	Std. err.	z	P>|z|	[95% conf.	interval]
wage						
education	.9899537	.0532565	18.59	0.000	.8855729	1.094334
age	.2131294	.0206031	10.34	0.000	.1727481	.2535108
_cons	.4857752	1.077037	0.45	0.652	-1.625179	2.59673
select						
married	.4451721	.0673954	6.61	0.000	.3130794	.5772647
children	.4387068	.0277828	15.79	0.000	.3842534	.4931601
education	.0557318	.0107349	5.19	0.000	.0346917	.0767718
age	.0365098	.0041533	8.79	0.000	.0283694	.0446502
_cons	-2.491015	.1893402	-13.16	0.000	-2.862115	-2.119915
/athrho	.8742086	.1014225	8.62	0.000	.6754241	1.072993
/lnsigma	1.792559	.027598	64.95	0.000	1.738468	1.84665
rho	.7035061	.0512264			.5885365	.7905862
sigma	6.004797	.1657202			5.68862	6.338548
lambda	4.224412	.3992265			3.441942	5.006881

```
LR test of indep. eqns. (rho = 0): chi2(1) = 61.20        Prob > chi2 = 0.0000
```

We then apply the bayes prefix to perform Bayesian estimation of the Heckman selection model.

```
. set seed 15
. bayes, dots: heckman wage educ age, select(married children educ age)
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  wage ~ heckman(xb_wage,xb_select,{athrho} {lnsigma})
Priors:
                     {wage:education age _cons} ~ normal(0,10000)          (1)
  {select:married children education age _cons} ~ normal(0,10000)          (2)
                                {athrho lnsigma} ~ normal(0,10000)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_wage.
(2) Parameters are elements of the linear form xb_select.
```

```
Bayesian Heckman selection model                MCMC iterations   =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in           =      2,500
                                                MCMC sample size  =     10,000
                                                Number of obs     =      2,000
                                                      Selected    =      1,343
                                                      Nonselected =        657
                                                Acceptance rate   =      .3484
                                                Efficiency:   min =     .02314
                                                              avg =     .03657
Log marginal-likelihood = -5260.2024                          max =     .05013
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
wage						
education	.9919131	.051865	.002609	.9931531	.8884407	1.090137
age	.2131372	.0209631	.001071	.2132548	.1720535	.2550835
_cons	.4696264	1.089225	.0716	.4406188	-1.612032	2.65116
select						
married	.4461775	.0681721	.003045	.4456493	.3178532	.5785857
children	.4401305	.0255465	.001156	.4402145	.3911135	.4903804
education	.0559983	.0104231	.000484	.0556755	.0360289	.076662
age	.0364752	.0042497	.000248	.0362858	.0280584	.0449843
_cons	-2.494424	.18976	.011327	-2.498414	-2.861266	-2.114334
athrho	.868392	.099374	.005961	.8699977	.6785641	1.062718
lnsigma	1.793428	.0269513	.001457	1.793226	1.740569	1.846779

```
Note: Default priors are used for model parameters.
```

The posterior mean estimates for the Bayesian model with default normal priors are similar to the ML estimates obtained with the `heckman` command.

We can calculate posterior summaries for the correlation parameter, ρ, and the standard error, σ, in their natural scale by inverse-transforming the model parameters `{athrho}` and `{lnsigma}` using the `bayesstats summary` command. We also include posterior summaries for the selectivity effect $\lambda = \rho\sigma$.

```
. bayesstats summary (rho:1-2/(exp(2*{athrho})+1))
> (sigma:exp({lnsigma}))
> (lambda:exp({lnsigma})*(1-2/(exp(2*{athrho})+1)))
Posterior summary statistics                    MCMC sample size =     10,000

         rho : 1-2/(exp(2*{athrho})+1)
       sigma : exp({lnsigma})
      lambda : exp({lnsigma})*(1-2/(exp(2*{athrho})+1))
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
rho	.6970522	.0510145	.003071	.701373	.5905851	.7867018
sigma	6.012205	.1621422	.008761	6.008807	5.700587	6.339366
lambda	4.196646	.3937209	.024351	4.212609	3.411479	4.946325

Again, the posterior mean estimates of ρ, σ, and λ agree with the ML estimates reported by `heckman`.

◁

Multilevel models

The bayes prefix supports several multilevel commands such as mixed and meglm; see [BAYES] **Bayesian estimation**. Multilevel models introduce effects at different levels of hierarchy such as hospital effects and doctor-nested-within-hospital effects, which are often high-dimensional. These effects are commonly referred to as random effects in frequentist models. Bayesian multilevel models estimate random effects together with other model parameters. In contrast, frequentist multilevel models integrate random effects out, but provide ways to predict them after estimation, conditional on other estimated model parameters. Thus, in addition to regression coefficients and variance components (variances and covariances of random effects), Bayesian multilevel models include random effects themselves as model parameters. With a slight abuse of the terminology, we will sometimes refer to regression coefficients as fixed effects, keeping in mind that they are still random quantities from a Bayesian perspective.

Multilevel models are more difficult to simulate from because of the existence of high-dimensional random-effects parameters. They typically require longer burn-in periods to achieve convergence and larger MCMC sample sizes to obtain precise estimates of random effects and variance components.

Prior specification is particularly important for multilevel models. Using noninformative priors for all model parameters will likely result in nonconvergence or high autocorrelation of the MCMC sample, especially with small datasets. The default priors provided by the bayes prefix are chosen to be fairly uninformative, which may often lead to low simulation efficiencies for model parameters and, especially, for variance components; see *Default priors*. So, do not be surprised to see high autocorrelation with default priors, and be prepared to investigate various prior specifications during your analysis. For example, you may need to use the iwishartprior() option to increase the degrees of freedom and to specify a different scale matrix of the inverse-Wishart prior distribution used for the covariance matrices of random effects.

To change the default priors, you will need to know the names of the model parameters. See *Likelihood model* to learn how the bayes prefix labels the parameters. You can specify your own name stubs for the groups of random-effects parameters using the restubs() option. After simulation, see *Different ways of specifying model parameters* for how to refer to individual random effects to evaluate MCMC convergence or to obtain their MCMC summaries.

By default, the bayes prefix does not compute or display MCMC summaries of individual random effects to conserve computation time and space. You can specify the showreffects() or show() option to compute and display them for chosen groups of random effects.

Also, the bayes prefix does not compute the log marginal-likelihood by default for multilevel models. The computation involves the inverse of the determinant of the sample covariance matrix of all parameters and loses accuracy as the number of parameters grows. For high-dimensional models such as multilevel models, the computation can be time consuming, and its accuracy may become unacceptably low. Because it is difficult to access the levels of accuracy of the computation for all multilevel models, the log marginal-likelihood is not computed by default. For multilevel models containing a small number of random effects, you can use the remargl option to compute and display it.

Assessing convergence of MCMC for multilevel models is challenging because of the high dimensionality. Technically, the convergence of all parameters, including the random-effects parameters, must be explored. In practice, this may not always be feasible. Many applications focus on the regression coefficients and variance components and treat random-effects parameters as nuisance. In this case, it may be sufficient to check convergence only for the parameters of interest, especially because their convergence is adversely affected whenever there are convergence problems for many of the random-effects parameters. If the random-effects parameters are of primary interest in your study, you should evaluate their convergence. For models with a small to moderate number of random-effects

parameters, it may be beneficial to always check the convergence of the random-effects parameters. Also see *Convergence of MCMC* in [BAYES] **bayesmh**.

Two-level models

Consider example 1 from [ME] **mixed** that analyzed the weight gain of 48 pigs over 9 successive weeks. Detailed Bayesian analysis of these data using `bayesmh` are presented in *Panel-data and multilevel models* in [BAYES] **bayesmh**. Here, we use `bayes: mixed` to fit Bayesian two-level random-intercept and random-coefficient models to these data.

```
. use https://www.stata-press.com/data/r18/pig
(Longitudinal analysis of pig weights)
```

▷ Example 12: Random-intercept model, using option melabel

We first consider a simple random-intercept model of dependent variable `weight` on covariate `week` with variable `id` identifying pigs. The random-intercept model assumes that all pigs share a common growth rate but have different initial weight.

For comparison purposes, we first use the `mixed` command to fit this model by maximum likelihood.

```
. mixed weight week || id:

Performing EM optimization ...

Performing gradient-based optimization:
Iteration 0:  Log likelihood = -1014.9268
Iteration 1:  Log likelihood = -1014.9268

Computing standard errors ...

Mixed-effects ML regression                     Number of obs     =        432
Group variable: id                              Number of groups  =         48
                                                Obs per group:
                                                              min =          9
                                                              avg =        9.0
                                                              max =          9
                                                Wald chi2(1)      =   25337.49
Log likelihood = -1014.9268                     Prob > chi2       =     0.0000
```

weight	Coefficient	Std. err.	z	P>|z|	[95% conf.	interval]
week	6.209896	.0390124	159.18	0.000	6.133433	6.286359
_cons	19.35561	.5974059	32.40	0.000	18.18472	20.52651

Random-effects parameters	Estimate	Std. err.	[95% conf.	interval]
id: Identity				
var(_cons)	14.81751	3.124225	9.801716	22.40002
var(Residual)	4.383264	.3163348	3.805112	5.04926

```
LR test vs. linear model: chibar2(01) = 472.65        Prob >= chibar2 = 0.0000
```

To fit a Bayesian analog of this model, we simply prefix the `mixed` command with `bayes`. We also specify the `melabel` option with `bayes` to label model parameters in the output table as `mixed` does.

```
. set seed 15
. bayes, melabel: mixed weight week || id:
note: Gibbs sampling is used for regression coefficients and variance
      components.
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Bayesian multilevel regression                  MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling          Burn-in          =      2,500
                                                MCMC sample size =     10,000
Group variable: id                              Number of groups =         48
                                                Obs per group:
                                                              min =          9
                                                              avg =        9.0
                                                              max =          9
                                                Number of obs    =        432
                                                Acceptance rate  =      .8112
                                                Efficiency:  min =    .007005
                                                             avg =      .5064
Log marginal-likelihood                                      max =          1
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
weight						
week	6.209734	.0390718	.000391	6.209354	6.133233	6.285611
_cons	19.46511	.6239712	.07455	19.48275	18.2534	20.67396
id						
var(_cons)	15.7247	3.436893	.049048	15.26104	10.31182	23.60471
var(Residual)	4.411155	.3193582	.004397	4.396044	3.834341	5.080979

```
Note: Default priors are used for model parameters.
```

The estimates of posterior means and posterior standard deviations are similar to the ML estimates and standard errors from `mixed`. The results are also close to those from `bayesmh` in example 23 in [BAYES] **bayesmh**.

The average efficiency of the simulation is about 51% and there is no indication of any immediate convergence problems, but we should investigate convergence more thoroughly; see, for example, example 5 in [BAYES] **Bayesian commands** and, more generally, *Convergence of MCMC* in [BAYES] **bayesmh**.

Because Bayesian multilevel models are generally slower than other commands, the `bayes` prefix displays dots by default with multilevel commands. You can specify the `nodots` option to suppress them.

Also, as we described in *Multilevel models*, the log marginal-likelihood is not computed for multilevel models by default because of the high dimensionality of the models. This is also described in the help file that appears when you click on `Log marginal-likelihood` in the output header in the Results window. For models with a small number of random effects, you can specify the `remargl` option to compute the log marginal-likelihood.

An important note about bayes: mixed is the default simulation method. Most bayes prefix commands use an adaptive MH algorithm to sample model parameters. The high-dimensional nature of multilevel models greatly decreases the simulation efficiency of this algorithm. For Gaussian multilevel models, such as bayes: mixed, model parameters can be sampled using a more efficient, albeit slower, Gibbs algorithm under certain prior distributions. The default priors used for regression coefficients and variance components allow the bayes prefix to use Gibbs sampling for these parameters with the mixed command. If you change the prior distributions or the default blocking structure for some parameters, Gibbs sampling may not be available for those parameters and an adaptive MH sampling will be used instead.

◁

▷ Example 13: Random-intercept model, default output

When we specified the melabel option with bayes in example 12, we intentionally suppressed some of the essential output from bayes: mixed. Here is what we would have seen had we not specified melabel.

```
. bayes
Multilevel structure
------------------------------------------------------------------------------
id
    {U0}: random intercepts
------------------------------------------------------------------------------

Model summary
------------------------------------------------------------------------------
Likelihood:
  weight ~ normal(xb_weight,{e.weight:sigma2})

Priors:
  {weight:week _cons} ~ normal(0,10000)                                   (1)
                {U0} ~ normal(0,{U0:sigma2})                              (1)
    {e.weight:sigma2} ~ igamma(.01,.01)

Hyperprior:
  {U0:sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_weight.
```

```
Bayesian multilevel regression                  MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling          Burn-in          =      2,500
                                                MCMC sample size =     10,000
Group variable: id                              Number of groups =         48
                                                Obs per group:
                                                              min =          9
                                                              avg =        9.0
                                                              max =          9
                                                Number of obs    =        432
                                                Acceptance rate  =      .8112
                                                Efficiency:  min =    .007005
                                                             avg =      .5064
Log marginal-likelihood                                      max =          1
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
weight						
week	6.209734	.0390718	.000391	6.209354	6.133233	6.285611
_cons	19.46511	.6239712	.07455	19.48275	18.2534	20.67396
id						
U0:sigma2	15.7247	3.436893	.049048	15.26104	10.31182	23.60471
e.weight						
sigma2	4.411155	.3193582	.004397	4.396044	3.834341	5.080979

```
Note: Default priors are used for model parameters.
```

Let's go over the default output in detail, starting with the model summary. For multilevel models, in addition to the model summary, which describes the likelihood model and prior distributions, the `bayes` prefix displays information about the multilevel structure of the model.

```
Multilevel structure
------------------------------------------------------------------------------
id
    {U0}: random intercepts
------------------------------------------------------------------------------
```

Our multilevel model has one set of random effects, labeled as `U0`, which represent random intercepts at the `id` level. Recall that in Bayesian models, random effects are not integrated out but estimated together with other model parameters. So, `{U0}`, or using its full name `{U0[id]}`, represent random-effects parameters in our model. See *Likelihood model* to learn about the default naming convention for random-effects parameters.

According to the model summary below, the likelihood of the model is a normal linear regression with the linear predictor containing regression parameters {weight:week} and {weight:_cons} and random-effects parameters {U0}, and with the error variance labeled as {e.weight:sigma2}. Regression coefficients {weight:week} and {weight:_cons} have default normal priors with zero means and variances of 10,000. The random intercepts {U0} are normally distributed with mean zero and variance {U0:sigma2}. The variance components, error variance {e.weight:sigma2}, and random-intercept variance {U0:sigma2} have default inverse-gamma priors, InvGamma$(0.01, 0.01)$. The random-intercept variance is a hyperparameter in our model.

```
Model summary
------------------------------------------------------------------------------
Likelihood:
  weight ~ normal(xb_weight,{e.weight:sigma2})
Priors:
  {weight:week _cons} ~ normal(0,10000)                                   (1)
                {U0} ~ normal(0,{U0:sigma2})                              (1)
    {e.weight:sigma2} ~ igamma(.01,.01)
Hyperprior:
  {U0:sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_weight.
```

The default output table of `bayes: mixed` uses the names of model parameters as they are defined by the `bayes` prefix.

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
weight						
week	6.209734	.0390718	.000391	6.209354	6.133233	6.285611
_cons	19.46511	.6239712	.07455	19.48275	18.2534	20.67396
id						
U0:sigma2	15.7247	3.436893	.049048	15.26104	10.31182	23.60471
e.weight						
sigma2	4.411155	.3193582	.004397	4.396044	3.834341	5.080979

Note: Default priors are used for model parameters.

Becoming familiar with the native parameter names of the `bayes` prefix is important for prior specification and for later postestimation. The `melabel` option is provided for easier comparison of the results between the `bayes` prefix and the corresponding frequentist multilevel command.

◁

▷ Example 14: Displaying random effects

By default, the `bayes` prefix does not compute or display MCMC summaries for the random-effects parameters to conserve space and computational time. You can specify the `showreffects` option to display all random effects or the `showreffects()` or `show()` option to display specific random effects. For example, continuing example 13, we can display the random-effects estimates for the first five pigs as follows.

```
. bayes, show({U0[1/5]}) noheader
```

U0[id]	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
1	-1.778442	.8873077	.074832	-1.761984	-3.542545	.0062218
2	.7831408	.8775376	.071421	.7961802	-.9547035	2.491798
3	-2.052634	.9038672	.072325	-2.061559	-3.822966	-.3246834
4	-1.891103	.878177	.075611	-1.858056	-3.642227	-.1028766
5	-3.316584	.8894319	.074946	-3.320502	-5.0469	-1.568927

These posterior mean estimates of random-effects parameters should be comparable with those predicted by `predict, reffects` after `mixed`. Posterior standard deviations, however, will generally be larger than the corresponding standard errors of random effects predicted after `mixed`, because the latter do not incorporate the uncertainty about the estimated model parameters.

You can also use [BAYES] **bayesstats summary** to obtain MCMC summaries of random-effects parameters after estimation:

```
. bayesstats summary {U0[1/5]}
(output omitted)
```

If you decide to use the `showreffects` option to display all random-effects parameters, beware of the increased computation time for models with many random effects. Then, the `bayes` prefix will compute and display the MCMC summaries for only the first M random-effects parameters, where M is the maximum matrix dimension (`c(max_matdim)`). The number of parameters displayed and stored in `e(b)` cannot exceed `c(max_matdim)`. You can specify the `show()` option with `bayes` or use `bayesstats summary` to obtain results for other random-effects parameters.

◁

▷ Example 15: Random-coefficient model

Continuing example 13, let's consider a random-coefficient model that allows the growth rate to vary among pigs.

Following `mixed`'s specification, we include the random slope for `week` at the `id` level by specifying the `week` variable in the random-effects equation.

```
. set seed 15
. bayes: mixed weight week || id: week
note: Gibbs sampling is used for regression coefficients and variance
      components.
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Multilevel structure
------------------------------------------------------------------------------
id
    {U0}: random intercepts
    {U1}: random coefficients for week
------------------------------------------------------------------------------
Model summary
------------------------------------------------------------------------------
Likelihood:
  weight ~ normal(xb_weight,{e.weight:sigma2})
Priors:
  {weight:week _cons} ~ normal(0,10000)                                   (1)
                {U0} ~ normal(0,{U0:sigma2})                              (1)
                {U1} ~ normal(0,{U1:sigma2})                              (1)
    {e.weight:sigma2} ~ igamma(.01,.01)
Hyperpriors:
  {U0:sigma2} ~ igamma(.01,.01)
  {U1:sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_weight.
Bayesian multilevel regression                  MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling          Burn-in          =      2,500
                                                MCMC sample size =     10,000
Group variable: id                              Number of groups =         48
                                                Obs per group:
                                                              min =          9
                                                              avg =        9.0
                                                              max =          9
                                                Number of obs    =        432
                                                Acceptance rate  =      .7473
                                                Efficiency:  min =    .003057
                                                             avg =     .07487
Log marginal-likelihood                                       max =      .1503
------------------------------------------------------------------------------
             |                                                      Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
weight       |
        week |  6.233977   .0801192    .01449   6.237648    6.05268   6.387741
       _cons |  19.44135   .3426786   .044377   19.44532   18.76211   20.11843
-------------+----------------------------------------------------------------
id           |
   U0:sigma2 |  7.055525   1.649394   .050935   6.844225   4.466329   10.91587
   U1:sigma2 |  .3941786   .0901945   .002717   .3825387   .2526756   .6044887
-------------+----------------------------------------------------------------
e.weight     |
      sigma2 |  1.613775   .1261213   .003254   1.609296   1.386427   1.880891
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
Note: There is a high autocorrelation after 500 lags.
```

In addition to random intercepts {U0}, we now have random coefficients for week, labeled as {U1}, with the corresponding variance parameter {U1:sigma2}. Compared with the random-intercept model, by capturing the variability of slopes on week, we reduced the estimates of the error variance and the random-intercept variance.

The average simulation efficiency decreased to only 7%, and we now see a note about a high autocorrelation after 500 lags. We can use, for example, bayesgraph diagnostics to verify that the high autocorrelation in this example is not an indication of nonconvergence but rather of a slow mixing of our MCMC sample. If we use bayesstats ess, we will see that the coefficient on weight and the constant term have the lowest efficiency, which suggests that these parameters are likely to be correlated with some of the random-effects estimates. If we want to reduce the autocorrelation and improve precision of the estimates for these parameters, we can increase the MCMC sample size by specifying the mcmcsize() option or thin the MCMC chain by specifying the thinning() option.

◁

▷ Example 16: Random-coefficient model, unstructured covariance

In example 15, we assumed independence between random intercepts {U0} and random slopes on week, {U1}. We relax this assumption here by specifying an unstructured covariance matrix.

Before we proceed with estimation, let's review our model summary first by specifying the dryrun option.

```
. bayes, dryrun: mixed weight week || id: week, covariance(unstructured)
Multilevel structure
------------------------------------------------------------------------------
id
    {U0}: random intercepts
    {U1}: random coefficients for week
------------------------------------------------------------------------------

Model summary
------------------------------------------------------------------------------
Likelihood:
  weight ~ normal(xb_weight,{e.weight:sigma2})

Priors:
  {weight:week _cons} ~ normal(0,10000)                                  (1)
              {U0 U1} ~ mvnormal(2,{U:Sigma,m})                          (1)
    {e.weight:sigma2} ~ igamma(.01,.01)

Hyperprior:
  {U:Sigma,m} ~ iwishart(2,3,I(2))
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_weight.
```

The prior distributions for random effects {U0} and {U1} are no longer independent. Instead, they have a joint prior—a bivariate normal distribution with covariance matrix parameter {U:Sigma,m}, which is short for {U:Sigma,matrix}. The random-effects stub U is used to label the covariance matrix. The covariance matrix {U:Sigma,m} is assigned a fairly uninformative inverse-Wishart prior with three degrees of freedom and an identity scale matrix; see *Default priors* for details.

Let's now fit the model but suppress the model summary for brevity.

```
. set seed 15
. bayes, nomodelsummary: mixed weight week || id: week, covariance(unstructured)
note: Gibbs sampling is used for regression coefficients and variance
      components.
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Multilevel structure
------------------------------------------------------------------------------
id
    {U0}: random intercepts
    {U1}: random coefficients for week
------------------------------------------------------------------------------

Bayesian multilevel regression                  MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling          Burn-in          =      2,500
                                                MCMC sample size =     10,000
Group variable: id                              Number of groups =         48
                                                Obs per group:
                                                              min =          9
                                                              avg =        9.0
                                                              max =          9
                                                Number of obs    =        432
                                                Acceptance rate  =      .7009
                                                Efficiency:  min =    .003683
                                                             avg =     .07461
Log marginal-likelihood                                      max =      .1602

------------------------------------------------------------------------------
             |                                                      Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
weight       |
        week |  6.207086   .0878022   .014469   6.204974   6.041093   6.384891
       _cons |  19.39551   .4077822   .050353   19.40187   18.53869    20.1993
-------------+----------------------------------------------------------------
id           |
 U:Sigma_1_1 |  6.872161   1.627769   .061568   6.673481   4.282284   10.62194
 U:Sigma_2_1 | -.0866373   .2702822   .009861  -.0796118   -.645439   .4341423
 U:Sigma_2_2 |   .399525   .0904532   .002488   .3885861   .2575883   .6104775
-------------+----------------------------------------------------------------
e.weight     |
      sigma2 |  1.611889   .1263131   .003155   1.605368   1.381651   1.872563
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
Note: There is a high autocorrelation after 500 lags.
```

The 95% credible interval for the covariance between {U0} and {U1}, labeled as {U:Sigma_2_1} in the output, is $[-.65, 0.43]$, which suggests independence between {U0} and {U1}.

The high autocorrelation note is due to the lower sampling efficiency of some of the regression coefficients as can be seen from the output of `bayesstats ess`:

```
. bayesstats ess
Efficiency summaries     MCMC sample size =    10,000
                         Efficiency:  min =   .003683
                                      avg =    .07461
                                      max =     .1602
```

	ESS	Corr. time	Efficiency
weight			
week	36.83	271.55	0.0037
_cons	65.58	152.48	0.0066
id			
U:Sigma_1_1	698.99	14.31	0.0699
U:Sigma_2_1	751.20	13.31	0.0751
U:Sigma_2_2	1321.67	7.57	0.1322
e.weight			
sigma2	1602.39	6.24	0.1602

We explore the impact of this high autocorrelation on MCMC convergence in example 17.

◁

▷ Example 17: Random-coefficient model, multiple chains

We continue with the random-coefficient model with unstructured covariance from example 16. Some of the parameters such as the coefficients `{weight:week}` and `{weight:_cons}` have low sampling efficiency, which raises convergence and precision concerns. Simulating multiple Markov chains of the model may help address these concerns.

We will simulate three chains by specifying the `nchains(3)` option. We will use the `rseed(15)` option to ensure reproducibility with multiple chains; see *Reproducing results* in [BAYES] **bayesmh**. We will also suppress various model summaries by specifying the `nomodelsummary` and `nomesummary` options.

When using multiple chains to assess convergence, it is important to apply overdispersed initial values for different chains. It is difficult to quantify overdispersion because it is specific to the data and model. The default initialization provided by the `bayes: mixed` command may or may not be sufficient. To be certain, we recommend that you provide initial values explicitly, at least for the main parameters of interest. In the following specification, we provide initial values for the two regression coefficients referred to as `{weight:}`, the variance parameter `{e.weight:sigma2}`, and the covariance matrix `{U:Sigma, matrix}`. We try to generate initial values that are sufficiently separated. For example, we use `rnormal(-10, 100)` for the regression coefficients in the second chain and `rnormal(10, 100)` in the third chain. Specifying initial values for the random effects `{U0}` and `{U1}` would be more tedious, so we let them be sampled from their corresponding prior distributions. Because the hyperparameters of these priors have overdispersed initial values, we indirectly provide some overdispersion for the initial random effects as well.

```
. bayes, nchains(3) rseed(15) nomodelsummary nomesummary
> init2({weight:} rnormal(-10,100) {e.weight:sigma2} 0.1 {U:Sigma,m} 100*I(2))
> init3({weight:} rnormal(10,100) {e.weight:sigma2} 100 {U:Sigma,m} (10,-5\-5,10)):
> mixed weight week || id: week, covariance(unstructured)
note: Gibbs sampling is used for regression coefficients and variance
      components.
Chain 1
  Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
  Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Chain 2
  Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
  Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Chain 3
  Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
  Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done

Bayesian multilevel regression              Number of chains    =          3
Metropolis-Hastings and Gibbs sampling      Per MCMC chain:
                                                 Iterations     =     12,500
                                                 Burn-in        =      2,500
                                                 Sample size    =     10,000
Group variable: id                          Number of groups    =         48
                                            Obs per group:
                                                          min =          9
                                                          avg =        9.0
                                                          max =          9
                                            Number of obs       =        432
                                            Avg acceptance rate =      .6981
                                            Avg efficiency: min =    .003059
                                                          avg =     .07659
                                                          max =      .1663
Log marginal-likelihood                     Max Gelman-Rubin Rc =      1.055
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
weight						
week	6.201475	.0874855	.009133	6.200176	6.032975	6.374917
_cons	19.3941	.4344171	.035266	19.38919	18.52954	20.2323
id						
U:Sigma_1_1	6.863804	1.6219	.035988	6.653249	4.329726	10.62575
U:Sigma_2_1	-.0799526	.2684949	.005546	-.0723027	-.6351419	.4354943
U:Sigma_2_2	.3983365	.0890525	.001378	.3869276	.258562	.6048894
e.weight						
sigma2	1.612452	.1254983	.001777	1.605632	1.383175	1.874105

```
Note: Default priors are used for model parameters.
Note: Default initial values are used for multiple chains.
Note: There is a high autocorrelation after 500 lags in at least one of the
      chains.
```

While the sampling efficiency of the chains is about the same as in example 16, having three MCMC samples instead of one improves the precision of the estimation results, as evident from the lower MCMC errors for all model parameters.

Let's compute Gelman–Rubin diagnostics as a convergence check. We can already see in the header of `bayes: mixed` that the maximum Gelman–Rubin statistic `Rc` of 1.055 is close to 1.

```
. bayesstats grubin
Gelman-Rubin convergence diagnostic
Number of chains     =            3
MCMC size, per chain =       10,000
Max Gelman-Rubin Rc  =     1.055383
```

	Rc
weight	
week	1.006404
_cons	1.055383
id	
U:Sigma_1_1	1.000567
U:Sigma_2_1	1.001168
U:Sigma_2_2	1.002119
e.weight	
sigma2	.9999899

```
Convergence rule: Rc < 1.1
```

The convergence diagnostic estimates `Rc` for all reported parameters are lower than 1.1, suggesting the convergence of the chains. We can also explore MCMC convergence visually; see [BAYES] **bayesgraph**.

◁

Crossed-effects model

Let's revisit example 4 from [ME] **meglm**, which analyzes salamander cross-breeding data. Two populations of salamanders are considered: whiteside males and females (variables `wsm` and `wsf`) and roughbutt males and females (variables `rbm` and `rbf`). Male and female identifiers are recorded in the `male` and `female` variables. The outcome binary variable `y` indicates breeding success or failure.

In example 4 of [ME] **meglm**, we fit a crossed-effects logistic regression for successful mating, in which the effects of `male` and `female` were crossed. For the purpose of illustration, we will fit a crossed-effects probit regression here using `meglm` with the probit link.

```
. use https://www.stata-press.com/data/r18/salamander
. meglm y wsm##wsf || _all: R.male || female:, family(bernoulli) link(probit)
note: crossed random-effects model specified; option intmethod(laplace)
      implied.
Fitting fixed-effects model:
Iteration 0:  Log likelihood = -223.01026
Iteration 1:  Log likelihood = -222.78736
Iteration 2:  Log likelihood = -222.78735
Refining starting values:
Grid node 0:  Log likelihood = -216.49485
Fitting full model:
Iteration 0:  Log likelihood = -216.49485  (not concave)
Iteration 1:  Log likelihood = -214.34477
Iteration 2:  Log likelihood = -209.96986
Iteration 3:  Log likelihood =  -208.2673
Iteration 4:  Log likelihood = -208.11936
Iteration 5:  Log likelihood =   -208.119  (not concave)
Iteration 6:  Log likelihood = -208.11897
Iteration 7:  Log likelihood = -208.11722
Iteration 8:  Log likelihood = -208.11342
Iteration 9:  Log likelihood = -208.11183
Iteration 10: Log likelihood = -208.11182
Mixed-effects GLM                               Number of obs     =        360
Family: Bernoulli
Link:   Probit
        Grouping information
```

Group variable	No. of groups	Observations per group Minimum	Average	Maximum
_all	1	360	360.0	360
female	60	6	6.0	6

```
Integration method: laplace

                                                Wald chi2(3)      =      45.09
Log likelihood = -208.11182                     Prob > chi2       =     0.0000
```

y	Coefficient	Std. err.	z	P>|z|	[95% conf.	interval]
1.wsm	-.4122695	.2658063	-1.55	0.121	-.9332403	.1087014
1.wsf	-1.720396	.3039435	-5.66	0.000	-2.316114	-1.124677
wsm#wsf						
1 1	2.121205	.3484936	6.09	0.000	1.43817	2.80424
_cons	.5951487	.2217643	2.68	0.007	.1604986	1.029799
_all>male						
var(_cons)	.3867562	.1779527			.1569589	.9529908
female						
var(_cons)	.4464295	.1952624			.1894299	1.0521

```
LR test vs. probit model: chi2(2) = 29.35                 Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

To fit the corresponding Bayesian model, we prefix the above command with `bayes:`.

```
. set seed 15
. bayes: meglm y wsm##wsf || _all: R.male || female:, family(bernoulli)
> link(probit)
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Multilevel structure
------------------------------------------------------------------------------
male
    {U0}: random intercepts
female
    {V0}: random intercepts
------------------------------------------------------------------------------
Model summary
------------------------------------------------------------------------------
Likelihood:
  y ~ meglm(xb_y)
Priors:
  {y:1.wsm 1.wsf 1.wsm#1.wsf _cons} ~ normal(0,10000)                    (1)
                              {U0} ~ normal(0,{U0:sigma2})               (1)
                              {V0} ~ normal(0,{V0:sigma2})               (1)
Hyperpriors:
  {U0:sigma2} ~ igamma(.01,.01)
  {V0:sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_y.
```

```
Bayesian multilevel GLM                          MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000

------------------------------------------------------------------------------
 Group variable |      No. of       Observations per group
                |      groups    Minimum     Average     Maximum
----------------+-------------------------------------------------------------
           _all |           1        360       360.0         360
        female |          60          6         6.0           6
------------------------------------------------------------------------------

Family: Bernoulli                                Number of obs    =        360
Link:   probit                                   Acceptance rate  =      .3223
                                                 Efficiency:  min =    .008356
                                                              avg =     .02043
Log marginal-likelihood                                       max =     .02773

------------------------------------------------------------------------------
             |                                                      Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
y            |
       1.wsm |  -.411886     .28122   .016889  -.4158334  -.9645049    .156521
       1.wsf | -1.722195   .3329918   .023312  -1.713574  -2.381169  -1.094443
             |
     wsm#wsf |
         1 1 |  2.110366   .3671998   .022643    2.09234   1.443113   2.831923
             |
       _cons |  .5858733   .2512646   .015407   .5906893   .0812177   1.077352
-------------+----------------------------------------------------------------
male         |
   U0:sigma2 |  .4291858   .2195246   .024015   .3876708   .1347684   .9648611
-------------+----------------------------------------------------------------
female       |
   V0:sigma2 |  .4928416   .2189307   .019043   .4576824   .1648551   1.003193
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

The variance components for `male` and `female`, `{U0:sigma2}` and `{V0:sigma2}`, are slightly higher than the corresponding ML estimates, but the regression coefficients are similar.

For an example of Bayesian estimation of a crossed-effects logistic regression model, see Rabe-Hesketh and Skrondal (2022, chap. 16).

Blocked-diagonal covariance structures

The 1989 fertility survey considered in example 5 of [ME] **me** analyzes the use of contraception among Bangladeshi women. The survey contains data from 60 districts, identified by the `district` variable, and includes demographic factors such as whether the woman is from an urban area (`urban`), mean-centered age (`age`), and number of children (`children`). Here `children` is a factor variable coded as `children` = 0 (no children), `children` = 1 (one child), `children` = 2 (two children), and `children` = 3 (three or more children). The outcome variable `c_use` is a binary indicator for the use of contraception.

We consider a two-level logit model for `c_use` with a random intercept and random coefficients for indicators of having one, two, or three or more `children`. As "fixed" predictor variables, we use `urban`, `age`, and `children`.

It seems reasonable to expect positive correlation between the three random coefficients. Following example 5 in [ME] **me**, we will use the `covariance(exchangeable)` option and repeat `district:` to specify a blocked-diagonal covariance structure for the random effects.

Let's first run `bayes: melogit` with the `dryrun` option to see the model parameters.

```
. use https://www.stata-press.com/data/r18/bangladesh
(Bangladesh Fertility Survey, 1989)
. bayes, dryrun: melogit c_use i.urban age i.children ||
> district: i.children, covariance(exchangeable) ||
> district:
Multilevel structure
------------------------------------------------------------------------------
district
    {U0}: random intercepts
    {U1}: random coefficients for 1.children
    {U2}: random coefficients for 2.children
    {U3}: random coefficients for 3.children
------------------------------------------------------------------------------

Model summary
------------------------------------------------------------------------------
Likelihood:
  c_use ~ melogit(xb_c_use)
Priors:
 {c_use:1.urban age i.children _cons} ~ normal(0,10000)                    (1)
                                {U0} ~ normal(0,{U0:sigma2})               (1)
                          {U1 U2 U3} ~ mvn0exchangeable(3,{U:sigma2},{U:rho})
                                       (1)
Hyperpriors:
      {U:rho} ~ uniform(-1,1)
  {U0:sigma2} ~ igamma(.01,.01)
   {U:sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_c_use.
```

The random coefficients `{U1}`, `{U2}`, and `{U3}` are assigned a multivariate normal prior with an exchangeable covariance structure, `mvn0exchangeable()`. This prior introduces two hyperparameters: `{U:sigma2}`, for the diagonal variance term of the covariance matrix, and `{U:rho}`, for the off-diagonal correlation term such that the covariance is equal to `{U:sigma2}`×`{U:rho}`. The random intercept `{U0}` is assigned a normal prior with hyperparameter `{U0:sigma2}` for its variance. It is recommended to assign informative priors to `{U0:sigma2}`, `{U:sigma2}`, and `{U:rho}`. For example, we believe the correlation parameter to be between 0 and 0.5 and thus assign the `uniform(0, 0.5)` prior to `{U:rho}`. In addition, let's say that, from historical data, the mean variability for children random coefficients was found to be about 0.2 and the mean variability for the random intercepts was found to be about 0.25. We may then assign the `igamma(11,2)` prior to `{U:sigma2}` and the `igamma(9,2)` prior to `{U0:sigma2}` to incorporate this prior knowledge. We will also add the `or` option to obtain estimates of the odds ratios.

```
. bayes, prior({U:rho}, uniform(0,0.5)) prior({U:sigma2}, igamma(11,2))
> prior({U0:sigma2}, igamma(9,2)) rseed(17):
> melogit c_use i.urban age i.children ||
> district: i.children, covariance(exchangeable) ||
> district:, or
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........5
> 000.........6000.........7000.........8000.........9000.........10000 done
Multilevel structure
------------------------------------------------------------------------------
district
    {U0}: random intercepts
    {U1}: random coefficients for 1.children
    {U2}: random coefficients for 2.children
    {U3}: random coefficients for 3.children
```

```
Model summary
------------------------------------------------------------------------------
Likelihood:
  c_use ~ melogit(xb_c_use)

Priors:
 {c_use:1.urban age i.children _cons} ~ normal(0,10000)                  (1)
                                {U0} ~ normal(0,{U0:sigma2})             (1)
                          {U1 U2 U3} ~ mvn0exchangeable(3,{U:sigma2},{U:rho})
                                       (1)

Hyperpriors:
      {U:rho} ~ uniform(0,0.5)
   {U:sigma2} ~ igamma(11,2)
  {U0:sigma2} ~ igamma(9,2)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_c_use.

Bayesian multilevel logistic regression          MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
Group variable: district                         Number of groups =         60
                                                 Obs per group:
                                                               min =          2
                                                               avg =       32.2
                                                               max =        118
Family: Bernoulli                                Number of obs    =      1,934
Link:   logit                                    Acceptance rate  =      .2401
                                                 Efficiency:  min =    .009968
                                                               avg =     .02371
Log marginal-likelihood                                        max =     .04605
```

	Odds ratio	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
c_use						
1.urban	2.153732	.2632265	.023028	2.135123	1.710943	2.728066
age	.9734474	.0076718	.000478	.9736178	.9585345	.9887891
children						
1	3.043873	.5490154	.03425	3.00129	2.119798	4.241168
2	4.030936	.7761135	.040228	3.949568	2.77722	5.714252
3	3.85945	.724596	.047131	3.778789	2.644804	5.448504
_cons	.1850523	.0271077	.002155	.1827656	.1395885	.242633
district						
U:rho	.3236901	.1286163	.010136	.3422138	.0326351	.4943052
U0:sigma2	.2147372	.0541223	.002522	.2069007	.1315863	.3416939
U:sigma2	.1736623	.0435398	.004361	.1676818	.1039366	.2793393

```
Note: Estimates are transformed only in the first equation to odds ratios.
Note: _cons estimates baseline odds (conditional on zero random effects).
Note: Default priors are used for some model parameters.
```

The posterior odds-ratio estimates for the fixed-effects parameters are close to the estimates reported by the `melogit` command in example 5. Our model reports an estimate of 0.32 for the correlation between random coefficients, a variance of 0.17 for the random coefficients, and a variance of 0.21 for the random intercepts.

Panel-data models

The bayes prefix supports several panel-data commands such as xtreg and xtlogit; see [BAYES] **Bayesian estimation**.

Panel-data models, also known as longitudinal-data models, are used for analyzing cross-sectional time series when there is an explicit time component. Panel-data models require that the panel variable be specified using the xtset command. See [XT] **xt** for details.

Panel-data models can also be viewed as two-level random-intercept models, so many comments from *Multilevel models* apply to these models too.

All Bayesian panel-data models include random intercepts, referred to as {U[*panelvar*]} or simply {U}, with the panel variable *panelvar* used as the grouping variable. These intercepts are commonly referred to as random effects in frequentist models.

Random intercepts are assigned default prior distributions specific to the likelihood family of the model. For linear and generalized linear models, the default prior is normal with zero mean and unknown variance {var_U}. Other models have special random-effects priors, and these are described in *Methods and formulas* of the command-specific bayes entries. Positive hyperparameters such as {var_U} are assigned default inverse-gamma priors. Categorical outcome models such as [BAYES] **bayes: xtmlogit** have multiple random effects. In cases when these random effects are correlated, the model includes a matrix hyperparameter {U:Sigma,m} that is assigned a default inverse-Wishart prior.

You can specify your own priors for regression coefficients, random effects, and auxiliary model parameters. To change the default priors, you will need to know the names of the model parameters. See *Likelihood model* to learn how the bayes prefix labels the parameters. You can also use the dryrun option to see the names of model parameters specific to each bayes model before estimation. After estimation, see *Different ways of specifying model parameters* for how to refer to individual random effects to evaluate MCMC convergence or to obtain their MCMC summaries.

Bayesian panel-data models estimate random effects together with regression coefficients and other model parameters. By default, the bayes prefix does not compute or display MCMC summaries of individual random effects to conserve computation time and space. You can specify the showreffects() or show() option to compute and display them for chosen subsets of random effects.

By default, all panel-data models use Gibbs sampling for variance components. Linear panel-data models, bayes: xtreg, additionally use Gibbs sampling for regression coefficients. With bayes: xtreg, we can specify Gibbs sampling also for random effects by using the gibbs option.

Unlike other bayes commands, panel-data models support the [BAYES] **bayespredict** postestimation command to compute Bayesian predictions; see examples in [BAYES] **bayes: xtpoisson** and [BAYES] **bayes: xtmlogit**.

▷ Example 18: Random-effects linear model

In example 12, we considered a random-intercept model analyzing the weight gain of pigs. In that example, the dependent variable, weight, is regressed on variable week, and random intercepts are introduced with respect to the group variable id. Let's fit the same random-intercept model but now using bayes: xtreg. First, we should declare our data as panel data.

```
. use https://www.stata-press.com/data/r18/pig
(Longitudinal analysis of pig weights)
. xtset id
Panel variable: id (balanced)
```

We can use `bayes: xtreg` to fit the same model that we previously fit using `bayes: mixed`. Both commands use the same default priors and the same default sampling method.

```
. bayes, rseed(17): xtreg weight week
note: Gibbs sampling is used for regression coefficients and variance
      components.
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done

Model summary
------------------------------------------------------------------------------
Likelihood:
  weight ~ normal(xb_weight,{sigma2})

Priors:
  {weight:week _cons} ~ normal(0,10000)                                   (1)
              {U[id]} ~ normal(0,{var_U})                                 (1)
             {sigma2} ~ igamma(0.01,0.01)

Hyperprior:
  {var_U} ~ igamma(0.01,0.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_weight.

Bayesian RE normal regression                   MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling          Burn-in          =      2,500
                                                MCMC sample size =     10,000
Group variable: id                              Number of groups =         48
                                                Obs per group:
                                                              min =          9
                                                              avg =        9.0
                                                              max =          9
                                                Number of obs    =        432
                                                Acceptance rate  =      .8089
                                                Efficiency:  min =    .008983
                                                             avg =      .5507
Log marginal-likelihood                                      max =          1

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
weight       |
        week |  6.209598   .0391057   .000391   6.209511   6.134362    6.28693
       _cons |   19.2624   .5480876   .057828   19.23869   18.18444   20.36098
-------------+----------------------------------------------------------------
       var_U |  15.75035   3.489106   .042737   15.31299   10.28186    23.8984
      sigma2 |  4.417614   .3188951   .004392   4.401373   3.837572    5.07726
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

The results are similar to those from example 12, up to MCMC sampling variation.

To improve efficiency, all panel-data models by default use Gibbs sampling for variance components. Panel-data linear models (`bayes: xtreg`) use Gibbs sampling also for regression coefficients. With `bayes: xtreg`, we can improve sampling efficiency further by specifying the `gibbs` option to use Gibbs sampling also for random effects. Beware that, depending on the number of random effects, this may increase the computation time substantially.

```
. bayes, gibbs rseed(17): xtreg weight week
note: Gibbs sampling is used for all parameters, including random effects.
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000...... ...9000.........10000 done

Model summary
------------------------------------------------------------------------------
Likelihood:
  weight ~ normal(xb_weight,{sigma2})

Priors:
  {weight:week _cons} ~ normal(0,10000)                                   (1)
              {U[id]} ~ normal(0,{var_U})                                 (1)
             {sigma2} ~ igamma(0.01,0.01)

Hyperprior:
  {var_U} ~ igamma(0.01,0.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_weight.

Bayesian RE normal regression                 MCMC iterations  =     12,500
Gibbs sampling                                Burn-in          =      2,500
                                              MCMC sample size =     10,000
Group variable: id                            Number of groups =         48
                                              Obs per group:
                                                           min =          9
                                                           avg =        9.0
                                                           max =          9
                                              Number of obs    =        432
                                              Acceptance rate  =          1
                                              Efficiency:  min =     .01606
                                                           avg =      .6605
Log marginal-likelihood                                    max =          1
------------------------------------------------------------------------------
                                                                Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
weight       |
        week |  6.209921   .0390177    .00039   6.209939    6.132542   6.285744
       _cons |  19.26382   .6209709   .048995   19.27342     18.0418    20.5063
-------------+----------------------------------------------------------------
       var_U |  15.80222   3.488439   .038688   15.33375     10.3458   24.03719
      sigma2 |  4.412905   .3236225    .00359   4.395282    3.821423   5.095022
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

Using full Gibbs sampling, we see that our estimates of regression coefficients and variance components are similar but that the minimum efficiency is increased to 0.016 from 0.009.

▷ Example 19: Random-effects ordered logit model

Consider example 1 from [XT] **xtologit**, which analyzes data from a smoking prevention project in schools. The dependent variable, tobacco and health knowledge score `thk`, has four categories. Predictor variables include preintervention score, `prethk`, classroom curriculum, `cc`, and television intervention, `tv`, as well as the interaction of the last two. The school identifier variable `school` is set as the panel variable.

```
. use https://www.stata-press.com/data/r18/tvsfpors
(Television, School, and Family Project)

. xtset school

Panel variable: school (unbalanced)
```

The `bayes: xtologit` command is used to fit a Bayesian model. The default prior distribution for regression coefficients is normal with zero mean and variances of 10,000. The default prior distribution for random effects is normal with mean zero and variance `{var_U}`. The hyperparameter `{var_U}` is assigned an inverse-gamma hyperprior. The three cutpoints for the ordered logit likelihood, `{_cut1}`, `{_cut2}`, and `{_cut3}`, are assigned a flat prior.

```
. bayes, rseed(17): xtologit thk prethk cc##tv
note: Gibbs sampling is used for variance components.
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000..... done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  thk ~ ologit(xb_thk,{_cut1 ... _cut3})
Priors:
  {thk:prethk 1.cc 1.tv 1.cc#1.tv} ~ normal(0,10000)                      (1)
                       {U[school]} ~ normal(0,{var_U})                    (1)
                {_cut1 _cut2 _cut3} ~ 1 (flat)
Hyperprior:
  {var_U} ~ igamma(0.01,0.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_thk.
Bayesian RE ordered logistic regression          MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling           Burn-in          =      2,500
                                                 MCMC sample size =     10,000
Group variable: school                           Number of groups =         28
                                                 Obs per group:
                                                               min =         18
                                                               avg =       57.1
                                                               max =        137
                                                 Number of obs    =      1,600
                                                 Acceptance rate  =       .506
                                                 Efficiency:  min =     .00404
                                                               avg =     .01548
Log marginal-likelihood                                        max =     .03692

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
thk          |
      prethk |   .4024205     .03817   .001987   .4016996    .3289603    .480875
        1.cc |   .9329812   .2127196   .019923   .9304351    .5156044   1.367753
        1.tv |   .3037174   .2089864    .03288   .2919775   -.0874367   .7099491
             |
       cc#tv |
        1 1  |  -.4663504   .2985113    .02669  -.4502481   -1.057705   .0993408
-------------+----------------------------------------------------------------
       _cut1 |  -.0960417   .1673066   .016383  -.0987278   -.4235516   .2458889
       _cut2 |   1.151299   .1739417   .020155   1.148734    .8009236    1.49998
       _cut3 |   2.340316   .1798423   .020381   2.338304    1.994793   2.696972
       var_U |   .1089538   .0529856   .002903   .0988449    .0351552   .2362116
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
Note: There is a high autocorrelation after 500 lags.
```

The command issues a high autocorrelation warning because of slower convergence for some of the parameters. You can use `bayesstats ess` to find that `{thk:1.tv}` is the parameter that has the lowest ESS. Slower convergence of panel-data models is often caused by the presence of many random effects, which indirectly influences the convergence of regression coefficients as well.

Sometimes, the sampling efficiency can be improved by simply increasing the burn-in period, thus prolonging the adaptation phase of the sampling algorithm. In the next run, we double the default burn-in period.

```
. bayes, burnin(5000) rseed(17): xtologit thk prethk cc##tv
note: Gibbs sampling is used for variance components.
Burn-in 5000 aaaaaaaaa1000aaaaaaaaa2000.........3000.........4000.........5000
> done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  thk ~ ologit(xb_thk,{_cut1 ... _cut3})
Priors:
  {thk:prethk 1.cc 1.tv 1.cc#1.tv} ~ normal(0,10000)                      (1)
                       {U[school]} ~ normal(0,{var_U})                    (1)
             {_cut1 _cut2 _cut3} ~ 1 (flat)
Hyperprior:
  {var_U} ~ igamma(0.01,0.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_thk.
Bayesian RE ordered logistic regression          MCMC iterations  =     15,000
Metropolis-Hastings and Gibbs sampling           Burn-in          =      5,000
                                                 MCMC sample size =     10,000
Group variable: school                           Number of groups =         28
                                                 Obs per group:
                                                               min =         18
                                                               avg =       57.1
                                                               max =        137
                                                 Number of obs    =      1,600
                                                 Acceptance rate  =      .5038
                                                 Efficiency:  min =    .003954
                                                               avg =       .015
Log marginal-likelihood                                        max =      .0366
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
thk						
prethk	.4043504	.0380502	.001989	.4033533	.3325402	.4827048
1.cc	.9352501	.2010255	.018787	.9288417	.5673248	1.348453
1.tv	.3041591	.2085135	.033158	.3009742	-.117611	.7077558
cc#tv						
1 1	-.4635365	.2798612	.027015	-.4525074	-1.028432	.0712566
_cut1	-.095777	.1627607	.016387	-.0969997	-.426459	.2438933
_cut2	1.15389	.1684856	.019615	1.154469	.8296157	1.499366
_cut3	2.344848	.1762402	.021575	2.34904	1.993787	2.685564
var_U	.1064932	.0524515	.002873	.0964727	.034738	.2305971

```
Note: Default priors are used for model parameters.
```

Compared with the frequentist estimates from example 1, the posterior mean estimates of the regression coefficients and cutpoints are not that different. The most noticeable difference is for the random-effects variance `{var_U}`, which has a posterior mean of about 0.11, slightly higher than the frequentist estimate of 0.07.

We can use `bayesstats summary` to display posterior estimates for the first five random effects `{U[school]}` or simply `{U}`.

```
. bayesstats summary {U[1/5]}
Posterior summary statistics                     MCMC sample size =    10,000
```

U[school]	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
193	.0983182	.2360735	.008371	.0949512	-.3319545	.5649471
194	.0910507	.2044525	.013411	.0850659	-.3085782	.5080763
196	.1609138	.2372827	.010454	.159283	-.3000192	.6540844
197	-.0351616	.2304207	.009844	-.036144	-.5106465	.4080927
198	-.1724522	.2164482	.019579	-.1666214	-.6123599	.2548694

We could also replace the default priors with more informative ones. There are two ways to do this. First, we can simply modify the parameters of the default prior without changing the family of the distribution. For example, we can use the `normalprior(1)` option to change the prior standard deviation for regression coefficients from 100 to 1.

```
. bayes, normalprior(1) rseed(17): xtologit thk prethk cc##tv
note: Gibbs sampling is used for variance components.
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  thk ~ ologit(xb_thk,{_cut1 ... _cut3})

Priors:
  {thk:prethk 1.cc 1.tv 1.cc#1.tv} ~ normal(0,1)                          (1)
                       {U[school]} ~ normal(0,{var_U})                    (1)
              {_cut1 _cut2 _cut3} ~ 1 (flat)

Hyperprior:
  {var_U} ~ igamma(0.01,0.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_thk.
```

```
Bayesian RE ordered logistic regression          MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling           Burn-in          =      2,500
                                                 MCMC sample size =     10,000
Group variable: school                           Number of groups =         28
                                                 Obs per group:
                                                              min =         18
                                                              avg =       57.1
                                                              max =        137
                                                 Number of obs    =      1,600
                                                 Acceptance rate  =      .5083
                                                 Efficiency:  min =    .005659
                                                              avg =     .01438
Log marginal-likelihood                                       max =      .0411
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
thk						
prethk	.3972503	.0386982	.003252	.3967045	.3240223	.4752994
1.cc	.8628827	.2182787	.029018	.8597381	.4505967	1.275168
1.tv	.2691059	.1952139	.020681	.2561737	-.064717	.6803609
cc#tv						
1 1	-.3874974	.2808	.030905	-.3749463	-.954762	.1415334
_cut1	-.1274545	.1812604	.017455	-.1252054	-.4761576	.2116238
_cut2	1.117835	.1811456	.017375	1.120978	.7740603	1.467072
_cut3	2.30662	.1859104	.015007	2.312644	1.958648	2.666062
var_U	.1104883	.0550946	.002718	.100217	.0357647	.239713

```
Note: Default priors are used for some model parameters.
```

The magnitudes of the regression coefficient estimates shrink slightly toward 0. Similarly, we can use the `igammaprior()` option to manipulate the shape and scale of the default inverse-gamma prior for `{var_U}`.

Another way of changing the default priors is to specify the `prior()` options for the selected groups of model parameters. For example, we can change the prior for cutpoints from the default flat to normal with mean 1 and variance 1.

```
. bayes, prior({_cut1 _cut2 _cut3}, normal(1, 1))
> normalprior(1) rseed(17): xtologit thk prethk cc##tv
note: Gibbs sampling is used for variance components.
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  thk ~ ologit(xb_thk,{_cut1 ... _cut3})
Priors:
  {thk:prethk 1.cc 1.tv 1.cc#1.tv} ~ normal(0,1)                          (1)
                       {U[school]} ~ normal(0,{var_U})                    (1)
                {_cut1 _cut2 _cut3} ~ normal(1,1)
Hyperprior:
  {var_U} ~ igamma(0.01,0.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_thk.

Bayesian RE ordered logistic regression          MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling           Burn-in          =      2,500
                                                 MCMC sample size =     10,000
Group variable: school                           Number of groups =         28
                                                 Obs per group:
                                                               min =         18
                                                               avg =       57.1
                                                               max =        137
                                                 Number of obs    =      1,600
                                                 Acceptance rate  =      .4909
                                                 Efficiency:  min =    .005571
                                                               avg =     .01344
Log marginal-likelihood                                        max =     .04221

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
thk          |
      prethk |   .3914625   .0344846    .00462   .3902991   .3256868   .4578337
        1.cc |    .832213   .2079096   .024539   .8433861   .4080022    1.20791
        1.tv |   .1969988   .2044468   .016094   .2080927  -.2166963   .5690862
             |
       cc#tv |
        1 1  |  -.3620582   .2739768   .032021   -.377875  -.9000601   .2192883
-------------+----------------------------------------------------------------
       _cut1 |  -.1775701   .1673107   .016436  -.1657233  -.5312352   .1188874
       _cut2 |   1.063019   .1684814   .018284   1.074538   .7075167    1.37078
       _cut3 |   2.240986   .1739471   .017195   2.251752   1.881608   2.556478
       var_U |   .1058796   .0550203   .002678   .0952031   .0334108   .2404828
------------------------------------------------------------------------------
Note: Default priors are used for some model parameters.
```

Time-series and DSGE models

The bayes prefix also supports vector autoregression ([BAYES] **bayes: var**), linear DSGE models ([BAYES] **bayes: dsge**), and nonlinear DSGE models ([BAYES] **bayes: dsgenl**). See the corresponding entries for examples of these commands.

Video examples

Introduction to Bayesian statistics, part 1: The basic concepts

Introduction to Bayesian statistics, part 2: MCMC and the Metropolis–Hastings algorithm

A prefix for Bayesian regression in Stata

Bayesian linear regression using the bayes prefix

Bayesian linear regression using the bayes prefix: How to specify custom priors

Bayesian linear regression using the bayes prefix: Checking convergence of the MCMC chain

Bayesian linear regression using the bayes prefix: How to customize the MCMC chain

Stored results

In addition to the results stored by bayesmh, the bayes prefix stores the following in e():

Scalars

e(priorsigma)	standard deviation of default normal priors
e(priorshape)	shape of default inverse-gamma priors
e(priorscale)	scale of default inverse-gamma priors
e(blocksize)	maximum size for blocks of model parameters

Macros

e(prefix)	bayes
e(cmdname)	command name from *estimation_command*
e(cmd)	same as e(cmdname)
e(command)	estimation command line

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

References

Balov, N. 2017. Bayesian logistic regression with Cauchy priors using the bayes prefix. *The Stata Blog: Not Elsewhere Classified.* https://blog.stata.com/2017/09/08/bayesian-logistic-regression-with-cauchy-priors-using-the-bayes-prefix/.

——. 2020. Bayesian inference using multiple Markov chains. *The Stata Blog: Not Elsewhere Classified.* https://blog.stata.com/2020/02/24/bayesian-inference-using-multiple-markov-chains/.

Rabe-Hesketh, S., and A. Skrondal. 2022. *Multilevel and Longitudinal Modeling Using Stata.* 4th ed. College Station, TX: Stata Press.

Also see

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

[U] **20 Estimation and postestimation commands**

Title

bayesmh — Bayesian models using Metropolis–Hastings algorithm

Description

`bayesmh` fits a variety of Bayesian models using an adaptive Metropolis–Hastings (MH) algorithm. It provides various likelihood models and prior distributions for you to choose from. Likelihood models include univariate normal linear and nonlinear regressions, multivariate normal linear and nonlinear regressions, generalized linear models such as logit and Poisson regressions, multiple-equations linear and nonlinear models, multilevel models, and more. Prior distributions include continuous distributions such as uniform, Jeffreys, normal, gamma, multivariate normal, and Wishart and discrete distributions such as Bernoulli and Poisson. You can also program your own Bayesian models; see [BAYES] **bayesmh evaluators**.

Also see [BAYES] **Bayesian estimation** for a list of Bayesian regression models that can be fit more conveniently with the `bayes` prefix ([BAYES] **bayes**).

Quick start

Bayesian normal linear regression of `y1` on `x1` with flat priors for coefficient on `x1` and the intercept and with a Jeffreys prior on the variance parameter `{var}`

```
bayesmh y1 x1, likelihood(normal({var}))  ///
     prior({y1: x1 _cons}, flat) prior({var}, jeffreys)
```

Add binary variable `a` using factor-variable notation

```
bayesmh y1 x1 i.a, likelihood(normal({var}))  ///
     prior({y1: x1 i.a _cons}, flat) prior({var}, jeffreys)
```

Same as above

```
bayesmh y1 x1 i.a, likelihood(normal({var}))  ///
     prior({y1:}, flat) prior({var}, jeffreys)
```

Specify a different prior for `a` = 1

```
bayesmh y1 x1 i.a, likelihood(normal({var}))                        ///
     prior({y1:x1  _cons}, flat) prior({y1: 1.a}, normal(0,100))  ///
     prior({var}, jeffreys)
```

Specify a starting value of 1 for parameter `{var}`

```
bayesmh y1 x1 i.a, likelihood(normal({var}))  ///
     prior({y1:}, flat) prior({var}, jeffreys) initial({var} 1)
```

Same as above

```
bayesmh y1 x1 i.a, likelihood(normal({var=1}))  ///
     prior({y1:}, flat) prior({var}, jeffreys)
```

A normal prior with $\mu = 2$ and $\sigma^2 = 0.5$ for the coefficient on x1, a normal prior with $\mu = -40$ and $\sigma^2 = 100$ for the intercept, and an inverse-gamma prior with shape parameter of 0.1 and scale parameter of 1 for {var}

```
bayesmh y1 x1, likelihood(normal({var})) ///
     prior({y1:x1}, normal(2,.5))        ///
     prior({y1:_cons}, normal(-40,100))  ///
     prior({var}, igamma(0.1,1))
```

Place {var} into a separate block

```
bayesmh y1 x1, likelihood(normal({var}))  ///
     prior({y1:x1}, normal(2,.5))         ///
     prior({y1:_cons}, normal(-40,100))   ///
     prior({var}, igamma(0.1,1)) block({var})
```

Same as above, but simulate four chains

```
bayesmh y1 x1, likelihood(normal({var}))  ///
     prior({y1:x1}, normal(2,.5))         ///
     prior({y1:_cons}, normal(-40,100))   ///
     prior({var}, igamma(0.1,1)) block({var}) ///
     nchains(4)
```

Zellner's g prior to allow {y1:x1} and {y1:_cons} to be correlated, specifying 2 dimensions, df $= 30$, $\mu = 2$ for {y1:x1}, $\mu = -40$ for {y1:_cons}, and variance parameter {var}

```
bayesmh y1 x1, likelihood(normal({var}))  ///
     prior({var}, igamma(0.1,1))          ///
     prior({y1:}, zellnersg(2,30,2,-40,{var}))
```

Model for dichotomous dependent variable y2 regressed on x1 with a logit likelihood

```
bayesmh y2 x1, likelihood(logit) prior({y2:}, normal(0,100))
```

Same as above, and save model results to simdata.dta, and store estimates in memory as m1

```
bayesmh y2 x1, likelihood(logit) prior({y2:},  ///
     normal(0,100)) saving(simdata.dta)
estimates store m1
```

Same as above, but save the results on replay

```
bayesmh y2 x1, likelihood(logit) prior({y2:}, normal(0,100))
bayesmh, saving(simdata.dta)
estimates store m1
```

Show model summary without performing estimation

```
bayesmh y2 x1, likelihood(logit) prior({y2:}, normal(0,100)) dryrun
```

Fit model without showing model summary

```
bayesmh y2 x1, likelihood(logit) prior({y2:}, normal(0,100))  ///
     nomodelsummary
```

Same as above, and specify the random-number seed for reproducibility

```
bayesmh y2 x1, likelihood(logit) prior({y2:}, normal(0,100))  ///
     rseed(1234)
```

Same as above (set seed method useful only for a single chain)

```
set seed 1234
bayesmh y2 x1, likelihood(logit) prior({y2:}, normal(0,100))
```

Specify 20,000 MCMC samples, and set length of the burn-in period to 5,000

```
bayesmh y2 x1, likelihood(logit) prior({y2:}, normal(0,100))  ///
     mcmcsize(20000) burnin(5000)
```

Specify that only observations $1 + 5k$, for $k = 0, 1, \ldots$, be saved to the MCMC sample

```
bayesmh y2 x1, likelihood(logit) prior({y2:}, normal(0,100))  ///
     thinning(5)
```

Set the maximum number of adaptive iterations of the MCMC procedure to 30, and specify that adaptation of the MCMC procedure be attempted every 25 iterations

```
bayesmh y2 x1, likelihood(logit) prior({y2:}, normal(0,100))  ///
     adaptation(maxiter(30) every(25))
```

Request that a dot be displayed every 100 simulations

```
bayesmh y2 x1, likelihood(logit) prior({y2:}, normal(0,100))  ///
     dots(100)
```

Also request that an iteration number be displayed every 1,000 iterations

```
bayesmh y2 x1, likelihood(logit) prior({y2:}, normal(0,100))  ///
     dots(100, every(1000))
```

Same as above

```
bayesmh y2 x1, likelihood(logit) prior({y2:}, normal(0,100))  ///
     dots
```

Request that the 90% equal-tailed credible interval be displayed

```
bayesmh y2 x1, likelihood(logit) prior({y2:}, normal(0,100))  ///
     clevel(90)
```

Request that the default 95% highest posterior density credible interval be displayed

```
bayesmh y2 x1, likelihood(logit) prior({y2:}, normal(0,100)) hpd
```

Use the batch-means estimator of MCSE with the length of the block of 5

```
bayesmh y2 x1, likelihood(logit) prior({y2:}, normal(0,100))  ///
     batch(5)
```

Multivariate normal regression of `y1` and `y3` on `x1` and `x2`, using normal priors with $\mu = 0$ and $\sigma^2 = 100$ for the regression coefficients and intercepts, an inverse-Wishart prior for the covariance matrix parameter `{S, matrix}` of dimension 2, df = 100, and an identity scale matrix

```
bayesmh y1 y3 = x1 x2, likelihood(mvnormal({S, matrix}))  ///
     prior({y1:} {y3:}, normal(0,100))                    ///
     prior({S, matrix}, iwishart(2,100,I(2)))
```

Same as above, but use abbreviated declaration for the covariance matrix

```
bayesmh y1 y3 = x1 x2, likelihood(mvnormal({S,m}))  ///
     prior({y1:} {y3:}, normal(0,100))              ///
     prior({S,m}, iwishart(2,100,I(2)))
```

Same as above, and specify starting values for matrix `{S,m}` using previously defined matrix `W`

```
bayesmh y1 y3 = x1 x2, likelihood(mvnormal({S,m}))  ///
     prior({y1:} {y3:}, normal(0,100))              ///
     prior({S,m}, iwishart(2,100,I(2))) initial({S,m} W)
```

Multivariate normal regression with outcome-specific regressors

```
bayesmh (y1 x1 x2) (y3 x1 x3), likelihood(mvnormal({S,m}))  ///
    prior({y1:} {y3:}, normal(0,100))                      ///
    prior({S,m}, iwishart(2,100,I(2)))
```

Linear multiple-equations model of y1 on x1 and of y3 on y1, x1, and x2 with separate variance parameters for each equation

```
bayesmh (y1 x1, likelihood(normal({var1})))      ///
     (y3 y1 x1 x2, likelihood(normal({var2}))),  ///
     prior({y1:} {y3:}, flat)                    ///
     prior({var1}, jeffreys) prior({var2}, jeffreys)
```

Nonlinear model with parameters {a}, {b}, {c}, and {var} specified using a substitutable expression

```
bayesmh y1 = ({a}+{b}*x1^{c}), likelihood(normal({var}))  ///
    prior({a b}, normal(0,100)) prior({c}, normal(0,2))   ///
    prior({var}, igamma(0.1,1))
```

Multivariate nonlinear model with distinct parameters in each equation

```
bayesmh (y1 = ({a1} + {b1}*x1^{c1}))                          ///
    (y3 = ({a2} + {b2}*x1^{c2})), likelihood(mvnormal({S,m}))  ///
    prior({a1 a2 b1 b2}, normal(0,100))                       ///
    prior({c1 c2}, normal(0,2)) prior({S,m}, iwishart(2,100,I(2)))
```

Random-intercept logistic regression of y1 on x1 with random intercepts U by level variable gr, with default zero-mean normal prior with variance parameter {var_U} for the random-intercept parameters {U[gr]}, and with Jeffreys prior for {var_U}

```
bayesmh y1 x1 U[gr], likelihood(logit) ///
     prior({y1: x1 _cons}, flat) prior({var_U}, jeffreys)
```

Menu

Statistics > Bayesian analysis > General estimation and regression

Syntax

Linear models

Univariate linear regression

```
bayesmh depvar [indepvarspec] [if] [in] [weight],
        likelihood(modelspec) prior(priorspec) [options]
```

Multivariate normal linear regression with common regressors

```
bayesmh depvars = [indepvarspec] [if] [in] [weight],
        likelihood(mvnormal(...)) prior(priorspec) [options]
```

Multivariate normal regression with outcome-specific regressors

```
bayesmh ([eqname1:]depvar1 [indepvarspec1])
        ([eqname2:]depvar2 [indepvarspec2]) [...] [if] [in] [weight],
        likelihood(mvnormal(...)) prior(priorspec) [options]
```

Nonlinear models

Univariate nonlinear regression

```
bayesmh nleqspec [if] [in] [weight],
        likelihood(modelspec) prior(priorspec) [options]
```

Multivariate normal nonlinear regression

```
bayesmh (nleqspec1) (nleqspec2) [...] [if] [in] [weight],
        likelihood(mvnormal(...)) prior(priorspec) [options]
```

Multilevel models

Any model can be fit as a multilevel model by including at least one random-effects term *respec*, such as random intercepts `U[id]` at the level variable `id`, in *indepvarspec*, *indepvarspec#*, *nlspec*, or *nlspec#*; see Random effects.

Multiple-equation models

```
bayesmh (eqspec) [(eqspec)] [...] [if] [in] [weight], prior(priorspec) [options]
```

Probability distributions

Univariate distributions

```
bayesmh depvar [if] [in] [weight],
        likelihood(distribution) prior(priorspec) [options]
```

Multiple-equation distribution specifications

```
bayesmh (deqspec) [(deqspec)] [...] [if] [in] [weight],
        prior(priorspec) [options]
```

indepvarspec is either *indepvars* or *respec*.

respec includes an optional list of independent variables *indepvars* and at least one of random-effects terms such as random intercepts `U[id]` at the level variable `id`. For instance, *respec* can be `x1 x2 U[id]`; see *Random effects*.

The syntax of *nleqspec* is *depvar* `=` `(`*subexprspec*`)`, where *subexprspec* is either *subexpr* or *resubexpr*.

subexpr is a substitutable expression; see *Substitutable expressions* for details.

resubexpr is a substitutable expression that contains model parameters and random effects specified in braces, `{}`, as in `exp({b}+{U[id]})`; see *Random effects* for details.

The syntax of *eqspec* is one of the following:

for linear models

varspec [*if*] [*in*] [*weight*], likelihood(*modelspec*) [noconstant]

for nonlinear models

nlspec [*if*] [*in*] [*weight*], likelihood(*modelspec*)

The syntax of *varspec* is one of the following:

for single outcome

[*eqname*:] *depvar* [*indepvarspec*]

for multiple outcomes with common regressors

depvars `=` [*indepvarspec*]

for multiple outcomes with outcome-specific regressors

`(`[*eqname1*:] *depvar1* [*indepvarspec1*]`)`
`(`[*eqname2*:] *depvar2* [*indepvarspec2*]`)` [...]

The syntax of *nlspec* is *nleqspec* for a single outcome or `(`*nleqspec1*`)` `(`*nleqspec2*`)` [...] for multiple outcomes.

The syntax of *deqspec* is

[*eqname*:] *depvar* [*if*] [*in*] [*weight*], likelihood(*distribution*)

The syntax of *modelspec* is

model [, *modelopts*]

model	Description
Model	
normal(*var*)	normal regression with variance *var*
t(*sigma2*, *df*)	*t* regression with squared scale *sigma2* and degrees of freedom *df*
lognormal(*var*)	lognormal regression with variance *var*
lnormal(*var*)	synonym for lognormal()
exponential	exponential regression
mvnormal(*Sigma*)	multivariate normal regression with covariance matrix *Sigma*
probit	probit regression
logit	logistic regression
logistic	logistic regression; synonym for logit
binomial(*n*)	binomial regression with logit link and number of trials *n*
binlogit(*n*)	synonym for binomial()
oprobit	ordered probit regression
ologit	ordered logistic regression
poisson	Poisson regression
stexponential	exponential survival regression
stgamma(*lns*)	gamma survival regression with log-scale parameter *lns*
stloglogistic(*lns*)	loglogistic survival regression with log-scale parameter *lns*
stlognormal(*lnstd*)	lognormal survival regression with log-standard-deviation parameter *lnstd*
stweibull(*lnp*)	Weibull survival regression with log-shape parameter *lnp*
llf(*subexpr*)	substitutable expression for observation-level log-likelihood function

A distribution argument is a number for scalar arguments such as *var*; a variable name, *varname* (except for matrix arguments); a matrix for matrix arguments such as *Sigma*; a model parameter, *paramspec*; an expression, *expr*; or a substitutable expression, *subexpr* or *resubexpr*. See *Specifying arguments of likelihood models and prior distributions*. For survival models, st*model*, a distribution argument can be only a scalar argument.

modelopts	Description
Model	
offset(*varname*$_o$)	include *varname*$_o$ in model with coefficient constrained to 1; not allowed with normal() and mvnormal()
exposure(*varname*$_e$)	include ln(*varname*$_e$) in model with coefficient constrained to 1; allowed only with poisson
survivalopts	options for survival models

survivalopts are allowed only with survival models stexponential, stgamma(), stloglogistic(), stlognormal(), and stweibull().

survivalopts	Description
Model	
[no]logparam	fit survival model using a scale, variance, or shape parameter in a log (the default) or original metric
ph	proportional hazards parameterization; default with survival models stexponential and stweibull()
aft	accelerated failure-time parameterization; default with survival models other than stexponential and stweibull()
time	synonym for aft
failure(*varname*)	indicator for failure event
ltruncated(*varname*|#)	lower limit for left-truncation

ph is allowed only with survival models stexponential and stweibull().

distribution	Description
Model	
dexponential(*beta*)	exponential distribution with scale parameter *beta*
dbernoulli(*p*)	Bernoulli distribution with success probability *p*
dbinomial(*p*,*n*)	binomial distribution with success probability *p* and number of trials *n*
dpoisson(*mu*)	Poisson distribution with mean *mu*

A distribution argument is a model parameter, *paramspec*, or a substitutable expression, *subexpr* or *resubexpr*, containing model parameters. An *n* argument may be a number; an expression, *expr*; or a variable name, *varname*. See *Specifying arguments of likelihood models and prior distributions*.

The syntax of *priorspec* is

paramref, *priordist* [split]

where the simplest specification of *paramref* is

paramspec [*paramspec* [...]]

Also see *Referring to model parameters* for other specifications. When *paramref* includes multiple model parameters, the prior suboption split is a convenience option for specifying the same prior distribution for multiple parameters but sampling them in separate blocks. Using the split option is equivalent to specifying a separate prior statement for each parameter.

The syntax of *paramspec* is

{ [*eqname*:]*param*[, matrix] }

where the parameter label *eqname* and parameter name *param* are valid Stata names. Model parameters are either scalars such as {var}, {mean}, and {shape:alpha} or matrices such as {Sigma, matrix} and {Scale:V, matrix}. For scalar parameters, you can use {*param*=#} to specify an initial value. For example, you can specify {var=1}, {mean=1.267}, or {shape:alpha=3}. *param* can also be a random-effects name; see *Random effects* for details.

priordist	Description
Model	
normal(*mu*,*var*)	normal with mean *mu* and variance *var*
t(*mu*,*sigma2*,*df*)	location–scale t with mean *mu*, squared scale *sigma2*, and degrees of freedom *df*
lognormal(*mu*,*var*)	lognormal with mean *mu* and variance *var*
lnormal(*mu*,*var*)	synonym for lognormal()
uniform(*a*,*b*)	uniform on (*a*, *b*)
gamma(*alpha*,*beta*)	gamma with shape *alpha* and scale *beta*
igamma(*alpha*,*beta*)	inverse gamma with shape *alpha* and scale *beta*
exponential(*beta*)	exponential with scale *beta*
beta(*a*,*b*)	beta with shape parameters *a* and *b*
laplace(*mu*,*beta*)	Laplace with mean *mu* and scale *beta*
cauchy(*loc*,*beta*)	Cauchy with location *loc* and scale *beta*
chi2(*df*)	central χ^2 with degrees of freedom *df*
pareto(*alpha*,*beta*)	Pareto with shape *alpha* and scale *beta*
jeffreys	Jeffreys prior for variance of a normal distribution
mvnormal(*d*,*mean*,*Sigma*)	multivariate normal of dimension *d* with mean vector *mean* and covariance matrix *Sigma*; *mean* can be a matrix name or a list of *d* means separated by comma: mu_1, mu_2, ..., mu_d
mvnormal0(*d*,*Sigma*)	multivariate normal of dimension *d* with zero mean vector and covariance matrix *Sigma*
mvn0(*d*,*Sigma*)	synonym for mvnormal0()
mvnexchangeable(*d*,*mean*,*var*,*rho*)	multivariate normal of dimension *d* with means *mean* and exchangeable covariance matrix with diagonal *var* and off-diagonal *var*×*rho*
mvn0exchangeable(*d*,*var*,*rho*)	as mvnexchangeable() but with zero mean vector
mvnindependent(*d*,*mean*,*vars*)	multivariate normal of dimension *d* with means *mean* and diagonal covariance matrix; *vars* can be a Stata vector of dimension *d* with fixed variances or a list of *d* variances (parameters or fixed values) separated by comma: var_1, var_2, ..., var_d
mvn0independent(*d*,*vars*)	as mvnindependent() but with zero mean vector
mvnidentity(*d*,*mean*,*var*)	multivariate normal of dimension *d* with means *mean* and identity covariance matrix with equal variances *var*
mvn0identity(*d*,*var*)	as mvnidentity() but with zero mean vector
mvnscaled(*d*,*mean*,*A*,{*var*})	multivariate normal of dimension *d* with mean vector *mean* and covariance matrix ({*var*}*A*); *mean* can be a matrix name or a list of *d* means separated by a comma: mu_1, mu_2, ..., mu_d; *A* is a positive-definite scale matrix; {*var*} is a variance parameter
mvn0scaled(*d*,*A*,{*var*})	as mvnscaled() but with zero mean vector

`zellnersg(`*d*`,`*g*`,`*mean*`,{`*var*`})`	Zellner's *g*-prior of dimension *d* with *g* degrees of freedom, mean vector *mean*, and variance parameter {*var*}; *mean* can be a matrix name or a list of *d* means separated by comma: mu_1, mu_2, ..., mu_d
`zellnersg0(`*d*`,`*g*`,{`*var*`})`	Zellner's *g*-prior of dimension *d* with *g* degrees of freedom, zero mean vector, and variance parameter {*var*}
`dirichlet(`a_1`,`a_2`,...,`a_d`)`	Dirichlet (multivariate beta) of dimension *d* with shape parameters a_1, a_2, ..., a_d
`wishart(`*d*`,`*df*`,`*V*`)`	Wishart of dimension *d* with degrees of freedom *df* and scale matrix *V*
`iwishart(`*d*`,`*df*`,`*V*`)`	inverse Wishart of dimension *d* with degrees of freedom *df* and scale matrix *V*
`jeffreys(`*d*`)`	Jeffreys prior for covariance of a multivariate normal distribution of dimension *d*
`bernoulli(`*p*`)`	Bernoulli with success probability *p*
`geometric(`*p*`)`	geometric for the number of failures before the first success with success probability on one trial *p*
`index(`p_1`,...,`p_k`)`	discrete indices 1, 2, ..., *k* with probabilities p_1, p_2, ..., p_k
`poisson(`*mu*`)`	Poisson with mean *mu*
`flat`	flat prior; equivalent to `density(1)` or `logdensity(0)`
`density(`*f*`)`	generic density *f*
`logdensity(`*logf*`)`	generic log density *logf*

Dimension *d* is a positive number #.

A distribution argument is a number for scalar arguments such as *var*, *alpha*, *beta*; a Stata matrix for matrix arguments such as *Sigma* and *V*; a model parameter, *paramspec*; an expression, *expr*; or a substitutable expression, *subexpr* or *resubexpr*. See *Specifying arguments of likelihood models and prior distributions*.

f is a nonnegative number, #; an expression, *expr*; or a substitutable expression, *subexpr* or *resubexpr*.

logf is a number, #; an expression, *expr*; or a substitutable expression, *subexpr* or *resubexpr*.

When `mvnormal()` or `mvnormal0()` of dimension *d* is applied to *paramref* with *n* parameters ($n \neq d$), *paramref* is reshaped into a matrix with *d* columns, and its rows are treated as independent samples from the specified `mvnormal()` distribution. If such reshaping is not possible, an error is issued. See example 25 for application of this feature.

options	Description
Model	
noconstant	suppress constant term; not allowed with ordered models, nonlinear models, and probability distributions
*likelihood(*lspec*)	distribution for the likelihood model
*prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Model 2	
define(*label*:*resubexpr*)	defines a function of model parameters; this option may be repeated
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
Initialization	
initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation

Adaptation

`adaptation(`*adaptopts*`)`	control the adaptive MCMC procedure
`scale(#)`	initial multiplier for scale factor; default is `scale(2.38)`
`covariance(`*cov*`)`	initial proposal covariance; default is the identity matrix

Reporting

`clevel(#)`	set credible interval level; default is `clevel(95)`
`hpd`	display HPD credible intervals instead of the default equal-tailed credible intervals
`eform[ (`*string*`) ]`	report exponentiated coefficients and, optionally, label as *string*
`remargl`	compute log marginal-likelihood for multilevel models
`batch(#)`	specify length of block for batch-means calculations; default is `batch(0)`
`saving(`*filename*`[ , replace ])`	save simulation results to *filename*`.dta`
`nomodelsummary`	suppress model summary
`noexpression`	suppress output of expressions from model summary
`chainsdetail`	display detailed simulation summary for each chain
`[no]dots`	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is `nodots`
`dots(#[ , every(#) ])`	display dots as simulation is performed
`[no]show(`*paramref*`)`	specify model parameters to be excluded from or included in the output
`showreffects[ (`*reref*`) ]`	specify that all or a subset of random-effects parameters be included in the output
`notable`	suppress estimation table
`noheader`	suppress output header
`title(`*string*`)`	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

`search(`*search_options*`)`	control the search for feasible initial values
`corrlag(#)`	specify maximum autocorrelation lag; default varies
`corrtol(#)`	specify autocorrelation tolerance; default is `corrtol(0.01)`

*Options `likelihood()` and `prior()` are required. `prior()` must be specified for all model parameters.

Options `prior()` and `block()` may be repeated.

indepvars and *paramref* may contain factor variables; see **[U] 11.4.3 Factor variables**.

indepvars and *paramref* may contain time-series operators; see **[U] 11.4.4 Time-series varlists**.

With multiple-equations specifications, a local *if* specified within an equation is applied together with the global *if* specified with the command.

`collect` is allowed; see **[U] 11.1.10 Prefix commands**.

Only `fweights` are allowed; see **[U] 11.1.6 weight**.

With multiple-equations specifications, local weights (weights specified within an equation) override global weights (weights specified with the command).

See **[U] 20 Estimation and postestimation commands** for more capabilities of estimation commands.

blockopts	Description
`gibbs`	requests Gibbs sampling; available for selected models only and not allowed with `scale()`, `covariance()`, or `adaptation()`
`split`	requests that all parameters in a block be treated as separate blocks
`reffects`	requests that all parameters in a block be treated as random-effects parameters
`scale(#)`	initial multiplier for scale factor for current block; default is `scale(2.38)`; not allowed with `gibbs`
`covariance(`*cov*`)`	initial proposal covariance for the current block; default is the identity matrix; not allowed with `gibbs`
`adaptation(`*adaptopts*`)`	control the adaptive MCMC procedure of the current block; not allowed with `gibbs`

Only `tarate()` and `tolerance()` may be specified in the `adaptation()` option.

adaptopts	Description
`every(#)`	adaptation interval; default is `every(100)`
`maxiter(#)`	maximum number of adaptation loops; default is `maxiter(25)` or $\max\{25, $ `floor(burnin()/every())` $\}$ whenever default values of these options are modified
`miniter(#)`	minimum number of adaptation loops; default is `miniter(5)`
`alpha(#)`	parameter controlling acceptance rate (AR); default is `alpha(0.75)`
`beta(#)`	parameter controlling proposal covariance; default is `beta(0.8)`
`gamma(#)`	parameter controlling adaptation rate; default is `gamma(0)`
* `tarate(#)`	target acceptance rate (TAR); default is parameter specific
* `tolerance(#)`	tolerance for AR; default is `tolerance(0.01)`

*Only starred options may be specified in the `adaptation()` option specified within `block()`.

Options

Model

`noconstant` suppresses the constant term (intercept) from the regression model. By default, `bayesmh` automatically includes a model parameter {*depname*`:_cons`} in all regression models except ordered and nonlinear models. Excluding the constant term may be desirable when there is a factor variable, the base level of which absorbs the constant term in the linear combination.

`likelihood(`*lspec*`)` specifies the distribution of the data. This option specifies the likelihood portion of the Bayesian model. This option is required. *lspec* is one of *modelspec* or *distribution*.

modelspec specifies one of the supported likelihood distributions for regression models. A location parameter of these distributions is automatically parameterized as a linear combination of the specified independent variables and needs not be specified. Other parameters may be specified as arguments to the distribution separated by commas. Each argument may be a real number (#), a variable name (except for matrix parameters), a predefined matrix, a model parameter specified in {}, a Stata expression, or a substitutable expression containing model parameters and, optionally, random effects; see *Declaring model parameters* and *Specifying arguments of likelihood models and prior distributions*. For survival models, a distribution argument may be only a real number or a model parameter.

distribution specifies one of the supported distributions for modeling the dependent variable. A distribution argument must be a model parameter specified in {} or a substitutable expression containing model parameters and, optionally, random effects; see *Declaring model parameters* and *Specifying arguments of likelihood models and prior distributions*. A number of trials, *n*, of the binomial distribution may be a real number (#), a Stata expression, or a variable name. For an example of modeling outcome distributions directly, see *Beta-binomial model*.

For some regression models, option `likelihood()` provides suboptions *subopts* in `likelihood(..., subopts)`. *subopts* are `offset()`, `exposure()`, and, for survival models, *survivalopts*.

`offset(`*varname*$_o$`)` specifies that *varname*$_o$ be included in the regression model with the coefficient constrained to be 1. This option is available with `probit`, `logit`, `binomial()`, `binlogit()`, `oprobit`, `ologit`, and `poisson`.

`exposure(`*varname*$_e$`)` specifies a variable that reflects the amount of exposure over which the *depvar* events were observed for each observation; ln(*varname*$_e$) with coefficient constrained to be 1 is entered into the log-link function. This option is available with `poisson`.

survivalopts are `logparam`, `nologparam`, `ph`, `aft`, `time` (synonym for `aft`), `failure(`*varname*`)`, and `ltruncated(`*varname*`|`#`)`.

`logparam` and `nologparam` specify the estimation metric for the auxiliary model parameter. `logparam` specifies that the survival model be fit using the log of the parameter controlling the shape of the distribution—scale for `stgamma()` and `stloglogistic()`, standard deviation for `stlognormal()`, and shape for `stweibull()`. This is the default. `nologparam` specifies that the model be fit using the parameter in the original metric. Which metric to use may depend on the desired prior distribution for the auxiliary parameter.

`ph`, `aft`, `failure()`, `ltruncated()`; see *survival* options in [SEM] **gsem family-and-link options**.

`prior(`*priorspec*`)` specifies a prior distribution for model parameters. This option is required and may be repeated. A prior must be specified for each model parameter. Model parameters may be scalars or matrices, but both types may not be combined in one prior statement. If multiple scalar parameters are assigned a single univariate prior, they are considered independent, and the specified prior is used for each parameter. You may assign a multivariate prior of dimension *d* to *d* scalar parameters. Also see *Referring to model parameters* and *Specifying arguments of likelihood models and prior distributions*.

All `likelihood()` and `prior()` combinations are allowed, but they are not guaranteed to correspond to proper posterior distributions. You need to think carefully about the model you are building and evaluate its convergence thoroughly; see *Convergence of MCMC*.

`dryrun` specifies to show the summary of the model that would be fit without actually fitting the model. This option is recommended for checking specifications of the model before fitting the model. The model summary reports the information about the likelihood model and about priors for all model parameters.

Model 2

`define(`*name*`:`*resubexpr*`)` is for use with nonlinear models. It defines a function of model parameters, *resubexpr*, and labels it as *name*. This option can be repeated to define multiple functions. The `define()` option is useful for expressions that appear multiple times in the main nonlinear specification: you define the expression once and then simply refer to it by using {*name*`:`} in the nonlinear specification. This option can also be used for notational convenience. See *Random effects* for how to specify *resubexpr*.

Simulation

`nchains(#)` specifies the number of Markov chains to simulate. You must specify at least two chains. By default, only one chain is produced. Simulating multiple chains is useful for convergence diagnostics and to improve precision of parameter estimates. Four chains are often recommended in the literature, but you can specify more or less depending on your objective. The reported estimation results are based on all chains. You can use `bayesstats summary` with option `sepchains` to see the results for each chain. The reported acceptance rate, efficiencies, and log marginal-likelihood are averaged over all chains. You can use option `chainsdetail` to see these simulation summaries for each chain. Also see *Convergence diagnostics using multiple chains* and *Gelman–Rubin convergence diagnostic* in [BAYES] **bayesstats grubin**.

`mcmcsize(#)` specifies the target MCMC sample size. The default MCMC sample size is `mcmcsize(10000)`. The total number of iterations for the MH algorithm equals the sum of the burn-in iterations and the MCMC sample size in the absence of thinning. If thinning is present, the total number of MCMC iterations is computed as $\texttt{burnin()} + (\texttt{mcmcsize()} - 1) \times \texttt{thinning()} + 1$. Computation time of the MH algorithm is proportional to the total number of iterations. The MCMC sample size determines the precision of posterior summaries, which may be different for different model parameters and will depend on the efficiency of the Markov chain. With multiple chains, `mcmcsize()` applies to each chain. Also see *Burn-in period and MCMC sample size*.

`burnin(#)` specifies the number of iterations for the burn-in period of MCMC. The values of parameters simulated during burn-in are used for adaptation purposes only and are not used for estimation. The default is `burnin(2500)`. Typically, burn-in is chosen to be as long as or longer than the adaptation period. With multiple chains, `burnin()` applies to each chain. Also see *Burn-in period and MCMC sample size* and *Convergence of MCMC*.

`thinning(#)` specifies the thinning interval. Only simulated values from every $(1 + k \times \#)$th iteration for $k = 0, 1, 2, \ldots$ are saved in the final MCMC sample; all other simulated values are discarded. The default is `thinning(1)`; that is, all simulation values are saved. Thinning greater than one is typically used for decreasing the autocorrelation of the simulated MCMC sample. With multiple chains, `thinning()` applies to each chain.

`rseed(#)` sets the random-number seed. This option can be used to reproduce results. With one chain, `rseed(#)` is equivalent to typing `set seed #` prior to calling `bayesmh`; see [R] **set seed**. With multiple chains, you should use `rseed()` for reproducibility; see *Reproducing results*.

`exclude(`*paramref*`)` specifies which model parameters should be excluded from the final MCMC sample. These model parameters will not appear in the estimation table, and postestimation features for these parameters and log marginal-likelihood will not be available. This option is useful for suppressing nuisance model parameters. For example, if you have a factor predictor variable with many levels but you are only interested in the variability of the coefficients associated with its levels, not their actual values, then you may wish to exclude this factor variable from the simulation results. If you simply want to omit some model parameters from the output, see the `noshow()` option. *paramref* can include individual random-effects parameters.

Blocking

`block(`*paramref*`[ , `*blockopts*`])` specifies a group of model parameters for the blocked MH algorithm. By default, all parameters except matrices are treated as one block, and each matrix parameter is viewed as a separate block. You can use the `block()` option to separate scalar parameters in multiple blocks. Technically, you can also use `block()` to combine matrix parameters in one block, but this is not recommended. The `block()` option may be repeated to define multiple blocks. Different types of model parameters, such as scalars and matrices, may not be specified in one `block()`. Parameters within one block are updated simultaneously, and each block of parameters is updated in the order it is specified; the first specified block is updated first, the second is updated second, and so on. See *Improving efficiency of the MH algorithm—blocking of parameters*.

blockopts include `gibbs`, `split`, `reffects`, `scale()`, `covariance()`, and `adaptation()`.

`gibbs` specifies to use Gibbs sampling to update parameters in the block. This option is allowed only for specific combinations of likelihood models and prior distributions; see *Gibbs sampling for some likelihood-prior and prior-hyperprior configurations*. For more information, see *Gibbs and hybrid MH sampling*. In the presence of multiple random effects, you may combine options `gibbs` and `split` to perform Gibbs sampling separately for each set of random-effects parameters. `gibbs` may not be combined with `reffects`, `scale()`, `covariance()`, or `adaptation()`.

`split` specifies that all parameters in a block are treated as separate blocks. This may be useful for levels of factor variables. Option `split` is convenient in combination with option `gibbs` with multiple random effects to perform Gibbs sampling separately for each set of random-effects parameters.

`reffects` specifies that the parameters associated with the levels of a factor variable included in the likelihood specification be treated as random-effects parameters. Random-effects parameters must be included in one prior statement and are assumed to be conditionally independent across levels of a grouping variable given all other model parameters. `reffects` requires that parameters be specified as {*depvar*`:i.`*varname*}, where `i.`*varname* is the corresponding factor variable in the likelihood specification, and may not be combined with `block()`'s suboptions `gibbs` and `split`. This option was useful for fitting hierarchical or multilevel models in previous versions and is now provided for historical reasons. See *Random effects* for how to fit multilevel models.

`scale(#)` specifies an initial multiplier for the scale factor corresponding to the specified block. The initial scale factor is computed as $\#/\sqrt{n_p}$ for continuous parameters and as $\#/n_p$ for discrete parameters, where n_p is the number of parameters in the block. The default is `scale(2.38)`. If specified, this option overrides the respective setting from the `scale()` option specified with the command. `scale()` may not be combined with `gibbs`.

`covariance(`*matname*`)` specifies a scale matrix *matname* to be used to compute an initial proposal covariance matrix corresponding to the specified block. The initial proposal covariance is computed as *rho*×*Sigma*, where *rho* is a scale factor and *Sigma* = *matname*. By default, *Sigma* is the identity matrix. If specified, this option overrides the respective setting from the `covariance()` option specified with the command. `covariance()` may not be combined with `gibbs`.

`adaptation(tarate())` and `adaptation(tolerance())` specify block-specific TAR and acceptance tolerance. If specified, they override the respective settings from the `adaptation()` option specified with the command. `adaptation()` may not be combined with `gibbs`.

`blocksummary` displays the summary of the specified blocks. This option is useful when `block()` is specified.

Initialization

`initial(`*initspec*`)` specifies initial values for the model parameters to be used in the simulation. With multiple chains, this option is equivalent to specifying option `init1()`. You can specify a parameter name, its initial value, another parameter name, its initial value, and so on. For example, to initialize a scalar parameter `alpha` to 0.5 and a 2x2 matrix `Sigma` to the identity matrix `I(2)`, you can type

```
bayesmh ... , initial({alpha} 0.5 {Sigma,m} I(2)) ...
```

You can also specify a list of parameters using any of the specifications described in *Referring to model parameters*. For example, to initialize all regression coefficients from equations `y1` and `y2` to zero, you can type

```
bayesmh ... , initial({y1:} {y2:} 0) ...
```

The general specification of *initspec* is

paramref initval [*paramref initval* [...]]

where *initval* is a number, a Stata expression that evaluates to a number, or a Stata matrix for initialization of matrix parameters.

Curly braces may be omitted for scalar parameters but must be specified for matrix parameters. Initial values declared using this option override the default initial values or any initial values declared during parameter specification in the `likelihood()` option. See *Specifying initial values* for details.

`init#(`*initspec*`)` specifies initial values for the model parameters for the #th chain. This option requires option `nchains()`. `init1()` overrides the default initial values for the first chain, `init2()` for the second chain, and so on. You specify initial values in `init#()` just like you do in option `initial()`. See *Specifying initial values* for details.

`initall(`*initspec*`)` specifies initial values for the model parameters for all chains. This option requires option `nchains()`. You specify initial values in `initall()` just like you do in option `initial()`. You should avoid specifying fixed initial values in `initall()` because then all chains will use the same initial values. `initall()` is useful to specify random initial values when you define your own priors within `prior()`'s `density()` and `logdensity()` suboptions. See *Specifying initial values* for details.

`nomleinitial` suppresses using maximum likelihood estimates (MLEs) as starting values for model parameters. With multiple chains, this option and discussion below apply only to the first chain. By default, when no initial values are specified, MLE values (when available) are used as initial values. If `nomleinitial` is specified and no initial values are provided, the command uses ones for positive scalar parameters, zeros for other scalar parameters, and identity matrices for matrix parameters. `nomleinitial` may be useful for providing an alternative starting state when checking convergence of MCMC. This option cannot be combined with `initrandom`.

`initrandom` specifies that the model parameters be initialized randomly. Random initial values are generated from the prior distributions of the model parameters. If you want to use fixed initial values for some of the parameters, you can specify them in the `initial()` option or during parameter declarations in the `likelihood()` option. Random initial values are not available for parameters with `flat`, `jeffreys`, `density()`, `logdensity()`, and `jeffreys()` priors; you must provide your own initial values for such parameters. This option cannot be combined with `nomleinitial`. See *Specifying initial values* for details.

`initsummary` specifies that the initial values used for simulation be displayed.

Adaptation

`adaptation(`*adaptopts*`)` controls adaptation of the MCMC procedure. Adaptation takes place every prespecified number of MCMC iterations and consists of tuning the proposal scale factor and proposal covariance for each block of model parameters. Adaptation is used to improve sampling efficiency. Provided defaults are based on theoretical results and may not be sufficient for all applications. See *Adaptation of the MH algorithm* for details about adaptation and its parameters.

adaptopts are any of the following options:

`every(#)` specifies that adaptation be attempted every #th iteration. The default is `every(100)`. To determine the adaptation interval, you need to consider the maximum block size specified in your model. The update of a block with k model parameters requires the estimation of a $k \times k$ covariance matrix. If the adaptation interval is not sufficient for estimating the $k(k+1)/2$ elements of this matrix, the adaptation may be insufficient.

`maxiter(#)` specifies the maximum number of adaptive iterations. Adaptation includes tuning of the proposal covariance and of the scale factor for each block of model parameters. Once the TAR is achieved within the specified tolerance, the adaptation stops. However, no more than # adaptation steps will be performed. The default is variable and is computed as $\max\{25, $ `floor(burnin()/adaptation(every()))` $\}$.

`maxiter()` is usually chosen to be no greater than (`mcmcsize()` + `burnin()`)/ `adaptation(every())`.

`miniter(#)` specifies the minimum number of adaptive iterations to be performed regardless of whether the TAR has been achieved. The default is `miniter(5)`. If the specified `miniter()` is greater than `maxiter()`, then `miniter()` is reset to `maxiter()`. Thus, if you specify `maxiter(0)`, then no adaptation will be performed.

`alpha(#)` specifies a parameter controlling the adaptation of the AR. `alpha()` should be in $[0, 1]$. The default is `alpha(0.75)`.

`beta(#)` specifies a parameter controlling the adaptation of the proposal covariance matrix. `beta()` must be in [0,1]. The closer `beta()` is to zero, the less adaptive the proposal covariance. When `beta()` is zero, the same proposal covariance will be used in all MCMC iterations. The default is `beta(0.8)`.

`gamma(#)` specifies a parameter controlling the adaptation rate of the proposal covariance matrix. `gamma()` must be in [0,1]. The larger the value of `gamma()`, the less adaptive the proposal covariance. The default is `gamma(0)`.

`tarate(#)` specifies the TAR for all blocks of model parameters; this is rarely used. `tarate()` must be in (0,1). The default AR is 0.234 for blocks containing continuous multiple parameters, 0.44 for blocks with one continuous parameter, and 1/*n_maxlev* for blocks with discrete parameters, where *n_maxlev* is the maximum number of levels for a discrete parameter in the block.

`tolerance(#)` specifies the tolerance criterion for adaptation based on the TAR. `tolerance()` should be in (0,1). Adaptation stops whenever the absolute difference between the current AR and TAR is less than `tolerance()`. The default is `tolerance(0.01)`.

`scale(#)` specifies an initial multiplier for the scale factor for all blocks. The initial scale factor is computed as $\#/\sqrt{n_p}$ for continuous parameters and $\#/n_p$ for discrete parameters, where n_p is the number of parameters in the block. The default is `scale(2.38)`.

`covariance(`*cov*`)` specifies a scale matrix *cov* to be used to compute an initial proposal covariance matrix. The initial proposal covariance is computed as $\rho \times \Sigma$, where ρ is a scale factor and $\Sigma =$ *matname*. By default, Σ is the identity matrix. Partial specification of Σ is also allowed.

The rows and columns of *cov* should be named after some or all model parameters. According to some theoretical results, the optimal proposal covariance is the posterior covariance matrix of model parameters, which is usually unknown. This option does not apply to the blocks containing random-effects parameters.

Reporting

`clevel(#)` specifies the credible level, as a percentage, for equal-tailed and HPD credible intervals. The default is `clevel(95)` or as set by [BAYES] **set clevel**.

`hpd` displays the HPD credible intervals instead of the default equal-tailed credible intervals.

`eform` and `eform(`*string*`)` specify that the coefficient table be displayed in exponentiated form and that `exp(b)` and *string*, respectively, be used to label the exponentiated coefficients in the table.

`remargl` specifies to compute the log marginal-likelihood for panel-data and multilevel models. It is not reported by default for these models. Bayesian panel-data and multilevel models contain many parameters because, in addition to regression coefficients and variance components, they also estimate individual random effects. The computation of the log marginal-likelihood involves the inverse of the determinant of the sample covariance matrix of all parameters and loses its accuracy as the number of parameters grows. For high-dimensional models such as multilevel models, the computation of the log marginal-likelihood can be time consuming, and its accuracy may become unacceptably low. Because it is difficult to access the levels of accuracy of the computation for all panel-data and multilevel models, the log marginal-likelihood is not reported by default. For models containing a small number of random effects, you can use the `remargl` option to compute and display the log marginal-likelihood.

`batch(#)` specifies the length of the block for calculating batch means and an MCSE using batch means. The default is `batch(0)`, which means no batch calculations. When `batch()` is not specified, the MCSE is computed using effective sample sizes instead of batch means. `batch()` may not be combined with `corrlag()` or `corrtol()`.

`saving(`*filename*`[ , replace ])` saves simulation results in *filename*`.dta`. The `replace` option specifies to overwrite *filename*`.dta` if it exists. If the `saving()` option is not specified, `bayesmh` saves simulation results in a temporary file for later access by postestimation commands. This temporary file will be overridden every time `bayesmh` is run and will also be erased if the current estimation results are cleared. `saving()` may be specified during estimation or on replay.

The saved dataset has the following structure. Variable `_chain` records chain identifiers. Variable `_index` records iteration numbers. `bayesmh` saves only states (sets of parameter values) that are different from one iteration to another and the frequency of each state in variable `_frequency`. (Some states may be repeated for discrete parameters.) As such, `_index` may not necessarily contain consecutive integers. Remember to use `_frequency` as a frequency weight if you need to obtain any summaries of this dataset. Values for each parameter are saved in a separate variable in the dataset. Variables containing values of parameters without equation names are named as `eq0_p#`, following the order in which parameters are declared in `bayesmh`. Variables containing values of parameters with equation names are named as `eq#_p#`, again following the order in which parameters are defined. Parameters with the same equation names will have the same variable prefix `eq#`. For example,

```
. bayesmh y x1, likelihood(normal({var})) saving(mcmc) ...
```

will create a dataset, `mcmc.dta`, with variable names `eq1_p1` for `{y:x1}`, `eq1_p2` for `{y:_cons}`, and `eq0_p1` for `{var}`. Also see macros `e(parnames)` and `e(varnames)` for the correspondence between parameter names and variable names.

In addition, bayesmh saves variable _loglikelihood to contain values of the log likelihood from each iteration and variable _logposterior to contain values of the log posterior from each iteration.

nomodelsummary suppresses the detailed summary of the specified model. The model summary is reported by default.

noexpression suppresses the output of expressions from the model summary. Expressions (when specified) are reported by default.

chainsdetail specifies that acceptance rates, efficiencies, and log marginal-likelihoods be reported separately for each chain. By default, the header reports these statistics averaged over all chains. This option requires option nchains().

nodots, dots, and dots(#) specify to suppress or display dots during simulation. With multiple chains, these options affect all chains. dots(#) displays a dot every # iterations. During the adaptation period, a symbol a is displayed instead of a dot. If dots(..., every(#)) is specified, then an iteration number is displayed every #th iteration instead of a dot or a. dots(, every(#)) is equivalent to dots(1, every(#)). dots displays dots every 100 iterations and iteration numbers every 1,000 iterations; it is a synonym for dots(100, every(1000)). By default, no dots are displayed (nodots or dots(0)).

show(*paramref*) or noshow(*paramref*) specifies a list of model parameters to be included in the output or excluded from the output, respectively. By default, all model parameters (except random-effects parameters) are displayed. Do not confuse noshow() with exclude(), which excludes the specified parameters from the MCMC sample. When the noshow() option is specified, for computational efficiency, MCMC summaries of the specified parameters are not computed or stored in e(). *paramref* can include individual random-effects parameters.

showreffects and showreffects(*reref*) are used with multilevel models and specify that all or a list *reref* of random-effects parameters be included in the output in addition to other model parameters. By default, all random-effects parameters are excluded from the output as if you have specified the noshow() option. This option computes, displays, and stores in e() MCMC summaries for the random-effects parameters.

notable suppresses the estimation table from the output. By default, a summary table is displayed containing all model parameters except those listed in the exclude() and noshow() options. Regression model parameters are grouped by equation names. The table includes six columns and reports the following statistics using the MCMC simulation results: posterior mean, posterior standard deviation, MCMC standard error or MCSE, posterior median, and credible intervals.

noheader suppresses the output header either at estimation or upon replay.

title(*string*) specifies an optional title for the command that is displayed above the table of the parameter estimates. The default title is specific to the specified likelihood model.

display_options: vsquish, noemptycells, baselevels, allbaselevels, nofvlabel, fvwrap(#), fvwrapon(*style*), and nolstretch; see [R] **Estimation options**.

Advanced

search(*search_options*) searches for feasible initial values. *search_options* are on, repeat(#), and off.

search(on) is equivalent to search(repeat(500)). This is the default.

search(repeat(k)), $k > 0$, specifies the number of random attempts to be made to find a feasible initial-value vector, or initial state. The default is repeat(500). An initial-value vector is feasible if it corresponds to a state with positive posterior probability. If feasible initial

values are not found after k attempts, an error will be issued. `repeat(0)` (rarely used) specifies that no random attempts be made to find a feasible starting point. In this case, if the specified initial vector does not correspond to a feasible state, an error will be issued.

`search(off)` prevents the command from searching for feasible initial values. We do not recommend specifying this option.

`corrlag(#)` specifies the maximum autocorrelation lag used for calculating effective sample sizes. The default is $\min\{500, \texttt{mcmcsize()}/2\}$. The total autocorrelation is computed as the sum of all lag-k autocorrelation values for k from 0 to either `corrlag()` or the index at which the autocorrelation becomes less than `corrtol()` if the latter is less than `corrlag()`. Options `corrlag()` and `batch()` may not be combined.

`corrtol(#)` specifies the autocorrelation tolerance used for calculating effective sample sizes. The default is `corrtol(0.01)`. For a given model parameter, if the absolute value of the lag-k autocorrelation is less than `corrtol()`, then all autocorrelation lags beyond the kth lag are discarded. Options `corrtol()` and `batch()` may not be combined.

Remarks and examples

Remarks are presented under the following headings:

Examples are presented under the following headings:

For a quick overview example of all Bayesian commands, see *Overview example* in [BAYES] **Bayesian commands**.

Using bayesmh

The `bayesmh` command for Bayesian analysis includes three functional components: setting up a posterior model, performing MCMC simulation, and summarizing and reporting results. The first component, the model-building step, requires some experience in the practice of Bayesian statistics and, as any modeling task, is probably the most demanding. You should specify a posterior model that is statistically correct and that represents the observed data. Another important aspect is the computational feasibility of the model in the context of the MH MCMC procedure implemented in `bayesmh`. The provided MH algorithm is adaptive and, to a degree, can accommodate various statistical models and data structures. However, careful model parameterization and well-specified initial values and MCMC sampling scheme are crucial for achieving a fast-converging Markov chain and consequently good results. Simulation of MCMC must be followed by a thorough investigation of the convergence of the MCMC algorithm. Once you are satisfied with the convergence of the simulated chains, you may proceed with posterior summaries of the results and their interpretation. Below we discuss the three major steps of using `bayesmh` and provide recommendations.

Setting up a posterior model

Any posterior model includes a likelihood model that specifies the conditional distribution of the data given model parameters and prior distributions for all model parameters. The prior distribution of a parameter can itself be specified conditional on other parameters, also referred to as *hyperparameters*. We will refer to their prior distributions as *hyperpriors*.

Likelihood model

The likelihood model describes the data. You build your likelihood model the same way you do this in frequentist likelihood-based analysis.

The `bayesmh` command provides various likelihood models, which are specified in the `likelihood()` option. For a univariate response, there are normal models, generalized linear models for binary and count response, and more. For a multivariate model, you may choose between a multivariate normal model with covariates common to all variables and with covariates specific to each variable. You can also build likelihood models for multiple variables by specifying a distribution and a regression function for each variable by using `bayesmh`'s multiple-equations specification.

bayesmh is primarily designed for fitting regression models. As we said above, you specify the likelihood or outcome distribution in the likelihood() option. The regression specification of the model is the same as for other regression commands. For a univariate response, you specify the dependent and all independent variables following the command name. (Here we also include the prior() option that specifies prior distributions to emphasize that it is required in addition to likelihood(). See the next subsection for details about this option.)

```
. bayesmh y x1 x2, likelihood() prior() ...
```

For a multivariate response, you separate the dependent variables from the independent variables with the equal sign.

```
. bayesmh y1 y2 = x1 x2, likelihood(mvnormal(...)) prior() ...
```

With multiple-equations specification, you follow the syntax for the univariate response, but you specify each equation in parentheses and you specify the likelihood() option within each equation.

```
. bayesmh (y1 x1, likelihood()) (y2 x2, likelihood()),  prior() ...
```

In the above models, the regression function is modeled using a linear combination of the specified independent variables and regression coefficients. The constant is included by default, but you can specify the noconstant option to omit it from the linear predictor.

bayesmh also allows you to model the regression function as a nonlinear function of independent variables and regression parameters. In this case, you must use the equal sign to separate the dependent variable from the expression and specify the expression in parentheses:

```
. bayesmh y = ({a}+{b}*x^{c}), likelihood(normal()) prior() ...

. bayesmh (y1 = ({a1}+{b1}*x^{c1})   ///
          (y2 = ({a2}+{b2}*x^{c2}), likelihood(mvnormal()) prior() ...
```

You can fit linear and nonlinear multilevel models by including random-effects terms in your regression specifications.

```
. bayesmh y x1 x2 U[id], likelihood() prior() ...
. bayesmh y = ({a}+{b}*x^{c}+{U[id]}), likelihood() prior() ...
```

Finally, you can model an outcome distribution directly by specifying one of the supported probability distributions.

For a not-supported or nonstandard likelihood, you can use the llf() option within likelihood() to specify a generic expression for the observation-level likelihood function; see *Substitutable expressions*. When you use the llf() option, it is your responsibility to ensure that the provided expression corresponds to a valid density. For more complicated Bayesian models, you may consider writing your own likelihood or posterior function evaluators; see [BAYES] **bayesmh evaluators**.

Prior distributions

In addition to the likelihood, you must also specify prior distributions for all model parameters in a Bayesian model (except random effects). Prior distributions or priors are key components in a Bayesian model specification and should be chosen carefully. They are used to quantify some expert knowledge or existing information about model parameters. For example, priors can be used for constraining the domain of some parameters to localize values that we think are more probable for reasons that are not considered in the likelihood specification. Improper priors (priors with densities that do not integrate to finite numbers) are also allowed, as long as they yield valid posterior distributions. Priors are often categorized as informative (subjective) or noninformative (objective). Noninformative priors

are also known as vague priors. Uniform distributions are often used as noninformative priors and can even be applied to parameters with unbounded domains, in which case they become improper priors. Normal and gamma distributions with very large variances relative to the expected values of the parameters are also used as noninformative priors. Another family of noninformative priors, often chosen for their invariance under reparameterization, are so-called Jeffreys priors, named after Harold Jeffreys (Jeffreys 1946). For example, the `bayesmh` command provides built-in Jeffreys priors for the normal family of distributions. Jeffreys priors are usually improper. As discussed by many researchers, however, the overuse of noninformative priors contradicts the principles of Bayesian approach—analysis of a posterior model with noninformative priors would be close to one based on the likelihood only. Noninformative priors may also negatively influence the MCMC convergence. It is thus important to find good priors based on earlier studies and use them in the model as well as perform sensitivity analysis for competing priors. A good choice of prior should minimize the MCMC standard errors of the parameter estimates.

As for likelihoods, the `bayesmh` command provides several priors you can choose from by specifying the `prior()` options. For example, continuous univariate priors include normal, lognormal, uniform, inverse gamma, and exponential; discrete priors include Bernoulli and Poisson; multivariate priors include multivariate normal and inverse Wishart. There are also special priors: `jeffreys` and `jeffreys(#)`, which specify Jeffreys priors for the variance of the normal and multivariate normal distributions, and `zellnersg()` and `zellnersg0()`, which specify multivariate priors for regression coefficients (Zellner and Revankar 1969).

The `prior()` option is required and may be repeated. You can use the `prior()` option for each parameter or you can combine multiple parameters in one `prior()` specification.

For example, we can specify different priors for parameters `{y:x}` and `{y:_cons}` by

```
. bayesmh y x, ... prior({y:x}, normal(10,100)) prior({y:_cons}, normal(20,200)) ...
```

or the same univariate prior using one `prior()` statement, using

```
. bayesmh y x, ... prior({y:x _cons}, normal(10,100)) ...
```

or a multivariate prior with zero mean and fixed variance–covariance `S`, as follows:

```
. bayesmh y x, ... prior({y:x _cons}, mvnormal0(2,S)) ...
```

In the `prior()` option, we list model parameters following any of the specifications described in *Referring to model parameters* and then, following the comma, we specify one of the prior distributions *priordist*.

If you want to specify a nonstandard prior or if the prior you need is not supported, you can use the `density()` or `logdensity()` option within the `prior()` option to specify an expression for a generic density or log density of the prior distribution; see *Substitutable expressions*. When you use the `density()` or `logdensity()` option, it is your responsibility to ensure that the provided expression corresponds to a valid density. For a complicated Bayesian model, you may consider writing your own posterior function evaluator; see [BAYES] **bayesmh evaluators**.

Sometimes, you may need to specify a flat prior (a prior with the density equal to one) for some of the parameters. This is often needed when specifying a noninformative prior. You can specify the `flat` option instead of the prior distribution in the `prior()` option to request the flat prior. This option is equivalent to specifying `density(1)` or `logdensity(0)` in `prior()`.

With multilevel models, random-effects parameters, such as random intercepts `{U[id]}` at the `id` levels, are assigned default normal priors with zero mean and an unknown variance, that is, `{var_U}`. You must, however, specify the priors for the unknown variance components. For instance, if we include random intercepts `{U[id]}` in our model, we will need to specify the prior for `{var_U}`.

You can use the `prior()` option to change the default priors for random effects, `prior({U}, ...)`. See *Random effects*.

The specified likelihood model for the data and prior distributions for the parameters are not guaranteed to result in proper posterior distributions of the parameters. Therefore, unless you are using one of the standard Bayesian models, you should always check the validity of the posterior model you specified.

Declaring model parameters

Model parameters are typically declared, meaning first introduced, in the arguments of distributions specified in options `likelihood()` and `prior()`. We will refer to model parameters that are declared in the prior distributions (and not the likelihood distributions) as hyperparameters. Model parameters may also be declared within the parameter specification of the `prior()` option, but this is more rare.

`bayesmh` distinguishes between two types of model parameters: scalar and matrix. There are also random-effects parameters, but we describe them in detail in *Random effects*. All parameters must be specified in curly braces, `{}`. There are two ways for declaring a scalar parameter: {*param*} and {*eqname*:*param*}, where *param* and *eqname* are valid Stata names.

The specification of a matrix parameter is similar, but you must use the `matrix` suboptions: {*param*, matrix} and {*eqname*:*param*, matrix}. The most common application of matrix model parameters is for specifying the variance–covariance matrix of a multivariate normal distribution.

All matrices are assumed to be symmetric and only the elements in the lower diagonal are reported in the output. Only a few multivariate prior distributions are available for matrix parameters: `wishart()`, `iwishart()`, and `jeffreys()`. In addition to being symmetric, these distributions require that the matrices be positive definite.

It is your responsibility to declare all parameters of your model, except regression coefficients in linear models. For a linear model, `bayesmh` automatically creates a regression coefficient with the name {*depvar*:*indepvar*} for each independent variable *indepvar* in the model and, if `noconstant` is not specified, an intercept parameter {*depvar*:_cons}. In the presence of factor variables, `bayesmh` will create a parameter {*depvar*:*level*} for each level indicator *level* and a parameter {*depvar*:*inter*} for each interaction indicator *inter*; see **[U] 11.4.3 Factor variables**. (It is still your responsibility, however, to specify prior distributions for the regression parameters.)

For example,

```
. bayesmh y x, ...
```

will automatically have two regression parameters: {y:x} and {y:_cons}, whereas

```
. bayesmh y x, noconstant ...
```

will have only one: {y:x}.

For a univariate normal linear regression, we may want to additionally declare the scalar variance parameter by

```
. bayesmh y x, likelihood(normal({sig2})) ...
```

We can label the variance parameter, as follows:

```
. bayesmh y x, likelihood(normal({var:sig2})) ...
```

We can declare a hyperparameter for {sig2} using

```
. bayesmh y x, likelihood(normal({sig2})) prior({sig2}, igamma({df},2)) ...
```

where the hyperparameter {df} is declared in the inverse-gamma prior distribution for {sig2}.

For a multivariate normal linear regression, in addition to four regression parameters declared automatically by bayesmh: {y1:x}, {y1:_cons}, {y2:x}, and {y2:_cons}, we may also declare a parameter for the variance–covariance matrix:

```
. bayesmh y1 y2 = x, likelihood(mvnormal({Sigma, matrix})) ...
```

or abbreviate matrix to m for short:

```
. bayesmh y1 y2 = x, likelihood(mvnormal({Sigma, m})) ...
```

For a two-level random-intercept model,

```
. bayesmh y x U[id], ...
```

in addition to regression coefficients {y:x} and {y:_cons}, bayesmh creates a variance component {var_U} associated with the included random effects {U[id]}. See *Random effects* for details.

Referring to model parameters

After a model parameter is declared, we may need to refer to it in our further model specification. We will definitely need to refer to it when we specify its prior distribution. We may also need to use it as an argument in the prior distributions of other parameters or need to specify it in the block() option for blocking of model parameters; see *Improving efficiency of the MH algorithm—blocking of parameters*.

To refer to one parameter, we simply use its definition: {*param*}, {*eqname*:*param*}, {*param*, matrix}, or {*eqname*:*param*, matrix}. There are several ways in which you can refer to multiple parameters. You can refer to multiple model parameters in the parameter specification *paramref* of the prior(*paramref*, ...) option, of the block(*paramref*, ...) option, or of the initial(*paramref* #) option.

The most straightforward way to refer to multiple scalar model parameters is to simply list them individually, as follows:

```
{param1} {param2} ...
```

but there are shortcuts.

For example, the alternative to the above is

```
{param1 param2} ...
```

where we simply list the names of all parameters inside one set of curly braces.

If parameters have the same equation name, you can refer to all the parameters with that equation name as follows. Suppose that we have three parameters with the same equation name eqname, then the specification

```
{eqname:param1} {eqname:param2} {eqname:param3}
```

is the same as the specification

```
{eqname:}
```

or the specification

```
{eqname:param1 param2 param3}
```

The above specification is useful if we want to refer to a subset of parameters with the same equation name. For example, in the above, if we wanted to refer to only param1 and param2, we could type

```
{eqname:param1 param2}
```

If a factor variable is used in the specification of the regression function, you can use the same factor-variable specification within *paramref* to refer to the coefficients associated with the levels of that factor variable; see [U] **11.4.3 Factor variables**.

You can mix and match all the specifications above in one parameter specification, *paramref*.

To refer to multiple matrix model parameters, you can use {*paramlist*, matrix} to refer to matrix parameters with names *paramlist* and {*eqname*:*paramlist*, matrix} to refer to matrix parameters with names in *paramlist* and with equation name *eqname*.

For example, the specification

```
{eqname:Sigma1,m} {eqname:Sigma2,m} {Sigma3,m} {Sigma4,m}
```

is the same as the specification

```
{eqname:Sigma1 Sigma2,m} {Sigma3 Sigma4,m}
```

See *Random effects* for how to refer to random-effects parameters.

You cannot refer to different types of parameters such as scalar and matrix parameters in one *paramref* specification.

For referring to model parameters in postestimation commands, see *Different ways of specifying model parameters* in [BAYES] **Bayesian postestimation**.

Specifying arguments of likelihood models and prior distributions

As previously mentioned, likelihood distributions (or more precisely, likelihood models), *modelspec*, are specified in the likelihood(*modelspec*) option and prior distributions *priordist* are specified following the comma in the prior(*paramref*, *priordist*) option. For a list of supported models and distributions, see the corresponding tables in the syntax diagram.

In a likelihood model, mean and location parameters are determined by the specified regression function and thus need not be specified in the likelihood distributions. For example, for a normal linear regression, we use likelihood(normal(*var*)), where we specify only the variance parameter—the mean is already parameterized as a linear combination of the specified independent variables. In the prior distributions, we must specify all parameters of the distribution. For example, for a normal prior specification, we use prior(*paramref*, normal(*mu*, *var*)), where we must specify both mean *mu* and variance *var*. In addition, all multivariate prior distributions require that you specify the dimension *d* as the first argument.

Scalar arguments of the distributions may be specified as a number or as a scalar expression *expr*. Matrix arguments of the distributions may be specified as a matrix or as a matrix expression *expr*. Both types of arguments may be specified as a parameter (see *Declaring model parameters*) or as a substitutable expression, *subexpr* or *resubexpr* (see *Substitutable expressions*). All distribution arguments, except the parameters of survival models and the dimension *d* of multivariate prior distributions, support the above specifications. For likelihood models, arguments of the distributions may also contain variable names.

For example, in a normal linear regression, we can specify the variance as a known value of 25,

```
. bayesmh y x, likelihood(normal(25)) ...
```

or as a squared standard deviation of 5 (scalar expression),

```
. bayesmh y x, likelihood(normal(5^2)) ...
```

or as an unknown variance parameter {var},

```
. bayesmh y x, likelihood(normal({var})) ...
```

or as a function of an unknown standard-deviation parameter {sd} (substitutable expression),

```
. bayesmh y x, likelihood(normal({sd}^2)) ...
```

In a multivariate normal linear regression, we can specify the variance–covariance matrix as a known matrix S,

```
. bayesmh y1 y2 = x, likelihood(mvnormal(S)) ...
```

or as a matrix function S = R*R' using its Cholesky decomposition,

```
. bayesmh y1 y2 = x, likelihood(mvnormal(R*R')) ...
```

or as an unknown matrix parameter {Sigma,m},

```
. bayesmh y1 y2 = x, likelihood(mvnormal({Sigma,m})) ...
```

or as a function of an unknown variance parameter {var} (substitutable expression),

```
. bayesmh y1 y2 = x, likelihood(mvnormal({var}*S)) ...
```

Substitutable expressions

You may use substitutable expressions in bayesmh to define nonlinear expressions *subexpr*, arguments of outcome distributions in option likelihood(), observation-level log likelihood in option llf(), arguments of prior distributions in option prior(), and generic prior distributions in prior()'s suboptions density() and logdensity(). Substitutable expressions are just like any other mathematical expression in Stata, except that they may include model parameters. Substitutable expressions may contain factor variables and time-series operators; see [U] **11.4.3 Factor variables** and [U] **11.4.4 Time-series varlists**.

To specify a substitutable expression in your bayesmh model, you must comply with the following rules:

1. Model parameters are bound in braces: {mu}, {var:sigma2}, {Sigma, matrix}, and {Cov:Sigma, matrix}.
2. Linear combinations can be specified using the notation

   { *eqname*: *varlist* [, xb noconstant] }

   For example, {lc:mpg price weight} is equivalent to

   {lc:mpg}*mpg + {lc:price}*price + {lc:weight}*weight + {mpg:_cons}

   The xb option is used to distinguish between the linear combination that contains one variable and a free parameter that has the same name as the variable and the same group name as the linear combination. For example, {lc:weight, xb} is equivalent to {lc:_cons} + {lc:weight}*weight, whereas {lc:weight} refers to either a free parameter weight with a group name lc or the coefficient of the weight variable, if {lc:} has been previously defined in the expression as a linear combination that involves variable weight. Thus the xb option indicates that the specification is a linear combination rather than a single parameter to be estimated.

   When you define a linear combination, a constant term is included by default. The noconstant option suppresses the constant.

   See *Linear combinations* in [ME] **menl** for details about specifying linear combinations.

3. Initial values are given by including an equal sign and the initial value inside the braces, for example, {b1=1.267}, {gamma=3}, etc. If you do not specify an initial value, that parameter is initialized to one for positive scalar parameters and to zero for other scalar parameters, or it is initialized to its MLE, if available. The initial() option overrides initial values provided in substitutable expressions. Initial values for matrices must be specified in the initial() option. By default, matrix parameters are initialized with identity matrices.

Specifying linear combinations. We can use substitutable expressions to specify linear combinations.

For example, a normal linear regression,

```
. bayesmh y x1 x2, likelihood(normal(1)) prior({y:}, normal(0,100))
```

may be equivalently (but less efficiently) fit using a nonlinear regression,

```
. bayesmh y = ({y:x1 x2}), likelihood(normal(1)) prior({y:}, normal(0,100))
```

The above nonlinear specification is essentially,

```
. bayesmh y = ({y:x1}*x1+{y:x2}*x2+{y:_cons}), likelihood(normal(1))
> prior({y:}, normal(0,100))
```

Specifying nonstandard densities. We can use substitutable expressions to define nonstandard or not-supported probability distributions.

For example, suppose we want to specify a Cauchy distribution with location a and scale b. We can specify the expression for the observation-level likelihood function in the llf() option within likelihood().

```
. bayesmh y, likelihood(llf(ln({b})-ln({b}^2+(y-{a})^2)-ln(_pi))) noconstant ...
```

You can also use substitutable expressions to define nonstandard or not-supported prior distributions. For example, as suggested by Gelman et al. (2014), we can specify a Cauchy prior with location $a = 0$ and scale $b = 2.5$ for logistic regression coefficients, where continuous covariate x is standardized to have mean 0 and standard deviation 0.5. If bayesmh did not support the Cauchy prior (option prior(, cauchy())), we could have specified this prior using the substitutable expressions as follows:

```
. bayesmh y x, likelihood(logit)
> prior({y:x}, logdensity(ln(2.5)-ln(2.5^2+{y:x}^2)-ln(_pi)))
> prior({y:_cons}, logdensity(ln(10)-ln(10^2+{y:_cons}^2)-ln(_pi)))
```

Including random effects. Substitutable expressions may also contain random effects; see *Random effects*.

Constraints on coefficients in linear combinations

If you wish to constrain a coefficient to a specific value, you can specify the @ symbol immediately after the variable whose coefficient is being constrained and then type the value. For instance,

```
. bayesmh y x1 x2@1, ...
```

will constrain the coefficient parameter {y:x2} to 1, which means that this parameter is a constant and will not be sampled.

You can also constrain a coefficient to a symbol, which is equivalent to renaming the corresponding parameter. For instance,

```
. bayesmh y x1 x2@a, ...
```

will replace {y:x2} with the free parameter {a}. This feature may be useful with multiple-equations models when we want the variable used in several linear combinations to have the same coefficient. For instance,

```
. bayesmh (y1 x1 x2@a, ...) (y2 x1 x2@a, ...)
```

will replace the parameters {y1:x2} and {y2:x2} with {a}, thus constraining the two original coefficients to be the same.

Random effects

You can include random effects in your bayesmh's specifications to fit multilevel models. Examples of random effects specified within the bayesmh syntax are U1[id], U2[id1>id2], U3[id1#id3], c.x1#U4[id], and 2.f1#U5[id], to name a few. These represent a random intercept at the id level, a random intercept at the id2-within-id1 level, a random interaction between the crossed levels id1 and id3, a random slope for the continuous variable x1, and a random slope associated with the second level of the factor variable f1, respectively. See the general syntax for the random-effects terms below.

To fit linear multilevel models, you include random-effects terms just as you include covariates—you simply list them following the dependent variable. For instance,

```
. bayesmh y x1 x2 U[id], ...
. bayesmh y x1 x2 U0[id] c.x1#U1[id], ...
```

In multiple-equations models, there are equation-specific coefficients associated with each random-effect term. The coefficient of the random effect in the first equation in which it appears is constrained to 1. For example,

```
. bayesmh (y1 x1 U[id1], ...) (y2 x1 U[id1] V[id2], ...)
```

constrains {y1:U} and {y2:V} to 1 because their associated random effects, {U[id1]} and {V[id2]}, appear for the first time in equations {y1:} and {y2:}, respectively. {y2:U} will be sampled because the associated random effect, {U[id1]}, had already appeared in the first equation.

The coefficients are constrained to 1 for the purpose of identifiability because you cannot identify both the coefficients and the variance component, which is introduced automatically by bayesmh, for each random effect. (Technically, you could identify both parameters with Bayesian models if you specify strong informative priors for them.)

You can override the coefficient constraints by using @*value* immediately following the random-effects term. For example,

```
. bayesmh (y1 x1 U[id1], ...) (y2 x1 U[id1]@1 V[id2], ...)
```

constrains {y2:U} to 1 and lets {y1:U} be sampled. You may also constrain a random effect to a symbol as follows:

```
. bayesmh (y1 x1 U[id1]@y1_U, ...) (y2 x1 U[id1] V[id2], ...)
```

Here both equations will contain coefficient parameters for U[id]: {y1_U} will be the coefficient in the first equation, and {y2:U} will continue to be the coefficient in the second equation. Notice that {y1_U} will be treated by bayesmh as a free parameter rather than its native regression coefficient. The above specification is useful when you want to constrain a variance component instead of one of the coefficients.

You can also include random effects in nonlinear models. You do this by creating a so-called random-effects substitutable expression—a substitutable expression that contains random effects. When you include random effects in substitutable expressions, you must enclose them in {}, just as you do this with other model parameters. For instance,

```
. bayesmh y = (({b1}+{U[id]})/(1+exp(-(x-{b2})/{b3}))), ...
. bayesmh y = (1/({b0}+{b1}*x1+{b2}*x2+{U0[id]}+{c.x1#U1[id]})), ...
```

The previous bayesmh model can be specified more elegantly by using a linear-combination specification within a substitutable expression:

```
. bayesmh y = (1/({xb:x1 x2 U0[id] c.x1#U1[id]})), ...
```

When random effects are specified within a linear-combination specification, as in the above example, the curly braces around each random effect are not needed. See *Random-effects substitutable expressions* in [ME] **menl** for examples of substitutable expressions containing random effects.

The general syntax for specifying random-effects terms, *reterm*, is provided below.

reterm	Description
{*rename*[*levelspec*]}	Random intercepts *rename* at hierarchy *levelspec*
{c.*varname*#*rename*[*levelspec*]}	Random coefficients *rename* for continuous variable *varname*
{#.*fvvarname*#*rename*[*levelspec*]}	Random coefficients *rename* for the #th level of factor variable *fvvarname*

rename is a random-effects name. It is a Stata name that starts with a capital letter. *levelspec* defines the level of hierarchy and is described below.

levelspec	Description
levelvar	variable identifying the group structure for the random effect at that level
lv2 > *lv1*	two-level nesting: levels of variable *lv1* are nested within *lv2*
lv3 > *lv2* > *lv1*	three-level nesting: levels of variable *lv1* are nested within *lv2*, which is nested within *lv3*
... > *lv3* > *lv2* > *lv1*	higher-level nesting
lv1#*lv2*	two-way interaction between crossed levels *lv1* and *lv2*
lv1#*lv2*#*lv3*	three-way interaction between crossed levels *lv1*, *lv2*, and *lv3*
lv1#*lv2*#*lv3*#...	higher-order interactions between crossed levels
_all	treat entire dataset as one big group
_n	treat each observation as its own group; defines a latent variable

You can equivalently specify levels in the opposite order, from the lowest level to the highest; for example, *lv1* < *lv2* < *lv3*, but they will be displayed in the canonical order, from the highest level to the lowest.

After you define a random-effects term once using its full specification *rename*[*levelspec*], you can refer to it further simply by name *rename*, or you can continue using the full name.

When you include a random effect in your regression model, bayesmh creates a parameter for each level of the grouping variable. For example, if you include U[id]—the random intercepts by level variable id that contains levels 1 through 10—bayesmh will create a separate scalar parameter for each level of id: {U[1.id]}, {U[2.id]}, ..., {U[10.id]}. These scalar parameters are sampled in one block using the sampling algorithm described in *Adaptive MH algorithm for random effects* in *Methods and formulas*.

When you use random effects with user-specified log-likelihood and log-posterior evaluators, they are sampled by default in one block as regular scalar parameters.

When you refer to random-effects parameters in bayesmh's specifications, you typically refer to them as a group. For example, suppose that you included random intercepts by level variable id in your model as U[id]. To specify a prior distribution for these random intercepts, you can refer to them by using the full definition {U[id]} or simply by name {U}. In postestimation commands or, for instance, in the showreffects() option, you may want to refer to individual random-effects parameters such as {U[1.id]} and {U[1]} or to the subsets of them such as {U[(1/5).id]} and {U[1/5]}. See *Different ways of specifying model parameters* in [BAYES] **Bayesian postestimation** for other ways of referring to individual random-effects parameters.

For each random effect {*rename*[*levelspec*]} you include in the model, bayesmh automatically assigns it a normal prior with zero mean and variance component {var_*rename*}. But it is your responsibility to specify a prior for each variance component {var_*rename*}. You can also use the prior() option to change the default prior for random effects. This is particularly useful for specifying a multivariate normal prior with an unstructured covariance matrix for correlated random effects; see example 25.

With multiple-equations models, you must specify a prior for each equation-specific coefficient associated with a random effect as long as the coefficient is not constrained. For example, if we write

```
. bayesmh (y1 x1 U[id1], ...) (y2 x1 U[id1] V[id2], ...)
```

then a prior must be specified for coefficient {y2:U} but not for coefficients {y1:U} and {y2:V} because these are constrained to 1.

Checking model specification

Specifying a Bayesian model may be a tedious task when there are many model parameters and possibly hyperparameters. It is thus essential to verify model specification before starting a potentially time-consuming estimation.

bayesmh displays the summary of the specified model as a part of its standard output. You can use the dryrun option to obtain the model summary without estimation or simulation. Once you are satisfied with the specified model, you can use the nomodelsummary option to suppress a potentially long model summary during estimation. Even if you specify nomodelsummary during estimation, you will still be able to see the model summary, if desired, by simply replaying the results:

```
. bayesmh
```

Specifying MCMC sampling procedure

Once you specify a correct posterior model, bayesmh uses an adaptive random-walk MH algorithm to obtain MCMC samples of model parameters from their posterior distribution.

Reproducing results

Because bayesmh uses MCMC simulation—a stochastic procedure for sampling from a complicated and possibly nontractable distribution—it will produce different results each time you run the command. If the MCMC algorithm converged, the results should not change drastically. To obtain reproducible results, you must specify the random-number seed.

To specify a random-number seed, you can use bayesmh's rseed() option. With a single chain, you can instead use set seed # prior to calling bayesmh; see [R] **set seed**. With multiple chains, you should use rseed() for reproducibility because, as we explain later, using set seed is no longer sufficient.

With a single chain, if you forgot to specify the random-number seed before calling bayesmh, you can retrieve the random-number state used by the command from e(rngstate) and use it later with set rngstate. With multiple chains, reproducing results after the simulation without specifying the seed is more difficult. We strongly recommend that you specify the rseed() option with bayesmh when simulating multiple chains.

When you specify the nchains() option to simulate multiple chains, each chain uses its own stream of random numbers; see [R] **set rngstream**. This is important to ensure that the chains are independent. To reproduce the simulation results, a random-number seed must be used for each stream. This is why using set seed prior to calling bayesmh will not be sufficient to reproduce results from multiple chains—set seed will affect only the first random-number stream. bayesmh's rseed() option, however, will use the specified random-number seed with each stream. If you forgot to specify the seed with multiple chains, you can retrieve chain-specific random-number states from stored scalars e(rngstate1), e(rngstate2), etc. and use them with chain-specific random-number streams; see [R] **set rngstream** and set rngstate in [R] **set seed**. For example, suppose you simulated two chains and forgot to specify the random-number seed:

```
. bayesmh ..., nchains(2) ...
```

You can type the following directly after the simulation to reproduce the results:

```
. set rng mt64s
. set rngstate 'e(rngstate2)'
. set rngstate 'e(rngstate1)'
. bayesmh ..., nchains(2) ...
```

Stata's default random-number generator is mt64; see [R] **set rng**. To simulate multiple chains, the nchains() option temporarily switches to the stream random-number generator mt64s. To manually reproduce the results from multiple chains, you need to use mt64s, but we recommend that you switch back to mt64 for the rest of your analysis. The set rngstate command sets the corresponding stream automatically; you do not need to use set rngstream to do this yourself. It is important, however, that you set the state of the first chain last, just before the next call to bayesmh, so that the stream used by the first chain is the current stream. Although you can reproduce results after estimation, we strongly recommend that you use the rseed() option during estimation if you want reproducibility.

Burn-in period and MCMC sample size

bayesmh has the default burn-in period of 2,500 iterations and the default MCMC sample size of 10,000 iterations. That is, the first 2,500 iterations of the MCMC sampler are discarded and the next 10,000 iterations are used to form the MCMC samples of values of model parameters. You can change these numbers by specifying options burnin() and mcmcsize().

The burn-in period must be long enough for the algorithm to reach convergence or, in other words, for the Markov chain to reach its stationary distribution or the desired posterior distribution of model parameters. The sample size for the MCMC sample is typically determined based on the autocorrelation present in the MCMC sample. The higher the autocorrelation, the larger the MCMC sample should be to achieve the same precision of the parameter estimates as obtained from the chain with low or negligible autocorrelation. Because of the nature of the sampling algorithm, all MCMC exhibit some autocorrelation and thus MCMC samples tend to have large sizes.

The defaults provided by bayesmh may not be sufficient for all Bayesian models and data types. You will need to explore the convergence of the MCMC algorithm for your particular data problem and modify the settings, if needed.

After the burn-in period, bayesmh includes every iteration in the MCMC sample. You can specify the thinning(#) option to store results from a subset of iterations. This option is useful if you want to subsample the chain to decrease autocorrelation in the final MCMC sample. If you use this option, bayesmh will perform a total of thinning() × (mcmcsize() − 1) + 1 iterations, excluding burn-in iterations, to obtain MCMC sample of size mcmcsize().

When you specify the nchains() option to produce multiple chains, the mcmcsize(), burnin(), and thinning() options apply to each chain.

Improving efficiency of the MH algorithm—blocking of parameters

Although the MH algorithm is very general and can be applied to any Bayesian model, it is not the most optimal sampler and may require tuning to achieve higher efficiency.

Efficiency describes mixing properties of the Markov chain. High efficiency means good mixing (low autocorrelation) in the MCMC sample, and low efficiency means bad mixing (high autocorrelation) in the MCMC sample. High autocorrelation is often present when fitting multilevel models; see *Multilevel models* in [BAYES] **bayes**.

An AR is the number of accepted proposals of model parameters relative to the total number of proposals. It should not be confused with sampling efficiency. High AR does not mean high efficiency.

An efficient MH sampler has an AR between 15% and 50% (Roberts and Rosenthal 2001) and low autocorrelation and thus relatively large effective sample size (ESS) for all model parameters.

One way to improve efficiency of the MH algorithm is by blocking of model parameters. Blocking of model parameters is an important functional aspect of the MH sampler. By default, all parameters are used as one block and their covariance matrix is used to adapt the proposal distribution. With many parameters, estimation of this covariance matrix becomes difficult and imprecise and may lead to the loss of efficiency of the MH algorithm. In many cases, this matrix has a block diagonal structure because of independence of some blocks or sets of model parameters and its estimation may be replaced with estimation of the corresponding blocks, which are typically of smaller dimension. This may improve the efficiency of the sampler. To achieve optimal blocking, you need to identify the sets of approximately independent (a posteriori) model parameters and specify them in separate blocks.

To achieve an optimal blocking, you need to know or have some idea about the dependence between the parameters as determined by the posterior distribution. To improve efficiency, follow this principle: correlated parameters should be specified together, while independent groups of parameters should be specified in separate blocks. Because the posterior is usually defined indirectly, the relationship between the parameters is generally unknown. Often, however, we have some knowledge, either deduced from the model specification or based on prior experience with the model, about which parameters are highly correlated. In the worst case, you may need to run some preliminary simulations and determine an optimal blocking by using trial and error.

An ideal case for the MH algorithm is when all model parameters are independent with respect to the posterior distribution and are thus placed in separate blocks and sampled independently. In practice, this is not a realistic or interesting case, but it gives us an idea that we should always try to parameterize the model in such a way that the correlation between model parameters is minimized.

With bayesmh, you can use options block() to perform blocking. You specify one block() option for each set of independent model parameters. Model parameters that are dependent with each other are specified in the same block() option.

To illustrate a typical case, consider the following simple linear regression model:

$$\mathtt{y} = \{\mathtt{a}\} + \{\mathtt{b}\} \times \mathtt{x} + \epsilon,\ \epsilon \sim N(0, \{\mathtt{var}\})$$

Even when {a} and {b} have independent prior specifications, the location parameters {a} and {b} are expected to be correlated a posteriori because of their common dependence on y. Alternatively, if the variance parameter {var} is independent of {a} and {b} a priori, it is generally less correlated with the location parameters a posteriori. A good blocking scheme is to use options block({a} {b}) and block({var}) with bayesmh. We can also reparameterize our model to reduce the correlation between {a} and {b} by recentering. To center the slope parameter, we replace {b} with {b} − #, where # is a constant close to the mean of {b}. Now {a} and {b} − # can also be placed in separate blocks. See, for example, Thompson (2014) for more discussion related to model parameterization.

Other options that control MCMC sampling efficiency are scale(), covariance(), and adaptation(); see *Adaptation of the MH algorithm* for details.

With multiple chains, the block() option and other options that control MCMC sampling efficiency apply to all chains.

Gibbs and hybrid MH sampling

In *Improving efficiency of the MH algorithm—blocking of parameters*, we discussed blocking of model parameters as a way of improving efficiency of the MH algorithm. For certain Bayesian models, further improvement is possible by using Gibbs sampling for certain blocks of parameters. This leads to what we call a hybrid MH sampling with Gibbs updates.

Gibbs sampling is the most effective sampling procedure with the maximum possible AR of one and with often very high efficiency. Using Gibbs sampling for some blocks of parameters will typically lead to higher efficiency of the hybrid MH sampling compared with the simple MH sampling.

To apply Gibbs sampling to a set of parameters, we need to know the full conditional distribution for each parameter and be able to generate random samples from it. Usually, the full conditionals are known in various special cases but are not available for general posterior distributions. Thus, Gibbs sampling is not available for all likelihood and prior combinations. bayesmh provides Gibbs sampling for Bayesian models with conjugate, or more specifically, semiconjugate prior distributions. See *Gibbs sampling for some likelihood-prior and prior-hyperprior configurations* for a list of supported models.

For a supported semiconjugate model, you can request Gibbs sampling for a block of parameters by specifying the gibbs suboption within option block(). In some cases, the gibbs suboption may be used in all parameter blocks, in which case we will have full Gibbs sampling.

To use Gibbs sampling for a set of parameters, you must first place them in separate prior() statements and specify semiconjugate prior distributions and then place them in a separate block and include the gibbs suboption, block(..., gibbs).

Here is a standard application of a full Gibbs sampling to a normal mean-only model. Under the normal–inverse-gamma prior, the conditional posterior distributions of the mean parameter is normal and of the variance parameter is inverse gamma.

```
. bayesmh y, likelihood(normal({var}))
>            prior({y:_cons},  normal(1,10))
>            prior({var},      igamma(10,1))
>            block({y:_cons},  gibbs)
>            block({var},      gibbs)
```

Because {y:_cons} and {var} are approximately independent a posteriori, we specified them in separate blocks.

Gibbs sampling can be applied to hyperparameters, which are not directly involved in the likelihood specification of the model. For example, we can use Gibbs sampling for the covariance matrix of regression coefficients.

```
. bayesmh y x, likelihood(normal(var))
>              prior(var,         igamma(10,1))
>              prior({y:_cons x}, mvnormal(2,1,0,{Sigma,m}))
>              prior({Sigma,m},   iwishart(2,10,V))
>              block({Sigma,m},   gibbs)
```

In the next example, the matrix parameter `{Sigma,m}` specifies the covariance matrix in the multivariate normal prior for a pair of model parameters, `{y:1.cat}` and `{y:2.cat}`. `{Sigma,m}` is a hyperparameter—it is not a model parameter of the likelihood but a parameter of a prior distribution, and it has an inverse-Wishart hyperprior distribution, which is a semiconjugate prior with respect to the multivariate normal prior distribution. Therefore, we can request a Gibbs sampler for `{Sigma,m}`.

```
bayesmh y x i.cat, likelihood(probit)
>                  prior(y:x _cons,     normal(0, 1000))
>                  prior(y:1.cat 2.cat, mvnormal0(2,{Sigma,m}))
>                  prior({Sigma,m}, iwishart(2,10,V))
>                  block({Sigma,m}, gibbs)
```

In general, Gibbs sampling, when available, is useful for covariance matrices because MH sampling has low efficiency for sampling positive-definite symmetric matrices. In a multivariate normal regression, the inverse Wishart distribution is a conjugate prior for the covariance matrix and thus inverse Wishart is the most common prior specification for a covariance matrix parameter. If an inverse-Wishart prior (`iwishart()`) is used for a covariance matrix, you can specify Gibbs sampling for the covariance matrix. You can do so by placing the matrix in a separate block and specifying the `gibbs` suboption in that block, as we showed above. Using Gibbs sampling for the covariance matrix usually greatly improves the sampling efficiency.

Adaptation of the MH algorithm

The MH algorithm simulates Markov chains by generating small moves or jumps from the current parameter values (or current state) according to the proposal distribution. At each iteration of the algorithm, the proposed new state is accepted with a probability that is calculated based on the newly proposed state and the current state. The choice of a proposal distribution is crucial for the mixing properties of the Markov chain, that is, the rate at which the chain explores its stationary distribution. (In a Bayesian context, a Markov chain state is a vector of model parameters, and a stationary distribution is the target posterior distribution.) If the jumps are too small, almost all moves will be accepted. If the jumps are too large, almost all moves will be rejected. Either case will cause the chain to explore the entire posterior domain slowly and will thus lead to poor mixing. Adaptive MH algorithms try to tune the proposal distribution so that some optimal AR is achieved (Haario, Saksman, and Tamminen [2001]; Roberts and Rosenthal [2009]; Andrieu and Thoms [2008]).

In the random-walk MH algorithm, the proposal distribution is a Gaussian distribution with a zero mean and is completely determined by its covariance matrix. It is useful to represent the proposal covariance matrix as a product of a (scalar) scale factor and a positive-definite scale matrix. Gelman, Gilks, and Roberts (1997) show that the optimal scale matrix is the true covariance matrix of the target distribution, and the optimal scale factor is inversely proportional to the number of parameters. Therefore, in the ideal case when the true covariance matrix is available, it can be used as a proposal covariance and an MCMC adaptation can be avoided altogether. In practice, the true covariance is rarely known and the adaptation is thus unavoidable.

In the `bayesmh` command, the scale factor and the scale matrix that form the proposal covariance are constantly tuned during the adaptation phase of an MCMC so that the current AR approaches some predefined value.

You can use `scale()`, `covariance()`, and `adaptation()` options to control adaptation of the MH algorithm. The TAR is controlled by option `adaptation(tarate())`. The initial scale factor and scale

matrix can be modified using the `scale()` and `covariance()` options. In the presence of blocks of parameters, these options can be specified separately for each block within the `block()` option. At each adaptation step, a new scale matrix is formed as a mixture (a linear combination) of the previous scale matrix and the current empirical covariance matrix of model parameters. The mixture of the two matrices is controlled by option `adaptation(beta())`. A positive `adaptation(beta())` is recommended to have a more stable scale matrix between adaptation periods. The adaptation lasts until the maximum number `adaptation(every())`×`adaptation(maxiter())` of adaptive iterations is reached or until `adaptation(tarate())` is reached within the `adaptation(tolerance())` limit. The default for `maxiter()` depends on the specified burn-in and `adaptation(every())` and is computed as $\max\{25, \texttt{floor(burnin()/adaptation(every()))}\}$. The default for `adaptation(every())` is 100. If you change the default values of these parameters, you may want to increase the `burnin()` to be as long as the specified adaptation period so that adaptation is finished before the final simulated sample is obtained. (There are adaptation regimes in which adaptation is performed during the simulation phase as well, such as continuous adaptation.) Two additional adaptation options, `adaptation(alpha())` and `adaptation(gamma())` control the AR and the adaptation rate. For a detailed description of the adaptation process, see *Adaptive random-walk Metropolis–Hastings* in [BAYES] **Intro** and *Adaptive MH algorithm* in *Methods and formulas*.

With multiple chains, adaptation options apply to all chains.

Specifying initial values

When exploring convergence of MCMC, it may be useful to try different initial values to verify that the convergence is unaffected by starting values. Using different initial values is also essential for multiple chains. We first describe how to specify initial values for a single chain and later for multiple chains.

Single chain. There are two different ways to specify initial values of model parameters in `bayesmh` for a single chain. First is by specifying an initial value when declaring a model parameter. Second is by specifying an initial value in the `initial()` option. Initial values for matrix model parameters may be specified only in the `initial()` option.

For example, below we initialize variance parameter `{var}` with a value of 1 using two equivalent ways, as follows:

```
. bayesmh y x, likelihood(normal({var=1})) ...
```

or

```
. bayesmh y x, likelihood(normal({var})) initial({var} 1) ...
```

If both initial-value specifications are used, initial values specified in the `initial()` option override any initial values specified during parameter declaration for the corresponding parameters.

You can initialize multiple parameters with the same value by supplying a list of parameters by using any of the specifications described in *Referring to model parameters* to `initial()`. For example, to initialize all regression coefficients from equations `y1` and `y2` to zero, you can type

```
. bayesmh ..., initial({y1:} {y2:} 0) ...
```

Stata expressions that evaluate to a number can also be used to specify initial values for scalar parameters. One particularly useful application of this is specifying random initial values using Stata's random-number functions; see [FN] **Random-number functions**. For example, we can generate random initial values for parameters `{y1:}` from a normal distribution with mean 0 and standard deviation 10 and for parameters `{y2:}` from a uniform on $(0, 1)$ distribution as follows:

```
. bayesmh ..., initial({y1:} rnormal(0,10) {y2:} runiform(0,1)) ...
```

You may also specify the initrandom option to request random initial values for all model parameters. In that case, initial values are generated from the prior distributions of the parameters, except for parameters that are assigned flat, jeffreys, density(), logdensity(), or jeffreys() prior distributions. For such parameters, you must specify your own initial values, or bayesmh will issue an error message.

Multiple chains. In the presence of multiple chains, you can use the init#() options to specify initial values for each chain: the init1() option specifies initial values for the first chain, init2() for the second chain, and so on. You specify initial values within the init#() options just like you do this within initial() for a single chain. (With multiple chains, initial() is synonymous to init1().)

For example,

```
. bayesmh y x, likelihood(normal({var})) nchains(2) init1({var} 1) init2({var} 10) ...
```

You can use the initall() option to specify initial values for all chains. This is useful, for instance, when you want to generate random initial values from the same distribution for all chains. You should avoid specifying fixed initial values within initall() because then all chains will use the same starting values.

Default initial values. By default, if no initial value is specified and option nomleinitial is not used, bayesmh uses MLEs, whenever available, as starting values for model parameters for a single chain. For random-effects parameters, bayesmh uses zeros as initial values and ones for their respective variance components. You can specify the initsummary option to see the default initial values used by bayesmh.

For example, for the previous regression model, bayesmh uses regression coefficients and mean squared error from linear regression regress y x as the respective starting values for the regression model parameters and variance parameter {var}.

If MLE is not available and an initial value is not provided, then a scalar model parameter is initialized with 1 for positive parameters and 0 for other parameters, and a matrix model parameter is initialized with an identity matrix. Note, however, that this default initialization is not guaranteed to correspond to the feasible state for the specified posterior model; that is, posterior probability of the initial state can be 0. When initial values are not feasible, bayesmh makes 500 random attempts to find a feasible initial-value vector. An initial-value vector is feasible if it corresponds to a state with positive posterior probability. If feasible initial values are not found after 500 attempts, bayesmh will issue the following error:

```
could not find feasible initial state
r(498);
```

You may use the search() option to modify the default settings for finding feasible initial values.

In the presence of multiple chains, each chain uses a different set of initial values for model parameters. The above description of default initial values applies to the first chain only. The subsequent chains use random initial values, which generally are generated from the prior distributions.

For improper priors flat, jeffreys, and jeffreys(#), bayesmh cannot draw random initial values directly from these priors. Doing so would typically produce extreme values for model parameters for which log likelihood would be missing. Instead, the command generates initial values from a normal distribution centered at the initial values of the first chain with standard deviations proportional to the magnitudes of the respective initial estimates. This approach is also used to generate default initial values with user-defined priors density() and logdensity().

Random initial values may not always be feasible. Extreme values may be produced for model parameters for some prior distributions, which may lead to missing log-likelihood values. bayesmh

will attempt to generate several different sets of initial values before terminating the simulation of a particular chain and issuing a warning message. In this case, you must specify your own initial values for that chain.

Default initial values are provided for convenience! To detect nonconvergence, overdispersed initial values should be used with multiple chains. Randomly generated default initial values are not guaranteed to produce overdispersed initial values for all chains. To fully explore convergence, we recommend that you specify your own initial values with multiple chains, especially with improper or noninformative priors.

See *Convergence diagnostics using multiple chains* for an example of specifying initial values with multiple chains.

You can use the `initsummary` option to see the initial values used for simulation. The initial values are also stored in the `e(init)` matrix after estimation.

Summarizing and reporting results

As we discussed in *Checking model specification*, it is useful to verify the details about your model specification before estimation. The `dryrun` model will display the model summary without estimation. Once you are satisfied with the model specification, you can use the `nomodelsummary` option during estimation to suppress a potentially long model summary from the final output.

In the presence of blocking, you may also display the information about specified blocks by using the `blocksummary` option.

Simulation may be time consuming for large datasets and for models with many parameters. You can specify one of `dots` or `dots(#)` option to display a dot every # iterations to see the simulation progress.

You can also use the `initsummary` option to see the initial values used in the simulation, which may be useful with multiple chains.

Posterior summaries and credible intervals

After simulation, `bayesmh` reports various summaries about the model parameters in the output table. The summaries include posterior mean and median estimates, estimates of posterior standard deviation and MCSE, and credible intervals. By default, 95% equal-tailed credible intervals are reported. You can use the `hpd` option to request HPD intervals instead. You can also use the `clevel()` option to change the default credible level.

`bayesmh` provides two estimators for MCSE: one using ESS and one using batch means. The ESS-based estimator is the default. You can request the batch-means estimator by specifying the `batch()` option. Options `corrlag()` and `corrtol()` affect how ESS is estimated when computing MCSE; see *Methods and formulas* in [BAYES] **bayesstats summary** for details.

For multilevel models, `bayesmh` does not report MCMC summaries for random-effects parameters by default, but you can use the `showreffects` or `showreffects()` option to display the summaries, respectively, for all of them or for a subset of them during either estimation or replay.

In the presence of multiple chains, all chains are used to produce posterior summaries. You can use `bayesstats summary`'s `sepchains` option to see the results for each chain separately. Also, the reported acceptance rate, efficiencies, and log marginal-likelihood are averaged over all chains. You can use the `chainsdetail` option to see these simulation summaries for each chain.

Saving MCMC results

In addition to postestimation summaries, bayesmh saves simulation results containing MCMC samples for all model parameters to a temporary Stata dataset. You can use the saving() option to save simulation results to a permanent dataset. In fact, if you want to store your estimation results in memory or save them to a disk, you must specify the saving() option with bayesmh; see *Storing estimation results after Bayesian estimation* in [BAYES] **Bayesian postestimation**. You can also specify the saving() option on replay.

```
. bayesmh, saving(...)
```

By default, all model parameters are saved in the dataset. If desired, you can exclude some of the parameters from the dataset by specifying the exclude() option. Beware that you will not be able to obtain posterior summaries for these parameters or use them in any way in your analysis, because no simulation results will be available for them. Also, the Laplace–Metropolis approximation for the log marginal-likelihood will not be available because its computation requires simulation results for all model parameters.

When fitting multilevel models containing many random effects, if you are interested only in the estimates of regression coefficients and variance components, you may consider using the exclude() option to exclude saving MCMC estimates of random-effects parameters to save time. If you do this, beware that some of the Bayesian postestimation features may not be available.

Convergence of MCMC

As we discuss in *Convergence diagnostics of MCMC* in [BAYES] **Intro**, checking convergence is an essential step of any MCMC simulation. Bayesian inference based on an MCMC sample is only valid if the Markov chain has converged and the sample is drawn from the desired posterior distribution. It is important to emphasize that we need to verify the convergence for all model parameters and not only for a subset of parameters of interest. Another difficulty in accessing convergence of MCMC is the lack of a single conclusive convergence criterion. The diagnostic usually involves checking for several necessary (but not necessarily sufficient) conditions for convergence. In general, the more aspects of the MCMC sample you inspect, the more reliable your results are.

An MCMC is said to have converged if it reached its stationary distribution. In the Bayesian context, the stationary distribution is the true posterior distribution of model parameters. Provided that the considered Bayesian model is well specified (that is, it defines a proper posterior distribution of model parameters), the convergence of MCMC is determined by the properties of its sampling algorithm.

The main component of the MH algorithm, or any MCMC algorithm, is the number of iterations it takes for the chain to approach its stationary distribution or for the MCMC sample to become representative of a sample from the true posterior distribution of model parameters. The period during which the chain is converging to its stationary distribution from its initial state is called the burn-in period. The iterations of the burn-in period are discarded from the MCMC sample used for analysis. Another complication is that adjacent observations from the MCMC sample tend to be positively correlated; that is, autocorrelation is typically present in MCMC samples. In theory, this should not be a problem provided that the MCMC sample size is sufficiently large. In practice, the autocorrelation in the MCMC sample may be so high that obtaining a sample of the necessary size becomes infeasible and finding ways to reduce autocorrelation becomes important.

Two aspects of the MH algorithm that affect the length of the burn-in (and convergence) are the starting values of model parameters or, in other words, a starting state and a proposal distribution. bayesmh has the default burn-in of 2,500 iterations, but you can change it by specifying the burnin() option. bayesmh uses a Gaussian normal distribution with a zero mean and a covariance matrix that

is updated with current sample values during the adaptation period. You can control the proposal distribution by changing the initial scale factor in option `scale()` and an initial scale matrix in option `covariance()`; see *Adaptation of the MH algorithm*.

For the starting values of a single chain, `bayesmh` uses MLEs whenever available, but you can specify your own initial values in option `initial()`; see *Specifying initial values*. Good initial values help to achieve fast convergence of MCMC and bad initial values may slow convergence down. A common approach for eliminating the dependence of the chain on the initial values is to discard an initial part of the simulated sample: a burn-in period. The burn-in period must be sufficiently large for a chain to "forget" its initial state and approach its stationary distribution or the desired posterior distribution.

There are some researchers (for example, Geyer [2011]) who advocate that any starting point in the posterior domain is equally good and there should be no burn-in. While this is a sensible approach for a fixed, nonadaptive MH algorithm, it may not be as sensible for an adaptive MH algorithm because the proposal distribution is changing (possibly drastically) during the adaptation period. Therefore, adaptive iterations are better discarded from the analysis MCMC sample and thus it is recommended that the burn-in period is at least as long as the adaptation period. (There are adaptive regimes such as continuous adaptation in which adaptation continues after the burn-in period as well.)

In addition to fast convergence, an "ideal" MCMC chain will also have good mixing (or low autocorrelation). A good mixing can be viewed as a rapid movement of the chain around the parameter space. High autocorrelation in MCMC and consequently low efficiencies are usually indications of bad mixing. To improve the mixing of the chain, you may need to improve the efficiency of the algorithm (see *Improving efficiency of the MH algorithm—blocking of parameters*) or sometimes reparameterize your model. In the presence of high autocorrelation, you may also consider subsampling or thinning the chain, option `thinning()`, to reduce autocorrelation, but this may not always be the best approach.

Even when the chain appears to have converged and has good mixing, you may still have a case of pseudoconvergence, which is common for multimodal posterior distributions. Specifying different sets of initial values may help detect pseudoconvergence.

Multiple chains are often used to assess the convergence of MCMC; see *Convergence diagnostics using multiple chains* and Balov (2016c). For more information about convergence of MCMC and its diagnostics, see *Convergence diagnostics of MCMC* in [BAYES] **Intro**, [BAYES] **bayesgraph**, [BAYES] **bayesstats ess**, and [BAYES] **bayesstats grubin**.

In what follows, we concentrate on demonstrating various specifications of `bayesmh`, which may not always correspond to the optimal Bayesian analysis for the considered problem. In addition, although we skip checking convergence for some of our models to keep the exposition short, it is important that you always check the convergence of all parameters in your model in your analysis before you make any inferential conclusions. If you are also interested in any functions of model parameters, you must check convergence of those functions as well.

Video examples

Introduction to Bayesian statistics, part 1: The basic concepts

Introduction to Bayesian statistics, part 2: MCMC and the Metropolis–Hastings algorithm

Getting started examples

We will use the familiar `auto.dta` for our introductory examples. This dataset contains information about 74 automobiles, including their make and model, price, and mileage (variable `mpg`). In our examples, we are interested in estimating the average fuel efficiency as measured by the `mpg` variable and its relationship with other automobile characteristics such as `weight`.

```
. use https://www.stata-press.com/data/r18/auto
(1978 automobile data)
. describe mpg weight length
Variable      Storage   Display    Value
    name         type    format    label      Variable label
------------------------------------------------------------------------------
mpg             int     %8.0g                 Mileage (mpg)
weight          int     %8.0gc                Weight (lbs.)
length          int     %8.0g                 Length (in.)
```

Mean of a normal distribution with a known variance

We start with an example of estimating the mean of a normal distribution with known variance. This corresponds to a constant-only normal linear regression with an unknown constant (or intercept) and a known error variance.

Suppose we are interested in estimating the average fuel efficiency as measured by the `mpg` variable. For illustration purposes, let's assume that `mpg` is normally distributed. We are interested in estimating its mean. Let's also assume that we know the variance of `mpg` and it is 36.

▷ Example 1: Noninformative prior for the mean when variance is known

To fit a Bayesian model, we must specify the likelihood model and priors for all model parameters. We have only one parameter in this model—the constant (or the mean) of `mpg`. We first consider a noninformative prior for the constant: the prior distribution with a density equal to one.

To specify this model in `bayesmh`, we use the likelihood specification `mpg, likelihood(normal(36))` and the prior specification `prior({mpg:_cons}, flat)`, where suboption `flat` requests a flat prior distribution with the density equal to one. This prior is an improper prior for the constant—the prior distribution does not integrate to one. `{mpg:_cons}`, the constant or the mean of `mpg`, is the only model parameter and is declared automatically by `bayesmh` as a part of the regression function. (For this reason, we also did not need to specify the mean of the `normal()` distribution in the likelihood specification.) All other simulation and reporting options are left at default.

Because `bayesmh` uses MCMC sampling, a stochastic procedure, to obtain results, we specify a random-number seed (for example, 14) for reproducibility of results.

```
. set seed 14
. bayesmh mpg, likelihood(normal(36)) prior({mpg:_cons}, flat)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},36)
Prior:
  {mpg:_cons} ~ 1 (flat)
------------------------------------------------------------------------------
```

```
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .4161
Log marginal-likelihood = -233.96144            Efficiency       =      .2292

------------------------------------------------------------------------------
             |                                                 Equal-tailed
         mpg |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
       _cons |   21.29812   .703431   .014693   21.28049   19.93155   22.69867
------------------------------------------------------------------------------
```

`bayesmh` first reports the summary of the model. The likelihood model specified for `mpg` is normal with mean `{mpg:_cons}` and fixed variance of 36. The prior for `{mpg:_cons}` is flat or completely noninformative.

Our model is very simple, so its summary is very short. For other models, the model summary may get very long. You can use the `nomodelsummary` option to suppress it from the output. It is useful, however, to review the model summary before estimation for models with many parameters and complicated specifications. You can use the `dryrun` option to see the model summary without estimation. Once you verified the correctness of your model specification, you can specify `nomodelsummary` during estimation.

Next, `bayesmh` reports the header including the title for the fitted model, the used MCMC algorithm, and various numerical summaries of the sampling procedure. `bayesmh` performed 12,500 MCMC iterations, of which 2,500 were discarded as burn-in iterations and the next 10,000 iterations were kept in the final MCMC sample. An overall AR is 0.42, meaning that 42% out of 10,000 proposal parameter values were excepted by the algorithm. This is a good AR for the MH algorithm. Values below 10% may be a cause for concern and may indicate problems with convergence of MCMC. Very low ARs may also mean high autocorrelation. The efficiency is 0.23 and is also considered good for the MH algorithm. Efficiencies below 1% should be investigated further and would require further tuning of the algorithm and possibly revisiting the considered model.

Finally, `bayesmh` reports an estimation table that includes the posterior mean, posterior standard deviation, MCMC standard error (MCSE), posterior median, and the 95% credible interval.

The estimated posterior mean for `{mpg:_cons}` is 21.298 with a posterior standard deviation of 0.70. The efficiency of the estimator of the posterior mean is about 23%, which is relatively high for the random-walk MH sampling. In general, you should expect to see lower efficiencies from this algorithm for models with more parameters. The MCSE, which is an approximation of the error in estimating the true posterior mean, is about 0.015. Therefore, provided that the MCMC simulation has converged, the posterior mean of the constant is accurate to 1 decimal position, 21.3. If you want an estimation precision of, say, 2 decimal positions, you may need to increase the MCMC sample size 10^1 times; that is, use `mcmcsize(100000)`.

The estimated posterior mean and medians are very close, suggesting that the posterior distribution of `{mpg:_cons}` may be symmetric. In fact, the posterior distribution of a mean in this model is known to be a normal distribution.

According to the reported 95% credible interval, the probability that the mean of `mpg` is between 19.9 and 22.7 is about 0.95. You can use the `clevel()` option to change the default credible level; also see [BAYES] **set clevel**.

Because we used a completely noninformative prior, our results should be the same as frequentist results. In this Bayesian model, the posterior distribution of the constant parameter is known to be normal with a mean equal to the sample average. In the frequentist domain, the MLE of the constant

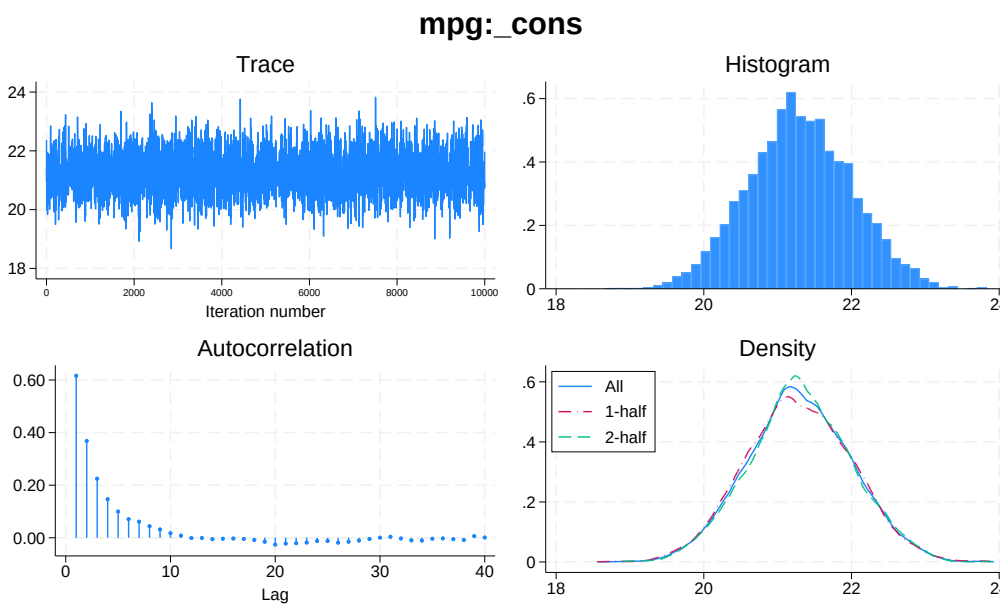
is also the sample average, so the posterior mean estimate and the MLE should be the same in this model.

The sample average of mpg is 21.2973. Our posterior mean estimate is 21.298, which is very close. The reason it is not exactly the same is because we estimated the posterior mean of the constant based on an MCMC sample simulated from its posterior distribution instead of using the known formula. Closed-form expressions for posterior mean estimators are available only for some Bayesian models. In general, posterior distributions of parameters are unknown and posterior summaries may only be estimated from the MCMC samples of parameters.

In practice, we must verify the convergence of MCMC before making any inferential conclusions about the obtained results.

We start by looking at various graphical diagnostics as produced by bayesgraph diagnostics.

```
. bayesgraph diagnostics {mpg:_cons}
```



The trace plot represents a "perfect" trace plot. It does not exhibit any trends, and it traverses the distribution quickly. The chain is centered around 21.3, but also explores the portions of the distribution where the density is low, which is indicative of good mixing of the chain. The autocorrelation dies off very quickly. The posterior distribution looks normal. The kernel density estimates based on the first and second halves of the sample are very similar to each other and are close to the overall density estimate. We can see that MCMC converged and mixes well. See [BAYES] **bayesgraph** for details about this command.

See *Convergence diagnostics using multiple chains* for an example of using multiple chains to assess convergence. Also see *Convergence diagnostics of MCMC* for more discussion about convergence of MCMC.

◁

▷ Example 2: Informative prior for the mean when variance is known

In example 1, we used a noninformative prior for {mpg:_cons}. Here, we consider a conjugate normal prior for {mpg:_cons}. A parameter is said to have a conjugate prior when the corresponding posterior belongs to the same family as the prior. In our example, if we assume a normal prior for the constant, its posterior is known to be normal too.

Suppose that based on previous studies, the distribution of the mean mileage was found to be normal with mean of 25 and variance of 10. We change the `flat` prior in `bayesmh`'s `prior()` option from example 1 with `normal(25,10)`.

```
. set seed 14
. bayesmh mpg, likelihood(normal(36)) prior({mpg:_cons}, normal(25,10))
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},36)
Prior:
  {mpg:_cons} ~ normal(25,10)
------------------------------------------------------------------------------

Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .4169
Log marginal-likelihood = -236.71627            Efficiency       =      .2293

------------------------------------------------------------------------------
             |                                                 Equal-tailed
         mpg |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
       _cons |  21.47952   .6820238   .014243   21.47745   20.13141   22.82153
------------------------------------------------------------------------------
```

Compared with example 1, our results change only slightly: the estimated posterior mean is 21.48 with a posterior standard deviation of 0.68. The 95% credible interval is $[20.1, 22.82]$.

The reason we obtained such similar results is that our specified prior is in close agreement with what we observed in this sample. The prior mean of 25 with a standard deviation of $\sqrt{10} = 3.16$ overlaps greatly with what we observe for {mpg:_cons} in the data.

If we place a very strong prior on the value for the mean by, for example, substantially decreasing the variance of the normal prior distribution,

```
. set seed 14
. bayesmh mpg, likelihood(normal(36)) prior({mpg:_cons}, normal(25,0.1))
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},36)
Prior:
  {mpg:_cons} ~ normal(25,0.1)
------------------------------------------------------------------------------

Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .4194
Log marginal-likelihood =  -246.2939            Efficiency       =      .2352

------------------------------------------------------------------------------
             |                                                 Equal-tailed
         mpg |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
       _cons |  24.37211    .292777   .006037   24.36588   23.79701   24.94403
------------------------------------------------------------------------------
```

we obtain very different results. Now the posterior mean and standard deviation estimates are very close to their prior values, as one would expect with such strong prior information.

Which results are correct? The answer depends on how confident we are in our prior knowledge. If we previously observed many samples in which the average mileage for the considered population of cars was essentially 25, our last results are consistent with this and the information about the mean of `{mpg:_cons}` contained in the observed sample was not enough to counteract our belief. If, on the other hand, we had no prior information about the mean mileage, then we would use a noninformative or mildly informative prior in our Bayesian analysis. Also, if we believe that our observed data should have more weight in our analysis, we would not specify a very strong prior.

◁

▷ Example 3: Noninformative normal prior for the mean when variance is known

In example 1, we used a completely noninformative, flat prior for `{mpg:_cons}`. In example 2, we considered a conjugate normal prior for `{mpg:_cons}`. We also saw that by varying the variance of the normal prior distribution, we could control the "informativeness" of our prior. The larger the variance, the less informative the prior. In fact, if we let the variance approach infinity, we will arrive at the same posterior distribution of the constant as with the flat prior.

For example, if we specify a very large variance in the normal prior,

```
. set seed 14
. bayesmh mpg, likelihood(normal(36)) prior({mpg:_cons}, normal(0,1000000))
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},36)
Prior:
  {mpg:_cons} ~ normal(0,1000000)
------------------------------------------------------------------------------

Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .4161
Log marginal-likelihood = -241.78836            Efficiency       =      .2292

------------------------------------------------------------------------------
             |                                                Equal-tailed
         mpg |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
       _cons |   21.29812   .7034313   .014693   21.28049   19.93155   22.69868
------------------------------------------------------------------------------
```

we will obtain results that are very similar to the results from example 1 with the flat prior.

We do not need to use such an extreme value of the variance for the results to become less sensitive to the prior specification. As we saw in example 2, using the variance of 10 in that example resulted in very little impact of the prior on the results.

◁

Mean of a normal distribution with an unknown variance

Let's now consider the case where both mean and variance of the normal distribution are unknown.

▷ Example 4: Noninformative Jeffreys prior when mean and variance are unknown

A noninformative prior commonly used for the normal model with unknown mean and variance is the Jeffreys prior, under which the prior for the mean is flat and the prior for the variance is the reciprocal of the variance. We use the same `flat` prior for `{mpg:_cons}` as in example 1 and specify the `jeffreys` prior for `{var}` using a separate `prior()` statement.

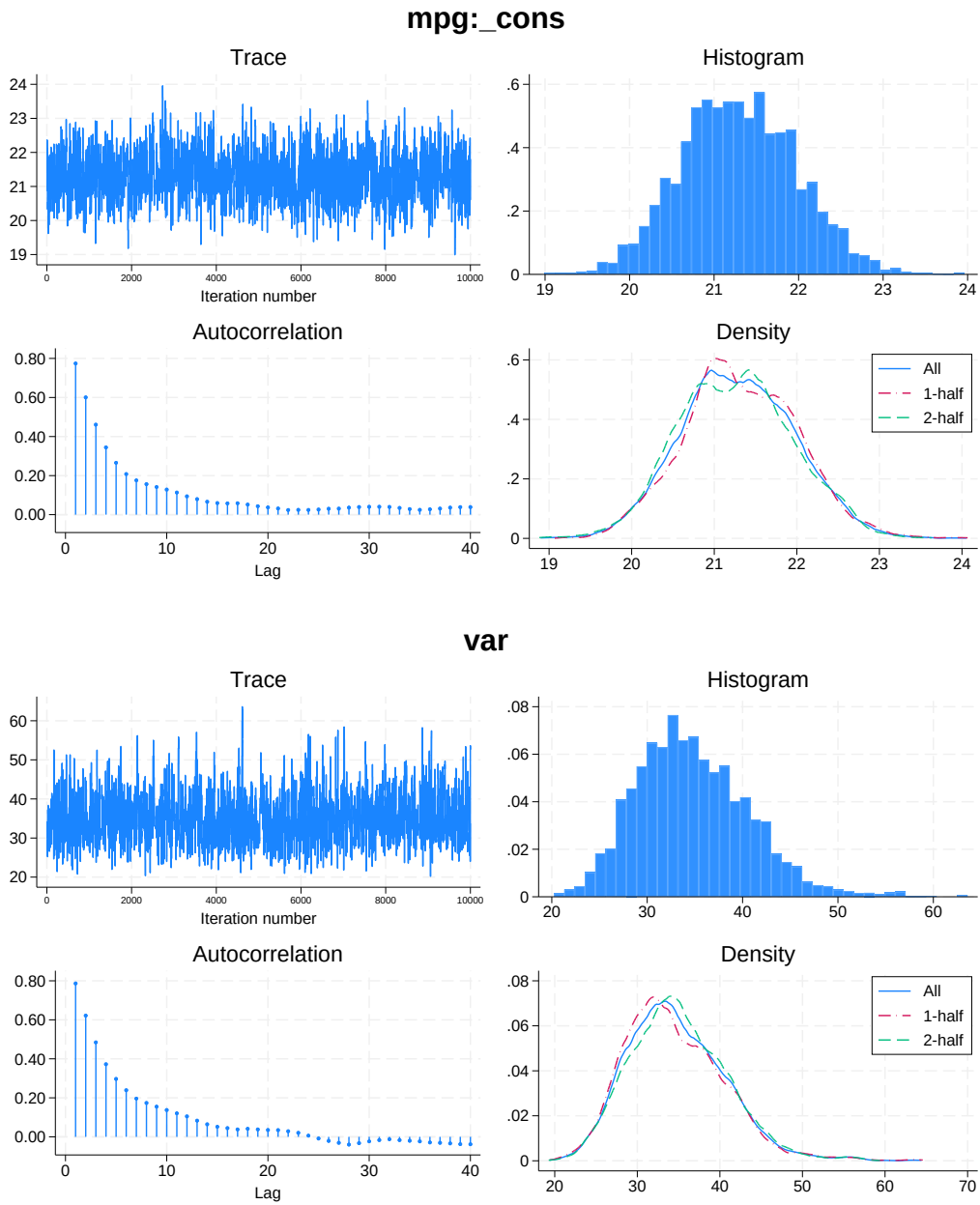
```
. set seed 14
. bayesmh mpg, likelihood(normal({var}))
> prior({mpg:_cons}, flat) prior({var}, jeffreys)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},{var})
Priors:
  {mpg:_cons} ~ 1 (flat)
        {var} ~ jeffreys
------------------------------------------------------------------------------
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .2668
                                                Efficiency:  min =     .09718
                                                             avg =      .1021
Log marginal-likelihood =   -234.645                         max =      .1071
------------------------------------------------------------------------------
                                                              Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |  21.29222   .6828864   .021906   21.27898   19.99152   22.61904
-------------+----------------------------------------------------------------
         var |  34.76572    5.91534   .180754   34.18391    24.9129   47.61286
------------------------------------------------------------------------------
```

Because we used a noninformative prior, our results should be similar to the frequentist results apart from simulation uncertainty. Compared with example 1, the average efficiency of the MH algorithm decreased to 10%, as is expected with more parameters, but is still considered a good efficiency for the MH algorithm.

The posterior mean estimate of {mpg:_cons} is close to the OLS estimate of 21.297, and the posterior standard deviation is close to the standard error of the OLS estimate 0.673. MCSE is slightly larger than in example 1 because we have lower efficiency. If we wanted to make MCSE smaller, we could increase our MCMC sample size. The posterior mean estimate of {var} agrees with the MLE of the variance 33.02, but we would not expect the two to be necessarily the same. We estimated the posterior mean of {var}, not the posterior mode, and because posterior distribution of {var} is not symmetric, the two estimates may not be the same.

Again, as with any MCMC analysis, we must verify the convergence of our MCMC sample before we can trust our results.

```
. bayesgraph diagnostics _all
```



Graphical diagnostic plots do not show any signs of nonconvergence for either of the parameters. We can also check convergence more formally using multiple chains; see [BAYES] **bayesstats grubin** and *Convergence diagnostics using multiple chains*.

Recall that to access convergence of MCMC, we must explore convergence for all model parameters. ◁

▷ Example 5: Informative conjugate prior when mean and variance are unknown

For a normal distribution with unknown mean and variance, the informative conjugate prior is a normal prior for the mean and an inverse-gamma prior for the variance. Specifically, if $y \sim N(\mu, \sigma^2)$, then the informative conjugate prior for the parameters is

$$\begin{aligned} \mu|\sigma^2 &\sim N(\mu_0, \sigma^2) \\ \sigma^2 &\sim \text{InvGamma}(\nu_0/2, \nu_0\sigma_0^2/2) \end{aligned}$$

where μ_0 is the prior mean of the normal distribution and ν_0 and σ_0^2 are the prior degrees of freedom and prior variance for the inverse-gamma distribution. Let's assume $\mu_0 = 25$, $\nu_0 = 10$, and $\sigma_0^2 = 30$.

Notice that in the specification of the prior for {mpg:_cons}, we specify the parameter {var} as the variance of the normal distribution. We use igamma(5,150) as the prior for the variance parameter {var}.

```
. set seed 14
. bayesmh mpg, likelihood(normal({var}))
> prior({mpg:_cons}, normal(25,{var}))
> prior({var}, igamma(5,150))
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},{var})
Priors:
  {mpg:_cons} ~ normal(25,{var})
        {var} ~ igamma(5,150)
------------------------------------------------------------------------------
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .1971
                                                Efficiency:  min =     .09822
                                                             avg =     .09923
Log marginal-likelihood = -237.77006                         max =      .1002
------------------------------------------------------------------------------
                                                              Equal-tailed
             |      Mean   Std. dev.      MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |    21.314   .6639278    .02097   21.29516   20.08292   22.63049
-------------+----------------------------------------------------------------
         var |   33.54699   5.382861   .171756   32.77635   24.88107    46.0248
------------------------------------------------------------------------------
```

Compared with example 4, the variance is slightly smaller, but the results are still very similar.

◁

▷ Example 6: Noninformative inverse-gamma prior when mean and variance are unknown

The Jeffreys prior for the variance from example 4 can be viewed as a limiting case of an inverse-gamma distribution with the degrees of freedom approaching zero.

Indeed, if we replace the `jeffreys` prior in example 4 with an inverse-gamma distribution with very small degrees of freedom,

```
. set seed 14
. bayesmh mpg, likelihood(normal({var}))
> prior({mpg:_cons}, flat)
> prior({var}, igamma(0.0001,0.0001))
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},{var})
Priors:
  {mpg:_cons} ~ 1 (flat)
        {var} ~ igamma(0.0001,0.0001)
------------------------------------------------------------------------------
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .2668
                                                Efficiency:  min =     .09718
                                                             avg =      .1021
Log marginal-likelihood = -243.85656                         max =      .1071
------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |  21.29223   .6828811   .021905   21.27899   19.99154   22.61903
-------------+----------------------------------------------------------------
         var |  34.76569   5.915305   .180753   34.18389   24.91294   47.61275
------------------------------------------------------------------------------
```

we obtain results that are very close to the results from example 4.

◁

Simple linear regression

In this example, we consider a simple linear regression with one independent variable. We continue with `auto.dta`, but this time we regress `mpg` on a rescaled covariate `weight`.

```
. use https://www.stata-press.com/data/r18/auto
(1978 automobile data)
. replace weight = weight/100
variable weight was int now float
(74 real changes made)
```

We will have three model parameters: the slope and the intercept for the linear predictor and the variance parameter for the error term. Regression parameters, `{mpg:weight}` and `{mpg:_cons}`, will be declared implicitly by `bayesmh`, but we will need to explicitly specify the variance parameter `{var}`. We will also need to assign appropriate priors for all parameters.

▷ Example 7: Noninformative prior for regression coefficients and variance

As in our earlier examples, we start with a noninformative prior. For this model, a common noninformative prior for the parameters includes flat priors for {mpg:weight} and {mpg:_cons} and a Jeffreys prior for {var}.

```
. set seed 14
. bayesmh mpg weight, likelihood(normal({var}))
> prior({mpg:}, flat)  prior({var}, jeffreys)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal(xb_mpg,{var})
Priors:
  {mpg:weight _cons} ~ 1 (flat)                                          (1)
               {var} ~ jeffreys
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .1768
                                                Efficiency:  min =     .04557
                                                             avg =     .06624
Log marginal-likelihood = -198.14389                         max =     .07961
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
mpg						
weight	-.6019838	.0512557	.001817	-.6018433	-.7015638	-.5021532
_cons	39.47227	1.589082	.058601	39.49735	36.26465	42.43594
var	12.22248	2.214665	.10374	11.92058	8.899955	17.47372

Our model summary shows the likelihood model for mpg, flat priors for the two regression coefficients, and a Jeffreys prior for the variance parameter. Now that we have a covariate in the model, the mean of the normal distribution is labeled as xb_mpg to emphasize that it is now a linear combination of independent variables. Regression coefficients involved in the linear predictor are marked with (1) on the right.

The results are again very similar to the frequentist results. Posterior mean estimates of the coefficients are very similar to the OLS estimates obtained by using regress below. Posterior standard deviations are similar to the standard errors from regress.

```
. regress mpg weight
      Source |       SS           df       MS      Number of obs   =        74
-------------+----------------------------------   F(1, 72)        =    134.62
       Model |  1591.99021         1  1591.99021   Prob > F        =    0.0000
    Residual |  851.469254        72  11.8259619   R-squared       =    0.6515
-------------+----------------------------------   Adj R-squared   =    0.6467
       Total |  2443.45946        73  33.4720474   Root MSE        =    3.4389

------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      weight |  -.6008687   .0517878   -11.60   0.000    -.7041058   -.4976315
       _cons |   39.44028   1.614003    24.44   0.000     36.22283    42.65774
------------------------------------------------------------------------------
```

Example 8: Conjugate prior for regression coefficients and variance

In this example, we use a conjugate prior for the parameters, which corresponds to normal priors for {mpg:weight} and {mpg:_cons} and an inverse-gamma prior for {var},

$$\begin{aligned}\beta_{\text{weight}}|\sigma^2 &\sim N(\mu_{\text{weight}}, \sigma^2)\\ \beta_{\text{cons}}|\sigma^2 &\sim N(\mu_{\text{cons}}, \sigma^2)\\ \sigma^2 &\sim \text{InvGamma}(\nu_0/2, \nu_0\sigma_0^2/2)\end{aligned}$$

where regression coefficients have different means but equal variances. μ_{weight} and μ_{cons} are the prior means of the normal distributions, and ν_0 and σ_0^2 are the prior degrees of freedom and prior variance for the inverse-gamma distribution. Let's assume $\mu_{\text{weight}} = -0.5$, $\mu_{\text{cons}} = 40$, $\nu_0 = 10$, and $\sigma_0^2 = 10$.

```
. set seed 14
. bayesmh mpg weight, likelihood(normal({var}))
> prior({mpg:weight}, normal(-0.5,{var}))
> prior({mpg:_cons},  normal(40,{var}))
> prior({var}, igamma(5,50))
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal(xb_mpg,{var})
Priors:
  {mpg:weight} ~ normal(-0.5,{var})                                        (1)
   {mpg:_cons} ~ normal(40,{var})                                          (1)
         {var} ~ igamma(5,50)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .1953
                                                Efficiency:  min =     .05953
                                                             avg =     .06394
Log marginal-likelihood = -202.74075                         max =     .06932
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
mpg						
weight	-.6074375	.0480685	.001916	-.6078379	-.6991818	-.5119767
_cons	39.65274	1.499741	.05696	39.63501	36.59486	42.47547
var	11.696	1.929562	.079083	11.52554	8.570938	16.26954

For this mildly informative prior, our regression coefficients are still very similar to the results obtained using the noninformative prior in example 7, but the variance estimate is slightly smaller.

◁

▷ Example 9: Zellner's g prior for regression coefficients

In example 8, we assumed that `{mpg:weight}` and `{mpg:_cons}` are independent a priori. We can specify Zellner's g prior (Zellner 1986), often used for regression coefficients in a multiple regression, which allows correlation between the regression coefficients.

The prior for the coefficients can be written as

$$\boldsymbol{\beta}|\sigma^2 \sim \text{MVN}(\boldsymbol{\mu}_0, g\sigma^2(X'X)^{-1})$$

where $\boldsymbol{\beta}$ is a vector of coefficients, $\boldsymbol{\mu}_0$ is the vector of prior means, g is the prior degrees of freedom, and X is the design matrix. Let's, for example, use $g = 30$ and $\boldsymbol{\mu}_0 = (\mu_{\text{weight}}, \mu_{\text{cons}}) = (-0.5, 40)$. Zellner's g prior is not strictly a conventional Bayesian prior because it depends on the data.

In `bayesmh`, we can use prior `zellnersg()` to specify this prior. The first argument for this prior is the dimension (2), the second argument is the degrees of freedom (30), the next parameters are prior means (-0.5 and 40), and the last parameter is the name of the parameter corresponding to the variance term (`{var}`).

```
. set seed 14
. bayesmh mpg weight, likelihood(normal({var}))
> prior({mpg:}, zellnersg(2,30,-0.5,40,{var}))
> prior({var},  igamma(5,50))
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal(xb_mpg,{var})
Priors:
  {mpg:weight _cons} ~ zellnersg(2,30,-0.5,40,{var})                    (1)
              {var} ~ igamma(5,50)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .2576
                                                Efficiency:  min =      .05636
                                                             avg =      .08661
Log marginal-likelihood =  -201.1662                         max =       .1025
------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
      weight |  -.6004123   .0510882   .001595  -.5998094  -.7040552  -.5058665
       _cons |   39.55017   1.590016   .050051   39.49377   36.56418   42.79701
-------------+----------------------------------------------------------------
         var |   12.18757   2.038488   .085865   11.90835   8.913695   16.88978
------------------------------------------------------------------------------
```

The results are now closer to the results using noninformative prior obtained in example 7, because we are introducing some information from the observed data by using $(X'X)^{-1}$.

◁

▷ Example 10: Specifying expressions as distributional arguments

We can actually reproduce what prior `zellnersg()` does in example 9 manually.

First, we need to create a matrix that contains $(X'X)^{-1}$, `S`.

```
. matrix accum xTx = weight
(obs=74)
. matrix S = invsym(xTx)
```

Then, we can use the multivariate normal prior `mvnormal()` with the variance specified as an expression `30*var*S`.

```
. set seed 14
. bayesmh mpg weight, likelihood(normal({var}))
> prior({mpg:}, mvnormal(2,-0.5,40,30*{var}*S))
> prior({var},  igamma(5,50))
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal(xb_mpg,{var})
Priors:
  {mpg:weight _cons} ~ mvnormal(2,-0.5,40,30*{var}*S)                    (1)
              {var} ~ igamma(5,50)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .2576
                                                Efficiency:  min =     .05636
                                                             avg =     .08661
Log marginal-likelihood =  -201.1662                         max =      .1025
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
mpg						
weight	-.6004123	.0510882	.001595	-.5998094	-.7040552	-.5058665
_cons	39.55017	1.590016	.050051	39.49377	36.56418	42.79701
var	12.18757	2.038488	.085865	11.90835	8.913695	16.88978

We obtain results identical to those from example 9.

An alternative way to specify the same model is by using the `mvnscaled()` prior distribution.

First, we create a Stata matrix `A` for the expression $30 \times (X'X)^{-1}$ using the `S` matrix we created above.

```
. matrix A = 30*S
```

Then, we use the `mvnscaled()` prior with mean values -0.5 and 40, scale matrix `A`, and variance parameter `{var}`.

```
. set seed 14
. bayesmh mpg weight, likelihood(normal({var}))
> prior({mpg:}, mvnscaled(2,-0.5,40,A,{var}))
> prior({var}, igamma(5,50))
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal(xb_mpg,{var})
Priors:
  {mpg:weight _cons} ~ mvnscaled(2,-0.5,40,A,{var})                       (1)
                {var} ~ igamma(5,50)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .2576
                                                Efficiency:  min =      .05636
                                                             avg =      .08661
Log marginal-likelihood =  -201.1662                         max =       .1025
------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
      weight |  -.6004123   .0510882   .001595  -.5998094  -.7040552  -.5058665
       _cons |   39.55017   1.590016   .050051   39.49377   36.56418   42.79701
-------------+----------------------------------------------------------------
         var |   12.18757   2.038488   .085865   11.90835   8.913695   16.88978
------------------------------------------------------------------------------
```

Again, we obtain results identical to those from example 9.

The `zellnersg()` prior is a special case of the `mvnscaled()` prior where the scaled matrix is proportional to $(X'X)^{-1}$. For a linear model with the `mvnscaled()` prior for regression coefficients and inverse Gamma prior for the error variance, `bayesmh` provides full Gibbs sampling for the parameters. In our example, Gibbs sampling can be requested by including the options `block({var}, gibbs)` and `block({mpg:}, gibbs)`.

◁

Multiple linear regression

For a detailed example of a multiple linear regression, see *Overview example* in [BAYES] **Bayesian commands**.

Improving efficiency of the MH sampling

In this section, we demonstrate how one can improve efficiency of the MH algorithm by using blocking of parameters and Gibbs sampling, whenever available. We continue with our simple linear regression of mpg on rescaled weight from *Simple linear regression*, but we use different values for the parameters of prior distributions. We also assume that regression coefficients and the variance parameter are independent a priori. We use the blocksummary option to include a summary about each block.

▷ Example 11: First simulation run

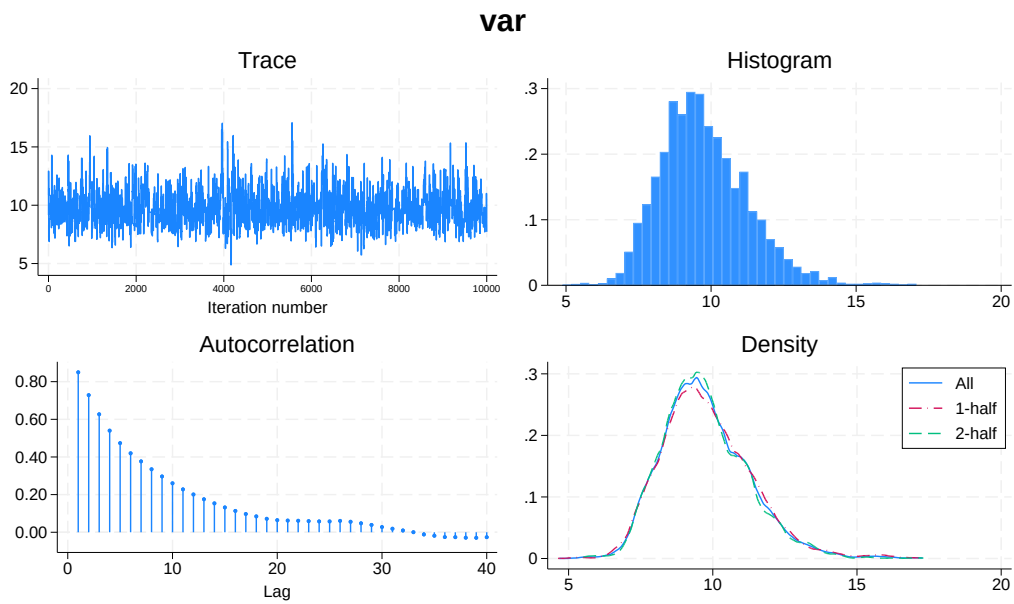
Our first simulation is performed using the default settings for the algorithm. Specifically, all three model parameters are placed in one simulation block and are updated simultaneously, as our block summary indicates.

```
. use https://www.stata-press.com/data/r18/auto
(1978 automobile data)
. replace weight = weight/100
variable weight was int now float
(74 real changes made)
. set seed 14
. bayesmh mpg weight, likelihood(normal({var}))
> prior({mpg:}, normal(0,100))
> prior({var}, igamma(10,10)) blocksummary
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal(xb_mpg,{var})
Priors:
  {mpg:weight _cons} ~ normal(0,100)                                      (1)
               {var} ~ igamma(10,10)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
Block summary
------------------------------------------------------------------------------
   1:  {mpg:weight _cons} {var}
------------------------------------------------------------------------------
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .2432
                                                Efficiency:  min =     .06871
                                                             avg =     .08318
Log marginal-likelihood = -226.63723                         max =     .09063
------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
      weight |  -.5759855   .0471288   .001569  -.5750919  -.6676517  -.4868595
       _cons |   38.65481   1.468605   .048784   38.70029   35.88062   41.49839
-------------+----------------------------------------------------------------
         var |   9.758003   1.514112   .057762   9.601339   7.302504   13.13189
------------------------------------------------------------------------------
```

The mean estimates based on the simulated sample are {mpg:weight} = −0.58, {mpg:_cons} = 38.65, and {var} = 9.8. The MH algorithm achieves an overall AR of 24% and an average efficiency of about 8%.

Our next step is to perform a visual inspection of the convergence of the chain.

```
. bayesgraph diagnostics {var}
```



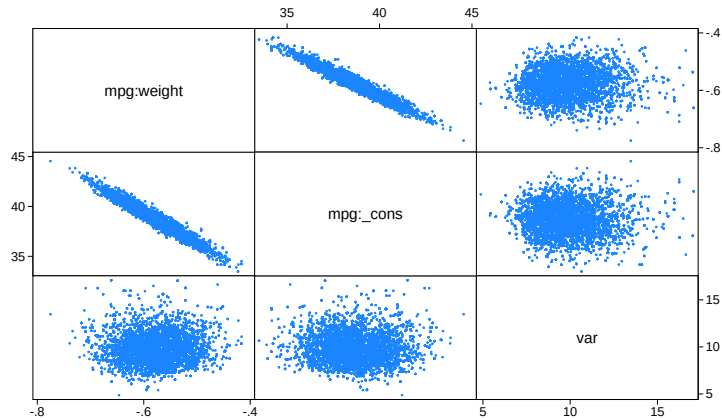
A graphical summary for the {var} parameter does not show any obvious problems. The trace plot reveals a good coverage of the domain of the marginal distribution, while the histogram and kernel density plots resemble the shape of an expected inverse-gamma distribution. The autocorrelation dies off after about lag 20.

◁

Example 12: Second simulation run—blocking of variance

Next, we show how to improve the mixing of the MCMC chain by using more careful blocking of model parameters. We can use the `bayesgraph matrix` command to view the scatterplots of the simulated values for {mpg:weight}, {mpg:_cons}, and {var}.

```
. bayesgraph matrix _all
```



The scatterplots reveal high correlation between {mpg:weight} and {mpg:_cons}. On the other hand, there is no significant correlation between {var} and the other two parameters.

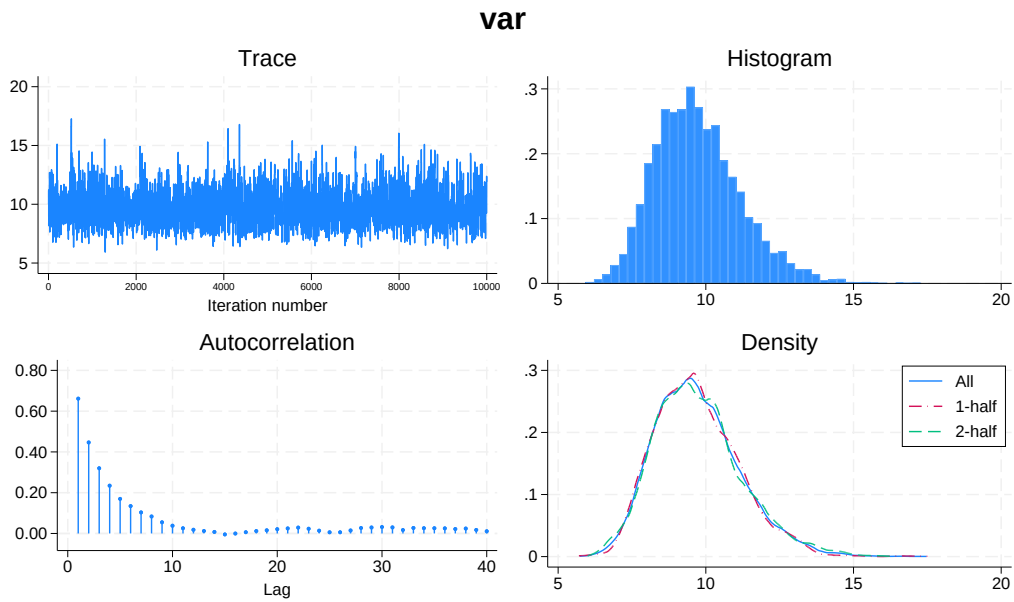
In cases like this, we can expect higher sampling efficiency if we place {var} in a separate block. We can do this by including the option `block({var})`. The other two parameters, {mpg:weight} and {mpg:_cons}, will be automatically considered as a second block.

```
. set seed 14
. bayesmh mpg weight, likelihood(normal({var}))
> prior({mpg:}, normal(0,100))
> prior({var}, igamma(10,10))
> block({var}) blocksummary
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal(xb_mpg,{var})
Priors:
  {mpg:weight _cons} ~ normal(0,100)                                      (1)
               {var} ~ igamma(10,10)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
Block summary
------------------------------------------------------------------------------
   1:  {var}
   2:  {mpg:weight _cons}
------------------------------------------------------------------------------
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .3309
                                                Efficiency:  min =     .09023
                                                             avg =      .1202
Log marginal-likelihood = -226.73992                         max =      .1784
------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
      weight |  -.5744536   .0450094   .001484   -.576579   -.663291  -.4853636
       _cons |   38.59206   1.397983    .04654   38.63252   35.80229   41.32773
-------------+----------------------------------------------------------------
         var |   9.721684   1.454193   .034432   9.570546   7.303129   12.95105
------------------------------------------------------------------------------
```

In this second run, we achieve higher simulation efficiency, about 12% on average. The MCSE for {var} is 0.034 and is about half the value of 0.058 from example 11, which leads to twice as much accuracy in the estimation of the posterior mean of {var}.

Again, we can verify the convergence of the MCMC run for {var} by inspecting the bayesgraph diagnostics plot.

```
. bayesgraph diagnostics {var}
```



The improved sampling efficiency for {var} is evident by observing that the autocorrelation becomes negligible after about lag 10. The trace plot reveals more rapid traversing of the marginal posterior domain as well.

◁

▷ Example 13: Third simulation run—Gibbs update of variance

Further improvement of the mixing can be achieved by requesting a Gibbs sampling for the variance parameter. This is possible because {var} has an inverse-gamma prior, which is independent of the mean and is a semiconjugate prior in this model.

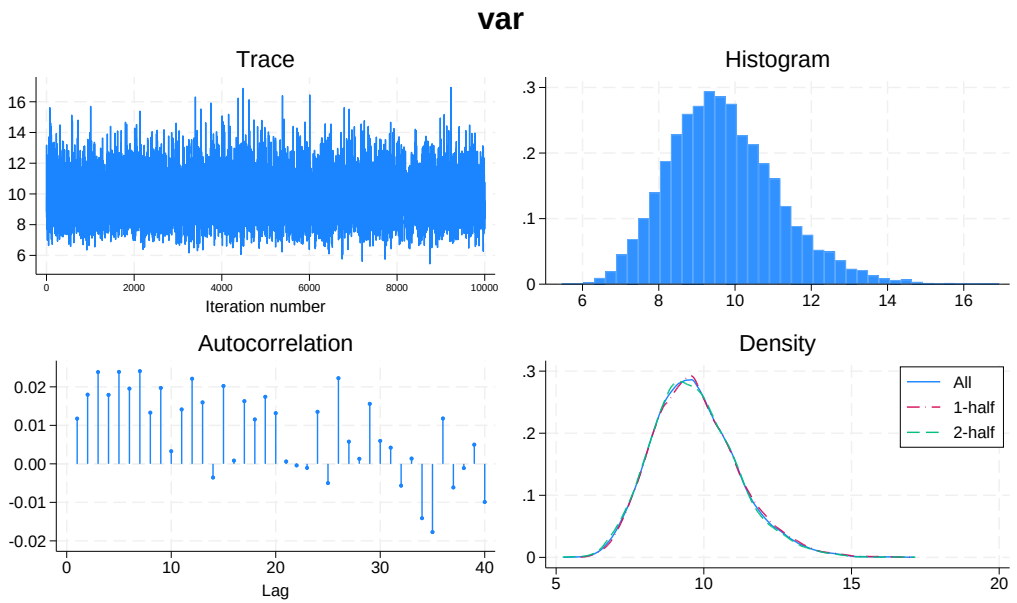
To request Gibbs sampling, we specify suboption `gibbs` within option `block()`.

```
. set seed 14
. bayesmh mpg weight, likelihood(normal({var}))
> prior({mpg:}, normal(0,100))
> prior({var}, igamma(10,10))
> block({var}, gibbs) blocksummary
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal(xb_mpg,{var})
Priors:
  {mpg:weight _cons} ~ normal(0,100)                                      (1)
              {var} ~ igamma(10,10)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
Block summary
------------------------------------------------------------------------------
   1:  {var}                                                        (Gibbs)
   2:  {mpg:weight _cons}
------------------------------------------------------------------------------
Bayesian normal regression                      MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling          Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .6285
                                                Efficiency:  min =      .1141
                                                             avg =      .3259
Log marginal-likelihood = -226.72192                         max =      .7441
------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
      weight |  -.5764752   .0457856   .001324  -.5764938  -.6654439   -.486788
       _cons |   38.64148   1.438705    .04259    38.6177   35.82136   41.38734
-------------+----------------------------------------------------------------
         var |   9.711499   1.454721   .016865   9.585728   7.236344   12.95503
------------------------------------------------------------------------------
```

The average efficiency is now 0.33 with the maximum of 0.74 corresponding to the variance parameter.

The diagnostics plot for {var} is an example of almost perfect mixing.

```
. bayesgraph diagnostics {var}
```



Example 14: Fourth simulation run—full Gibbs sampling

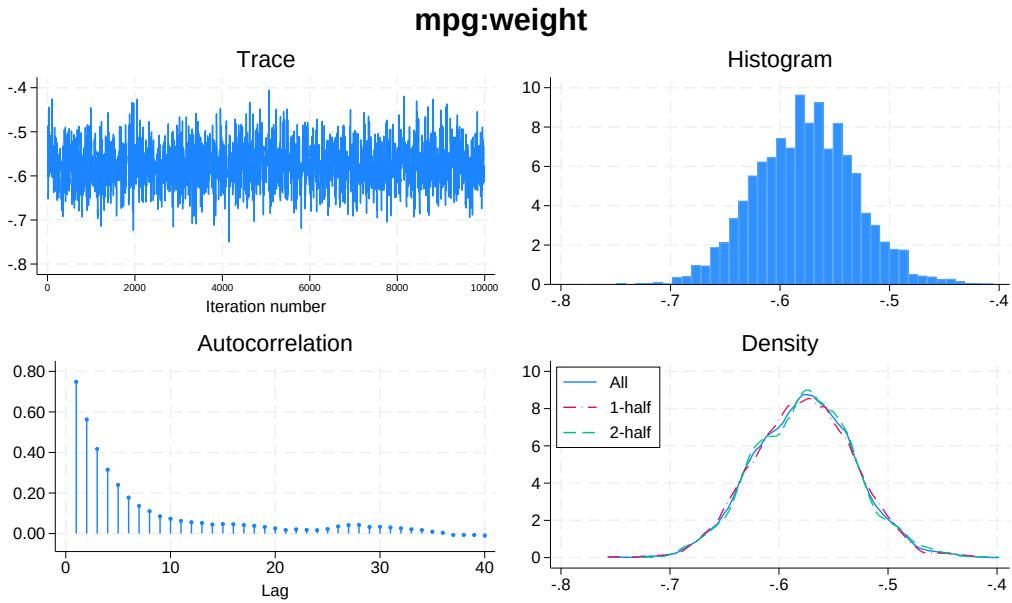
Continuing example 13, there is still room for improvement in our model in terms of sampling efficiency. The efficiency of the regression coefficients is now low relative to the variance efficiency.

```
. bayesstats ess
Efficiency summaries     MCMC sample size =    10,000
                         Efficiency:  min =     .1141
                                      avg =     .3259
                                      max =     .7441
```

	ESS	Corr. time	Efficiency
mpg			
weight	1195.57	8.36	0.1196
_cons	1141.12	8.76	0.1141
var	7440.67	1.34	0.7441

For example, diagnostic plots for {weight:_cons} do not look as good as diagnostic plots for the variance parameter in example 13.

```
. bayesgraph diagnostics {mpg:weight}
```



Further improvement of the mixing can be achieved by requesting Gibbs sampling for the two blocks of parameters: regression coefficients and variance. Again, this is possible only because {mpg:weight}, {mpg:_cons}, and {var} have normal and an inverse-gamma priors, which are independent and are semiconjugate in this model.

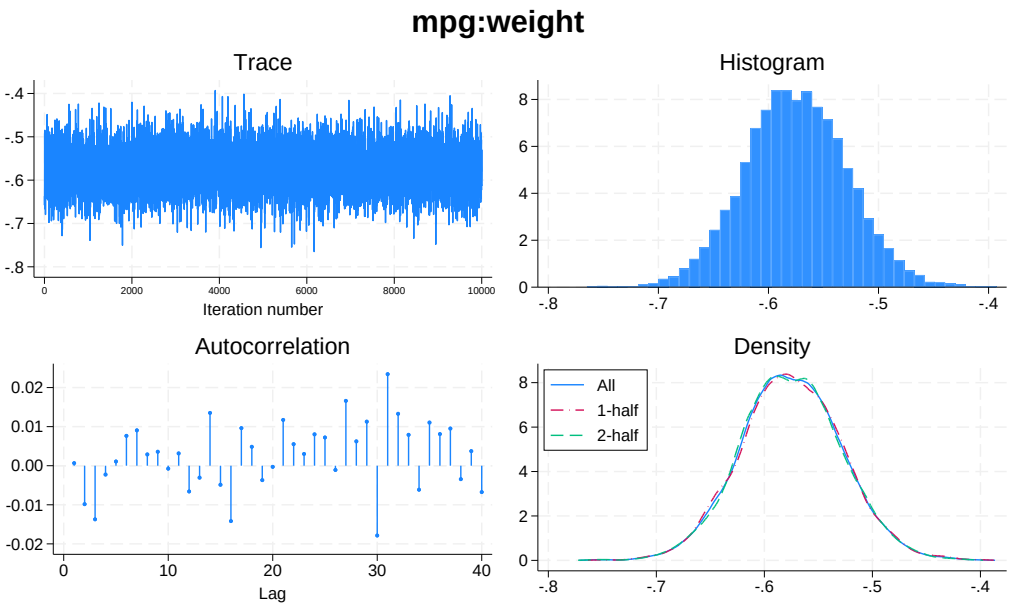
To request Gibbs sampling for the regression coefficients, we must place them in a separate block.

```
. set seed 14
. bayesmh mpg weight, likelihood(normal({var}))
> prior({mpg:}, normal(0,100))
> prior({var}, igamma(10,10))
> block({var}, gibbs)
> block({mpg:}, gibbs) blocksummary
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal(xb_mpg,{var})
Priors:
  {mpg:weight _cons} ~ normal(0,100)                                      (1)
               {var} ~ igamma(10,10)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
Block summary
------------------------------------------------------------------------------
   1:  {var}                                                          (Gibbs)
   2:  {mpg:weight _cons}                                             (Gibbs)
------------------------------------------------------------------------------
Bayesian normal regression                      MCMC iterations  =     12,500
Gibbs sampling                                  Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =          1
                                                Efficiency:  min =      .9423
                                                             avg =      .9808
Log marginal-likelihood = -226.67227                         max =          1
------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
      weight |  -.5751071   .0467837   .000468  -.5757037  -.6659412  -.4823263
       _cons |   38.61033   1.459511   .014595   38.61058   35.79156   41.45336
-------------+----------------------------------------------------------------
         var |   9.703432   1.460435   .015045   9.564502   7.216982   12.96369
------------------------------------------------------------------------------
```

Now we have perfect sampling efficiency (with an average of 0.98) with essentially no autocorrelation. The estimators of posterior means have the lowest MCSEs among the four simulations.

For example, diagnostic plots for {mpg:weight} now look noticeably better.

```
. bayesgraph diagnostics {mpg:weight}
```



You can verify that the diagnostic plots of all parameters demonstrate almost perfect mixing as well.

```
. bayesgraph diagnostics _all
(output omitted)
```

Convergence diagnostics using multiple chains

To assess the convergence of MCMC simulations of a Bayesian model, the literature often recommends comparing the results of multiple simulation sequences or multiple chains; see, for example, Gelman et al. (2014, chap. 11.4). In this section, we show how one can simulate multiple chains using bayesmh, visually compare the results using trace and density plots, and perform formal tests for convergence.

To simulate multiple Markov chains, you can use the nchains() option with bayesmh. When running multiple chains, it is essential for the chains to have different initial values dispersed over the range of values of model parameters. bayesmh, nchains() provides default initial values that are different for each chain, but these values are not guaranteed to be overdispersed and are provided strictly for your convenience. Often, you may want to specify your own initial values, which you can do using the init#() options; see *Specifying initial values* and *Multiple chains using overdispersed initial values*.

Multiple chains using default initial values

Let's continue with the Bayesian multiple linear regression model from example 11. We specify the `nchains(4)` option to simulate four Markov chains of default size 10,000. We use the `rseed()` option to ensure reproducibility when running multiple chains. Specifying `set seed` is not sufficient in this case; see *Reproducing results*. We also use `nomodelsummary` to suppress the output of the model summary.

```
. bayesmh mpg weight, likelihood(normal({var}))
> prior({mpg:}, normal(0,100)) prior({var}, igamma(10,10))
> nomodelsummary nchains(4) rseed(16)
Chain 1
  Burn-in ...
  Simulation ...
Chain 2
  Burn-in ...
  Simulation ...
Chain 3
  Burn-in ...
  Simulation ...
Chain 4
  Burn-in ...
  Simulation ...
Bayesian normal regression                      Number of chains    =          4
Random-walk Metropolis-Hastings sampling        Per MCMC chain:
                                                     Iterations     =     12,500
                                                     Burn-in        =      2,500
                                                     Sample size    =     10,000
                                                Number of obs       =         74
                                                Avg acceptance rate =      .2275
                                                Avg efficiency: min =     .07897
                                                                avg =     .08265
                                                                max =     .08827
Avg log marginal-likelihood = -226.73271        Max Gelman-Rubin Rc =      1.002
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
mpg						
weight	-.5749136	.0463642	.000816	-.5760212	-.6649088	-.4847602
_cons	38.59661	1.447703	.025758	38.62636	35.7311	41.40999
var	9.713168	1.431891	.024098	9.605324	7.332055	12.84306

```
Note: Default initial values are used for multiple chains.
```

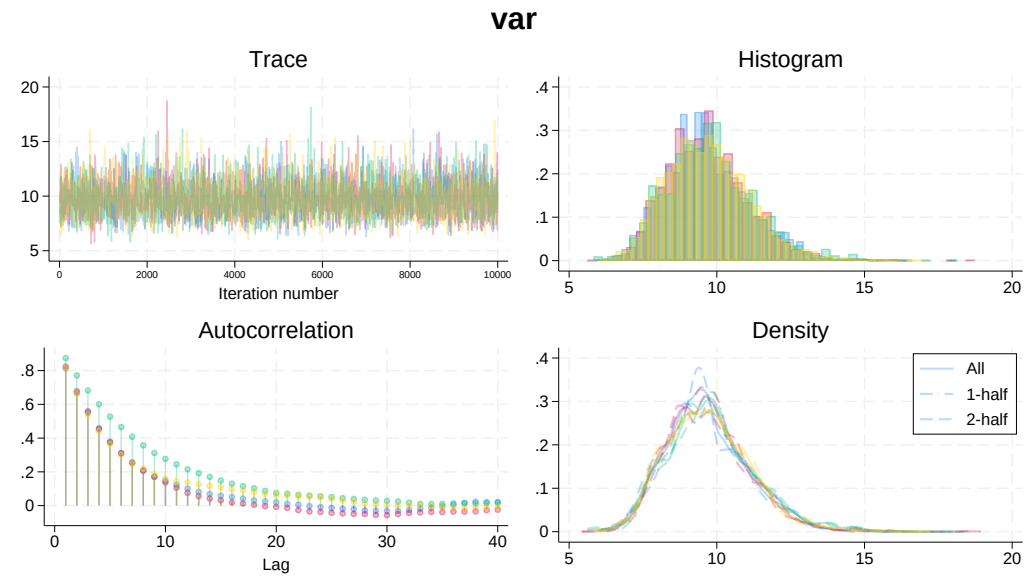
The important change in the output header of `bayesmh` with multiple chains is the presence of the maximum Gelman–Rubin convergence statistic, `Max Gelman-Rubin Rc`. This is the maximum value of the statistics across all model parameters. A convergence rule often used in practice is to declare convergence when convergence statistics of all model parameters are less than 1.1. In our example, the maximum statistic of 1.002 is less than 1.1, so the convergence rule is satisfied. See [BAYES] **bayesstats grubin** for details. Of course, it is important to also inspect convergence visually, as we demonstrate later in this example.

Because there are multiple simulation chains, `bayesmh` reports the simulation summaries averaged over the chains such as the average acceptance rate, average efficiencies, and the average log marginal-likelihood. You can use the `chainsdetail` option to see those summaries separately for each chain.

The average simulation efficiency for all chains is above 8% and seems adequate. The Gelman–Rubin convergence rule is met. There is no indication of convergence problems. Nevertheless, inspecting the simulation chains visually can provide additional reassurance. For instance, by comparing the trace plots of different simulation sequences for a model parameter, we can detect convergence irregularities and assess the overlap of the simulated marginal distributions for this parameter. If Markov chains have converged, we should not observe substantial differences between the trace plots or between the sampled marginal distributions.

For a single chain, we used `bayesgraph diagnostics` to explore the convergence of MCMC visually. We can use this command with multiple chains as well. Let's plot graphical summaries for the variance parameter `{var}`.

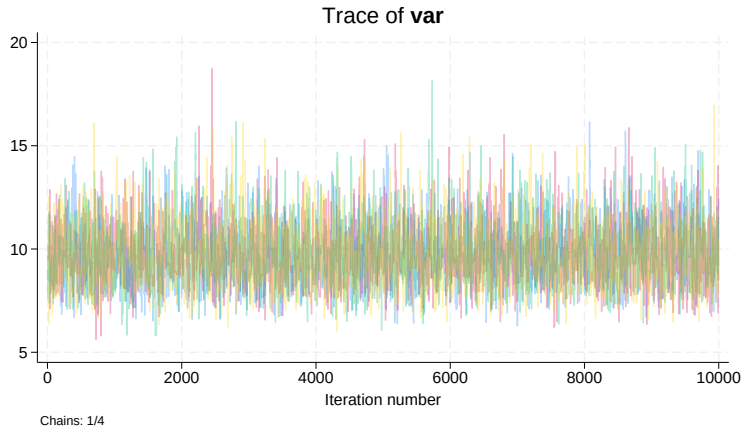
```
. bayesgraph diagnostics {var}
```



Graphical diagnostics look somewhat messy for multiple chains, but the main takeaway from this graph is that the results of the chains do not look drastically different. The trace plots overlap, the autocorrelations die off, and the histograms and density plots are similar for all chains. If desired, you can produce separate plots or graphs for each chain using `bayesgraph`'s `bychain()` or `sepchains` option; see [BAYES] **bayesgraph**.

You can also focus separately on each type of plot. For instance, let's look more closely at the trace and density plots.

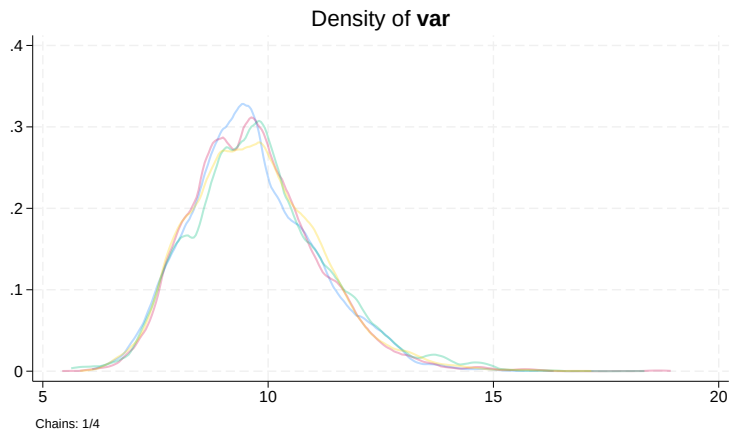
```
. bayesgraph trace {var}
```



The `bayesgraph trace` command overlays the traces of the simulated chains for convenient visual comparison of the chains. The trace plots are similar in terms of coverage and variation.

The overlaid density plots shown by `bayesgraph kdensity` provide another aspect of comparing multiple simulation sequences.

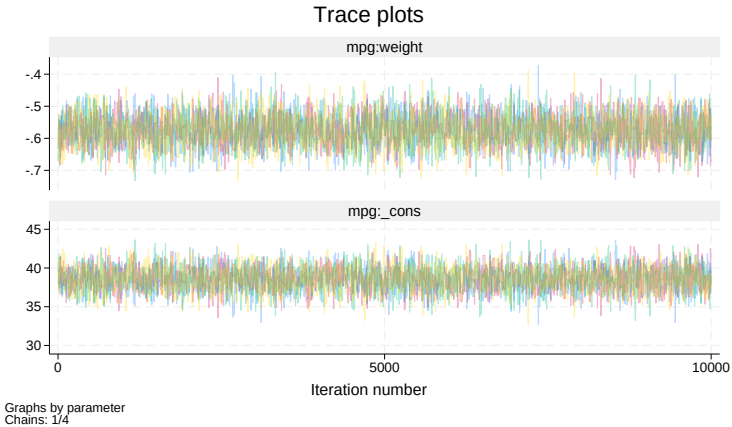
```
. bayesgraph kdensity {var}
```



The density plots of `{var}` from all chains mostly overlap with some variations about the marginal mode.

Similarly, we can explore the MCMC convergence visually for other parameters. For example, we can draw the trace plots for the coefficient parameters {mpg:_cons} and {mpg:weight} and use bayesgraph's byparm option to place plots of both parameters on one graph.

```
. bayesgraph trace {mpg:}, byparm
```



Again, the overlaid trace plots of {mpg:_cons} and {mpg:weight} do not show any substantial differences and indicate good mixing of the chains.

We can use the bayesstats grubin command to compute Gelman–Rubin convergence diagnostics using multiple chains.

```
. bayesstats grubin
Gelman-Rubin convergence diagnostic
Number of chains     =            4
MCMC size, per chain =       10,000
Max Gelman-Rubin Rc  =     1.002068

------------------------------------
             |                   Rc
-------------+----------------------
mpg          |
      weight |    1.000783
       _cons |    1.000557
-------------+----------------------
         var |    1.002068
------------------------------------
Convergence rule: Rc < 1.1
```

Estimates of convergence statistics, Rc, larger than 1.2 indicate possible nonconvergence. In our case, the Rc estimates for all parameters are very close to 1 and do not raise any convergence concerns. Note that the largest estimate, 1.002, as reported by bayesmh, corresponds to parameter {var}.

Once MCMC convergence is established, we can proceed with our estimation results. We replay them here for your convenience (without the table header information).

```
. bayesmh, noheader
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
mpg						
weight	-.5749136	.0463642	.000816	-.5760212	-.6649088	-.4847602
_cons	38.59661	1.447703	.025758	38.62636	35.7311	41.40999
var	9.713168	1.431891	.024098	9.605324	7.332055	12.84306

The summary results in the estimation table are based on all chains. Because we used more chains, our results are now more precise (have smaller MCSEs) compared with example 11.

To inspect posterior summaries of each chain, we can use the `bayesstats summary` command with the `sepchains` option.

```
. bayesstats summary, sepchains
Posterior summary statistics
```

Chain 1 — MCMC sample size = 10,000

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
mpg						
weight	-.5736929	.0458934	.001611	-.5745238	-.6629738	-.4877666
_cons	38.5649	1.425768	.052564	38.60731	35.75694	41.37725
var	9.64884	1.386373	.044099	9.513188	7.251423	12.70699

Chain 2 — MCMC sample size = 10,000

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
mpg						
weight	-.5747026	.0456178	.001699	-.5759074	-.6618918	-.4851731
_cons	38.59502	1.441276	.053339	38.57138	35.72466	41.40902
var	9.683921	1.39533	.043302	9.60479	7.420058	12.73925

Chain 3 — MCMC sample size = 10,000

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
mpg						
weight	-.5740745	.0468218	.00169	-.576532	-.6631272	-.4817094
_cons	38.57018	1.469792	.053026	38.62822	35.68724	41.37469
var	9.802202	1.508294	.059519	9.68037	7.339275	13.32406

Chain 4 MCMC sample size = 10,000

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
mpg						
weight	-.5771844	.0470114	.001543	-.5773599	-.6678485	-.4862513
_cons	38.65634	1.451485	.047729	38.69004	35.82901	41.49365
var	9.717709	1.428596	.048662	9.614184	7.33145	12.89246

The results from all chains are similar. The differences between posterior means, for instance, are within the ranges of the MCMC standard errors of the estimates.

In the presence of multiple chains, `bayesmh` displays a note beneath the estimation table about default initial values being used for the chains. The default initial values are provided for convenience, and often you may want to specify your own; see *Specifying initial values* for details. Also see *Multiple chains using overdispersed initial values* next.

Multiple chains using overdispersed initial values

We continue with our multiple-chains example from *Multiple chains using default initial values*, but here we simulate Markov chains using overdispersed initial values. We specify random initial values manually using the `init#()` options.

For simplicity, we use only two chains. We generate initial values that are highly overdispersed and are far away from the maximum-likelihood estimates of model parameters. For the first chain, we generate initial values for the regression coefficients from the normal distribution with mean 10 and standard deviation 10 and for the variance from the gamma distribution with shape 1 and scale 50. For the second chain, we use the same distributions but different parameters, except for the standard deviation: we use the mean of -10, the standard deviation of 10, the shape of 50, and the scale of 1. We use the `init1()` and `init2()` options, respectively, to specify these initial values. To see the initial values used, we also specify the `initsummary` option.

```
. bayesmh mpg weight, likelihood(normal({var}))
> prior({mpg:}, normal(0,100)) prior({var}, igamma(10,10))
> init1({mpg:} rnormal( 10, 10) {var} rgamma(50, 1))
> init2({mpg:} rnormal(-10, 10) {var} rgamma(1, 50))
> nomodelsummary nchains(2) rseed(16) initsummary
Chain 1
  Burn-in ...
  Simulation ...
Chain 2
  Burn-in ...
  Simulation ...

Initial values:
Chain 1:  {mpg:weight} .168372 {mpg:_cons} 10.2646 {var} 46.3212
Chain 2:  {mpg:weight} -9.07515 {mpg:_cons} -22.1665 {var} 39.3092

Bayesian normal regression                  Number of chains    =          2
Random-walk Metropolis-Hastings sampling    Per MCMC chain:
                                                 Iterations     =     12,500
                                                 Burn-in        =      2,500
                                                 Sample size    =     10,000
                                            Number of obs       =         74
                                            Avg acceptance rate =      .2256
                                            Avg efficiency: min =      .04544
                                                            avg =      .07662
                                                            max =      .09876
Avg log marginal-likelihood = -245.37212    Max Gelman-Rubin Rc =      42.57
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
mpg						
weight	-.5334204	.0939955	.002271	-.5468147	-.6670521	-.3335525
_cons	37.27179	2.977634	.067	37.70683	30.95118	41.41418
var	27.45511	25.17659	.835183	30.3807	7.549151	45.8256

```
Note: There is a high autocorrelation after 500 lags in at least one of the
      chains.
```

The reported maximum Gelman–Rubin convergence statistic, 42.57, is very high and is much larger than 1. A note beneath the table reports high autocorrelation in one of the chains. Clearly, we have a problem.

We check the sampling efficiency of the parameters for each chain separately:

```
. bayesstats ess, sepchains
Efficiency summaries
Chain 1                  MCMC sample size =    10,000
                         Efficiency:  min =    .07407
                                      avg =    .07956
                                      max =    .08962
```

	ESS	Corr. time	Efficiency
mpg			
weight	749.91	13.33	0.0750
_cons	740.66	13.50	0.0741
var	896.19	11.16	0.0896

```
Chain 2                  MCMC sample size =    10,000
                         Efficiency:  min =   .001253
                                      avg =    .07369
                                      max =     .1234
```

	ESS	Corr. time	Efficiency
mpg			
weight	963.73	10.38	0.0964
_cons	1234.44	8.10	0.1234
var	12.53	798.09	0.0013

The {var} parameter in the second chain has the lowest ESS of 12.53.

Let's check the Gelman–Rubin convergence statistics for all parameters.

```
. bayesstats grubin
Gelman-Rubin convergence diagnostic
Number of chains     =            2
MCMC size, per chain =       10,000
Max Gelman-Rubin Rc  =     42.57122
```

	Rc
mpg	
weight	1.622996
_cons	1.665635
var	42.57122

```
Convergence rule: Rc < 1.1
```

The Rc estimates for all three parameters exceed 1, confirming nonconvergence, but {var} has a particularly large value of the convergence statistic of 42.57.

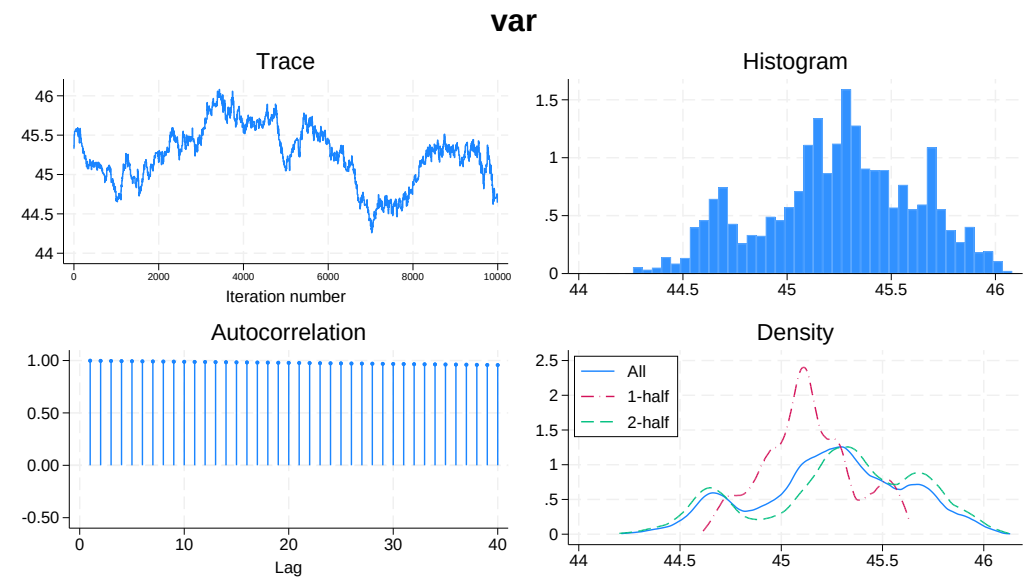
To investigate the convergence problem further visually, we inspect the trace plots of the {var} parameter from each chain.

```
. bayesgraph trace {var}
```

The two trace plots are completely separated and show that the chains explore different domains of the posterior distribution. The trace plot of the second chain, shown in red, has a mean value of about 45. Given a large initial value for {var} and the stochastic nature of the algorithm, the second chain did not converge by the default number of 2,500 burn-in iterations.

If we look at graphical diagnostics of {var} for the second chain,

```
. bayesgraph diagnostics {var}, chains(2)
```



Chain 2

we notice that the autocorrelation stays close to 1 and the trace plot exhibits a slow random walk behavior, failing to stabilize in a particular region.

When you specify overdispersed initial values, you should give the chains enough time to converge. This second chain simply has not run long enough to converge to the domain with a high posterior density. To fix this, we can use a longer burn-in of 10,000, `burnin(10000)`, and longer adaptation by lowering the adaptation tolerance to 0.002, `adaptation(tolerance(0.002))`.

```
. bayesmh mpg weight, likelihood(normal({var}))
> prior({mpg:}, normal(0,100)) prior({var}, igamma(10,10))
> nomodelsummary nchains(2) rseed(16)
> init1({mpg:} rnormal( 10, 10) {var} rgamma(50, 1))
> init2({mpg:} rnormal(-10, 10) {var} rgamma(1, 50))
> burnin(10000) adapt(tolerance(0.002))
Chain 1
  Burn-in ...
  Simulation ...
Chain 2
  Burn-in ...
  Simulation ...
Bayesian normal regression                      Number of chains    =          2
Random-walk Metropolis-Hastings sampling        Per MCMC chain:
                                                     Iterations     =     20,000
                                                     Burn-in        =     10,000
                                                     Sample size    =     10,000
                                                Number of obs       =         74
                                                Avg acceptance rate =       .296
                                                Avg efficiency: min =     .08096
                                                                avg =     .09193
                                                                max =      .1002
Avg log marginal-likelihood = -226.70215        Max Gelman-Rubin Rc =      1.001
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
mpg						
weight	-.5759702	.0461691	.001061	-.5772111	-.665917	-.4826217
_cons	38.64229	1.440565	.032185	38.66686	35.73169	41.42428
var	9.691232	1.472907	.036603	9.530698	7.264868	13.0381

The maximum Gelman–Rubin statistic is now only 1.001. We use `bayesstats grubin` for details.

```
. bayesstats grubin
Gelman-Rubin convergence diagnostic
Number of chains     =           2
MCMC size, per chain =      10,000
Max Gelman-Rubin Rc  =    1.001315
```

	Rc
mpg	
weight	1.001315
_cons	1.00095
var	1.000061

```
Convergence rule: Rc < 1.1
```

All `Rc` estimates satisfy the convergence rule, $\texttt{Rc} < 1.1$.

Bayesian predictions

Bayesian predictions provide a powerful set of tools for model evaluation and assessing goodness of fit, in addition to predicting future observations; see *Overview of Bayesian predictions* in [BAYES] **bayespredict** for details. You can use `bayespredict`, `bayesreps`, and `bayesstats ppvalues` to obtain Bayesian predictions and perform model checks. Here we illustrate some of the features of Bayesian predictions, which are available after fitting a model using `bayesmh`. We continue with the Bayesian multiple linear regression model from example 11.

Simulating replicated outcomes

As a quick model check, we can explore the distribution of the replicated outcomes and compare them with the observed outcome distribution. Replicated outcomes are new outcome values simulated from the posterior predictive distribution conditional on the observed set of covariates. Generally, replicated outcomes compose a sample of T observations, MCMC replicates, and n variables, one for each observation in the original data. The entire prediction sample is rarely needed in most applications. Often, it is sufficient to explore a small random subset from all T MCMC replicates. We can use `bayesreps` to generate such a subset and save the generated replicates as new variables in our dataset.

To use `bayesreps` and `bayespredict`, we must first save the simulation results from `bayesmh`. Let's refit the linear regression model and save the simulation results in `linregsim.dta`. We suppress the output with `quietly`.

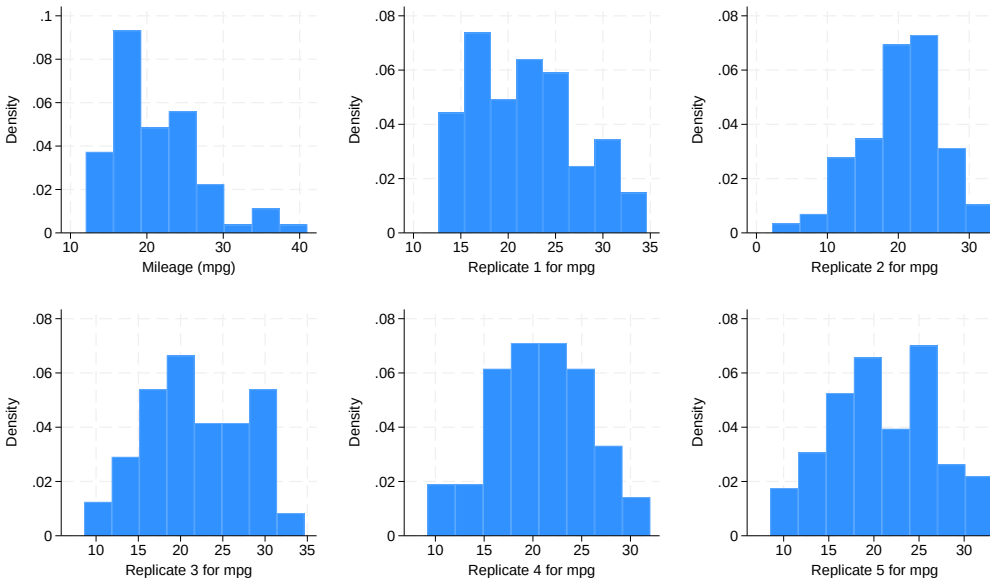
```
. quietly bayesmh mpg weight, likelihood(normal({var}))
> prior({mpg:}, normal(0,100)) prior({var}, igamma(10,10))
> saving(linregsim) rseed(16)
```

We can now use `bayesreps` to generate the replicated outcomes for variable `mpg`. These will be samples from the posterior predictive distribution of `mpg` conditioned on the observed set of explanatory variables, `weight`. Each replication sample will be of the same size, 74, as the original outcome `mpg`. Let's generate 5 replication samples and save them in the original dataset as new variables, `mpgrep1` through `mpgrep5`, specified as the stub `mpgrep*`.

```
. bayesreps mpgrep*, nreps(5) rseed(16)
Computing predictions ...
```

We can visually inspect the histograms of the replicated samples and compare them with the histogram for the observed mpg.

```
. quietly histogram mpg, name(hist0) nodraw
. local histlist hist0
. forvalues i = 1/5 {
  2.         quietly histogram mpgrep`i', name(hist`i') nodraw
  3.         local histlist `histlist' hist`i'
  4. }
. graph combine `histlist'
```



The histogram of mpg (top, left) looks different from those of the replications. All of them cover the range of $(10, 30)$, but the observed mpg is skewed to the right and has heavier tails. The normal model does not appear to capture the observed distribution well. After these initial checks, we proceed with a more quantitative assessment of model fit.

Posterior predictive checks

A posterior predictive check is one of the main applications of Bayesian predictions. It starts with defining test statistics that represent different aspects of the outcome distribution. Then, these test statistics are computed using the observed and replicated outcomes, and their values are compared. For example, the mean, minimum, and maximum statistics can be used for assessing how well the model represents the outcome distribution with respect to its center and extremes.

We can simulate the mean, minimum, and maximum statistics using bayespredict, which supports the use of Mata functions to compute functions of simulated outcomes. Thus, we can use Mata functions mean(), min(), and max() to compute the desired statistics. We specify the argument {_ysim} with the functions to request statistics of the simulated outcomes (we can also use {_resid} for residuals). We save the prediction results in mpgsim.dta. See [BAYES] **bayespredict** for details about the specification.

```
. bayespredict (prmean:@mean({_ysim})) (prmin:@min({_ysim}))
> (prmax:@max({_ysim})), saving(mpgsim) rseed(16)
Computing predictions ...
file mpgsim.dta saved.
file mpgsim.ster saved.
```

We can now access the prediction results within other Bayesian postestimation commands such as `bayesstats summary` and `bayesstats ppvalues`.

Let's compare the agreement for the mean, minimum, and maximum between the replicated data and observed data. The `bayesstats ppvalues` command makes such comparisons easy. It reports the proportion of cases when the simulated statistics are greater than or equal to the observed values of statistics, which is an estimate of the so-called posterior predictive p-value.

```
. bayesstats ppvalues {prmean} {prmin} {prmax} using mpgsim
Posterior predictive summary   MCMC sample size =    10,000
```

T	Mean	Std. dev.	E(T_obs)	P(T>=T_obs)
prmean	21.24042	.5016505	21.2973	.4511
prmin	8.372033	2.159442	12	.027
prmax	32.92524	1.802402	41	.0004

```
Note: P(T>=T_obs) close to 0 or 1 indicates lack of fit.
```

The posterior predictive p-value is 0.45 for the mean statistic, 0.03 for the minimum, and less than 0.001 for the maximum. Our normal model captures the center of the distribution of `mpg` well but fails to capture the extreme values. The posterior predictive p-value for the maximum statistic is particularly small, which agrees with our earlier conclusion based on the histograms that the maximum values are not well represented by the model. If we believe that the extremely large observations of `mpg` are not aberrant outliers, we may need to look for a better-fitting likelihood model than the normal model.

As the final step, we remove the files generated by `bayesmh` and `bayespredict` because we no longer need them.

```
. erase linregsim.dta
. erase mpgsim.dta
. erase mpgsim.ster
```

See [BAYES] **bayespredict** and [BAYES] **bayesstats ppvalues** for more examples.

Logistic regression model: A case of nonidentifiable parameters

We use the heart disease dataset from the UCI Machine Learning Repository (Lichman 2013) and, in particular, we consider a subset of the Switzerland data created by William Steinbrunn, M.D. of University Hospital in Zurich, Switzerland, and by Matthias Pfisterer, M.D. of University Hospital in Basel, Switzerland. The dataset is named `heartswitz.dta` and contains 6 variables, of which `num` is the predicted attribute that takes values from 0 (no heart disease) to 4. We dichotomized `num` to create a new binary variable `disease` as an indicator for the presence of a heart disease.

```
. use https://www.stata-press.com/data/r18/heartswitz, clear
(Subset of Switzerland heart disease data from UCI Machine Learning Repository)
. describe
Contains data from https://www.stata-press.com/data/r18/heartswitz.dta
 Observations:           123                  Subset of Switzerland heart
                                                disease data from UCI Machine
                                                Learning Repository
    Variables:             6                  5 Feb 2022 16:55
                                              (_dta has notes)
-------------------------------------------------------------------------------
Variable      Storage   Display    Value
    name         type    format    label      Variable label
-------------------------------------------------------------------------------
age             byte    %9.0g                 Age (in years)
male            byte    %9.0g      malelab    1 = male, 0 = female
isfbs           byte    %9.0g      fbslab     Indicator for fasting blood sugar
                                                > 120 mg/dl: 0 = no, 1 = yes
restecg         byte    %28.0g     ecglab     Resting electrocardiographic
                                                results (3 categories)
num             byte    %9.0g                 Presence of heart disease: 0 =
                                                absent and 1,2,3,4 = present
disease         byte    %9.0g      dislab     Indicator for heart disease: 0 =
                                                absent, 1 = present (num>0)
-------------------------------------------------------------------------------
Sorted by:
```

Our goal is to investigate the relationship between the presence of a heart disease and covariates `restecg`, `isfbs`, `age`, and `male`.

First, we fit a standard logistic regression model using the `logit` command.

```
. logit disease restecg isfbs age male
note: restecg != 0 predicts success perfectly;
      restecg omitted and 17 obs not used.
note: isfbs != 0 predicts success perfectly;
      isfbs omitted and 3 obs not used.
note: male != 1 predicts success perfectly;
      male omitted and 2 obs not used.
Iteration 0:  Log likelihood = -4.2386144
Iteration 1:  Log likelihood = -4.2358116
Iteration 2:  Log likelihood = -4.2358076
Iteration 3:  Log likelihood = -4.2358076
Logistic regression                                     Number of obs =     26
                                                        LR chi2(1)    =   0.01
                                                        Prob > chi2   = 0.9403
Log likelihood = -4.2358076                             Pseudo R2     = 0.0007
------------------------------------------------------------------------------
     disease | Coefficient  Std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
     restecg |          0  (omitted)
       isfbs |          0  (omitted)
         age |  -.0097846   .1313502    -0.07   0.941    -.2672263    .2476572
        male |          0  (omitted)
       _cons |   3.763893   7.423076     0.51   0.612    -10.78507    18.31285
------------------------------------------------------------------------------
```

We encounter collinearity and dropping of observations because of perfect prediction. As a result, the regression coefficients corresponding to `restecg`, `isfbs`, and `male` are essentially excluded from the model. The standard logistic analysis is limited because of the small size of the dataset.

Next we consider Bayesian analysis of the same data. We fit the same logistic regression model using `bayesmh` and apply fairly noninformative normal priors $N(0, 1e4)$ for all regression parameters.

```
. set seed 14
. bayesmh disease restecg isfbs age male, likelihood(logit)
> prior({disease:}, normal(0,10000))
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  disease ~ logit(xb_disease)
Prior:
  {disease:restecg isfbs age male _cons} ~ normal(0,10000)                (1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_disease.
Bayesian logistic regression                    MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         48
                                                Acceptance rate  =      .2661
                                                Efficiency:  min =     .01685
                                                             avg =     .02389
Log marginal-likelihood = -16.709588                         max =     .02966
```

disease	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
restecg	81.22007	63.87998	4.29587	68.31417	2.518447	237.8033
isfbs	81.65967	60.07603	4.03945	70.37466	2.035696	229.4291
age	-.0191681	.1777758	.013695	-.0154955	-.3833187	.3242438
male	-53.69173	42.4866	2.50654	-44.93144	-154.439	.7090207
_cons	59.39037	43.5938	2.53139	51.31836	.1225503	161.2943

The estimated posterior means of `{disease:restecg}`, `{disease:isfbs}`, `{disease:male}`, and `{disease:_cons}` are fairly large, roughly on the same scale as the prior standard deviation of 100.

Indeed, if we decrease the standard deviation of the priors to 10, we observe that the scale of the estimates decreases by the same order of magnitude.

```
. set seed 14
. bayesmh disease restecg isfbs age male, likelihood(logit)
> prior({disease:}, normal(0,100))
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  disease ~ logit(xb_disease)
Prior:
  {disease:restecg isfbs age male _cons} ~ normal(0,100)                (1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_disease.
Bayesian logistic regression                    MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         48
                                                Acceptance rate  =      .3161
                                                Efficiency:  min =     .02287
                                                             avg =      .0331
Log marginal-likelihood = -12.418273                         max =     .05204
------------------------------------------------------------------------------
             |                                                      Equal-tailed
     disease |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
     restecg |   8.559131       6.71   .443681   7.447336   -.889714   23.93564
       isfbs |   6.322615   6.411998   .281084   5.504684   -3.85021   20.56641
         age |   .0526448   .1226056    .00718   .0468937  -.1734675   .3050607
        male |  -3.831954    5.31727   .279435  -3.048654  -15.77187   4.451594
       _cons |   5.624899   6.641158   .417961   5.181183  -6.408041    20.1234
------------------------------------------------------------------------------
```

We can, therefore, conclude that the regression parameters are highly sensitive to the choice of priors and their scale cannot be determined by the data alone; that is, it cannot be determined by the likelihood of the model. In other words, these model parameters are not identifiable from the likelihood alone. This conclusion is in agreement with the results of the `logit` command.

We may consider applying an informative prior. We can use information from other heart disease studies from Lichman (2013). For example, we use a subset of the Hungarian data created by Andras Janosi, M.D. of Hungarian Institute of Cardiology in Budapest, Hungary. `hearthungary.dta` contains the same attributes as in `heartswitz.dta` but from a Hungarian population.

We fit bayesmh with noninformative priors to hearthungary.dta and obtain the following posterior mean estimates for the regression parameters:

```
. use https://www.stata-press.com/data/r18/hearthungary
(Subset of Hungarian heart disease data from UCI Machine Learning Repository)
. set seed 14
. bayesmh disease restecg isfbs age male, likelihood(logit)
> prior({disease:}, normal(0,1000))
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  disease ~ logit(xb_disease)
Prior:
  {disease:restecg isfbs age male _cons} ~ normal(0,1000)                (1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_disease.
Bayesian logistic regression                    MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =        285
                                                Acceptance rate  =      .2341
                                                Efficiency:  min =     .03088
                                                             avg =     .04524
Log marginal-likelihood =  -195.7454                         max =     .06362
------------------------------------------------------------------------------
                                                              Equal-tailed
     disease |      Mean   Std. dev.      MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
     restecg |  -.1076298   .2931371   .013664  -.1036111  -.6753464   .4471483
       isfbs |   1.182073    .541182   .030797   1.169921   .2267485   2.268314
         age |    .042955   .0170492   .000676   .0432923   .0103757   .0763747
        male |   1.488844   .3612114   .018399   1.484816   .7847398   2.244648
       _cons |  -3.866674   .8904101   .041022  -3.869567  -5.658726  -2.112237
------------------------------------------------------------------------------
```

With this additional information, we can form more informative priors for the 5 parameters of interest—we center {restecg} and {age} at 0, {disease:isfbs} and {disease:male} at 1, and {disease:_cons} at −4, and we use a prior variance of 10 for all coefficients.

```
. use https://www.stata-press.com/data/r18/heartswitz
(Subset of Switzerland heart disease data from UCI Machine Learning Repository)
. set seed 14
. bayesmh disease restecg isfbs age male, likelihood(logit)
> prior({disease:restecg age}, normal( 0,10))
> prior({disease:isfbs male}, normal( 1,10))
> prior({disease:_cons}, normal(-4,10))
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  disease ~ logit(xb_disease)
Priors:
  {disease:restecg age} ~ normal(0,10)                                    (1)
   {disease:isfbs male} ~ normal(1,10)                                    (1)
        {disease:_cons} ~ normal(-4,10)                                   (1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_disease.
Bayesian logistic regression                    MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         48
                                                Acceptance rate  =       .247
                                                Efficiency:  min =     .03691
                                                             avg =     .05447
Log marginal-likelihood = -11.021903                         max =     .06737
```

disease	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
restecg	1.74292	2.21888	.097001	1.385537	-2.065912	6.584702
isfbs	1.885653	2.792842	.145375	1.595679	-2.976167	7.976913
age	.1221246	.0698409	.002691	.1174274	-.0078114	.2706446
male	.2631	2.201574	.089281	.2667496	-4.125275	4.646742
_cons	-2.304595	2.706482	.115472	-2.256248	-7.785531	3.098357

We now obtain more reasonable results that also agree with the Hungarian results. For the final analysis, we may consider other heart disease datasets to verify the reasonableness of our prior specifications and to check the sensitivity of the parameters to other prior specifications.

Ordered probit regression

Ordered probit and ordered logit regressions are appropriate for modeling ordinal response variables. You can perform Bayesian analysis of an ordinal outcome by specifying the `oprobit` or `ologit` likelihood function. In addition to regression coefficients in ordered models, `bayesmh` automatically introduces parameters representing the cutpoints for the linear predictor. The cutpoint parameters are declared as {*depname*:`_cut1`}, {*depname*:`_cut2`}, and so on, where *depname* is the name of the response variable.

In the next example, we consider the full auto dataset and model the ordinal variable `rep77`, the repair record, as a function of independent variables `foreign`, `length`, and `mpg`. The variable `rep77` has 5 levels, so the cutpoint parameters are {`rep77:_cut1`}, {`rep77:_cut2`}, {`rep77:_cut3`}, and {`rep77:_cut4`}. The independent variables are all positive, so it seems reasonable to use exponential prior for the cutpoint parameters. The exponential prior is controlled by a hyperparameter {`lambda`}. Based on the range of the independent predictors, we assign {`lambda`} a prior that is uniform in

the 10 to 40 range. We assign $N(0,1)$ prior for regression coefficients. To monitor the progress, we specify `dots` to request that `bayesmh` displays dots every 100 iterations and iteration numbers every 1,000 iterations.

```
. use https://www.stata-press.com/data/r18/fullauto
(Automobile models)
. replace length = length/10
variable length was int now float
(74 real changes made)
. set seed 14
. bayesmh rep77 foreign length mpg, likelihood(oprobit)
> prior({rep77: foreign length mpg}, normal(0,1))
> prior({rep77:_cut1 _cut2 _cut3 _cut4}, exponential({lambda=30}))
> prior({lambda}, uniform(10,40)) block(lambda) dots
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  rep77 ~ oprobit(xb_rep77,{rep77:_cut1 ... _cut4})
Priors:
  {rep77:foreign length mpg} ~ normal(0,1)                                (1)
     {rep77:_cut1 ... _cut4} ~ exponential({lambda})
Hyperprior:
  {lambda} ~ uniform(10,40)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_rep77.
Bayesian ordered probit regression              MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         66
                                                Acceptance rate  =      .3422
                                                Efficiency:  min =     .02171
                                                             avg =      .0355
Log marginal-likelihood = -102.82883                         max =      .1136
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
rep77						
foreign	1.338071	.3750768	.022296	1.343838	.6331308	2.086062
length	.3479392	.1193329	.00787	.3447806	.1277292	.5844067
mpg	.1048089	.0356498	.002114	.1022382	.0373581	.1761636
_cut1	7.204502	2.910222	.197522	7.223413	1.90771	13.07034
_cut2	8.290923	2.926149	.197229	8.258871	2.983281	14.16535
_cut3	9.584845	2.956191	.197144	9.497836	4.23589	15.52108
_cut4	10.97314	3.003014	.192244	10.89227	5.544563	17.06189
lambda	18.52477	7.252342	.215137	16.40147	10.21155	36.44309

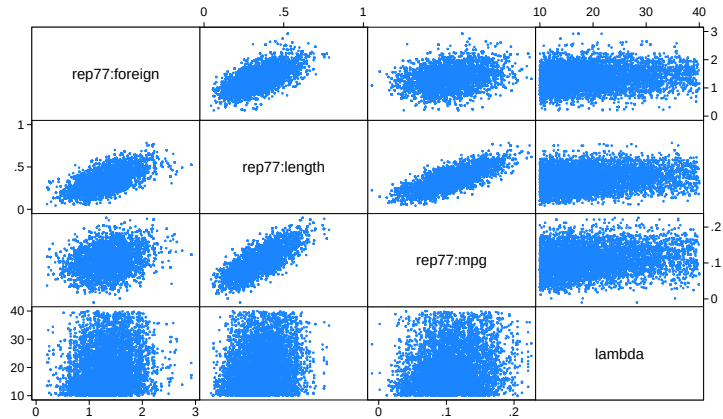
When we specify `dots` or `dots()`, `bayesmh` displays dots as simulation is performed. The burn-in and simulation iterations are displayed separately. During the adaptation period, iterations are displayed with a symbol `a` instead of a dot. This indicates the period during which the proposal distribution is still changing and thus may not be suitable for sampling from yet. Typically, adaptation is performed during the burn-in period, the iterations of which are discarded from the MCMC sample. You should pay closer attention to your results if you see adaptive iterations during the simulation period. This may happen, for example, if you increase `adaptation(maxiter())` without increasing `burnin()`

correspondingly. In this case, you may need to perform additional checks to verify that the part of the MCMC sample corresponding to the adaptation period is similar to the rest of the sample.

Posterior credible intervals suggest that `foreign`, `length`, and `mpg` are among the explanatory factors for `rep77`. Based on MCSEs, their posterior mean estimates are fairly precise. The posterior mean estimates of cutpoints, as expected, are not as precise. The estimated posterior mean for `{lambda}` is 18.52.

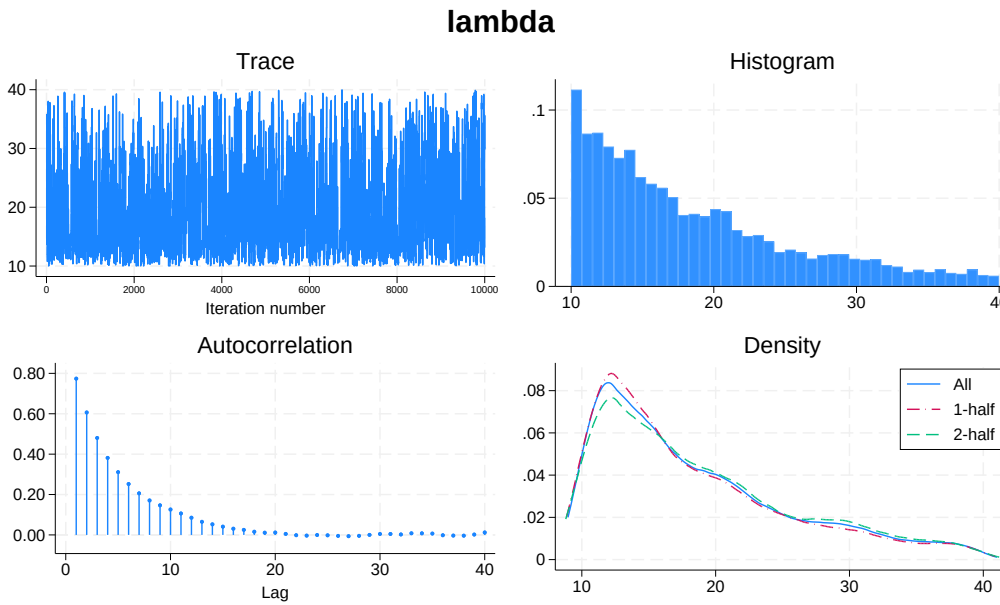
We placed the hyperparameter `{lambda}` in a separate block because we wanted to sample this nuisance parameter independently from the other model parameters. Based on the bivariate scatterplots, this parameter does appear to be independent of other model parameters a posteriori.

```
. bayesgraph matrix {rep77:foreign} {rep77:length} {rep77:mpg} {lambda}
```



As with any MCMC analysis, we should verify convergence of all of our parameters. Here we show diagnostic plots only for {lambda}.

```
. bayesgraph diagnostics {lambda}
```



The diagnostic plots for {lambda} do not cause any concern.

Beta-binomial model

bayesmh is a regression command, which models the mean of the outcome distribution as a function of predictors. There are cases when we do not have any predictors and want to model the outcome distribution directly. For example, we may want to fit a Poisson distribution or a binomial distribution to our outcome. We can do this by specifying one of the four distributions supported by bayesmh in the likelihood() option: dexponential(), dbernoulli(), dbinomial(), or dpoisson().

Let's revisit the example from *What is Bayesian analysis?* in [BAYES] **Intro**, originally from Hoff (2009, 3), of estimating the prevalence of a rare infectious disease in a small city. The outcome variable y is the number of infected subjects in a city of 20 subjects, and our data consist of only one observation, $y = 0$. We assume a binomial distribution for the outcome y, Binom(20,θ), where the infection probability θ is a parameter of interest. Based on some previous studies, the model parameter θ is assigned a Beta$(2, 20)$ prior. For this model, the posterior distribution of θ is known to be Beta$(2, 40)$.

To fit a binomial distribution to y using bayesmh, we specify the option likelihood(dbinomial({theta},20)). The infection probability θ is represented by {theta}.

```
. set obs 1
Number of observations (_N) was 0, now 1.
. generate y = 0
. set seed 14
. bayesmh y, likelihood(dbinomial({theta},20))
> prior({theta}, beta(2,20)) initial({theta} 0.01)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  y ~ binomial({theta},20)
Prior:
  {theta} ~ beta(2,20)
------------------------------------------------------------------------------

Bayesian binomial model                         MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =          1
                                                Acceptance rate  =      .4527
Log marginal-likelihood = -1.1658052            Efficiency       =      .1549

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
       theta |  .0467973   .0317862   .000808   .039931   .0051255   .1277823
------------------------------------------------------------------------------
```

The estimated posterior mean for {theta} is 0.0468, which is close to the theoretical value of $2/(2+40) = 0.0476$ and is within the range of the MCSE of 0.0008.

Multivariate regression

We consider a simple multivariate normal regression model without covariates. We use auto.dta, and we fit a multivariate normal distribution to variables mpg, weight, and length.

We rescale these variables to have approximately equal ranges. Equalizing the range of model variables is always recommended, because this makes the model computationally more stable.

```
. use https://www.stata-press.com/data/r18/auto, clear
(1978 automobile data)
. quietly replace weight = weight/1000
. quietly replace length = length/100
. quietly replace mpg = mpg/10
```

▷ Example 15: Default MH sampling with inverse-Wishart prior for the covariance

For a multivariate normal distribution, an inverse-Wishart prior is commonly used as a prior for the covariance matrix. Let's fit our multivariate model using bayesmh.

We specify the multivariate normal likelihood likelihood(mvnormal({Sigma,m})) for the three variables mpg, weight, and length, where {Sigma,m} is a matrix parameter for the covariance matrix. We use vague normal priors normal(0,100) for all three means of the variables. For a covariance matrix {Sigma,m}, which is of dimension three, we specify an inverse-Wishart prior with the identity scale matrix. We also specify the mean parameters and the covariance parameter in two separate blocks. To monitor the simulation process, we specify dots.

```
. set seed 14
. bayesmh (mpg) (weight) (length), likelihood(mvnormal({Sigma,m}))
> prior({mpg:_cons} {weight:_cons} {length:_cons}, normal(0,100))
> prior({Sigma,m}, iwishart(3,100,I(3)))
> block({mpg:_cons} {weight:_cons} {length:_cons})
> block({Sigma,m}) dots
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg weight length ~ mvnormal(3,{mpg:},{weight:},{length:},{Sigma,m})
Priors:
     {mpg:_cons} ~ normal(0,100)
  {weight:_cons} ~ normal(0,100)
  {length:_cons} ~ normal(0,100)
       {Sigma,m} ~ iwishart(3,100,I(3))
------------------------------------------------------------------------------

Bayesian multivariate normal regression          MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         74
                                                 Acceptance rate  =      .3255
                                                 Efficiency:  min =    .001396
                                                              avg =     .04166
Log marginal-likelihood = -254.88899                          max =      .1111

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |   2.13089   .0455363   .001763   2.129007    2.04435   2.223358
-------------+----------------------------------------------------------------
weight       |
       _cons |  3.018691   .0671399    .00212   3.020777   2.880051   3.149828
-------------+----------------------------------------------------------------
length       |
       _cons |  1.879233   .0210167    .00063   1.879951   1.837007   1.920619
-------------+----------------------------------------------------------------
   Sigma_1_1 |  .1571554   .0038157   .000183   .1570586   .1499028   .1648159
   Sigma_2_1 | -.1864936   .0024051   .000343  -.1864259  -.1912537    -.18194
   Sigma_3_1 | -.0533863   .0033667   .000199   -.053342  -.0601722  -.0468986
   Sigma_2_2 |  .3293518   .0044948   .001203    .329703   .3193904   .3366703
   Sigma_3_2 |  .0894404   .0040487   .000471   .0894156   .0816045   .0976702
   Sigma_3_3 |  .0329253    .002521    .00024   .0328027   .0285211   .0383005
------------------------------------------------------------------------------
Note: There is a high autocorrelation after 500 lags.
```

In this first run, we do not achieve good mixing of the MCMC chain. `bayesmh` issues a note about significant autocorrelation of the simulated parameters.

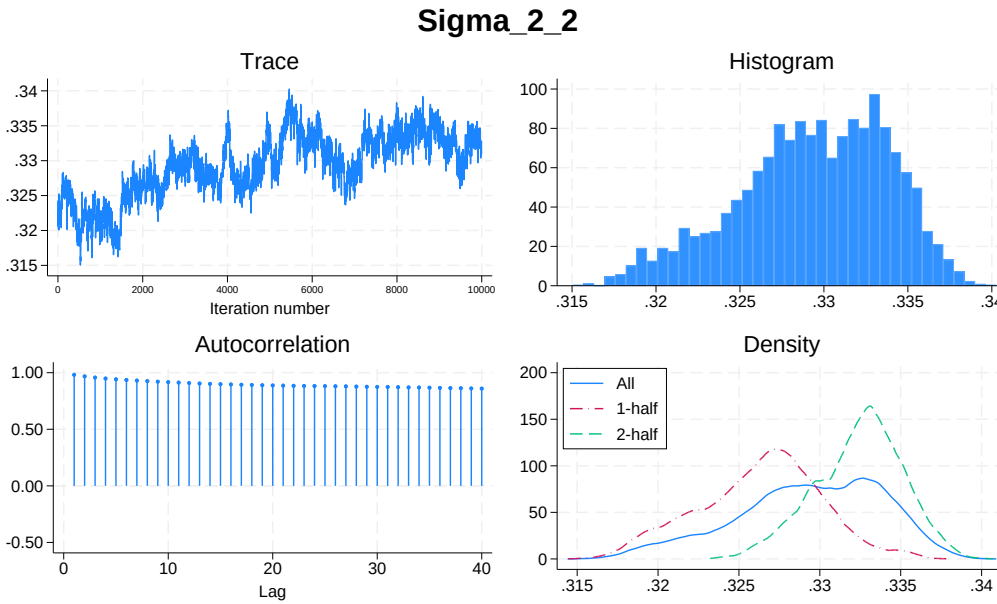
A closer inspection of the ESS table reveals very low sampling efficiencies for the elements of the covariance matrix `{Sigma}`.

```
. bayesstats ess
Efficiency summaries     MCMC sample size =    10,000
                         Efficiency:  min =   .001396
                                      avg =    .04166
                                      max =     .1111
```

	ESS	Corr. time	Efficiency
mpg			
_cons	667.48	14.98	0.0667
weight			
_cons	1002.92	9.97	0.1003
length			
_cons	1111.14	9.00	0.1111
Sigma_1_1	433.25	23.08	0.0433
Sigma_2_1	49.03	203.96	0.0049
Sigma_3_1	287.03	34.84	0.0287
Sigma_2_2	13.96	716.45	0.0014
Sigma_3_2	73.76	135.57	0.0074
Sigma_3_3	110.41	90.58	0.0110

For example, the diagnostic plots for {Sigma_2_2} provide visual confirmation of the convergence issues—very poorly mixing trace plot, high autocorrelation, and a bimodal posterior distribution.

```
. bayesgraph diagnostics Sigma_2_2
```



Here, we see a general problem associated with the simulation of covariance matrices. Random-walk MH algorithm is not well suited for sampling positive-definite matrices. This is why even an adaptive version of the MH algorithm, as implemented in bayesmh, may not achieve good mixing. ◁

Example 16: Adaptation of MH sampling with inverse-Wishart prior for the covariance

Continuing example 15, we can specify longer adaptation and burn-in periods to improve convergence.

```
. set seed 14
. bayesmh (mpg) (weight) (length), likelihood(mvnormal({Sigma,m}))
> prior({mpg:_cons} {weight:_cons} {length:_cons}, normal(0,100))
> prior({Sigma,m}, iwishart(3,100,I(3)))
> block({mpg:_cons} {weight:_cons} {length:_cons})
> block({Sigma,m}) dots burnin(5000) adaptation(maxiter(50))
Burn-in 5000 aaaaaaaaa1000aaaaaaaaa2000aaaaaaaaa3000aaaa.....4000.........5000
> done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg weight length ~ mvnormal(3,{mpg:},{weight:},{length:},{Sigma,m})
Priors:
     {mpg:_cons} ~ normal(0,100)
  {weight:_cons} ~ normal(0,100)
  {length:_cons} ~ normal(0,100)
       {Sigma,m} ~ iwishart(3,100,I(3))
------------------------------------------------------------------------------
Bayesian multivariate normal regression          MCMC iterations  =     15,000
Random-walk Metropolis-Hastings sampling         Burn-in          =      5,000
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         74
                                                 Acceptance rate  =      .2382
                                                 Efficiency:  min =     .02927
                                                              avg =     .05053
Log marginal-likelihood = -245.83844                          max =     .07178
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
mpg						
_cons	2.13051	.0475691	.001809	2.13263	2.038676	2.220953
weight						
_cons	3.017943	.0626848	.00234	3.016794	2.898445	3.143252
length						
_cons	1.878912	.019905	.000769	1.878518	1.840311	1.918476
Sigma_1_1	.1711394	.0089943	.000419	.1706437	.1548036	.1898535
Sigma_2_1	-.1852432	.002432	.000126	-.1852973	-.1898398	-.1803992
Sigma_3_1	-.0517404	.0035831	.000201	-.051688	-.058747	-.0449874
Sigma_2_2	.3054418	.0144859	.000551	.3055426	.2783409	.3340654
Sigma_3_2	.0809091	.0057474	.000314	.080709	.0698331	.0924053
Sigma_3_3	.030056	.002622	.000153	.0299169	.0251627	.0355171

There is no note about high autocorrelation, and the average efficiency increases slightly from 4% to 5%.

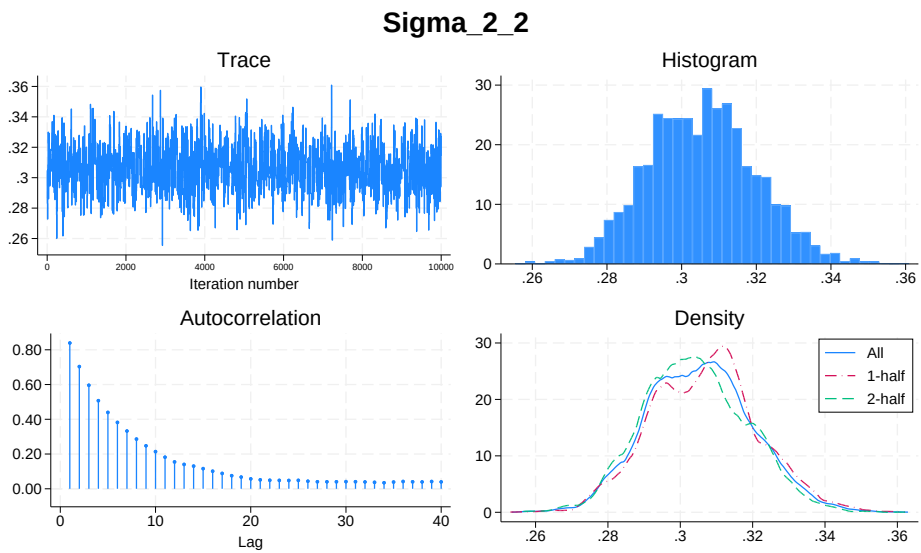
Sampling efficiencies of the elements of the covariance matrix improved substantially.

```
. bayesstats ess
Efficiency summaries      MCMC sample size =    10,000
                          Efficiency:  min =    .02927
                                       avg =    .05053
                                       max =    .07178
```

	ESS	Corr. time	Efficiency
mpg			
_cons	691.54	14.46	0.0692
weight			
_cons	717.82	13.93	0.0718
length			
_cons	670.63	14.91	0.0671
Sigma_1_1	459.78	21.75	0.0460
Sigma_2_1	370.45	26.99	0.0370
Sigma_3_1	318.91	31.36	0.0319
Sigma_2_2	692.06	14.45	0.0692
Sigma_3_2	334.08	29.93	0.0334
Sigma_3_3	292.70	34.16	0.0293

The diagnostic plots for {Sigma_2_2} look much better.

```
. bayesgraph diagnostics Sigma_2_2
```



▷ Example 17: Gibbs sampling of a covariance matrix

Continuing example 15, the convergence of the chain can be greatly improved if we use Gibbs sampling for the covariance matrix parameter. For a multivariate normal model, inverse Wishart is a conjugate prior, or more precisely semiconjugate prior, for the covariance matrix and thus Gibbs sampling is available. To request Gibbs sampling, we only need to add the `gibbs` suboption to the block specification of `{Sigma,m}`. The mean parameters are still updated by the random-walk MH algorithm.

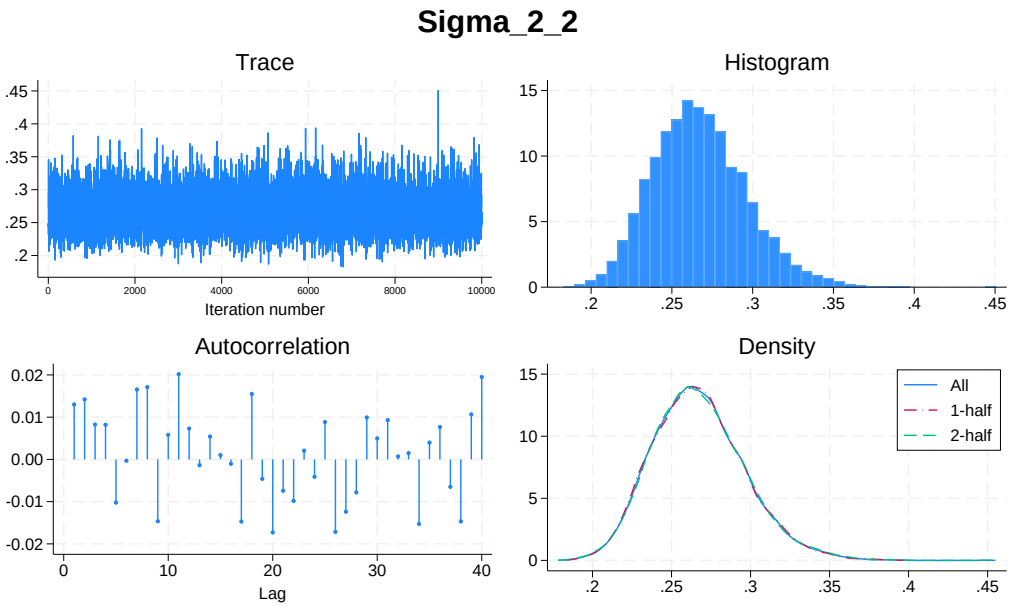
```
. set seed 14
. bayesmh (mpg) (weight) (length), likelihood(mvnormal({Sigma,m}))
> prior({mpg:_cons} {weight:_cons} {length:_cons}, normal(0,100))
> prior({Sigma,m}, iwishart(3,100,I(3)))
> block({mpg:_cons} {weight:_cons} {length:_cons})
> block({Sigma,m}, gibbs) dots
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaa.. done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg weight length ~ mvnormal(3,{mpg:},{weight:},{length:},{Sigma,m})
Priors:
     {mpg:_cons} ~ normal(0,100)
  {weight:_cons} ~ normal(0,100)
  {length:_cons} ~ normal(0,100)
       {Sigma,m} ~ iwishart(3,100,I(3))
------------------------------------------------------------------------------
Bayesian multivariate normal regression          MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling           Burn-in          =      2,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         74
                                                 Acceptance rate  =      .5942
                                                 Efficiency:  min =     .06842
                                                              avg =      .6659
Log marginal-likelihood = -240.48717                          max =      .9781
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
mpg						
_cons	2.128801	.0457224	.00164	2.128105	2.041016	2.215
weight						
_cons	3.020533	.0609036	.002328	3.021561	2.908383	3.143715
length						
_cons	1.880409	.0197061	.000725	1.881133	1.843106	1.918875
Sigma_1_1	.150733	.0164464	.000166	.1495231	.1219304	.1869429
Sigma_2_1	-.1571622	.0196803	.000201	-.156005	-.1995812	-.1224243
Sigma_3_1	-.0443725	.0060229	.000061	-.0439466	-.0571876	-.0338685
Sigma_2_2	.2673525	.029205	.0003	.2654589	.2163041	.3305366
Sigma_3_2	.0708095	.0085435	.000087	.0702492	.0557448	.0893794
Sigma_3_3	.0273506	.0029932	.000031	.0271362	.0220723	.0337994

Compared with example 15, the results improved substantially. Compared with example 16, the minimum efficiency increases from about 3% to 7% and the average efficiency from 5% to 67%. MCSEs of posterior mean estimates, particularly for elements of `{Sigma}`, are lower.

The diagnostic plots, for example, for `Sigma_2_2` also indicate a very good convergence.

```
. bayesgraph diagnostics Sigma_2_2
```



▷ Example 18: Gibbs sampling of a covariance matrix with the Jeffreys prior

In this example, we perform a sensitivity analysis of the model by replacing the inverse-Wishart prior for the covariance matrix with a Jeffreys prior.

```
. set seed 14
. bayesmh (mpg) (weight) (length), likelihood(mvnormal({Sigma,m}))
> prior({mpg:} {weight:} {length:}, normal(0,100))
> prior({Sigma,m}, jeffreys(3))
> block({mpg:} {weight:} {length:})
> block({Sigma,m}, gibbs) dots
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg weight length ~ mvnormal(3,{mpg:},{weight:},{length:},{Sigma,m})
Priors:
     {mpg:_cons} ~ normal(0,100)
  {weight:_cons} ~ normal(0,100)
  {length:_cons} ~ normal(0,100)
       {Sigma,m} ~ jeffreys(3)
------------------------------------------------------------------------------
Bayesian multivariate normal regression          MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling           Burn-in          =      2,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         74
                                                 Acceptance rate  =      .6223
                                                 Efficiency:  min =     .08573
                                                              avg =      .6886
Log marginal-likelihood = -42.728723                          max =          1
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
mpg						
_cons	2.130704	.0709095	.002185	2.129449	1.989191	2.267987
weight						
_cons	3.019323	.0950116	.003245	3.019384	2.834254	3.208017
length						
_cons	1.879658	.0271562	.000892	1.879859	1.827791	1.933834
Sigma_1_1	.3596673	.0628489	.000628	.3526325	.2575809	.5028854
Sigma_2_1	-.3905511	.0772356	.000772	-.3824458	-.5668251	-.2654059
Sigma_3_1	-.1103824	.0220164	.000223	-.1077659	-.1611913	-.0751177
Sigma_2_2	.6503219	.1141333	.001141	.6378476	.466738	.9140429
Sigma_3_2	.1763159	.0318394	.000323	.1725042	.1248434	.2507866
Sigma_3_3	.0533981	.0093631	.000095	.0522228	.0382405	.0748096

```
Note: Adaptation tolerance is not met in at least one of the blocks.
```

Compared with example 17, the estimates of the means of the multivariate distribution do not change much, but the estimates of the elements of the covariance matrix do change. The estimates for `{Sigma,m}` obtained using the Jeffreys prior are approximately twice as big as the estimates obtained using the inverse-Wishart prior. If we compute correlation matrices corresponding to `{Sigma,m}` from the two models, they will be similar. This can be explained by the fact that both the Jeffreys prior and the inverse-Wishart prior with identity scale matrix are not informative for the correlation structure

because they only depend on the determinant and the trace of {Sigma,m} whereas the correlation structure is determined by the data alone.

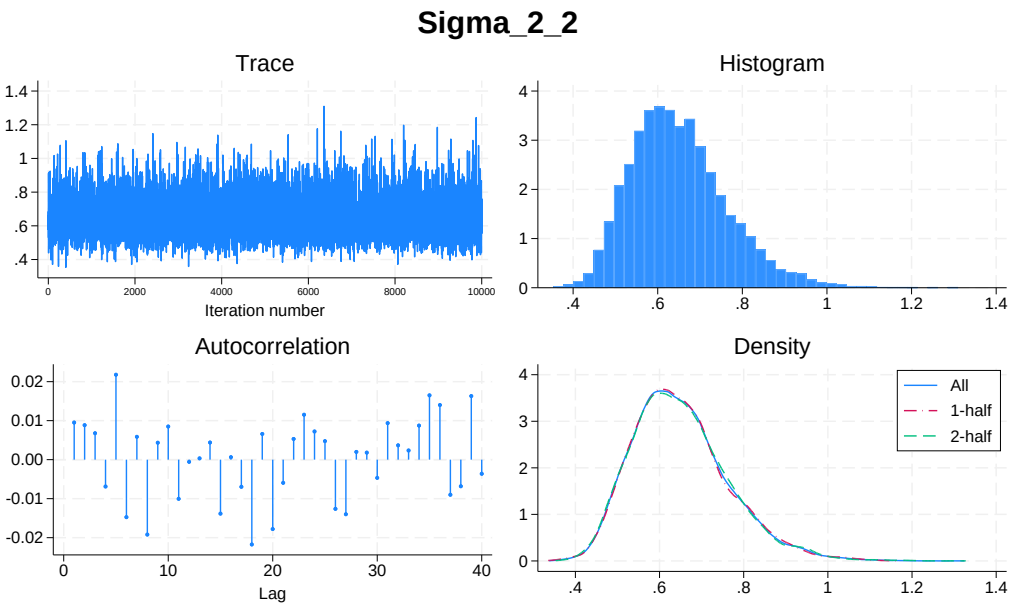
❑ Technical note: Adaptation tolerance is not met

At the bottom of the table in the previous output, the note about the adaptation tolerance not being met in one of the blocks is displayed. Adaptation is part of MH sampling, so the note refers to the block of regression coefficients. This note does not necessarily indicate a problem. It simply notifies you that the default target acceptance rate as specified in adaptation(tarate()) has not been reached within the tolerance specified in adaptation(tolerance()). The used default for the target acceptance rate corresponds to the theoretical asymptotically optimal acceptance rate of 0.44 for a block with one parameter and 0.234 for a block with multiple parameters. The rate is derived for a specific class of models and does not necessarily represent the optimal rate for all models. If your MCMC converged, you can safely ignore this note. Otherwise, you need to investigate your model further. One remedy is to increase the burn-in period, which automatically increases the adaptation period, or more specifically, the number of adaptive iterations as controlled by adaptation(maxiter()). For example, if we increase burn-in to 3,000 by specifying option burnin(3000) in the above example, we will meet the adaptation tolerance.

❑

The diagnostic plots of Sigma_2_2 demonstrate excellent mixing properties.

```
. bayesgraph diagnostics Sigma_2_2
```



◁

Panel-data and multilevel models

Let's fit two-level random-intercept and random-coefficients models. A two-level random-intercept model is also known as a panel-data model. Also see [BAYES] **Bayesian estimation** for fitting panel-data and multilevel models more conveniently by using the `bayes` prefix.

Two-level random-intercept model or panel-data model

Ruppert, Wand, and Carroll (2003) and Diggle et al. (2002) analyzed a longitudinal dataset consisting of `weight` measurements of 48 pigs on 9 successive `weeks`. Pigs were identified by the group variable `id`.

The following two-level model was considered:

$$\texttt{weight}_{ij} = \beta_0 + \beta_1 \texttt{week}_{ij} + u_j + \epsilon_{ij}$$

where u_j is the random effect for pig j, $j = 1, \ldots, 48$, and the counter $i = 1, \ldots, 9$ identifies the weeks.

We first use `mixed` to fit this model by using maximum likelihood for comparison purposes; see [ME] **mixed**.

```
. use https://www.stata-press.com/data/r18/pig, clear
(Longitudinal analysis of pig weights)
. mixed weight week || id:
Performing EM optimization ...
Performing gradient-based optimization:
Iteration 0:  Log likelihood = -1014.9268
Iteration 1:  Log likelihood = -1014.9268
Computing standard errors ...
Mixed-effects ML regression                     Number of obs     =        432
Group variable: id                              Number of groups  =         48
                                                Obs per group:
                                                              min =          9
                                                              avg =        9.0
                                                              max =          9
                                                Wald chi2(1)      =   25337.49
Log likelihood = -1014.9268                     Prob > chi2       =     0.0000
```

weight	Coefficient	Std. err.	z	P>|z|	[95% conf.	interval]
week	6.209896	.0390124	159.18	0.000	6.133433	6.286359
_cons	19.35561	.5974059	32.40	0.000	18.18472	20.52651

Random-effects parameters	Estimate	Std. err.	[95% conf.	interval]
id: Identity				
var(_cons)	14.81751	3.124225	9.801716	22.40002
var(Residual)	4.383264	.3163348	3.805112	5.04926

```
LR test vs. linear model: chibar2(01) = 472.65        Prob >= chibar2 = 0.0000
```

Consider the following Bayesian model for these data:

$$\texttt{weight}_{ij} = \beta_0 + \beta_1 \texttt{week}_{ij} + u_j + \epsilon_{ij}$$

$$\epsilon_{ij} \sim \text{i.i.d. } N(0, \sigma_0^2)$$
$$u_j \sim \text{i.i.d. } N(0, \sigma_u^2)$$
$$\beta_0 \sim N(0, 100)$$
$$\beta_1 \sim N(0, 100)$$
$$\sigma_0^2 \sim \text{InvGamma}(0.001, 0.001)$$
$$\sigma_u^2 \sim \text{InvGamma}(0.001, 0.001)$$

The model has four main parameters of interest: regression coefficients β_0 and β_1 and variance components σ_0^2 and σ_u^2. The pig random effects u_j's are considered nuisance parameters. We use normal priors for the regression coefficients and random effects and inverse-gamma priors for the variance parameters. The chosen priors are fairly noninformative, so we would expect results to be similar to the frequentist results.

To fit this model using `bayesmh`, we need to include random effects for pig in our regression model. This can be done simply by adding the random-effects term `U[id]` to the list of variables.

In addition to two regression coefficients and two variance components, we have 48 random-effects parameters. As for other models, `bayesmh` will automatically create parameters of the regression function: `{weight:week}` for the regression coefficient of `week` and `{weight:_cons}` for the constant term. It will also create random-effects parameters `{U:1.id}`, `{U:2.id}`, ..., `{U:48.id}` and the corresponding variance component `{var_U}`. So, we only need to create one remaining parameter for the error variance. We will use `{var_0}` to match our math notation.

We will perform five simulations for the specified Bayesian model to illustrate some common difficulties in applying MH MCMC to multilevel models.

▷ Example 19: First simulation—default MH settings

In the first simulation, we use default simulation settings of the MH algorithm. We have many parameters in our model, so the simulation will take a few moments. For exploration purposes and to expedite results, here we use a smaller MCMC size of 5,000 instead of the default of 10,000. To monitor the progress of the simulation, we also specify `dots`. And we use the `rseed()` option to specify the random-number seed instead of `set seed`.

```
. bayesmh weight week U[id], likelihood(normal({var_0}))
>         prior({weight:_cons}, normal(0, 100))
>         prior({weight:week},  normal(0, 100))
>         prior({var_0},        igamma(0.001, 0.001))
>         prior({var_U},        igamma(0.001, 0.001))
>         mcmcsize(5000) dots rseed(14)
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aa... done
Simulation 5000 .........1000.........2000.........3000.........4000.........
> 5000 done

Model summary
------------------------------------------------------------------------------
Likelihood:
  weight ~ normal(xb_weight,{var_0})

Priors:
  {weight:_cons week} ~ normal(0,100)                                       (1)
              {U[id]} ~ normal(0,{var_U})                                   (1)
              {var_0} ~ igamma(0.001,0.001)

Hyperprior:
  {var_U} ~ igamma(0.001,0.001)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_weight.

Bayesian normal regression                      MCMC iterations  =      7,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =      5,000
                                                Number of obs    =        432
                                                Acceptance rate  =      .2689
                                                Efficiency:  min =    .004996
                                                             avg =     .03269
Log marginal-likelihood                                      max =     .05366

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
weight       |
        week |  6.214207    .038642   .002359   6.213394    6.139342    6.289956
       _cons |  19.32073   .4780961   .095658   19.33685    18.36352    20.16849
-------------+----------------------------------------------------------------
       var_0 |  4.422389   .3193947   .020177   4.397903    3.847674    5.129631
       var_U |  15.14296   3.299171   .314644   14.65057    10.17046    23.11491
------------------------------------------------------------------------------
```

`bayesmh` reports results that are similar to those from `mixed`, but the low minimum efficiency of 0.005 may indicate problems with MCMC convergence for some of the parameters. `bayesmh` does not report the estimates of random effects by default, but you can use the `showreffects` option to display them.

We use `bayesstats ess` to identify the main model parameter that has the lowest efficiency.

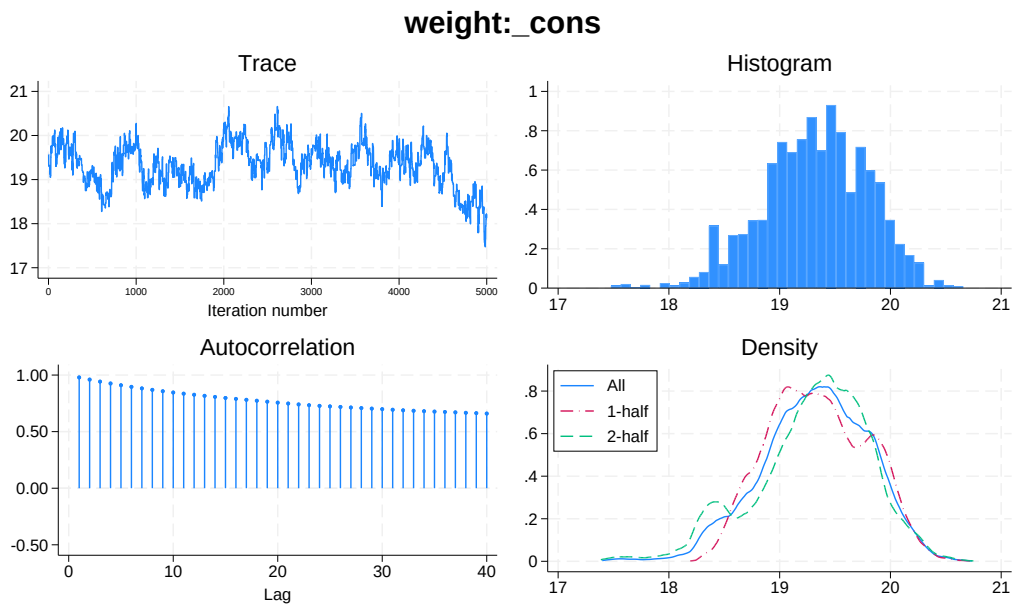
```
. bayesstats ess
Efficiency summaries      MCMC sample size =     5,000
                          Efficiency:  min =   .004996
                                       avg =   .03269
                                       max =   .05366
```

	ESS	Corr. time	Efficiency
weight			
week	268.29	18.64	0.0537
_cons	24.98	200.16	0.0050
var_0	250.58	19.95	0.0501
var_U	109.94	45.48	0.0220

The `{weight:_cons}` parameter has the lowest efficiency of 0.005.

If we look at diagnostic plots for `{weight:_cons}`,

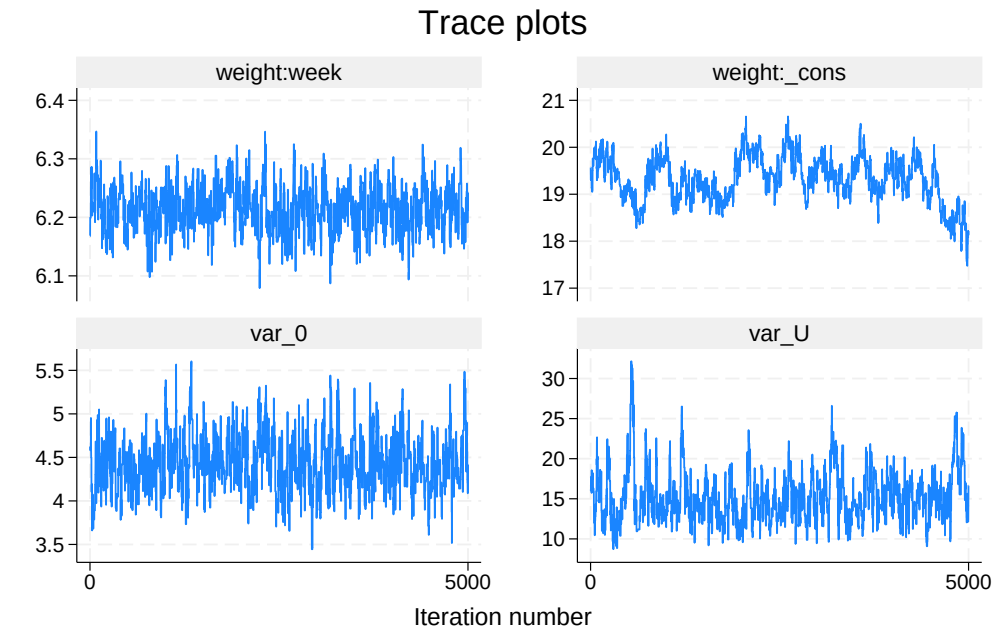
```
. bayesgraph diagnostics {weight:_cons}
```



we see that the trace plot exhibits some trend and does not show good mixing and that the autocorrelation is high. Our MCMC does not seem to converge and thus we should be cautious about the obtained results.

We can also look at the trace and autocorrelation plots of all main parameters.

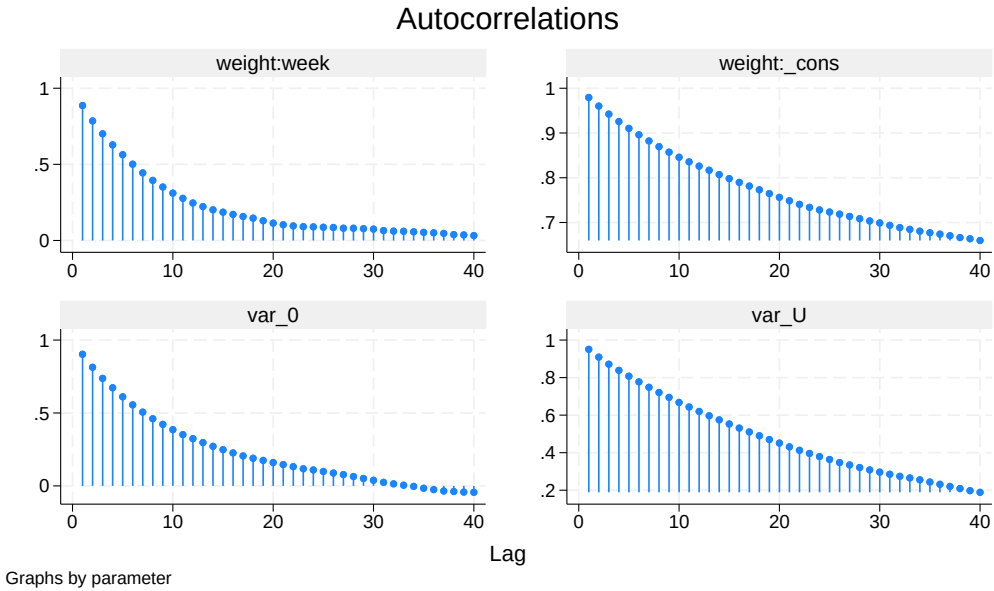
```
. bayesgraph trace _all, byparm(cols(2))
```



Graphs by parameter

The trace plots of all parameters other than the constant do not appear to have any trend.

```
. bayesgraph ac _all, byparm
```



The autocorrelation for the constant {weight:_cons} and variance component {var_U} is high.

▷ Example 20: Second simulation—blocking of parameters

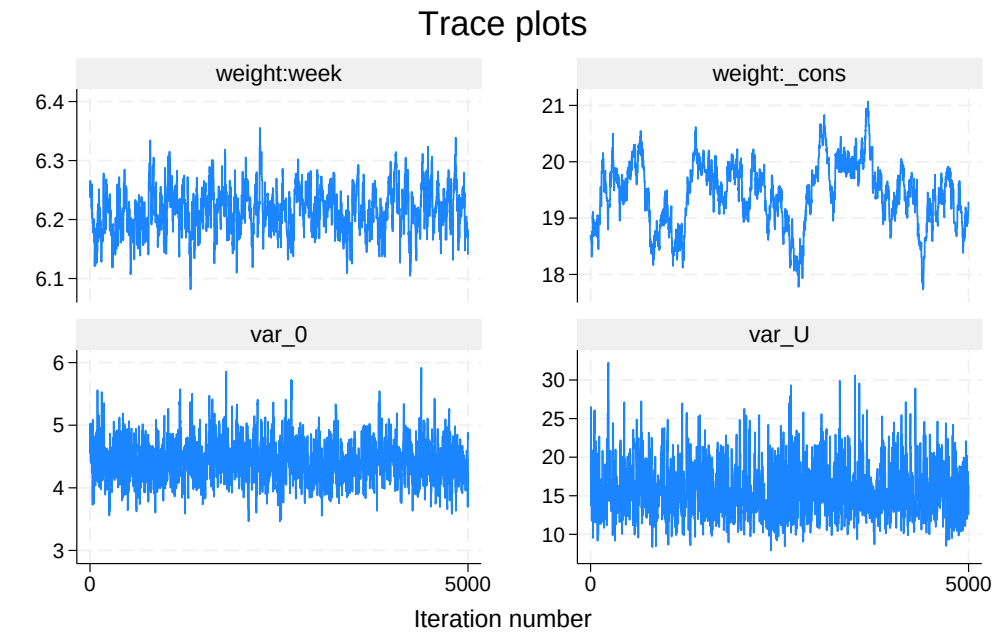
Continuing example 19, we can improve efficiency of the MH algorithm by separating model parameters into blocks to be sampled independently. We consider a separate block for each model parameter; random-effects parameters automatically share the same separate block. We also specify `nomodelsummary` to suppress the model summary of `bayesmh`. To block parameters, we can either specify a separate `block()` option for each parameter or group all parameters in one `block()` option and use `block()`'s suboption `split`. We use the second approach.

```
. bayesmh weight week U[id], likelihood(normal({var_0}))
>         prior({weight:_cons}, normal(0, 100))
>         prior({weight:week},  normal(0, 100))
>         prior({var_0},        igamma(0.001, 0.001))
>         prior({var_U},        igamma(0.001, 0.001))
>         block({weight:} {var_0 var_U}, split)
>         mcmcsize(5000) dots rseed(14) nomodelsummary
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 5000 .........1000.........2000.........3000.........4000.........
> 5000 done

Bayesian normal regression                      MCMC iterations  =      7,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =      5,000
                                                Number of obs    =        432
                                                Acceptance rate  =      .4046
                                                Efficiency:  min =    .004964
                                                             avg =     .08105
Log marginal-likelihood                                      max =      .1597

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
weight       |
        week |  6.215408   .0381479   .002808   6.214654   6.140876   6.293443
       _cons |  19.41979   .5741026    .11524   19.46862   18.24166   20.44603
-------------+----------------------------------------------------------------
       var_0 |  4.425198   .3318405     .0134   4.408941    3.84317   5.117833
       var_U |   15.8305   3.499092   .123841   15.28998   10.28572   23.73757
------------------------------------------------------------------------------
```

Blocking certainly improved efficiencies: the average efficiency is now 0.08, but the minimum efficiency is still low.

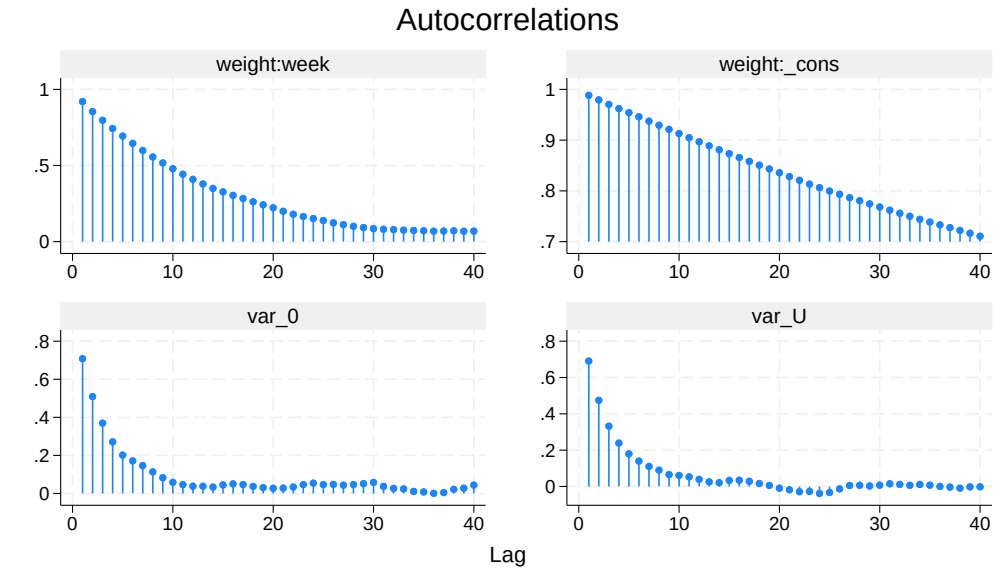
The trace and autocorrelation plots below have improved for variance components but not for regression coefficients.

```
. bayesgraph trace _all, byparm(cols(2))
```



Graphs by parameter

```
. bayesgraph ac _all, byparm
```



▷ Example 21: Third simulation—Gibbs sampling

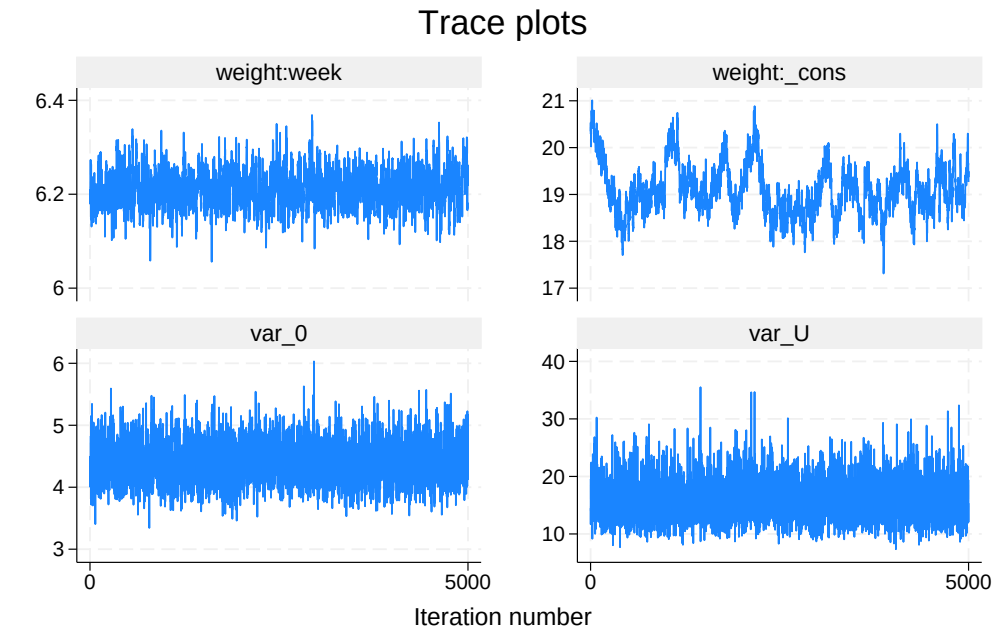
The most efficient MCMC procedure for our Bayesian model is Gibbs sampling, which can be set up as follows. To request a Gibbs sampling for a block of model parameters, we must first define them in a separate `prior()` statement and then put them in a separate `block()` with the `gibbs` suboption.

```
. bayesmh weight week U[id], likelihood(normal({var_0}))
>         prior({weight:_cons}, normal(0, 100))
>         prior({weight:week},  normal(0, 100))
>         prior({var_0},        igamma(0.001, 0.001))
>         prior({var_U},        igamma(0.001, 0.001))
>         block({weight:} {var_0 var_U}, split gibbs)
>         mcmcsize(5000) dots rseed(14) nomodelsummary
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 5000 .........1000.........2000.........3000.........4000.........
> 5000 done

Bayesian normal regression                      MCMC iterations  =      7,500
Metropolis-Hastings and Gibbs sampling          Burn-in          =      2,500
                                                MCMC sample size =      5,000
                                                Number of obs    =        432
                                                Acceptance rate  =      .8455
                                                Efficiency:  min =    .007933
                                                             avg =      .3116
Log marginal-likelihood                                      max =      .6695

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
weight       |
        week |   6.211245   .0394854   .001513   6.211084   6.136556   6.290471
       _cons |   19.10077   .5413931   .085962    19.0496   18.20506   20.29911
-------------+----------------------------------------------------------------
       var_0 |   4.405236    .320582    .00689   4.391879    3.81231   5.076974
       var_U |   15.76448    3.44687   .059575   15.34651   10.16291    23.5736
------------------------------------------------------------------------------
```

The average efficiency increased dramatically to 0.31 but the minimum efficiency is still low.

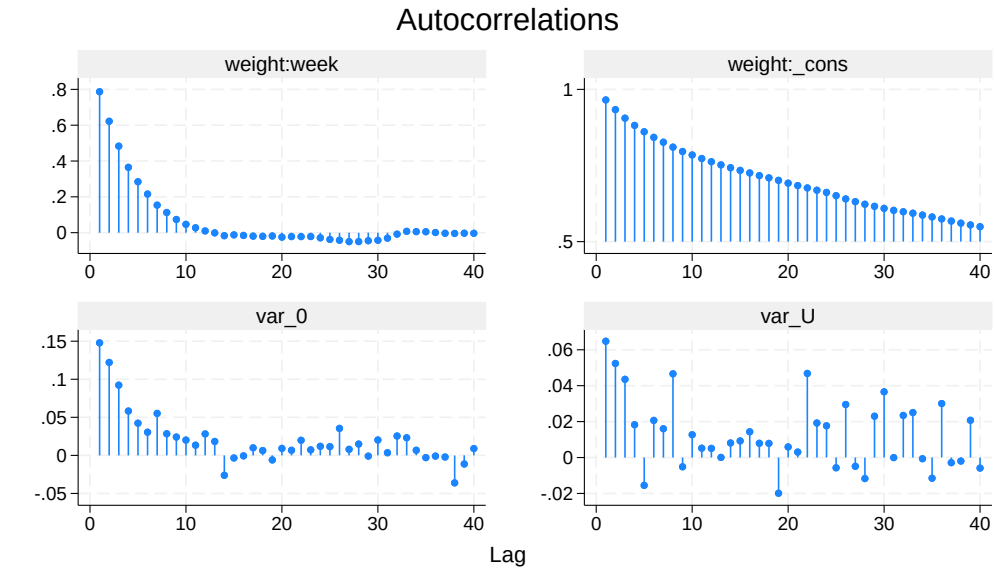
If we again inspect the diagnostic plots for main model parameters,

```
. bayesgraph trace _all, byparm(cols(2))
```



Graphs by parameter

```
. bayesgraph ac _all, byparm
```



we will see that all but the constant term show nearly perfect mixing.

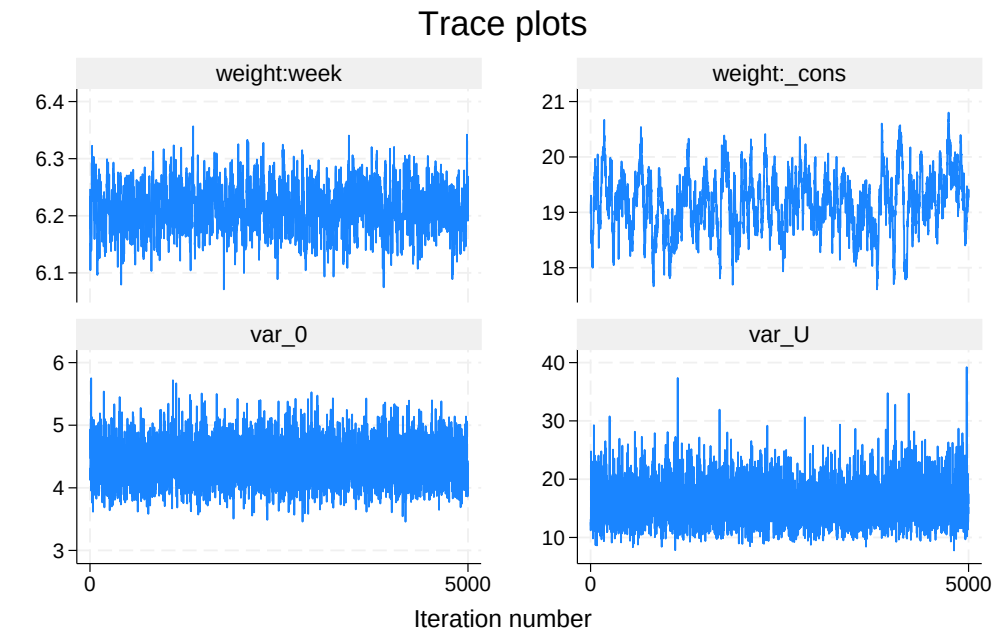
For linear multilevel models, we can further improve mixing by specifying Gibbs sampling also for random effects.

```
. bayesmh weight week U[id], likelihood(normal({var_0}))
>         prior({weight:_cons}, normal(0, 100))
>         prior({weight:week},  normal(0, 100))
>         prior({var_0},        igamma(0.001, 0.001))
>         prior({var_U},        igamma(0.001, 0.001))
>         block({weight:} {var_0 var_U}, split gibbs)
>         block({U}, gibbs)
>         mcmcsize(5000) dots rseed(14) nomodelsummary
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 5000 .........1000.........2000.........3000.........4000.........
> 5000 done
Bayesian normal regression                      MCMC iterations  =      7,500
Gibbs sampling                                  Burn-in          =      2,500
                                                MCMC sample size =      5,000
                                                Number of obs    =        432
                                                Acceptance rate  =          1
                                                Efficiency:  min =     .02462
                                                             avg =      .4626
Log marginal-likelihood                                      max =      .8788
```

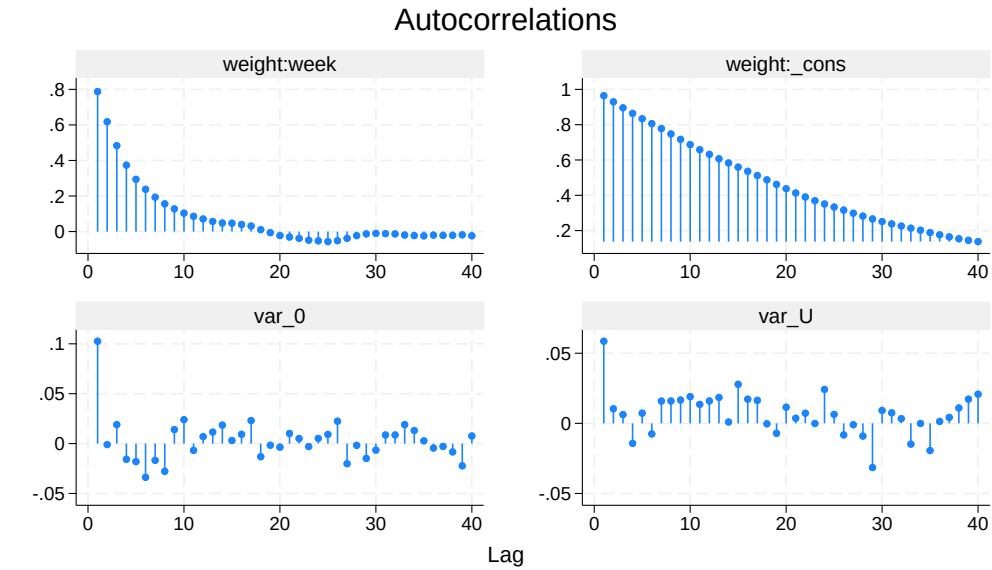
	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
weight						
week	6.212522	.0391656	.001618	6.212953	6.135002	6.287983
_cons	19.17706	.527013	.047497	19.19138	18.0913	20.1664
var_0	4.412689	.3197871	.004965	4.395271	3.827182	5.094548
var_U	15.76501	3.421817	.051622	15.30836	10.33911	23.6702

The minimum efficiency is now increased to 0.025, and the diagnostics plots for the constant term look much better:

```
. bayesgraph trace _all, byparm(cols(2))
```



```
. bayesgraph ac _all, byparm
```



Example 22: Fourth simulation—splitting random-effects parameters

Gibbs sampling typically provides the most efficient sampling of parameters. Full Gibbs sampling is not always available; see, for example, *Multilevel logistic regression* below.

In the absence of Gibbs sampling for random effects, `block()`'s suboption `split` provides the next most efficient albeit much slower way of sampling the random-effects parameters in `bayesmh`. Taking into account conditional independence of individual random effects, random-effects parameters associated with levels of the grouping variable can be sampled sequentially (as separate blocks) instead of being sampled jointly from a high-dimensional proposal distribution (as in example 20).

For example, instead of using Gibbs sampling for the random effects (as in example 21), we use `block()`'s suboption `split` for the random-effects parameters `{U[id]}`.

```
. bayesmh weight week U[id], likelihood(normal({var_0}))
>         prior({weight:_cons}, normal(0, 100))
>         prior({weight:week},  normal(0, 100))
>         prior({var_0},        igamma(0.001, 0.001))
>         prior({var_U},        igamma(0.001, 0.001))
>         block({weight:} {var_0 var_U}, split gibbs)
>         block({U}, split)
>         mcmcsize(5000) dots rseed(14) nomodelsummary
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 5000 .........1000.........2000.........3000.........4000.........
> 5000 done
Bayesian normal regression                      MCMC iterations  =      7,500
Metropolis-Hastings and Gibbs sampling          Burn-in          =      2,500
                                                MCMC sample size =      5,000
                                                Number of obs    =        432
                                                Acceptance rate  =      .8455
                                                Efficiency:  min =    .007933
                                                             avg =      .3116
Log marginal-likelihood                                      max =      .6695
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
weight						
week	6.211245	.0394854	.001513	6.211084	6.136556	6.290471
_cons	19.10077	.5413931	.085962	19.0496	18.20506	20.29911
var_0	4.405236	.320582	.00689	4.391879	3.81231	5.076974
var_U	15.76448	3.44687	.059575	15.34651	10.16291	23.5736

The average sampling efficiency, 39%, is lower than with the full Gibbs sampling in example 21 but is higher compared with the model that did not use Gibbs sampling for random effects. For models that do not support Gibbs sampling, splitting on random effects may be a good alternative.

◁

▷ Example 23: Fifth simulation—alternative parameterization

In our pig-data example, the difficulty of sampling the constant term efficiently may be explained by the presence of a high correlation between the constant and one or more random effects. In such cases, an alternative parameterization of a multilevel model may be useful.

Consider the following formulation of an earlier random-intercept model:

$$\texttt{weight}_{ij} = \beta_0 + \beta_1\texttt{week}_{ij} + u_j + \epsilon_{ij} = \beta_1\texttt{week}_{ij} + \tau_j + \epsilon_{ij},$$

$$\begin{aligned}
\epsilon_{ij} &\sim \text{i.i.d. } N(0, \sigma_0^2)\\
\tau_j &\sim \text{i.i.d. } N(\beta_0, \sigma_u^2)\\
\beta_0 &\sim N(0, 100)\\
\beta_1 &\sim N(0, 100)\\
\sigma_0^2 &\sim \text{InvGamma}(0.001, 0.001)\\
\sigma_u^2 &\sim \text{InvGamma}(0.001, 0.001)
\end{aligned}$$

Here, the constant term is absorbed into the prior for the random effects τ_j's, which have a mean of β_0 instead of a zero, as for random effects u_j's.

To specify the above model with `bayesmh`, we need to use the `noconstant` option, and we need to specify the prior for random effects manually.

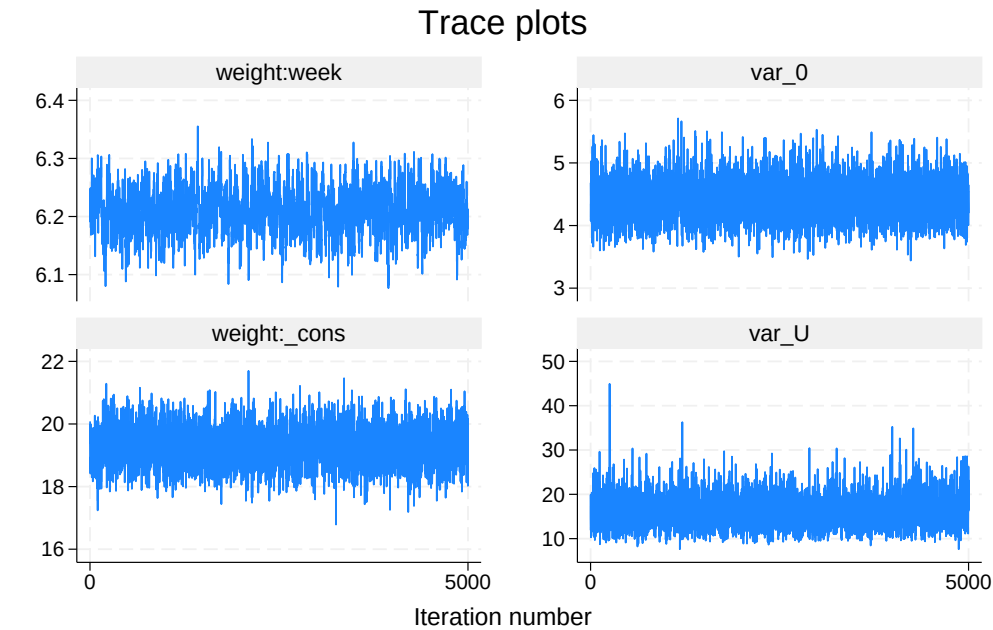
Continuing with example 21, we now fit a reparameterized model:

```
. bayesmh weight week U[id], likelihood(normal({var_0})) noconstant
>         prior({U[id]},        normal({weight:_cons},{var_U}))
>         prior({weight:_cons}, normal(0, 100))
>         prior({weight:week},  normal(0, 100))
>         prior({var_0},        igamma(0.001, 0.001))
>         prior({var_U},        igamma(0.001, 0.001))
>         block({weight:} {var_0 var_U}, split gibbs)
>         block({U}, gibbs)
>         mcmcsize(5000) dots rseed(14)
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 5000 .........1000.........2000.........3000.........4000.........
> 5000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  weight ~ normal(xb_weight,{var_0})

Priors:
   {weight:week} ~ normal(0,100)                                          (1)
         {U[id]} ~ normal({weight:_cons},{var_U})                         (1)
         {var_0} ~ igamma(0.001,0.001)
  {weight:_cons} ~ normal(0,100)

Hyperprior:
  {var_U} ~ igamma(0.001,0.001)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_weight.

Bayesian normal regression                      MCMC iterations  =      7,500
Gibbs sampling                                  Burn-in          =      2,500
                                                MCMC sample size =      5,000
                                                Number of obs    =        432
                                                Acceptance rate  =          1
                                                Efficiency:  min =      .1139
                                                             avg =      .6008
Log marginal-likelihood                                      max =      .9366

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
weight       |
        week |  6.210628   .0389494   .001632   6.21117   6.133097   6.286066
       _cons |  19.28477    .607197   .012616   19.28279   18.10872   20.50361
-------------+----------------------------------------------------------------
       var_0 |  4.412291   .3191009   .004663   4.398022   3.827661   5.090693
       var_U |  15.82342   3.484342   .052251   15.38458   10.29349   23.88555
------------------------------------------------------------------------------
```

The average efficiency increased dramatically to 60% with the minimum efficiency of 11% now.

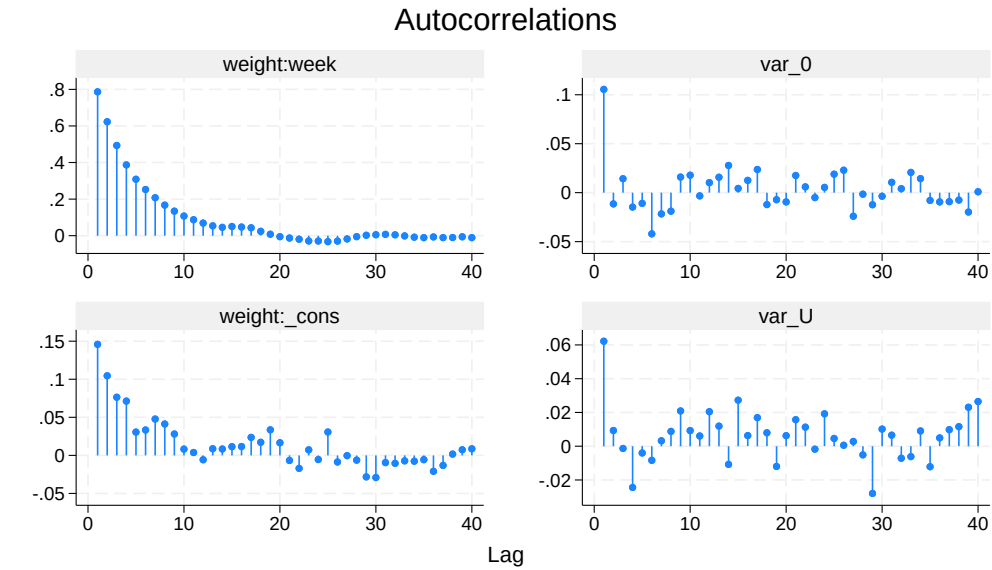
The diagnostic plots now show perfect mixing for all main model parameters:

```
. bayesgraph trace _all, byparm(cols(2))
```



Graphs by parameter

```
. bayesgraph ac _all, byparm
```



All estimates are very close to the MLEs obtained earlier with the `mixed` command.

◁

Linear growth curve model—a random-coefficient model

Continuing our pig data example from *Two-level random-intercept model or panel-data model*, we extend the random-intercept model to include random coefficients for `week` by using

$$\texttt{weight}_{ij} = \beta_0 + \beta_1\texttt{week}_{ij} + u_{0j} + u_{1j}\texttt{week}_{ij} + \epsilon_{ij}$$

where u_{0j} is the random effect for pig and u_{1j} is the pig-specific random coefficient on `week` for $j = 1, \ldots, 48$ and $i = 1, \ldots, 9$.

▷ Example 24: Independent covariance structure for the random effects

Let us first assume that the random effects u_{0j}'s and u_{1j}'s are independent. We can use `mixed` to fit this model by using maximum likelihood.

```
. use https://www.stata-press.com/data/r18/pig
(Longitudinal analysis of pig weights)
. mixed weight week || id: week
Performing EM optimization ...
Performing gradient-based optimization:
Iteration 0:  Log likelihood = -869.03825
Iteration 1:  Log likelihood = -869.03825
Computing standard errors ...
Mixed-effects ML regression                     Number of obs     =        432
Group variable: id                              Number of groups  =         48
                                                Obs per group:
                                                              min =          9
                                                              avg =        9.0
                                                              max =          9
                                                Wald chi2(1)      =    4689.51
Log likelihood = -869.03825                     Prob > chi2       =     0.0000
```

weight	Coefficient	Std. err.	z	P>|z|	[95% conf.	interval]
week	6.209896	.0906819	68.48	0.000	6.032163	6.387629
_cons	19.35561	.3979159	48.64	0.000	18.57571	20.13551

Random-effects parameters	Estimate	Std. err.	[95% conf.	interval]
id: Independent				
var(week)	.3680668	.0801181	.2402389	.5639103
var(_cons)	6.756364	1.543503	4.317721	10.57235
var(Residual)	1.598811	.1233988	1.374359	1.85992

```
LR test vs. linear model: chi2(2) = 764.42                Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

Consider the following Bayesian model for these data:

$$\texttt{weight}_{ij} = \beta_0 + \beta_1\texttt{week}_{ij} + u_{0j} + u_{1j}\texttt{week}_{ij} + \epsilon_{ij} = \tau_{0j} + \tau_{1j}\texttt{week}_{ij} + \epsilon_{ij},$$

$$\begin{aligned}
\epsilon_{ij} &\sim \text{i.i.d. } N(0, \sigma_0^2)\\
\tau_{0j} &\sim \text{i.i.d. } N(\beta_0, \sigma^2_{\tau_0})\\
\tau_{1j} &\sim \text{i.i.d. } N(\beta_1, \sigma^2_{\tau_1})\\
\beta_0 &\sim N(0, 100)\\
\beta_1 &\sim N(0, 100)\\
\sigma_0^2 &\sim \text{InvGamma}(0.001, 0.001)\\
\sigma^2_{\tau_0} &\sim \text{InvGamma}(0.001, 0.001)\\
\sigma^2_{\tau_1} &\sim \text{InvGamma}(0.001, 0.001)
\end{aligned}$$

The model has five main parameters of interest: regression coefficients β_0 and β_1 and variance components σ_0^2, $\sigma_{\tau_0}^2$, and $\sigma_{\tau_1}^2$. β_0 and β_1 are technically hyperparameters because they are specified as mean parameters of the prior distributions for random effects τ_{0j}'s and τ_{1j}'s, respectively. Random effects τ_{0j} and τ_{1j} are considered nuisance parameters. We again use normal priors for the regression coefficients and random effects and inverse-gamma priors for the variance parameters. We specify fairly noninformative priors.

To fit this model using `bayesmh`, we include random effects for pig and their interaction with `week` in our regression model. Following *Random effects*, we add random intercepts for the `id` variable as `T0[id]`, and we include random coefficients on `week` as `c.week#T1[id]`, where `T0` and `T1` stand for τ_0 and τ_1.

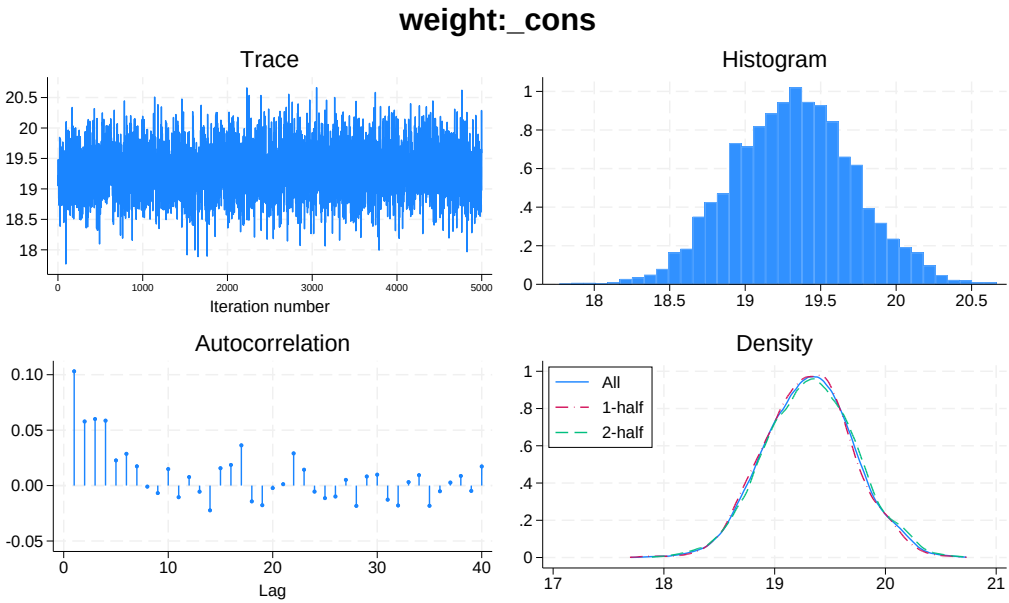
We fit our model using `bayesmh`. Following example 21, we perform blocking of parameters and use Gibbs sampling for the blocks. For brevity, we also combine the same prior specifications in one statement but use `prior()`'s `split` suboption to continue treating the parameters from the same `prior()` statement as separate blocks during simulation.

```
. bayesmh weight T0[id] c.week#T1[id], likelihood(normal({var_0})) noconstant
>         prior({T0[id]}, normal({weight:_cons}, {var_T0}))
>         prior({T1[id]}, normal({weight:week},  {var_T1}))
>         prior({weight:week _cons}, normal(0, 1e2) split)
>         prior({var_0 var_T0 var_T1}, igamma(0.001, 0.001) split)
>         block({var_0 var_T0 var_T1}, gibbs split)
>         block({weight:}, gibbs split)
>         block({T0}, gibbs) block({T1}, gibbs)
>         mcmcsize(5000) rseed(17) dots notable
Burn-in 2500 .........1000.........2000..... done
Simulation 5000 .........1000.........2000.........3000.........4000.........
> 5000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  weight ~ normal(xb_weight,{var_0})

Priors:
             {T0[id]} ~ normal({weight:_cons},{var_T0})                    (1)
             {T1[id]} ~ normal({weight:week},{var_T1})                     (1)
              {var_0} ~ igamma(0.001,0.001)
  {weight:week _cons} ~ normal(0,1e2)

Hyperprior:
  {var_T0 var_T1} ~ igamma(0.001,0.001)
------------------------------------------------------------------------------
(1) Parameter is an element of the linear form xb_weight.

Bayesian normal regression                      MCMC iterations  =      7,500
Gibbs sampling                                  Burn-in          =      2,500
                                                MCMC sample size =      5,000
                                                Number of obs    =        432
                                                Acceptance rate  =          1
                                                Efficiency:  min =      .4104
                                                             avg =      .5277
Log marginal-likelihood                                      max =      .6875
```

Our AR is good and efficiencies are high. We do not have a reason to suspect nonconvergence. Nevertheless, it is important to perform graphical convergence diagnostics to confirm this. We used the `notable` option to suppress the estimation summary to focus on checking the MCMC convergence first and to redisplay the coefficients in the same order as in `mixed`.

Let's look at diagnostic plots. We show only diagnostic plots for the mean of random intercepts, but convergence should be established for all parameters before any inference can be made. We leave it to you to verify convergence of the remaining parameters.

```
. bayesgraph diagnostics {weight:_cons}
```



The diagnostic plots look good.

Our posterior mean estimates of the main model parameters are in agreement with maximum likelihood results from `mixed`, as is expected with noninformative priors.

```
. bayesstats summary {weight:week _cons} {var_T1 var_T0 var_0}
Posterior summary statistics                       MCMC sample size =     5,000
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
weight						
week	6.213062	.0950649	.001621	6.213753	6.029047	6.401924
_cons	19.31661	.4041825	.007445	19.32041	18.54005	20.13218
var_T1	.3940673	.0927395	.001937	.3815496	.2522003	.6080756
var_T0	7.176892	1.719979	.037968	6.956708	4.424175	11.31125
var_0	1.604662	.1229856	.002478	1.600799	1.377464	1.857627

▷ Example 25: Unstructured covariance structure for the random effects

In this example, we assume that the random effects τ_{0j}'s and τ_{1j}'s are correlated. Again we can use the `mixed` command to fit this model by using maximum likelihood.

```
. mixed weight week || id: week, cov(unstructured)
Performing EM optimization ...
Performing gradient-based optimization:
Iteration 0:  Log likelihood = -868.96185
Iteration 1:  Log likelihood = -868.96185
Computing standard errors ...
Mixed-effects ML regression                     Number of obs     =        432
Group variable: id                              Number of groups  =         48
                                                Obs per group:
                                                              min =          9
                                                              avg =        9.0
                                                              max =          9
                                                Wald chi2(1)      =    4649.17
Log likelihood = -868.96185                     Prob > chi2       =     0.0000
```

weight	Coefficient	Std. err.	z	P>|z|	[95% conf.	interval]
week	6.209896	.0910745	68.18	0.000	6.031393	6.388399
_cons	19.35561	.3996387	48.43	0.000	18.57234	20.13889

Random-effects parameters	Estimate	Std. err.	[95% conf.	interval]
id: Unstructured				
var(week)	.3715251	.0812958	.2419532	.570486
var(_cons)	6.823363	1.566194	4.351297	10.69986
cov(week,_cons)	-.0984378	.2545767	-.5973991	.4005234
var(Residual)	1.596829	.123198	1.372735	1.857505

```
LR test vs. linear model: chi2(3) = 764.58                Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

We modify the previous Bayesian model to account for the correlation between the random effects:

$$(\tau_{0j}, \tau_{1j}) \sim \text{i.i.d. MVN}(\beta_0, \beta_1, \Sigma)$$
$$\Sigma \sim \text{InvWishart}\{3, I(2)\}$$

$$\Sigma = \begin{bmatrix} \sigma^2_{\tau_0} & \sigma^2_{12} \\ \sigma^2_{21} & \sigma^2_{\tau_1} \end{bmatrix}$$

The elements $\sigma^2_{\tau_0}$ and $\sigma^2_{\tau_1}$ of Σ represent the variances of τ_{0j}'s and τ_{1j}'s, respectively, while σ_{21} is the covariance between them. We apply a weakly informative inverse-Wishart prior with degree of freedom 3 and identity scale matrix.

Gibbs sampling is not available in bayesmh for the mean parameters ({weight:_cons} and {weight:week}) of the multivariate normal distribution with an unstructured covariance. We thus remove gibbs from the corresponding block() option.

```
. bayesmh weight T0[id] c.week#T1[id], likelihood(normal({var_0})) noconstant
>         prior({T0 T1}, mvnormal(2, {weight:_cons}, {weight:week}, {Sigma,m}))
>         prior({weight:week _cons}, normal(0, 1e2) split)
>         prior({var_0},   igamma(0.001,0.001))
>         prior({Sigma,m}, iwishart(2,3,I(2)))
>         block({var_0} {Sigma,m}, gibbs split)
>         block({weight:}, split)
>         block({T0}, gibbs) block({T1}, gibbs)
>         mcmcsize(5000) rseed(17) dots
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 5000 .........1000.........2000.........3000.........4000.........
> 5000 done

Model summary
------------------------------------------------------------------------------
Likelihood:
  weight ~ normal(xb_weight,{var_0})

Priors:
              {var_0} ~ igamma(0.001,0.001)
      {T0[id] T1[id]} ~ mvnormal(2,{weight:_cons},{weight:week},{Sigma,m}) (1)
  {weight:week _cons} ~ normal(0,1e2)

Hyperprior:
  {Sigma,m} ~ iwishart(2,3,I(2))
------------------------------------------------------------------------------
(1) Parameter is an element of the linear form xb_weight.

Bayesian normal regression                      MCMC iterations  =      7,500
Metropolis-Hastings and Gibbs sampling          Burn-in          =      2,500
                                                MCMC sample size =      5,000
                                                Number of obs    =        432
                                                Acceptance rate  =      .8146
                                                Efficiency:  min =       .177
                                                             avg =      .3942
Log marginal-likelihood                                      max =      .5378

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
weight       |
       _cons |   19.32651   .3922638   .013186   19.32816   18.54339   20.11928
        week |   6.207807   .0986948   .003086    6.20779   6.009859   6.402211
-------------+----------------------------------------------------------------
       var_0 |   1.608075   .1253061   .002416    1.60557   1.377569   1.859606
   Sigma_1_1 |   6.845693   1.643541   .034744   6.637035   4.250556   10.62172
   Sigma_2_1 |  -.0947838   .2706155   .005435  -.0897511   -.654002   .4270949
   Sigma_2_2 |   .4021311     .09014   .001798   .3894671   .2606943   .6142174
------------------------------------------------------------------------------
```

The average sampling efficiency is about 40% with no indications for convergence problems. The posterior mean estimates of the main model parameters are close to the maximum likelihood results from mixed. For example, the estimates of variance components $\sigma^2_{\tau_0}$, σ_{21}, and $\sigma^2_{\tau_1}$ are 6.85, -0.095, and 0.40, respectively, from bayesmh and 6.82, -0.098, and 0.37, respectively, from mixed.

◁

Multilevel logistic regression

Here we revisit example 1 [ME] **melogit**. The example analyzes data from the 1989 Bangladesh fertility survey (Huq and Cleland 1990). A logistic regression model applied to the response variable `c_use` uses fixed-effects variables `urban`, `age`, and `i.children` and a random-effects variable, `district`, to account for the between-district variability.

A Bayesian analog of this two-level, random-intercept model using `bayesmh` is as follows. We include `U[district]` in the list of covariates to specify the random intercepts for the group variable `district`. The corresponding random-effects parameters `{U[district]}` are assigned a zero-mean normal prior distribution with variance `{var_U}`. A relatively weak `normal(0,100)` prior is applied to the fixed-effects parameters `{c_use:urban}`, `{c_use:age}`, `{c_use:i.children}`, and `{c_use:_cons}`. The variance parameter `{var_U}` is assigned a noninformative `igamma(0.01,0.01)` prior, and a Gibbs sampler is used for it.

```
. use https://www.stata-press.com/data/r18/bangladesh
(Bangladesh Fertility Survey, 1989)

. bayesmh c_use urban age i.children U[district], likelihood(logit)
>         prior({c_use:urban age i.children _cons}, normal(0, 100))
>         prior({var_U}, igamma(0.01,0.01))
>         block({var_U}, gibbs) dots rseed(17)
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done

Model summary
------------------------------------------------------------------------------
Likelihood:
  c_use ~ logit(xb_c_use)

Priors:
  {c_use:urban age i.children _cons} ~ normal(0,100)                      (1)
                       {U[district]} ~ normal(0,{var_U})                  (1)

Hyperprior:
  {var_U} ~ igamma(0.01,0.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_c_use.

Bayesian logistic regression                    MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling          Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =      1,934
                                                Acceptance rate  =      .4517
                                                Efficiency:  min =     .01859
                                                             avg =     .02813
Log marginal-likelihood                                      max =     .04373

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
c_use        |
       urban |   .7364239   .1120843   .007943   .7393282   .4993958   .9511179
         age |  -.0262663   .0076378    .00056    -.02666  -.0418213  -.0116904
             |
    children |
    1 child  |   1.129249   .1530869   .010718   1.127919   .8263055   1.432189
 2 children  |   1.368097   .1678695    .01045   1.361876   1.040911   1.690345
3 or more..  |   1.340399   .1773981   .009683   1.337075   .9809634   1.692562
             |
       _cons |  -1.688619   .1480851   .007926  -1.692551  -1.966011  -1.388868
-------------+----------------------------------------------------------------
       var_U |   .2295154   .0797827   .003815   .2180827   .1098954   .4199566
------------------------------------------------------------------------------
```

Although the average efficiency of 0.03 is not that high, there are no indications for convergence problems. (We can verify this by looking at convergence diagnostics using `bayesgraph diagnostics`.)

Our estimates of the main regression parameters are close to those obtained with the `melogit` command. The posterior mean estimate of variance parameter `{var_U}`, 0.23, is slightly larger than the corresponding estimate of 0.22 from `melogit`.

Three-level nonlinear model

We revisit example 20 from [ME] **menl** analyzing the affect of dietary additive guar on blood glucose level after alcohol consumption. A total of seven subjects participated in the study, identified by the `subject` variable. Their blood glucose was measured at time points given by the variable `time`. The binary variable `guar` identifies experiments with and without the dietary additive.

```
. use https://www.stata-press.com/data/r18/glucose
(Glucose levels following alcohol ingestion (Hand and Crowder, 1996))
. describe
Contains data from https://www.stata-press.com/data/r18/glucose.dta
 Observations:           196                  Glucose levels following
                                                alcohol ingestion (Hand and
                                                Crowder, 1996)
    Variables:             4                  16 Feb 2023 14:16
-------------------------------------------------------------------------------
Variable      Storage   Display    Value
    name         type    format    label      Variable label
-------------------------------------------------------------------------------
subject         byte    %9.0g                 Subject ID
time            byte    %9.0g                 Time since alcohol ingestion
                                                (min/10)
glucose         double  %9.0g                 Blood glucose level (mg/dl)
guar            byte    %12.0g     guarlbl    Experiment with and without guar
-------------------------------------------------------------------------------
Sorted by:
```

The expected glucose level is analyzed according to a model proposed in Hand and Crowder (1996). It is a three-level nonlinear model that includes subject-level random effects `U1[subject]` and `U2[subject]` and guar-within-subject level random effects `UU1[subject>guar]` and `UU2[subject>guar]`. See example 20 for a full description of the model. We consider the model from that example in which the pairs `U1` and `U2`, and `UU1` and `UU2`, are assumed to be independent.

We fit a Bayesian version of the model using `bayesmh`. The likelihood specification is similar to the one used by the `menl` command, but with `bayesmh`, we also specify the prior distributions for the model parameters. Random effects are assigned normal priors by default with the corresponding variance components `{var_U1}`, `{var_U2}`, `{var_UU1}`, and `{var_UU2}`. The parameters `{phi1:_cons}`, `{phi2:_cons}`, and `{phi3}` are assigned `normal(0, 100)` priors, and all variance components are assigned `igamma(0.01, 0.01)` priors. Gibbs sampling is used for variance components, and `{phi1:_cons}`, `{phi2:_cons}`, and `{phi3}` are sampled in separate blocks. We use the `define()` option to define parameters `{phi1:}` and `{phi2:}` as a linear combination of the corresponding random effects, including the constant term.

We suppress the estimation table and redisplay results later by using `bayesstats summary` to match the output from `menl` more closely. The model contains many parameters, so it takes about a minute to run.

```
. bayesmh glucose = ({phi1:} + {phi2:}*c.time#c.time#c.time*exp(-{phi3}*time)),
> likelihood(normal({var}))
> define(phi1: U1[subject] UU1[subject>guar])
> define(phi2: U2[subject] UU2[subject>guar])
> prior({phi1:_cons} {phi2:_cons} {phi3}, normal(0, 100) split)
> prior({var var_U1 var_UU1 var_U2 var_UU2}, igamma(0.01, 0.01) split)
> block({phi1:_cons} {phi2:_cons}, split)
> block({var var_U1 var_UU1 var_U2 var_UU2}, gibbs split)
> mcmcsize(5000) rseed(17) notable
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 5000 .........1000.........2000.........3000.........4000.........
> 5000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  glucose ~ normal(xb_phi1 + xb_phi2*c.time#c.time#c.time*exp(-{phi3}*time),{v
            ar})

Priors:
         {var} ~ igamma(0.01,0.01)
        {phi3} ~ normal(0,100)
  {phi1:_cons} ~ normal(0,100)
  {phi2:_cons} ~ normal(0,100)

Hyperpriors:
  {var_U1 var_UU1 var_U2 var_UU2} ~ igamma(0.01,0.01)
                     {U1[subject]} ~ normal(0,{var_U1})
               {UU1[subject>guar]} ~ normal(0,{var_UU1})
                     {U2[subject]} ~ normal(0,{var_U2})
               {UU2[subject>guar]} ~ normal(0,{var_UU2})
------------------------------------------------------------------------------

Bayesian normal regression                      MCMC iterations  =      7,500
Metropolis-Hastings and Gibbs sampling          Burn-in          =      2,500
                                                MCMC sample size =      5,000
                                                Number of obs    =        196
                                                Acceptance rate  =      .6232
                                                Efficiency:  min =    .006257
                                                             avg =      .1226
Log marginal-likelihood                                      max =      .7002
```

The `bayesmh` command reports a reasonable average sampling efficiency of about 12% but the minimum efficiency is below 1%, so we may look into improving sampling efficiency for some parameters. There is no obvious indication of nonconvergence, but it is important to assess MCMC convergence visually by using, for instance, `bayesgraph diagnostics` or more formally by running multiple chains and evaluating the Gelman–Rubin statistics; see *Convergence diagnostics using multiple chains*.

Let's look at the results and compare them with the results reported by the menl command. We report variance components as standard deviations to more easily match the results from menl

```
. bayesstats summary {phi1:_cons} {phi2:_cons} {phi3}
> (sd_U1:sqrt({var_U1})) (sd_U2:sqrt({var_U2}))
> (sd_UU1:sqrt({var_UU1})) (sd_UU2:sqrt({var_UU2}))
> (sd:sqrt({var}))
Posterior summary statistics                       MCMC sample size =     5,000

       sd_U1 : sqrt({var_U1})
       sd_U2 : sqrt({var_U2})
      sd_UU1 : sqrt({var_UU1})
      sd_UU2 : sqrt({var_UU2})
          sd : sqrt({var})
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
phi1						
_cons	3.675754	.1233928	.013441	3.675342	3.426524	3.933746
phi2						
_cons	.4454892	.075955	.01358	.443041	.2921755	.6014314
phi3	.5990691	.0131787	.001021	.5991885	.5745415	.6255063
sd_U1	.2937574	.1372631	.007882	.2697849	.1069155	.6306559
sd_U2	.1445083	.0633264	.005947	.1322361	.0626003	.2953982
sd_UU1	.1754194	.0793246	.0065	.1606835	.0717868	.3715494
sd_UU2	.1453472	.0411391	.002454	.1393845	.0828334	.2437548
sd	.5847464	.033378	.000565	.583425	.5251977	.6544421

The posterior mean estimates for the coefficients {phi1:_cons}, {phi2:_cons}, and {phi3} and the residual standard deviation are close to the estimates from menl. The Bayesian estimates of variance components are higher. In particular, the posterior means for the standard deviations of {U2} and {UU1} are not only higher but also more concentrated with 95% credible intervals of [0.06, 0.30] and [0.07, 0.37]. In comparison, the corresponding 95% confidence intervals from menl are rather wide, [0.0003, 6.3] and [0.0007, 6], which indicates less reliable estimates.

To improve sampling efficiency in this example, we can reparameterize the model by recentering the random effects U1 and U2 around constants {phi1:_cons} and {phi2:_cons} so that these constants become the prior means for the random effects U1 and U2. This will allow us to use Gibbs sampling for {phi1:_cons} and {phi2:_cons}.

We fit the reparameterized model using bayesmh with the Gibbs sampling for the prior means.

```
. bayesmh glucose = ({phi1:} + {phi2:}*c.time#c.time#c.time*exp(-{phi3}*time)),
> likelihood(normal({var}))
> define(phi1: U1[subject] UU1[subject>guar], noconstant)
> define(phi2: U2[subject] UU2[subject>guar], noconstant)
> prior({U1[subject]}, normal({phi1:_cons}, {var_U1}))
> prior({U2[subject]}, normal({phi2:_cons}, {var_U2}))
> prior({phi1:_cons} {phi2:_cons} {phi3}, normal(0, 100) split)
> prior({var var_U1 var_UU1 var_U2 var_UU2}, igamma(0.01, 0.01) split)
> block({phi1:_cons} {phi2:_cons}, gibbs split)
> block({var var_U1 var_UU1 var_U2 var_UU2}, gibbs split)
> mcmcsize(5000) rseed(17) notable
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 5000 .........1000.........2000.........3000.........4000.........
> 5000 done
```

```
Model summary
------------------------------------------------------------------------------
Likelihood:
  glucose ~ normal(xb_phi1 + xb_phi2*c.time#c.time#c.time*exp(-{phi3}*time),{v
            ar})

Priors:
         {var} ~ igamma(0.01,0.01)
        {phi3} ~ normal(0,100)
  {phi1:_cons} ~ normal(0,100)
  {phi2:_cons} ~ normal(0,100)

Hyperpriors:
                    {U1[subject]} ~ normal({phi1:_cons},{var_U1})
                    {U2[subject]} ~ normal({phi2:_cons},{var_U2})
  {var_U1 var_UU1 var_U2 var_UU2} ~ igamma(0.01,0.01)
              {UU1[subject>guar]} ~ normal(0,{var_UU1})
              {UU2[subject>guar]} ~ normal(0,{var_UU2})
------------------------------------------------------------------------------

Bayesian normal regression                      MCMC iterations  =      7,500
Metropolis-Hastings and Gibbs sampling          Burn-in          =      2,500
                                                MCMC sample size =      5,000
                                                Number of obs    =        196
                                                Acceptance rate  =      .7143
                                                Efficiency:  min =     .02353
                                                             avg =      .1242
Log marginal-likelihood                                      max =      .5715
```

The minimum efficiency is now increased to about 2%, but the maximum efficiency is decreased. On average, we are still at 12%.

```
. bayesstats summary {phi1:_cons} {phi2:_cons} {phi3}
> (sd_U1:sqrt({var_U1})) (sd_U2:sqrt({var_U2}))
> (sd_UU1:sqrt({var_UU1})) (sd_UU2:sqrt({var_UU2}))
> (sd:sqrt({var}))

Posterior summary statistics                       MCMC sample size =     5,000

       sd_U1 : sqrt({var_U1})
       sd_U2 : sqrt({var_U2})
      sd_UU1 : sqrt({var_UU1})
      sd_UU2 : sqrt({var_UU2})
          sd : sqrt({var})
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
phi1						
_cons	3.668967	.1514235	.00922	3.671296	3.361262	3.968073
phi2						
_cons	.4433111	.0754776	.005946	.4447485	.2940002	.5930835
phi3	.6000894	.0115797	.001068	.5994865	.5779582	.6232038
sd_U1	.3106145	.1466302	.008729	.2839151	.1113562	.6797507
sd_U2	.1422476	.0632357	.003645	.1288667	.06242	.30695
sd_UU1	.1805265	.0826131	.007787	.1635459	.0715432	.3957199
sd_UU2	.1508045	.0443954	.003536	.1445271	.0815014	.2546343
sd	.5753598	.0314809	.000588	.5737936	.5181599	.6412948

We obtain very similar results to the above.

Survival models

bayesmh provides several likelihood models (stexponential, stgamma(), stloglogistic(), stlognormal(), and stweibull()) in the likelihood() option to analyze survival-time or failure-time data. Also see [BAYES] **bayes: streg** and [BAYES] **bayes: mestreg**.

You can use these models to analyze failures-only data as well as to account for right-censoring when you specify the failure() suboption within likelihood() and for left-truncation when you specify the ltruncated() suboption. You can also choose between the proportional hazards (PH) and accelerated failure-time (AFT) parameterizations with stexponential and stweibull() via suboptions ph (the default) and aft.

When fitting survival models, you have two options for the metric of the ancillary parameters of the survival distributions. For instance, for the Weibull distribution, you can model the shape parameter p in the log metric by using likelihood(stweibull(*lnp*)) or likelihood(stweibull(*lnp*), logparam) (the default) or in the original metric by using likelihood(stweibull(*p*), nologparam). Similarly, for the lognormal distribution, you can model the log-standard deviation by using likelihood(stlognormal(*lnstd*)) (the default) or the variance by using likelihood(stlognormal(*var*), nologparam), and so on. Which parameterization to use for the ancillary parameters often depends on the chosen priors. For example, in a Weibull model, we may use a normal prior for the log-shape parameter *lnp* and a uniform prior for the shape parameter *p*.

Let's look at a couple of examples below.

Consider cancer.dta, which records patient survival in a cancer drug trial. Of the 48 participants, 20 receive a placebo (drug = 1), 14 receive one type of treatment (drug = 2), and 14 receive another type of treatment (drug = 3). We want to analyze time until death, measured in months (variable studytime), as a function of treatment adjusted for age. The died variable records the failure status for each subject, where died = 1 means a subject died and died = 0 means a subject is still alive and is thus considered right-censored.

Initially, let's ignore the failure status died and assume that studytime records failure times for all subjects.

For a reference, let's fit a classical Weibull regression model first by using `streg`.

```
. use https://www.stata-press.com/data/r18/cancer
(Patient survival in drug trial)
. stset studytime
Survival-time data settings
         Failure event: (assumed to fail at time=studytime)
Observed time interval: (0, studytime]
     Exit on or before: failure
------------------------------------------------------------------------------
         48  total observations
          0  exclusions
------------------------------------------------------------------------------
         48  observations remaining, representing
         48  failures in single-record/single-failure data
        744  total analysis time at risk and under observation
                                                At risk from t =         0
                                     Earliest observed entry t =         0
                                          Last observed exit t =        39
. streg i.drug age, distribution(weibull) nolog
        Failure _d: 1 (meaning all fail)
  Analysis time _t: studytime
Weibull PH regression
No. of subjects =  48                                 Number of obs =     48
No. of failures =  48
Time at risk    = 744
                                                      LR chi2(3)    =  27.52
Log likelihood = -42.840673                           Prob > chi2   = 0.0000
```

_t	Haz. ratio	Std. err.	z	P>|z|	[95% conf.	interval]
drug						
Other	.3979255	.1428204	-2.57	0.010	.1969223	.8040971
NA	.1526351	.0595183	-4.82	0.000	.0710785	.3277712
age	1.078185	.0309445	2.62	0.009	1.019209	1.140573
_cons	.0001469	.0002668	-4.86	0.000	4.18e-06	.0051652
/ln_p	.6848375	.1139204	6.01	0.000	.4615576	.9081174
p	1.983449	.2259554			1.586543	2.47965
1/p	.5041722	.0574355			.4032827	.6303011

Note: **_cons** estimates baseline hazard.

We now fit a Bayesian Weibull model by using `bayesmh`. To compare results with `streg`, we use vague priors for model parameters and specify the `eform()` option to report hazard ratios (exponentiated coefficients) instead of the coefficients reported by default by `bayesmh`. We also sample the shape parameter separately from the coefficients to improve efficiency.

```
. bayesmh studytime i.drug age, likelihood(stweibull({lnp}))
> prior({studytime:} {lnp}, normal(0,10000))
> rseed(17) eform(Haz. ratio) block({lnp})
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  studytime ~ stweibull(xb_studytime,{lnp})

Priors:
  {studytime:i.drug age _cons} ~ normal(0,10000)                          (1)
                         {lnp} ~ normal(0,10000)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_studytime.

Bayesian Weibull PH regression                  MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
No. of subjects =         48                    Number of obs    =         48
No. of failures =         48
Time at risk    =        744
                                                Acceptance rate  =      .3523
                                                Efficiency:  min =     .00462
                                                             avg =     .02827
Log marginal-likelihood = -200.03961                         max =     .04609

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             | Haz. ratio   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
studytime    |
        drug |
      Other  |  .4093515   .1455973   .008398   .3880567   .1930648   .7578985
         NA  |  .1586529   .0625765   .004121   .1507637   .0661176    .305668
             |
         age |   1.07599   .0314129   .001621   1.076738   1.014651   1.138556
       _cons |  .0008647   .0027453   .000128    .000166   4.69e-06   .0064232
-------------+----------------------------------------------------------------
         lnp |  .6707761   .1215257    .01788   .6717002   .4291893   .8990958
------------------------------------------------------------------------------
Note: _cons estimates baseline hazard.
```

The results between `bayesmh` and `streg` are similar, as expected with weak priors.

By default, `bayesmh` fits a Weibull model by using the log of the shape parameter. We can use `bayesstats summary` to display this parameter in the original metric and also to report its reciprocal.

```
. bayesstats summary (p:exp({lnp})) (reciprocal: 1/exp({lnp}))

Posterior summary statistics                    MCMC sample size =     10,000

           p : exp({lnp})
  reciprocal : 1/exp({lnp})

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
           p |  1.970195   .2388086   .034966   1.957563   1.536012    2.45738
  reciprocal |  .5151116   .0630406   .009313   .5108393   .4069374   .6510367
------------------------------------------------------------------------------
```

Depending on the data and desired prior, we may want to parameterize the model to use the shape parameter in the original metric. We can do this by specifying the `nologparam` suboption within `likelihood()`.

Let's refit the above model by using the direct parameterization of the shape parameter and specify a uniform prior for it.

```
. bayesmh studytime i.drug age, likelihood(stweibull({p}), nologparam)
> prior({studytime:}, normal(0,10000)) prior({p}, uniform(0,10))
> rseed(17) eform(Haz. ratio) block({p}) initial({p} 1)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  studytime ~ stweibull_nolog(xb_studytime,{p})
Priors:
  {studytime:i.drug age _cons} ~ normal(0,10000)                          (1)
                          {p} ~ uniform(0,10)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_studytime.
Bayesian Weibull PH regression                  MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
No. of subjects =         48                    Number of obs    =         48
No. of failures =         48
Time at risk    =        744
                                                Acceptance rate  =      .3121
                                                Efficiency:  min =    .003827
                                                             avg =     .01719
Log marginal-likelihood = -197.19456                         max =      .0247
------------------------------------------------------------------------------
                                                              Equal-tailed
             |  Haz. ratio   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
studytime    |
        drug |
       Other |   .4254684   .1642118   .011746   .4001081   .1856402   .7999705
          NA |   .1571577   .0637717   .005037   .1477305   .0634229   .3087045
             |
         age |   1.081398   .0315245   .002132   1.080576   1.023548   1.148237
       _cons |   .0003976   .0009806   .000062   .0000991   2.99e-06   .0029425
-------------+----------------------------------------------------------------
           p |   2.058852   .2210333    .03573    2.06263   1.635212   2.464803
------------------------------------------------------------------------------
Note: _cons estimates baseline hazard.
```

We obtain similar results.

Continuing with the cancer dataset, let's now account for right-censoring, when `died = 0`.

As before, let's fit a classical Weibull model first for comparison.

```
. stset studytime, failure(died)
Survival-time data settings
         Failure event: died!=0 & died<.
Observed time interval: (0, studytime]
     Exit on or before: failure
------------------------------------------------------------------------------
         48  total observations
          0  exclusions
------------------------------------------------------------------------------
         48  observations remaining, representing
         31  failures in single-record/single-failure data
        744  total analysis time at risk and under observation
                                                At risk from t =         0
                                     Earliest observed entry t =         0
                                          Last observed exit t =        39

. streg i.drug age, distribution(weibull) nolog
        Failure _d: died
  Analysis time _t: studytime
Weibull PH regression
No. of subjects =  48                                 Number of obs =     48
No. of failures =  31
Time at risk    = 744
                                                      LR chi2(3)    =  37.07
Log likelihood = -42.090672                           Prob > chi2   = 0.0000
```

_t	Haz. ratio	Std. err.	z	P>|z|	[95% conf.	interval]
drug						
Other	.1705633	.0831449	-3.63	0.000	.0656067	.4434277
NA	.0782594	.0402588	-4.95	0.000	.0285532	.2144953
age	1.124439	.0410087	3.22	0.001	1.046869	1.207757
_cons	.0000254	.0000583	-4.60	0.000	2.80e-07	.0022994
/ln_p	.5573333	.1402154	3.97	0.000	.2825163	.8321504
p	1.74601	.2448175			1.326463	2.298256
1/p	.5727343	.0803062			.4351126	.7538844

Note: **_cons** estimates baseline hazard.

With bayesmh, we specify the failure indicator in the failure() suboption within likelihood().

```
. bayesmh studytime i.drug age, likelihood(stweibull({lnp}), failure(died))
> prior({studytime:} {lnp}, normal(0,1000))
> rseed(17) eform(Haz. ratio)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  studytime ~ stweibull(xb_studytime,{lnp})

Priors:
  {studytime:i.drug age _cons} ~ normal(0,1000)                          (1)
                         {lnp} ~ normal(0,1000)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_studytime.

Bayesian Weibull PH regression                  MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
No. of subjects =         48                    Number of obs    =         48
No. of failures =         31
Time at risk    =        744
                                                Acceptance rate  =      .2097
                                                Efficiency:  min =     .02624
                                                             avg =     .05735
Log marginal-likelihood = -144.93174                         max =      .1121
------------------------------------------------------------------------------
             |                                                Equal-tailed
             | Haz. ratio   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
studytime    |
       drug  |
     Other   |  .1812423   .0873363   .004128   .1646181   .0552102   .3888732
        NA   |  .0862965   .0467029   .001991   .0761287    .023666   .2074524
             |
         age |   1.12242   .0409687   .001859   1.122171   1.048103   1.207311
       _cons |  .0003249   .0017001   .000051   .0000297   2.47e-07   .0023124
-------------+----------------------------------------------------------------
         lnp |  .5360872   .1458155   .009001   .5467961   .2352398   .8087516
------------------------------------------------------------------------------
Note: _cons estimates baseline hazard.
```

The results are again similar to those from streg after accounting for right-censoring.

As with right-censoring, we can account for left-truncation by specifying the ltruncated() option. We can also specify the aft option to fit a Weibull (or exponential) model using the AFT parameterization instead of the default PH parameterization.

Bayesian analysis of change-point problem

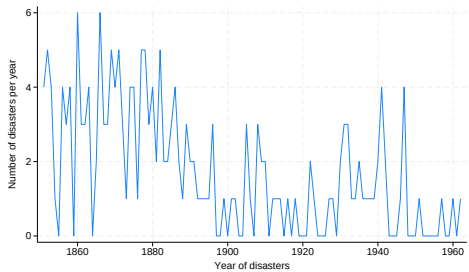
Change-point problems deal with stochastic data, usually time-series data, that undergo some abrupt change at some time point. It is of interest to localize the point of change and estimate the properties of the stochastic process before and after the change.

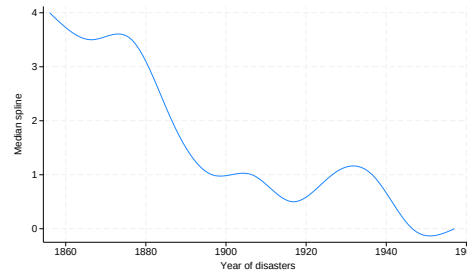
Here we analyze the British coal mining disaster data for the years 1851 to 1962 as given in table 5 in Carlin, Gelfand, and Smith (1992). The data are originally from Maguire, Pearson, and Wynn (1952) with updates from Jarrett (1979).

coal.dta contains 112 observations, and it includes the variables id, which records observation identifiers; count, which records the number of coal mining disasters involving 10 or more deaths; and year, which records the years corresponding to the disasters.

```
. use https://www.stata-press.com/data/r18/coal
(British coal-mining disaster data, 1851-1962)
. describe
Contains data from https://www.stata-press.com/data/r18/coal.dta
 Observations:           112                  British coal-mining disaster
                                                data, 1851-1962
    Variables:             3                  5 Feb 2022 18:03
                                              (_dta has notes)
-------------------------------------------------------------------------------
Variable      Storage   Display    Value
    name         type    format    label      Variable label
-------------------------------------------------------------------------------
id                int     %9.0g                Observation identifier
year              int     %9.0g                Year of disasters
count             byte    %9.0g                Number of disasters per year
-------------------------------------------------------------------------------
Sorted by:
```

The figures below suggest a fairly abrupt decrease in the rate of disasters around the 1887–1895 period, possibly because of the decline in labor productivity in coal mining (Raftery and Akman 1986). The line plot of count versus year is shown in the left pane and its smoothed version in the right pane.





To find the change-point parameter (cp) in the rate of disasters, we apply the following Bayesian model with noninformative priors for the parameters (accounting for the restricted range of cp):

$$\begin{aligned}
\texttt{counts}_i &\sim \text{Poisson}(\mu_1),\ \texttt{if year}_i < \text{cp}\\
\texttt{counts}_i &\sim \text{Poisson}(\mu_2),\ \texttt{if year}_i \geq \text{cp}\\
\mu_1 &\sim 1\\
\mu_2 &\sim 1\\
\text{cp} &\sim \text{Uniform}(1851, 1962)
\end{aligned}$$

The model has three parameters: μ_1, μ_2, and cp, which we will declare as `{mu1}`, `{mu2}`, and `{cp}` with `bayesmh`. One interesting feature of this model is the specification of a mixture distribution for `count`. To accommodate this, we specify the substitutable expression

```
({mu1}*sign(year<{cp})+{mu2}*sign(year>={cp}))
```

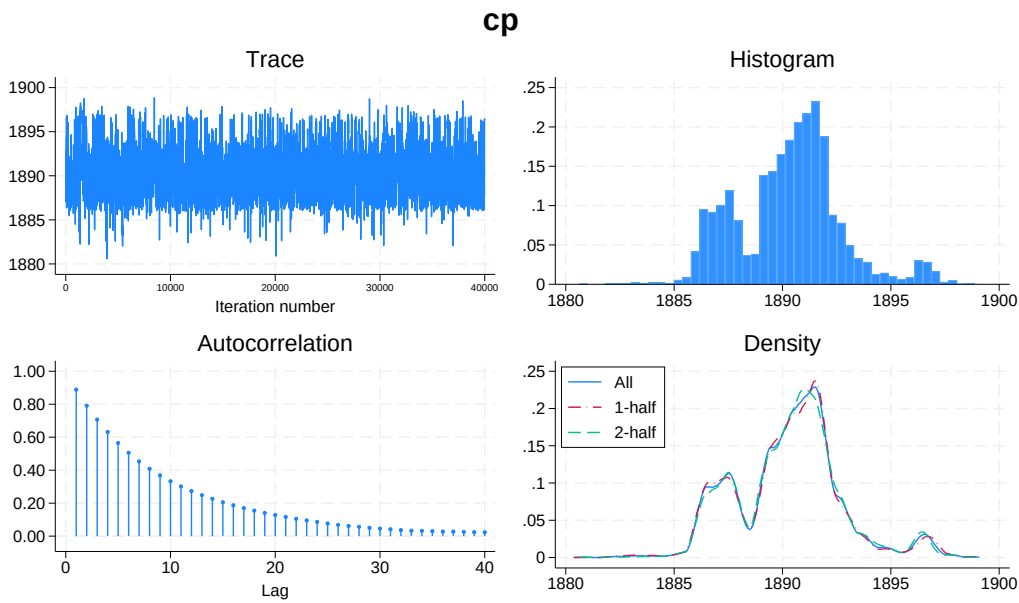
as the mean of a Poisson distribution `dpoisson()`. To ensure the feasibility of the initial state, we specify the desired initial values in option `initial()`. Because of high autocorrelation in the MCMC chain, we increase the MCMC size to achieve higher precision of our estimates. We change the default title to the title specific to our analysis. To monitor the progress of simulation, we request that `bayesmh` display a dot every 500 iterations and an iteration number every 5,000 iterations.

```
. set seed 14

. bayesmh count,
> likelihood(dpoisson({mu1}*sign(year<{cp})+{mu2}*sign(year>={cp})))
> prior({mu1} {mu2}, flat)
> prior({cp}, uniform(1851,1962))
> initial({mu1} 1 {mu2} 1 {cp} 1906)
> mcmcsize(40000) title(Change-point analysis) dots(500, every(5000))
Burn-in 2500 a.... done
Simulation 40000 .........5000.........10000.........15000.........20000.......
> ..25000.........30000.........35000.........40000 done

Model summary
------------------------------------------------------------------------------
Likelihood:
  count ~ poisson({mu1}*sign(year<{cp})+{mu2}*sign(year>={cp}))

Priors:
  {mu1 mu2} ~ 1 (flat)
       {cp} ~ uniform(1851,1962)
------------------------------------------------------------------------------

Change-point analysis                           MCMC iterations  =     42,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     40,000
                                                Number of obs    =        112
                                                Acceptance rate  =       .215
                                                Efficiency:  min =     .04909
                                                             avg =     .07177
Log marginal-likelihood = -173.39572                         max =     .09142

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
          cp |  1890.309    2.43097   .05486   1890.523   1886.126   1896.411
         mu1 |  3.151979   .2894379  .005291   3.137662   2.620379   3.741032
         mu2 |   .934086   .1162233  .001922   .9286517   .7184804   1.175782
------------------------------------------------------------------------------
```

According to our results, the change occurred in the first half of 1890. The drop of the disaster rate was significant, from an estimated average of 3.2 to 0.9.

The diagnostic plots, for example, for {cp} do not indicate any convergence problems. (This is also true for other parameters.)

```
. bayesgraph diagnostics {cp}
```



The simulated marginal density of {cp} shown in the right bottom corner provides more details. Apart from the main peak, there are 2 smaller bumps around the years 1886 and 1896, which correspond to local peaks in the number of disasters at these years: 4 in 1886 and 3 in 1896.

We may be interested in estimating the ratio between the two means. We can use bayesstats summary to estimate this ratio.

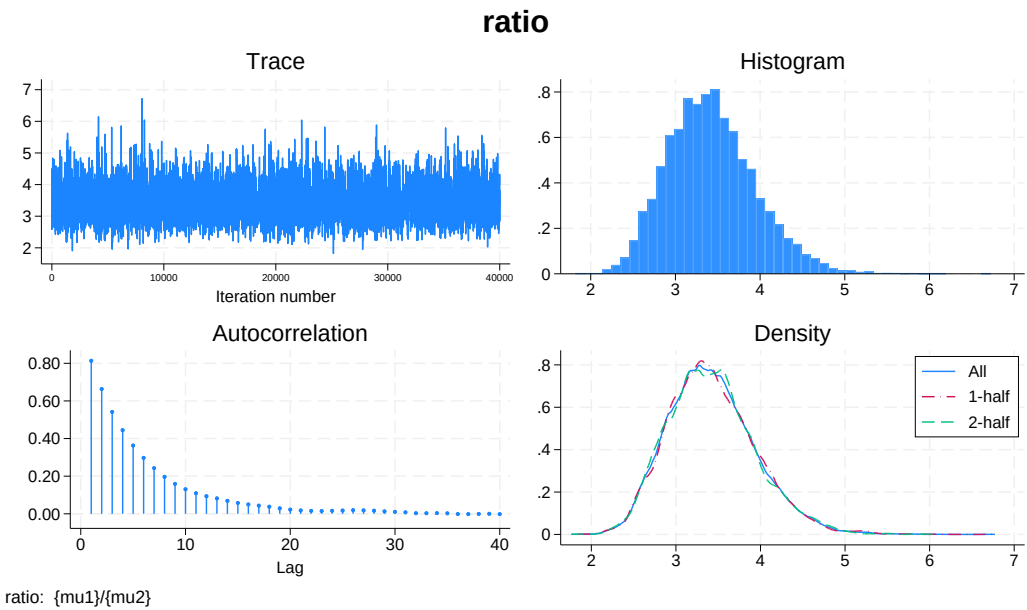
```
. bayesstats summary (ratio:{mu1}/{mu2})
Posterior summary statistics                         MCMC sample size =    40,000
       ratio : {mu1}/{mu2}
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
ratio	3.424565	.5169099	.008259	3.381721	2.541948	4.554931

The posterior mean estimate of the ratio and its 95% credible intervals confirm the change between the two means. After 1890, the mean number of disasters decreased by a factor of about 3.4 with a 95% credible range of [2.5, 4.6].

Remember that convergence must be verified not only for all model parameters but also for the functions of interest. The diagnostic plots for `ratio` look good.

```
. bayesgraph diagnostics (ratio:{mu1}/{mu2})
```



Bioequivalence in a crossover trial

Balanced crossover designs are widely used in the pharmaceutical industry for testing the efficacy of new drugs. Gelfand et al. (1990) analyzed a two-treatment, two-period crossover trial comparing two Carbamazepine tablets. The data consist of log-concentration measurements and are originally described in Maas et al. (1987).

A random-effect two-treatment, two-period crossover design is given by

$$y_{i(jk)} = \mu + (-1)^{j-1}\frac{\phi}{2} + (-1)^{k-1}\frac{\pi}{2} + d_i + \epsilon_{i(jk)} = \mu_{i(jk)} + \epsilon_{i(jk)}$$

$$\epsilon_{i(jk)} \sim \text{i.i.d. } N(0, \sigma^2)$$
$$d_i \sim \text{i.i.d. } N(0, \tau^2)$$

where $i = 1, \ldots, n$ is the subject index, $j = 1, 2$ is the treatment group, and $k = 1, 2$ is the period.

bioequiv.dta has four main variables: subject identifier id from 1 to 10, treatment identifier treat containing values 1 or 2, period identifier period containing values 1 or 2, and outcome y measuring log concentration for the two tablets.

```
. use https://www.stata-press.com/data/r18/bioequiv
(Bioequivalent study of Carbamazepine tablets)
. describe
Contains data from https://www.stata-press.com/data/r18/bioequiv.dta
 Observations:            20                  Bioequivalent study of
                                                Carbamazepine tablets
    Variables:             5                  5 Feb 2022 23:45
                                              (_dta has notes)
-------------------------------------------------------------------------------
Variable      Storage   Display    Value
    name         type    format    label      Variable label
-------------------------------------------------------------------------------
obsid           byte    %9.0g                 Observation identifier
id              byte    %9.0g                 Subject identifier
treat           byte    %9.0g                 Assigned treatment
period          byte    %9.0g                 Period identifier
y               float   %9.0g                 Log-concentration measurement
-------------------------------------------------------------------------------
Sorted by: id  period
```

The outcome is assumed to be normally distributed with mean $\mu_{i(jk)}$ and variance σ^2. To accommodate the specific structure of the regression function, we use a nonlinear specification of bayesmh. We specify the expression for the mean function $\mu_{i(jk)}$ as a nonlinear expression following the outcome y. We include subject-specific random effects d_i as {D[id]} in the nonlinear expression. We specify noninformative priors for parameters and use Gibbs sampling for variance components {tau} and {var}. To improve convergence, we increase the burn-in period to 5,000. We also specify the showreffects option to display the estimates of subject-specific effects {D[id]}.

```
. bayesmh y = ({mu}+(-1)^(treat-1)*{phi}/2+(-1)^(period-1)*{pi}/2+{D[id]}),
> likelihood(normal({var}))
> prior({D[id]},         normal(0,{tau}))
> prior({tau},           igamma(0.001,0.001))
> prior({var},           igamma(0.001,0.001))
> prior({mu} {phi} {pi}, normal(0,1e6))
> block({tau}, gibbs)
> block({var}, gibbs)
> burnin(5000) rseed(17) showreffects
Burn-in 5000 aaaaaaaaa1000aaaaaaaaa2000aaaaaaaaa3000aaaaaaaaa4000aaaaaaaaa5000
> done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
-------------------------------------------------------------------------------
Likelihood:
  y ~ normal({mu}+(-1)^(treat-1)*{phi}/2+(-1)^(period-1)*{pi}/2+{D[id]},{var})
Priors:
        {var} ~ igamma(0.001,0.001)
      {D[id]} ~ normal(0,{tau})
  {mu phi pi} ~ normal(0,1e6)
Hyperprior:
  {tau} ~ igamma(0.001,0.001)
-------------------------------------------------------------------------------
```

```
Bayesian normal regression                      MCMC iterations  =     15,000
Metropolis-Hastings and Gibbs sampling          Burn-in          =      5,000
                                                MCMC sample size =     10,000
                                                Number of obs    =         20
                                                Acceptance rate  =       .641
                                                Efficiency:  min =     .01171
                                                             avg =     .03912
Log marginal-likelihood                                      max =      .1168
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
mu	1.425404	.056644	.005234	1.427506	1.294818	1.527516
phi	-.0083643	.0495315	.00145	-.0091141	-.1069416	.0918596
pi	-.1800847	.0491643	.00164	-.1808839	-.2760931	-.0797408
var	.0124764	.00785	.000371	.0101862	.0041796	.0331787
tau	.0242893	.0211577	.000873	.0191958	.0027104	.0766
D[id]						
1	.0744192	.0831627	.004779	.074302	-.0849912	.2504312
2	.1364082	.0882816	.00521	.1365127	-.0359345	.3141966
3	.0640035	.0843961	.005008	.0596878	-.0939025	.2507555
4	.0708824	.0797542	.004431	.067086	-.0787817	.2440256
5	.1828674	.0937784	.005368	.184261	.0040691	.3700767
6	-.1694658	.0876467	.006416	-.1729349	-.3306482	.0033349
7	-.1212957	.0836953	.005709	-.1226434	-.2772058	.0448479
8	-.0603565	.0796002	.005112	-.0613437	-.218101	.1017121
9	-.0769446	.0800835	.00564	-.0762672	-.2324788	.088155
10	-.0076075	.0778637	.004483	-.0097928	-.1540721	.1496486

Sampling efficiencies look reasonable considering the number of model parameters. The diagnostic plots of the main model parameters (not shown here) look reasonable, except there is a high autocorrelation in the MCMC for `{mu}`, so you may consider increasing the MCMC size or using thinning.

Parameter $\theta = \exp(\phi)$ is commonly used as a measure of bioequivalence. Bioequivalence is declared whenever θ lies in the interval $[0.8, 1.2]$ with a high posterior probability.

We use `bayesstats summary` to calculate this probability and to also display other main parameters.

```
. bayesstats summary {mu} {phi} {pi} {tau} {var}
> (theta:exp({phi})) (equiv:exp({phi})>0.8 & exp({phi})<1.2)
Posterior summary statistics                    MCMC sample size =     10,000

       theta : exp({phi})
       equiv : exp({phi})>0.8 & exp({phi})<1.2
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
mu	1.425404	.056644	.005234	1.427506	1.294818	1.527516
phi	-.0083643	.0495315	.00145	-.0091141	-.1069416	.0918596
pi	-.1800847	.0491643	.00164	-.1808839	-.2760931	-.0797408
tau	.0242893	.0211577	.000873	.0191958	.0027104	.0766
var	.0124764	.00785	.000371	.0101862	.0041796	.0331787
theta	.9928879	.0492324	.001441	.9909273	.8985782	1.096211
equiv	.9999	.01	.0001	1	1	1

We obtain an estimate of 0.9999 for the posterior probability of bioequivalence specified as an expression `equiv`. So we would conclude bioequivalence between the two tablets.

Random-effects meta-analysis of clinical trials

In meta-analysis of clinical trials, one considers several distinct studies estimating an effect of interest. It is convenient to consider the true effect as varying randomly between the studies. A detailed description of the random-effects meta-analysis can be found in, for example, Carlin (1992). For traditional meta-analysis, see [META] **meta**.

We illustrate Bayesian random-effects meta-analysis of 2×2 tables for the beta-blockers dataset analyzed in Carlin (1992). These data are also analyzed in Yusuf, Simon, and Ellenberg (1987). The data summarize the results of 22 clinical trials of beta-blockers used as postmyocardial infarction treatment.

▷ Example 26: Normal–normal analysis

Here we follow the approach of Carlin (1992) for the normal–normal analysis of the beta-blockers data.

For our normal–normal analysis, we consider data in wide form and concentrate on modeling estimates of log odds-ratios from 22 studies.

```
. use https://www.stata-press.com/data/r18/betablockers_wide
(Beta-blockers data in wide form)
. describe
Contains data from https://www.stata-press.com/data/r18/betablockers_wide.dta
 Observations:            22                  Beta-blockers data in wide form
    Variables:             7                  5 Feb 2022 19:02
                                              (_dta has notes)
------------------------------------------------------------------------------
Variable      Storage   Display    Value
    name         type    format    label      Variable label
------------------------------------------------------------------------------
study           byte    %9.0g                 Study identifier
deaths0         int     %9.0g                 Number of deaths in the control
                                                group
total0          int     %9.0g                 Number of subjects in the control
                                                group
deaths1         int     %9.0g                 Number of deaths in the treatment
                                                group
total1          int     %9.0g                 Number of subjects in the
                                                treatment group
D               double  %10.0g                Log odds-ratio (based on
                                                empirical logits)
var             double  %10.0g                Squared standard error of log
                                                odds-ratio
------------------------------------------------------------------------------
Sorted by:
```

The estimates of log odds-ratios and their squared standard errors are recorded in variables `D` and `var`, respectively. They are computed from variables `deaths0`, `total0`, `deaths1`, and `total1` based on empirical logits; see Carlin [1992, eq. (3) and (4)]. The `study` variable records study identifiers.

In a normal–normal model, we assume a random-effects model for estimates of log odds-ratios with normally distributed errors and normally distributed random effects. Specifically,

$$\mathtt{D}_i = d + u_i + \epsilon_i = d_i + \epsilon_i$$

where $\epsilon_i \sim N(0, \mathtt{var}_i)$ and $d_i \sim N(d, \sigma^2)$. Errors ϵ_i's represent uncertainty about estimates of log odds-ratios in each study i and are assumed to have known study-specific variances, $\mathtt{var}_i$'s. Random

effects d_i's represent differences in estimates of log odds-ratios from study to study. The estimates of their mean and variance are of interest in meta-analysis: d estimates a true effect, and σ^2 estimates variation in estimating this effect across studies. Small values of σ^2 imply that the estimates of a true effect agree among studies.

In Bayesian analysis, we additionally specify prior distributions for d and σ^2. Following Carlin (1992), we use noninformative priors for these parameters: normal with large variance for d and inverse gamma with very small degrees of freedom for σ^2.

$$d \sim N(0, 1000)$$
$$\sigma^2 \sim \text{InvGamma}(0.001, 0.001)$$

We specify `normal()` likelihood with `bayesmh` and request observation-specific variances by specifying variable `var` as `normal()`'s variance argument. We include `D[study]` in the list of covariates to specify the random effects d_i. We follow the above model formulation for specifying prior distributions. To improve efficiency, we request that all parameters be placed in separate blocks and use Gibbs sampling for the mean parameter `{d}` and the variance parameter `{sig2}`.

```
. bayesmh D D[study], likelihood(normal(var)) noconstant
> prior({D[study]}, normal({d},{sig2}))
> prior({d},        normal(0,1000))
> prior({sig2},     igamma(0.001,0.001))
> block({sig2},     gibbs)
> block({d},        gibbs)
> rseed(17)
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  D ~ normal(xb_D,var)
Prior:
  {D[study]} ~ normal({d},{sig2})                                        (1)
Hyperpriors:
     {d} ~ normal(0,1000)
  {sig2} ~ igamma(0.001,0.001)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_D.
Bayesian normal regression                      MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling          Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         22
                                                Acceptance rate  =      .7623
                                                Efficiency:  min =     .02206
                                                             avg =     .02348
Log marginal-likelihood                                      max =     .02491

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
           d |  -.2537001   .0648291   .004107  -.2574083   -.371893  -.1213832
        sig2 |   .0191485   .0212749   .001433   .0115096   .0013426    .078143
------------------------------------------------------------------------------
```

Our posterior mean estimates `d` and `sig2` of mean d and variance σ^2 are -0.25 and 0.019, respectively, with posterior standard deviations of 0.06 and 0.02. The estimates are close to those reported by Carlin (1992). Considering the number of parameters, the AR and efficiency summaries look good.

We can obtain the efficiencies for the main parameters by using `bayesstats ess`.

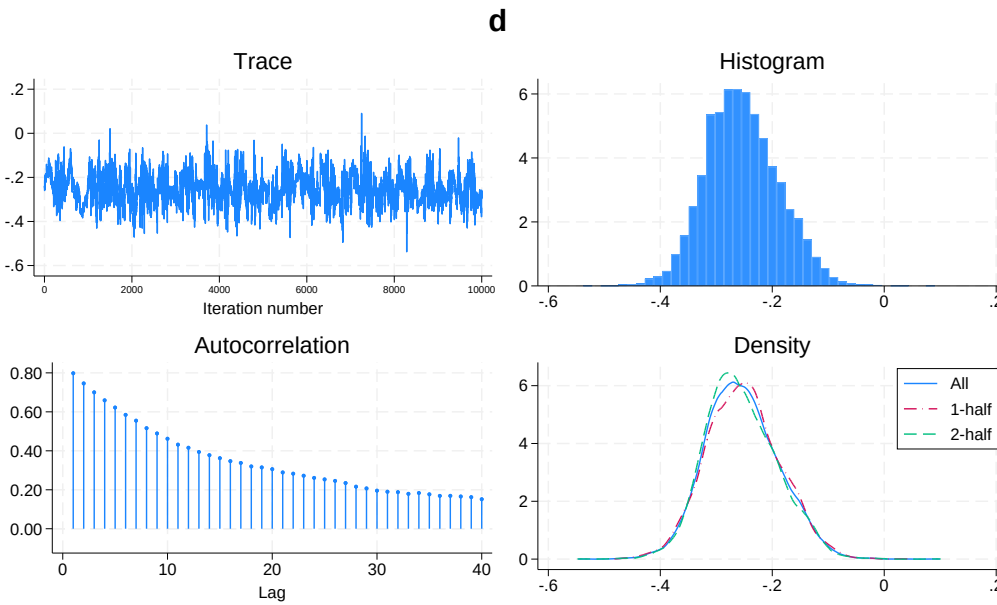
```
. bayesstats ess {d} {sig2}
Efficiency summaries     MCMC sample size =     10,000
                         Efficiency:  min =     .02206
                                      avg =     .02348
                                      max =     .02491
```

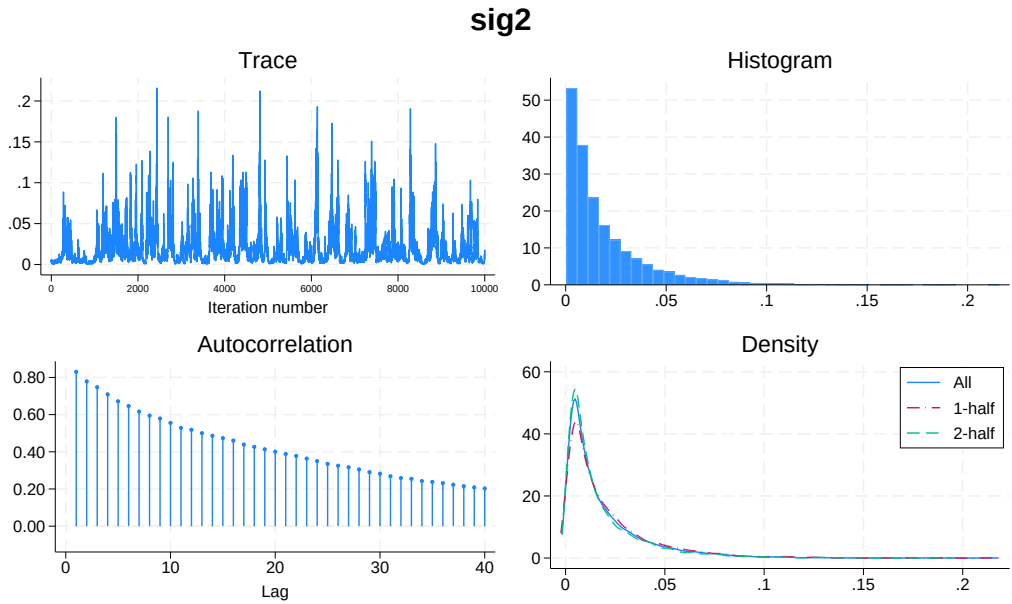
	ESS	Corr. time	Efficiency
d	249.13	40.14	0.0249
sig2	220.55	45.34	0.0221

The efficiencies are acceptable, but based on the correlation times, the autocorrelation becomes small only after lag 40 or so. The precision of the mean and variance estimates is comparable with those based on 249 independent observations for the mean and 220 independent observations for the variance.

We explore convergence visually.

```
. bayesgraph diagnostics {d} {sig2}
```





The diagnostic plots look reasonable for both parameters, but autocorrelation is high. You may consider increasing the default MCMC size to obtain more precise estimates of posterior means.

◁

▷ Example 27: Binomial-normal model

There is an alternative but equivalent way of formulating the meta-analysis model from example 26 as a binomial-normal model. Instead of modeling estimates of log odds-ratios directly, one can model probabilities of success (an event of interest) in each group.

Let p_i^T and p_i^C be the probabilities of success for the treatment and control groups in the ith trial. The random-effects meta-analysis model can be given as

$$\text{logit}(p_i^C) = \mu_i$$
$$\text{logit}(p_i^T) = \mu_i + d_i$$

where μ_i is log odds of success in the control group in study i and $\mu_i + d_i$ is log odds of success in the treatment group. d_i's are viewed as random effects and are assumed to be normally distributed as

$$d_i \sim \text{i.i.d. } N(d, \sigma^2)$$

where d is the population effect and σ^2 is its variability across trials.

Suppose that we observe y_i^C successes out of n_i^C events in the control group and y_i^T successes out of n_i^T events in the treatment group from the ith trial. Then,

$$y_i^C \sim \text{Binomial}(p_i^C, n_i^C)$$
$$y_i^T \sim \text{Binomial}(p_i^T, n_i^T)$$

The random effects are usually assumed to be normally distributed as

$$d_i \sim \text{i.i.d. } N(d, \sigma^2)$$

where d is the population effect and is the main parameter of interest in the model and σ^2 is its variability across trials.

We can rewrite the model above assuming the data are in long form as

$$\text{logit}(p_i) = \mu_i + (T_i == 1)d_i$$
$$y_i \sim \text{Binomial}(p_i, n_i)$$
$$d_i \sim \text{i.i.d. } N(d, \sigma^2)$$

where T_i is a binary treatment with $T_i = 0$ for the control group and $T_i = 1$ for the treatment group.

In Bayesian analysis, we additionally specify prior distributions for μ_i, d, and σ^2. We use noninformative priors.

$$\mu_i \sim 1$$
$$d \sim N(0, 1000)$$
$$\sigma^2 \sim \text{InvGamma}(0.001, 0.001)$$

We continue our analysis of beta-blockers data. The analysis of these data using a binomial-normal model is also provided as an example in OpenBUGS (Thomas et al. 2006).

For this analysis, we use the beta-blockers data in long form.

```
. use https://www.stata-press.com/data/r18/betablockers_long
(Beta-blockers data in long form)
. describe
Contains data from https://www.stata-press.com/data/r18/betablockers_long.dta
 Observations:            44                  Beta-blockers data in long form
    Variables:             4                  5 Feb 2022 19:02
                                              (_dta has notes)
------------------------------------------------------------------------------
Variable      Storage   Display    Value
    name         type    format    label      Variable label
------------------------------------------------------------------------------
study           byte    %9.0g                 Study identifier
treat           byte    %9.0g      treatlab   Treatment group: 0 - control, 1 -
                                                treatment
deaths          int     %9.0g                 Number of deaths in each group
total           int     %9.0g                 Number of subjects in each group
------------------------------------------------------------------------------
Sorted by: study  treat
```

Variable `treat` records the binary treatment: `treat==0` identifies the control group, and `treat==1` identifies the treatment group.

We include `M[study]` to specify the random effects μ_i's and `1.treat#D[study]` for the random effects $(T_i == 1)d_i$'s. We use a `binomial()` likelihood model for the number of `deaths`. We split the hyperparameters and random effects `{D[study]}` into separate blocks and request Gibbs sampling for `sig2` to improve efficiency of the algorithm.

```
. bayesmh deaths M[study] 1.treat#D[study], likelihood(binomial(total))
> noconstant
> prior({M[study]}, flat)
> prior({D[study]}, normal({d},{sig2}))
> prior({d},        normal(0,1000))
> prior({sig2},     igamma(0.001,0.001))
> block({D[study]}, split)
> block({d sig2},   gibbs split)
> rseed(17)
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  deaths ~ binlogit(xb_deaths,total)
Priors:
  {M[study]} ~ 1 (flat)                                                   (1)
  {D[study]} ~ normal({d},{sig2})                                         (1)
Hyperpriors:
     {d} ~ normal(0,1000)
  {sig2} ~ igamma(0.001,0.001)
------------------------------------------------------------------------------
(1) Parameter is an element of the linear form xb_deaths.
Bayesian binomial regression                    MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling          Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         44
                                                Acceptance rate  =      .4846
                                                Efficiency:  min =     .01025
                                                             avg =     .01398
Log marginal-likelihood                                      max =     .01771
------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
           d |  -.2497927   .0655042   .004923  -.2496163  -.3739794  -.1159871
        sig2 |   .0188492   .0225658   .002229   .0117471   .0005956    .079379
------------------------------------------------------------------------------
Note: Adaptation tolerance is not met in at least one of the blocks.
```

This model has 22 more parameters than the model in example 26. The posterior mean estimates `d` and `sig2` of mean d and variance σ^2 are -0.25 and 0.019, respectively, with posterior standard deviations of 0.07 and 0.02. The estimates of the mean and variance are again close to the ones reported by Carlin (1992).

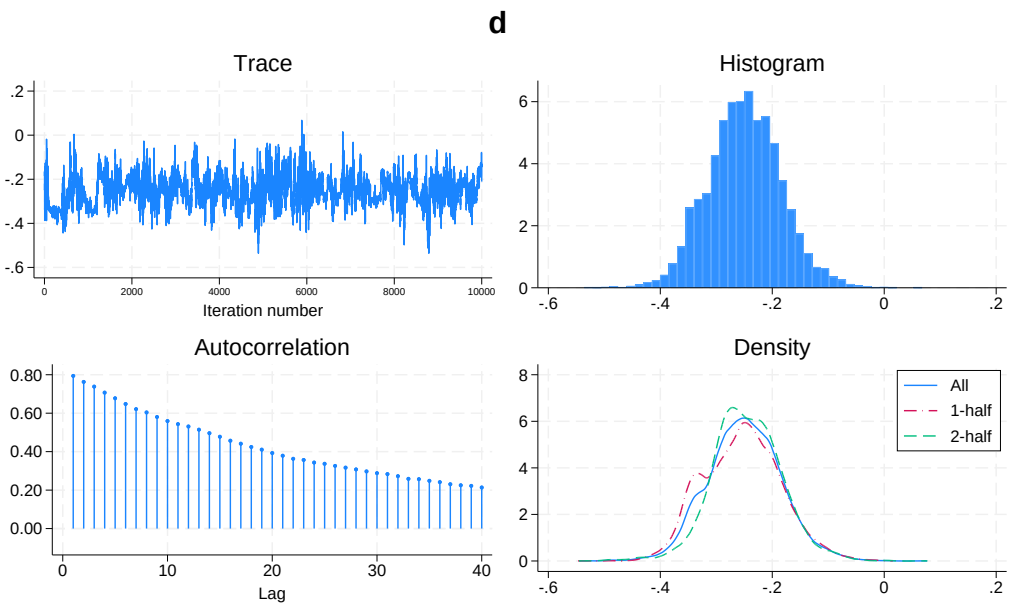
Compared with example 26, the efficiencies and other statistics for the main parameters are similar.

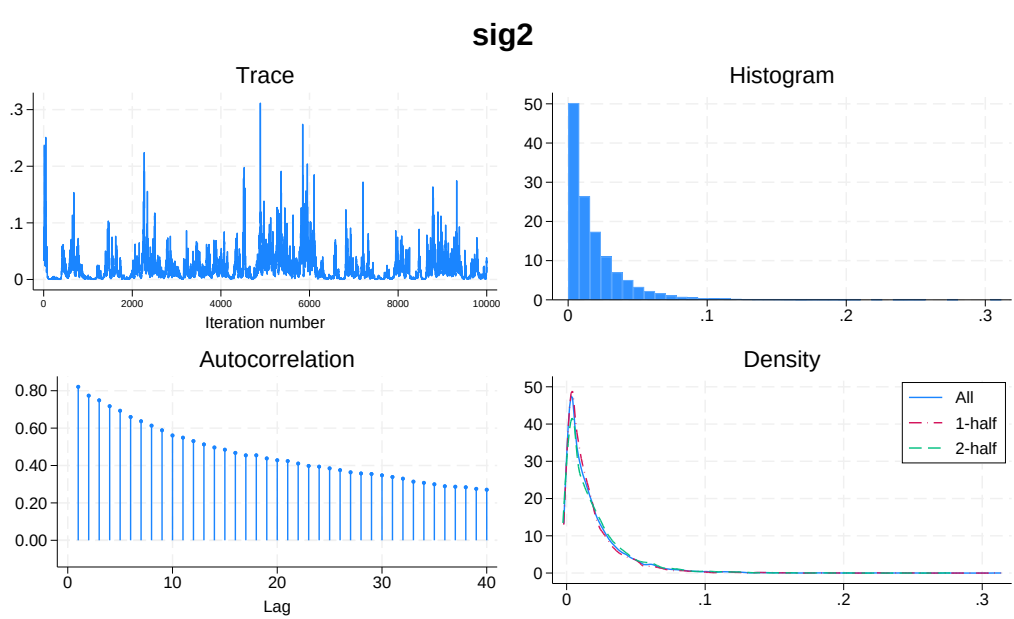
```
. bayesstats ess {d} {sig2}
Efficiency summaries     MCMC sample size =     10,000
                         Efficiency:  min =     .01025
                                      avg =     .01398
                                      max =     .01771
```

	ESS	Corr. time	Efficiency
d	177.07	56.47	0.0177
sig2	102.47	97.59	0.0102

The diagnostic plots look similar to those shown in example 26.

```
. bayesgraph diagnostics {d} {sig2}
```





Item response theory

▷ Example 28: 1PL IRT model—Rasch model

If you are not familiar with IRT, see [IRT] **irt** for an introduction to IRT concepts and terminology. Here we revisit example 1 of [IRT] **irt 1pl**. The example analyzes student responses to nine test questions and uses an abridged version of the mathematics and science data from De Boeck and Wilson (2004). The goal of the analysis is to estimate the common discrimination of the questions (items) and their individual difficulties.

An alternative formulation of the one-parameter IRT model is the Rasch (1960) model with logit link; see, for example, *Methods and formulas* of [IRT] **irt 1pl**. A typical IRT dataset consists of binary outcomes (success or failure) of J subjects, where each subject is tested on I items. Let the observation y_{ij} represent the binary outcome for item i, where $i = 1, \ldots, I$, and subject j, where $j = 1, \ldots, J$. Each item i is characterized by a level of difficulty b_i. The difficulties are not observed and must be estimated. Associated with each subject j is a latent trait level, θ_j, that characterizes the ability of the subject. The model likelihood has a generalized linear regression form

$$\text{logit}\{\Pr(y_{ij} = 1|b_i, \theta_j)\} = a(\theta_j - b_i)$$

where a is a discrimination parameter. According to this likelihood model, the probability of success increases with the subject ability and decreases with item difficulty. The discrimination parameter a represents the slope of the item characteristic curves. The subject abilities are assumed to be standardized so that

$$\theta_j \sim \text{ i.i.d. } N(0,1)$$

The discrimination parameter a can be absorbed into θ_j and b_i so that the model is reparameterized as

$$\text{logit}\{\Pr(y_{ij}=1|\widetilde{b}_i,\widetilde{\theta}_j)\} = \widetilde{\theta}_j + \widetilde{b}_i \tag{1}$$

$$\widetilde{\theta}_j \sim \text{ i.i.d. } N(0,\sigma^2)$$

where $\sigma = a$ and $\widetilde{b}_i = -ab_i$. In addition to the above, a Bayesian formulation of the model requires prior specifications for parameters σ^2 and $\widetilde{b}_i$. In the following example, we use

$$\sigma^2 \sim \text{InvGamma}(0.01, 0.01)$$

$$\widetilde{b}_i \sim N(0,10)$$

To fit this model using `bayesmh`, we first need to reshape the data from example 1 of [IRT] **irt 1pl** in long format so that the answers to the nine questions are represented by the response variable `y`, while the `item` and `id` variables encode the questions and students, respectively.

```
. use https://www.stata-press.com/data/r18/masc1, clear
(Data from De Boeck & Wilson (2004))
. generate id = _n
. quietly reshape long q, i(id) j(item)
. rename q y
```

The Rasch likelihood model can be specified with `bayesmh` using `y` as a dependent variable and `U[item]` and `V[id]` as crossed random effects. We use the `noconstant` option in the likelihood specification to include all levels of `U[item]` and `V[id]`. The random-effects parameters `{V[id]}` are assigned a zero-mean normal prior with variance `{var}` [σ^2 in model specification (1)]. The parameter `{var}` is assigned a noninformative inverse-gamma prior with shape 0.01 and scale 0.01, whereas the parameters `{U[item]}` [$\widetilde{b}_i$'s in model (1)] are applied ad hoc informative `normal(0,10)` priors.

```
. bayesmh y U[item] V[id], noconstant likelihood(logit)
> prior({U[item]}, normal(0, 10))
> prior({V[id]}, normal(0, {var}))
> prior({var}, igamma(0.01,0.01))
> block({var}) rseed(17) showreffects(U[item])
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaa.. done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  y ~ logit(xb_y)
Priors:
  {U[item]} ~ normal(0,10)                                              (1)
    {V[id]} ~ normal(0,{var})                                           (1)
Hyperprior:
  {var} ~ igamma(0.01,0.01)
------------------------------------------------------------------------------
```

```
(1) Parameter is an element of the linear form xb_y.
Bayesian logistic regression                    MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =      7,200
                                                Acceptance rate  =      .3078
                                                Efficiency:  min =     .01974
                                                             avg =      .1056
Log marginal-likelihood                                      max =      .1371
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
var	.7292225	.0742153	.005282	.7267709	.5849949	.8788834
U[item]						
1	.6027924	.0848417	.002727	.6033436	.4383438	.7676613
2	.1047865	.0817006	.002411	.1017675	-.0494946	.2691851
3	1.551305	.0953048	.002574	1.549129	1.362338	1.745973
4	-.2759237	.0791898	.002193	-.2752539	-.4319626	-.121707
5	-1.408907	.0940374	.002999	-1.40848	-1.590385	-1.224282
6	-.5913131	.0837824	.002701	-.5902511	-.7540854	-.431315
7	-1.128982	.0921381	.002597	-1.129163	-1.311912	-.9454393
8	2.054062	.1130098	.003294	2.052132	1.842889	2.278157
9	1.018282	.091037	.002634	1.015498	.8454456	1.195609

In the simulation summary, `bayesmh` reports a modest average efficiency of about 11% with no indication of any convergence problems. We could have omitted the prior specification for `{V[id]}`, in which case `bayesmh` would have labeled the variance component as `{var_V}`.

To match the discrimination and question difficulty parameters of the `irt 1pl` command, we can apply the following transformation to the `bayesmh` model parameters. The common discrimination parameter equals the square-root of `{var}`, and the individual question difficulties equal the negative `{U[item]}`'s parameters, normalized by their common discrimination. We can obtain estimates of these parameters using the `bayesstats summary` command.

```
. bayesstats summary (discr:sqrt({var}))
>                    (diff1:-{U[item]:1}/sqrt({var}))
>                    (diff2:-{U[item]:2}/sqrt({var}))
>                    (diff3:-{U[item]:3}/sqrt({var}))
>                    (diff4:-{U[item]:4}/sqrt({var}))
>                    (diff5:-{U[item]:5}/sqrt({var}))
>                    (diff6:-{U[item]:6}/sqrt({var}))
>                    (diff7:-{U[item]:7}/sqrt({var}))
>                    (diff8:-{U[item]:8}/sqrt({var}))
>                    (diff9:-{U[item]:9}/sqrt({var})), nolegend
Posterior summary statistics                       MCMC sample size =    10,000
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
discr	.8528361	.043511	.003121	.8525086	.7648496	.9374878
diff1	-.708256	.1030494	.003739	-.7075444	-.9076266	-.5087035
diff2	-.1229125	.0957599	.0028	-.1200833	-.3128214	.0586056
diff3	-1.823084	.1372403	.00629	-1.822315	-2.111938	-1.567898
diff4	.3244352	.0946774	.002831	.3225444	.140814	.5142564
diff5	1.655759	.1318078	.005645	1.655727	1.397132	1.91738
diff6	.6948282	.1024367	.003553	.6955096	.500485	.9021124
diff7	1.326701	.1219158	.005173	1.324991	1.092751	1.569114
diff8	-2.413647	.165384	.006845	-2.408337	-2.762421	-2.10808
diff9	-1.196676	.1190397	.004515	-1.194314	-1.438426	-.9766857

We observe that the reported posterior means for the common discrimination and question difficulties are close to those obtained with `irt 1pl`, within the limits of the MCMC standard errors.

◁

In this example, we fit the Rasch model and use transformation to estimate parameters of the corresponding 1PL IRT model. To avoid reparameterization, we could have fit the 1PL model directly using a nonlinear specification of `bayesmh`, as we demonstrate in example 29 for the 2PL IRT model. The shortcoming of the nonlinear specification is slower execution.

▷ Example 29: 2PL IRT model

A more comprehensive IRT model is the 2PL model introduced by Birnbaum (1968), which allows the discrimination and difficulty parameters to vary between items. For a detailed description and examples of the model, see [IRT] **irt 2pl**.

A Bayesian formulation of the 2PL model allows the item-specific discrimination and difficulty parameters as well as the subject abilities to be modeled, either individually or as groups, using prior distributions.

The 2PL model likelihood has the following form,

$$\Pr(Y_{ij}=1)=\frac{\exp\{a_i(\theta_j-b_i)\}}{1+\exp\{a_i(\theta_j-b_i)\}}$$

where a_i's and b_i's are discrimination and difficulty parameters and θ_j's are subject abilities. This is a logistic regression model with probability of success modeled using the linear form $a_i(\theta_j-b_i)$. We assume that the probability of success increases with subject ability, which implies $a_i>0$. Subject ability parameters are assumed independent and distributed according to the standard normal distribution

$$\theta_j\sim N(0,1)$$

For Bayesian modeling, we additionally assume the following prior specifications:

$$\ln(a_i) \sim N(\mu_a, \sigma_a^2)$$

$$b_i \sim N(\mu_b, \sigma_b^2)$$

$$\mu_a, \mu_b \sim N(0, 1)$$

$$\sigma_a^2, \sigma_b^2 \sim \text{Gamma}(1, 1)$$

In the absence of prior knowledge about parameters a_i's and b_i's, we want to specify proper priors that are not subjective. Because a_i's must be positive, a common choice is to assume that $\ln(a_i)$'s are normally distributed with mean μ_a and variance σ_a^2. We assume that b_i's are normally distributed with mean μ_b and variance σ_b^2. Our prior assumption is that the questions in the study are fairly balanced in terms of discrimination and difficulty, and we express this expectation by specifying $N(0, 1)$ hyperpriors for μ_a and μ_b; that is, we assume that μ_a and μ_b are not that different from zero. We also put a slight prior constraint on the variability of the discrimination and difficulty parameters by assigning a gamma distribution with shape 1 and scale 1 as hyperprior distributions for σ_a^2 and σ_b^2. To demonstrate a Bayesian 2PL model, we use again the mathematics and science dataset `masc1`, reshaped in long format as in example 28.

```
. bayesmh y = ({Discr[item]}*({V[id]}-{Diff[item]})), likelihood(logit)
> prior({V[id]},       normal(0, 1))
> prior({Discr[item]}, lognormal({mua}, {vara}))
> prior({D[iffitem]},  normal({mub}, {varb}))
> prior({vara varb},   gamma(1, 1))
> prior({mua mub},     normal(0, 1))
> ...
```

To specify the 2PL model likelihood in `bayesmh`, we need to use a nonlinear specification to accommodate the varying coefficients a_i's. For `masc1.dta`, we have 9 items, where $i = 1, \ldots, 9$, and 800 subjects, where $j = 1, \ldots, 800$. A straightforward nonlinear specification is `({Discr[item]}*({V[id]}-{Diff[item]}))`, where random effects `Discr[item]`, `Diff[item]`, and `V[id]` represent discrimination, item difficulty, and student ability, respectively.

To achieve better sampling efficiency, we place the hyperparameters `{mua}`, `{mub}`, `{vara}`, and `{varb}` into separate blocks using the `block()`'s suboption `split`. We also initialize the discrimination and difficulty random effects with 1 because the default 0s result in an invalid initial state. Because the random effects are not shown by default, we use the `showreffects()` option to display the discrimination and difficulty parameters.

```
. bayesmh y = ({Discr[item]}*({V[id]}-{Diff[item]})), likelihood(logit)
> prior({V[id]}, normal(0, 1))
> prior({Discr}, lognormal({mua}, {vara}))
> prior({Diff}, normal({mub}, {varb}))
> prior({vara varb},gamma(1, 1)) prior({mua mub}, normal(0, 1))
> block({vara varb mua mub}, split) init({Discr} 1 {Diff} 1)
> showreffects({Discr} {Diff}) rseed(17)
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  y ~ logit({Discr[item]}*({V[id]}-{Diff[item]}))

Priors:
        {V[id]} ~ normal(0,1)
  {Discr[item]} ~ lognormal({mua},{vara})
   {Diff[item]} ~ normal({mub},{varb})

Hyperpriors:
  {vara varb} ~ gamma(1,1)
    {mua mub} ~ normal(0,1)
------------------------------------------------------------------------------

Bayesian logistic regression                    MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =      7,200
                                                Acceptance rate  =      .3681
                                                Efficiency:  min =    .008642
                                                             avg =     .04421
Log marginal-likelihood                                      max =      .2174
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
mua	-.1532513	.172939	.006185	-.1512495	-.5066464	.1898917
vara	.2459257	.1732519	.009683	.1981045	.0580936	.7308169
mub	-.067519	.4272602	.009163	-.068848	-.905363	.7854128
varb	1.954127	.8517321	.030869	1.810081	.8276775	4.021905
Discr[item]						
1	1.474051	.226756	.016747	1.461149	1.085353	1.977109
2	.6710171	.1110106	.004925	.6675754	.4590724	.8893063
3	.9238635	.1454797	.011848	.9209288	.6422116	1.217656
4	.8076416	.1221467	.006042	.8019258	.5810136	1.057661
5	.8825339	.1445803	.011687	.8722941	.6319481	1.197729
6	.9497897	.1401296	.007687	.944759	.6944811	1.236898
7	.4846824	.0881389	.006968	.4791858	.3258165	.6695858
8	1.353603	.219108	.023569	1.362743	.9303272	1.772465
9	.6649918	.1198973	.01178	.6650413	.444871	.90068
Diff[item]						
1	-.5069895	.0818094	.004323	-.5031544	-.6849757	-.3521039
2	-.1502343	.121276	.003424	-.1455632	-.407207	.0784043
3	-1.742259	.2430085	.019752	-1.706428	-2.331342	-1.357637
4	.3328318	.1101783	.003805	.3282234	.1280959	.555568
5	1.638084	.2356449	.018557	1.616757	1.247654	2.160822
6	.6465024	.116495	.005363	.6380789	.4409175	.8947524
7	2.158884	.4045901	.031847	2.101079	1.528233	3.101399
8	-1.779656	.2166062	.022939	-1.742365	-2.300026	-1.453126
9	-1.490028	.2781509	.025778	-1.451536	-2.13252	-1.065914

bayesmh reports an acceptable average efficiency of about 4%. A close inspection of the estimation table shows that the posterior mean estimates for item discrimination and difficulty are similar to the MLE estimates obtained with the irt 2pl command; see example 1 in [IRT] **irt 2pl**.

◁

Latent growth model

We revisit [SEM] **Example 18**, which analyzes crime rate in four quarters of 1995. The crime-rate variables lncrime0 through lncrime3 record measurements of crime rate on the log scale. The observed crime rates are assumed to follow a linear growth model with random intercept I and random slope S,

$$\texttt{lncrime}_i = \texttt{I} + i\texttt{S} + \epsilon,$$

where I and S are latent variables and ϵ is a vector of error terms that are normally distributed with mean zero and variance σ^2. The coefficients for the random intercepts are fixed to 1, and the coefficients for the slopes are fixed to 0, 1, 2, and 3, corresponding to the 4 quarters. I and S are assumed to be correlated.

```
. use https://www.stata-press.com/data/r18/sem_lcm
. describe
Contains data from https://www.stata-press.com/data/r18/sem_lcm.dta
 Observations:           359
    Variables:             4                  25 May 2022 11:08
                                              (_dta has notes)
------------------------------------------------------------------------------
Variable      Storage   Display    Value
    name         type    format    label      Variable label
------------------------------------------------------------------------------
lncrime0        float   %9.0g                 ln(crime rate) in Jan & Feb
lncrime1        float   %9.0g                 ln(crime rate) in Mar & Apr
lncrime2        float   %9.0g                 ln(crime rate) in May & Jun
lncrime3        float   %9.0g                 ln(crime rate) in Jul & Aug
------------------------------------------------------------------------------
Sorted by:
```

To fit the model using bayesmh, we need to specify four normal likelihood equations, one for each crime-rate variable, that include latent variables {I[_n]} and {S[_n]} (see *Random effects*). The error variance σ^2 is given by the parameter {var}. As in a classical SEM model, the latent variables are assumed to have a bivariate normal distribution, which we will model using the mvnormal() prior with means {meani} and {means} and variance–covariance matrix {Sigma,m}. In a Bayesian model, we additionally specify prior distributions for all other model parameters. Specifically, the error variance is assigned the inverse-gamma prior, igamma(1, 1). The hyperparameters {meani} and {means} are assigned normal(0, 100) priors. And the covariance {Sigma,m} matrix hyperparameter is assigned an inverse-Wishart prior, iwishart(2,3,I(2)).

We place parameters in separate blocks and use Gibbs sampling for the covariance {Sigma,m}. To do this, we must specify each parameter in separate prior() and block() options. More conveniently, we can use prior()'s and block()'s split suboptions to combine similar parameters in one prior() and one block() specifications.

```
. bayesmh (lncrime0 I[_n]@1 S[_n]@0, likelihood(normal({var})) noconstant)
>         (lncrime1 I[_n]@1 S[_n]@1, likelihood(normal({var})) noconstant)
>         (lncrime2 I[_n]@1 S[_n]@2, likelihood(normal({var})) noconstant)
>         (lncrime3 I[_n]@1 S[_n]@3, likelihood(normal({var})) noconstant),
> prior({I} {S}, mvnormal(2, {meani}, {means}, {Sigma,m}))
> prior({var}, igamma(1, 1)) prior({meani} {means}, normal(0, 100) split)
> prior({Sigma,m}, iwishart(2, 3, I(2)))
> block({meani means var}, split) block({Sigma,m}, gibbs) rseed(17) dots
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done

Model summary
------------------------------------------------------------------------------
Likelihood:
  lncrime0 ~ normal(xb_lncrime0,{var})
  lncrime1 ~ normal(xb_lncrime1,{var})
  lncrime2 ~ normal(xb_lncrime2,{var})
  lncrime3 ~ normal(xb_lncrime3,{var})

Priors:
          {var} ~ igamma(1,1)
  {I[_n] S[_n]} ~ mvnormal(2,{meani},{means},{Sigma,m})                   (1)

Hyperpriors:
  {meani means} ~ normal(0,100)
      {Sigma,m} ~ iwishart(2,3,I(2))
------------------------------------------------------------------------------
(1) Parameter is an element of the linear form xb_lncrime0.

Bayesian normal regression                      MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling          Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =        359
                                                Acceptance rate  =      .4568
                                                Efficiency:  min =     .02935
                                                             avg =     .06287
Log marginal-likelihood                                      max =       .112
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
lncrime0						
I	1	0	0	1	1	1
S	0	0	0	0	0	0
lncrime1						
I	1	0	0	1	1	1
S	1	0	0	1	1	1
lncrime2						
I	1	0	0	1	1	1
S	2	0	0	2	2	2
lncrime3						
I	1	0	0	1	1	1
S	3	0	0	3	3	3
var	.0980241	.0052328	.000288	.0977252	.0883533	.1092536
meani	5.337768	.0414444	.001238	5.338614	5.255186	5.415398
means	.1429141	.0113074	.000523	.1430148	.1208266	.1648296
Sigma_1_1	.5346687	.0447749	.001346	.5324011	.4528704	.6270454
Sigma_2_1	-.0389518	.0094347	.000443	-.0388106	-.0580931	-.0212465
Sigma_2_2	.027595	.0032268	.000188	.0274319	.0216741	.0342223

The average sampling efficiency is about 6% with no signs of convergence problems. The posterior mean estimates are similar to the maximum likelihood estimates reported by the sem command.

As expected, there is a negative correlation between the latent variables I and S of about −0.32.

```
. bayesstats summary (corr:{Sigma_1_2}/sqrt({Sigma_1_1}*{Sigma_2_2}))
Posterior summary statistics                       MCMC sample size =    10,000
       corr :  { Sigma_1_2 } /sqrt( { Sigma_1_1 } * { Sigma_2_2 } )
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
corr	-.3193145	.064091	.002767	-.3212176	-.4389513	-.1889672

Because the linear growth model assumes that the slope coefficients are constrained to 0, 1, 2, and 3, it may be interesting to check how well the observed average quarterly crime rates are explained by the model. We can formally address this question by simulating the posterior predictive crime-rate means from the model and comparing them with the observed quarterly averages. We use the bayespredict command to simulate the expected outcomes from the posterior predictive distribution. For example, in the specification below, the first expected outcome is obtained by applying the mean function to {_ysim1}, pmean0:@mean({_ysim1}), and saving it as {pmean0} in a new prediction dataset predmeans.dta. Once {pmean0}, {pmean1}, {pmean2}, and {pmean3} are simulated, we use the bayesstats ppvalues command to compute the corresponding posterior predictive p-values to check model fit. Before using bayespredict, however, we must save our simulation results in a permanent Stata dataset.

```
. bayesmh, saving(semex18sim)
note: file semex18sim.dta saved.

. bayespredict (pmean0:@mean({_ysim1})) (pmean1:@mean({_ysim2}))
> (pmean2:@mean({_ysim3})) (pmean3:@mean({_ysim4})),
> saving(predmeans) rseed(17) dots

Computing predictions 10000 .........1000.........2000.........3000.........
> 4000.........5000.........6000.........7000.........8000.........9000.........
> 10000 done

file predmeans.dta saved.
file predmeans.ster saved.

. bayesstats ppvalues {pmean0} {pmean1} {pmean2} {pmean3} using predmeans
Posterior predictive summary   MCMC sample size =    10,000
```

T	Mean	Std. dev.	E(T_obs)	P(T>=T_obs)
pmean0	5.338168	.0211914	5.318657	.8196
pmean1	5.481137	.0188344	5.515685	.0341
pmean2	5.623649	.0187776	5.610934	.7465
pmean3	5.766436	.0211988	5.762558	.5764

```
Note: P(T>=T_obs) close to 0 or 1 indicates lack of fit.
```

All expected quarterly crime rates except the second one are consistent with the observed data. For the second-quarter crime rate, we have a low posterior p-value of 3%. We could relax the assumption of a linear growth for the second quarter and check whether this improves model fit.

Stored results

bayesmh stores the following in e():

Scalars

e(N)	number of observations
e(N_sub)	number of subjects (only with survival models)
e(N_fail)	number of failures (only with survival models)
e(risk)	total time at risk (only with survival models)
e(k)	number of parameters
e(k_sc)	number of scalar parameters
e(k_mat)	number of matrix parameters
e(n_eq)	number of equations
e(nchains)	number of MCMC chains
e(mcmcsize)	MCMC sample size
e(burnin)	number of burn-in iterations
e(mcmciter)	total number of MCMC iterations
e(thinning)	thinning interval
e(arate)	overall AR
e(eff_min)	minimum efficiency
e(eff_avg)	average efficiency
e(eff_max)	maximum efficiency
e(Rc_max)	maximum Gelman–Rubin convergence statistic (only with nchains())
e(clevel)	credible interval level
e(hpd)	1 if hpd is specified; 0 otherwise
e(batch)	batch length for batch-means calculations
e(corrlag)	maximum autocorrelation lag
e(corrtol)	autocorrelation tolerance
e(dic)	deviance information criterion
e(lml_lm)	log marginal-likelihood using Laplace–Metropolis method
e(scale)	initial multiplier for scale factor; scale()
e(block#_gibbs)	1 if Gibbs sampling is used in #th block, 0 otherwise
e(block#_reffects)	1 if the parameters in #th block are random effects, 0 otherwise
e(block#_scale)	#th block initial multiplier for scale factor
e(block#_tarate)	#th block target adaptation rate
e(block#_tolerance)	#th block adaptation tolerance
e(adapt_every)	adaptation iterations adaptation(every())
e(adapt_maxiter)	maximum number of adaptive iterations adaptation(maxiter())
e(adapt_miniter)	minimum number of adaptive iterations adaptation(miniter())
e(adapt_alpha)	adaptation parameter adaptation(alpha())
e(adapt_beta)	adaptation parameter adaptation(beta())
e(adapt_gamma)	adaptation parameter adaptation(gamma())
e(adapt_tolerance)	adaptation tolerance adaptation(tolerance())
e(repeat)	number of attempts used to find feasible initial values

Macros

e(cmd)	bayesmh
e(cmdline)	command as typed
e(method)	sampling method
e(depvars)	names of dependent variables
e(eqnames)	names of equations
e(likelihood)	likelihood distribution (one equation)
e(likelihood#)	likelihood distribution for #th equation
e(prior)	prior distribution
e(prior#)	prior distribution, if more than one prior() is specified
e(priorparams)	parameter specification in prior()
e(priorparams#)	parameter specification from #th prior(), if more than one prior() is specified
e(parnames)	names of model parameters except exclude()
e(postvars)	variable names corresponding to model parameters in e(parnames)
e(subexpr)	substitutable expression
e(subexpr#)	substitutable expression, if more than one
e(wtype)	weight type (one equation)
e(wtype#)	weight type for #th equation
e(wexp)	weight expression (one equation)

e(wexp#)	weight expression for #th equation
e(block#_names)	parameter names from #th block
e(exclude)	names of excluded parameters
e(filename)	name of the file with simulation results
e(scparams)	scalar model parameters
e(matparams)	matrix model parameters
e(pareqmap)	model parameters in display order
e(title)	title in estimation output
e(rngstate)	random-number state at the time of simulation (only with single chain)
e(rngstate#)	random-number state for #th chain (only with nchains())
e(search)	on, repeat(), or off

Matrices

e(mean)	posterior means
e(sd)	posterior standard deviations
e(mcse)	MCSE
e(median)	posterior medians
e(cri)	credible intervals
e(Cov)	variance–covariance matrix of parameters
e(ess)	effective sample sizes
e(init)	initial values vector
e(dic_chains)	deviance information criterion for each chain (only with nchains())
e(arate_chains)	acceptance rate for each chain (only with nchains())
e(eff_min_chains)	minimum efficiency for each chain (only with nchains())
e(eff_avg_chains)	average efficiency for each chain (only with nchains())
e(eff_max_chains)	maximum efficiency for each chain (only with nchains())
e(lml_lm_chains)	log marginal-likelihood for each chain (only with nchains())

Functions

e(sample)	mark estimation sample

Methods and formulas

Methods and formulas are presented under the following headings:

Adaptive MH algorithm

The bayesmh command implements an adaptive random-walk Metropolis–Hastings algorithm with optional blocking of parameters. Providing an efficient MH procedure for simulating from a general posterior distribution is a difficult task, and various adaptive methods have been proposed (Haario, Saksman, and Tamminen 2001; Giordani and Kohn 2010; Roberts and Rosenthal 2009; Andrieu and Thoms 2008). The essence of the problem is in choosing an optimal proposal covariance matrix and a scale for parameter updates. Below we describe the implemented adaptation algorithm, assuming one block of parameters. In the presence of multiple blocks, the adaptation is applied to each block independently. The adaptation() option of bayesmh controls all the tuning parameters for the adaptation algorithm.

Let $\boldsymbol{\theta}$ be a vector of d scalar model parameters. Let T_0 be the length of a burn-in period (iterations that are discarded) as specified in `burnin()` and T be the size of the MCMC sample (iterations that are retained) as specified in `mcmcsize()`. The total number of MCMC iterations is then $T_{\text{total}} = T_0 + (T-1) \times \texttt{thinning()} + 1$. Also, let ALEN be the length of the adaptation interval (option `adaptation(every())`) and AMAX be the maximum number of adaptations (option `adaptation(maxiter())`).

The steps of the adaptive MH algorithm are the following. At $t = 0$, we initialize $\boldsymbol{\theta}_t = \boldsymbol{\theta}_0^f$, where $\boldsymbol{\theta}_0^f$ is the initial feasible state, and we set adaptation counter $k = 1$ and initialize $\rho_0 = 2.38/\sqrt{d}$, where d is the number of considered parameters. Σ_0 is the identity matrix. For $t = 1, \ldots, T_{\text{total}}$, do the following:

1. Generate proposal parameters: $\boldsymbol{\theta}_* = \boldsymbol{\theta}_{t-1} + \mathbf{e}$, $\mathbf{e} \sim N(\mathbf{0}, \rho_k^2 \Sigma_k)$, where ρ_k and Σ_k are current values of the proposal scale and covariance for adaptation iteration k.
2. Calculate the acceptance probability using

$$\alpha(\boldsymbol{\theta}_* | \boldsymbol{\theta}_{t-1}) = \min\left\{ \frac{p(\boldsymbol{\theta}_* | \mathbf{y})}{p(\boldsymbol{\theta}_{t-1} | \mathbf{y})}, 1 \right\}$$

   where $p(\boldsymbol{\theta}|\mathbf{y}) = f(\mathbf{y}|\boldsymbol{\theta}) p(\boldsymbol{\theta})$ is the posterior distribution of $\boldsymbol{\theta}$ corresponding to the likelihood function $f(\mathbf{y}|\boldsymbol{\theta})$ and prior $p(\boldsymbol{\theta})$.
3. Draw $u \sim \text{Uniform}(0, 1)$ and set $\boldsymbol{\theta}_t = \boldsymbol{\theta}_*$ if $u < \alpha(\boldsymbol{\theta}_* | \boldsymbol{\theta}_{t-1})$ or $\boldsymbol{\theta}_t = \boldsymbol{\theta}_{t-1}$, otherwise.
4. Perform adaptive iteration k. This step is performed only if $k \leq$ AMAX and t mod ALEN $= 0$. Update ρ_k according to (2), update Σ_k according to (3), and set $k = k + 1$.
5. Repeat steps 1–4. Note that the adaptation in step 4 is not performed at every MCMC iteration.

The output is the MCMC sequence $\{\boldsymbol{\theta}_t\}_{t=T_0+1}^{T_{\text{total}}}$ or $\boldsymbol{\theta}_1, \boldsymbol{\theta}_{1+l}, \boldsymbol{\theta}_{1+2l}, \ldots$, where l is the thinning interval as specified in the `thinning()` option.

If the parameter vector $\boldsymbol{\theta}$ is split into B blocks $\boldsymbol{\theta}^1$, $\boldsymbol{\theta}^2$, …, $\boldsymbol{\theta}^B$, then steps 1 through 3 are repeated for each $\boldsymbol{\theta}^b$, $b = 1, \ldots, B$ sequentially. The adaptation in step 4 is then applied sequentially to each block $b = 1, 2, \ldots, B$. See *Blocking of parameters* in [BAYES] **Intro** for details about blocking.

Initialization. We recommend that you carefully choose starting values for model parameters, $\boldsymbol{\theta}_0$, to be within the domain of the posterior distribution; see *Specifying initial values*. By default, for a single chain, MLEs are used as initial values, whenever available. If MLEs are not available, parameters with positive support are initialized with 1, probabilities are initialized with 0.5, and the remaining parameters are initialized with 0. Matrix parameters are initialized as identity matrices. If specified initial values $\boldsymbol{\theta}_0$ are within the domain of the posterior, then $\boldsymbol{\theta}_0^f = \boldsymbol{\theta}_0$. Otherwise, `bayesmh` performs 500 attempts (or as specified in `search(repeat())`) to find a feasible state $\boldsymbol{\theta}_0^f$, which is used as the initial state in the algorithm. If the command cannot find feasible values, it exits with an error.

You can specify the `initrandom` option to request random initial values for all model parameters. In this case, `bayesmh` generates random initial values from the corresponding prior distributions of the parameters, except for those that are assigned improper priors such as `flat` and `jeffreys()` or user-defined priors using the `density()` and `logdensity()` prior options. You must specify your own initial values for all model parameters for which random initial values cannot be generated.

With multiple chains, the initial values for the first chain are generated as described above and random initial values are generally generated from prior distributions for subsequent chains.

See *Specifying initial values* for details.

Adaptation. The adaptation step is performed as follows. At each adaptive iteration k of the tth MCMC iteration, the proposal covariance Σ_k and scale ρ_k are tuned to achieve an optimal AR. Some asymptotic results (for example, Gelman, Gilks, and Roberts [1997]) show that the optimal AR, hereafter referred to as a TAR, for a single model parameter is 0.44 and is 0.234 for a block of multiple parameters.

Adaptation is performed periodically after a constant number of iterations as specified by the `adaptation(every())` option. At least `adaptation(miniter())` adaptive iterations are performed not to exceed `adaptation(maxiter())`. `bayesmh` does not perform adaptation if the absolute difference between the current AR and TAR is within the tolerance given by `adaptation(tolerance())`.

The `bayesmh` command allows you to control the calculation of AR through the `adaptation(alpha())` option with the default of 0.75, as follows,

$$\text{AR}_k = (1-\alpha)\text{AR}_{k-1} + \alpha\widehat{\text{AR}}_k$$

where $\widehat{\text{AR}}_k$ is the expected acceptance probability, which is computed as the average of the acceptance probabilities, $\alpha(\boldsymbol{\theta}_*|\boldsymbol{\theta}_{t-1})$, since the last adaptive iteration (for example, Andrieu and Thoms [2008]), and AR_0 is defined as described in the `adaptation(tarate())` option. Choosing $\alpha \in (0,1)$ allows for smoother change in the current AR between adaptive iterations.

The tuning of the proposal scale ρ is based on results in Gelman, Gilks, and Roberts (1997), Roberts and Rosenthal (2001), and Andrieu and Thoms (2008). The initial ρ_0 is set to $2.38/\sqrt{d}$, where d is the number of parameters in the considered block. Then, ρ_k is updated according to

$$\rho_k = \rho_{k-1} e^{\beta_k\left\{\Phi^{-1}(\text{AR}_k/2)-\Phi^{-1}(\text{TAR}/2)\right\}} \tag{2}$$

where $\Phi(\cdot)$ is the standard normal cumulative distribution function and β_k is defined below.

The adaptation of the covariance matrix is performed when multiple parameters are in the block and is based on Andrieu and Thoms (2008). You may specify an initial proposal covariance matrix Σ_0 in `covariance()` or use the identity matrix by default. Then, at time of adaptation k, the proposal covariance Σ_k is recomputed according to the formula

$$\Sigma_k = (1-\beta_k)\Sigma_{k-1} + \beta_k\widehat{\Sigma}_k, \quad \beta_k = \frac{\beta_0}{k^\gamma} \tag{3}$$

where $\widehat{\Sigma}_k = (\Theta_{t_k} - \boldsymbol{\mu}_{k-1})(\Theta_{t_k} - \boldsymbol{\mu}_{k-1})'/(t_k - t_{k-1})$ is the empirical covariance of the recent MCMC sample $\Theta_{t_k} = \{\boldsymbol{\theta}_s\}_{s=t_{k-1}}^{t_k}$ and t_{k-1} is the MCMC iteration corresponding to the adaptive iteration $k-1$ or 0 if adaptation did not take place. $\boldsymbol{\mu}_k$ is defined as

$$\boldsymbol{\mu}_k = \boldsymbol{\mu}_{k-1} + \beta_k(\overline{\Theta}_{t_k} - \boldsymbol{\mu}_{k-1}),\ k > 1$$

and $\boldsymbol{\mu}_1 = \overline{\Theta}_{t_k}$, where $\overline{\Theta}_{t_k}$ is the sample mean of Θ_{t_k}.

The constants $\beta_0 \in [0,1]$ and $\gamma \in [0,1]$ in (3) are specified in the options `adaptation(beta())` and `adaptation(gamma())`, respectively. The default values are 0.8 and 0, respectively. When $\gamma > 0$, we have a diminishing adaptation regime, which means that Σ_k is not changing much from one adaptive iteration to another. Random-walk Metropolis–Hastings algorithms with diminishing adaptation are shown to preserve the ergodicity of the Markov chain (Roberts and Rosenthal 2007; Andrieu and Moulines 2006; Atchadé and Rosenthal 2005).

The above algorithm is also used for discrete parameters, but discretization is used to obtain samples of discrete values. The default initial scale factor ρ_0 is set to $2.38/d$ for a block of d discrete parameters. The default TAR for discrete parameters with priors `bernoulli()` and `index()` is $\max\{0.1353, 1/n_{\text{maxbins}}\}$, where n_{maxbins} is the maximum number of discrete values a parameter can take among all the parameters specified in the same block. Blocks containing a mixture of continuous and discrete parameters are not allowed.

Adaptive MH algorithm for random effects

Suppose that u is a random-effects variable that takes discrete values $1, \ldots, m$. For an independent sample $Y = \{y_{ij}\}$, where $j = 1, \ldots, m$ and where $i = 1, \ldots, n_j$, we assume that u takes value j for all y_{ij}, where $i = 1, \ldots, n_j$. Consider a two-level Bayesian model that includes random-effect parameters η_j, where $j = 1, \ldots, m$, one for each level of u, and additional parameter vector $\boldsymbol{\theta}$. We assume that, with respect to the posterior distribution of the model, the random-effects parameters η_j are conditionally independent given $\boldsymbol{\theta}$ and the data sample Y. The latter can be ensured the prior distribution of η_j's satisfies the conditional independence condition

$$\pi(\eta_1, \ldots, \eta_m|\boldsymbol{\theta}) = \prod_{j=1}^{m} \pi(\eta_j|\boldsymbol{\theta})$$

In this case, the posterior distribution admits the following factorization,

$$\Pr(\eta_1, \ldots, \eta_m, \boldsymbol{\theta}|Y) = \pi(\boldsymbol{\theta})\left\{\prod_{j=1}^{m} \pi(\eta_j|\boldsymbol{\theta}) \prod_{i=1}^{n_j} \Pr(y_{ij}|\eta_j, \boldsymbol{\theta})\right\}$$

where $\pi(\boldsymbol{\theta})$ is the prior distribution of $\boldsymbol{\theta}$. This form of the posterior allows the parameters η_j's to be placed in one block and steps 1, 2, and 3 of the adaptive MH algorithm to be performed for all of them simultaneously in a vector form, as if they were a single scalar parameter.

To request the random-effects MH algorithm in `bayesmh`, use `block`'s suboption `reffects`. The same algorithm is used if one includes the random effects in the model. A random-effects block of parameters has a default acceptance rate of 0.44, performs adaptation of the scale ρ_k according to (2), but uses a fixed identity matrix for the proposal covariance Σ_k.

Gibbs sampling for some likelihood-prior and prior-hyperprior configurations

In some cases, when a block of parameters $\boldsymbol{\theta}^b$ has a conjugate prior, or more appropriately, a semiconjugate prior, with respect to the respective likelihood distribution for this block, you can request Gibbs sampling instead of random-walk MH sampling. Then, steps 1 through 4 of the algorithm described in *Adaptive MH algorithm* are replaced with just one step of Gibbs sampling as follows:

1'. Simulate proposal parameters: $\boldsymbol{\theta}^b_* \sim F_b(\boldsymbol{\theta}^b|\boldsymbol{\theta}^1_*, \ldots, \boldsymbol{\theta}^{b-1}_*, \boldsymbol{\theta}^{b+1}_*, \ldots, \boldsymbol{\theta}^B_*, \mathbf{y})$

Here $F_b(\cdot|\cdot)$ is the full conditional distribution of $\boldsymbol{\theta}^b$ with respect to the rest of the parameters.

Below we list the full conditional distributions for the likelihood-prior specifications for which `bayesmh` provides Gibbs sampling. All priors except Jeffreys priors are semiconjugate, meaning that full conditional distributions belong to the same family as the specified prior distributions for the chosen data model. This contrasts with a concept of conjugacy under which the posterior distribution of all parameters belongs to the same family as the joint prior distribution. All the combinations below assume prior independence; that is, all parameters are independent a priori. Thus their joint prior distribution is simply the product of the individual prior distributions.

Likelihood-prior configurations

Let $\mathbf{y} = (y_1, y_2, \ldots, y_n)'$ be a data sample of size n. For multivariate data, $Y = (\mathbf{y}_1, \mathbf{y}_2, \ldots, \mathbf{y}_n)' = \{y_{ij}\}_{i,j=1}^{n,d}$ is an $n \times d$ data matrix.

1. **Normal–normal model**: θ^b is a mean of a normal distribution of y_i's with a variance σ^2; mean and variance are independent a priori,

$$\begin{aligned} y_i|\theta^b, \sigma^2 &\sim N(\theta^b, \sigma^2),\ i = 1, 2, \ldots, n \\ \theta^b &\sim N(\mu_0, \tau_0^2) \\ \theta^b|\sigma^2, \mathbf{y} &\sim F_b = N(\mu_n, \tau_n^2) \end{aligned}$$

   where μ_0 and τ_0^2 are hyperparameters (prior mean and prior variance) of a normal prior distribution for θ^b and

$$\begin{aligned} \mu_n &= \left(\mu_0\tau_0^{-2} + \sum y_i\sigma^{-2}\right)\tau_n^2 \\ \tau_n^2 &= (\tau_0^{-2} + n\sigma^{-2})^{-1} \end{aligned}$$

2. **Normal–normal regression**: $\boldsymbol{\theta}^b$ is a $p_1 \times 1$ subvector of a $p \times 1$ vector of regression coefficients $\boldsymbol{\beta}$ from a normal linear regression model for $\mathbf{y}$ with an $n \times p$ design matrix $X = (\mathbf{x}_1', \mathbf{x}_2', \ldots, \mathbf{x}_n')'$ and with a variance σ^2; regression coefficients and variance are independent a priori,

$$\begin{aligned} y_i|\boldsymbol{\theta}^b, \sigma^2 &\sim N(\mathbf{x}_i'\boldsymbol{\beta}, \sigma^2),\ i = 1, 2, \ldots, n \\ \theta_k^b &\sim \text{i.i.d. } N(\beta_0, \tau_0^2),\ k = 1, 2, \ldots, p_1 \\ \boldsymbol{\theta}^b|\sigma^2, \mathbf{y} &\sim F_b = \text{MVN}(\boldsymbol{\mu}_n, \Lambda_n) \end{aligned}$$

   where β_0 and τ_0^2 are hyperparameters (prior regression coefficient and prior variance) of normal prior distributions for θ_k^b and

$$\begin{aligned} \boldsymbol{\mu}_n &= (\boldsymbol{\beta}_0\tau_0^{-2} + X_b'\mathbf{y}\sigma^{-2})\Lambda_n \\ \Lambda_n &= (\tau_0^{-2}I_{p_1} + \sigma^{-2}X_b'X_b)^{-1} \end{aligned}$$

   In the above, I_{p_1} is a $p_1 \times p_1$ identity matrix, and $X_b = (\mathbf{x}_{1b}', \mathbf{x}_{2b}', \ldots, \mathbf{x}_{nb}')'$ is an $n \times p_1$ submatrix of X corresponding to the regression coefficients $\boldsymbol{\theta}^b$.

3. **Normal–inverse-gamma model**: θ^b is a variance of a normal distribution of y_i's with a mean μ; mean and variance are independent a priori,

$$\begin{aligned} y_i|\mu, \theta^b &\sim N(\mu, \theta^b),\ i = 1, 2, \ldots, n \\ \theta^b &\sim \text{InvGamma}(\alpha, \beta) \\ \theta^b|\mu, \mathbf{y} &\sim F_b = \text{InvGamma}(\alpha + n/2, \beta + \sum_{i=1}^{n}(y_i - \mu)^2/2) \end{aligned}$$

   where α and β are hyperparameters (prior shape and prior scale) of an inverse-gamma prior distribution for θ^b.

4. **Multivariate-normal–multivariate-normal model**: $\boldsymbol{\theta}^b$ is a mean vector of a multivariate normal distribution of $\mathbf{y}$'s with a $d \times d$ covariance matrix Σ; mean and covariance are independent a priori,

$$\begin{aligned}\mathbf{y}_i|\boldsymbol{\theta}^b, \Sigma &\sim \text{MVN}(\boldsymbol{\theta}^b, \Sigma),\ i = 1, 2, \ldots, n\\ \boldsymbol{\theta}^b &\sim \text{MVN}(\boldsymbol{\mu}_0, \Lambda_0)\\ \boldsymbol{\theta}^b|\Sigma, Y &\sim F_b = \text{MVN}(\boldsymbol{\mu}_n, \Lambda_n)\end{aligned}$$

where $\boldsymbol{\mu}_0$ and Λ_0 are hyperparameters (prior mean vector and prior covariance) of a multivariate normal prior distribution for $\boldsymbol{\theta}^b$ and

$$\begin{aligned}\boldsymbol{\mu}_n &= \Lambda_n\Lambda_0^{-1}\boldsymbol{\mu}_0 + \Lambda_n\Sigma^{-1}\left(\sum_{i=1}^{n}\mathbf{y}_i\right)\\ \Lambda_n &= (\Lambda_0^{-1} + n\Sigma^{-1})^{-1}\end{aligned}$$

5. **Multivariate-normal–inverse-Wishart model**: Θ^b is a $d \times d$ covariance matrix of a multivariate normal distribution of $\mathbf{y}$'s with a mean vector $\boldsymbol{\mu}$; mean and covariance are independent a priori,

$$\begin{aligned}\mathbf{y}_i|\boldsymbol{\mu}, \Theta^b &\sim \text{MVN}(\boldsymbol{\mu}, \Theta^b),\ i = 1, 2, \ldots, n\\ \Theta^b &\sim \text{InvWishart}(\nu, \Psi)\\ \Theta^b|\boldsymbol{\mu}, Y &\sim F_b = \text{InvWishart}(n + \nu, \Psi + \sum_{i=1}^{n}(\mathbf{y}_i - \boldsymbol{\mu})(\mathbf{y}_i - \boldsymbol{\mu})')\end{aligned}$$

where ν and Ψ are hyperparameters (prior degrees of freedom and prior scale matrix) of an inverse-Wishart prior distribution for Θ^b.

6. **Multivariate-normal–Jeffreys model**: Θ^b is a $d \times d$ covariance matrix of a multivariate normal distribution of $\mathbf{y}$'s with a mean vector $\boldsymbol{\mu}$; mean and covariance are independent a priori,

$$\begin{aligned}\mathbf{y}_i|\boldsymbol{\mu}, \Theta^b &\sim \text{MVN}(\boldsymbol{\mu}, \Theta^b),\ i = 1, 2, \ldots, n\\ \Theta^b &\sim |\Theta^b|^{-\frac{d+1}{2}}\ \text{(multivariate Jeffreys)}\\ \Theta^b|\boldsymbol{\mu}, Y &\sim F_b = \text{InvWishart}(n - 1, \sum_{i=1}^{n}(\mathbf{y}_i - \boldsymbol{\mu})(\mathbf{y}_i - \boldsymbol{\mu})')\end{aligned}$$

where $|\cdot|$ denotes the determinant of a matrix.

7. **Normal–scaled-multivariate-normal regression**: $\boldsymbol{\theta}^b$ is the vector of regression coefficients $\boldsymbol{\beta}$ from a normal linear regression model for $\mathbf{y}$ with an $n \times p$ design matrix $X = (\mathbf{x}_1', \mathbf{x}_2', \ldots, \mathbf{x}_n')'$ and variance σ^2,

$$y_i|\boldsymbol{\theta}^b, \sigma^2 \sim N(\mathbf{x}_i'\boldsymbol{\beta}, \sigma^2),\ i = 1, 2, \ldots, n$$

The prior for $\boldsymbol{\theta}^b$ conditional on σ^2 is multivariate normal with covariance Λ_0 proportional to σ^2 with a scale matrix A (`mvnscaled()` prior distribution),

$$\boldsymbol{\theta}^b|\sigma^2 \sim \text{MVN}(\boldsymbol{\mu}_0, \Lambda_0 = \sigma^2 A)$$

The posterior for $\boldsymbol{\theta}^b$ conditional on σ^2 is also multivariate normal,

$$\boldsymbol{\theta}^b|\sigma^2, \mathbf{y} \sim F_b = \text{MVN}(\boldsymbol{\mu}_n, \Lambda_n = \sigma^2 B)$$

where

$$\boldsymbol{\mu}_n = B(X'\mathbf{y} + A^{-1}\boldsymbol{\mu}_0)$$
$$\Lambda_n = \sigma^2 B = \sigma^2(X'X + A^{-1})^{-1}$$

8. **Probit–multivariate-normal model**: $\boldsymbol{\theta}^b$ is the vector of regression coefficients $\boldsymbol{\beta}$ from a probit regression model for $\mathbf{y}$,

$$P(y_i = 1|\boldsymbol{\theta}^b) = \Phi(\mathbf{x}_i'\boldsymbol{\beta}),\ i = 1, 2, \ldots, n$$
$$\boldsymbol{\theta}^b \sim \text{MVN}(\boldsymbol{\mu}_0, \Lambda_0)$$
$$\boldsymbol{\theta}^b|\mathbf{y} \sim F_b = \text{MVN}(\boldsymbol{\mu}_n, \Lambda_n)$$

where

$$\boldsymbol{\mu}_n = \Lambda_n(X'\mathbf{y}^* + \Lambda_0^{-1}\boldsymbol{\mu}_0)$$
$$\Lambda_n = (X'X + \Lambda_0^{-1})^{-1}$$

and $\mathbf{y}^* = (y_1^*, y_2^*, \ldots, y_n^*)'$ is an auxiliary vector such that

$$y_i^* \sim \text{TruncatedNormal}_{(-\infty,0)}(\mathbf{x}_i'\boldsymbol{\beta}, 1),\ y_i = 0$$
$$y_i^* \sim \text{TruncatedNormal}_{(0,\infty)}(\mathbf{x}_i'\boldsymbol{\beta}, 1),\ y_i = 1$$

Prior-hyperprior configurations

Suppose that a prior distribution of a parameter of interest $\boldsymbol{\theta}$ has hyperparameters $\boldsymbol{\theta}_h$ for which a prior distribution is specified. We refer to the former prior distribution as a hyperprior. You can also request Gibbs sampling for the following prior-hyperprior combinations.

We use θ_h^b and $\boldsymbol{\theta}_h^b$ to refer to the hyperparameters from the block b.

1. **Normal–normal model**: θ_h^b is a mean of a normal prior distribution of θ with a variance σ_h^2; mean and variance are independent a priori,

$$\theta|\theta_h^b, \sigma_h^2 \sim N(\theta_h^b, \sigma_h^2)$$
$$\theta_h^b \sim N(\mu_0, \tau_0^2)$$
$$\theta_h^b|\sigma_h^2, \theta \sim F_b = N(\mu_1, \tau_1^2)$$

where μ_0 and τ_0^2 are the prior mean and prior variance of a normal hyperprior distribution for θ_h^b and

$$\mu_1 = \left(\mu_0\tau_0^{-2} + \theta\sigma_h^{-2}\right)\tau_1^2$$
$$\tau_1^2 = (\tau_0^{-2} + \sigma_h^{-2})^{-1}$$

2. **Normal–inverse-gamma model**: θ_h^b is a variance of a normal prior distribution of θ with a mean μ_h; mean and variance are independent a priori,

$$\theta|\mu_h, \theta_h^b \sim N(\mu_h, \theta_h^b)$$
$$\theta_h^b \sim \text{InvGamma}(\alpha, \beta)$$
$$\theta_h^b|\mu_h, \theta \sim F_b = \text{InvGamma}(\alpha + 0.5, \beta + (\theta - \mu)^2/2)$$

where α and β are the prior shape and prior scale, respectively, of an inverse-gamma hyperprior distribution for θ_h^b.

3. **Bernoulli–beta model**: θ_h^b is a probability of success of a Bernoulli prior distribution of θ,

$$\begin{aligned}\theta|\theta_h^b &\sim \text{Bernoulli}(\theta_h^b)\\ \theta_h^b &\sim \text{Beta}(\alpha,\beta)\\ \theta_h^b|\theta &\sim F_b = \text{Beta}(\alpha+\theta,\beta+1-\theta)\end{aligned}$$

where α and β are the prior shape and prior scale, respectively, of a beta hyperprior distribution for θ_h^b.

4. **Poisson–gamma model**: θ_h^b is a mean of a Poisson prior distribution of θ,

$$\begin{aligned}\theta|\theta_h^b &\sim \text{Poisson}(\theta_h^b)\\ \theta_h^b &\sim \text{Gamma}(\alpha,\beta)\\ \theta_h^b|\theta &\sim F_b = \text{Gamma}(\alpha+\theta,\beta/(\beta+1))\end{aligned}$$

where α and β are the prior shape and prior scale, respectively, of a gamma hyperprior distribution for θ_h^b.

5. **Multivariate-normal–multivariate-normal model**: $\boldsymbol{\theta}_h^b$ is a mean vector of a multivariate normal prior distribution of $\boldsymbol{\theta}$ with a $d\times d$ covariance matrix Σ_h; mean and covariance are independent a priori,

$$\begin{aligned}\boldsymbol{\theta}|\boldsymbol{\theta}_h^b,\Sigma_h &\sim \text{MVN}(\boldsymbol{\theta}_h^b,\Sigma_h)\\ \boldsymbol{\theta}_h^b &\sim \text{MVN}(\boldsymbol{\mu}_0,\Lambda_0)\\ \boldsymbol{\theta}_h^b|\Sigma_h,\boldsymbol{\theta} &\sim F_b = \text{MVN}(\boldsymbol{\mu}_1,\Lambda_1)\end{aligned}$$

where $\boldsymbol{\mu}_0$ and Λ_0 are the prior mean vector and prior covariance of a multivariate normal hyperprior distribution for $\boldsymbol{\theta}_h^b$ and

$$\begin{aligned}\boldsymbol{\mu}_1 &= \Lambda_1\Lambda_0^{-1}\boldsymbol{\mu}_0 + \Lambda_1\Sigma_h^{-1}\boldsymbol{\theta}\\ \Lambda_1 &= (\Lambda_0^{-1}+\Sigma_h^{-1})^{-1}\end{aligned}$$

6. **Multivariate-normal–inverse-Wishart model**: Θ_h^b is a $d\times d$ covariance matrix of a multivariate normal prior distribution of $\boldsymbol{\theta}$ with a mean vector $\boldsymbol{\mu}_h$; mean and covariance are independent a priori,

$$\begin{aligned}\boldsymbol{\theta}|\boldsymbol{\mu}_h,\Theta_h^b &\sim \text{MVN}(\boldsymbol{\mu}_h,\Theta_h^b)\\ \Theta_h^b &\sim \text{InvWishart}(\nu,\Psi)\\ \Theta_h^b|\boldsymbol{\mu}_h,\boldsymbol{\theta} &\sim F_b = \text{InvWishart}(\nu+1,\Psi+(\boldsymbol{\theta}-\boldsymbol{\mu}_h)(\boldsymbol{\theta}-\boldsymbol{\mu}_h)')\end{aligned}$$

where ν and Ψ are the prior degrees of freedom and prior scale matrix of an inverse-Wishart hyperprior distribution for Θ_h^b.

Marginal likelihood

The marginal likelihood is defined as

$$m(\mathbf{y}) = \int p(\mathbf{y}|\boldsymbol{\theta})\pi(\boldsymbol{\theta})d\boldsymbol{\theta}$$

where $p(\mathbf{y}|\boldsymbol{\theta})$ is the probability density of data $\mathbf{y}$ given $\boldsymbol{\theta}$ and $\pi(\boldsymbol{\theta})$ is the density of the prior distribution for $\boldsymbol{\theta}$.

Marginal likelihood $m(\mathbf{y})$, being the denominator term in the posterior distribution, has a major role in Bayesian analysis. It is sometimes referred to as "model evidence", and it is used as a goodness-of-fit criterion. For example, marginal likelihoods are used in calculating Bayes factors for the purpose of model comparison; see *Methods and formulas* in [BAYES] **bayesstats ic**.

The simplest approximation to $m(\mathbf{y})$ is provided by the Monte Carlo integration,

$$\widehat{m}_p = \frac{1}{M}\sum_{s=1}^{M} p(\mathbf{y}|\boldsymbol{\theta}_s)$$

where $\{\boldsymbol{\theta}_s\}_{s=1}^{M}$ is an independent sample from the prior distribution $\pi(\boldsymbol{\theta})$. This estimation is very inefficient, however, because of the high variance of the likelihood function. MCMC samples are not independent and cannot be used directly for calculating $\widehat{m}_p$.

An improved estimation of the marginal likelihood can be obtained by using importance sampling. For a sample $\{\boldsymbol{\theta}_t\}_{t=1}^{T}$, not necessarily independent, from the posterior distribution, the harmonic mean of the likelihood values,

$$\widehat{m}_h = \left\{\frac{1}{T}\sum_{t=1}^{T} p(\mathbf{y}|\boldsymbol{\theta}_t)^{-1}\right\}^{-1}$$

approximates $m(\mathbf{y})$ (Geweke 1989).

Another method for estimating $m(\mathbf{y})$ uses the Laplace approximation,

$$\widehat{m}_l = (2\pi)^{p/2}|-\widetilde{H}|^{-1/2} p(\mathbf{y}|\widetilde{\boldsymbol{\theta}})\pi(\widetilde{\boldsymbol{\theta}})$$

where p is the number of parameters (or dimension of $\boldsymbol{\theta}$), $\widetilde{\boldsymbol{\theta}}$ is the posterior mode, and $\widetilde{H}$ is the Hessian matrix of $l(\boldsymbol{\theta}) = p(\mathbf{y}|\boldsymbol{\theta})\pi(\boldsymbol{\theta})$ calculated at the mode $\widetilde{\boldsymbol{\theta}}$.

Using the fact that the posterior sample covariance matrix, which we denote as $\widehat{\Sigma}$, is asymptotically equal to $(-\widetilde{H})^{-1}$, Raftery (1996) proposed what he called the Laplace–Metropolis estimator (implemented by `bayesmh`):

$$\widehat{m}_{lm} = (2\pi)^{p/2}|\widehat{\Sigma}|^{1/2} p(\mathbf{y}|\widetilde{\boldsymbol{\theta}})\pi(\widetilde{\boldsymbol{\theta}})$$

Raftery (1996) recommends that a robust and consistent estimator be used for the posterior covariance matrix.

Estimation of the log marginal-likelihood becomes unstable for high-dimensional models such as multilevel models and may result in a missing value.

With multiple chains, an average of the log-marginal-likelihood values over the chains is reported.

Nicholas Constantine Metropolis (1915–1999) was born in Chicago. He completed his PhD in experimental physics at the University of Chicago in 1941. In 1943, Metropolis moved to Los Alamos, where he spent much of his time working on computers and computational algorithms. He first worked with analog and then IBM punch card machines. Beginning in 1948, he helped design the MANIAC I computer, one of the first digital computers. He later oversaw the construction of the MANIAC II and MANIAC III. He collaborated with Stanislaw Ulam to develop the Monte Carlo method, and he coauthored a paper in 1953 introducing the Monte Carlo algorithm. The algorithm would later be extended to general cases by W. K. Hastings and would be known as the Metropolis–Hastings algorithm. In 1957, Metropolis returned to the University of Chicago, where he taught physics and helped found the Institute for Computer Research.

The American Physical Society elected Metropolis as a fellow in 1953 and created an award in his honor that recognizes extraordinary work in computational physics. Also, in 1984, the Institute of Electrical and Electronics Engineers (IEEE) awarded him the Computer Pioneer Award. In his late 70s, Metropolis appeared in a Woody Allen film, portraying a scientist.

Wilfred Keith Hastings (1930–2016) was born in Toronto, Ontario, Canada. He studied applied mathematics at the University of Toronto, obtaining his bachelors in 1953 and later working as a computer applications consultant. In this position, he was exposed to statistics and gained experience with simulations. In 1962, he obtained his PhD, also from the University of Toronto. His dissertation was on fiducial distributions, but after attending a statistics conference, he learned that people were abandoning the study of fiducial probability. Shortly after graduation, he joined the faculty at the University of Canterbury for two years and then worked at the research company Bell Labs for two years as well. In 1966, he became an associate professor at his alma mater, and three years later he published his work on the Markov chain Monte Carlo (MCMC) method. His publication on Monte Carlo sampling methods was an extension of the algorithm introduced in the 1953 publication by Nicholas Metropolis et al. The idea originated from his interactions and consultations with the chemistry department's application of the Metropolis algorithm to estimating the energy of particles. Hastings's publication was cited over 2,000 times and gave rise to the Metropolis–Hastings algorithm. After this publication, Hastings served as a professor at the University of Victoria for 21 years and conducted research with multiple grants from the Natural Sciences and Engineering Research Council of Canada (NSERC).

Harold Jeffreys (1891–1989) was born near Durham, England, and spent more than 75 years studying and working at the University of Cambridge, principally on theoretical and observational problems in geophysics, astronomy, mathematics, and statistics. He developed a systematic Bayesian approach to inference in his monograph *Theory of Probability*.

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Also see

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **bayesmh evaluators** — User-defined evaluators with bayesmh

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

[BMA] **bmaregress** — Bayesian model averaging for linear regression

Title

bayesmh evaluators — User-defined evaluators with bayesmh

Description

`bayesmh` provides two options, `evaluator()` and `llevaluator()`, that facilitate user-defined evaluators for fitting general Bayesian regression models. `bayesmh, evaluator()` accommodates log-posterior evaluators. `bayesmh, llevaluator()` accommodates log-likelihood evaluators, which are combined with built-in prior distributions to form the desired posterior density. For a catalog of built-in likelihood models and prior distributions, see [BAYES] **bayesmh**.

Syntax

Single-equation models

User-defined log-posterior evaluator

`bayesmh` *depvar* [*indepvars*] [*if*] [*in*] [*weight*], `evaluator(`*evalspec*`)` [*options*]

User-defined log-likelihood evaluator

`bayesmh` *depvar* [*indepvars*] [*if*] [*in*] [*weight*], `llevaluator(`*evalspec*`)`
`prior(`*priorspec*`)` [*options*]

Multiple-equations models

User-defined log-posterior evaluator

`bayesmh (`*eqspecp*`)` [`(`*eqspecp*`)` [...]] [*if*] [*in*] [*weight*], `evaluator(`*evalspec*`)`
[*options*]

User-defined log-likelihood evaluator

`bayesmh (`*eqspecll*`)` [`(`*eqspecll*`)` [...]] [*if*] [*in*] [*weight*], `prior(`*priorspec*`)`
[*options*]

The syntax of *eqspecp* is

varspec [, noconstant]

The syntax of *eqspecll* for built-in likelihood models is

varspec, likelihood(*modelspec*) [noconstant]

The syntax of *eqspecll* for user-defined log-likelihood evaluators is

varspec, llevaluator(*evalspec*) [noconstant]

The syntax of *varspec* is one of the following:

for single outcome

[*eqname*:]*depvar* [*indepvars*]

for multiple outcomes with common regressors

depvars = [*indepvars*]

for multiple outcomes with outcome-specific regressors

([*eqname1*:]*depvar1* [*indepvars1*]) ([*eqname2*:]*depvar2* [*indepvars2*]) [...]

The syntax of *evalspec* is

progname, parameters(*paramlist*) [extravars(*varlist*) passthruopts(*string*)]

where *progname* is the name of a Stata program that you write to evaluate the log-posterior density or the log-likelihood function (see *Program evaluators*), and *paramlist* is a list of model parameters:

paramdef [*paramdef* [...]]

The syntax of *paramdef* is

{[*eqname*:]*param* [*param* [...]] [, matrix]}

where the parameter label *eqname* and parameter names *param* are valid Stata names. Model parameters are either scalars such as {var}, {mean}, and {shape:alpha} or matrices such as {Sigma, matrix} and {Scale:V, matrix}. For scalar parameters, you can use {param=#} in the above to specify an initial value. For example, you can specify {var=1}, {mean=1.267}, or {shape:alpha=3}. You can specify the multiple parameters with same equation as {eq:p1 p2 p3} or {eq: S1 S2, matrix}. Also see *Declaring model parameters* in [BAYES] **bayesmh**.

options	Description
*`evaluator(`*evalspec*`)`	specify log-posterior evaluator; may not be combined with `llevaluator()` and `prior()`
*`llevaluator(`*evalspec*`)`	specify log-likelihood evaluator; requires `prior()` and may not be combined with `evaluator()`
*`prior(`*priorspec*`)`	prior for model parameters; required with log-likelihood evaluator and may be repeated
`likelihood(`*modelspec*`)`	distribution for the likelihood model; allowed within an equation of a multiple-equations model only
`noconstant`	suppress constant term; not allowed with ordered models specified in `likelihood()` with multiple-equations models
bayesmhopts	any options of [BAYES] **bayesmh** except `likelihood()` and `prior()`

*Option `evaluator()` is required for log-posterior evaluators, and options `llevaluator()` and `prior()` are required for log-likelihood evaluators. With log-likelihood evaluators, `prior()` must be specified for all model parameters and may be repeated.

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

Only `fweights` are allowed; see [U] **11.1.6 weight**.

Options

`evaluator(`*evalspec*`)` specifies the name and the attributes of the log-posterior evaluator; see *Program evaluators* for details. This option may not be combined with `llevaluator()` or `likelihood()`.

`llevaluator(`*evalspec*`)` specifies the name and the attributes of the log-likelihood evaluator; see *Program evaluators* for details. This option may not be combined with `evaluator()` or `likelihood()` and requires the `prior()` option.

`prior(`*priorspec*`)`; see [BAYES] **bayesmh**.

`likelihood(`*modelspec*`)`; see [BAYES] **bayesmh**. This option is allowed within an equation of a multiple-equations model only.

`noconstant`; see [BAYES] **bayesmh**.

bayesmhopts specify any *options* of [BAYES] **bayesmh**, except `likelihood()` and `prior()`.

Remarks and examples

Remarks are presented under the following headings:

Program evaluators

If your likelihood model or prior distributions are particularly complex and cannot be represented by one of the predefined sets of distributions or by substitutable expressions provided with bayesmh, you can program these functions by writing your own evaluator program.

Evaluator programs can be used for programming the full posterior density by specifying the evaluator() option or only the likelihood portion of your Bayesian model by specifying the llevaluator() option. For likelihood evaluators, prior() option(s) must be specified for all model parameters. Your program is expected to calculate and return an overall log-posterior or a log-likelihood density value.

It is allowed for the return values to match the log density up to an additive constant, in which case, however, some of the reported statistics such as DIC and log marginal-likelihood may not be applicable.

Your program evaluator *progname* must be a Stata program; see [U] 18 Programming Stata. The program must follow the style below.

```
program progname
    args lnden xb1 [xb2 ...] [modelparams]
    ... computations ...
    scalar 'lnden' = ...
end
```

Here lnden contains the name of a temporary scalar to be filled in with an overall log-posterior or log-likelihood value;

xb# contains the name of a temporary variable containing the linear predictor from the #th equation; and

modelparams is a list of names of scalars or matrices to contain the values of model parameters specified in suboption parameters() of evaluator() or llevaluator(). For matrix parameters, the specified names will contain the names of temporary matrices containing current values. For scalar parameters, these are the names of temporary scalars containing current values. The order in which names are listed should correspond to the order in which model parameters are specified in parameters().

Also see *Global macros* for a list of global macros available to the program evaluator.

After you write a program evaluator, you specify its name in the option evaluator() for log-posterior evaluators,

```
. bayesmh ..., evaluator(progname, evalopts)
```

or option llevaluator() for log-likelihood evaluators,

```
. bayesmh ..., llevaluator(progname, evalopts)
```

Evaluator options *evalopts* include parameters(), extravars(), and passthruopts().

parameters(*paramlist*) specifies model parameters. Model parameters can be scalars or matrices. Each parameter must be specified in curly braces {}. Multiple parameters with the same equation names may be specified within one set of {}.

For example,

```
parameters({mu} {var:sig2} {S,matrix} {cov:Sigma, matrix} {prob:p1 p2})
```

specifies a scalar parameter with name mu without an equation label, a scalar parameter with name sig2 and label var, a matrix parameter with name S, a matrix parameter with name Sigma and label cov, and two scalar parameters {prob:p1} and {prob:p2}.

`extravars(`*varlist*`)` specifies any variables in addition to dependent and independent variables that you may need in your program evaluator. Examples of such variables are offset variables, exposure variables for count-data models, and failure or censoring indicators for survival-time models. See *Cox proportional hazards regression* for an example.

`passthruopts(`*string*`)` specifies a list of options you may want to pass to your program evaluator. For example, these options may contain fixed values of model parameters and hyperparameters. See *Multivariate normal regression model* for an example.

`bayesmh` automatically creates parameters for regression coefficients: {*depname*:*varname*} for every *varname* in *indepvars*, and a constant parameter {*depname*:_cons} unless `noconstant` is specified. These parameters are used to form linear predictors used by the program evaluator. If you need to access values of the parameters in the evaluator, you can use `$MH_b`; see the log-posterior evaluator in *Cox proportional hazards regression* for an example. With multiple dependent variables, regression coefficients are defined for each dependent variable.

Simple linear regression model

Suppose that we want to fit a Bayesian normal regression where we program the posterior distribution ourselves. The `normaljeffreys` program below computes the log-posterior density for the normal linear regression with flat priors for the coefficients and the Jeffreys prior for the variance parameter.

```
. program normaljeffreys
  1.         version 18.0
  2.         args lnp xb var
  3.         /* compute log likelihood */
.         tempname sd
  4.         scalar `sd' = sqrt(`var')
  5.         tempvar lnfj
  6.         quietly generate double `lnfj'=lnnormalden($MH_y,`xb',`sd')
>                                       if $MH_touse
  7.         quietly summarize `lnfj', meanonly
  8.         if r(N) < $MH_n {
  9.                 scalar `lnp' = .
 10.                 exit
 11.         }
 12.         tempname lnf
 13.         scalar `lnf' = r(sum)
 14.         /* compute log prior */
.         tempname lnprior
 15.         scalar `lnprior' = -2*ln(`sd')
 16.         /* compute log posterior */
.         scalar `lnp' = `lnf' + `lnprior'
 17. end
```

The program accepts three parameters: a temporary name `` `lnp' `` of a scalar to contain the log-posterior value, a temporary name `` `xb' `` of the variable that contains the linear predictor, and a temporary name `` `var' `` of a scalar that contains the values of the variance parameter.

The first part of the program calculates the overall log likelihood of the normal regression. The second part of the program calculates the log of prior distributions of the parameters. Because the coefficients have flat prior distributions with densities of 1, their log is 0 and does not contribute to the overall prior. The only contribution is from the Jeffreys prior $\ln(1/\sigma^2) = -2\ln(\sigma)$ for the variance σ^2. The third and final part of the program computes the values of the posterior density as the sum of the overall log likelihood and the log of the prior.

The substantial portion of this program is the computation of the overall log likelihood. The global macro `$MH_y` contains the name of the dependent variable, `$MH_touse` contains a temporary marker

variable identifying observations to be used in computations, and $MH_n contains the total number of observations in the sample identified by the $MH_touse variable.

We used the built-in function lnnormalden() to compute observation-specific log likelihood and used summarize to obtain the overall value. Whenever a temporary variable is needed for calculations, such as 'lnfj' in our program, it is important to create it of type double to ensure the highest precision of the results. It is also important to perform computations using only the relevant subset of observations as identified by the marker variable stored in $MH_touse. This variable contains the value of 1 for observations to be used in the computations and 0 for the remaining observations. Missing values in used variables, if, and in affect this variable. After we compute the log-likelihood value, we should verify that the number of nonmissing observation-specific contributions to the log likelihood equals $MH_n. If it does not, the log-posterior value (or log-likelihood value in a log-likelihood evaluator) must be set to missing.

We can now specify the normaljeffreys evaluator in the evaluator() option of bayesmh. In addition to the regression coefficients, we have one extra parameter, the variance of the normal distribution, which we must specify in the parameters() suboption of evaluator().

We use auto.dta to illustrate the command. We specify a simple regression of mpg on rescaled weight.

```
. use https://www.stata-press.com/data/r18/auto
(1978 automobile data)
. quietly replace weight = weight/100
. set seed 14
. bayesmh mpg weight, evaluator(normaljeffreys, parameters({var}))
Burn-in ...
note: invalid initial state.
Simulation ...
Model summary
------------------------------------------------------------------------------
Posterior:
  mpg ~ normaljeffreys(xb_mpg,{var})
------------------------------------------------------------------------------

Bayesian regression                             MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .1433
                                                Efficiency:  min =     .06246
                                                             avg =     .06669
Log marginal-likelihood =   -198.247                         max =     .07091

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
      weight |  -.6052218    .053604   .002075  -.6062666  -.7121237  -.4992178
       _cons |   39.56782   1.658124   .066344   39.54211   36.35645   42.89876
-------------+----------------------------------------------------------------
         var |   12.19046   2.008871   .075442   12.03002   8.831172   17.07787
------------------------------------------------------------------------------
```

The output of bayesmh with user-defined evaluators is the same as the output of bayesmh with built-in distributions, except the title and the model summary. The generic title Bayesian regression is used for all evaluators, but you can change it by specifying the title() option. The model summary provides the name of the posterior evaluator.

Following the command line, there is a note about invalid initial state. For program evaluators, `bayesmh` initializes all parameters with zeros, except for positive parameters used in prior specifications, which are initialized with ones. This may not be sensible for all parameters, such as the variance parameter in our example. We may consider using, for example, OLS estimates as initial values of the parameters.

```
. regress mpg weight
```

Source	SS	df	MS	Number of obs	=	74
				F(1, 72)	=	134.62
Model	1591.99021	1	1591.99021	Prob > F	=	0.0000
Residual	851.469254	72	11.8259619	R-squared	=	0.6515
				Adj R-squared	=	0.6467
Total	2443.45946	73	33.4720474	Root MSE	=	3.4389

mpg	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
weight	-.6008687	.0517878	-11.60	0.000	-.7041058	-.4976315
_cons	39.44028	1.614003	24.44	0.000	36.22283	42.65774

```
. display e(rmse)^2
11.825962
```

We specify initial values in the `initial()` option.

```
. set seed 14
. bayesmh mpg weight, evaluator(normaljeffreys, parameters({var}))
> initial({mpg:weight} -0.6 {mpg:_cons} 39 {var} 11.83)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Posterior:
  mpg ~ normaljeffreys(xb_mpg,{var})
------------------------------------------------------------------------------
Bayesian regression                             MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .1668
                                                Efficiency:  min =     .04114
                                                             avg =     .04811
Log marginal-likelihood = -198.14302                         max =     .05938
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
mpg						
weight	-.6025616	.0540995	.002667	-.6038729	-.7115221	-.5005915
_cons	39.50491	1.677906	.080156	39.45537	36.2433	43.14319
var	12.26586	2.117858	.086915	12.05298	8.827655	17.10703

We can compare our results with `bayesmh` that uses a built-in normal likelihood and flat and Jeffreys priors. To match the results, we must use the same initial values, because `bayesmh` has a different initialization logic for built-in distributions.

```
. set seed 14
. bayesmh mpg weight, likelihood(normal({var}))
> prior({mpg:}, flat) prior({var}, jeffreys)
> initial({mpg:weight} -0.6 {mpg:_cons} 39 {var} 11.83)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal(xb_mpg,{var})
Priors:
  {mpg:weight _cons} ~ 1 (flat)                                          (1)
               {var} ~ jeffreys
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .1668
                                                Efficiency:  min =     .04114
                                                             avg =     .04811
Log marginal-likelihood = -198.14302                         max =     .05938
------------------------------------------------------------------------------
                                                                Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
      weight |  -.6025616   .0540995   .002667  -.6038729  -.7115221  -.5005915
       _cons |   39.50491   1.677906   .080156   39.45537   36.2433   43.14319
-------------+----------------------------------------------------------------
         var |   12.26586   2.117858   .086915   12.05298   8.827655   17.10703
------------------------------------------------------------------------------
```

If your Bayesian model uses prior distributions that are supported by `bayesmh` but the likelihood model is not supported, you can write only the likelihood evaluator and use built-in prior distributions.

For example, we extract the portion of the `normaljeffreys` program computing the overall log likelihood into a separate program and call it `normalreg`.

```
. program normalreg
  1.         version 18.0
  2.         args lnf xb var
  3.                                              /* compute log likelihood */
.         tempname sd
  4.         scalar `sd' = sqrt(`var')
  5.         tempvar lnfj
  6.         quietly generate double `lnfj' = lnnormalden($MH_y,`xb',`sd')
>                                       if $MH_touse
  7.         quietly summarize `lnfj', meanonly
  8.         if r(N) < $MH_n {
  9.             scalar `lnf' = .
 10.             exit
 11.         }
 12.         scalar `lnf' = r(sum)
 13. end
```

We can now specify this program in the `llevaluator()` option and use `prior()` options to specify built-in flat priors for the coefficients and the Jeffreys prior for the variance.

```
. set seed 14
. bayesmh mpg weight, llevaluator(normalreg, parameters({var}))
> prior({mpg:}, flat) prior({var}, jeffreys)
> initial({mpg:weight} -0.6 {mpg:_cons} 39 {var} 11.83)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normalreg(xb_mpg,{var})
Priors:
  {mpg:weight _cons} ~ 1 (flat)                                          (1)
                {var} ~ jeffreys
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
Bayesian regression                             MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .1668
                                                Efficiency:  min =     .04114
                                                             avg =     .04811
Log marginal-likelihood = -198.14302                         max =     .05938
------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
      weight |  -.6025616   .0540995   .002667  -.6038729  -.7115221  -.5005915
       _cons |   39.50491   1.677906   .080156   39.45537    36.2433   43.14319
-------------+----------------------------------------------------------------
         var |   12.26586   2.117858   .086915   12.05298   8.827655   17.10703
------------------------------------------------------------------------------
```

We obtain the same results as earlier.

Logistic regression model

Some models, such as logistic regression, do not have any additional parameters except regression coefficients. Here we show how to use a program evaluator for fitting a Bayesian logistic regression model.

We start by creating a program for computing the log likelihood.

```
. program logitll
  1.         version 18.0
  2.         args lnf xb
  3.         tempvar lnfj
  4.         quietly generate `lnfj' = ln(invlogit( `xb'))
>                                       if $MH_y == 1 & $MH_touse
  5.         quietly replace `lnfj'  = ln(invlogit(-`xb'))
>                                       if $MH_y == 0 & $MH_touse
  6.         quietly summarize `lnfj', meanonly
  7.         if r(N) < $MH_n {
  8.             scalar `lnf' = .
  9.             exit
 10.         }
 11.         scalar `lnf' = r(sum)
 12. end
```

The structure of our log-likelihood evaluator is similar to the one described in *Simple linear regression model*, except we have no extra parameters.

We continue with `auto.dta` and regress `foreign` on `mpg`. For simplicity, we assume a flat prior for the coefficients and use `bayesmh, llevaluator()` to fit this model.

```
. use https://www.stata-press.com/data/r18/auto, clear
(1978 automobile data)
. set seed 14
. bayesmh foreign mpg, llevaluator(logitll) prior({foreign:}, flat)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  foreign ~ logitll(xb_foreign)
Prior:
  {foreign:mpg _cons} ~ 1 (flat)                                          (1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_foreign.
Bayesian regression                             MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .2216
                                                Efficiency:  min =     .09293
                                                             avg =     .09989
Log marginal-likelihood = -41.626028                         max =      .1068
------------------------------------------------------------------------------
             |                                                Equal-tailed
     foreign |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
         mpg |     .16716   .0545771    .00167   .1644019    .0669937   .2790017
       _cons |  -4.560637   1.261675   .041387  -4.503921   -7.107851  -2.207665
------------------------------------------------------------------------------
```

The results from the program-evaluator version match the results from `bayesmh` with a built-in logistic model.

```
. set seed 14
. bayesmh foreign mpg, likelihood(logit) prior({foreign:}, flat)
> initial({foreign:} 0)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  foreign ~ logit(xb_foreign)
Prior:
  {foreign:mpg _cons} ~ 1 (flat)                                         (1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_foreign.
Bayesian logistic regression                    MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .2216
                                                Efficiency:  min =     .09293
                                                             avg =     .09989
Log marginal-likelihood = -41.626029                         max =      .1068
------------------------------------------------------------------------------
                                                              Equal-tailed
     foreign |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
         mpg |     .16716   .0545771    .00167   .1644019   .0669937   .2790017
       _cons |  -4.560636   1.261675   .041387  -4.503921  -7.10785  -2.207665
------------------------------------------------------------------------------
```

Because we assumed a flat prior with the density of 1, the log prior is 0, so the log-posterior evaluator for this model is the same as the log-likelihood evaluator.

```
. set seed 14
. bayesmh foreign mpg, evaluator(logitll)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Posterior:
  foreign ~ logitll(xb_foreign)
------------------------------------------------------------------------------
Bayesian regression                             MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .2216
                                                Efficiency:  min =     .09293
                                                             avg =     .09989
Log marginal-likelihood = -41.626028                         max =      .1068
------------------------------------------------------------------------------
                                                              Equal-tailed
     foreign |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
         mpg |     .16716   .0545771    .00167   .1644019   .0669937   .2790017
       _cons |  -4.560637   1.261675   .041387  -4.503921  -7.107851  -2.207665
------------------------------------------------------------------------------
```

Multivariate normal regression model

Here we demonstrate how to write a program evaluator for a multivariate response. We consider a bivariate normal regression, and we again start with a log-likelihood evaluator. In this example, we also use Mata to speed up our computations.

```
. program mvnregll
  1.         version 18.0
  2.         args lnf xb1 xb2
  3.         tempvar diff1 diff2
  4.         quietly generate double `diff1' = $MH_y1 - `xb1' if $MH_touse
  5.         quietly generate double `diff2' = $MH_y2 - `xb2' if $MH_touse
  6.         local d $MH_yn
  7.         local n $MH_n
  8.         mata: st_numscalar("`lnf'", mvnll_mata(`d',`n',"`diff1'","`diff2'"))
  9. end
.
. mata:
------------------------------------------------- mata (type end to exit) -----
: real scalar mvnll_mata(real scalar d, n, string scalar sdiff1, sdiff2)
> {
>         real matrix Diff
>         real scalar trace, lnf
>         real matrix Sigma
>
>         Sigma = st_matrix(st_global("MH_m1"))
>         st_view(Diff=.,.,(sdiff1,sdiff2),st_global("MH_touse"))
>
>         /* compute log likelihood */
>         trace = trace(cross(cross(Diff',invsym(Sigma))',Diff'))
>         lnf = -0.5*n*(d*ln(2*pi())+ln(det(Sigma)))-0.5*trace
>
>         return(lnf)
> }
: end
------------------------------------------------------------------------------
```

The `mvnregll` program has three arguments: a scalar to store the log-likelihood values and two temporary variables containing linear predictors corresponding to each of the two dependent variables. It creates deviations `` `diff1' `` and `` `diff2' `` and passes them, along with other parameters, to the Mata function `mvnll_mata()` to compute the bivariate normal log-likelihood value.

The extra parameter in this model is a covariance matrix of a bivariate response. In *Simple linear regression model*, we specified an extra parameter, variance, which was a scalar, as an additional argument of the evaluator. This is not allowed with matrix parameters. They should be accessed via globals `$MH_m1`, `$MH_m2`, and so on for each matrix model parameters in the order they are specified in option `parameters()`. In our example, we have only one matrix and we access it via `$MH_m1`. `$MH_m1` contains the temporary name of a matrix containing the current value of the covariance matrix parameter.

To demonstrate, we again use `auto.dta`. We rescale the variables to be used in our example to stabilize the results.

```
. use https://www.stata-press.com/data/r18/auto
(1978 automobile data)
. replace weight = weight/100
variable weight was int now float
(74 real changes made)
. replace length = length/10
variable length was int now float
(74 real changes made)
```

We fit a bivariate normal regression of `mpg` and `weight` on `length`. We specify the extra covariance parameter as a matrix model parameter `{Sigma,m}` in suboption `parameters()` of `llevaluator()`. We specify flat priors for the coefficients and an inverse-Wishart prior for the covariance matrix.

```
. set seed 14
. bayesmh mpg weight = length, llevaluator(mvnregll, parameters({Sigma,m}))
> prior({mpg:} {weight:}, flat)
> prior({Sigma,m}, iwishart(2,12,I(2))) mcmcsize(1000)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg weight ~ mvnregll(xb_mpg,xb_weight,{Sigma,m})
Priors:
     {mpg:length _cons} ~ 1 (flat)                                       (1)
  {weight:length _cons} ~ 1 (flat)                                       (2)
              {Sigma,m} ~ iwishart(2,12,I(2))
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
(2) Parameters are elements of the linear form xb_weight.
Bayesian regression                             MCMC iterations  =      3,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =      1,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .1728
                                                Efficiency:  min =     .02882
                                                             avg =     .05012
Log marginal-likelihood = -415.01504                         max =      .1275
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
mpg						
length	-2.040162	.2009062	.037423	-2.045437	-2.369287	-1.676332
_cons	59.6706	3.816341	.705609	59.63619	52.54652	65.84583
weight						
length	3.31773	.1461644	.026319	3.316183	3.008416	3.598753
_cons	-32.19877	2.79005	.484962	-32.4154	-37.72904	-26.09976
Sigma_1_1	11.49666	1.682975	.149035	11.3523	8.691888	14.92026
Sigma_2_1	-2.33596	1.046729	.153957	-2.238129	-4.414118	-.6414916
Sigma_2_2	5.830413	.9051206	.121931	5.630011	4.383648	8.000739

To reduce computation time, we used a smaller MCMC sample size of 1,000 in our example. In your analysis, you should always verify whether a smaller MCMC sample size results in precise enough estimates before using it for final results.

We can check our results against `bayesmh` using the built-in multivariate normal regression after adjusting the initial values.

```
. set seed 14
. bayesmh mpg weight = length, likelihood(mvnormal({Sigma,m}))
> prior({mpg:} {weight:}, flat)
> prior({Sigma,m}, iwishart(2,12,I(2)))
> mcmcsize(1000) initial({mpg:} {weight:} 0)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg weight ~ mvnormal(2,xb_mpg,xb_weight,{Sigma,m})
Priors:
     {mpg:length _cons} ~ 1 (flat)                                        (1)
  {weight:length _cons} ~ 1 (flat)                                        (2)
              {Sigma,m} ~ iwishart(2,12,I(2))
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
(2) Parameters are elements of the linear form xb_weight.
Bayesian multivariate normal regression          MCMC iterations  =      3,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =      1,000
                                                 Number of obs    =         74
                                                 Acceptance rate  =      .1728
                                                 Efficiency:  min =     .02882
                                                              avg =     .05012
Log marginal-likelihood = -415.01504                          max =      .1275
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
mpg						
length	-2.040162	.2009062	.037423	-2.045437	-2.369287	-1.676332
_cons	59.6706	3.816341	.705609	59.63619	52.54652	65.84583
weight						
length	3.31773	.1461644	.026319	3.316183	3.008416	3.598753
_cons	-32.19877	2.79005	.484962	-32.4154	-37.72904	-26.09976
Sigma_1_1	11.49666	1.682975	.149035	11.3523	8.691888	14.92026
Sigma_2_1	-2.33596	1.046729	.153957	-2.238129	-4.414118	-.6414916
Sigma_2_2	5.830413	.9051206	.121931	5.630011	4.383648	8.000739

We obtain the same results.

Similarly, we can define the log-posterior evaluator. We already have the log-likelihood evaluator, which we can reuse in our log-posterior evaluator. The only additional portion is to compute the log of the inverse-Wishart prior density for the covariance parameter.

```
. program mvniWishart
  1.         version 18.0
  2.         args lnp xb1 xb2
  3.         tempvar diff1 diff2
  4.         quietly generate double `diff1' = $MH_y1 - `xb1' if $MH_touse
  5.         quietly generate double `diff2' = $MH_y2 - `xb2' if $MH_touse
  6.         local d $MH_yn
  7.         local n $MH_n
  8.         mata:
>             st_numscalar("`lnp'", mvniWish_mata(`d',`n',"`diff1'","`diff2'"))
  9. end
.
. mata:
------------------------------------------------- mata (type end to exit) -----
: real scalar mvniWish_mata(real scalar d, n, string scalar sdiff1, sdiff2)
> {
>         real scalar lnf, lnprior
>         real matrix Sigma
>
>         /* compute log likelihood */
>         lnf = mvnll_mata(d,n,sdiff1,sdiff2)
>         /* compute log of inverse-Wishart prior for Sigma */
>         Sigma = st_matrix(st_global("MH_m1"))
>         lnprior = lniwishartden(12,I(2),Sigma)
>         return(lnf + lnprior)
> }
: end
------------------------------------------------------------------------------
```

The results of the log-posterior evaluator match our earlier results.

```
. set seed 14
. bayesmh mpg weight = length, evaluator(mvniWishart, parameters({Sigma,m}))
> mcmcsize(1000)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Posterior:
  mpg weight ~ mvniWishart(xb_mpg,xb_weight,{Sigma,m})
------------------------------------------------------------------------------

Bayesian regression                             MCMC iterations  =      3,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =      1,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .1728
                                                Efficiency:  min =     .02882
                                                             avg =     .05012
Log marginal-likelihood = -415.01504                         max =      .1275

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
      length |  -2.040162   .2009062   .037423  -2.045437  -2.369287  -1.676332
       _cons |    59.6706   3.816341   .705609   59.63619   52.54652   65.84583
-------------+----------------------------------------------------------------
weight       |
      length |   3.31773   .1461644   .026319   3.316183   3.008416   3.598753
       _cons |  -32.19877    2.79005   .484962   -32.4154  -37.72904  -26.09976
-------------+----------------------------------------------------------------
   Sigma_1_1 |   11.49666   1.682975   .149035    11.3523   8.691888   14.92026
   Sigma_2_1 |  -2.33596   1.046729   .153957  -2.238129  -4.414118  -.6414916
   Sigma_2_2 |   5.830413   .9051206   .121931   5.630011   4.383648   8.000739
------------------------------------------------------------------------------
```

Sometimes, it may be useful to be able to pass options to our evaluators. For example, we used the identity `I(2)` matrix as a scale matrix of the inverse Wishart distribution. Suppose that we want to check the sensitivity of our results to other choices of the scale matrix. We can pass the name of a matrix we want to use in an option. In our example, we use the `vmatrix()` option to pass the name of the scale matrix. We later specify this option within suboption `passthruopts()` of the `evaluator()` option. The options passed this way are stored in the `$MH_passthruopts` global macro.

```
. program mvniWishartV
  1.         version 18.0
  2.         args lnp xb1 xb2
  3.         tempvar diff1 diff2
  4.         quietly generate double `diff1' = $MH_y1 - `xb1' if $MH_touse
  5.         quietly generate double `diff2' = $MH_y2 - `xb2' if $MH_touse
  6.         local d $MH_yn
  7.         local n $MH_n
  8.         local 0 , $MH_passthruopts
  9.         syntax, vmatrix(string)
 10.         mata: st_numscalar("`lnp'",
>               mvniWishV_mata(`d',`n',"`diff1'","`diff2'","`vmatrix'"))
 11. end
```

```
. mata:
------------------------------------------------- mata (type end to exit) -----
: real scalar mvniWishV_mata(real scalar d, n, string scalar sdiff1, sdiff2,
> vmat)
> {
>         real scalar lnf, lnprior
>         real matrix Sigma
>
>         /* compute log likelihood */
>         lnf = mvnll_mata(d,n,sdiff1,sdiff2)
>         /* compute log of inverse-Wishart prior for Sigma */
>         Sigma = st_matrix(st_global("MH_m1"))
>         lnprior = lniwishartden(12,st_matrix(vmat),Sigma)
>         return(lnf + lnprior)
> }
: end
--------------------------------------------------------------------------------
```

We now define the scale matrix `V` (as the identity matrix to match our previous results) and specify `vmatrix(V)` in suboption `passthruopts()` of `evaluator()`.

```
. set seed 14
. matrix V = I(2)
. bayesmh mpg weight = length,
> evaluator(mvniWishartV, parameters({Sigma,m}) passthruopts(vmatrix(V)))
> mcmcsize(1000)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Posterior:
  mpg weight ~ mvniWishartV(xb_mpg,xb_weight,{Sigma,m})
------------------------------------------------------------------------------

Bayesian regression                             MCMC iterations  =      3,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =      1,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .1728
                                                Efficiency:  min =     .02882
                                                             avg =     .05012
Log marginal-likelihood = -415.01504                         max =      .1275

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
      length |  -2.040162   .2009062   .037423  -2.045437  -2.369287  -1.676332
       _cons |    59.6706   3.816341   .705609   59.63619   52.54652   65.84583
-------------+----------------------------------------------------------------
weight       |
      length |    3.31773   .1461644   .026319   3.316183   3.008416   3.598753
       _cons |  -32.19877    2.79005   .484962   -32.4154  -37.72904  -26.09976
-------------+----------------------------------------------------------------
   Sigma_1_1 |   11.49666   1.682975   .149035    11.3523   8.691888   14.92026
   Sigma_2_1 |   -2.33596   1.046729   .153957  -2.238129  -4.414118  -.6414916
   Sigma_2_2 |   5.830413   .9051206   .121931   5.630011   4.383648   8.000739
------------------------------------------------------------------------------
```

The results are the same as before.

Cox proportional hazards regression

Some evaluators may require additional variables, apart from the dependent and independent variables, for computation. For example, in a Cox proportional hazards model such variable is a failure or censoring indicator. The `coxphll` program below computes partial log likelihood for the Cox proportional hazards regression. The failure indicator will be passed to the evaluator as an extra variable in suboption `extravars()` of option `llevaluator()` or option `evaluator()` and can be accessed from the global macro `$MH_extravars`.

```
. program coxphll
  1.         version 18.0
  2.         args lnf xb
  3.         tempvar negt
  4.         quietly generate double `negt' = -$MH_y1
  5.         local d "$MH_extravars"
  6.         sort $MH_touse `negt' `d'
  7.         tempvar B A sumd last L
  8.         local byby "by $MH_touse `negt' `d'"
  9.         quietly {
 10.                gen double `B' = sum(exp(`xb')) if $MH_touse
 11.                `byby': gen double `A' = cond(_n==_N, sum(`xb'), .)
>                                         if `d'==1 & $MH_touse
 12.                `byby': gen `sumd' = cond(_n==_N, sum(`d'), .) if $MH_touse
 13.                `byby': gen byte `last' = (_n==_N & `d' == 1) if $MH_touse
 14.                gen double `L' = `A' - `sumd'*ln(`B') if `last' & $MH_touse
 15.                quietly count if $MH_touse & `last'
 16.                local n = r(N)
 17.                summarize `L' if `last' & $MH_touse, meanonly
 18.         }
 19.         if r(N) < `n' {
 20.             scalar `lnf' = .
 21.             exit
 22.         }
 23.         scalar `lnf' = r(sum)
 24. end
```

We demonstrate the command using the survival-time `cancer` dataset. The survival-time variable is `studytime` and the failure indicator is `died`. The regressor of interest in this model is `age`. We use a fairly noninformative normal prior with a zero mean and a variance of 100 for the regression coefficient of `age`. (The constant in the Cox proportional hazards model is not likelihood-identifiable, so we omit it from this model with a noninformative prior.)

```
. use https://www.stata-press.com/data/r18/cancer, clear
(Patient survival in drug trial)
. gsort -studytime died
. set seed 14
. bayesmh studytime age, llevaluator(coxphll, extravars(died))
> prior({studytime:}, normal(0,100)) noconstant mcmcsize(1000)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  studytime ~ coxphll(xb_studytime)
Prior:
  {studytime:age} ~ normal(0,100)                                           (1)
------------------------------------------------------------------------------
(1) Parameter is an element of the linear form xb_studytime.
```

```
Bayesian regression                               MCMC iterations  =      3,500
Random-walk Metropolis-Hastings sampling          Burn-in          =      2,500
                                                  MCMC sample size =      1,000
                                                  Number of obs    =         48
                                                  Acceptance rate  =      .4066
Log marginal-likelihood = -103.04797              Efficiency       =      .3568

------------------------------------------------------------------------------
             |                                                 Equal-tailed
   studytime |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
         age |    .076705   .0330669   .001751   .077936   .0099328   .1454275
------------------------------------------------------------------------------
```

We specified the failure indicator `died` in suboption `extravars()` of `llevaluator()`. We again used a smaller value for the MCMC sample size only to reduce computation time.

For the log-posterior evaluator, we add the log of the normal prior of the `age` coefficient to the log-likelihood value to obtain the final log-posterior value. We did not need to specify the loop in the log-prior computation in this example, but we did this to be general, in case more than one regressor is included in the model.

```
. program coxphnormal
  1.         version 18.0
  2.         args lnp xb
.         /* compute log likelihood */
.         tempname lnf
  3.         scalar `lnf' = .
  4.         quietly coxphll `lnf' `xb'
.         /* compute log priors of regression coefficients */
.         tempname lnprior
  5.         scalar `lnprior' = 0
  6.         forvalues i = 1/$MH_bn {
  7.             scalar `lnprior' = `lnprior' + lnnormalden($MH_b[1,`i'], 10)
  8.         }
  9.         /* compute log posterior */
.         scalar `lnp' = `lnf' + `lnprior'
 10. end
```

As expected, we obtain the same results as previously.

```
. set seed 14
. bayesmh studytime age, evaluator(coxphnormal, extravars(died))
> noconstant mcmcsize(1000)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Posterior:
  studytime ~ coxphnormal(xb_studytime)
------------------------------------------------------------------------------

Bayesian regression                               MCMC iterations  =      3,500
Random-walk Metropolis-Hastings sampling          Burn-in          =      2,500
                                                  MCMC sample size =      1,000
                                                  Number of obs    =         48
                                                  Acceptance rate  =      .4066
Log marginal-likelihood = -103.04797              Efficiency       =      .3568

------------------------------------------------------------------------------
             |                                                 Equal-tailed
   studytime |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
         age |    .076705   .0330669   .001751   .077936   .0099328   .1454275
------------------------------------------------------------------------------
```

Global macros

Global macros	Description
`$MH_n`	number of observations
`$MH_yn`	number of dependent variables
`$MH_touse`	variable containing 1 for the observations to be used; 0 otherwise
`$MH_w`	variable containing weight associated with the observations
`$MH_extravars`	*varlist* specified in `extravars()`
`$MH_passthruopts`	options specified in `passthruopts()`
One outcome	
`$MH_y1`	name of the dependent variable
`$MH_x1`	name of the first independent variable
`$MH_x2`	name of the second independent variable
...	
`$MH_xn`	number of independent variables
`$MH_xb`	name of a temporary variable containing the linear combination
Multiple outcomes	
`$MH_y1`	name of the first dependent variable
`$MH_y2`	name of the second dependent variable
...	
`$MH_y1x1`	name of the first independent variable modeling `y1`
`$MH_y1x2`	name of the second independent variable modeling `y1`
...	
`$MH_y1xn`	number of independent variables modeling `y1`
`$MH_y1xb`	name of a temporary variable containing the linear combination modeling `y1`
`$MH_y2x1`	name of the first independent variable modeling `y2`
`$MH_y2x2`	name of the second independent variable modeling `y2`
...	
`$MH_y2xn`	number of independent variables modeling `y2`
`$MH_y2xb`	name of a temporary variable containing the linear combination modeling `y2`
...	
Scalar and matrix parameters	
`$MH_b`	name of a temporary vector of coefficients; stripes are properly named after the name of the coefficients
`$MH_bn`	number of coefficients
`$MH_p`	name of a temporary vector of additional scalar model parameters, if any; stripes are properly named
`$MH_pn`	number of additional scalar model parameters
`$MH_m1`	name of a temporary matrix of the first matrix parameter, if any
`$MH_m2`	name of a temporary matrix of the second matrix parameter, if any
...	
`$MH_mn`	number of matrix model parameters

Stored results

In addition to the results stored by `bayesmh`, `bayesmh, evaluator()` and `bayesmh, llevaluator()` store the following in `e()`:

Macros

`e(evaluator)`	program evaluator (one equation)
`e(evaluator#)`	program evaluator for the #th equation
`e(evalparams)`	evaluator parameters (one equation)
`e(evalparams#)`	evaluator parameters for the #th equation
`e(extravars)`	extra variables (one equation)
`e(extravars#)`	extra variables for the #th equation
`e(passthruopts)`	pass-through options (one equation)
`e(passthruopts#)`	pass-through options for the #th equation

Reference

Marchenko, Y. V. 2015. Bayesian modeling: Beyond Stata's built-in models. *The Stata Blog: Not Elsewhere Classified.* http://blog.stata.com/2015/05/26/bayesian-modeling-beyond-statas-built-in-models/.

Also see

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

Bayesian postestimation — Postestimation tools for bayesmh and the bayes prefix

Postestimation commands Remarks and examples Also see

Postestimation commands

The following Bayesian postestimation commands are available after the `bayesmh` command ([BAYES] **bayesmh**) and the `bayes` prefix ([BAYES] **bayes**):

Command	Description
`bayesgraph`	graphical summaries and convergence diagnostics
`bayesstats grubin`	Gelman–Rubin convergence diagnostics
`bayesstats ess`	effective sample sizes and related statistics
† `bayesstats ppvalues`	Bayesian predictive p-values
`bayesstats summary`	Bayesian summary statistics for model parameters and their functions
`bayesstats ic`	Bayesian information criteria and Bayes factors
`bayestest model`	hypothesis testing using model posterior probabilities
`bayestest interval`	interval hypothesis testing
† `bayespredict`	Bayesian predictions
* `estimates`	cataloging estimation results

† `bayesstats ppvalues` and `bayespredict` are available only after `bayesmh`, `bayes: var`, `bayes: xtreg`, `bayes: xtlogit`, `bayes: xtprobit`, `bayes: xtologit`, `bayes: xtoprobit`, `bayes: xtpoisson`, `bayes: xtnbreg`, or `bayes: xtmlogit`.

* `estimates table` and `estimates stats` are not appropriate with `bayesmh` and `bayes:` estimation results.

The following postestimation commands are available after `bayes: var`:

Command	Description
`bayesfcast`	Bayesian dynamic forecasts
`bayesirf`	Bayesian impulse–response functions, dynamic-multiplier functions, and FEVDs
`bayesvarstable`	check stability condition of estimates

See [BAYES] **bayes: var postestimation**.

The following postestimation command is available after `bayes: dsge` and `bayes: dsgenl`:

Command	Description
`bayesirf`	Bayesian impulse–response functions

See [BAYES] **bayes: dsge postestimation**.

Remarks and examples

Remarks are presented under the following headings:

After estimation, you can use `bayesgraph` to check convergence of MCMC visually. If you simulated multiple chains, you can use `bayesstats grubin` to compute Gelman–Rubin convergence diagnostics. Once convergence is established, you can use `bayespredict` and `bayesstats ppvalues` to perform model checking after `bayesmh`. Once you are satisfied with the model, you can use `bayesstats summary` to obtain Bayesian summaries such as posterior means and standard deviations of model parameters and functions of model parameters; `bayesstats ess` to compute effective sample sizes and related statistics for model parameters and functions of model parameters; and `bayesstats ic` to compute Bayesian information criteria and Bayes factors for model parameters and their functions. You can use `bayestest model` to test hypotheses by comparing posterior probabilities of models. You can also use `bayestest interval` to test interval hypotheses about parameters and functions of parameters. After `bayesmh`, you can also use `bayespredict` to predict future outcome values.

For an overview example of postestimation commands, see *Overview example* in [BAYES] **Bayesian commands**.

Different ways of specifying model parameters

Many Bayesian postestimation commands such as `bayesstats summary` and `bayesgraph` allow you to specify model parameters for which you want to see the results. To see results for all parameters, simply type a postestimation command without arguments after estimation using `bayesmh` or the `bayes` prefix, for example,

```
. bayesstats summary
```

or you could type

```
. bayesstats summary _all
```

To manually list all model parameters, type

```
. bayesstats summary {param1} {param2} ...
```

or

```
. bayesstats summary {param1 param2} ...
```

The only exception is the `bayesgraph` command when there is more than one model parameter. In that case, `bayesgraph` requires that you either specify `_all` to request all model parameters or specify the model parameters of interest.

You can refer to a single model parameter in the same way you define parameters in, say, the `bayesmh` command. For example, for a parameter with name `param` and no equation name, you can use `{param}`. For a parameter with name `param` and equation name `eqname`, you can use its full name `{eqname:name}`, where the equation name and the parameter name are separated with a colon. With postestimation commands, you can also omit the equation name when referring to the parameter with an equation name.

In the presence of more than one model parameter, you have several ways for referring to multiple parameters at once. If parameters have the same equation name, you can refer to all the parameters with that equation name as follows.

Suppose that you have three parameters with the same equation name `eqname`. Then the specification

```
. bayesstats summary {eqname:param1} {eqname:param2} {eqname:param3}
```

is the same as the specification

```
. bayesstats summary {eqname:}
```

or the specification

```
. bayesstats summary {eqname:param1 param2 param3}
```

The above specification is useful if we want to refer to a subset of parameters with the same equation name. For example, in the above, if we wanted to use only `param1` and `param2`, we could type

```
. bayesstats summary {eqname:param1 param2}
```

There is also a convenient way to refer to the parameters with the same name but different equation names. For example, typing

```
. bayesstats summary {eqname1:param} {eqname2:param}
```

is the same as simply typing

```
. bayesstats summary {param}
```

You can mix and match all the specifications above in one call to a postestimation command. You can also specify expressions of model parameters; see *Specifying functions of model parameters* for details.

Note that if `param` refers to a matrix model parameter, then the results will be provided for all elements of the matrix. For example, if `param` is the name of a 2×2 matrix, then typing

```
. bayesstats summary {param}
```

implies the following:

```
. bayesstats summary {param_1_1} {param_1_2} {param_2_1} {param_2_2}
```

For multilevel models, there are various ways, *reref*, in which you can refer to individual random-effects parameters. Suppose that your model has random intercepts at the `id` level, which are labeled as `{U0[id]}` or `{U0}` for short. To refer to all random intercepts, you can use `{U0}`, `{U0[.]}`, and `{U0[id]}`. To refer to specific random intercepts, you can use `{U0[#]}`, where # refers to the #th element of the random-effects vector, or use `{U0[#.id]}`, where # refers to the #th level of the `id` variable. You can also refer to a subset *numlist* of random intercepts by using `{U0[`*numlist*`]}` or `{U0[(`*numlist*`).id]}`. For nested random effects, for example, `{UU0[id1>id2]}`, you can refer to all random effects as `{UU0}` or `{UU0[.,.]}` and to subsets of random effects as `{UU0[`*numlist*`,`*numlist*`]}` or `{UU0[(`*numlist*`).id1,(`*numlist*`).id2]}`.

Specifying functions of model parameters

You can use Bayesian postestimation commands to obtain results for functions or expressions of model parameters. Each expression must be specified in parentheses. An expression can be any Stata expression, but it may not include matrix model parameters. However, you may include individual elements of matrix model parameters. You may provide labels for your expressions.

For example, we can obtain results for the exponentiated parameter `{param}` as follows:

```
. bayesstats summary (exp({param}))
```

Note that we specified the expression in parentheses.

We can include a label, say, myexp, in the above by typing

```
. bayesstats summary (myexp: exp({param}))
```

We can specify multiple expressions by typing

```
. bayesstats summary (myexp: exp({param}) (sd: sqrt({var})))
```

If param is a matrix, we can specify expressions, including its elements, but not the matrix itself in the following:

```
. bayesstats summary (exp({param_1_1})) (exp({param_1_2})) ...
```

Storing estimation results after Bayesian estimation

The bayesmh command and the bayes prefix store various e() results such as scalars, macros, and matrices in memory like any other estimation command. Unlike other estimation commands, these commands also save the resulting simulation dataset containing MCMC samples of parameters to disk. Many Bayesian postestimation commands such as bayesstats summary and bayesstats ess require access to this file. If you do not specify the saving() option with bayesmh or the bayes prefix, the commands save simulation results in a temporary Stata dataset. This file is being replaced with the new simulation results each time bayesmh or the bayes prefix is run. To save your simulation results, you must specify the saving() option with bayesmh or the bayes prefix, in which case your simulation results are saved to the specified file in the specified location and will not be overridden by the next call to these commands.

You can specify the saving() option during estimation by typing

```
. bayesmh ..., likelihood() prior() ... saving()
```

or

```
. bayes, saving(): ...
```

or on replay by typing

```
. bayesmh, saving()
```

or

```
. bayes, saving()
```

As you can with other estimation commands, you can use estimates store to store Bayesian estimation results in memory and estimates save to save them to disk, but you must first use the saving() option with bayesmh or the bayes prefix to save simulation data in a permanent dataset. For example, type

```
. bayesmh ..., likelihood() prior() ... saving(bmh_simdata)
. estimates store model1
```

or, after bayesmh estimation, type

```
. bayesmh, saving(bmh_simdata)
. estimates store model1
```

Once you create a permanent dataset, it is your responsibility to erase it after it is no longer needed. estimates drop and estimates clear will drop estimation results only from memory; they will not erase the simulation files you saved.

```
. estimates drop model1
. erase bmh_simdata.dta
```

See [R] **estimates** for more information about commands managing estimation results. estimates table and estimates stats are not appropriate after bayesmh and the bayes prefix.

Different ways of specifying predictions and their functions

After bayesmh (except for survival models), you can use the bayespredict command to simulate outcome variables, residuals, and other test quantities; see [BAYES] **bayespredict**. Bayesian postestimation commands bayesgraph, bayesstats summary, bayesstats ppvalues, bayesstats ess, and bayestest interval can then be used to obtain graphs, posterior summaries, and so on for these prediction quantities.

In this section, we describe various specifications of prediction results with Bayesian postestimation commands mentioned above. We use bayesstats summary in our examples, but the same specifications may be used with other postestimation commands, except that bayestest interval allows only specifications containing individual observations.

Suppose that we use the bayesmh command to fit a model with two outcome variables.

```
. bayesmh y1 y2 = x1 x2, ... saving(mcmcfile)
```

We then use bayespredict to simulate samples for these two outcome variables and save them in a prediction dataset, predfile.dta.

```
. bayespredict {_ysim1} {_ysim2}, saving(predfile)
```

To access prediction results, all postestimation commands must specify the prediction dataset in the using specification. In fact, this is all postestimation commands need to produce results for the prediction quantities. (Technically, the auxiliary estimation file generated by bayespredict, for example, predfile.ster, must also exist.) That is, they do not rely on the estimation results or the simulation data from bayesmh.

When the prediction dataset contains simulated outcomes, in addition to accessing these outcomes (for instance, {_ysim1} and {_ysim2} in our example), postestimation commands may also access the residuals ({_resid1} and {_resid2}), expected values ({_mu1} and {_mu2}), and Stata expressions of simulated outcomes, residuals, and expected values. You can also call Mata functions within command specifications to compute functions of simulated outcomes, residuals, and expected values.

Let's calculate posterior summaries for all observations of the first outcome and for all residuals of the second outcome.

```
. bayesstats summary {_ysim1} {_resid2} using predfile
```

You can refer to a subset of predicted observations, say, from 1 to 10 for the observations and from 1 to 5 for the residuals.

```
. bayesstats summary {_ysim1[1/10]} {_resid2[1/5]} using predfile
```

You can compute expressions of individual simulated outcome observations and their residuals.

```
. bayesstats summary (exp({_ysim1[1]})) ({_resid2[1]}^2) using predfile
```

You can test whether the residual for the first observation of the second outcome variable is greater than zero by using bayestest interval to calculate the corresponding posterior probability.

```
. bayestest interval {_resid2[1]} using predfile, lower(0)
```

As we mentioned earlier, you can use Mata functions of predicted outcomes and residuals. These functions operate across observations. For example, to summarize the mean of the first simulated outcome and the variance of the second simulated outcome, type

```
. bayesstats summary (@mean({_ysim1})) (@variance({_ysim2})) using predfile
```

Instead of using the default labels for the computed quantities, you can specify your own. Below, we use `mean` and `var` to label the corresponding predictions.

```
. bayesstats summary (mean:@mean({_ysim1})) (var:@variance({_ysim2})) using predfile
```

You cannot specify Mata functions with `bayestest interval`, and, unlike `bayespredict`, you cannot specify Stata programs within the postestimation commands.

If you need to access individual values of the predicted quantity computed using a Mata function or specify an expression of this quantity, you need to compute and save this quantity with `bayespredict`.

Suppose that you wish to compute the sum of the two outcome variances. You simulate these variances by using `bayespredict` first.

```
. bayespredict (prvar1:@variance({_ysim1})) (prvar2:@variance({_ysim2})),  ///
        saving(predfile)
```

In the above, we labeled the computed variances as `prvar1` and `prvar2`.

Then, you can call `bayesstats summary` to compute the sum of the predicted quantities.

```
. bayesstats summary ({prvar1} + {prvar2}) using predfile
```

Or you can obtain summaries of each predicted quantity.

```
. bayesstats summary {prvar1} {prvar2} using predfile
```

You can combine various specifications in one call to the postestimation command. For example, let's save the following prediction quantities with `bayespredict`.

```
. bayespredict {_ysim1} {_ysim2} (mean1:@mean({_ysim1}))  ///
        (var2:@variance({_ysim2})), saving(predfile)
```

You can specify multiple prediction quantities in one call to `bayesstats summary` or other postestimation commands.

```
. bayesstats summary ({_ysim1}) ({_resid[1/5]}) ({mean1})    ///
        ({var2}) (mean2:@mean({_ysim2})) using predfile
```

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

[BAYES] **bayesmh evaluators** — User-defined evaluators with bayesmh

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

[U] **20 Estimation and postestimation commands**

Title

bayesgraph — Graphical summaries and convergence diagnostics

Description

`bayesgraph` provides graphical summaries and convergence diagnostics for simulated posterior distributions (MCMC samples) of model parameters and functions of model parameters obtained after Bayesian estimation. Graphical summaries include trace plots, autocorrelation plots, and various distributional plots.

Quick start

Trace plot, histogram, autocorrelation plot, and density plot for parameter {p}

```
bayesgraph diagnostics {p}
```

Add plots for parameter {y:x1}

```
bayesgraph diagnostics {p} {y:x1}
```

Same as above, but for all model parameters

```
bayesgraph diagnostics _all
```

Same as above, but for a function of model parameters {y:x1} and {p}

```
bayesgraph diagnostics ({y:x1}/{p})
```

Specify a blue trace plot line for all plots

```
bayesgraph diagnostics {p} {y:x1} {y:x2}, traceopts(lcolor(blue))
```

Specify a blue trace plot line only for the second trace plot

```
bayesgraph diagnostics {p} {y:x1} {y:x2}, trace2opts(lcolor(blue))
```

Trace plots for all parameters in a single graph

```
bayesgraph trace _all, byparm
```

Cumulative sum plot for parameter {p}

```
bayesgraph cusum {p}
```

Scatterplot matrix for parameters {p} and {y:x1}

```
bayesgraph matrix {p} {y:x1}
```

Autocorrelation plots for elements 1,1 and 2,1 of matrix parameter {S}

```
bayesgraph ac {S_1_1} {S_2_1}
```

Diagnostic plots for all parameters in the model and pause at least 3 seconds before displaying the next graph

```
bayesgraph diagnostics _all, sleep(3)
```

Same as above, but pause until the user presses any key

```
bayesgraph diagnostics _all, wait
```

Same as above, but close the current Graph window when the next graph is displayed

```
bayesgraph diagnostics _all, close
```

Histogram of the first 10 observations of the first simulated outcome plotted on one graph

```
bayespredict {_ysim}, saving(predres)
bayesgraph histogram {_ysim[1/10]} using predres, byparm
```

Density plot of the mean across observations of the simulated outcome labeled as `mymean`

```
bayesgraph kdensity (mymean: @mean({_ysim})) using predres
```

Menu

Statistics > Bayesian analysis > Graphical summaries

Syntax

Syntax is presented under the following headings:

Graphical summaries for model parameters
Graphical summaries for predictions

Graphical summaries for model parameters

Graphical summaries and convergence diagnostics for a single parameter

`bayesgraph` *graph scalar_param* [`,` *singleopts*]

Graphical summaries and convergence diagnostics for multiple parameters

`bayesgraph` *graph spec* [*spec* ...] [`,` *multiopts*]

`bayesgraph matrix` *spec spec* [*spec* ...] [`,` *singleopts*]

Graphical summaries and convergence diagnostics for all parameters

`bayesgraph` *graph* `_all` [`,` *multiopts* `showreffects` [`(`*reref*`)`]]

scalar_param is a scalar model parameter specified as `{param}` or `{eqname:param}` or an expression *exprspec* of scalar model parameters. Matrix model parameters are not allowed, but you may refer to their individual elements.

exprspec is an optionally labeled expression of model parameters specified in parentheses:

`(` [*exprlabel* `:`] *expr*`)`

exprlabel is a valid Stata name, and *expr* is a scalar expression that may not contain matrix model parameters. See *Specifying functions of model parameters* in [BAYES] **Bayesian postestimation** for examples.

spec is either *scalar_param* or *exprspec*.

Graphical summaries for predictions

Graphical summaries for an individual prediction

```
bayesgraph graph predspecsc using predfile [ , singleopts ]
```

Graphical summaries for multiple predictions

```
bayesgraph graph predspec [predspec ...] using predfile [ , multiopts ]
```

```
bayesgraph matrix predspec predspec [predspec ...] using predfile [ , singleopts ]
```

predfile is the name of the dataset created by `bayespredict` that contains prediction results.

predspecsc may contain individual observations of simulated outcomes, `{_ysim#[#]}`; individual expected outcome values, `{_mu#[#]}`; individual simulated residuals, `{_resid#[#]}`; and other scalar predictions, {*label*}.

predspec is one of *yspec*, (*yexprspec*), or (*funcspec*). See *Different ways of specifying predictions and their functions* in [BAYES] **Bayesian postestimation**.

yspec is {*ysimspec* | *residspec* | *muspec* | *label*}.

ysimspec is `{_ysim#}` or `{_ysim#[`*numlist*`]}`, where `{_ysim#}` refers to all observations of the #th simulated outcome and `{_ysim#[`*numlist*`]}` refers to the selected observations, *numlist*, of the #th simulated outcome. `{_ysim}` is a synonym for `{_ysim1}`.

residspec is `{_resid#}` or `{_resid#[`*numlist*`]}`, where `{_resid#}` refers to all residuals of the #th simulated outcome and `{_resid#[`*numlist*`]}` refers to the selected residuals, *numlist*, of the #th simulated outcome. `{_resid}` is a synonym for `{_resid1}`.

muspec is `{_mu#}` or `{_mu#[`*numlist*`]}`, where `{_mu#}` refers to all expected values of the #th outcome and `{_mu#[`*numlist*`]}` refers to the selected expected values, *numlist*, of the #th outcome. `{_mu}` is a synonym for `{_mu1}`.

label is the name of the function simulated using `bayespredict`.

With large datasets, specifications `{_ysim#}`, `{_resid#}`, and `{_mu#}` may use a lot of time and memory and should be avoided. See *Generating and saving simulated outcomes* in [BAYES] **bayespredict**.

yexprspec is [*exprlabel*`:`]*yexpr*, where *exprlabel* is a valid Stata name and *yexpr* is a scalar expression that may contain individual observations of simulated outcomes, `{_ysim#[#]}`; individual expected outcome values, `{_mu#[#]}`; individual simulated residuals, `{_resid#[#]}`; and other scalar predictions, {*label*}.

funcspec is [*label*`:`]`@`*func*`(`*arg1*[`,` *arg2*]`)`, where *label* is a valid Stata name; *func* is an official or user-defined Mata function that operates on column vectors and returns a real scalar; and *arg1* and *arg2* are one of `{_ysim[#]}`, `{_resid[#]}`, or `{_mu[#]}`. *arg2* is primarily for use with user-defined Mata functions; see *Defining test statistics using Mata functions* in [BAYES] **bayespredict**.

graph	Description
diagnostics	multiple diagnostics in compact form
trace	trace plots
ac	autocorrelation plots
histogram	histograms
kdensity	density plots
cusum	cumulative sum plots
matrix	scatterplot matrix

bayesgraph matrix requires at least two parameters. diagnostics, trace, ac, and cusum are not relevant for predictions.

singleopts	Description
Chains	
chainopts	options controlling multiple chains
Options	
skip(#)	skip every # observations from the MCMC sample; default is skip(0)
name(*name*, ...)	specify name of graph
saving(*filename*, ...)	save graph in file
graphopts	graph-specific options

multiopts	Description
Chains	
chainopts	options controlling multiple chains
Options	
byparm[(*grbyparmopts*)]	specify the display of plots on one graph; default is separate graph for each plot; not allowed with graphs diagnostics and matrix or with options combine() and bychain()
combine[(*grcombineopts*)]	specify the display of plots on one graph; recommended when the number of parameters is large; not allowed with graphs diagnostics and matrix or with options byparm() and bychain()
sleep(#)	pause for # seconds between multiple graphs; default is sleep(0)
wait	pause until the —more— condition is cleared
[no]close	(do not) close Graph windows when the next graph is displayed with multiple graphs; default is noclose
skip(#)	skip every # observations from the MCMC sample; default is skip(0)
name(*namespec*, ...)	specify names of graphs
saving(*filespec*, ...)	save graphs in files
graphopts(*graphopts*)	control the look of all graphs; not allowed with byparm()
graph#opts(*graphopts*)	control the look of #th graph; not allowed with byparm()
graphopts	equivalent to graphopts(*graphopts*); only one may be specified

chainopts	Description
`chains(_all | `*numlist*`)`	specify which chains to plot; default is to plot the first 10 chains
`sepchains`	draw a separate graph for each chain; default is to overlay chains
`chainslegend`	show legend keys corresponding to chain numbers; not allowed with graphs `diagnostics` and `matrix` or with options `combine()` and `byparm()`
`bychain[ (`*grbychainopts*`) ]`	plot each chain as a subgraph on one graph; default is all chains overlayed on one graph; not allowed with graphs `diagnostics` and `matrix` or with options `combine()` and `byparm()`
`chainopts(`*graphopts*`)`	control the look of all chains
`chain#opts(`*graphopts*`)`	control the look of #th chain

Options *chainopts* are relevant only when option `nchains()` is used with `bayesmh` or the `bayes` prefix.

graphopts	Description
diagnosticsopts	options for `bayesgraph diagnostics`
tslineopts	options for `bayesgraph trace` and `bayesgraph cusum`
acopts	options for `bayesgraph ac`
histopts	options for `bayesgraph histogram`
kdensityopts	options for `bayesgraph kdensity`
grmatrixopts	options for `bayesgraph matrix`

diagnosticsopts	Description
`traceopts(`*tslineopts*`)`	affect rendition of all trace plots
`trace#opts(`*tslineopts*`)`	affect rendition of #th trace plot
`acopts(`*acopts*`)`	affect rendition of all autocorrelation plots
`ac#opts(`*acopts*`)`	affect rendition of #th autocorrelation plot
`histopts(`*histopts*`)`	affect rendition of all histogram plots
`hist#opts(`*histopts*`)`	affect rendition of #th histogram plot
`kdensopts(`*kdensityopts*`)`	affect rendition of all density plots
`kdens#opts(`*kdensityopts*`)`	affect rendition of #th density plot
grcombineopts	any option documented in [G-2] **graph combine**

acopts	Description
`ci`	plot autocorrelations with confidence intervals; not allowed with `byparm()`
acopts	any options other than `generate()` documented for the `ac` command in [TS] **corrgram**

kdensityopts	Description
kdensopts	options for the overall kernel density plot
`show(`*showspec*`)`	show first-half density (`first`), second-half density (`second`), `both`, or `none`; default varies
`kdensfirst(`*kdens1opts*`)`	affect rendition of the first-half density plot
`kdenssecond(`*kdens2opts*`)`	affect rendition of the second-half density plot

Options

Chains

`chains(_all` | *numlist*`)` specifies which chains from the MCMC sample to plot. The default is to plot the first 10 chains. You can use `chains(_all)` to plot all chains.

`sepchains` specifies that a separate graph be drawn for each chain. This option is implied for `bayesgraph matrix` and may not be combined with `bychain()`.

`chainslegend` specifies that the graph be plotted with a legend showing keys corresponding to chain numbers. This option is not allowed with graphs `diagnostics` and `matrix` or with options `combine()` and `byparm()`.

`bychain`[`(`*grbychainopts*`)`] specifies that each chain be plotted as a subgraph on one graph. By default, all chains are displayed overlayed on one graph. This option is not allowed with graphs `diagnostics` and `matrix` or with options `combine()`, `byparm()`, and `sepchains`.

grbychainopts is any of the suboptions of `by()` documented in [G-3] ***by_option***.

`chainopts(`*graphopts*`)` and `chain#opts(`*graphopts*`)` control the look of chains. `chainopts()` controls the look of all chains but may be overridden for specific chains by using the `chain#opts()` option.

Chain-specific options are ignored if option `nchains()` is not specified with `bayesmh` or the `bayes` prefix.

Options

`byparm`[`(`*grbyparmopts*`)`] specifies the display of all plots of parameters as subgraphs on one graph. By default, a separate graph is produced for each plot when multiple parameters are specified. This option is not allowed with `bayesgraph diagnostics` or `bayesgraph matrix` and may not be combined with options `combine()` and `bychain()`. When many parameters or expressions are specified, this option may fail because of memory constraints. In that case, you may use option `combine()` instead.

grbyparmopts is any of the suboptions of `by()` documented in [G-3] ***by_option***.

`byparm()` allows y scales to differ for all graph types and forces x scales to be the same only for `bayesgraph trace` and `bayesgraph cusum`. Use `noyrescale` within `byparm()` to specify a common y axis, and use `xrescale` or `noxrescale` to change the default behavior for the x axis.

`byparm()` with `bayesgraph trace` and `bayesgraph cusum` defaults to displaying multiple plots in one column to accommodate the x axis with many iterations. Use `norowcoldefault` within `byparm()` to switch back to the default behavior of options `rows()` and `cols()` of the [G-3] ***by_option***.

`combine`[(*grcombineopts*)] specifies the display of all plots of parameters as subgraphs on one graph and is an alternative to `byparm()` with a large number of parameters. By default, a separate graph is produced for each plot when multiple parameters are specified. This option is not allowed with `bayesgraph diagnostics` or `bayesgraph matrix` and may not be combined with option `byparm()`. It can be used in cases where a large number of parameters or expressions are specified and the `byparm()` option would cause an error because of memory constraints.

grcombineopts is any of the options documented in [G-2] **graph combine**.

`sleep(#)` specifies pausing for # seconds before producing the next graph. This option is allowed only when multiple parameters are specified. This option may not be combined with `wait`, `combine()`, or `byparm()`.

`wait` causes `bayesgraph` to display —`more`— and pause until any key is pressed before producing the next graph. This option is allowed when multiple parameters are specified. This option may not be combined with `sleep()`, `combine()`, or `byparm()`. `wait` temporarily ignores the global setting that is specified using `set more off`.

[`no`]`close` specifies that, for multiple graphs, the Graph window be closed when the next graph is displayed. The default is `noclose` or to not close any Graph windows.

`skip(#)` specifies that every # observations from the MCMC sample not be used for computation. The default is `skip(0)` or to use all observations in the MCMC sample. Option `skip()` can be used to subsample or thin the chain. `skip(#)` is equivalent to a thinning interval of #+1. For example, if you specify `skip(1)`, corresponding to the thinning interval of 2, the command will skip every other observation in the sample and will use only observations 1, 3, 5, and so on in the computation. If you specify `skip(2)`, corresponding to the thinning interval of 3, the command will skip every 2 observations in the sample and will use only observations 1, 4, 7, and so on in the computation. `skip()` does not thin the chain in the sense of physically removing observations from the sample, as is done by, for example, `bayesmh`'s `thinning()` option. It only discards selected observations from the computation and leaves the original sample unmodified.

`name(`*namespec*[`, replace`]`)` specifies the name of the graph or multiple graphs. See [G-3] ***name_option*** for a single graph. If multiple graphs are produced, then the argument of `name()` is either a list of names or a *stub*, in which case graphs are named *stub*`1`, *stub*`2`, and so on. With multiple graphs, if `name()` is not specified and neither `sleep()` nor `wait` is specified, `name(Graph__#, replace)` is assumed, and thus the produced graphs may be replaced by subsequent `bayesgraph` commands.

The `replace` suboption causes existing graphs with the specified name or names to be replaced.

`saving(`*filespec*[`, replace`]`)` specifies the filename or filenames to use to save the graph or multiple graphs to disk. See [G-3] ***saving_option*** for a single graph. If multiple graphs are produced, then the argument of `saving()` is either a list of filenames or a *stub*, in which case graphs are saved with filenames *stub*`1`, *stub*`2`, and so on.

The `replace` suboption specifies that the file (or files) may be replaced if it already exists.

`showreffects` and `showreffects(`*reref*`)` are for use after multilevel models, and they specify that the results for all or a list *reref* of random-effects parameters be provided in addition to other model parameters. By default, all random-effects parameters are excluded from the results to conserve computation time.

`graphopts(`*graphopts*`)` and `graph#opts(`*graphopts*`)` affect the rendition of graphs. `graphopts()` affects the rendition of all graphs but may be overridden for specific graphs by using the `graph#opts()` option. The options specified within `graph#opts()` are specific for each type of graph.

The two specifications

```
bayesgraph ..., graphopts(graphopts)
```

and

```
bayesgraph ..., graphopts
```

are equivalent, but you may specify one or the other.

These options are not allowed with `byparm()` and when only one parameter is specified.

graphopts specifies options specific to each graph type.

diagnosticsopts specifies options for use with `bayesgraph diagnostics`. See the corresponding table in the syntax diagram for a list of options.

tslineopts specifies options for use with `bayesgraph trace` and `bayesgraph cusum`. See the options of [TS] **tsline** except `by()`.

acopts specifies options for use with `bayesgraph ac`.

`ci` requests that the graph of autocorrelations with confidence intervals be plotted. By default, confidence intervals are not plotted. This option is not allowed with `byparm()`.

acopts specifies any options except `generate()` of the `ac` command in [TS] **corrgram**.

histopts specifies options for use with `bayesgraph histogram`. See options of [R] **histogram** except `by()`.

kdensityopts specifies options for use with `bayesgraph kdensity`.

kdensopts specifies options for the overall kernel density plot. See the options documented in [R] **kdensity** except `generate()` and `at()`.

`show(`*showspec*`)` specifies which kernel density curves to plot. *showspec* is one of `first`, `second`, `both`, or `none`. If `show(first)` is specified, only the first-half density curve, obtained from the first half of an MCMC sample, is plotted. If `show(second)` is specified, only the second-half density curve, obtained from the second half of an MCMC sample, is plotted. `show(both)`, the default with graph `diagnostics`, overlays both the first-half density curve and the second-half density curve with the overall kernel density curve. `show(none)`, the default with graph `kdensity`, shows only the overall kernel density curve.

`kdensfirst(`*kdens1opts*`)` specifies options of [G-2] **graph twoway kdensity** except `by()` to affect rendition of the first-half kernel density plot.

`kdenssecond(`*kdens2opts*`)` specifies options of [G-2] **graph twoway kdensity** except `by()` to affect rendition of the second-half kernel density plot.

grmatrixopts specifies options for use with `bayesgraph matrix`. See the options of [G-2] **graph matrix** except `by()`.

Remarks and examples

Remarks are presented under the following headings:

Using bayesgraph

`bayesgraph` requires specifying at least one parameter with all graph types except matrix, which requires at least two parameters. To request graphs for all parameters, use `_all`.

When multiple graphs are produced, they are automatically stored in memory with names `Graph__#` and will all appear on the screen. After you are done reviewing the graphs, you can type

```
. graph close Graph__*
```

to close these graphs or type

```
. graph drop Graph__*
```

to close the graphs and drop them from memory.

If you would like to see only one graph at a time, you can specify option `close` to close the Graph window when the next graph is displayed. You can also use option `sleep()` or option `wait` to pause between the subsequent graphs. The `sleep(#)` option causes each graph to pause for # seconds. The `wait` option causes `bayesgraph` to wait until a key is pressed before producing the next graph.

You can combine separate graphs into one by specifying one of `byparm()` or `combine()`. These options are not allowed with diagnostics or matrix graphs. The `byparm()` option produces more compact graphs, but it may not be feasible with many parameters or expressions and large sizes of MCMC samples.

With multiple graphs, you can control the look of each individual graph with `graph#opts()`. Options common to all graphs may be specified in `graphopts()` or passed directly to the command as with single graphs.

With multiple chains, `bayesgraph` plots only the first 10 chains by default. If you have more than 10 chains, although only four chains are commonly used in practice, you can use the `chains(_all)` option to plot all the chains. You can also use the `chains()` option to handpick the chains you want to be plotted. For example, `chains(1/3 5)` will plot chains 1, 2, 3, and 5. If desired, you can see which plot corresponds to which chain by using the `chainslegend` option.

By default, the chains will be plotted overlaid on one graph. You can specify the `sepchains` option to plot each chain on a separate graph, in which case the graphs will be automatically stored in memory with names `Graph__#` and will all appear on the screen. Or, you can use the `bychain` option to plot each chain separately but one graph.

To control the look of an individual chain, you can use the `chain#opts()` options. For example, to change the line color to red for chain 2, you would specify the `chain2opts(lcolor(red))` option. To control the look of all chains, you can use the `chainopts()` option.

You can use bayesgraph to plot predicted quantities when you supply the prediction dataset generated by bayespredict in the using specification. Also see *Different ways of specifying predictions and their functions* in [BAYES] **Bayesian postestimation**.

Examples

We demonstrate the bayesgraph command using an example of Bayesian normal linear regression applied to auto.dta. We model the mpg variable using a normal distribution with unknown mean and variance. Our Bayesian model thus has two parameters, {mpg:_cons} and {var}, for which we need to specify prior distributions. We consider fairly noninformative prior distributions for these parameters: $N(0, 1000)$ for the constant and inverse gamma with shape and scale of 0.1 for the variance. Because the specified prior distributions are independent and semiconjugate relative to the normal data distribution, we can use Gibbs sampling for both parameters instead of the default MH sampling. To illustrate, we will use Gibbs sampling for the variance and MH sampling (default) for the mean.

We use bayesmh to fit our model.

```
. use https://www.stata-press.com/data/r18/auto
(1978 automobile data)
. bayesmh mpg, likelihood(normal({var}))
> prior({mpg:_cons}, normal(0,1000))
> prior({var}, igamma(0.1,0.1)) block({var}, gibbs) rseed(14)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},{var})
Priors:
  {mpg:_cons} ~ normal(0,1000)
        {var} ~ igamma(0.1,0.1)
------------------------------------------------------------------------------
Bayesian normal regression                      MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling          Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .7133
                                                Efficiency:  min =      .2331
                                                             avg =      .6166
Log marginal-likelihood =  -242.1155                         max =          1
------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |   21.29231   .6648867   .013771   21.29419   19.94367   22.56746
-------------+----------------------------------------------------------------
         var |    34.2805   5.844213   .058442   33.6464   24.65882    47.5822
------------------------------------------------------------------------------
```

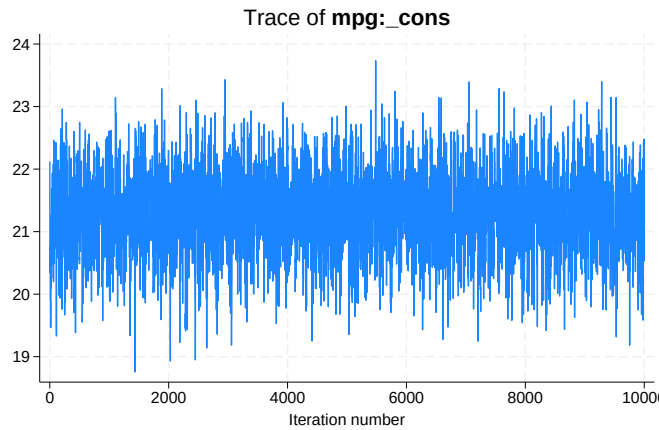
The MCMC simulation has a fairly high efficiency for the MH algorithm of 23% for the mean and an efficiency of 1 for the variance because of the Gibbs sampling. The output suggests no convergence problems. However, it is important to verify this and to also inspect various other graphical summaries of the parameters. This example demonstrates graphical summaries for a well-mixing MCMC chain that has converged and that generates samples from the posterior distribution of the model. For examples of poor-mixing MCMC chains, see *Convergence diagnostics in* MCMC in [BAYES] **Intro**.

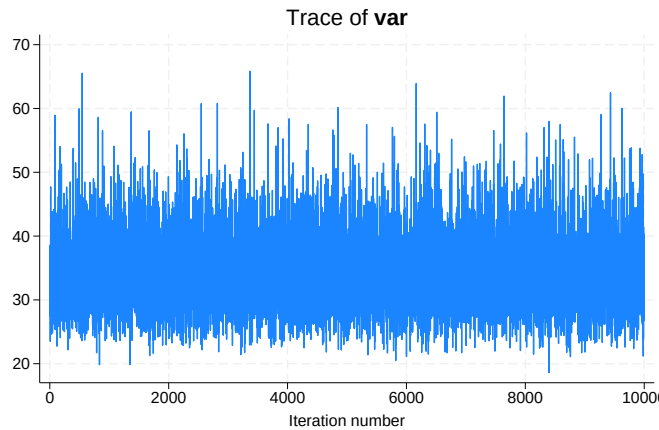
Trace plots

We start with trace plots, which plot the values of the simulated parameters against the iteration number and connect consecutive values with a line. For a well-mixing parameter, the range of the parameter is traversed rapidly by the MCMC chain, which makes the drawn lines look almost vertical and dense. Sparseness and trends in the trace plot of a parameter suggest convergence problems.

Let's use `bayesgraph trace` to obtain trace plots for `{mpg:_cons}` and `{var}`. We specify `_all` to request both plots at once.

```
. bayesgraph trace _all
```

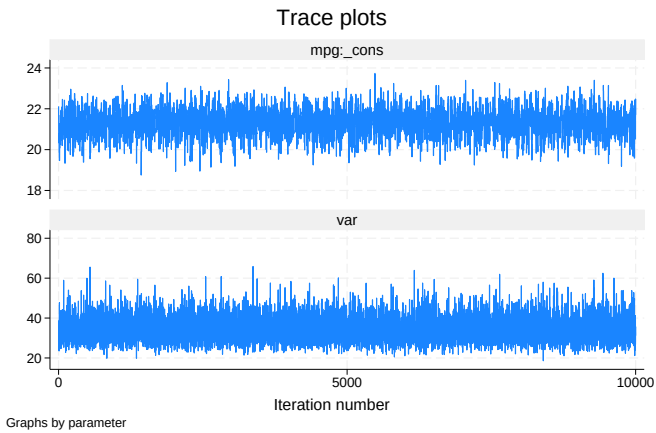




The mean parameter mixes very well and the variance parameter mixes perfectly.

Alternatively, we can use the `byparm()` option to plot results on one graph.

```
. bayesgraph trace _all, byparm
```



`bayesgraph trace` (as well as `bayesgraph cusum`) with option `byparm()` displays multiple plots in one column to accommodate an x axis with many iterations. You can specify `byparm(norowcoldefault)` to switch to the default behavior of options `rows()` and `cols()` documented in [G-3] ***by_option***.

Also see *Convergence diagnostics using multiple chains* in [BAYES] **bayesmh** for an example of trace plots with multiple chains.

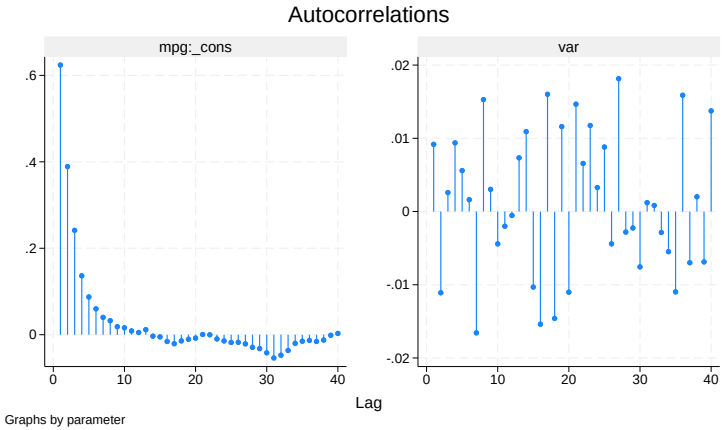
Autocorrelation plots

The second graphical summary we demonstrate is an autocorrelation plot. This plot shows the degree of autocorrelation in an MCMC sample for a range of lags, starting from lag 0. At lag 0, the plotted value corresponds to the sample variance of MCMC.

Autocorrelation is usually present in any MCMC sample. Typically, autocorrelation starts from some positive value for lag 0 and decreases toward 0 as the lag index increases. For a well-mixing MCMC chain, autocorrelation dies off fairly rapidly.

For example, autocorrelation for {mpg:_cons} becomes negligible after about lag 8 and is basically nonexistent for {var}.

```
. bayesgraph ac _all, byparm
```



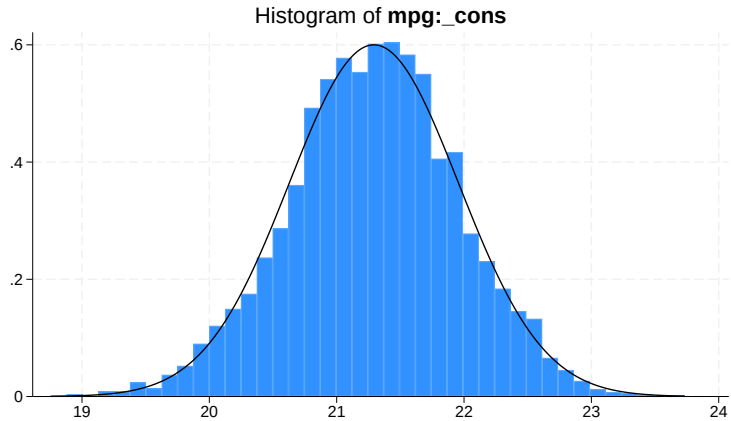
Autocorrelation lags are approximated by correlation times of parameters as reported by the bayesstats ess command; see [BAYES] **bayesstats ess** for details. Autocorrelation lags are also used to determine the batch size for the batch-means estimator of the MCMC standard errors; see [BAYES] **bayesstats summary**.

Histogram plots

Graphical posterior summaries such as histograms and kernel density estimates provide useful additions to the various numerical statistics (see [BAYES] **bayesstats summary**) for summarizing MCMC output. It is always a good practice to inspect the histogram and kernel density estimates of the marginal posterior distributions of parameters to ensure that these empirical distributions behave as expected. These plots can be used to compare the empirical posterior and the specified prior distributions to visualize the impact of the data.

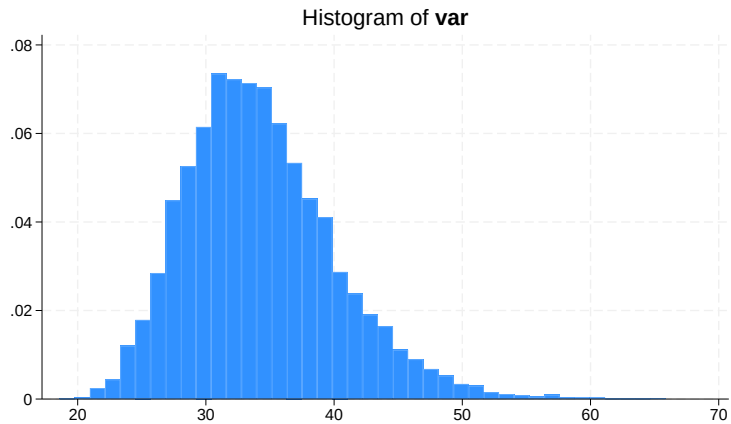
A histogram depicts the general shape of the marginal posterior distribution of a model parameter. Let's look at histograms of our parameters.

```
. bayesgraph histogram {mpg:_cons}, normal
```



The distribution of {mpg:_cons} is in good agreement with the normal distribution. This is not surprising, because the specified conjugate normal prior implies that the marginal posterior for {mpg:_cons} is a normal distribution. The unimodal histogram is also another confirmation that we have obtained a good simulation of the marginal posterior distribution of {mpg:_cons}.

```
. bayesgraph histogram {var}
```



The histogram for {var} is also unimodal but is slightly skewed to the right. This is also in agreement with the specified prior because the marginal posterior for the variance is inverse gamma for the specified model.

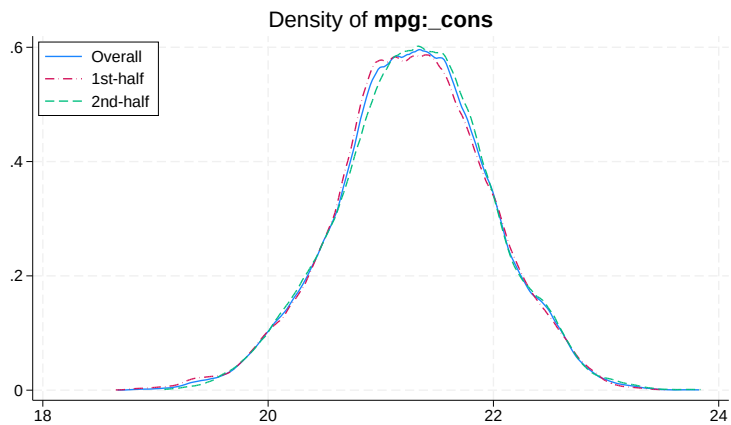
For examples of histograms for prediction quantities, see example 4 and example 7 in [BAYES] **bayespredict** and example 1 and example 3 in [BAYES] **bayesstats ppvalues**.

Kernel density plots

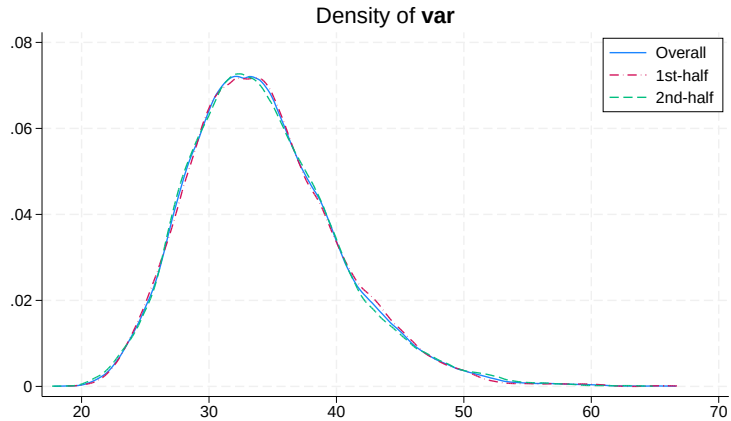
Kernel density plots provide alternative visualizations of the simulated marginal posterior distributions. They may be viewed as smoothed histograms. By default, the `bayesgraph kdensity` command shows an overall density of the entire MCMC sample. To explore convergence, the command provides the `show(both)` option, which additionally plots two density curves: the first-half density obtained using the first half of the MCMC sample and the second-half density obtained using the second half of the MCMC sample. If the chain has converged and mixes well, we expect the three density curves to be close to each other. Large discrepancies between the first-half curve and the second-half curve suggest convergence problems.

Let's look at the three kernel density curves for our two parameters.

```
. bayesgraph kdensity {mpg:_cons}, show(both)
```



```
. bayesgraph kdensity {var}, show(both)
```



Kernel density plots for {mpg:_cons} and {var} are similar in shape to the histograms' plots from the previous section. All three density curves are close to each other for both parameters.

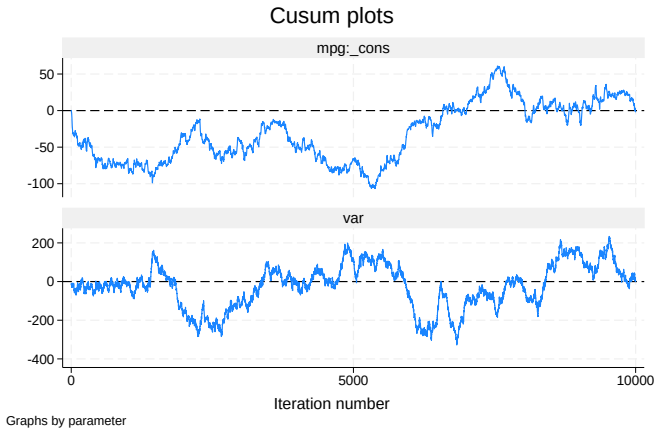
Also see *Convergence diagnostics using multiple chains* in [BAYES] **bayesmh** for an example of kernel density plots with multiple chains.

Cumulative sum plots

Cumulative sum (cusum) plots are useful graphical summaries for detecting persistent trends in MCMC chains. All cusum plots start and end at 0 and may or may not cross the x axis. There is great variability in the looks of cusum plots, which make them difficult to interpret sometimes. Typically, if the cusum line never crosses the x axis, this may indicate a problem. See, for example, *Convergence diagnostics of* MCMC in [BAYES] **Intro** for a cusum plot demonstrating convergence problems.

By inspecting a cusum plot, we may detect an early drift in the simulated sample because of an insufficient burn-in period. In cases of pronounced persistent trends, the cusum curve may stay either in the positive or in the negative y plane. For a well-mixing parameter, the cusum curve typically crosses the x axis several times. This is the case for the cusum plots of {mpg:_cons} and {var}.

```
. bayesgraph cusum _all, byparm
```



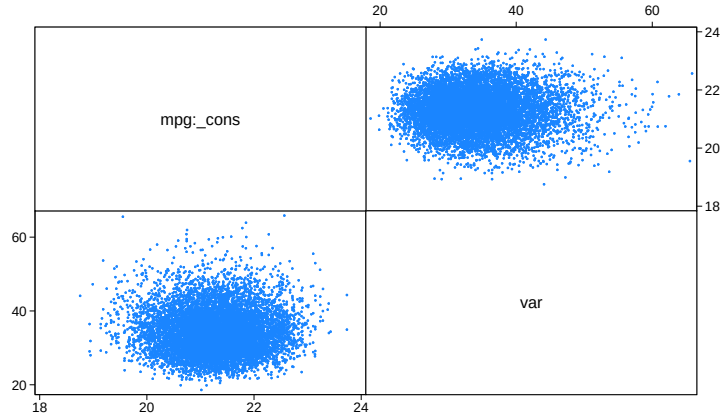
Bivariate scatterplots

The `bayesgraph matrix` command draws bivariate scatterplots of model parameters based on MCMC samples. A bivariate scatterplot represents a joint sample posterior distribution for pairs of parameters. It may reveal correlation between parameters and characterize a general shape of a multivariate posterior distribution. For example, bivariate scatterplots are useful for detecting multimodal posterior distributions.

Typically, scatterplots depict clouds of points. Sparseness and irregularities in the scatterplots can be strong indications of nonconvergence of an MCMC. For a well-mixing chain, the scatterplots have an ellipsoidal form with an increasing concentration around the posterior mode.

This scatterplot of {mpg:_cons} and {var} is an example of a well-behaved scatterplot.

```
. bayesgraph matrix {mpg:_cons} {var}
```

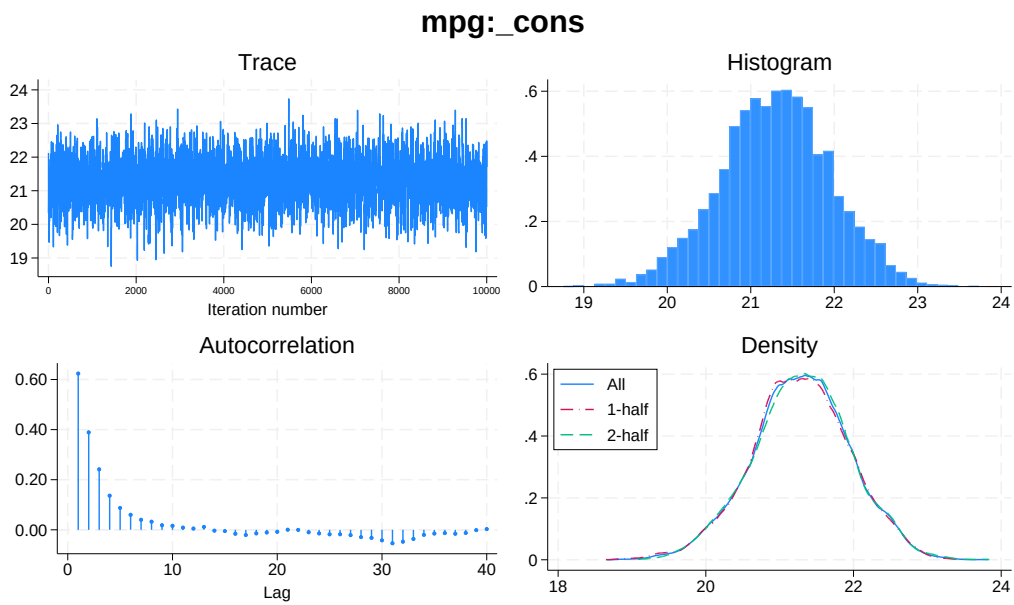


Diagnostic plots

Finally, we demonstrate the `bayesgraph diagnostics` command, which combines the trace, histogram, autocorrelation, and kernel density plots compactly on one graph. We already discussed the individual plots in the previous sections. Diagnostic plots are convenient for inspecting the overall behavior of a particular model parameter. We recommend that diagnostic plots for all parameters be inspected routinely as a part of the convergence-checking process.

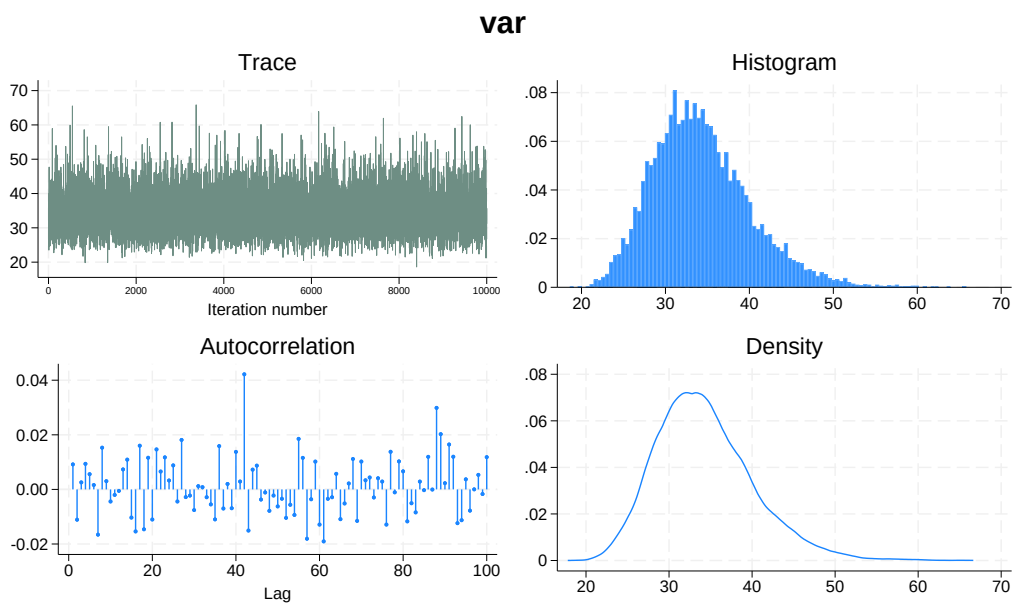
Let's obtain the diagnostic plot for {mpg:_cons}.

```
. bayesgraph diagnostics {mpg:_cons}
```



In the diagnostics plot for {var}, let's also demonstrate the use of several options of the depicted plots.

```
. bayesgraph diagnostics {var}, traceopts(lwidth(0.2) lcolor(teal))
> acopts(lag(100)) histopts(bins(100)) kdensopts(show(none))
```



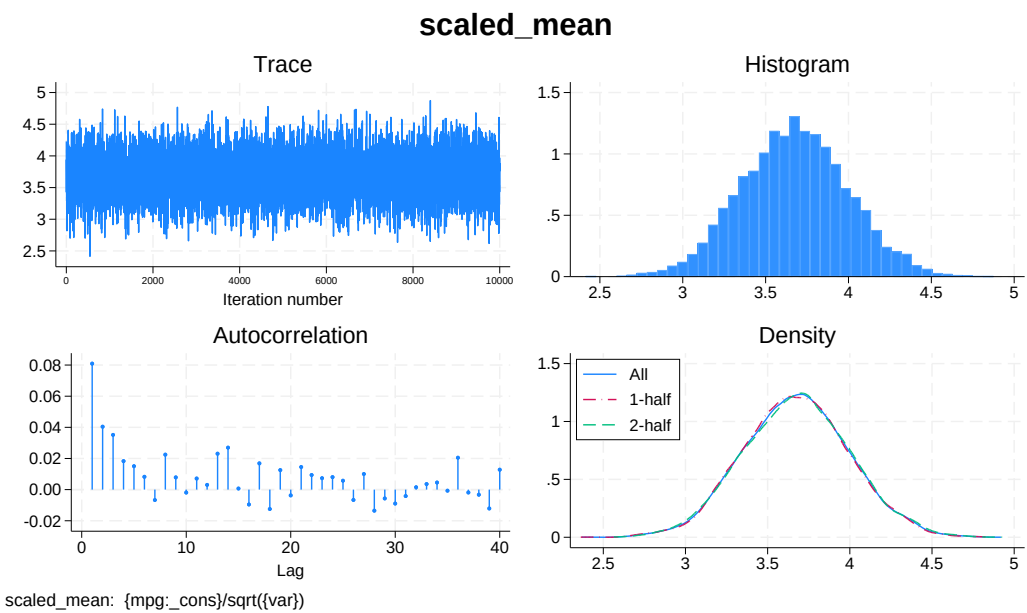
In the above, we changed the width and color of the trace line, the maximum lag for calculating the autocorrelation, the number of bins for the histogram, and requested that the two subsample kernel densities not be shown on the kernel density plot.

Also see *Convergence diagnostics using multiple chains* in [BAYES] **bayesmh** for an example of diagnostics plots with multiple chains.

Functions of model parameters

All `bayesgraph` subcommands can provide graphical summaries of functions of model parameters. Below we apply `bayesgraph diagnostics` to the expression `{mpg:_cons}/sqrt({var})`, which we label as `scaled_mean`.

```
. bayesgraph diagnostics (scaled_mean: {mpg:_cons}/sqrt({var}))
```



If you detect convergence problems in a function of parameters, you must inspect every parameter used in the expression individually. In fact, we recommend that you inspect all model parameters before you proceed with any postestimation analysis.

Methods and formulas

Let θ be a scalar model parameter and $\{\theta_t\}_{t=1}^{T}$ be an MCMC sample of size T drawn from the marginal posterior distribution of θ.

The trace plot of θ plots θ_t against t with connecting lines for $t = 1, \ldots, T$.

The autocorrelation plot of θ shows the autocorrelation in the $\{\theta_t\}_{t=1}^{T}$ sample for lags from 0 to the `lag(#)` option of the `ac` command.

The histogram and kernel density plots of θ are drawn using the `histogram` and `kdensity` commands.

Yu and Mykland (1998) proposed a graphical procedure for assessing the convergence of individual parameters based on cumulative sums, also known as a cusum plot. The cusum plot for θ plots S_t against t for $t = 1, \ldots, T$ and connects the successive points. S_t is the cumulative sum at time t:

$$S_t = \sum_{k=1}^{t} (\theta_k - \widehat{\theta}), \quad \widehat{\theta} = \frac{1}{T} \sum_{k=1}^{T} \theta_k$$

and $S_0 = 0$.

The scatterplot of two model parameters θ^1 and θ^2 plots points (θ_t^1, θ_t^2) for $t = 1, \ldots, T$.

With multiple chains, the plots are produced separately for each chain.

References

Huber, C. 2016. Introduction to Bayesian statistics, part 2: MCMC and the Metropolis–Hastings algorithm. *The Stata Blog: Not Elsewhere Classified.* http://blog.stata.com/2016/11/15/introduction-to-bayesian-statistics-part-2-mcmc-and-the-metropolis-hastings-algorithm/.

Yu, B., and P. Mykland. 1998. Looking at Markov samplers through cusum path plots: A simple diagnostic idea. *Statistics and Computing* 8: 275–286. https://doi.org/10.1023/A:1008917713940.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **bayesstats ess** — Effective sample sizes and related statistics

[BAYES] **bayesstats summary** — Bayesian summary statistics

[G-2] **graph matrix** — Matrix graphs

[G-2] **graph twoway kdensity** — Kernel density plots

[R] **histogram** — Histograms for continuous and categorical variables

[R] **kdensity** — Univariate kernel density estimation

[TS] **corrgram** — Tabulate and graph autocorrelations

[TS] **tsline** — Time-series line plots

Title

bayesstats — Bayesian statistics after Bayesian estimation

Description Also see

Description

The following subcommands are available with `bayesstats` after `bayesmh` and the `bayes` prefix:

Command	Description
`bayesstats ess`	effective sample sizes and related statistics
`bayesstats summary`	Bayesian summary statistics for model parameters and their functions
`bayesstats ic`	Bayesian information criteria and Bayes factors
`bayesstats grubin`	Gelman–Rubin convergence diagnostics
`bayesstats ppvalues`	Bayesian predictive p-values (available only after `bayesmh`)

Also see

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

Title

bayesstats ess — Effective sample sizes and related statistics

Description

`bayesstats ess` calculates effective sample sizes (ESS), correlation times, and efficiencies for model parameters and functions of model parameters using current Bayesian estimation results.

Quick start

Effective sample sizes for all model parameters after a Bayesian regression model

```
bayesstats ess
```

Same as above, but only for model parameters `{y:x1}` and `{var}`

```
bayesstats ess {y:x1} {var}
```

Same as above, but skip every 5 observations from the full MCMC sample

```
bayesstats ess {y:x1} {var}, skip(5)
```

Effective sample sizes for functions of scalar model parameters

```
bayesstats ess ({y:x1}-{y:_cons}) (sd:sqrt({var}))
```

Same as above, and include `{y:x1}` and `{var}`

```
bayesstats ess {y:x1} {var} ({y:x1}-{y:_cons}) (sd:sqrt({var}))
```

Menu

Statistics > Bayesian analysis > Effective sample sizes

Syntax

Syntax is presented under the following headings:

Statistics for model parameters

Statistics for all model parameters

```
bayesstats ess [, options showreffects[(reref)]]

bayesstats ess _all [, options showreffects[(reref)]]
```

Statistics for selected model parameters

```
bayesstats ess paramspec [, options]
```

Statistics for expressions of model parameters

```
bayesstats ess exprspec [, options]
```

Full syntax

```
bayesstats ess spec [spec ...] [, options]
```

paramspec can be one of the following:

{*eqname*:*param*} refers to a parameter *param* with equation name *eqname*;

{*eqname*:} refers to all model parameters with equation name *eqname*;

{*eqname*:*paramlist*} refers to parameters with names in *paramlist* and with equation name *eqname*; or

{*param*} refers to all parameters named *param* from all equations.

In the above, *param* can refer to a matrix name, in which case it will imply all elements of this matrix. See *Different ways of specifying model parameters* in [BAYES] **Bayesian postestimation** for examples.

exprspec is an optionally labeled expression of model parameters specified in parentheses:

(*[exprlabel:]expr*)

exprlabel is a valid Stata name, and *expr* is a scalar expression that may not contain matrix model parameters. See *Specifying functions of model parameters* in [BAYES] **Bayesian postestimation** for examples.

spec is one of *paramspec* or *exprspec*.

Statistics for predictions

Statistics for simulated outcomes, residuals, and more

```
bayesstats ess yspec [yspec ...] using predfile [, options]
```

Statistics for expressions of simulated outcomes, residuals, and more

```
bayesstats ess (yexprspec) [(yexprspec) ...] using predfile [, options]
```

Statistics for Mata functions of simulated outcomes, residuals, and more

```
bayesstats ess (funcspec) [(funcspec) ...] using predfile [, options]
```

Full syntax

```
bayesstats ess predspec [predspec ...] using predfile [, options]
```

predfile is the name of the dataset created by `bayespredict` that contains prediction results.

yspec is {*ysimspec* | *residspec* | *muspec* | *label*}.

ysimspec is `{_ysim#}` or `{_ysim#[`*numlist*`]}`, where `{_ysim#}` refers to all observations of the #th simulated outcome and `{_ysim#[`*numlist*`]}` refers to the selected observations, *numlist*, of the #th simulated outcome. `{_ysim}` is a synonym for `{_ysim1}`.

residspec is `{_resid#}` or `{_resid#[`*numlist*`]}`, where `{_resid#}` refers to all residuals of the #th simulated outcome and `{_resid#[`*numlist*`]}` refers to the selected residuals, *numlist*, of the #th simulated outcome. `{_resid}` is a synonym for `{_resid1}`.

muspec is `{_mu#}` or `{_mu#[`*numlist*`]}`, where `{_mu#}` refers to all expected values of the #th outcome and `{_mu#[`*numlist*`]}` refers to the selected expected values, *numlist*, of the #th outcome. `{_mu}` is a synonym for `{_mu1}`.

label is the name of the function simulated using `bayespredict`.

With large datasets, specifications `{_ysim#}`, `{_resid#}`, and `{_mu#}` may use a lot of time and memory and should be avoided. See *Generating and saving simulated outcomes* in [BAYES] **bayespredict**.

yexprspec is [*exprlabel*`:`]*yexpr*, where *exprlabel* is a valid Stata name and *yexpr* is a scalar expression that may contain individual observations of simulated outcomes, `{_ysim#[#]}`; individual expected outcome values, `{_mu#[#]}`; individual simulated residuals, `{_resid#[#]}`; and other scalar predictions, {*label*}.

funcspec is [*label*`:`]`@`*func*`(`*arg1*[`,` *arg2*]`)`, where *label* is a valid Stata name; *func* is an official or user-defined Mata function that operates on column vectors and returns a real scalar; and *arg1* and *arg2* are one of `{_ysim[#]}`, `{_resid[#]}`, or `{_mu[#]}`. *arg2* is primarily for use with user-defined Mata functions; see *Defining test statistics using Mata functions* in [BAYES] **bayespredict**.

predspec is one of *yspec*, (*yexprspec*), or (*funcspec*). See *Different ways of specifying predictions and their functions* in [BAYES] **Bayesian postestimation**.

options	Description
Main	
* `chains(_all | numlist)`	specify which chains to use for computation; default is `chains(_all)`
* `sepchains`	compute results separately for each chain
`skip(#)`	skip every # observations from the MCMC sample; default is `skip(0)`
`nolegend`	suppress table legend
display_options	control spacing, line width, and base and empty cells
Advanced	
`corrlag(#)`	specify maximum autocorrelation lag; default varies
`corrtol(#)`	specify autocorrelation tolerance; default is `corrtol(0.01)`

*Options `chains()` and `sepchains` are relevant only when option `nchains()` is used with `bayesmh` or the `bayes` prefix.

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

Options

Main

`chains(_all | numlist)` specifies which chains from the MCMC sample to use for computation. The default is `chains(_all)` or to use all simulated chains. Using multiple chains, provided the chains have converged, generally improves MCMC summary statistics. Option `chains()` is relevant only when option `nchains()` is specified with `bayesmh` or the `bayes` prefix.

`sepchains` specifies that the results be computed separately for each chain. The default is to compute results using all chains as determined by option `chains()`. Option `sepchains` is relevant only when option `nchains()` is specified with `bayesmh` or the `bayes` prefix.

`showreffects` and `showreffects(`*reref*`)` are for use after multilevel models, and they specify that the results for all or a list *reref* of random-effects parameters be provided in addition to other model parameters. By default, all random-effects parameters are excluded from the results to conserve computation time.

`skip(#)` specifies that every # observations from the MCMC sample not be used for computation. The default is `skip(0)` or to use all observations in the MCMC sample. Option `skip()` can be used to subsample or thin the chain. `skip(#)` is equivalent to a thinning interval of #+1. For example, if you specify `skip(1)`, corresponding to the thinning interval of 2, the command will skip every other observation in the sample and will use only observations 1, 3, 5, and so on in the computation. If you specify `skip(2)`, corresponding to the thinning interval of 3, the command will skip every 2 observations in the sample and will use only observations 1, 4, 7, and so on in the computation. `skip()` does not thin the chain in the sense of physically removing observations from the sample, as is done by, for example, `bayesmh`'s `thinning()` option. It only discards selected observations from the computation and leaves the original sample unmodified.

`nolegend` suppresses the display of the table legend, which identifies the rows of the table with the expressions they represent.

display_options: `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `nofvlabel`, `fvwrap(#)`, `fvwrapon(`*style*`)`, and `nolstretch`; see [R] **Estimation options**.

Advanced

`corrlag(#)` specifies the maximum autocorrelation lag used for calculating effective sample sizes. The default is $\min\{500, \texttt{mcmcsize()}/2\}$. The total autocorrelation is computed as the sum of

all lag-k autocorrelation values for k from 0 to either `corrlag()` or the index at which the autocorrelation becomes less than `corrtol()` if the latter is less than `corrlag()`.

`corrtol(#)` specifies the autocorrelation tolerance used for calculating effective sample sizes. The default is `corrtol(0.01)`. For a given model parameter, if the absolute value of the lag-k autocorrelation is less than `corrtol()`, then all autocorrelation lags beyond the kth lag are discarded.

Remarks and examples

Remarks are presented under the following headings:

Effective sample size and MCMC sampling efficiency
Using bayesstats ess

Effective sample size and MCMC sampling efficiency

It is well known that for a random sample of T independent subjects, the standard error of the sample mean estimator is proportional to $1/\sqrt{T}$. In Bayesian inference, it is of interest to estimate the standard error of the posterior mean estimator. The posterior mean of a parameter of interest is typically estimated as a sample mean from an MCMC sample obtained from the marginal posterior distribution of the parameter of interest. Observations from an MCMC sample are not independent and are usually positively correlated, which must be taken into account when computing the standard error. Thus the standard error of the posterior mean estimator is proportional to $1/\sqrt{\text{ESS}}$, where ESS is the effective sample size for the parameter of interest. Typically, ESS is less than T, the total number of observations in the MCMC sample. We can thus interpret the posterior mean estimate as a sample mean estimate from an independent sample of size ESS. In other words, the effective sample size is an estimate of the number of independent observations that the MCMC chain represents. We say that MCMC samples with higher ESS are more efficient.

Effective sample size is directly related to the convergence properties of an MCMC sample—very low ESS relative to T suggests nonconvergence. In the extreme case of a perfectly correlated MCMC observation, ESS is 1. It is thus a standard practice to assess the quality of an MCMC sample by inspecting ESS values for all involved model parameters. Note, however, that high ESS values are not generally sufficient for declaring convergence of MCMC because pseudoconvergence, which may occur when MCMC does not explore the entire distribution, may also lead to high ESS values.

Using bayesstats ess

`bayesstats ess` reports effective sample sizes, correlation times, and efficiencies for model parameters and their functions using the current Bayesian estimation results. When typed without arguments, the command displays results for all model parameters. Alternatively, you can specify a subset of model parameters following the command name; see *Different ways of specifying model parameters* in [BAYES] **Bayesian postestimation**. You can also obtain results for scalar functions of model parameters; see *Specifying functions of model parameters* in [BAYES] **Bayesian postestimation**. You can obtain the summaries for prediction quantities when you specify the prediction dataset in the `using` specification; see *Different ways of specifying predictions and their functions* in [BAYES] **Bayesian postestimation** for how to specify prediction quantities within `bayesstats ess`.

Consider our analysis of auto.dta from example 4 in [BAYES] **bayesmh** using the mean-only normal model for mpg with a noninformative prior.

```
. use https://www.stata-press.com/data/r18/auto
(1978 automobile data)
. set seed 14
. bayesmh mpg, likelihood(normal({var}))
> prior({mpg:_cons}, flat) prior({var}, jeffreys)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},{var})
Priors:
  {mpg:_cons} ~ 1 (flat)
        {var} ~ jeffreys
------------------------------------------------------------------------------
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .2668
                                                Efficiency:  min =     .09718
                                                             avg =      .1021
Log marginal-likelihood =   -234.645                         max =      .1071
------------------------------------------------------------------------------
                                                              Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |   21.29222   .6828864   .021906   21.27898   19.99152   22.61904
-------------+----------------------------------------------------------------
         var |   34.76572    5.91534   .180754   34.18391    24.9129   47.61286
------------------------------------------------------------------------------
```

▷ Example 1: Effective sample sizes for all parameters

To compute effective sample sizes and other related statistics for all model parameters, we type `bayesstats ess` without arguments after the `bayesmh` command.

```
. bayesstats ess
Efficiency summaries    MCMC sample size =    10,000
                        Efficiency:  min =    .09718
                                     avg =     .1021
                                     max =     .1071
```

	ESS	Corr. time	Efficiency
mpg			
_cons	971.82	10.29	0.0972
var	1070.99	9.34	0.1071

The closer the ESS estimates are to the MCMC sample size, the better. Also, the lower the correlation times are and the higher the efficiencies are, the better. ESS estimates can be interpreted as follows. In a sample of 10,000 MCMC observations, we have only about 972 independent observations to obtain estimates for `{mpg:_cons}` and only about 1,071 independent observations to obtain estimates for `{var}`. Correlation times are the reciprocal of efficiencies. You can interpret them as an estimated lag after which autocorrelation in an MCMC sample is small. In our example, the estimated lag is roughly 10 for both parameters. In general, efficiencies above 10% are considered good for the MH algorithm. In our example, they are about 10% for both parameters.

Alternatively, we could have listed all parameters manually:

```
. bayesstats ess {mpg:_cons} {var}
  (output omitted)
```

◁

▷ Example 2: Effective sample sizes for functions of model parameters

Similarly to other Bayesian postestimation commands, `bayesstats ess` accepts expressions to compute results for functions of model parameters. For example, we can use expression `(sd:sqrt({var}))` with a label, `sd`, to compute effective sample sizes for the standard deviation of `mpg` in addition to the variance.

```
. bayesstats ess (sd:sqrt({var})) {var}
Efficiency summaries    MCMC sample size =    10,000
                        Efficiency:  min =     .1071
                                     avg =     .1082
                                     max =     .1094

          sd : sqrt({var})
```

	ESS	Corr. time	Efficiency
sd	1093.85	9.14	0.1094
var	1070.99	9.34	0.1071

ESS and efficiency are higher for the standard deviation than for the variance, which means that we need slightly more iterations to estimate `{var}` with the same precision as `sd`.

If we wanted, we could have suppressed the `sd` legend in the output above by specifying the `nolegend` option.

◁

Stored results

`bayesstats ess` stores the following in `r()`:

Scalars

`r(mcmcsize)`	MCMC sample size used in the computation
`r(skip)`	number of MCMC observations to skip in the computation; every `r(skip)` observations are skipped
`r(corrlag)`	maximum autocorrelation lag
`r(corrtol)`	autocorrelation tolerance
`r(nchains)`	number of chains used in the computation

Macros

`r(names)`	names of model parameters and expressions
`r(expr_#)`	#th expression
`r(exprnames)`	expression labels
`r(chains)`	chains used in the computation, if `chains()` is specified

Matrices

`r(ess)`	matrix with effective sample sizes, correlation times, and efficiencies for parameters in `r(names)`
`r(ess_chain#)`	matrix `ess` for chain #, if `sepchains` is specified

Methods and formulas

Let θ be a scalar model parameter and $\{\theta_t\}_{t=1}^{T}$ be an MCMC sample of size T drawn from the marginal posterior distribution of θ. The effective sample size of the MCMC sample of θ is given by

$$\text{ESS} = T/(1 + 2 \sum_{k=1}^{\text{max\_lags}} \rho_k)$$

where ρ_k is the lag-k autocorrelation of the MCMC sample, and max_lags is the maximum number less than or equal to ρ_{lag} such that for all $k = 1, \ldots, \text{max\_lags}$, $|\rho_k| > \rho_{\text{tol}}$, where ρ_{lag} and ρ_{tol} are specified in options `corrlag()` and `corrtol()` with the respective default values of 500 and 0.01.

The lag-k autocorrelation is $\rho_k = \gamma_k/\gamma_0$, where

$$\gamma_k = \frac{1}{T} \sum_{t=1}^{T-k} (\theta_t - \widehat{\theta})(\theta_{t+k} - \widehat{\theta})$$

is the empirical autocovariance of lag k, and γ_0 simplifies to the sample variance. $\widehat{\theta}$ is the posterior mean estimator.

Correlation time is defined as T/ESS, and efficiency is defined as the reciprocal of the correlation time, ESS/T. Because ESS is between 0 and T, inclusively, the efficiency is always between 0 and 1.

In the presence of multiple chains, the overall ESS is computed as the sum of the individual ESS statistics calculated using each chain independently. Correlation times and efficiencies are then computed using the overall ESS and the total MCMC sample size, $M \times T$, where M is the number of chains.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **bayesstats summary** — Bayesian summary statistics

Title

bayesstats grubin — Gelman–Rubin convergence diagnostics

Description

`bayesstats grubin` calculates Gelman–Rubin convergence diagnostics for model parameters and functions of model parameters using current Bayesian estimation results containing at least two Markov chains.

Quick start

Gelman–Rubin convergence diagnostics for all model parameters after a Bayesian regression model using four chains

```
bayes, nchains(4): regress y x1
bayesstats grubin
```

Same as above, but only for model parameters `{y:x1}` and `{sigma2}`

```
bayesstats grubin {y:x1} {sigma2}
```

Gelman–Rubin convergence diagnostics for functions of scalar model parameters

```
bayesstats grubin ({y:x1}-{y:_cons}) (sd:sqrt({sigma2}))
```

Menu

Statistics > Bayesian analysis > Gelman–Rubin convergence diagnostics

Syntax

Convergence statistics for all model parameters

```
bayesstats grubin [ , options showreffects[ (reref) ] ]

bayesstats grubin _all [ , options showreffects[ (reref) ] ]
```

Convergence statistics for selected model parameters

```
bayesstats grubin paramspec [ , options ]
```

Convergence statistics for functions of model parameters

```
bayesstats grubin exprspec [ , options ]
```

Full syntax

```
bayesstats grubin spec [spec ...] [ , options ]
```

paramspec can be one of the following:

{*eqname*:*param*} refers to a parameter *param* with equation name *eqname*;

{*eqname*:} refers to all model parameters with equation name *eqname*;

{*eqname*:*paramlist*} refers to parameters with names in *paramlist* and with equation name *eqname*; or

{*param*} refers to all parameters named *param* from all equations.

In the above, *param* can refer to a matrix name, in which case it will imply all elements of this matrix. See *Different ways of specifying model parameters* in [BAYES] **Bayesian postestimation** for examples.

exprspec is an optionally labeled expression of model parameters specified in parentheses:

([*exprlabel*:] *expr*)

exprlabel is a valid Stata name, and *expr* is a scalar expression that may not contain matrix model parameters. See *Specifying functions of model parameters* in [BAYES] **Bayesian postestimation** for examples.

spec is one of *paramspec* or *exprspec*.

options	Description
`sort`	list parameters in descending order of their convergence statistics
`skip(#)`	skip every # observations from the MCMC sample; default is `skip(0)`
`nolegend`	suppress table legend
display_options	control spacing, line width, and base and empty cells

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

Options

`sort` specifies that model parameters be listed in descending order of their Gelman–Rubin convergence statistics. This option is useful for models with many parameters, such as multilevel models, to more easily identify the set of parameters with large values of convergence statistics.

`showreffects` and `showreffects(`*reref*`)` are for use after multilevel models, and they specify that the results for all or a list *reref* of random-effects parameters be provided in addition to other model parameters. By default, all random-effects parameters are excluded from the results to conserve computation time. If random-effects parameters are of interest in your study, you should use option `showreffects` to check their convergence diagnostics.

`skip(#)` specifies that every # observations from the MCMC sample not be used for computation. The default is `skip(0)` or to use all observations in the MCMC sample. Option `skip()` can be used to subsample or thin the chain. `skip(#)` is equivalent to a thinning interval of #+1. For example, if you specify `skip(1)`, corresponding to the thinning interval of 2, the command will skip every other observation in the sample and will use only observations 1, 3, 5, and so on in the computation. If you specify `skip(2)`, corresponding to the thinning interval of 3, the command will skip every 2 observations in the sample and will use only observations 1, 4, 7, and so on in the computation. `skip()` does not thin the chain in the sense of physically removing observations from the sample, as is done by, for example, `bayesmh`'s `thinning()` option. It only discards selected observations from the computation and leaves the original sample unmodified.

`nolegend` suppresses the display of the table legend, which identifies the rows of the table with the expressions they represent.

display_options: `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `nofvlabel`, `fvwrap(#)`, `fvwrapon(`*style*`)`, and `nolstretch`; see [R] **Estimation options**.

Remarks and examples

Remarks are presented under the following headings:

Gelman–Rubin convergence diagnostic
Using bayesstats grubin

Gelman–Rubin convergence diagnostic

The Gelman–Rubin convergence diagnostic, R_c, assesses MCMC convergence by analyzing differences between multiple Markov chains. The convergence is assessed by comparing the estimated between-chains and within-chain variances for each model parameter. Large differences between these variances indicate nonconvergence. See Gelman and Rubin (1992) and Brooks and Gelman (1998) for details.

Large values of R_c indicate nonconvergence of MCMC. Literature suggests that the values of this diagnostic should be less than 1.2 for all model parameters to declare MCMC convergence. In practice, a more stringent convergence rule, $R_c < 1.1$, is often used.

Gelman–Rubin diagnostic relies on a Student's t approximation of the marginal posterior distribution of a model parameter. When this assumption is suspect, it is recommended to transform the parameter such that its marginal posterior distribution is better approximated by a Student's t distribution before obtaining the diagnostic. For example, for the variance parameter, it is better to compute the diagnostic for the log variance.

Using bayesstats grubin

The `bayesstats grubin` command computes the Gelman–Rubin convergence diagnostic for each model parameter using multiple MCMC samples or chains from a common posterior model. This command requires at least two chains. Multiple chains can be obtained by using the `nchains()` option with the `bayesmh` command ([BAYES] **bayesmh**) or with the `bayes` prefix ([BAYES] **bayes**). When you simulate multiple chains to assess convergence, it is important to use overdispersed initial values (Gelman and Rubin 1992, Brooks and Gelman 1998). See *Specifying initial values* in [BAYES] **bayesmh** and *Initial values* in [BAYES] **bayes** for details.

When typed without arguments, the command displays results for all model parameters. Alternatively, you can specify a subset of model parameters following the command name; see *Different ways of specifying model parameters* in [BAYES] **Bayesian postestimation**. You can also obtain results for scalar functions of model parameters; see *Specifying functions of model parameters* in [BAYES] **Bayesian postestimation**. Also see example 2.

For multilevel models, similarly to other Bayesian postestimation commands, `bayesstats grubin` does not report convergence statistics for the random-effects parameters by default. You can use the `showreffects` option to see them for all random-effects parameters or the `showreffects(`*reref*`)` option for a subset *reref* of random-effects parameters of interest. See *Multilevel models* in [BAYES] **bayes** for more information about MCMC convergence in multilevel models.

For models with many parameters such as multilevel models, you can use the `sort` option to list model parameters in descending order of their convergence statistics `Rc`. The parameters with the largest values of `Rc` will be listed first, making it easier to verify their convergence.

▷ Example 1: Convergence diagnostics for all parameters

Recall our analysis of `womenwage.dta` using the `bayes: regress` command from example 1 in [BAYES] **bayes**. We fit a linear regression model to the response variable `wage` with predictor `age`. Here we use option `nchains(3)` to simulate three Markov chains to formally check convergence of model parameters. To ensure reproducibility of multiple chains, we also specify the `rseed(15)` option. Specifying `set seed` is not sufficient for reproducibility with multiple chains; see *Reproducing results* in [BAYES] **bayesmh** for details.

```
. use https://www.stata-press.com/data/r18/womenwage
(Wages of women)
. bayes, nchains(3) rseed(15): regress wage age
Chain 1
  Burn-in ...
  Simulation ...
Chain 2
  Burn-in ...
  Simulation ...
Chain 3
  Burn-in ...
  Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  wage ~ regress(xb_wage,{sigma2})
Priors:
  {wage:age _cons} ~ normal(0,10000)                                      (1)
          {sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_wage.
Bayesian linear regression                  Number of chains    =          3
Random-walk Metropolis-Hastings sampling    Per MCMC chain:
                                                 Iterations     =     12,500
                                                 Burn-in        =      2,500
                                                 Sample size    =     10,000
                                            Number of obs       =        488
                                            Avg acceptance rate =      .3673
                                            Avg efficiency: min =      .1409
                                                            avg =      .1735
                                                            max =      .2294
Avg log marginal-likelihood = -1810.1557    Max Gelman-Rubin Rc =          1
------------------------------------------------------------------------------
                                                              Equal-tailed
             |      Mean   Std. dev.      MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
wage         |
         age |   .4003528   .0599411   .000922   .4002037   .2804134   .5188627
       _cons |   5.999502   1.769855   .026358   6.025288   2.571305   9.517341
-------------+----------------------------------------------------------------
      sigma2 |   90.80977   5.822896   .070195   90.49567   79.92114   102.7621
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
Note: Default initial values are used for multiple chains.
```

Compared with example 1 in [BAYES] **bayes**, the precision of the posterior means almost doubled with more chains, judging by the MCMC standard errors. For example, the MCSE estimate for `{sigma2}` drops from 0.12 to 0.07.

In the presence of multiple chains, the `bayes` prefix automatically reports in the header the maximum value of the Gelman–Rubin convergence statistics across all parameters. In practice, we want to see this value be close to 1; if it is less than 1.1, the chains are considered to have converged. This convergence rule is satisfied in our example.

To compute the Gelman–Rubin statistics for all model parameters, we type `bayesstats grubin` without arguments after the `bayes` prefix.

```
. bayesstats grubin
Gelman-Rubin convergence diagnostic
Number of chains     =            3
MCMC size, per chain =       10,000
Max Gelman-Rubin Rc  =     1.000323
------------------------------------
             |          Rc
-------------+----------------------
wage         |
         age |   1.000062
       _cons |   1.000323
-------------+----------------------
      sigma2 |   1.000253
------------------------------------
Convergence rule: Rc < 1.1
```

Just like the `bayes` prefix, the `bayesstats grubin` command reports in the header the maximum value of `Rc` across all parameters. This is particularly useful as a quick convergence check for models with many parameters: if the maximum `Rc` is less than 1.2 or 1.1, then this convergence rule is satisfied by all parameters. In our example, the maximum `Rc` is 1.0003 and is less than 1.1, so the convergence criterion is met for all parameters.

The table reports the `Rc` estimates for each model parameter. As we already determined based on the maximum `Rc`, the convergence diagnostics for all model parameters are less than 1.1. This suggests that all chains have converged.

◁

▷ Example 2: Convergence diagnostics for functions of parameters

Continuing with example 1, we can compute the Gelman–Rubin statistics for functions of parameters. Let's compute the convergence diagnostic for the log-transformed variance parameter `{sigma2}`.

```
. bayesstats grubin (lnsigma2: ln({sigma2}))
Gelman-Rubin convergence diagnostic
Number of chains     =            3
MCMC size, per chain =       10,000
Max Gelman-Rubin Rc  =     1.000268
    lnsigma2 : ln({sigma2})
------------------------------------
             |          Rc
-------------+----------------------
    lnsigma2 |   1.000268
------------------------------------
Convergence rule: Rc < 1.1
```

Again, the convergence diagnostic for the log-transformed variance is less than 1.1 indicating no convergence problems with the transformed parameter. This also suggests that `{sigma2}` does not have convergence problems.

◁

In our examples, we used the default initial values provided by `bayes:` with multiple chains; see *Initial values* in [BAYES] **bayes**. To fully explore MCMC convergence, particularly when a posterior distribution is suspected to have multiple modes, you should use overdispersed initial values. See

Multiple chains using overdispersed initial values in [BAYES] **bayesmh** for an example of how to specify overdispersed initial values.

Of course, it is important to explore convergence visually as well; see *Convergence diagnostics using multiple chains* in [BAYES] **bayesmh**.

Stored results

`bayesstats grubin` stores the following in `r()`:

Scalars

`r(mcmcsize)`	MCMC sample size of each chain
`r(nchains)`	number of MCMC chains
`r(Rc_max)`	maximum convergence diagnostic

Matrices

`r(Rc)`	convergence diagnostics `Rc`
`r(t_df)`	degrees of freedom of a t distribution
`r(B)`	between-chains variances
`r(W)`	within-chain variances
`r(V)`	total variances

Methods and formulas

Suppose we have M chains of length T. For a model parameter θ, let $\{\theta_{jt}\}_{t=1}^{T}$ be the jth simulated chain drawn from the marginal posterior distribution of θ, $j = 1, \ldots, M$. Let $\widehat{\theta}_j$ and $\widehat{s}_j^2$ be the respective sample posterior mean and variance of the mth chain, and let the overall sample posterior mean be $\widehat{\theta} = (1/M)\sum_{j=1}^{M}\widehat{\theta}_j$. The between-chains and within-chain variances are given by

$$B = \frac{T}{M-1}\sum_{j=1}^{M}(\widehat{\theta}_j - \widehat{\theta})^2$$

$$W = \frac{1}{M}\sum_{j=1}^{M}\widehat{s}_j^2$$

When the chains are strongly stationary, that is, all chains draw samples from the target posterior distribution, the weighted average of W and B

$$\widehat{\sigma}^2 = \frac{T-1}{T}W + \frac{1}{T}B$$

is an unbiased estimator of the marginal posterior variance of θ.

Gelman and Rubin (1992) approximate the target distribution of θ by a Student's t distribution with mean $\widehat{\theta}$ and scale $\sqrt{\widehat{V}}$, where

$$\widehat{V} = \frac{T-1}{T}W + \frac{M+1}{MT}B$$

They define the so-called "scale" reduction factor as the ratio of $\widehat{V}$ and $\sigma^2 = \mathrm{Var}(\theta)$. They further estimate σ^2 by W and use the ratio of $\widehat{V}$ and W as an estimator of the scale reduction factor, known as the potential scale reduction factor. If the M chains have converged to the target posterior distribution, then the potential scale reduction factor should be close to 1.

Brooks and Gelman (1998) propose the corrected estimator of the potential scale reduction factor, R_c, that accounts for sampling variability:

$$R_c = \sqrt{\frac{\widehat{d}+3}{\widehat{d}+1}\frac{\widehat{V}}{W}}$$

where $\widehat{d}$ is the estimated degrees of freedom of the approximating Student's t distribution for θ

$$\widehat{d} = \frac{2\widehat{V}^2}{\widehat{\mathrm{Var}}(\widehat{V})}$$

and

$$\widehat{\mathrm{Var}}(\widehat{V}) = \left(\frac{T-1}{T}\right)^2 \frac{1}{M}\widehat{\mathrm{Var}}(\widehat{s}_j^2) + \left(\frac{M+1}{MT}\right)^2 \frac{2}{M-1}B^2 + 2\frac{(M+1)(T-1)}{M^2T}\left\{\widehat{\mathrm{Cov}}(\widehat{s}_j^2, \widehat{\theta}_j^2) - 2\widehat{\theta}\,\widehat{\mathrm{Cov}}(\widehat{s}_j^2, \widehat{\theta}_j)\right\}$$

$\widehat{\mathrm{Var}}(\widehat{s}_j^2)$ is the sample variance of $\widehat{s}_j^2$'s, $j = 1, \ldots, M$. $\widehat{\mathrm{Cov}}(\widehat{s}_j^2, \widehat{\theta}_j^2)$ and $\widehat{\mathrm{Cov}}(\widehat{s}_j^2, \widehat{\theta}_j)$ are the sample covariances of $\widehat{s}_j^2$'s and $\widehat{\theta}_j^2$'s and $\widehat{s}_j^2$'s and $\widehat{\theta}_j$'s, respectively.

Brooks and Gelman (1998) suggested to use the criterion $R_c < 1.2$ for all model parameters to declare MCMC convergence. In practice, a more stringent convergence criterion, $R_c < 1.1$, is often used. If a convergence criterion is not met, longer chains or other means for improving the convergence are needed.

References

Balov, N. 2016. Gelman–Rubin convergence diagnostic using multiple chains. *The Stata Blog: Not Elsewhere Classified.* http://blog.stata.com/2016/05/26/gelman-rubin-convergence-diagnostic-using-multiple-chains/.

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Brooks, S. P., and A. Gelman. 1998. General methods for monitoring convergence of iterative simulations. *Journal of Computational and Graphical Statistics* 7: 434–455. https://doi.org/10.1080/10618600.1998.10474787.

Gelman, A., and D. B. Rubin. 1992. Inference from iterative simulation using multiple sequences. *Statistical Science* 7: 457–472. https://doi.org/10.1214/ss/1177011136.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **bayesstats summary** — Bayesian summary statistics

Title

bayesstats ic — Bayesian information criteria and Bayes factors

Description

`bayesstats ic` calculates and reports model-selection statistics, including the deviance information criterion (DIC), log marginal-likelihood, and Bayes factors (BFs), using current Bayesian estimation results. BFs can be displayed in the original metric or in the log metric. The command also provides two different methods to approximate marginal likelihood.

Quick start

Information criteria for previously saved estimation results `A` and `B` with `A` used as the base model by default

```
bayesstats ic A B
```

Same as above, but use `B` as the base model instead of `A`

```
bayesstats ic A B, basemodel(B)
```

Report BFs instead of the default log BFs

```
bayesstats ic A B, bayesfactor
```

Menu

Statistics > Bayesian analysis > Information criteria

Syntax

```
bayesstats ic [namelist] [, options]
```

namelist is a name, a list of names, `_all`, or `*`. A name may be `.`, meaning the current (active) estimates. `_all` and `*` mean the same thing.

options	Description
Main	
`basemodel(`*name*`)`	specify a base or reference model; default is the first-listed model
`bayesfactor`	report BFs instead of the default log BFs
`diconly`	report only DIC
* `chains(_all | `*numlist*`)`	specify which chains to use for computation; default is `chains(_all)`
* `sepchains`	compute results separately for each chain
Advanced	
`marglmethod(`*method*`)`	specify marginal-likelihood approximation method; default is to use Laplace–Metropolis approximation, `lmetropolis`; rarely used

*Options `chains()` and `sepchains` are relevant only when option `nchains()` is used with `bayesmh` or the `bayes` prefix.

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

method	Description
`lmetropolis`	Laplace–Metropolis approximation; the default
`hmean`	harmonic-mean approximation

Options

Main

`basemodel(`*name*`)` specifies the name of the model to be used as a base or reference model when computing BFs. By default, the first-listed model is used as a base model.

`bayesfactor` specifies that BFs be reported instead of the default log BFs.

`diconly` specifies that only DIC be reported in the table and that the log marginal-likelihood and Bayes factors be omitted from the table. Options `basemodel()`, `basefactor`, and `marglmethod()` have no effect when the `diconly` option is specified.

`chains(_all | `*numlist*`)` specifies which chains from the MCMC sample to use for computation. The default is `chains(_all)` or to use all simulated chains. Using multiple chains, provided the chains have converged, generally improves MCMC summary statistics. Option `chains()` is relevant only when option `nchains()` is specified with `bayesmh` or the `bayes` prefix.

`sepchains` specifies that the results be computed separately for each chain. The default is to compute results using all chains as determined by option `chains()`. Option `sepchains` is relevant only when option `nchains()` is specified with `bayesmh` or the `bayes` prefix.

Advanced

`marglmethod(`*method*`)` specifies a method for approximating the marginal likelihood. *method* is either `lmetropolis`, the default, for Laplace–Metropolis approximation or `hmean` for harmonic-mean approximation. This option is rarely used.

Remarks and examples

Remarks are presented under the following headings:

Bayesian information criteria

Bayesian information criteria are used for selecting a model among a set of candidate models that best fits the data. Likelihood-based inference is known to be prone to overfitting the data. Indeed, it is often possible to increase the likelihood by simply including more parameters in a model. Bayesian information criteria address this problem by applying a penalty proportional to the complexity of the models to the likelihood.

Consider a finite set of Bayesian models $M_1, \ldots, M_r$, which we want to compare with a base model M_b. All models M_js are fit to the same dataset but may differ in their likelihood or prior specification.

Three commonly used information criteria are Akaike information criterion (AIC), Bayesian information criterion (BIC), and DIC. All three criteria are likelihood based and include a goodness-of-fit term proportional to the negative likelihood of the model and a penalty term proportional to the number of parameters in the model. Models with smaller values of these criteria are preferable.

The BIC, originally derived for the exponential family of distributions, is based on the assumption that the model has a flat, noninformative prior. In frequentist statistics, BIC is widely used as a variable-selection criterion, particularly in linear regression. In BIC, the penalty term is a product of the number of parameters in the model and the log of the sample size. The penalty of BIC thus increases not only with the number of parameters but also with the sample size. In the AIC, the penalty term is two times the number of parameters and does not depend on the sample size. As a result, BIC is more conservative than AIC and prefers simpler models. DIC is similar to AIC, but its penalty term is based on a complexity term that measures the difference between the expected log likelihood and the log likelihood at the posterior mean point. DIC is designed specifically for Bayesian estimation that involves MCMC simulations.

The limitation of all three criteria is that they either ignore prior distributions or assume that prior distributions are noninformative. They are thus not well suited for Bayesian sensitivity analysis, when models with the same parameters but different priors are being compared.

The `bayesstats ic` command reports DIC. See [R] **estat ic** after the corresponding maximum likelihood estimation command for values of AIC and BIC.

Bayes factors

In Bayesian inference, BFs are preferred to model-selection criteria because, unlike BIC, AIC, and DIC, they incorporate the information about model priors. Taking into account prior information is essential for Bayesian sensitivity analysis, when models with the same parameters but different priors are being compared.

The BF of two models is just the ratio of their marginal likelihoods calculated using the same dataset. Unlike BIC, AIC, and DIC, BFs include all information about the specified Bayesian model. Thus BFs are not applicable to models with improper priors, whereas BIC, AIC, and DIC are still applicable because they ignore prior information. BFs, however, are often difficult to compute reliably because of the difficulty in computing marginal likelihoods.

BFs also require that posterior distributions be completely specified, including the normalizing constants. The latter is especially important in Bayesian estimation using MCMC simulations, when the normalizing constants are often omitted from the specification of a posterior distribution. The Bayesian estimation commands always simulate from a complete posterior distribution when you select one of the supported Bayesian models, but you need to make sure to include all normalizing constants with your posterior distribution when you are programming your own Bayesian model (see [BAYES] **bayesmh evaluators**) and would like to use BFs during postestimation.

Let BF_{jb}, $j = 1, \ldots, r$, be the BF of model M_j with respect to the base model M_b. All models M_j are fit to the same dataset; otherwise, BFs are meaningless. The `bayesstats ic` command calculates BF_{jb}'s and reports them in log metric or in absolute metric when the `bayesfactor` option is specified.

Jeffreys (1961) proposes the following interpretation of the values of BF_{jb} based on half-units of the log metric:

$\log_{10}(\text{BF}_{jb})$	BF_{jb}	Evidence against M_b
0 to 1/2	1 to 3.2	Bare mention
1/2 to 1	3.2 to 10	Substantial
1 to 2	10 to 100	Strong
>2	>100	Decisive

Kass and Raftery (1995) suggest using twice the natural logarithm of the BF to make it have the same scale as the DIC and likelihood-ratio test statistic. They suggest the following interpretation table:

$2\log_e(\text{BF}_{jb})$	BF_{jb}	Evidence against M_b
0 to 2	1 to 3	Bare mention
2 to 6	3 to 20	Positive
6 to 10	20 to 150	Strong
>10	>150	Very strong

Typically, the worst-fitting model is chosen as a base model. If the base model happens to be better than the comparison model, the corresponding BF will be negative. In this case, you can apply results above to the absolute value of the BF.

BFs compute relative probabilities of how well each model fits the data compared with the base model. Being relative quantities, BFs cannot be used to measure goodness of fit of a particular model unless one assumes that the base model fits the data well. Some researchers view this as a limitation of BFs (Gelman et al. 2014). Kass and Raftery (1995), on the other hand, show that BFs can be

viewed as differences between predictive scores and thus can be used to measure success of different models at predicting the data.

BFs have several advantages over the more traditional, frequentist testing methods. For example, they do not have the limitation of the p-value approach to systematically reject the null hypothesis in large samples. BFs are also suitable for comparing both nonnested and nested models. Also see *Comparing Bayesian models* in [BAYES] **Intro** for more information about Bayesian model comparison.

A key element in computing BFs is calculating the marginal likelihood. Except for some rare cases, marginal likelihood does not have a closed form and needs to be approximated. A detailed review of different approximation methods is given by Kass and Raftery (1995). The default method implemented in `bayesstats ic` (and `bayesmh`) is the Laplace–Metropolis approximation (Lewis and Raftery 1997). The harmonic-mean approximation of the marginal likelihood is also available via the `marglmethod(hmean)` option, but we recommend that you use the default method. See *Methods and formulas* in [BAYES] **bayesmh** for technical details.

Using bayesstats ic

▷ Example 1

The `bayesstats ic` command provides several model-selection statistics that can be used to compare models. To illustrate the use of `bayesstats ic`, we consider `auto.dta`. We model the fuel-efficiency variable `mpg` using a normal distribution with fixed variance but unknown, random mean. There is only one random parameter in this model—`{mpg:_cons}`. We compare the models with three different prior distributions to find the best one among them. We fit the three models using `bayesmh` and save the corresponding estimation results as `uniform1`, `uniform2`, and `normal`.

First, for comparison purposes, let's obtain the maximum likelihood estimate (MLE) of the mean of `mpg`, which is simply the sample mean in our example:

```
. use https://www.stata-press.com/data/r18/auto
(1978 automobile data)
. summarize mpg
```

Variable	Obs	Mean	Std. dev.	Min	Max
mpg	74	21.2973	5.785503	12	41

The sample mean of `mpg` is roughly 21.3.

Next, we use bayesmh to fit our first model of interest. We fix the variance of the normal distribution to 30, which is close to the estimated variance of mpg of $5.79^2 = 33.52$.

```
. set seed 14
. bayesmh mpg, likelihood(normal(30))
> prior({mpg:_cons}, uniform(-10, 10))
> initial({mpg:_cons} 2) saving(uniform1_simdata)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},30)
Prior:
  {mpg:_cons} ~ uniform(-10,10)
------------------------------------------------------------------------------

Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .4102
Log marginal-likelihood = -397.42978            Efficiency       =     .08018

------------------------------------------------------------------------------
             |                                                 Equal-tailed
         mpg |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
       _cons |  9.965511   .0342812   .001211   9.975729   9.871825   9.998796
------------------------------------------------------------------------------

file uniform1_simdata.dta saved.
. estimates store uniform1
```

In the first model, we deliberately chose a prior for {mpg:_cons}, uniform(-10,10), that does not include the value of the sample mean. We thus expect this model to fit poorly. Because of the restricted domain of the specified uniform prior, we also needed to specify an initial value for {mpg:_cons} for MCMC to start from a point of positive posterior probability.

We also specified the saving() option to save the MCMC simulation dataset so that we could use estimates store to store our estimation results for future use. See *Storing estimation results after Bayesian estimation* in [BAYES] **Bayesian postestimation** for details.

```
. set seed 14
. bayesmh mpg, likelihood(normal(30))
> prior({mpg:_cons}, uniform(10, 30))
> initial({mpg:_cons} 20) saving(uniform2_simdata)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},30)
Prior:
  {mpg:_cons} ~ uniform(10,30)
------------------------------------------------------------------------------

Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .4272
Log marginal-likelihood = -237.08583            Efficiency       =      .2414

------------------------------------------------------------------------------
             |                                                 Equal-tailed
         mpg |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
       _cons |  21.31085   .6447073   .013123   21.31485   20.06381   22.57936
------------------------------------------------------------------------------

file uniform2_simdata.dta saved.
. estimates store uniform2
```

In the second model, we used a uniform prior that included the value of the sample mean in its domain.

```
. set seed 14
. bayesmh mpg, likelihood(normal(30))
> prior({mpg:_cons}, normal(30)) saving(normal_simdata)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},30)
Prior:
  {mpg:_cons} ~ normal(0,30)
------------------------------------------------------------------------------

Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .4295
Log marginal-likelihood = -244.16624            Efficiency       =      .2319

------------------------------------------------------------------------------
             |                                                 Equal-tailed
         mpg |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
       _cons |   21.01901   .6461194   .013417   21.01596   19.76637    22.3019
------------------------------------------------------------------------------

file normal_simdata.dta saved.
. estimates store normal
```

In the third model, we used a normal prior with a variance fixed at 30. Note that we did not need to specify an initial value for `{mpg:_cons}` in this model, because the domain of the normal distribution is the whole real line.

Both the `uniform2` and `normal` models yield estimates close to the MLE of 21.3. According to their credible intervals, the domain of the posterior distribution of `{mpg:_cons}` is concentrated around MLE. For example, the 95% credible interval for the `uniform2` model is [20.06, 22.58].

Now, let's use `bayesstats ic` to compare the three models. We list all the models following the command name and use the `normal` model as a reference model.

```
. bayesstats ic uniform1 uniform2 normal, basemodel(normal)
Bayesian information criteria
------------------------------------------------------------------------------
             |       DIC     log(ML)      log(BF)
-------------+----------------------------------------------------------------
    uniform1 |   785.8891  -397.4298   -153.2635
    uniform2 |   471.1909  -237.0858    7.080404
      normal |   471.3905  -244.1662           .
------------------------------------------------------------------------------
Note: Marginal likelihood (ML) is computed
      using Laplace-Metropolis approximation.
```

The `uniform1` model performs worse than the other two models according to the log marginal-likelihood, `log(ML)`, and DIC—the `DIC` value is much larger, and the `log(ML)` value is much smaller for the `uniform1` model. The other two models have only slightly different values for `DIC` and `log(ML)`, according to which the `uniform2` model is preferable.

Although the `uniform2` and `normal` models have different prior distributions, they have almost identical posterior domain, that is, the range of values of `{mpg:_cons}` where the posterior is strictly positive. As such, they will have the same values for AIC and BIC, and we will not be able to discriminate between the two models based on these information criteria.

The most decisive factor between the `uniform2` and `normal` models is the BF. The value of log BF, `log(BF)`, is 7.08, which provides very strong evidence in favor of the `uniform2` model.

We thus conclude that `uniform2` is the best model among the three considered models. This may be explained by the fact that the specified `uniform(10,30)` prior is in more agreement with the likelihood of the data than the specified `normal(0,30)` prior.

After your analysis, remember to erase the saved simulation datasets you no longer need. For example, we erase all of them by typing

```
. erase uniform1_simdata.dta
. erase uniform2_simdata.dta
. erase normal_simdata.dta
```

◁

Stored results

`bayesstats ic` stores the following in `r()`:

Scalars

`r(bayesfactor)`	`1` if `bayesfactor` is specified, `0` otherwise
`r(nchains)`	number of chains used in the computation

Macros

`r(names)`	names of estimation results used
`r(basemodel)`	name of the base or reference model
`r(marglmethod)`	method for approximating marginal likelihood: `lmetropolis` or `hmean`
`r(chains)`	chains used in the computation, if `chains()` is specified

Matrices

`r(ic)`	matrix reporting `DIC`, `log(ML)`, and `log(BF)` or `BF`, if `bayesfactor` is specified
`r(ic_chain#)`	matrix `ic` for chain `#`, if `sepchains` is specified

Methods and formulas

DIC was introduced by Spiegelhalter et al. (2002) for Bayesian model selection using MCMC simulations. DIC is based on the deviance statistics

$$D(\boldsymbol{\theta}) = -2\{\log f(\mathbf{y};\boldsymbol{\theta}) - \log f^*(\mathbf{y};\boldsymbol{\theta}^*)\}$$

where $f(\cdot;\cdot)$ is the likelihood function of the model and $f^*(\mathbf{y};\boldsymbol{\theta}^*)$ is the likelihood of the full model that fits data perfectly. Because $f^*(\mathbf{y};\boldsymbol{\theta}^*)$ is constant across models fit to the same data, it is ignored in the actual calculation of DIC. Given an MCMC sample $\{\boldsymbol{\theta}_t\}_{t=1}^T$, the expected deviance can be estimated by the sample average $\overline{D}(\boldsymbol{\theta}) = 1/T\sum_{t=1}^T D(\boldsymbol{\theta}_t)$. Similarly to AIC and BIC, DIC is a sum of two components: the goodness-of-fit term $\overline{D}(\boldsymbol{\theta})$ and the model complexity term p_D: DIC $= \overline{D}(\boldsymbol{\theta}) + p_D$. The complexity is defined as the difference between the expected deviance and the deviance at the sample posterior mean: $p_D = \overline{D}(\boldsymbol{\theta}) - D(\overline{\boldsymbol{\theta}})$. We thus have

$$\text{DIC} = D(\overline{\boldsymbol{\theta}}) + 2p_D$$

Models with smaller values of DIC are preferred to models with larger values of DIC.

With multiple chains, the `bayesstats ic` command reports the average DIC and the average log marginal-likelihood computed over the chains. If the `sepchains` option is specified, these statistics are reported separately for each chain.

BFs were introduced by Jeffreys (1961). The BF of two models, M_1 and M_2, is given by

$$\text{BF}_{12} = \frac{P(\mathbf{y}|M_1)}{P(\mathbf{y}|M_2)} = \frac{m_1(\mathbf{y})}{m_2(\mathbf{y})}$$

where $m_1(\cdot)$ and $m_2(\cdot)$ are the corresponding marginal likelihoods associated with models M_1 and M_2. (See *Methods and formulas* in [BAYES] **bayesmh** for details about computing marginal likelihood.) BFs are defined only for proper marginal densities. Comparing models with improper priors is allowed as long as the resulting marginal densities are proper. The methodological importance of BFs comes from the fact that the so-called posterior odds is a product of prior odds and BF:

$$\frac{P(M_1|\mathbf{y})}{P(M_2|\mathbf{y})} = \frac{P(M_1)}{P(M_2)} \times \text{BF}_{12}$$

Therefore, if we assume that M_1 and M_2 are equally probable a priori, the posterior odds will be equal to the BF. We thus prefer model M_1 if $\text{BF}_{12} > 1$ and model M_2 otherwise. In practice, because of the higher numerical stability, we often calculate BFs in the (natural) log metric and compare its value against 0.

$$\log\text{BF}_{12} = \log m_1(\mathbf{y}) - \log m_2(\mathbf{y})$$

With multiple chains, BFs are computed using the average log marginal-likelihoods. If the `sepchains` option is specified, BFs are calculated and reported separately for each chain.

References

Gelman, A., J. B. Carlin, H. S. Stern, D. B. Dunson, A. Vehtari, and D. B. Rubin. 2014. *Bayesian Data Analysis*. 3rd ed. Boca Raton, FL: Chapman and Hall/CRC.

Jeffreys, H. 1961. *Theory of Probability*. 3rd ed. Oxford: Oxford University Press.

Kass, R. E., and A. E. Raftery. 1995. Bayes factors. *Journal of the American Statistical Association* 90: 773–795. https://doi.org/10.1080/01621459.1995.10476572.

Lewis, S. M., and A. E. Raftery. 1997. Estimating Bayes factors via posterior simulation with the Laplace–Metropolis estimator. *Journal of the American Statistical Association* 92: 648–655. https://doi.org/10.1080/01621459.1997.10474016.

Spiegelhalter, D. J., N. G. Best, B. P. Carlin, and A. Van Der Linde. 2002. Bayesian measures of model complexity and fit. *Journal of the Royal Statistical Society, Series B* 64: 583–639. https://doi.org/10.1111/1467-9868.00353.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **bayestest model** — Hypothesis testing using model posterior probabilities

[R] **estimates** — Save and manipulate estimation results

Title

bayesstats ppvalues — Bayesian predictive p-values and other predictive summaries

Description

`bayesstats ppvalues` performs posterior predictive checking of the goodness of fit of a Bayesian model. It computes posterior predictive p-values (PPPs) for functions of replicated outcomes produced by `bayespredict`. PPPs measure the agreement between replicated and observed data. PPPs close to 0 or 1 indicate lack of model fit. The command also reports other summary statistics related to posterior predictive checking.

Quick start

Posterior predictive summaries of replicated outcomes

Bayesian predictions for all outcome variables after fitting a two-equation Bayesian model using `bayesmh`

```
bayespredict {_ysim1} {_ysim2}, saving(prdata)
```

Posterior predictive summaries for the first replicated outcome

```
bayesstats ppvalues {_ysim} using prdata
```

Posterior predictive summaries for the simulated residuals of the first outcome

```
bayesstats ppvalues {_resid} using prdata
```

Posterior predictive summaries for both replicated outcomes

```
bayesstats ppvalues {_ysim1} {_ysim2} using prdata
```

Posterior predictive summaries for the first observation of the second replicated outcome squared

```
bayesstats ppvalues ({_ysim2[1]}^2) using prdata
```

Posterior predictive summaries for test statistics of replicated outcomes

Posterior predictive summaries for the maximum and minimum across observations of the second replicated outcome

```
bayesstats ppvalues (y2max:@max({_ysim2})) (y2min:@min({_ysim2}))  ///
     using prdata
```

Posterior predictive summaries for the maximum and minimum across observations of the residuals for the first outcome variable

```
bayesstats ppvalues (rmax:@max({_resid1})) (rmin:@min({_resid1}))  ///
     using prdata
```

Menu

Statistics > Bayesian analysis > Posterior predictive p-values

Syntax

Posterior predictive summaries for replicated outcomes, residuals, and more

```
bayesstats ppvalues yspec [yspec ...] using predfile [, options]
```

Posterior predictive summaries for expressions of replicated outcomes, residuals, and more

```
bayesstats ppvalues (yexprspec) [(yexprspec) ...] using predfile [, options]
```

Posterior predictive summaries for Mata functions of replicated outcomes, residuals, and more

```
bayesstats ppvalues (funcspec) [(funcspec) ...] using predfile [, options]
```

Full syntax

```
bayesstats ppvalues predspec [predspec ...] using predfile [, options]
```

predfile is the name of the dataset created by `bayespredict` that contains prediction results.

yspec is {*ysimspec* | *residspec* | *label*}.

ysimspec is `{_ysim#}` or `{_ysim#[`*numlist*`]}`, where `{_ysim#}` refers to all observations of the #th replicated outcome and `{_ysim#[`*numlist*`]}` refers to the selected observations, *numlist*, of the #th replicated outcome. `{_ysim}` is a synonym for `{_ysim1}`.

residspec is `{_resid#}` or `{_resid#[`*numlist*`]}`, where `{_resid#}` refers to all residuals of the #th replicated outcome and `{_resid#[`*numlist*`]}` refers to the selected residuals, *numlist*, of the #th replicated outcome. `{_resid}` is a synonym for `{_resid1}`.

label is the name of the function simulated using `bayespredict`.

With large datasets, specifications `{_ysim#}` and `{_resid#}` may use a lot of time and memory and should be avoided. See *Generating and saving simulated outcomes* in [BAYES] **bayespredict**.

yexprspec is [*exprlabel*`:`]*yexpr*, where *exprlabel* is a valid Stata name and *yexpr* is a scalar expression that may contain individual observations of simulated outcomes, `{_ysim#[#]}`; individual expected outcome values, `{_mu#[#]}`; individual simulated residuals, `{_resid#[#]}`; and other scalar predictions, {*label*}.

funcspec is [*label*`:`]`@`*func*`(`*arg1*[`,` *arg2*]`)`, where *label* is a valid Stata name; *func* is an official or user-defined Mata function that operates on column vectors and returns a real scalar; and *arg1* and *arg2* are one of `{_ysim[#]}`, `{_resid[#]}`, or `{_mu[#]}`. *arg2* is primarily for use with user-defined Mata functions; see *Defining test statistics using Mata functions* in [BAYES] **bayespredict**.

predspec is one of *yspec*, (*yexprspec*), or (*funcspec*). See *Different ways of specifying predictions and their functions* in [BAYES] **Bayesian postestimation**.

options	Description
* `chains(_all | `*numlist*`)`	specify which chains to use for computation; default is `chains(_all)`
* `sepchains`	compute results separately for each chain
`nolegend`	suppress table legend

*Options `chains()` and `sepchains` are relevant only when option `nchains()` is used with `bayesmh`. `collect` is allowed; see [U] **11.1.10 Prefix commands**.

Options

`chains(_all | `*numlist*`)` specifies which chains from the MCMC sample to use for computation. The default is `chains(_all)` or to use all simulated chains. Using multiple chains, provided the chains have converged, generally improves MCMC summary statistics. Option `chains()` is relevant only when option `nchains()` is specified with `bayesmh`.

`sepchains` specifies that the results be computed separately for each chain. The default is to compute results using all chains as determined by option `chains()`. Option `sepchains` is relevant only when option `nchains()` is specified with `bayesmh`.

`nolegend` suppresses the display of the table legend, which identifies the rows of the table with the expressions they represent.

Remarks and examples

Remarks are presented under the following headings:

Posterior predictive checks
PPPs
Nonlinear effect of labor and capital on companies' output

Posterior predictive checks

Posterior predictive checks, or model checks, are graphical and quantitative methods for comparing observed and replicated outcomes to assess goodness of fit of a Bayesian model. See Box (1980), Zellner (1975), West (1986), Gelman, Meng, and Stern (1996), and Gelman and Rubin (1992) for historical remarks and more in-depth discussions.

Replicated outcomes are outcome values that are simulated from the posterior predictive distribution using the observed covariate data; see *Overview of Bayesian predictions* and *Methods and formulas* in [BAYES] **bayespredict**. The distribution of replicated outcomes or its various summaries are compared with those of the observed outcomes. If they are similar, the Bayesian model is considered to fit the observed data well.

One of the graphical model checks uses quantile–quantile plots to compare observed and replicated residuals. These plots reveal misspecifications of the error distribution of a model. Histograms are commonly used to compare the distributions of the observed and replicated outcomes. More formally, the so-called PPPs, which we describe in the next section, are used to quantify the discrepancy between the summaries of the observed and replicated data.

PPPs

The notion of a PPP was introduced by Rubin (1984) as a Bayesian version of the classical p-value. The role of p-values in classical hypothesis testing is to quantify the discrepancy between the observed sample and population quantities. Test statistics, which are scalar functions of a sample, are commonly used as discrepancy measures. The p-value is defined as the probability to obtain a value of the test statistic as or more extreme than its observed value if the null hypothesis is true. This probability is computed with respect to the sampling distribution of the test statistic.

In a Bayesian setting, the discrepancy between the model and the observed data is measured by test quantities, which are scalar functions of a sample and model parameters. A test statistic is a special case of a test quantity that depends only on the sample. The distribution of a test quantity is defined with respect to the posterior predictive distribution of the replicated data and posterior distribution of model parameters. A PPP (or a Bayesian p-value or a Bayesian predictive p-value) is then defined as the probability that a test quantity for the replicated data could be as or more extreme than for the observed data. You can think of a PPP as a classical p-value averaged over the posterior distribution (Meng 1994). For more information about PPPs, see Tsui and Weerahandi (1989), Gelman, Meng, and Stern (1996), and Gelman et al. (2014), among others.

One of the advantages of PPPs over their classical counterparts is that they automatically handle nuisance parameters by averaging over the posterior distribution of all model parameters. In contrast, classical p-values are conditional on fixed model parameters, typically MLEs. Also, PPPs are not defined conditional on the null hypothesis being true and can be viewed simply as probabilities of model misfit. Values of PPPs close to zero or one indicate lack of fit. For a well-fitting model, the PPP should, ideally, be close to 0.5, although values between 0.05 and 0.95 are often considered acceptable in the literature (Gelman et al. 2014, 150; Congdon 2010, sec. 2.5.2).

One criticism of PPPs is that their distribution under the correct model specification is generally not uniform (for example, Bayarri and Berger [2000] and Robins, van der Vaart, and Ventura [2000]). The distribution tends to be more concentrated around 0.5 when the model is correct. Gelman (2013) argues that this property may be desirable in some cases and discusses the cases when it is not desirable. The author concludes that although it is difficult to provide general recommendations for how best to interpret PPPs, he suggests that they are still useful in practice to discover systematic discrepancies between the observed data and the fitted model.

When you check model fit, it is important to consider different test quantities that describe various aspects of the distribution of the replicated data. Certain distinctive aspects of the assumed model distribution such as symmetry and weight of the tails are commonly used as test quantities. For example, for assumed normal errors, it is appropriate to test the skewness and kurtosis of replicated residuals and compare them with the skewness and kurtosis of a normal distribution. When you use test quantities, Gelman (2013) suggests to use "caution in interpreting diagnostics that strongly depend on parameters or latent data". In addition to test quantities, you can use PPPs to compare individual observations, that is, compare the sample of replicated outcomes for a particular observation with the corresponding observed outcome value.

Nonlinear effect of labor and capital on companies' output

In this example, we show an application of PPPs to assess goodness of fit of a Bayesian model. We adapt an example described in Koop (2003, sec. 5.9) about the effect of labor and capital on companies' production. The dataset, `coutput.dta`, includes data for 123 companies with variables `output`, `labor`, and `capital`. The variables are scaled.

```
. use https://www.stata-press.com/data/r18/coutput
(Company output data)
. describe
Contains data from https://www.stata-press.com/data/r18/coutput.dta
 Observations:           123                  Company output data
    Variables:             3                  22 Feb 2023 13:24
                                              (_dta has notes)
------------------------------------------------------------------------------
Variable      Storage   Display    Value
    name         type    format    label      Variable label
------------------------------------------------------------------------------
output          float   %9.0g                 Output
labor           float   %9.0g                 Labor
capital         float   %9.0g                 Capital
------------------------------------------------------------------------------
Sorted by:
```

Koop (2003) proposes the following nonlinear model for describing companies' output:

$$\texttt{output}_i = \alpha + (\beta_1 \texttt{labor}_i^{\lambda} + \beta_2 \texttt{capital}_i^{\lambda})^{1/\lambda} + \epsilon_i,\ \epsilon_i \sim_{\text{i.i.d.}} N(0,\sigma^2)$$

A nonlinear model ($\lambda > 1$) is expected to provide a better fit for the data than the linear model ($\lambda = 1$). We explore this by using posterior predictive checks.

Without concrete prior knowledge about the parameters α, β_1, β_2, and λ, we specify weakly informative priors for them. We use the $N(0, 100)$ prior for the coefficients, which is noninformative because the variables are scaled to be in the $(0, 2)$ range. We apply exponential prior, $\exp(1)$, for λ because λ is a positive parameter with 1 being a highly probable value for it. Below is the full model specification using `bayesmh`:

```
. bayesmh output =
> ({alpha}+({beta1}*labor^{lambda}+{beta2}*capital^{lambda})^(1/{lambda})),
> likelihood(normal({sig2}))
> prior({alpha beta1 beta2}, normal(0,100))
> prior({lambda}, exp(1)) prior({sig2}, igamma(0.1,0.1))
> init({alpha beta1 beta2 lambda} 1)
> saving(coutput_mcmc) mcmcsize(5000) rseed(16)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  output ~ normal(<expr1>,{sig2})
Priors:
               {sig2} ~ igamma(0.1,0.1)
  {alpha beta1 beta2} ~ normal(0,100)
            {lambda} ~ exponential(1)
Expression:
  expr1 : {alpha}+({beta1}*labor^{lambda}+{beta2}*capital^{lambda})^
  > (1/{lambda})
------------------------------------------------------------------------------
```

```
Bayesian normal regression                      MCMC iterations  =      7,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =      5,000
                                                Number of obs    =        123
                                                Acceptance rate  =      .2176
                                                Efficiency:  min =     .02226
                                                             avg =     .03045
Log marginal-likelihood =  6.9478788                         max =     .03524
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
alpha	1.028072	.0549225	.004364	1.028156	.9300813	1.137604
beta1	.6838483	.0990207	.007467	.6736414	.5037749	.8903975
beta2	.9578192	.140161	.013285	.9413369	.7197326	1.25467
lambda	1.270644	.2435384	.020624	1.255252	.8222015	1.78508
sig2	.0390367	.0052749	.000397	.038495	.0301147	.0503593

```
file coutput_mcmc.dta saved.
```

We generated an MCMC sample of size 5,000 with an average efficiency of about 3%. `bayesmh` estimated the posterior mean of λ, 1.3, to be larger than 1, which implies that labor and capital do have a nonlinear effect on companies' output.

Model assumptions can be assessed through residual analysis. We follow Koop (2003) and use PPPs to compare various aspects of the distribution of residuals simulated from the fitted model and observed residuals. By construction, the distribution of the simulated residuals is $N(0, \sigma^2)$.

▷ Example 1: PPPs for simple test statistics

One simple check is to compare the means and variances of the simulated residuals, $\mathbf{r}^{\text{sim}}$, with those of the observed residuals, $\mathbf{r}^{\text{obs}}$. Let

$$T_1(\mathbf{y}) = \overline{y} = \frac{1}{n}\sum_{i=1}^{n} y_i \text{ and } T_2(\mathbf{y}) = \frac{1}{n-1}\sum_{i=1}^{n}(y_i - \overline{y})^2$$

denote the mean and variance test statistics. We want to compare $T_1(\mathbf{r}^{\text{sim}})$ with $T_1(\mathbf{r}^{\text{obs}})$ and $T_2(\mathbf{r}^{\text{sim}})$ with $T_2(\mathbf{r}^{\text{obs}})$.

We first use `bayespredict` to generate MCMC samples of means and variances of simulated and observed residuals.

```
. bayespredict (mean:@mean({_resid})) (var:@variance({_resid})),
> saving(coutput_pred) rseed(16)

Computing predictions ...

file coutput_pred.dta saved.
file coutput_pred.ster saved.
```

We used built-in Mata functions `mean()` and `variance()` to compute the means and variances; the Mata function specification is designated with `@`. We specified `{_resid}` as the argument to these functions to compute the means and variances of the simulated residuals. We labeled the resulting means as `mean` and variances as `var`; we can use these labels later within `bayesstats ppvalues` to refer to these prediction results. And we saved the simulated results in the prediction dataset, `coutput_pred.dta`. As we discussed in *Prediction dataset* of [BAYES] **bayespredict**, the generated prediction dataset includes, among other variables, the `mean` variable containing 5,000 means of simulated residuals, $\{T_1(\mathbf{r}^{\text{sim},1}), T_1(\mathbf{r}^{\text{sim},2}), \ldots, T_1(\mathbf{r}^{\text{sim},5000})\}$, where $\mathbf{r}^{\text{sim,t}}$ is the column vector

containing 123 residuals simulated from the fitted model using the tth set of MCMC estimates of model parameters. (We saved our MCMC estimates of model parameters in `couput_mcmc.dta` with `bayesmh`.) Additionally, `bayespredict` generated 5,000 means of the observed residuals, $\{T_1(\mathbf{r}^{\text{obs},1}), T_1(\mathbf{r}^{\text{obs},2}), \ldots, T_1(\mathbf{r}^{\text{obs},5000})\}$, and stored them in the `_obs_mean` variable in the prediction dataset. Similarly, `bayespredict` generated variances of simulated and observed residuals and saved them in variables `var` and `_obs_var` in the prediction dataset. See [BAYES] **bayespredict** for details.

We can now access the simulated means and variances within `bayesstats ppvalues`. For example, we specify `{mean}` to compute PPPs for the mean test statistic. We also specify the prediction dataset, `coutput_pred.dta`, containing the simulated means in the required `using` specification.

```
. bayesstats ppvalues {mean} using coutput_pred
Posterior predictive summary    MCMC sample size =      5,000
```

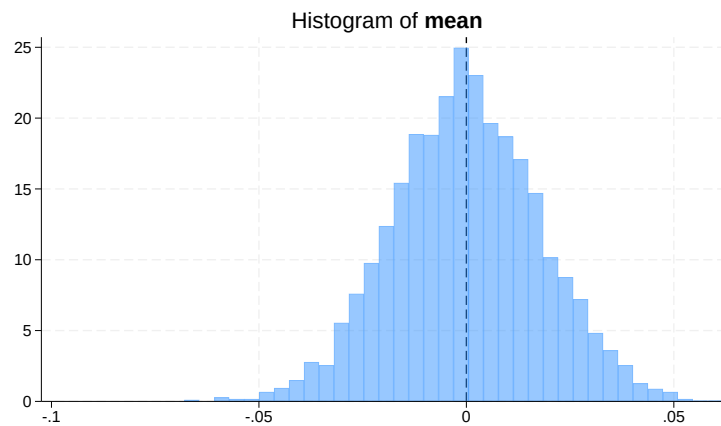
T	Mean	Std. dev.	E(T_obs)	P(T>=T_obs)
mean	-.00007	.0177143	.0000147	.4978

```
Note: P(T>=T_obs) close to 0 or 1 indicates lack of fit.
```

`T` and `T_obs` denote the test statistics computed using the replicated data and observed data, respectively. In our example, `T` is $T_1(\mathbf{r}^{\text{sim}})$ and `T_obs` is $T_1(\mathbf{r}^{\text{obs}})$. The posterior mean estimate, `Mean`, of $T_1(\mathbf{r}^{\text{sim}})$ from the MCMC sample of means of simulated residuals is -0.00007. The posterior mean estimate, `E(T_obs)`, of $T_1(\mathbf{r}^{\text{obs}})$ from the MCMC sample of means of observed residuals is 0.0000147. Both are close to zero. The estimated PPP is about 0.5, which indicates a perfect agreement between the two means. This p-value represents the proportion of times the mean of simulated residuals was greater than or equal to the mean of the observed residuals in the MCMC sample.

The PPP can be also visualized using a histogram with the reference line at the observed mean, which is essentially 0 in our example.

```
. bayesgraph histogram {mean} using coutput_pred, color(%50) xline(0)
```



The PPP is the area of the histogram to the right of the observed value, which is about 50% in our example.

As with the mean, we can compare the variances.

```
. bayesstats ppvalues {var} using coutput_pred
Posterior predictive summary   MCMC sample size =     5,000
```

T	Mean	Std. dev.	E(T_obs)	P(T>=T_obs)
var	.038952	.0073444	.03694	.5762

```
Note: P(T>=T_obs) close to 0 or 1 indicates lack of fit.
```

Posterior mean estimates of the variances of the simulated and observed residuals are similar and are close to the error variance {sig2} of 0.39, as estimated by bayesmh. The estimated PPP is 0.58 and again indicates very good agreement between the variances.

It is not surprising that the means and variances of simulated and observed residuals are in such good agreement. This tends to be true for many models in which the parameters directly model means and variances. In example 3, we explore other discrepancy measures such as skewness and kurtosis. ◁

▷ Example 2: Specifying Mata functions directly with bayesstats ppvalues

In example 1, we computed the mean and variance test statistics with bayespredict. Such specification is preferable with large datasets because it does not save a typically large sample of replicated outcomes. With moderate-sized datasets, you may save the replicated outcomes first and compute the functions within bayesstats ppvalues.

For example, here we simulate replicated outcomes using bayespredict. We replace the earlier coutput_pred.dta with new results.

```
. bayespredict {_ysim}, saving(coutput_pred, replace) rseed(16)
Computing predictions ...
file coutput_pred.dta saved.
file coutput_pred.ster saved.
```

In this case, the generated prediction dataset contains 5,000 MCMC replicates for each observation of our outcome output. That is, the dataset has 123 variables and 5,000 observations (and other auxiliary variables). We can now compute PPPs for any function of the replicated outcomes or their residuals.

We use the same specification of Mata functions with bayesstats ppvalues as we did with bayespredict in example 1.

```
. bayesstats ppvalues (mean:@mean({_resid})) (var:@variance({_resid}))
> using coutput_pred
Posterior predictive summary   MCMC sample size =     5,000
```

T	Mean	Std. dev.	E(T_obs)	P(T>=T_obs)
mean	-.00007	.0177143	.0000147	.4978
var	.038952	.0073444	.03694	.5762

```
Note: P(T>=T_obs) close to 0 or 1 indicates lack of fit.
```

We obtain identical results to example 1. Notice that we can combine various specifications in one call to bayesstats ppvalues.

`bayesstats ppvalues` used the replicated outcomes from `coutput_pred.dta` to compute the simulated residuals, which resulted in an intermediate sample of 5,000 MCMC residuals for each of the 123 observations. It then produced yet another intermediate sample of 5,000 means of the residuals over 123 observations. Finally, it used the sample of 5,000 means to compute the posterior predictive summaries as displayed in the output table. The command performed the same computations for the variances, `var`.

Using `bayespredict` to save the entire sample of replicated outcomes, whenever feasible, is convenient because you can explore various discrepancy measures without having to predefine them. However, there are two other advantages of the earlier specification, in addition to speed and storage efficiency. When you compute functions using `bayespredict`, you can specify expressions of these functions with `bayesstats ppvalues` (or other Bayesian postestimation commands). Also, you can compute your own functions within Stata programs and specify them with `bayespredict`, whereas the use of Stata programs is not allowed within `bayesstats ppvalues` and other Bayesian postestimation commands. But you can define your own Mata functions and use them with `bayesstats ppvalues`, as we demonstrate in the next example.

◁

▷ Example 3: PPPs for user-defined test statistics

Continuing with example 2, we explore other discrepancy measures for the simulated and observed residuals. Given that we expect our residuals to be normally distributed when the model fits the data, we can explore their skewness and kurtosis.

Skewness and kurtosis are related to the third and fourth moments of a distribution. The skewness statistic measures the symmetry of a distribution about its mean. The kurtosis statistic measures the weight of the tails of a distribution. A normal distribution has skewness of 0 and kurtosis of 3.

There are no built-in Mata functions to compute these measures, so we need to define our own.

```
. mata:
------------------------------------------------- mata (type end to exit) -----
: real scalar skew(real colvector vresid) {
>         return (sqrt(length(vresid))*sum(vresid:^3)/(sum(vresid:^2)^1.5))
> }
: real scalar kurtosis(real colvector vresid) {
>         return (length(vresid)*sum(vresid:^4)/(sum(vresid:^2)^2) - 3)
> }
: end
--------------------------------------------------------------------------------
```

Mata function `skew()` computes sample skewness, and `kurtosis()` computes sample kurtosis, but it subtracts 3 from the formula so that the kurtosis of a normally distributed sample is 0. Both functions accept a column vector of residuals as an argument and calculate and return the overall test statistic as a scalar.

We can now use these two functions to compute PPPs for skewness and kurtosis of residuals.

```
. bayesstats ppvalues (sy:@skew({_resid})) (ky:@kurtosis({_resid}))
> using coutput_pred
Posterior predictive summary   MCMC sample size =     5,000
```

T	Mean	Std. dev.	E(T_obs)	P(T>=T_obs)
sy	.0014651	.3420932	.1763123	.3464
ky	-.0368386	.423227	-.3171961	.7304

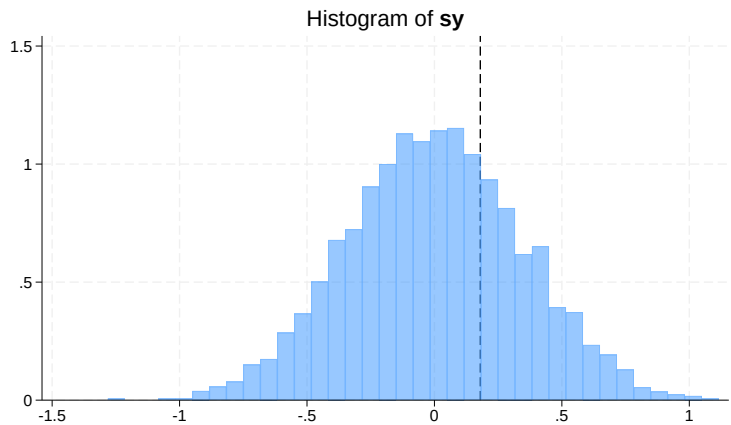
```
Note: P(T>=T_obs) close to 0 or 1 indicates lack of fit.
```

The posterior mean estimates for the skewness and kurtosis of the observed residuals are not as close to zero as their counterparts simulated from the model. Nevertheless, according to the estimated PPPs of 0.35 for skewness and of 0.73 for kurtosis, the observed discrepancies can be explained by sampling variation. For instance, 35% of simulated skewnesses are greater than or equal to the observed skewnesses.

A PPP close to 0 or 1 indicates model misfit. Although there are no definitive recommendations, some literature suggests that PPPs less than 0.05 or larger than 0.95 be considered indicative of lack of fit (Gelman et al. 2014). However, it is important to consider PPPs in the context of your research question, such as whether the observed discrepancy is practically meaningful.

To visualize once again the PPP, we can plot the histogram of the simulated skewness with the reference line at the expected observed value of 0.18.

```
. bayesgraph histogram (sy:@skew({_resid})) using coutput_pred, xline(0.18)
> color(%50)
```



About 35% of the histogram area is on the right of the mean observed skewness of 0.18.

In conclusion, our residual analysis revealed good agreement between the simulated and observed residuals with respect to several test statistics. Therefore, there do not appear to be any violations of the normality assumption for the error terms in the model.

We want to emphasize the importance of the choice of test statistics when assessing model fit. You should avoid using sufficient statistics such as sample mean and variance, which are usually well behaved because they are often directly modeled by parameters. Instead, you should focus on statistics that measure more specific distribution properties such as quantiles, skewness, kurtosis, maximum and minimum, and more.

Stored results

`bayesstats ppvalues` stores the following in `r()`:

Scalars

`r(mcmcsize)`	MCMC sample size used in the computation
`r(nchains)`	number of chains used in the computation

Macros

`r(names)`	names of model parameters and expressions
`r(expr_#)`	#th expression
`r(exprnames)`	expression labels
`r(chains)`	chains used in the computation, if `chains()` is specified

Matrices

`r(summary)`	matrix with predictive statistics for parameters in `r(names)`
`r(summary_chain#)`	matrix `summary` for chain #, if `sepchains` is specified

Methods and formulas

See *Methods and formulas* of [BAYES] **bayespredict** for general definitions and for formulas related to replicated outcomes, $\mathbf{y}^{\text{rep}}$.

Let $T_q(\mathbf{y}, \boldsymbol{\theta})$ be a test quantity. The PPP, $q(T_q)$, is defined as the probability that $T_q(\mathbf{y}^{\text{rep}}, \boldsymbol{\theta})$ is greater than or equal to the observed $T(\mathbf{y}^{\text{obs}}, \boldsymbol{\theta})$ (Rubin 1984, Gelman et al. 2014). Specifically,

$$\begin{aligned} q(T_q) &= \Pr\left\{T_q(\mathbf{y}^{\text{rep}}, \boldsymbol{\theta}) \geq T_q(\mathbf{y}^{\text{obs}}, \boldsymbol{\theta}) | \mathbf{y}^{\text{obs}}, X^{\text{obs}}\right\} \\ &= \int\int 1_{T_q(\mathbf{y}^{\text{rep}}, \boldsymbol{\theta}) \geq T_q(\mathbf{y}^{\text{obs}}, \boldsymbol{\theta})} p(\mathbf{y}^{\text{rep}}, \boldsymbol{\theta} | \mathbf{y}^{\text{obs}}, X^{\text{obs}}) d\mathbf{y}^{\text{rep}} d\boldsymbol{\theta} \\ &= \int\int 1_{T_q(\mathbf{y}^{\text{rep}}, \boldsymbol{\theta}) \geq T_q(\mathbf{y}^{\text{obs}}, \boldsymbol{\theta})} p(\mathbf{y}^{\text{rep}} | \boldsymbol{\theta}, X^{\text{obs}}) p(\boldsymbol{\theta} | \mathbf{y}^{\text{obs}}, X^{\text{obs}}) d\mathbf{y}^{\text{rep}} d\boldsymbol{\theta} \end{aligned}$$

and $1_{(A)}$ is an indicator function of A being true.

In practice, the joint posterior distribution $p(\mathbf{y}^{\text{rep}}, \boldsymbol{\theta} | \mathbf{y}^{\text{obs}}, X^{\text{obs}})$ is not available. Instead, we have a simulated sample $\left\{(\mathbf{y}^{\text{rep},1}, \boldsymbol{\theta}^1), (\mathbf{y}^{\text{rep},2}, \boldsymbol{\theta}^2), \ldots, (\mathbf{y}^{\text{rep},\text{T}}, \boldsymbol{\theta}^T)\right\}$, where T is the MCMC sample size. Then $q(T_q)$ is estimated as

$$\widehat{q}(T_q) = \frac{1}{T}\sum_{t=1}^{T} 1_{T_q(\mathbf{y}^{\text{rep},\text{t}}, \boldsymbol{\theta}^t) \geq T_q(\mathbf{y}^{\text{obs}}, \boldsymbol{\theta}^t)}$$

`bayesstats ppvalues` reports $\widehat{q}(T_q)$ in the output table and labels it `P(T>=T_obs)`. `bayesstats ppvalues` also reports the average observed test quantity, `E(T_obs)`,

$$\widehat{E}\left\{T_q(\mathbf{y}^{\text{obs}}, \boldsymbol{\theta})\right\} = \frac{1}{T}\sum_{t=1}^{T} T_q(\mathbf{y}^{\text{obs}}, \boldsymbol{\theta}^t)$$

and the sample mean and standard deviation of the sample of replicated test quantities, $\left\{T_q(\mathbf{y}^{\text{rep},1}, \boldsymbol{\theta}^1), T_q(\mathbf{y}^{\text{rep},2}, \boldsymbol{\theta}^2), \ldots, T_q(\mathbf{y}^{\text{rep,T}}, \boldsymbol{\theta}^T)\right\}$.

For a special case of test statistics, $T_q(\mathbf{y}, \boldsymbol{\theta}) = T_s(\mathbf{y})$, the above formulas simplify correspondingly.

M. J. Bayarri (1956–2014) was born in Valencia, Spain. She received a bachelor's, master's, and doctorate degree in mathematics, all from the University of Valencia. She began as an assistant professor and then became a full professor at her alma mater.

Bayarri won a Fulbright fellowship to attend Carnegie Mellon University in 1984, which marked the beginning of routine visits to the United States. She became a visiting professor at Purdue University, an adjunct professor at Duke University, and leader of the research program at the Statistical and Applied Mathematical Sciences Institute (SAMSI). She coauthored books on Bayesian statistics and biostatistics, and coauthored numerous research articles, including some award-winning papers. Her main areas of research included selection models, weighted distributions, and Bayesian analysis of queuing systems.

Aside from her published contributions, she held multiple leadership roles. For example, Bayarri served as President of the International Society for Bayesian Analysis (ISBA) and as the principal investigator of Biostatnet, a network of biostatistical researchers. Her critical skills shined as Coordinating Editor of the *Journal of Statistical Planning and Inference* and as an award-winning food critic. In 1997, she was elected as a fellow of the American Statistical Association, and in 2008, she was elected as a fellow of the Institute of Mathematical Statistics.

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Also see

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

[BAYES] **bayespredict** — Bayesian predictions

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

Title

bayesstats summary — Bayesian summary statistics

Description

`bayesstats summary` calculates and reports posterior summary statistics for model parameters and functions of model parameters using current Bayesian estimation results. Posterior summary statistics include posterior means, posterior standard deviations, MCMC standard errors (MCSE), posterior medians, and equal-tailed credible intervals or highest posterior density (HPD) credible intervals.

Quick start

Posterior summaries for all model parameters after a Bayesian regression model

```
bayesstats summary
```

Same as above, but only for parameters `{y:x1}` and `{y:x2}`

```
bayesstats summary {y:x1} {y:x2}
```

Same as above

```
bayesstats summary {y:x1 x2}
```

Posterior summaries for elements 1,1 and 2,1 of matrix parameter `{S}`

```
bayesstats summary {S_1_1 S_2_1}
```

Posterior summaries for all elements of matrix parameter `{S}`

```
bayesstats summary {S}
```

Posterior summaries with HPD instead of equal-tailed credible intervals and with credible level of 90%

```
bayesstats summary, hpd clevel(90)
```

Posterior summaries with MCSE calculated using batch means

```
bayesstats summary, batch(100)
```

Posterior summaries for functions of scalar model parameters

```
bayesstats summary ({y:x1}-{y:_cons}) (sd:sqrt({var}))
```

Posterior summaries for the log-likelihood and log-posterior functions

```
bayesstats summary _loglikelihood _logposterior
```

Posterior summaries for selected model parameters and functions of model parameters and for log-likelihood and log-posterior functions using abbreviated syntax

```
bayesstats summary {var} ({y:x1}-{y:_cons}) _ll _lp
```

Posterior summaries of the simulated outcome

```
bayespredict {_ysim}, saving(predres)
bayesstats summary {_ysim} using predres
```

Posterior summaries of the mean across observations of the simulated outcome labeled as `mymean`

```
bayesstats summary (mymean: @mean({_ysim})) using predres
```

Menu

Statistics > Bayesian analysis > Summary statistics

Syntax

Syntax is presented under the following headings:

Summary statistics for model parameters

Summary statistics for all model parameters

```
bayesstats summary [, options showreffects[(reref)]]

bayesstats summary _all [, options showreffects[(reref)]]
```

Summary statistics for selected model parameters

```
bayesstats summary paramspec [, options]
```

Summary statistics for expressions of model parameters

```
bayesstats summary exprspec [, options]
```

Summary statistics of log-likelihood or log-posterior functions

```
bayesstats summary _loglikelihood|_logposterior [, options]
```

Full syntax

```
bayesstats summary spec [spec ...] [, options]
```

paramspec can be one of the following:

{*eqname*:*param*} refers to a parameter *param* with equation name *eqname*;

{*eqname*:} refers to all model parameters with equation name *eqname*;

{*eqname*:*paramlist*} refers to parameters with names in *paramlist* and with equation name *eqname*; or

{*param*} refers to all parameters named *param* from all equations.

In the above, *param* can refer to a matrix name, in which case it will imply all elements of this matrix. See *Different ways of specifying model parameters* in [BAYES] **Bayesian postestimation** for examples.

exprspec is an optionally labeled expression of model parameters specified in parentheses:

([*exprlabel* :] *expr*)

exprlabel is a valid Stata name, and *expr* is a scalar expression that may not contain matrix model parameters. See *Specifying functions of model parameters* in [BAYES] **Bayesian postestimation** for examples.

`_loglikelihood` and `_logposterior` also have respective synonyms `_ll` and `_lp`.

spec is one of *paramspec*, *exprspec*, `_loglikelihood` (or `_ll`), or `_logposterior` (or `_lp`).

Summary statistics for predictions

Summary statistics for simulated outcomes, residuals, and more

`bayesstats summary` *yspec* [*yspec* ...] `using` *predfile* [`,` *options*]

Summary statistics for expressions of simulated outcomes, residuals, and more

`bayesstats summary` (*yexprspec*) [(*yexprspec*) ...] `using` *predfile* [`,` *options*]

Summary statistics for Mata functions of simulated outcomes, residuals, and more

`bayesstats summary` (*funcspec*) [(*funcspec*) ...] `using` *predfile* [`,` *options*]

Full syntax

`bayesstats summary` *predspec* [*predspec* ...] `using` *predfile* [`,` *options*]

predfile is the name of the dataset created by `bayespredict` that contains prediction results.

yspec is {*ysimspec* | *residspec* | *muspec* | *label*}.

ysimspec is `{_ysim#}` or `{_ysim#[`*numlist*`]}`, where `{_ysim#}` refers to all observations of the #th simulated outcome and `{_ysim#[`*numlist*`]}` refers to the selected observations, *numlist*, of the #th simulated outcome. `{_ysim}` is a synonym for `{_ysim1}`.

residspec is `{_resid#}` or `{_resid#[`*numlist*`]}`, where `{_resid#}` refers to all residuals of the #th simulated outcome and `{_resid#[`*numlist*`]}` refers to the selected residuals, *numlist*, of the #th simulated outcome. `{_resid}` is a synonym for `{_resid1}`.

muspec is `{_mu#}` or `{_mu#[`*numlist*`]}`, where `{_mu#}` refers to all expected values of the #th outcome and `{_mu#[`*numlist*`]}` refers to the selected expected values, *numlist*, of the #th outcome. `{_mu}` is a synonym for `{_mu1}`.

label is the name of the function simulated using `bayespredict`.

With large datasets, specifications `{_ysim#}`, `{_resid#}`, and `{_mu#}` may use a lot of time and memory and should be avoided. See *Generating and saving simulated outcomes* in [BAYES] **bayespredict**.

yexprspec is [*exprlabel* :] *yexpr*, where *exprlabel* is a valid Stata name and *yexpr* is a scalar expression that may contain individual observations of simulated outcomes, `{_ysim#[#]}`; individual expected outcome values, `{_mu#[#]}`; individual simulated residuals, `{_resid#[#]}`; and other scalar predictions, {*label*}.

funcspec is [*label*:]@*func*(*arg1*[, *arg2*]), where *label* is a valid Stata name; *func* is an official or user-defined Mata function that operates on column vectors and returns a real scalar; and *arg1* and *arg2* are one of {_ysim[#]}, {_resid[#]}, or {_mu[#]}. *arg2* is primarily for use with user-defined Mata functions; see *Defining test statistics using Mata functions* in [BAYES] **bayespredict**.

predspec is one of *yspec*, (*yexprspec*), or (*funcspec*). See *Different ways of specifying predictions and their functions* in [BAYES] **Bayesian postestimation**.

options	Description
Main	
clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
batch(#)	specify length of block for batch-means calculations; default is batch(0)
* chains(_all | *numlist*)	specify which chains to use for computation; default is chains(_all)
* sepchains	compute results separately for each chain
skip(#)	skip every # observations from the MCMC sample; default is skip(0)
nolegend	suppress table legend
display_options	control spacing, line width, and base and empty cells
Advanced	
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Options chains() and sepchains are relevant only when option nchains() is used with bayesmh or the bayes prefix.

collect is allowed; see [U] **11.1.10 Prefix commands**.

Options

Main

clevel(#) specifies the credible level, as a percentage, for equal-tailed and HPD credible intervals. The default is clevel(95) or as set by [BAYES] **set clevel**.

hpd displays the HPD credible intervals instead of the default equal-tailed credible intervals.

batch(#) specifies the length of the block for calculating batch means and an MCSE using batch means. The default is batch(0), which means no batch calculations. When batch() is not specified, the MCSE is computed using effective sample sizes instead of batch means. batch() may not be combined with corrlag() or corrtol().

chains(_all | *numlist*) specifies which chains from the MCMC sample to use for computation. The default is chains(_all) or to use all simulated chains. Using multiple chains, provided the chains have converged, generally improves MCMC summary statistics. Option chains() is relevant only when option nchains() is specified with bayesmh or the bayes prefix.

sepchains specifies that the results be computed separately for each chain. The default is to compute results using all chains as determined by option chains(). Option sepchains is relevant only when option nchains() is specified with bayesmh or the bayes prefix.

showreffects and showreffects(*reref*) are for use after multilevel models, and they specify that the results for all or a list *reref* of random-effects parameters be provided in addition to other model parameters. By default, all random-effects parameters are excluded from the results to conserve computation time.

skip(#) specifies that every # observations from the MCMC sample not be used for computation. The default is skip(0) or to use all observations in the MCMC sample. Option skip() can be used to subsample or thin the chain. skip(#) is equivalent to a thinning interval of #+1. For example, if you specify skip(1), corresponding to the thinning interval of 2, the command will skip every other observation in the sample and will use only observations 1, 3, 5, and so on in the computation. If you specify skip(2), corresponding to the thinning interval of 3, the command will skip every 2 observations in the sample and will use only observations 1, 4, 7, and so on in the computation. skip() does not thin the chain in the sense of physically removing observations from the sample, as is done by, for example, bayesmh's thinning() option. It only discards selected observations from the computation and leaves the original sample unmodified.

nolegend suppresses the display of the table legend, which identifies the rows of the table with the expressions they represent.

display_options: vsquish, noemptycells, baselevels, allbaselevels, nofvlabel, fvwrap(#), fvwrapon(*style*), and nolstretch; see [R] **Estimation options**.

Advanced

corrlag(#) specifies the maximum autocorrelation lag used for calculating effective sample sizes. The default is $\min\{500, \texttt{mcmcsize()}/2\}$. The total autocorrelation is computed as the sum of all lag-k autocorrelation values for k from 0 to either corrlag() or the index at which the autocorrelation becomes less than corrtol() if the latter is less than corrlag(). Options corrlag() and batch() may not be combined.

corrtol(#) specifies the autocorrelation tolerance used for calculating effective sample sizes. The default is corrtol(0.01). For a given model parameter, if the absolute value of the lag-k autocorrelation is less than corrtol(), then all autocorrelation lags beyond the kth lag are discarded. Options corrtol() and batch() may not be combined.

Remarks and examples

Remarks are presented under the following headings:

Introduction

bayesstats summary reports posterior summary statistics for model parameters and their functions using the current Bayesian estimation results. When typed without arguments, the command displays results for all model parameters. Alternatively, you can specify a subset of model parameters following the command name; see *Different ways of specifying model parameters* in [BAYES] **Bayesian postestimation**. You can also obtain results for scalar functions of model parameters; see *Specifying functions of model parameters* in [BAYES] **Bayesian postestimation**.

Sometimes, it may be useful to obtain posterior summaries of log-likelihood and log-posterior functions. This can be done by specifying _loglikelihood and _logposterior (or the respective synonyms _ll and _lp) following the command name.

You can also obtain the posterior summaries for prediction quantities when you specify the prediction dataset in the using specification; see *Different ways of specifying predictions and their functions* in [BAYES] **Bayesian postestimation** for how to specify prediction quantities with bayesstats summary.

`bayesstats summary` reports the following posterior summary statistics: posterior mean, posterior standard deviation, MCMC standard error, posterior median, and equal-tailed credible intervals or, if the `hpd` option is specified, HPD credible intervals. The default credible level is set to 95%, but you can change this by specifying the `clevel()` option. Equal-tailed and HPD intervals may produce very different results for asymmetric or highly skewed marginal posterior distributions. The HPD intervals are preferable in this situation.

You should not confuse the term "HPD interval" with the term "HPD region". A $\{100\times(1-\alpha)\}\%$ HPD interval is defined such that it contains $\{100\times(1-\alpha)\}\%$ of the posterior density. A $\{100\times(1-\alpha)\}\%$ HPD region also satisfies the condition that the density inside the region is never lower than that outside the region. For multimodal univariate marginal posterior distributions, the HPD regions may include unions of nonintersecting HPD intervals. For unimodal univariate marginal posterior distributions, HPD regions are indeed simply HPD intervals. The `bayesstats summary` command thus calculates HPD intervals assuming unimodal marginal posterior distributions (Chen and Shao 1999).

Some authors use the term "posterior intervals" instead of "credible intervals" and the term "central posterior intervals" instead of "equal-tailed credible intervals" (for example, Gelman et al. [2014]).

Bayesian summaries for an auto data example

Recall our analysis of `auto.dta` from example 4 in [BAYES] **bayesmh** using the mean-only normal model for `mpg` with a noninformative prior.

```
. use https://www.stata-press.com/data/r18/auto
(1978 automobile data)
. set seed 14
. bayesmh mpg, likelihood(normal({var}))
> prior({mpg:_cons}, flat) prior({var}, jeffreys)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},{var})
Priors:
  {mpg:_cons} ~ 1 (flat)
        {var} ~ jeffreys
------------------------------------------------------------------------------
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .2668
                                                Efficiency:  min =     .09718
                                                             avg =      .1021
Log marginal-likelihood =   -234.645                         max =      .1071
------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |   21.29222   .6828864   .021906   21.27898   19.99152   22.61904
-------------+----------------------------------------------------------------
         var |   34.76572    5.91534   .180754   34.18391    24.9129   47.61286
------------------------------------------------------------------------------
```

Example 1: Summaries for all parameters

If we type `bayesstats summary` without arguments after the `bayesmh` command, we will obtain the same summary table as reported by `bayesmh`.

```
. bayesstats summary
Posterior summary statistics                         MCMC sample size =    10,000
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
mpg						
_cons	21.29222	.6828864	.021906	21.27898	19.99152	22.61904
var	34.76572	5.91534	.180754	34.18391	24.9129	47.61286

The posterior mean of `{mpg:_cons}` is 21.29 and of `{var}` is 34.8. They are close to their respective frequentist analogs (the sample mean of `mpg` is 21.297, and the sample variance is 33.47), because we used a noninformative prior. Posterior standard deviations are 0.68 for `{mpg:_cons}` and 5.92 for `{var}`, and they are comparable to frequentist standard errors under this noninformative prior. The standard error estimates of the posterior means, MCSEs, are low. For example, MCSE is 0.022 for `{mpg:_cons}`. This means that the precision of our estimate is, up to one decimal point, 21.3 provided that MCMC converged. The posterior means and medians of `{mpg:_cons}` are close, which suggests that the posterior distribution for `{mpg:_cons}` may be symmetric. According to the credible intervals, we are 95% certain that the posterior mean of `{mpg:_cons}` is roughly between 20 and 23 and that the posterior mean of `{var}` is roughly between 25 and 48. We can infer from this that `{mpg:_cons}` is greater than, say, 15, and that `{var}` is greater than, say, 20, with a very high probability. (We can use [BAYES] **bayestest interval** to compute the actual probabilities.)

The above is also equivalent to typing

```
. bayesstats summary {mpg:_cons} {var}
  (output omitted)
```

Example 2: Credible intervals

By default, `bayesstats summary` reports 95% equal-tailed credible intervals. We can change the default credible level by specifying the `clevel()` option.

```
. bayesstats summary, clevel(90)
Posterior summary statistics                         MCMC sample size =    10,000
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [90% cred. interval]	
mpg						
_cons	21.29222	.6828864	.021906	21.27898	20.18807	22.44172
var	34.76572	5.91534	.180754	34.18391	26.28517	44.81732

As expected, 90% credible intervals are more narrow.

To calculate and report HPD intervals, we specify the `hpd` option.

```
. bayesstats summary, hpd
Posterior summary statistics                     MCMC sample size =    10,000
```

	Mean	Std. dev.	MCSE	Median	HPD [95% cred. interval]	
mpg						
_cons	21.29222	.6828864	.021906	21.27898	19.94985	22.54917
var	34.76572	5.91534	.180754	34.18391	24.34876	46.12339

The posterior distribution of {mpg:_cons} is symmetric about the posterior mean; thus there is little difference between the 95% equal-tailed credible interval from example 1 and this 95% HPD credible interval for {mpg:_cons}. The 95% HPD interval for {var} has a smaller width than the corresponding equal-tailed interval in example 1.

◁

▷ Example 3: Batch-means estimator

`bayesstats summary` provides two estimators for MCSE: effective-sample-size and batch-means. Estimation using effective sample sizes is the default. You can use the `batch(#)` option to request the batch-means estimator, where # is the batch size. The optimal batch size depends on the autocorrelation in the MCMC sample. For example, if we observe that the autocorrelation for the parameters of interest is negligible after lag 100, we can specify `batch(100)` to estimate MCSE.

In our example, autocorrelation dies out after about lag 10 (see, for example, *Autocorrelation plots* in [BAYES] **bayesgraph** and example 1 in [BAYES] **bayesstats ess**), so we use 10 as our batch size:

```
. bayesstats summary, batch(10)
Posterior summary statistics                     MCMC sample size =    10,000
                                                 Batch size       =        10
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
mpg						
_cons	21.29222	.6828864	.015315	21.27898	19.99152	22.61904
var	34.76572	5.91534	.135295	34.18391	24.9129	47.61286

```
Note: Mean and MCSE are estimated using batch means.
```

The batch-means MCSE estimates are somewhat smaller than those obtained by default using effective sample sizes.

Use caution when choosing the batch size for the batch-means method. For example, if you use the batch size of 1, you will obtain MCSE estimates under the assumption that the draws in the MCMC sample are independent, which is not true.

◁

▷ Example 4: Subsampling or thinning the chain

You can reduce correlation between MCMC draws by thinning or subsampling the MCMC chain. You can use the `skip(#)` option to skip every # observations from the MCMC sample, which is equivalent to a thinning interval of $\# + 1$. For example, if you specify `skip(1)`, corresponding to the thinning interval of 2, `bayesstats summary` will skip every other observation in the sample and will use only observations 1, 3, 5, and so on in the computation. If you specify `skip(2)`, corresponding to the thinning interval of 3, `bayesstats summary` will skip every two observations in the sample and will use only observations 1, 4, 7, and so on in the computation. By default, no observations are skipped—`skip(0)`. Note that `skip()` does not thin the chain in the sense of physically removing observations from the sample, as is done by `bayesmh`'s `thinning()` option. It discards only selected observations from the computation and leaves the original sample unmodified.

```
. bayesstats summary, skip(9)
note: skipping every 9 sample observations; using observations 1,11,21,....
Posterior summary statistics                       MCMC sample size =     1,000
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
mpg						
_cons	21.29554	.6813796	.029517	21.27907	19.98813	22.58582
var	34.7396	5.897313	.206269	33.91782	24.9554	48.11452

We selected to skip every 9 observations, which led to a significant reduction of the MCMC sample size and thus increased our standard deviations. In some cases, with larger MCMC sample sizes, subsampling may decrease standard deviations because of the decreased autocorrelation in the reduced MCMC sample.

◁

▷ Example 5: Summaries for expressions of model parameters

`bayesstats summary` accepts expressions to provide summaries of functions of model parameters. For example, we can use expression `(sd:sqrt({var}))` with a label, `sd`, to summarize the standard deviation of `mpg` in addition to the variance.

```
. bayesstats summary (sd:sqrt({var})) {var}
Posterior summary statistics                       MCMC sample size =     10,000
          sd : sqrt({var})
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
sd	5.87542	.4951654	.014972	5.846701	4.991282	6.900207
var	34.76572	5.91534	.180754	34.18391	24.9129	47.61286

Expressions can also be used for calculating posterior probabilities, although this can be more easily done using `bayestest interval` (see [BAYES] **bayestest interval**). For illustration, let's verify the probability that `{var}` is within the endpoints of the reported credible interval, indeed 0.95.

```
. bayesstats summary (prob:{var}>24.913 & {var}<47.613)
Posterior summary statistics                       MCMC sample size =    10,000
        prob : {var}>24.913 & {var}<47.613
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
prob	.9502	.2175424	.005301	1	0	1

Example 6: Summaries for log likelihood and log posterior

We can use reserved names `_loglikelihood` (or the synonym `_ll`) and `_logposterior` (or the synonym `_lp`) to obtain summaries of the log likelihood and log posterior for the simulated MCMC sample.

```
. bayesstats summary _ll _lp
Posterior summary statistics                       MCMC sample size =    10,000
         _ll : _loglikelihood
         _lp : _logposterior
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
_ll	-235.4162	.990654	.032232	-235.1379	-238.1236	-234.4345
_lp	-238.9507	1.037785	.034535	-238.6508	-241.7889	-237.9187

Example 7: Summaries for predicted outcomes

We continue our series of examples by computing summaries for Bayesian predictions. Let's generate Bayesian predictions of `mpg` and summarize them.

We use `bayespredict` to simulate outcome values for `mpg` for the first 10 observations from the fitted `bayesmh` model. To use `bayespredict`, we must first save the simulation results from `bayesmh` in a Stata dataset, `autosim.dta`. We then use `bayespredict` to save the prediction results in the dataset `mpgreps.dta`.

```
. bayesmh, saving(autosim)
note: file autosim.dta saved.
. bayespredict {_ysim[1/10]}, saving(mpgreps) rseed(16)
Computing predictions ...
file mpgreps.dta saved.
file mpgreps.ster saved.
```

We can now summarize the prediction results by using `bayesstats summary`. We specify the prediction quantity we wish to summarize, the simulated outcome `{_ysim}` in our example, and the prediction dataset, `mpgreps.dta`, which contains the prediction quantity, in the `using` specification.

```
. bayesstats summary {_ysim} using mpgreps
Posterior summary statistics                       MCMC sample size =    10,000
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
_ysim1_1	21.24878	6.018783	.062648	21.23939	9.444973	33.07051
_ysim1_2	21.2539	5.944206	.060415	21.21638	9.421932	32.90605
_ysim1_3	21.3256	5.910363	.061595	21.31499	9.801655	33.02746
_ysim1_4	21.40651	5.963456	.059479	21.45933	9.794156	33.39388
_ysim1_5	21.19781	5.926335	.061197	21.26437	9.759916	32.80291
_ysim1_6	21.34776	5.94413	.059441	21.32314	9.771529	33.30251
_ysim1_7	21.34043	5.898474	.058985	21.34119	9.821613	33.07709
_ysim1_8	21.25329	5.957051	.05886	21.26176	9.476474	32.96236
_ysim1_9	21.25284	5.866096	.05962	21.3052	9.714165	32.82636
_ysim1_10	21.3464	5.931401	.060853	21.30528	9.670334	33.10769

`bayesstats summary` reports posterior summaries for all simulated outcomes in the prediction dataset, `mpgreps.dta`. Estimated posterior means and standard deviations are similar to the corresponding observed values for `mpg`, 21.30 and 5.79, respectively.

We can specifically examine the first observation of the replicated sample, `{_ysim_1}`, and compare it with the observed value, `mpg[1]`, of 22.

```
. bayesstats summary ({_ysim_1}>=`=mpg[1]') using mpgreps
Posterior summary statistics                       MCMC sample size =    10,000
       expr1 : _ysim1_1>=22
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
expr1	.4479	.497303	.004973	0	0	1

We find that 45% of the replicates of `mpg[1]` are greater than 22. The reported probability of 0.45 is known as the posterior predictive p-value and is used for goodness-of-fit checking; see [BAYES] **bayesstats ppvalues**.

◁

Stored results

`bayesstats summary` stores the following in `r()`:

Scalars

`r(mcmcsize)`	MCMC sample size used in the computation
`r(clevel)`	credible interval level
`r(hpd)`	`1` if `hpd` is specified, `0` otherwise
`r(batch)`	batch length for batch-means calculations
`r(skip)`	number of MCMC observations to skip in the computation; every `r(skip)` observations are skipped
`r(corrlag)`	maximum autocorrelation lag
`r(corrtol)`	autocorrelation tolerance
`r(nchains)`	number of chains used in the computation

Macros

`r(names)`	names of model parameters and expressions
`r(expr_#)`	#th expression
`r(exprnames)`	expression labels
`r(chains)`	chains used in the computation, if `chains()` is specified

Matrices

`r(summary)`	matrix with posterior summaries statistics for parameters in `r(names)`
`r(summary_chain#)`	matrix `summary` for chain #, if `sepchains` is specified

Methods and formulas

Methods and formulas are presented under the following headings:

Most of the summary statistics employed in Bayesian analysis are based on the marginal posterior distributions of individual model parameters or functions of model parameters.

Let θ be a scalar model parameter and $\{\theta_t\}_{t=1}^T$ be an MCMC chain of size T drawn from the marginal posterior distribution of θ. For a function $g(\theta)$, substitute $\{\theta_t\}_{t=1}^T$ with $\{g(\theta_t)\}_{t=1}^T$ in the formulas below. If θ is a covariance matrix model parameter, the formulas below are applied to each element of the lower-diagonal portion of θ.

Point estimates

Marginal posterior moments are approximated using the Monte Carlo integration applied to the simulated samples $\{\theta_t\}_{t=1}^T$.

Sample posterior mean and sample posterior standard deviation are defined as follows,

$$\widehat{\theta} = \frac{1}{T}\sum_{t=1}^{T}\theta_t,\ \ \widehat{s}^2 = \frac{1}{T-1}\sum_{t=1}^{T}(\theta_t - \widehat{\theta})^2$$

where $\widehat{\theta}$ and $\widehat{s}^2$ are sample estimators of the population posterior mean $E(\theta_t)$ and posterior variance $\mathrm{Var}(\theta_t)$.

With multiple chains, the posterior mean and standard deviation are estimated using the combined sample of all chains or of those that are requested in the `chains()` option as follows. Let $\{\theta_{jt}\}_{t=1}^T$ be the jth Markov chain, $j = 1, \ldots, M$, with sample mean $\widehat{\theta}_j$ and variance $\widehat{s}_j^2$. The overall sample posterior mean is

$$\widehat{\theta} = \frac{1}{MT}\sum_{j=1}^{M}\sum_{t=1}^{T}\theta_{jt}$$

and equals the average of the sample means of individual chains. Let B and W be the respective between-chains and within-chain variances

$$B = \frac{T}{M-1}\sum_{j=1}^{M}(\widehat{\theta}_j - \widehat{\theta})^2,\ \ W = \frac{1}{M}\sum_{j=1}^{M}\widehat{s}_j^2$$

The estimator of the posterior variance is

$$\widehat{s}^2 = \frac{T-1}{T}W + \frac{1}{T}B \tag{1}$$

When the chains are strongly stationary, $\widehat{s}^2$ is an unbiased estimator of the marginal posterior variance of θ (Gelman et al. 2014, sec. 11.4).

The precision of the sample posterior mean is evaluated by its standard error, also known as the Monte Carlo standard error (MCSE). Note that MCSE cannot be estimated using the classical formula for the standard error, $\widehat{s}/\sqrt{T}$, because of the dependence between θ_t's.

Let

$$\sigma^2 = \text{Var}(\theta_t) + 2\sum_{k=1}^{\infty} \text{Cov}(\theta_t, \theta_{t+k})$$

Then, $\sqrt{T}\times$MCSE approaches σ asymptotically in T.

`bayesstats summary` provides two different approaches for estimating MCSE. Both approaches try to adjust for the existing autocorrelation in the MCMC sample. The first one uses the so-called effective sample size (ESS), and the second one uses batch means (Roberts 1996; Jones et al. 2006).

The ESS-based estimator for MCSE, the default in `bayesstats summary`, is given by

$$\text{MCSE}(\widehat{\theta}) = \widehat{s}/\sqrt{\text{ESS}}$$

ESS is defined as

$$\text{ESS} = T/(1 + 2\sum_{k=1}^{\text{max\_lags}} \rho_k)$$

where ρ_k is the lag-k autocorrelation, and max_lags is the maximum number less than or equal to ρ_{lag} such that for all $k = 1, \ldots, \text{max\_lags}$, $|\rho_k| > \rho_{\text{tol}}$, where ρ_{lag} and ρ_{tol} are specified in options `corrlag()` and `corrtol()` with the respective default values of 500 and 0.01. ρ_k is estimated as γ_k/γ_0, where

$$\gamma_k = \frac{1}{T}\sum_{t=1}^{T-k}(\theta_t - \widehat{\theta})(\theta_{t+k} - \widehat{\theta})$$

is the lag-k empirical autocovariance.

With multiple chains, the overall ESS is given by the sum of the effective sample sizes of individual chains. The MCSE is then calculated using the formula

$$\text{MCSE}(\widehat{\theta}) = \widehat{s}/\sqrt{\sum_{j=1}^{M} \text{ESS}_j}$$

where $\widehat{s}$ is computed using (1) and ESS_j is the effective sample size of the jth chain.

The batch-means estimator of MCSE is obtained as follows. For a given batch of length b, the initial MCMC chain is split into m batches of size b,

$$\{\theta_{j'+1}, \ldots, \theta_{j'+b}\}\ \{\theta_{j'+b+1}, \ldots, \theta_{j'+2b}\}\ \ldots\ \{\theta_{T-b+1}, \ldots, \theta_T\}$$

where $j' = T - m \times b$ and m batch means $\widehat{\mu}_1, \ldots, \widehat{\mu}_m$ are calculated as sample means of each batch. m is chosen as the maximum number such that $m \times b \leq T$. If m is not a divisor of T, the first $T - m \times b$ observations of the sample are not used in the batch-means computation. The batch-means estimator of the posterior variance, $\widehat{s}^2_{\text{batch}}$, is based on the assumption that $\widehat{\mu}_j$s are much less correlated than the original sample draws.

The batch-means estimator of the posterior mean is

$$\widehat{\theta}_{\text{batch}} = \frac{1}{m}\sum_{j=1}^{m} \widehat{\mu}_j$$

We have $\widehat{\theta}_{\text{batch}} = \widehat{\theta}$, whenever $m \times b = T$. Under the assumption that the batch means are uncorrelated, $\widehat{s}^2_{\text{batch}} = \{1/(m-1)\} \sum_{j=1}^{m} (\widehat{\mu}_j - \widehat{\theta}_{\text{batch}})^2$ can be used as an estimator of σ^2/b. This fact justifies the batch-means estimator of MCSE given by

$$\text{MCSE}_{\text{batch}}(\widehat{\theta}) = \frac{\widehat{s}_{\text{batch}}}{\sqrt{m}}$$

The accuracy of the batch-means estimator depends on the choice of the batch length b. The higher the autocorrelation in the original MCMC sample, the larger the batch length b should be, provided that the number of batches m does not become too small; $\sqrt{T}$ is typically used as the maximum value for b. The batch length is commonly determined by inspecting the autocorrelation plot for θ. Under certain assumptions, Flegal and Jones (2010) establish that an asymptotically optimal batch size is of order $T^{1/3}$.

With multiple chains, the batch-means estimator is calculated using the combined sample of all chains or of those that are requested in the `chains()` option.

Credible intervals

Let $\theta_{(1)}, \ldots, \theta_{(T)}$ be an MCMC sample ordered from smallest to largest. Let $(1-\alpha)$ be a credible level. Then, a $\{100 \times (1-\alpha)\}\%$ equal-tailed credible interval is

$$(\theta_{([T\alpha/2])}, \theta_{([T(1-\alpha/2)])})$$

where $[\,]$ in the above imply an integer number.

A $\{100 \times (1-\alpha)\}\%$ HPD interval is defined as the shortest interval among the $\{100 \times (1-\alpha)\}\%$ credible intervals $(\theta_{(j)}, \theta_{(j+[T(1-\alpha)])})$, $j = 1, \ldots, T - [T(1-\alpha)]$.

With multiple chains, credible intervals are computed using the combined sample of all chains or of those requested with the `chains()` option; see Brooks and Gelman (1998, sec. 1.1).

References

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Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **bayesgraph** — Graphical summaries and convergence diagnostics

[BAYES] **bayespredict** — Bayesian predictions

[BAYES] **bayesstats ess** — Effective sample sizes and related statistics

[BAYES] **bayesstats ppvalues** — Bayesian predictive p-values and other predictive summaries

[BAYES] **bayestest interval** — Interval hypothesis testing

Title

bayestest — Bayesian hypothesis testing

Description Remarks and examples Also see

Description

`bayestest` provides two types of Bayesian hypothesis testing, interval hypothesis testing and model hypothesis testing, using current Bayesian estimation results.

`bayestest interval` performs interval hypothesis tests for model parameters and functions of model parameters; see [BAYES] **bayestest interval**.

`bayestest model` tests hypotheses about models by computing posterior probabilities of the models; see [BAYES] **bayestest model**.

Remarks and examples

Bayesian hypothesis testing is fundamentally different from the conventional frequentist hypothesis testing using p-values. Frequentist hypothesis testing is based on the deterministic decision of whether to reject a null hypothesis against an alternative hypothesis based on the obtained p-value. Bayesian hypothesis testing is built upon a probabilistic formulation for a parameter of interest. For example, it can provide a probabilistic summary of how likely that parameter of interest belongs to some prespecified set of values. Also, Bayesian testing can assign a probability to a hypothesis of interest or model of interest given the observed data. This cannot be done in the frequentist testing. The ability to assign a probability to a hypothesis often provides a more natural interpretation of the results. For example, Bayesian hypothesis testing provides a direct answer to the following questions. How likely is it that the mean height of males is larger than six feet? What is the probability that a person is guilty versus being innocent? How likely is one model over the other model? Frequentist hypothesis testing cannot be used to answer these questions.

We consider two forms of Bayesian hypothesis testing: interval hypothesis testing and what we call model hypothesis testing.

The goal of interval hypothesis testing is to estimate the probability that a model parameter lies in a certain interval; see [BAYES] **bayestest interval** for details.

The goal of model hypothesis testing is to test hypotheses about models by computing probabilities of the specified models given the observed data; see [BAYES] **bayestest model** for details.

Also see

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **bayestest interval** — Interval hypothesis testing

[BAYES] **bayestest model** — Hypothesis testing using model posterior probabilities

Title

bayestest interval — Interval hypothesis testing

Description

`bayestest interval` performs interval hypothesis tests for model parameters and functions of model parameters using current Bayesian estimation results. `bayestest interval` reports mean estimates, standard deviations, and MCMC standard errors of posterior probabilities associated with an interval hypothesis.

Quick start

Posterior probability of the hypothesis that $45 <$ `{y:_cons}` < 50

```
bayestest interval {y:_cons}, lower(45) upper(50)
```

Same as above, but skip every 5 observations from the full MCMC sample

```
bayestest interval {y:_cons}, lower(45) upper(50) skip(5)
```

Posterior probability of a hypothesis about a function of model parameter `{y:x1}`

```
bayestest interval (OR:exp({y:x1})), lower(1.1) upper(1.5)
```

Posterior probability of hypotheses $45 <$ `{y:_cons}` < 50 and $0 <$ `{var}` < 10 tested independently

```
bayestest interval ({y:_cons}, lower(45) upper(50))   ///
     ({var}, lower(0) upper(10))
```

Same as above, but tested jointly

```
bayestest interval (({y:_cons}, lower(45) upper(50))  ///
     ({var}, lower(0) upper(10)), joint)
```

Posterior probability of the hypothesis `{mean}` $= 2$ for discrete parameter `{mean}`

```
bayestest interval ({mean}==2)
```

Posterior probability of the interval hypothesis $0 \leq$ `{mean}` ≤ 4

```
bayestest interval {mean}, lower(0, inclusive) upper(4, inclusive)
```

Posterior probability that the first observation of the first simulated outcome is positive (after `bayesmh`)

```
bayespredict {_ysim}, saving(predres)
bayestest interval {_ysim[1]} using predres, lower(0)
```

Posterior probability that the predicted test statistic `chi2stat` is less than 1

```
bayespredict (chi2stat: @chi2stat({_ysim})), saving(predres)
bayestest interval {chi2stat} using predres, upper(1)
```

Menu

Statistics > Bayesian analysis > Interval hypothesis testing

Syntax

Test one interval hypothesis about continuous or discrete parameter

```
bayestest interval exspec [using predfile] [, luspec options]
```

Test one point hypothesis about discrete parameter

```
bayestest interval exspec==# [using predfile] [, options]
```

Test multiple hypotheses separately

```
bayestest interval (testspec) [(testspec) ...] [using predfile] [, options]
```

Test multiple hypotheses jointly

```
bayestest interval (jointspec) [using predfile] [, options]
```

Full syntax

```
bayestest interval (spec) [(spec) ...] [using predfile] [, options]
```

exspec is optionally labeled expression of model parameters, [*prlabel*:]*expr*, where *prlabel* is a valid Stata name (or `prob#` by default), and *expr* is a scalar model parameter or scalar expression (parentheses are optional) containing scalar model parameters. The expression *expr* may not contain variable names.

predfile is the name of the dataset created by `bayespredict` that contains prediction results. When you specify `using` *predfile*, *expr* may contain individual observations of simulated outcomes `{_ysim#[#]}`, expected outcome values `{_mu#[#]}`, simulated residuals `{_resid#[#]}`, and their expressions as described in *Functions of simulated outcomes, expected values, and residuals* in *Syntax* of [BAYES] **bayespredict**. *expr* may also contain {*label*}, which is the name of the function simulated using [BAYES] **bayespredict**. See *Different ways of specifying predictions and their functions* in [BAYES] **Bayesian postestimation**. *expr* may not contain model parameters when `using` *predfile* is specified.

testspec is *exspec*[, *luspec*] or *exspec*`==#` for discrete parameters only.

jointspec is [*prlabel:*](*testspec*) (*testspec*) ..., `joint`. The labels (if any) of *testspec* are ignored.

spec is one of *testspec* or *jointspec*. *spec* may not contain model parameters when `using` *predfile* is specified.

luspec	Null hypothesis
lower(#) [upper(.)]	$\theta > \#$
lower(#, inclusive) [upper(.)]	$\theta \geq \#$
[lower(.)] upper(#)	$\theta < \#$
[lower(.)] upper(#, inclusive)	$\theta \leq \#$
lower($\#_l$) upper($\#_u$)	$\#_l < \theta < \#_u$
lower($\#_l$) upper($\#_u$, inclusive)	$\#_l < \theta \leq \#_u$
lower($\#_l$, inclusive) upper($\#_u$)	$\#_l \leq \theta < \#_u$
lower($\#_l$, inclusive) upper($\#_u$, inclusive)	$\#_l \leq \theta \leq \#_u$

lower(*intspec*) and upper(*intspec*) specify the lower- and upper-interval values, respectively.

intspec is # [, inclusive]

where # is the interval value, and suboption inclusive specifies that this value should be included in the interval, meaning a closed interval. Closed intervals make sense only for discrete parameters.

intspec may also contain a dot (.), meaning negative infinity for lower() and positive infinity for upper(). Either option lower(.) or option upper(.) must be specified.

options	Description
Main	
* chains(_all | *numlist*)	specify which chains to use for computation; default is chains(_all)
* sepchains	compute results separately for each chain
skip(#)	skip every # observations from the MCMC sample; default is skip(0)
nolegend	suppress table legend
Advanced	
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Options chains() and sepchains are relevant only when option nchains() is used with bayesmh or the bayes prefix.

collect is allowed; see [U] 11.1.10 Prefix commands.

Options

Main

chains(_all | *numlist*) specifies which chains from the MCMC sample to use for computation. The default is chains(_all) or to use all simulated chains. Using multiple chains, provided the chains have converged, generally improves MCMC summary statistics. Option chains() is relevant only when option nchains() is specified with bayesmh or the bayes prefix.

sepchains specifies that the results be computed separately for each chain. The default is to compute results using all chains as determined by option chains(). Option sepchains is relevant only when option nchains() is specified with bayesmh or the bayes prefix.

skip(#) specifies that every # observations from the MCMC sample not be used for computation. The default is skip(0) or to use all observations in the MCMC sample. Option skip() can be used to subsample or thin the chain. skip(#) is equivalent to a thinning interval of #+1. For

example, if you specify `skip(1)`, corresponding to the thinning interval of 2, the command will skip every other observation in the sample and will use only observations 1, 3, 5, and so on in the computation. If you specify `skip(2)`, corresponding to the thinning interval of 3, the command will skip every 2 observations in the sample and will use only observations 1, 4, 7, and so on in the computation. `skip()` does not thin the chain in the sense of physically removing observations from the sample, as is done by, for example, `bayesmh`'s `thinning()` option. It only discards selected observations from the computation and leaves the original sample unmodified.

`nolegend` suppresses the display of the table legend, which identifies the rows of the table with the expressions they represent.

Advanced

`corrlag(#)` specifies the maximum autocorrelation lag used for calculating effective sample sizes. The default is $\min\{500, \texttt{mcmcsize()}/2\}$. The total autocorrelation is computed as the sum of all lag-k autocorrelation values for k from 0 to either `corrlag()` or the index at which the autocorrelation becomes less than `corrtol()` if the latter is less than `corrlag()`.

`corrtol(#)` specifies the autocorrelation tolerance used for calculating effective sample sizes. The default is `corrtol(0.01)`. For a given model parameter, if the absolute value of the lag-k autocorrelation is less than `corrtol()`, then all autocorrelation lags beyond the kth lag are discarded.

Remarks and examples

Remarks are presented under the following headings:

Introduction

In this entry, we describe interval hypothesis testing, the goal of which is to estimate the probability that a model parameter lies in a certain interval. Interval hypothesis testing is inversely related to credible intervals. For example, if we have a 95% credible interval for θ with endpoints U and L, then the probability of a hypothesis H_0: $\theta \in [U, L]$ is 0.95. For hypothesis testing using model posterior probabilities, see [BAYES] **bayestest model**.

In frequentist hypothesis testing, we often consider a point hypothesis such as H_0: $\theta = \theta_0$ versus H_a: $\theta \neq \theta_0$. In Bayesian hypothesis testing, the probability $P(\theta = \theta_0)$ is 0 whenever θ has a continuous posterior distribution. A point hypothesis is relevant only to parameters with discrete posterior distributions. For continuous parameters, all hypotheses should be formulated as intervals. One possibility is to consider an interval hypothesis H_0: $\theta \in (\theta_0 - \epsilon, \theta_0 + \epsilon)$, where ϵ is some small value.

Note that Bayesian hypothesis testing does not really need a distinction between the null and alternative hypotheses, in the sense that they are defined in a frequentist statistic. There is no need to "protect" the null hypothesis: if $P\{H_0\text{: } \theta \in (a, b)\} = p$, then $P\{H_a\text{: } \theta \notin (a, b)\} = 1 - p$. In what follows, when we refer to H_0, we imply a hypothesis of interest H_0: $\theta \in \Theta$, and when we refer to H_a, we imply the complement hypothesis H_a: $\theta \in \Theta^c$, where Θ is a set of points from the domain of θ and Θ^c is its complement.

The `bayestest interval` command estimates the posterior probability of a null interval hypothesis H_0 using the simulated posterior distributions of model parameters produced by Bayesian estimation. Essentially, `bayestest interval` reports posterior summaries for a dichotomous expression that represents H_0.

For example, suppose we would like to test the following hypothesis: H_0: $\theta \in (a, b)$. Then,

```
bayestest interval ({theta}, lower(a) upper(b))
```

is equivalent to

```
bayesstats summary ({theta} > a & {theta} < b)
```

`bayestest interval` reports the estimated posterior mean probability for H_0, which is not a p-value—as reported by classical frequentist tests—used to decide whether to reject H_0 in favor of the alternative H_a. The p-value interpretation is based on the dichotomous problem formulation of H_0 versus H_a, assuming that one of these two alternatives is actually true. The answer in the Bayesian context is a probability statement about θ that is free of any deterministic presumptions. For example, if you estimate $P(H_0)$ to be 0.15, you cannot ask whether this value is significant or whether you can reject the null hypothesis. Bayesian interpretation of this probability is that if you draw θ from the specified prior distribution and update your knowledge about θ based on the observed data, then there is a 15% chance that θ will belong to the interval (a, b). So the conclusion of Bayesian hypothesis testing is not an acceptance or rejection of the null hypothesis but an explicit probability statement about the tested hypothesis.

Interval tests for continuous parameters

Let's continue our analysis of `auto.dta` from example 4 in [BAYES] **bayesmh** using the mean-only normal model for `mpg` with a noninformative prior.

```
. use https://www.stata-press.com/data/r18/auto
(1978 automobile data)
. set seed 14
. bayesmh mpg, likelihood(normal({var}))
> prior({mpg:_cons}, flat) prior({var}, jeffreys)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},{var})
Priors:
  {mpg:_cons} ~ 1 (flat)
        {var} ~ jeffreys
------------------------------------------------------------------------------
```

```
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .2668
                                                Efficiency:  min =     .09718
                                                             avg =      .1021
Log marginal-likelihood =   -234.645                         max =      .1071
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
mpg						
_cons	21.29222	.6828864	.021906	21.27898	19.99152	22.61904
var	34.76572	5.91534	.180754	34.18391	24.9129	47.61286

▷ Example 1: Interval hypothesis and credible intervals

In the introduction, we commented on the inverse relationship that exists between interval hypothesis tests and credible intervals. Let's verify this using `bayestest interval`. We are interested in a hypothesis H_0: {mpg:_cons} $\in (19.992, 22.619)$, where the specified numbers are the endpoints of the credible interval for {mpg:_cons} from the `bayesmh` output. To compute the posterior probability for this hypothesis, we specify the parameter following the command line and specify interval endpoints in `lower()` and `upper()`.

```
. bayestest interval {mpg:_cons}, lower(19.992) upper(22.619)
Interval tests     MCMC sample size =    10,000
       prob1 : 19.992 < {mpg:_cons} < 22.619
```

	Mean	Std. dev.	MCSE
prob1	.9496	0.21878	.0053652

The estimated posterior probability is close to 0.95, as we expected, because we used the endpoints of the 95% credible intervals for {mpg:_cons}.

By default, `bayestest interval` labels probabilities as `prob#` (`prob1` in our example). You can specify your own label as long as you enclose the parameter in parentheses:

```
. bayestest interval (mean:{mpg:_cons}), lower(19.992) upper(22.619)
Interval tests     MCMC sample size =    10,000
        mean : 19.992 < {mpg:_cons} < 22.619
```

	Mean	Std. dev.	MCSE
mean	.9496	0.21878	.0053652

◁

Example 2: Testing multiple hypotheses separately

Continuing example 1, we can verify that the probability associated with the credible interval for {var} is also close to 0.95.

We can specify multiple hypotheses with bayestest interval, but we must enclose them in parentheses.

```
. bayestest interval ({mpg:_cons}, lower(19.992) upper(22.619))
>                    ({var}, lower(24.913) upper(47.613))
Interval tests     MCMC sample size =    10,000
       prob1 : 19.992 < {mpg:_cons} < 22.619
       prob2 : 24.913 < {var} < 47.613
```

	Mean	Std. dev.	MCSE
prob1	.9496	0.21878	.0053652
prob2	.9502	0.21754	.0053011

The estimated posterior probability prob2 is also close to 0.95.

Example 3: Testing multiple hypotheses jointly

We can perform joint tests of multiple hypotheses by enclosing hypothesis to be tested jointly in parentheses and by specifying suboption joint. Notice that each individual hypothesis must also be enclosed in parentheses.

```
. bayestest interval (({mpg:_cons}, lower(19.992) upper(22.619))
>                     ({var}, lower(24.913) upper(47.613)), joint)
Interval tests     MCMC sample size =    10,000
       prob1 : 19.992 < {mpg:_cons} < 22.619,
               24.913 < {var} < 47.613
```

	Mean	Std. dev.	MCSE
prob1	.9034	0.29543	.0076789

The joint posterior probability of both {mpg:_cons} and {var} belonging to their respective intervals is 0.9 with a posterior variance of 0.3 and MCSE of 0.008.

Example 4: Full syntax

We can specify multiple separate hypotheses and hypotheses tested jointly in one call to `bayestest interval`.

```
. bayestest interval (({mpg:_cons}, lower(19.992) upper(22.619))
>                     ({var}, lower(24.913) upper(47.613)), joint)
>                    ({mpg:_cons}, lower(21))
>                    ({var}, upper(40))
Interval tests     MCMC sample size =    10,000
       prob1 : 19.992 < {mpg:_cons} < 22.619,
               24.913 < {var} < 47.613
       prob2 : {mpg:_cons} > 21
       prob3 : {var} < 40
------------------------------------------------------------------------------
             |      Mean    Std. dev.      MCSE
-------------+----------------------------------------------------------------
       prob1 |      .9034     0.29543   .0076789
       prob2 |      .6505     0.47684    .015786
       prob3 |      .8136     0.38945   .0110613
------------------------------------------------------------------------------
```

In addition to the joint hypothesis from the previous example, we specified two new separate interval hypotheses for testing {mpg:_cons} $>$ 21 and for testing {var} $<$ 40. The estimated posterior probabilities for these hypotheses are 0.65 and 0.81, respectively.

◁

Example 5: Point hypothesis for continuous parameters

As we discussed in *Introduction* above, point hypothesis for continuous parameters do not make sense, because the corresponding probability is 0:

```
. bayestest interval ({mpg:_cons}==21)
Interval tests     MCMC sample size =    10,000
       prob1 : {mpg:_cons}==21
------------------------------------------------------------------------------
             |      Mean    Std. dev.      MCSE
-------------+----------------------------------------------------------------
       prob1 |         0      0.00000         0
------------------------------------------------------------------------------
```

We can consider a small window around the value of interest and test an interval hypothesis instead:

```
. bayestest interval ({mpg:_cons}, lower(20.5) upper(21.5))
Interval tests     MCMC sample size =    10,000
       prob1 : 20.5 < {mpg:_cons} < 21.5
------------------------------------------------------------------------------
             |      Mean    Std. dev.      MCSE
-------------+----------------------------------------------------------------
       prob1 |      .4932     0.49998   .0138391
------------------------------------------------------------------------------
```

The probability that {mpg:_cons} is between 20.5 and 21.5 is about 50%.

Note that the probability of a continuous parameter belonging to a closed interval or semiclosed interval is the same as that for the open interval. Below we use suboption `inclusive` within `lower()` and `upper()` to request the closed interval.

```
. bayestest interval ({mpg:_cons}, lower(20.5,inclusive) upper(21.5,inclusive))
Interval tests     MCMC sample size =    10,000
       prob1 : 20.5 <= {mpg:_cons} <= 21.5
```

	Mean	Std. dev.	MCSE
prob1	.4932	0.49998	.0138391

We obtain the same results as above for the corresponding open interval.

◁

▷ Example 6: Functions of parameters

We can test functions of model parameters. For example, let's compute the probability that the posterior standard deviation is greater than 6.

```
. bayestest interval (sd: sqrt({var}), lower(6))
Interval tests     MCMC sample size =    10,000
          sd : sqrt({var}) > 6
```

	Mean	Std. dev.	MCSE
sd	.3793	0.48524	.0143883

The estimated probability is 0.38.

◁

Interval tests for discrete parameters

In this section, we demonstrate how to perform hypothesis testing for a discrete parameter.

First, we simulate data from the Poisson distribution with a mean of 2.

```
. clear
. set seed 12345
. set obs 20
Number of observations (_N) was 0, now 20.
. generate double y = rpoisson(2)
```

We fit a Bayesian Poisson model to the data and specify a discrete prior for the mean $P(\mu = k) = 0.25$ for $k = 1, 2, 3, 4$.

```
. set seed 14
. bayesmh y, likelihood(dpoisson({mu}))
> prior({mu}, index(0.25,0.25,0.25,0.25)) initial({mu} 2)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  y ~ poisson({mu})
Prior:
  {mu} ~ index(0.25,0.25,0.25,0.25)
------------------------------------------------------------------------------
Bayesian Poisson model                          MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         20
                                                Acceptance rate  =      .2552
Log marginal-likelihood =  -31.58903            Efficiency       =      .4428
------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
          mu |   2.0014   .1039188   .001562          2           2           2
------------------------------------------------------------------------------
```

▷ Example 7: Point hypotheses for discrete parameters

We can compute probabilities for each of the four discrete values of {mu}.

```
. bayestest interval ({mu}==1) ({mu}==2) ({mu}==3) ({mu}==4)
Interval tests     MCMC sample size =    10,000
       prob1 : {mu}==1
       prob2 : {mu}==2
       prob3 : {mu}==3
       prob4 : {mu}==4
------------------------------------------------------------------------------
             |      Mean    Std. dev.       MCSE
-------------+----------------------------------------------------------------
       prob1 |      .0047     0.06840   .0013918
       prob2 |      .9892     0.10337   .0027909
       prob3 |      .0061     0.07787   .0017691
       prob4 |         0     0.00000          0
------------------------------------------------------------------------------
```

The posterior probability that {mu} equals 2 is 0.99.

◁

▷ Example 8: Interval hypotheses for discrete parameters

As we can with continuous parameters, we can test interval hypotheses for discrete parameters. For example, we can compute the probability of whether {mu} is between 2 and 4.

```
. bayestest interval {mu}, lower(2) upper(4)
Interval tests     MCMC sample size =    10,000
       prob1 : 2 < {mu} < 4
------------------------------------------------
             |      Mean    Std. dev.      MCSE
-------------+----------------------------------
       prob1 |      .0061     0.07787   .0017691
------------------------------------------------
```

The estimated probability is very small.

Note that unlike hypotheses for continuous parameters, hypotheses including open intervals and closed or semiclosed intervals for discrete parameters may have different probabilities.

```
. bayestest interval {mu}, lower(2, inclusive) upper(4, inclusive)
Interval tests     MCMC sample size =    10,000
       prob1 : 2 <= {mu} <= 4
------------------------------------------------
             |      Mean    Std. dev.      MCSE
-------------+----------------------------------
       prob1 |      .9953     0.06840   .0013918
------------------------------------------------
```

The estimated posterior probability that {mu} is between 2 and 4, inclusively, is drastically different compared with the results for the corresponding open interval.

◁

Stored results

bayestest interval stores the following in r():

Scalars

r(mcmcsize)	MCMC sample size used in the computation
r(skip)	number of MCMC observations to skip in the computation; every r(skip) observations are skipped
r(corrlag)	maximum autocorrelation lag
r(corrtol)	autocorrelation tolerance
r(nchains)	number of chains used in the computation

Macros

r(names)	names of probability expressions
r(expr_#)	#th probability expression
r(chains)	chains used in the computation, if chains() is specified

Matrices

r(summary)	test results for parameters in r(names)
r(summary_chain#)	matrix summary for chain #, if sepchains is specified

Methods and formulas

Let θ be a model parameter and $\{\theta_t\}_{t=1}^{T}$ be an MCMC sample of size T drawn from the marginal posterior distribution of θ. It is often of interest to test how likely it is that θ belongs to a particular range of values. Note that testing a point null hypothesis such as H_0: $\theta = \theta_0$ is usually of no interest for parameters with continuous posterior distributions, because the posterior probability $P(H_0)$ is 0.

To perform an open-interval test of the form

$$H_0\colon\ \theta \in (a,b) \text{ versus } H_a\colon\ \theta \notin (a,b)$$

we estimate the posterior probability of H_0 from the given MCMC sample. The `bayestest interval` command calculates the probability $P(H_0)$ based on the simulated marginal posterior distribution of θ. The estimate is given by the frequency of inclusion of θ_ts in the test interval

$$\widehat{P}(H_0) = \frac{1}{T}\sum_{t=1}^{T} 1_{\{\theta_t \in (a,b)\}} \tag{1}$$

where $1_{\{A\}}$ is an indicator function and equals 1 if A is true and 0 otherwise.

When a model parameter θ is discrete, the following closed- and semiclosed-interval tests may be of interest in addition to open-interval tests:

$$H_0\colon\ \theta = a \text{ versus } H_a\colon\ \theta \neq a$$

$$H_0\colon\ \theta \in [a,b] \text{ versus } H_a\colon\ \theta \notin [a,b]$$

$$H_0\colon\ \theta \in [a,b) \text{ versus } H_a\colon\ \theta \notin [a,b)$$

$$H_0\colon\ \theta \in (a,b] \text{ versus } H_a\colon\ \theta \notin (a,b]$$

The corresponding probabilities are calculated as follows:

$$\widehat{P}(H_0) = \frac{1}{T}\sum_{t=1}^{T} 1_{\{\theta_t = a\}}$$

$$\widehat{P}(H_0) = \frac{1}{T}\sum_{t=1}^{T} 1_{\{\theta_t \in [a,b]\}}$$

$$\widehat{P}(H_0) = \frac{1}{T}\sum_{t=1}^{T} 1_{\{\theta_t \in [a,b)\}}$$

$$\widehat{P}(H_0) = \frac{1}{T}\sum_{t=1}^{T} 1_{\{\theta_t \in (a,b]\}}$$

The probability of an alternative hypothesis is always given by $P(H_a) = 1 - P(H_0)$.

The formulas above can be modified to accommodate joint hypotheses tests by multiplying the indicator functions of the individual hypothesis statements. For example, for a joint hypothesis $H_0\colon \theta_1 > a, \theta_2 < b$, we would replace the indicator function with $1_{\{\theta_{1t} > a\}} \times 1_{\{\theta_{2t} < b\}}$ in (1), where $\{\theta_{1t}\}_{t=1}^{T}$ and $\{\theta_{2t}\}_{t=1}^{T}$ are the corresponding MCMC samples for θ_1 and θ_2.

With multiple chains, the `bayestest interval` command performs computation using all simulated chains or those specified in the `chains()` option. The calculations are the same as for `bayesstats summary` in the presence of multiple chains; see *Methods and formulas* in [BAYES] **bayesstats summary**.

Reference

Huber, C. 2016. Introduction to Bayesian statistics, part 1: The basic concepts. *The Stata Blog: Not Elsewhere Classified*. http://blog.stata.com/2016/11/01/introduction-to-bayesian-statistics-part-1-the-basic-concepts/.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **bayespredict** — Bayesian predictions

[BAYES] **bayesstats summary** — Bayesian summary statistics

[BAYES] **bayestest model** — Hypothesis testing using model posterior probabilities

Title

bayestest model — Hypothesis testing using model posterior probabilities

Description

`bayestest model` computes posterior probabilities of Bayesian models fit using the `bayesmh` command or the `bayes` prefix. These posterior probabilities can be used to test hypotheses about model parameters. The command reports marginal likelihoods, prior probabilities, and posterior probabilities for all tested models.

Quick start

Compute posterior probabilities of models corresponding to previously saved estimation results `M1` and `M2`

```
bayestest model M1 M2
```

Same as above, but specify prior probabilities for models

```
bayestest model M1 M2, prior(0.3 0.7)
```

Menu

Statistics > Bayesian analysis > Hypothesis testing using model posterior probabilities

Syntax

```
bayestest model [namelist] [, options]
```

where *namelist* is a name, a list of names, `_all`, or `*`. A name may be `.`, meaning the current (active) estimates. `_all` and `*` mean the same thing.

options	Description
Main	
`prior(`*numlist*`)`	specify prior probabilities for tested models; default is all models are equally likely
* `chains(_all | `*numlist*`)`	specify which chains to use for computation; default is `chains(_all)`
* `sepchains`	compute results separately for each chain
Advanced	
`marglmethod(`*method*`)`	specify marginal-likelihood approximation method; default is to use Laplace–Metropolis approximation, `lmetropolis`; rarely used

*Options `chains()` and `sepchains` are relevant only when option `nchains()` is used with `bayesmh` or the `bayes` prefix.

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

method	Description
`lmetropolis`	Laplace–Metropolis approximation; default
`hmean`	harmonic-mean approximation

Options

Main

`prior(`*numlist*`)` specifies prior probabilities for models. By default, all models are assumed to be equally likely. You may specify probabilities for all tested models, in which case the probabilities must sum to one. Alternatively, you may specify probabilities for all but the last model, in which case the sum of the specified probabilities must be less than one, and the probability for the last model is computed as one minus this sum.

`chains(_all | `*numlist*`)` specifies which chains from the MCMC sample to use for computation. The default is `chains(_all)` or to use all simulated chains. Using multiple chains, provided the chains have converged, generally improves MCMC summary statistics. Option `chains()` is relevant only when option `nchains()` is specified with `bayesmh` or the `bayes` prefix.

`sepchains` specifies that the results be computed separately for each chain. The default is to compute results using all chains as determined by option `chains()`. Option `sepchains` is relevant only when option `nchains()` is specified with `bayesmh` or the `bayes` prefix.

Advanced

`marglmethod(`*method*`)` specifies a method for approximating the marginal likelihood. *method* is either `lmetropolis`, the default, for Laplace–Metropolis approximation or `hmean` for harmonic-mean approximation. This option is rarely used.

Remarks and examples

Remarks are presented under the following headings:

Introduction

In this entry, we describe hypothesis testing by computing model posterior probabilities, probabilities of Bayesian models given observed data. For interval hypothesis testing, see [BAYES] **bayestest interval**.

The `bayestest model` command computes posterior probabilities for specified models. The computed probabilities can be used to compare which model is more likely among considered models given observed data. You can compare models that differ only in several covariates or models with completely different regression functions, such as linear and nonlinear models. You can compare models with different outcome distributions or with different prior distributions or both. The only requirements are that the considered models have proper posterior distributions and that the same data are used to fit the models. If MCMC is used to approximate posterior distributions, convergence of MCMC should also be verified before model comparison.

The results reported by `bayestest model` are related to Bayes factors; see [BAYES] **bayesstats ic** to compute Bayes factors.

To use `bayestest model`, you must store estimation results after each Bayesian model of interest. You can use `estimates store` (see [R] **estimates store**) to store estimation results after `bayesmh` or the `bayes` prefix, as you can with other estimation commands, provided you also saved simulation results from `bayesmh` or the `bayes` prefix using the `saving()` option. See *Storing estimation results after Bayesian estimation* in [BAYES] **Bayesian postestimation** for details.

Testing nested hypotheses

Consider the following Bayesian regression model for `auto.dta`,

$$\texttt{mpg} = \beta_0 + \beta_1\texttt{weight1} + \beta_2\texttt{length1} + \epsilon$$

where `weight1` and `length1` are the original `weight` and `length` variables rescaled to have similar scale as `mpg`.

We assume that errors are normally distributed: $\epsilon \sim \text{normal}(0, \sigma^2)$. We also assume a noninformative Jeffreys prior for the parameters: $(\boldsymbol{\beta}, \sigma^2) \sim 1/\sigma^2$. Suppose that we are interested in testing whether there is a relationship between mileage and weight and length of cars. We will consider four models: the mean-only model, the model with weight only, the model with length only, and the full model with both covariates.

In a frequentist setting, the four models correspond to the following hypotheses: H_0: $\beta_1 = 0$, $\beta_2 = 0$, H_0: $\beta_1 = 0$, and H_0: $\beta_2 = 0$. In a Bayesian setting, we cannot formulate point hypotheses for parameters with continuous distributions; see [BAYES] **bayestest interval** for examples. However, we can compute probabilities of how likely each of the four models is given the observed data.

Let's load auto.dta and generate rescaled versions of weight and length.

```
. use https://www.stata-press.com/data/r18/auto
(1978 automobile data)
. generate weight1 = weight/100
. generate length1 = length/10
```

Next, we fit the four models using bayesmh. We use the saving() option to save the simulation datasets so that we can store estimation results of each model for later use with bayestest model.

The first model we fit is the mean-only model. We store its estimation results as meanonly.

```
. set seed 14
. bayesmh mpg, likelihood(normal({var}))
> prior({mpg:}, flat) prior({var}, jeffreys)
> saving(meanonly_simdata) burnin(3500)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},{var})
Priors:
  {mpg:_cons} ~ 1 (flat)
        {var} ~ jeffreys
------------------------------------------------------------------------------
Bayesian normal regression                      MCMC iterations  =     13,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      3,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .2627
                                                Efficiency:  min =       .105
                                                             avg =      .1064
Log marginal-likelihood = -234.64617                         max =      .1078
------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |   21.29355   .6768607   .020887   21.28059   20.00132   22.61904
-------------+----------------------------------------------------------------
         var |   34.80707   5.963995   .181615   34.23247    24.9129    47.6883
------------------------------------------------------------------------------
file meanonly_simdata.dta saved.
. estimates store meanonly
```

To accommodate the Jeffreys prior for the parameters, we specify suboption flat within the prior() option for coefficients to request the flat prior with the density of 1 and suboption jeffreys within prior() for the variance parameter to request a Jeffreys prior. We also specify a longer burn-in period to improve convergence of MCMC samples for all examples. (Remember to use bayesgraph to check convergence of MCMC.)

We fit the second model containing only covariate `length1` and store its results as `length`:

```
. set seed 14
. bayesmh mpg length1, likelihood(normal({var}))
> prior({mpg:}, flat) prior({var}, jeffreys)
> saving(length_simdata) burnin(3500)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal(xb_mpg,{var})
Priors:
  {mpg:length1 _cons} ~ 1 (flat)                                        (1)
                {var} ~ jeffreys
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
Bayesian normal regression                      MCMC iterations  =     13,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      3,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .2865
                                                Efficiency:  min =      .0771
                                                             avg =      .07938
Log marginal-likelihood =  -198.7678                         max =      .08286
------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
     length1 |  -2.069861   .1882345   .006539  -2.068094   -2.44718  -1.706264
       _cons |   60.20346   3.562119   .127411   60.20927   53.34306   67.22423
-------------+----------------------------------------------------------------
         var |   12.88852   2.273808   .081887   12.62042   9.169482   18.16685
------------------------------------------------------------------------------
file length_simdata.dta saved.
. estimates store length
```

We fit the third model containing only covariate weight1 and store its results as weight:

```
. set seed 14
. bayesmh mpg weight1, likelihood(normal({var}))
> prior({mpg:}, flat) prior({var}, jeffreys)
> saving(weight_simdata) burnin(3500)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal(xb_mpg,{var})
Priors:
  {mpg:weight1 _cons} ~ 1 (flat)                                          (1)
                {var} ~ jeffreys
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
Bayesian normal regression                      MCMC iterations  =     13,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      3,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .1735
                                                Efficiency:  min =      .0463
                                                             avg =      .06694
Log marginal-likelihood = -198.20751                         max =      .07989
------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
     weight1 |  -.6014409   .0506121   .001791  -.6013071  -.6996976    -.50121
       _cons |   39.45934   1.574673   .057646   39.49735   36.31386   42.33547
-------------+----------------------------------------------------------------
         var |   12.13997   2.141741   .099534   11.87332   8.883221   17.14041
------------------------------------------------------------------------------
file weight_simdata.dta saved.
. estimates store weight
```

Finally, we fit the last model containing both covariates and store its results as `full`:

```
. set seed 14
. bayesmh mpg weight1 length1, likelihood(normal({var}))
> prior({mpg:}, flat) prior({var}, jeffreys)
> saving(full_simdata) burnin(3500)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal(xb_mpg,{var})
Priors:
  {mpg:weight1 length1 _cons} ~ 1 (flat)                                  (1)
                        {var} ~ jeffreys
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
Bayesian normal regression                      MCMC iterations  =     13,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      3,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .2323
                                                Efficiency:  min =     .05455
                                                             avg =     .06647
Log marginal-likelihood = -196.86195                         max =     .08085
------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
     weight1 |  -.3977027   .1580411   .005558  -.401646  -.6965175  -.0721332
     length1 |  -.7599159   .5546754   .021944  -.7502182  -1.907818   .3106868
       _cons |   47.5913   6.132597   .262563   47.5656   35.89593   60.18002
-------------+----------------------------------------------------------------
         var |  11.81753    1.96315    .07608   11.59273   8.729182   16.14065
------------------------------------------------------------------------------
file full_simdata.dta saved.
. estimates store full
```

▷ Example 1: Computing posterior probabilities of models

We now use `bayestest model` to compute posterior probabilities of the four models.

```
. bayestest model meanonly length weight full
Bayesian model tests
------------------------------------------------
             |   log(ML)       P(M)     P(M|y)
-------------+----------------------------------
    meanonly | -234.6462     0.2500     0.0000
      length | -198.7678     0.2500     0.1055
      weight | -198.2075     0.2500     0.1848
        full | -196.8619     0.2500     0.7097
------------------------------------------------
Note: Marginal likelihood (ML) is computed using
      Laplace-Metropolis approximation.
```

The mean-only model is very unlikely compared with other models. The length and weight models are somewhat likely with the respective posterior probabilities of 0.11 and 0.18, and the full model has the highest posterior probability of 0.71.

◁

▷ Example 2: Specifying prior probabilities of models

If we have some prior knowledge about each of the models, we can use the `prior()` option to specify prior probabilities for each model. For example, suppose that we have prior knowledge that the weight model is much more likely than the full model so that the prior probabilities are 0.1 for the mean-only model and the length model, 0.6 for the weight model, and only 0.2 for the full model.

```
. bayestest model meanonly length weight full, prior(0.1 0.1 0.6 0.2)
Bayesian model tests
```

	log(ML)	P(M)	P(M|y)
meanonly	-234.6462	0.1000	0.0000
length	-198.7678	0.1000	0.0401
weight	-198.2075	0.6000	0.4210
full	-196.8619	0.2000	0.5389

```
Note: Marginal likelihood (ML) is computed using
      Laplace-Metropolis approximation.
```

Under the specified prior, posterior probabilities of the weight and full models are now more similar: 0.42 and 0.54, respectively, but the full model is still preferable.

The above is equivalent to the following prior specification:

```
. bayestest model meanonly length weight full, prior(0.1 0.1 0.6)
  (output omitted)
```

◁

Using our results, we conclude that `mpg` is related to both `weight` and `length` and would proceed with the full model.

After your analysis, remember to erase the saved simulation datasets you no longer need. For example, we erase all of them by typing

```
. erase meanonly_simdata.dta
. erase weight_simdata.dta
. erase length_simdata.dta
. erase full_simdata.dta
```

Comparing models with different priors

In the previous section, we used `bayestest model` to compare nested hypotheses about which covariates to include in the regression function. We can use `bayestest model` to compare models with not only different covariates but also different outcome distributions and priors for parameters.

We continue our analysis of `auto.dta`, but for simplicity, we now consider the mean-only model for `mpg`. Let's compare models with two slightly different informative priors. We use an informative normal–inverse-gamma prior for both models,

$$(\beta_0|\sigma^2) \sim N(\mu_0, \sigma^2/n_0)$$
$$\sigma^2 \sim \text{InvGamma}(\nu_0/2, \nu_0\sigma_0^2/2)$$

with $\mu_0 = 25$, $n_0 = 10$, and $\sigma_0^2 = 30$, but we consider two different values for the degrees of freedom: $\nu_0 = 5$ and $\nu_0 = 1$.

We use bayesmh to fit our models. Following the formulas, we specify a normal() prior for the constant {mpg:_cons} (mean parameter) and an inverse-gamma prior igamma() for the variance parameter {var}. We specify an expression for the variance of the normal prior distribution in parentheses.

We fit the first model with $\nu_0 = 5$ and store its estimation results as informative1.

```
. set seed 14
. bayesmh mpg, likelihood(normal({var}))
> prior({mpg:}, normal(25,{var}/10))
> prior({var}, igamma(2.5,75)) saving(inf1_simdata)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},{var})
Priors:
  {mpg:_cons} ~ normal(25,{var}/10)
        {var} ~ igamma(2.5,75)
------------------------------------------------------------------------------
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .2548
                                                Efficiency:  min =     .09065
                                                             avg =      .1049
Log marginal-likelihood = -238.55856                         max =      .1192
------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |  21.71853   .6592655   .019091   21.69554   20.44644   23.04896
-------------+----------------------------------------------------------------
         var |  35.47405   5.823372   .193417   34.72454   25.84419     48.228
------------------------------------------------------------------------------
file inf1_simdata.dta saved.
. estimates store informative1
```

We fit the second model with $\nu_0 = 1$ and store its estimation results as `informative2`.

```
. set seed 14
. bayesmh mpg, likelihood(normal({var}))
> prior({mpg:}, normal(25,{var}/10))
> prior({var}, igamma(0.5,15)) saving(inf2_simdata)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},{var})
Priors:
  {mpg:_cons} ~ normal(25,{var}/10)
        {var} ~ igamma(0.5,15)
------------------------------------------------------------------------------

Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .2261
                                                Efficiency:  min =      .0941
                                                             avg =       .109
Log marginal-likelihood =  -239.4049                         max =      .1239

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |   21.7175   .6539814   .021319    21.7295   20.47311   23.02638
-------------+----------------------------------------------------------------
         var |  35.89504   6.288571   .178665   35.17056   25.86084   50.21624
------------------------------------------------------------------------------

file inf2_simdata.dta saved.
. estimates store informative2
```

▷ Example 3: Comparing models with informative priors

We now use `bayestest model` to compare our models with two different informative priors.

```
. bayestest model informative1 informative2
Bayesian model tests

------------------------------------------------------
             |   log(ML)       P(M)      P(M|y)
-------------+----------------------------------------
informative1 | -238.5586     0.5000     0.6998
informative2 | -239.4049     0.5000     0.3002
------------------------------------------------------
Note: Marginal likelihood (ML) is computed using
      Laplace-Metropolis approximation.
```

Assuming that both models are equally likely a priori, the posterior probability of the `informative1` stored results, 0.70, is much higher than the probability of the `informative2` stored results, 0.3.

◁

▷ Example 4: Comparing a model with noninformative prior

A note of caution regarding comparing models with informative and noninformative priors—models with noninformative priors will often win because they are typically in most agreement with the observed data. For models with noninformative priors, most of the information about parameters is contained in a likelihood. As such, any model with an informative prior that is not in perfect agreement with the data will not fit data as well as a model with a noninformative prior.

For example, let's fit our constant-only model using a noninformative Jeffreys prior for the parameters.

```
. set seed 14
. bayesmh mpg, likelihood(normal({var}))
> prior({mpg:}, flat) prior({var}, jeffreys)
> saving(jeffreys_simdata)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},{var})
Priors:
  {mpg:_cons} ~ 1 (flat)
        {var} ~ jeffreys
------------------------------------------------------------------------------
Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .2668
                                                Efficiency:  min =     .09718
                                                             avg =      .1021
Log marginal-likelihood =   -234.645                         max =      .1071
------------------------------------------------------------------------------
                                                              Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |  21.29222   .6828864   .021906   21.27898   19.99152   22.61904
-------------+----------------------------------------------------------------
         var |  34.76572    5.91534   .180754   34.18391    24.9129   47.61286
------------------------------------------------------------------------------
file jeffreys_simdata.dta saved.
. estimates store jeffreys
```

Let's now compare this model with our two informative models.

```
. bayestest model informative1 informative2 jeffreys
Bayesian model tests
------------------------------------------------
             |   log(ML)       P(M)      P(M|y)
-------------+----------------------------------
informative1 | -238.5586     0.3333     0.0194
informative2 | -239.4049     0.3333     0.0083
    jeffreys | -234.6450     0.3333     0.9723
------------------------------------------------
Note: Marginal likelihood (ML) is computed using
      Laplace-Metropolis approximation.
```

The posterior probability of the Jeffreys model is 0.97.

◁

Finally, at the end of our analysis, we erase all the simulation datasets we no longer need. We erase all of them by typing

```
. erase inf1_simdata.dta
. erase inf2_simdata.dta
. erase jeffreys_simdata.dta
```

Stored results

`bayestest model` stores the following in `r()`:

Macros

`r(names)`	names of estimation results used
`r(marglmethod)`	method for approximating marginal likelihood: `lmetropolis` or `hmean`
`r(chains)`	chains used in the computation, if `chains()` is specified

Matrices

`r(test)`	test results for models in `r(names)`
`r(test_chain#)`	matrix `test` for chain #, if `sepchains` is specified

Methods and formulas

Suppose we have r models M_j for $j = 1, \ldots, r$ with prior probabilities $P(M_j)$ such that $\sum_{j=1}^{r} p(M_j) = 1$. Then, posterior probability for model J is

$$P(M_j|\mathbf{y}) = \frac{P(\mathbf{y}|M_j)P(M_j)}{P(\mathbf{y})}$$

where $P(\mathbf{y}|M_j) = m_j(y)$ is the marginal likelihood of M_j with respect to $\mathbf{y}$, and $P(\mathbf{y}) = \sum_{j=1}^{r} P(\mathbf{y}|M_j)P(M_j)$. See *Methods and formulas* in [BAYES] **bayesmh** for details about computing marginal likelihood.

With multiple chains, the `bayestest model` command uses the averaged across chains log marginal-likelihood for calculations. If the `sepchains` option is specified, the results are calculated and reported separately for each chain.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **bayesstats ic** — Bayesian information criteria and Bayes factors

[BAYES] **bayesstats summary** — Bayesian summary statistics

[BAYES] **bayestest interval** — Interval hypothesis testing

Title

bayespredict — Bayesian predictions

Description

`bayespredict` computes Bayesian predictions using current estimation results produced by `bayesmh` with built-in likelihood models or by `bayes: var`, `bayes: xtreg`, `bayes: xtlogit`, `bayes: xtprobit`, `bayes: xtologit`, `bayes: xtoprobit`, `bayes: xtpoisson`, `bayes: xtnbreg`, or `bayes: xtmlogit`. The Bayesian predictions are saved in a separate Stata dataset. Bayesian predictions include simulated outcomes, which are samples from the posterior predictive distribution of the fitted Bayesian model, and their functions. You can also compute posterior summaries of simulated outcomes and store them as new variables in the current dataset.

`bayesreps` generates a random subset of MCMC replicates of simulated outcomes from the entire MCMC sample and stores them as new variables in the current dataset. This command is useful for checking model fit.

`bayespredict` and `bayesreps` require that you first save MCMC results by using the `saving()` option with the `bayesmh` command or the `bayes` prefix.

Quick start

Simulated outcomes

Predictions for the first outcome variable after fitting a two-equation Bayesian model using `bayesmh`

```
bayespredict {_ysim}, saving(prdata)
```

Same as above, but for the second outcome variable, replacing `prdata.dta` with new prediction results

```
bayespredict {_ysim2}, saving(prdata, replace)
```

Predictions for the first outcome variable and observations 2 through 5

```
bayespredict {_ysim1[2/5]}, saving(prdata, replace)
```

Test statistics for simulated outcomes

Maximums and minimums of simulated outcomes computed over observations for the first outcome variable

```
bayespredict (rmax:@max({_ysim1})) (rmin:@min({_ysim1})),    ///
     saving(prdata, replace)
```

Maximums and minimums of residuals for the second outcome variable

```
bayespredict (rmax:@max({_resid2})) (rmin:@min({_resid2})),  ///
     saving(prdata, replace)
```

Posterior summaries of simulated outcomes

Posterior means for the two outcomes stored in new variables `pmean1` and `pmean2` in the current dataset

```
bayespredict pmean1 pmean2, mean
```

Same as above, but calculating posterior medians and storing them in new variables `pmedian1` and `pmedian2` specified as a variable stub `pmedian*`

```
bayespredict pmedian*, median
```

95% credible intervals for the second outcome variable `y2`; the lower and upper bounds are stored in `cril2` and `criu2`, respectively

```
bayespredict cril2 criu2, cri outcome(y2)
```

Simulate and save MCMC replicates of simulated outcomes

Generate 10 MCMC replicates for the first outcome in the model, and store them as new variables `y1rep1`, ..., `y1rep10` in the current dataset

```
bayesreps y1rep*, nreps(10)
```

Same as above, but for the second outcome `y2` and storing the results in new variables `y2rep1`, ..., `y2rep10`

```
bayesreps y2rep*, nreps(10) outcome(y2)
```

Menu

Statistics > Bayesian analysis > Predictions

Syntax

Syntax is presented under the following headings:

Compute predictions

Prediction of selected outcome variables and observations

```
bayespredict ysimspec [ysimspec ...] [if] [in], saving(filespec) [simopts]
```

Functions of simulated outcomes, expected values, and residuals

```
bayespredict (funcspec) [(funcspec) ...] [if] [in], saving(filespec) [simopts]
```

ysimspec is `{_ysim#}` or `{_ysim#[`*numlist*`]}`, where `{_ysim#}` refers to all observations of the #th simulated outcome and `{_ysim#[`*numlist*`]}` refers to the selected observations, *numlist*, of the #th simulated outcome. `{_ysim}` is a synonym for `{_ysim1}`. With large datasets, specification `{_ysim#}` may use a lot of time and memory and should be avoided. See *Generating and saving simulated outcomes*.

funcspec is one of the following,

```
[label:]@func(arg1 [, arg2])
[label:]@userprog arg1 [arg2] [, extravars(varlist) passthruopts(string)]
```

where *label* is a valid Stata name; *func* is an official or user-defined Mata function that operates on column vectors and returns a real scalar; *userprog* is a user-defined Stata program; and *arg1* and *arg2* are one of `{_ysim[#]}`, `{_resid[#]}`, or `{_mu[#]}`. `{_mu#}` refers to expected values, and `{_resid#}` refers to residuals for the #th outcome, where the latter is defined as the difference between `{_ysim#}` and `{_mu#}`. *arg2* is primarily for use with user-defined Mata functions; see *Defining test statistics using Mata functions*.

Compute posterior summaries of simulated outcomes

Posterior mean of simulated outcomes

```
bayespredict [type] newvarspec [if] [in], mean
    [outcome(depvar) meanopts simopts]
```

Posterior median or posterior standard deviation of simulated outcomes

```
bayespredict [type] newvarspec [if] [in], median|std
    [outcome(depvar) simopts]
```

Credible intervals for simulated outcomes

```
bayespredict [type] newvar_l newvar_u [if] [in], cri
    [outcome(depvar) criopts simopts]
```

newvarspec is *newvar* for single-outcome models and *newvarlist* or *stub*`*` for multiple-outcome models.

Generate a subset of MCMC replicates of simulated outcomes

`bayesreps` [*type*] *newrepspec* [*if*] [*in*], `nreps(#)` [`outcome(`*depvar*`)` *simopts*]

newrepspec is *newvar* with `nreps(1)` for a single replicate and *stub*`*` with `nreps(#)`, where # is greater than 1, for multiple replicates.

meanopts	Description
Main	
`mcse(`*newvar*`)`	create *newvar* containing MCSEs
Advanced	
`batch(#)`	specify length of block for batch-means calculations; default is `batch(0)`
`corrlag(#)`	specify maximum autocorrelation lag; default varies
`corrtol(#)`	specify autocorrelation tolerance; default is `corrtol(0.01)`

simopts	Description
Simulation	
`rseed(#)`	random-number seed
* `chains(_all` | *numlist*`)`	specify which chains to use for computation; default is `chains(_all)`
`dots`	display dots every 100 iterations and iteration numbers every 1,000 iterations
`dots(#[, every(#)])`	display dots as simulation is performed

*Option `chains()` is relevant only when option `nchains()` is used with `bayesmh`.

criopts	Description
Main	
`clevel(#)`	set credible interval level; default is `clevel(95)`
`hpd`	calculate HPD credible intervals instead of the default equal-tailed credible intervals

Options

Options are presented under the following headings:

Options for predictions
Options for posterior summaries
Options for bayesreps

Options for predictions

Main

`saving(`*filename*`[ , replace ])` saves the requested predictions such as simulated outcomes and residuals in *filename*`.dta`. It also saves auxiliary estimation results in *filename*`.ster`, which is accessible by specifying `estimates use` *filename*. The `replace` option specifies to overwrite *filename*`.dta` and *filename*`.ster` if they exist. `saving()` is required when computing predictions. The results are saved only for the outcome variables, observations, and functions that are specified with `bayespredict`. See *Prediction dataset* for details.

`extravars(`*varlist*`)` is for use with user-defined Stata programs. It specifies any variables in addition to dependent and independent variables that you may need to calculate predictions. For example, such variables are offset variables and exposure variables for count-data models.

`passthruopts(`*string*`)` is for use with user-defined Stata programs. It specifies a list of options you may want to pass to your program when calculating predictions. For example, these options may contain fixed values of model parameters and hyperparameters.

Simulation

`rseed(#)` sets the random-number seed. This option can be used to reproduce results. With one chain, `rseed(#)` is equivalent to typing `set seed #` prior to calling `bayespredict`; see [R] **set seed**. With multiple chains, you should use `rseed()` for reproducibility; see *Reproducing results* in [BAYES] **bayesmh**.

`chains(_all | `*numlist*`)` specifies which chains from the MCMC sample to use for computation. The default is `chains(_all)` or to use all simulated chains. Using multiple chains, provided the chains have converged, generally improves MCMC summary statistics. Option `chains()` is relevant only when option `nchains()` is specified with `bayesmh`.

`dots` and `dots(#)` specify to display dots during simulation. With multiple chains, these options affect all chains. `dots(#)` displays a dot every # iterations. If `dots(..., every(#))` is specified, then an iteration number is displayed every #th iteration instead of a dot. `dots(, every(#))` is equivalent to `dots(1, every(#))`. `dots` displays dots every 100 iterations and iteration numbers every 1,000 iterations; it is a synonym for `dots(100, every(1000))`.

Options for posterior summaries

Main

`mean` calculates posterior means of a simulated outcome variable and stores them as a new variable in the current dataset.

`median` calculates posterior medians of a simulated outcome variable and stores them as a new variable in the current dataset.

`std` calculates posterior standard deviations of a simulated outcome variable and stores them as a new variable in the current dataset.

`mean`, `median`, and `std` can compute results for all simulated outcome variables or for a specific one. To compute results for all simulated outcome variables, you specify p new variables, where p is the number of dependent variables. Alternatively, you can specify *stub*`*`, in which case these options will store the results in variables *stub*`1`, *stub*`2`, ..., *stubp*. To compute the results for a specific simulated outcome variable, you specify one new variable and, optionally, the outcome variable name in option `outcome()`; if you omit `outcome()`, the first outcome variable is assumed.

cri calculates credible intervals for a simulated outcome variable and stores the corresponding lower and upper bounds in two new variables in the current dataset. For multiple-outcome models, it computes the results for the outcome variable as specified in option outcome() or, by default, for the first outcome variable.

outcome(*depvar*) is for use with multiple-outcome models when computing posterior summaries of simulated outcomes. It specifies for which simulated outcome posterior summaries are to be calculated. outcome() should contain a name of the outcome (dependent) variable. The default is the first outcome variable. outcome() may not be combined with the *newvarlist* or *stub** specification.

mcse(*newvar*) is for use in a combination with option mean. It adds *newvar* of storage type *type* containing MCSEs for the posterior means of a simulated outcome variable. If multiple variables are specified with bayespredict, *newvar* is used as a stub *newvar**.

clevel(#) specifies the credible level, as a percentage, for equal-tailed and HPD credible intervals. The default is clevel(95) or as set by [BAYES] **set clevel**. This option requires that cri also be specified.

hpd calculates the HPD credible intervals instead of the default equal-tailed credible intervals. This option requires that cri also be specified.

Simulation

rseed(#) sets the random-number seed. This option can be used to reproduce results. With one chain, rseed(#) is equivalent to typing set seed # prior to calling bayespredict; see [R] **set seed**. With multiple chains, you should use rseed() for reproducibility; see *Reproducing results* in [BAYES] **bayesmh**.

chains(_all | *numlist*) specifies which chains from the MCMC sample to use for computation. The default is chains(_all) or to use all simulated chains. Using multiple chains, provided the chains have converged, generally improves MCMC summary statistics. Option chains() is relevant only when option nchains() is specified with bayesmh.

dots and dots(#) specify to display dots during simulation. With multiple chains, these options affect all chains. dots(#) displays a dot every # iterations. If dots(..., every(#)) is specified, then an iteration number is displayed every #th iteration instead of a dot. dots(, every(#)) is equivalent to dots(1, every(#)). dots displays dots every 100 iterations and iteration numbers every 1,000 iterations; it is a synonym for dots(100, every(1000)).

Advanced

The advanced options are available only in a combination with option mean.

batch(#) specifies the length of the block for calculating batch means and an MCSE using batch means. The default is batch(0), which means no batch calculations. When batch() is not specified, the MCSE is computed using effective sample sizes instead of batch means. batch() may not be combined with corrlag() or corrtol().

corrlag(#) specifies the maximum autocorrelation lag used for calculating effective sample sizes. The default is $\min\{500, \texttt{mcmcsize()}/2\}$. The total autocorrelation is computed as the sum of all lag-k autocorrelation values for k from 0 to either corrlag() or the index at which the autocorrelation becomes less than corrtol() if the latter is less than corrlag(). Options corrlag() and batch() may not be combined.

corrtol(#) specifies the autocorrelation tolerance used for calculating effective sample sizes. The default is corrtol(0.01). For a given model parameter, if the absolute value of the lag-k

autocorrelation is less than corrtol(), then all autocorrelation lags beyond the kth lag are discarded. Options corrtol() and batch() may not be combined.

Options for bayesreps

Main

nreps(#) specifies the number of MCMC replicates of simulated outcomes to be drawn at random from the entire sample of MCMC replicates. # must be an integer between 1 and the MCMC sample size, inclusively. The generated replicates are stored as new variables in the current dataset. For a single replicate, nreps(1), you specify one new variable name. For multiple replicates, you specify a *stub**, in which case the replicates will be stored in variables *stub*1, *stub*2, ..., *stub*R, where R is the number of replicates specified in nreps().

outcome(*depvar*) is for use with multiple-outcomes models when generating MCMC replicates of simulated outcomes using bayesreps. It specifies for which simulated outcome MCMC replicates are to be generated. The default is to use the first outcome variable. You can specify other outcome (dependent) variable names in outcome().

Simulation

rseed(#) sets the random-number seed. This option can be used to reproduce results. With one chain, rseed(#) is equivalent to typing set seed # prior to calling bayespredict; see [R] **set seed**. With multiple chains, you should use rseed() for reproducibility; see *Reproducing results* in [BAYES] **bayesmh**.

chains(_all | *numlist*) specifies which chains from the MCMC sample to use for computation. The default is chains(_all) or to use all simulated chains. Using multiple chains, provided the chains have converged, generally improves MCMC summary statistics. Option chains() is relevant only when option nchains() is specified with bayesmh.

dots and dots(#) specify to display dots during simulation. With multiple chains, these options affect all chains. dots(#) displays a dot every # iterations. If dots(..., every(#)) is specified, then an iteration number is displayed every #th iteration instead of a dot. dots(, every(#)) is equivalent to dots(1, every(#)). dots displays dots every 100 iterations and iteration numbers every 1,000 iterations; it is a synonym for dots(100, every(1000)).

Remarks and examples

Remarks are presented under the following headings:

Examples are presented under the following headings:

Overview of Bayesian predictions

Bayesian analysis rests on the assumptions that model parameters are random quantities distributed according to some prior beliefs and that the data, once observed, are fixed. The main goal of Bayesian inference is to estimate the posterior distribution of model parameters, which combines the prior beliefs with evidence from the observed data, and form inferences about these parameters. But what if we want to estimate a future outcome value? This is one of the goals of Bayesian prediction.

Bayesian predictions are useful in a wide range of applications. They can be used as optimal predictors in forecasting, optimal classifiers in classification problems, imputations for missing data, and more. They are also important for checking model goodness of fit.

Bayesian prediction differs from frequentist prediction. Prediction, in a frequentist sense, is a deterministic function of estimated model parameters. For example, in a linear regression, the linear predictor, which is a linear combination of estimated regression coefficients and observed covariates, is used to predict values of continuous outcomes. Bayesian predictions, on the other hand, are functions of simulated outcomes and are thus stochastic quantities. Simulated outcomes are new outcome values generated from the so-called posterior predictive distribution, which we describe next.

Prior and posterior predictive distributions

Before the data $\mathbf{y}$ are observed, the distribution of $\mathbf{y}$ is

$$p(\mathbf{y}) = \int p(\mathbf{y}, \boldsymbol{\theta}) d\boldsymbol{\theta} = \int p(\mathbf{y}|\boldsymbol{\theta}) p(\boldsymbol{\theta}) d\boldsymbol{\theta} \tag{1}$$

where $p(\mathbf{y}|\boldsymbol{\theta})$ is the likelihood of $\mathbf{y}$ given model parameters $\boldsymbol{\theta}$ and $p(\boldsymbol{\theta})$ is the prior distribution for $\boldsymbol{\theta}$. $p(\mathbf{y})$ is the so-called prior predictive distribution, which is more commonly known as the marginal distribution of $\mathbf{y}$.

Suppose that $\mathbf{y}^{\text{obs}}$ are observed data and $\mathbf{y} = \mathbf{y}^{\text{new}}$ are new, unobserved (future) data. The posterior predictive distribution of $\mathbf{y}^{\text{new}}$ is

$$p(\mathbf{y}^{\text{new}}|\mathbf{y}^{\text{obs}}) = \int p(\mathbf{y}^{\text{new}}|\boldsymbol{\theta}) p(\boldsymbol{\theta}|\mathbf{y}^{\text{obs}}) d\boldsymbol{\theta} \tag{2}$$

where $p(\boldsymbol{\theta}|\mathbf{y}^{\text{obs}})$ is the posterior distribution of $\boldsymbol{\theta}$. You can think of a posterior predictive distribution (2) as a prior predictive distribution (1) updated after observing the data $\mathbf{y}^{\text{obs}}$.

Simulated outcomes

Like the posterior distribution of model parameters, the predictive distribution $p(\mathbf{y}^{\text{new}}|\mathbf{y}^{\text{obs}})$ usually does not have a closed form and must be approximated. The goal of Bayesian prediction is to simulate data from $p(\mathbf{y}^{\text{new}}|\mathbf{y}^{\text{obs}})$. We will refer to these data as *simulated outcomes*, $\mathbf{y}^{\text{sim}}$.

Formula (2) provides a way of simulating new outcome values by using a two-step procedure. First, model parameters $\boldsymbol{\theta}^{\star}$ are simulated from their posterior distribution $p(\boldsymbol{\theta}|\mathbf{y}^{\text{obs}})$. Then, the new outcome values $\mathbf{y}^{\text{sim}}$ are simulated from the likelihood model $p(\mathbf{y}^{\text{sim}}|\boldsymbol{\theta}^{\star})$ using the simulated model parameters from step 1. These two steps are repeated for a prespecified number of MCMC iterations, T. The result is an MCMC sample of simulated outcomes, $(\mathbf{y}^{\text{sim},1}, \mathbf{y}^{\text{sim},2}, \ldots, \mathbf{y}^{\text{sim},\text{T}})$. This sample is used to estimate the posterior predictive distribution.

Thus, unlike classical prediction, which produces a single value for each observation, Bayesian prediction produces a sample of T simulated values for each observation. If you have n observations in the dataset, the result of a Bayesian prediction will be a $T \times n$ matrix (for each outcome or dependent variable). Therefore, Bayesian predictions are often computed for a subset of observations or for various summaries over observations such as means, quantiles, minimum and maximum values, and so on. Sometimes, a smaller sample of $R << T$ MCMC replicates of simulated outcomes is used to explore the posterior distribution of simulated outcomes. In other cases, posterior summaries over the MCMC replicates such as posterior means and medians of simulated outcomes may be of interest.

Posterior predictive checking and replicated outcomes

In addition to predicting future observations, Bayesian prediction is useful for model checking. Model checking is accomplished by performing the so-called posterior predictive checks, which compare various characteristics of the posterior predictive distribution with those observed in the data.

The concept of replicated data or replicated outcomes arises in the context of posterior predictive checking for regression-type models. In a regression setting, the posterior predictive distribution also depends on the covariate-data matrix X, $p(\mathbf{y}^{\text{new}}|\mathbf{y}^{\text{obs}}) = p(\mathbf{y}^{\text{new}}|\mathbf{y}^{\text{obs}}, X)$. The data matrix X may contain the observed values that were used to fit the Bayesian model, X^{obs}, or the new values, X^{new}. *Replicated outcomes* are outcomes simulated from the posterior predictive distribution, $p(\mathbf{y}^{\text{new}}|\mathbf{y}^{\text{obs}}, X^{\text{obs}})$, using the observed covariate data. In other words, the replicated outcomes are the outcomes we would observe if we repeated our experiment again. We will denote replicated outcomes as $\mathbf{y}^{\text{rep}}$.

Replicated outcomes are also known as in-sample predictions, whereas outcomes simulated using new covariate data, X^{new}, are known as out-of-sample predictions. In-sample predictions are useful for diagnostic checks. Out-of-sample predictions can be used for forecasting and model validation. In the latter case, the data are split into training and test subsamples: the training subsample is used to fit a Bayesian model, and the test subsample is used to assess prediction accuracy of the fitted model.

Posterior predictive checking is performed by comparing the distribution (or certain aspects of it) of the replicated data to that of the observed data. This can be done visually by examining histograms and quantile plots. More formally, discrepancy measures such as a mean, minimum, and maximum statistics computed for the replicated data and for the observed data can be compared using posterior predictive p-values; see [BAYES] **bayesstats ppvalues** for details.

It is important to realize the difference between MCMC diagnostic checks (*Convergence of MCMC* in [BAYES] **bayesmh**) and posterior predictive checks. The former examines the properties of MCMC sampling, whereas the latter inspects how well the specified Bayesian model describes the observed data. But these two types of checks are related—an ill-fitting model lowers the MCMC sampling efficiency and may even lead to nonconvergence of the MCMC algorithm.

For in-depth coverage of Bayesian predictions and posterior predictive inference, see Meng (1994), West (1986), Tsui and Weerahandi (1989), Gelman, Meng, and Stern (1996), Gelman and Rubin (1992), and Gelman et al. (2014), to name a few.

Using bayespredict and bayesreps

`bayespredict` computes Bayesian predictions using current estimation results produced by the `bayesmh` command with built-in likelihood models and saves them in a separate Stata dataset. Bayesian predictions include simulated outcomes, which are samples from the posterior predictive distribution of the fitted Bayesian model, and their functions. You can also compute posterior summaries of simulated outcomes and store them as new variables in the current dataset.

To compute Bayesian predictions, you must specify the `saving()` option with `bayespredict` to save the prediction results; see *Generating and saving simulated outcomes*. To compute posterior summaries, you must specify one or more new variable names and the corresponding option such as `mean` for posterior mean and `std` for posterior standard deviation; see *Posterior summaries of simulated outcomes*.

`bayesreps` generates a random subset of MCMC replicates of simulated outcomes from the entire MCMC sample and stores them as new variables in the current dataset. This command is useful for checking model fit. The number of replicates is specified in the `nreps(`$\#_{\text{reps}}$`)` option. With multiple replicates, you must specify a variable *stub*`*` with `bayesreps`, and the command will generate new variables *stub*1, *stub*2, ..., *stub*$\#_{\text{reps}}$ in the current dataset. For multiple-outcome models, the replicates are produced for one outcome at a time. The first outcome is the default, but you can specify a different outcome variable in the `outcome()` option.

Both `bayespredict` and `bayesreps` require that `bayesmh`'s MCMC simulation dataset be saved prior to their execution. You can save MCMC simulation results by specifying the `saving()` option with `bayesmh` during or after estimation; see *Storing estimation results after Bayesian estimation* in [BAYES] **Bayesian postestimation**.

Both commands produce stochastic results. Use the `rseed()` option for reproducibility. Depending on the number of observations, the specified MCMC sample size, and model complexity, the computations may be time consuming. Options `dots` and `dots()` may be useful in this case to monitor the progress. They display a dot for each simulation performed.

`bayespredict` and `bayesreps` can be used to make in-sample or out-of-sample predictions; see *Description* in [R] **predict** for how to specify such predictions.

Generating and saving simulated outcomes

Generating and saving simulated outcomes is the main usage of `bayespredict`, which requires the `saving()` option when generating simulated outcomes. The simplest specification is

```
. bayespredict {_ysim1}, saving(filename)
```

which generates the simulated values for the first outcome variable and saves them in *filename*`.dta`. You can also use `{_ysim}` as a synonym for `{_ysim1}`.

The above specification produces the prediction dataset *filename*`.dta`, which contains T observations and n variables, where T is the MCMC sample size used by `bayesmh` and n is the number of observations in the original dataset. That is, an MCMC sample of size T is generated for each observation of the outcome variable.

For example, if our dataset has 100 observations and we use an MCMC sample of size 10,000 during simulation, `bayespredict` will produce the prediction dataset *filename*`.dta` with 10,000 observations and 100 variables. This specification may not always be feasible, especially for large datasets, or even necessary.

You would rarely need to simulate and store all observations for all outcome variables. More likely, if you are performing model diagnostics, you may be interested only in several test statistics, which you can simulate without storing the simulated outcomes; see *Defining test statistics using Mata functions*. Or you may be interested only in posterior summaries of simulated outcomes; see *Posterior summaries of simulated outcomes*. Or you may need to explore only a small random subset of MCMC replicates of simulated outcomes, which you can obtain by using the `bayesreps` command. Or if you are interested in forecasting, you may need to simulate values for only a few new data points.

For example, suppose we want to simulate outcome values for 10 new observations only, which are stored in observations 101 through 110 in our original dataset. We can do this using

```
. bayespredict {_ysim1[101/110]}, saving(filename)
```

or, equivalently, using

```
. bayespredict {_ysim1} in 101/110, saving(filename)
```

The two specifications above are more efficient with respect to execution time and storage.

The full syntax of `bayespredict` for simulating all variables and all observations is

```
. bayespredict {_ysim1} {_ysim2} ..., saving(filename)
```

where you specify `{_ysim#}` for the #th outcome variable. The order of variables is determined by the order in which they were specified with `bayesmh`.

If you need to predict multiple outcomes, it may be more efficient with regard to storage to simulate them separately. Remember that the total number of variables in the prediction dataset may not exceed the current `c(maxvar)` setting. Because `bayespredict` stores additional variables, the number of specified outcome observations may not exceed `floor((c(maxvar)-3)/2)`; see *Prediction dataset*.

By default, `bayespredict` computes out-of-sample predictions. This may sometimes lead to missing predicted observations, for instance, when some of the covariates contain missing values. In the context of `bayespredict` when simulating outcomes, residuals, and expected values, this implies that the prediction dataset may contain variables containing all missing observations. Recall that the variables in the prediction dataset correspond to the observations in the original dataset. In such cases, to reduce the size of the prediction dataset, you may consider restricting the prediction sample to the estimation sample, `if e(sample)`; or specifying a subset of observations using *numlist*, for example, `_ysim[`*numlist*`]`; or specifying the subset of interest by using `if` and `in`.

Defining test statistics using Mata functions

Instead of simulating all observations for your outcomes of interest, you may be interested in obtaining only some summary statistics such as sample means, medians, smallest and largest observations, and standard deviations calculated over these observations. This is commonly used when performing posterior predictive checks; see *Posterior predictive inference*.

Test statistics are scalar functions of observed (or simulated) outcome values. Let `y` be an outcome variable in a dataset of size n and let $\mathbf{y}^{\text{sim}} = (y_1^{\text{sim}}, y_2^{\text{sim}}, \ldots, y_n^{\text{sim}})^T$ denote one simulated outcome sample given as a column vector. A test statistic $T(\mathbf{y}^{\text{sim}})$ summarizes the column vector $\mathbf{y}^{\text{sim}}$ by a single number. For example, the mean statistic is defined as

$$T(\mathbf{y}^{\text{sim}}) = \frac{1}{n}(y_1^{\text{sim}} + \cdots + y_n^{\text{sim}}) = \overline{\mathbf{y}}^{\text{sim}}$$

In `bayespredict`, test statistics can be defined using Mata functions or Stata programs. Here we focus on the specifications using Mata functions; see *User-defined Stata programs* for Stata programs. Note that if you need to compute a test quantity, $T(\mathbf{y}, \boldsymbol{\theta})$, that directly uses model parameters $\boldsymbol{\theta}$, you must use Stata programs.

`bayespredict` supports Mata functions that return a scalar and accept one or two column vectors as arguments. You can specify the following as the arguments to the Mata functions: simulated outcomes, `{_ysim#}`; simulated residuals, `{_resid#}`; and expected outcome values, `{_mu#}`. `{_resid#}` is defined as the difference between `{_ysim#}` and `{_mu#}`. (Specifications `{_resid#}` and `{_mu#}` are not available for ordinal models.) You can also use `{_ysim}`, `{_resid}`, and `{_mu}` as synonyms

for {_ysim1}, {_resid1}, and {_mu1}, respectively. If you used if or in with bayespredict to restrict the prediction sample or specified only a subset of observations, that is, {_ysim[1/10]}, the column vectors passed to Mata functions as arguments will contain only the available observations.

Suppose we want to produce an MCMC sample of means of the first simulated outcome. We can specify

```
. bayespredict (@mean({_ysim1}), saving(...)
```

Similarly, we can produce an MCMC sample of means for the residuals of the first simulated outcome

```
. bayespredict (resmean: @mean({_resid1}), saving(...)
```

In the above, we also labeled our prediction as resmean. We can use this label to refer to this prediction in other Bayesian postestimation commands such as bayesstats ppvalues and bayesstats summary. If we do not specify our own labels, the default labels will be used for each prediction. The default label is *arg1_func*, where *arg1* is the first function argument and *func* is the name of the function. For instance, in our first example, the default label _ysim1_mean will be used.

You will typically specify only one argument with most official Mata functions. The support of two arguments is provided primarily for calculating more complicated test statistics using user-defined Mata functions. For example, let's define a new Mata function that calculates the sum of squared Pearson residuals assuming a Poisson model.

We define a Mata function, sumpresid(), that calculates the squared Pearson residuals as the squared difference between the simulated outcome vector, ysim, and expected values, mu, divided by the variance, which is also mu for a Poisson model. The result is the sum of these squared standardized differences.

```
mata:
    real scalar sumpresid(real colvector ysim, real colvector mu) {
        return (sum((ysim-mu):^2:/mu))
    }
end
```

Then, we can call bayespredict with the following specification to compute the sum of squared Pearson residuals for the first outcome in the model:

```
. bayespredict (@sumpresid({_ysim1}, {_mu1})), saving(...)
```

Mata functions can be used only with one outcome at a time. That is, specifications that refer to two outcomes such as @myprog({_ysim1}, {_ysim2}), @myprog({_ysim1}, {_mu2}), or @myprog({_ysim1}, {_resid2}) are not allowed.

Mata functions are preferable to Stata programs because of speed, but Stata programs provide more flexibility to compute complicated functions; see *User-defined Stata programs* below.

User-defined Stata programs

Mata functions (see *Defining test statistics using Mata functions*) are more efficient and faster in computing simple test statistics and test quantities, but they have limitations. For example, you cannot access model parameters within Mata functions. You can within Stata programs. Although executing Stata programs may be much slower, they provide more flexibility for computing test quantities.

A Stata program must have the following format in order to be used by bayespredict:

```
program userprog
        version 18.0
        args res simvar1 [simvar2]
        ... computation ...
        scalar 'res' = ...
end
```

The first argument, *res*, contains the name of a temporary scalar to store the final result. The second argument, *simvar1*, and the third (optional) argument, *simvar2*, contain the names of temporary variables, which store the simulation results for the quantities specified as program arguments *arg1* and *arg2* with bayespredict:

```
. bayespredict ([label]: @userprog arg1 [arg2]), saving(...) ...
```

arg1 and *arg2* may be one of {_ysim#}, {_mu#}, or {_resid#}, but they should refer to the same outcome variable; that is, they must use the same #. *label* is the label for the computed prediction result that can be used later to refer to this result within other Bayesian postestimation commands such as bayesstats summary. If we do not specify our own label, the default label will be used for each prediction. The default label is *arg1_userprog*, where *arg1* is the first program argument and *userprog* is the name of the program.

Recall the sumpresid() Mata function defined in the previous section. Below, we replicate the same computation but now using the Stata program.

```
program sumpresidprog
        version 18.0
        args sum ysim mu
        tempvar presid
        generate double 'presid' = ('ysim'-'mu')^2/'mu'
        summarize 'presid', meanonly
        scalar 'sum' = r(sum)
end
```

We can then call bayespredict with the following specification,

```
. bayespredict (@sumpresidprog {_ysim1} {_mu1}), saving(...)
```

to compute this statistic for the first outcome. Because we did not specify our own label in the above, the default label _ysim1_sumpresidprog will be used.

Generally, our Stata program should use a proper "touse" variable, which marks the prediction sample of bayespredict. Unlike Mata functions, the prediction results passed to Stata programs as arguments will contain all observations. However, the observations outside the prediction sample will contain missing values. Nevertheless, it is good practice to always use the touse variable in the calculations.

```
program sumpresidprog
        version 18.0
        args sum ysim mu
        local touse $BAYESPR_touse
        tempvar presid
        generate double 'presid' = ('ysim'-'mu')^2/'mu' if 'touse'
        summarize 'presid' if 'touse', meanonly
        scalar 'sum' = r(sum)
end
```

The global macro $BAYESPR_touse contains a temporary name of a binary variable that marks the prediction sample, which we now use in our calculations.

One flexibility of Stata programs is that we can access model parameters within them. In the above programs, we used precomputed expected values, `mu`. We can compute these values manually by using the simulated model parameters and observed variables.

```
program sumpresidprogmu
        version 18.0
        args sum ysim
        local touse $BAYESPR_touse
        local theta $BAYESPR_theta                              //<--New line
        tempvar xb mu                                           //<--New line
        matrix score double `xb' = `theta' if `touse'           //<--New line
        qui generate double `mu' = invlogit(`xb') if `touse' //<--New line
        tempvar presid
        generate double `presid' = (`ysim'-`mu')^2/`mu' if `touse'
        summarize `presid' if `touse', meanonly
        scalar `sum' = r(sum)
end
```

To compute expected values, we need to compute the linear predictor. To compute the linear predictor, we need coefficient estimates. The coefficient estimates are provided in a temporary matrix (row vector) with the name stored in the global macro `$BAYESPR_theta`. The columns of this temporary matrix are labeled properly with the names of the corresponding predictors, so we can use `matrix score` (see [P] **matrix score**) to easily compute the linear predictor. We then use the inverse-logit function to compute expected values (probabilities) from the linear predictions. The rest of the program is the same as earlier.

We call the above program using the following `bayespredict` specification:

```
. bayespredict (@sumpresidprogmu {_ysim1}), saving(...)
```

See example 8.

For some programs, you may need to pass additional variables or contents of command options. You can use `extravars()` and `passthruopts()` for that; see *Options for predictions*.

You can access the following global macros from the Stata programs used with `bayespredict`.

Global macros	Description
`$BAYESPR_theta`	name of a temporary matrix (row vector) of scalar parameters; stripes are properly named after the names of model parameters
`$BAYESPR_matrix_`*mname*	name of a temporary matrix containing simulated matrix parameter *mname*
`$BAYESPR_touse`	variable containing 1 for the observations to be used; 0 otherwise
`$BAYESPR_extravars`	*varlist* specified in `extravars()`
`$BAYESPR_passthruopts`	options specified in `passthruopts()`

Posterior summaries of simulated outcomes

In some applications, we may not need the actual simulated outcomes but rather their posterior summaries such as posterior means, medians, and standard deviations. For this purpose, `bayespredict` offers the `mean`, `median`, `std`, and `cri` options to compute posterior means, medians, standard deviations, and credible intervals. When you specify these options, the prediction results are stored in the specified new variables in the current dataset. You do not need to specify the `saving()` option in this case because the high-dimensional simulation outcomes are not saved, only their posterior summaries.

With mean, median, and std, you can compute results for one outcome variable at a time or for all outcome variables. In the first case, you specify a new variable name and the name of the outcome (dependent) variable in the outcome() option. If you omit outcome(), the first outcome variable will be used. To compute results for all outcome variables, you specify a new variable name for each outcome or *stub**, in which case the new variables will be named *stub*1, *stub*2, and so on.

When you compute posterior means, you can also specify the mcse(*newvar*) option to compute their corresponding MCSEs. If posterior means are computed for multiple outcome variables, *newvar* is used as *stub** to store MCSEs for each outcome in *newvar*1, *newvar*2, and so on.

With cri, you specify two new variable names to contain the lower and upper credible bounds. You can compute results only for one outcome variable at a time, which you specify in the outcome() option. If you omit this option, the first outcome variable is assumed. You can specify the clevel() option to change the default 95% credible level and the hpd option to calculate HPD credible intervals instead of the default equal-tailed intervals.

All computed results are stochastic. You should specify the rseed() option for reproducibility. Also see *Syntax* for other available simulation options, *simopts*.

Prediction dataset

bayespredict saves prediction results in a dataset *filename*.dta as specified in the saving(*filename*) option. In addition, bayespredict stores auxiliary estimation results, described in *Stored results*, in *filename*.ster. This file is used by other postestimation commands such as bayesstats summary when summarizing the simulated prediction quantities.

The format of the *filename*.dta file is similar to the simulation dataset created by the bayesmh command. The first two variables are _chain and _index, which store the respective chain and MCMC iteration identifiers. Following are the variables containing simulated values for the $\#_1$th outcome variable and the $\#_2$th observation, _ysim$\#_1$_$\#_2$, if any, and the corresponding expected outcome values, _mu$\#_1$_$\#_2$. For any function of simulated outcomes or residuals specified with bayespredict, there are two variables in the dataset named *label* and _obs_*label*, where *label* is the specified function or program label. Variable *label* contains the MCMC sample of values of the function. Variable _obs_*label* contains the observed values of the function, which are computed by substituting the simulated outcome for the observed outcome variable in the function specification. This variable is consumed by [BAYES] **bayesstats ppvalues**. Finally, the _frequency variable is the last variable in the prediction dataset. It always contains one in the prediction dataset and is provided purely for the consistency with the simulation dataset, where it records the frequency of duplicate sets of model parameters.

If bayespredict is specified with p simulated outcomes, each with n observations, and with k functions or programs, then the prediction dataset will contain $2pn + 2k + 3$ variables. The number of observations in the prediction dataset is determined by the MCMC sample size, T, used by bayesmh.

After your analysis, if you no longer need the prediction dataset, remember to remove both *filename*.dta and *filename*.ster.

Bayesian predictions

Consider the rare infectious disease example from Hoff (2009) that we analyzed in *Beta-binomial model* of [BAYES] **bayesmh**. A small random sample of 20 subjects from a city is checked for infection, and none is observed to be infected. The parameter of interest θ, $\theta \in [0, 1]$, is the proportion of infected individuals in the city. The outcome y is the number of infected subjects in the sample of 20. The sampling distribution for the outcome y is thus assumed to be binomial, $y|\theta \sim \text{binomial}(20, \theta)$.

Our observed data contain one observation that is zero because we did not observe any infected subjects in our sample. We can easily generate these data as follows:

```
. set obs 1
Number of observations (_N) was 0, now 1.
. generate byte y = 0
```

Following the examples in *Beta-binomial model* (except we are using a different random-number seed here), we assume a beta$(2, 20)$ prior for θ and use `bayesmh` to fit the resulting beta-binomial model.

```
. bayesmh y, likelihood(dbinomial({theta}, 20))
> prior({theta}, beta(2, 20)) saving(betabin_mcmc) rseed(16)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  y ~ binomial({theta},20)
Prior:
  {theta} ~ beta(2,20)
------------------------------------------------------------------------------

Bayesian binomial model                         MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =          1
                                                Acceptance rate  =      .4627
Log marginal-likelihood = -1.1575104            Efficiency       =      .1446

------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
       theta |  .0476128   .0320509   .000843   .0406464   .0057875   .1251631
------------------------------------------------------------------------------
file betabin_mcmc.dta saved.
```

The posterior mean for `{theta}`, which is also the probability that a subject from a sample of 20 will be infected, is estimated to be 0.0476. Thus, we would expect $20 \times 0.0476 = 0.952$ infected subjects in a sample of 20.

Let's explore various Bayesian predictions for this beta-binomial model. The relevant examples are presented under the following headings:

▷ Example 1: Predicting the number of infected subjects

Let's predict the number of infected subjects, our outcome, assuming the fitted beta-binomial model. To do this in a Bayesian framework, we need to simulate the outcome from its posterior predictive distribution. We can use `bayespredict` to do this.

To use `bayespredict`, we must first save our MCMC simulation results from `bayesmh` in a dataset, which we already did by specifying the `saving(betabin_mcmc)` option with `bayesmh`. If you forget to specify this option during estimation, you can always do it after by typing

```
. bayesmh, saving(betabin_mcmc)
```

We simulate the outcome by specifying {_ysim} with bayespredict and save the simulated data in betabin_pred.dta; the saving() option is required with bayespredict when simulating Bayesian predictions. Because the command uses simulation, we also specify the rseed() option for reproducibility.

```
. bayespredict {_ysim}, saving(betabin_pred) rseed(16)
Computing predictions ...
file betabin_pred.dta saved.
file betabin_pred.ster saved.
```

The computation may be time consuming, so the command displays Computing predictions ... to inform you that the computation is in progress. You may also specify the dots or dots() option to see the dots as simulations are performed.

In addition to saving prediction results in a Stata dataset, bayespredict also saves auxiliary estimation results in the betabin_pred.ster file. This file is used by other postestimation commands such as bayesstats summary when summarizing the simulated prediction quantities. Remember to remove this file in addition to your prediction dataset when you no longer need them.

The bayespredict command simulates T outcome values for each specified outcome and for each specified observation. T is the MCMC sample size used by bayesmh. The outcome values are simulated for each set of T MCMC estimates of model parameters generated by bayesmh. Our bayespredict specification {_ysim} is equivalent to {_ysim1} and refers to all observations of the first outcome. In our example, we have only one observation and one outcome, and the default MCMC sample size is 10,000. Thus, betabin_pred.dta contains one simulated variable, _ysim1_1, and 10,000 observations, in addition to other auxiliary variables such as chain and iteration number identifiers; see *Prediction dataset*.

```
. describe using betabin_pred
Contains data
 Observations:        10,000                  23 Mar 2023 15:27
    Variables:             5
-------------------------------------------------------------------------------
Variable      Storage   Display    Value
    name         type    format    label      Variable label
-------------------------------------------------------------------------------
_chain          int     %8.0g                 Chain identifier
_index          int     %8.0g                 Iteration number
_ysim1_1        double  %10.0g                Simulated y, obs #1
_mu1_1          double  %10.0g                Expected values for y, obs #1
_frequency      byte    %8.0g                 Frequency weight
-------------------------------------------------------------------------------
Sorted by:
```

In this dataset, _ysim1_1 represents an MCMC sample of size 10,000 from the posterior predictive distribution of y for the first observation. If we had more observations, say, 100, the dataset would have contained 100 variables, _ysim1_1, _ysim1_2, ..., _ysim1_100, one for each observation. In the prediction dataset, the observations are MCMC replicates, and the variables are outcome values for each observation and each outcome from the data that were used to fit the model.

◁

▷ Example 2: Summarizing prediction results

We can summarize our prediction results like any other Bayesian model parameter. For example, we can calculate standard posterior summaries for {_ysim} by using bayesstats summary.

```
. bayesstats summary {_ysim} using betabin_pred
Posterior summary statistics                       MCMC sample size =    10,000
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
_ysim1_1	.9526	1.145899	.020218	1	0	4

The calculated posterior predictive mean is 0.95, which agrees with our earlier computation of $20 \times 0.0476 = 0.952$ using the posterior mean estimate of θ, 0.0476. Under our Bayesian model, we should expect to observe roughly 1 infected individual in a sample of 20, which is comparable with our observed data with no infected subjects.

Generally, we should be careful when using {_ysim} with Bayesian postestimation commands because it refers to all observations of the outcome variable. A better approach is to use a subset of observations, {_ysim[*numlist*]}, such as {_ysim[1/10]}. In our example, we have only one observation, so this specification is equivalent to specifying only the first observation, {_ysim[1]}.

◁

▷ Example 3: Expressions of individual prediction results

We can compute posterior summaries for the expressions involving the individual values, {_ysim[#]}, where # refers to an observation. For instance, let's calculate the probability of observing 0 infected subjects in our sample of 20. Recall that our only observation records the number of observed infected subjects. We can estimate the probability that the outcome value is 0 as a proportion of 0 values of our simulated outcome in a sample of 10,000 MCMC replicates. We can do this by specifying the expression {_ysim[1]}==0 in bayesstats summary.

```
. bayesstats summary (prob0:{_ysim[1]}==0) using betabin_pred
Posterior summary statistics                       MCMC sample size =    10,000
       prob0 : _ysim1_1==0
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
prob0	.4479	.497303	.00708	0	0	1

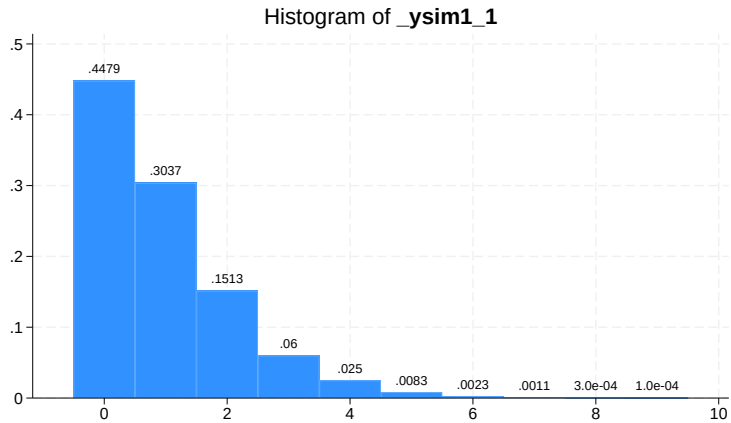
The posterior predictive mean (probability) for observing 0 infected subjects in the sample of 20 is 0.45, with a posterior predictive standard deviation of 0.5.

◁

Example 4: Visualizing prediction results

We can use graphical tools such as the histogram to summarize the posterior predictive distribution.

```
. bayesgraph histogram {_ysim[1]} using betabin_pred, discrete addlabels
```



The mass of the posterior predictive distribution for the number of infected subjects is concentrated on small numbers such as 0, 1, and 2 and thus agrees with what we observed in our sample.

Example 5: Posterior summaries of simulated outcomes

We can compute the posterior mean of the simulated outcome and save it in the current dataset as a new variable.

```
. bayespredict pmean, mean rseed(16)
Computing predictions ...
. summarize pmean
```

Variable	Obs	Mean	Std. dev.	Min	Max
pmean	1	.9526	.	.9526	.9526

The sample mean of `pmean` is an estimate of the posterior predictive mean of the outcome y and is the same as the one we obtained earlier by using `bayesstats summary`. Notice that we obtained the exact same values only because we used the same random-number seed, `rseed(16)`, with `bayespredict` when simulating the outcome `{_ysim}` and the posterior mean `pmean`.

If you need only posterior summaries of simulated outcomes, the above approach is preferable because it does not create a potentially large prediction dataset containing all MCMC replicates.

As the final step, we remove all the datasets created by `bayesmh` and `bayespredict` because we no longer need them, but you may choose to keep yours.

```
. erase betabin_mcmc.dta
. erase betabin_pred.dta
. erase betabin_pred.ster
```

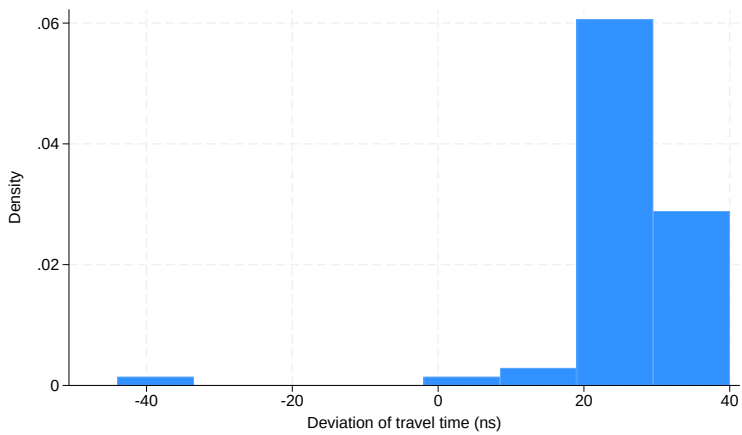
Posterior predictive inference

To illustrate posterior predictive checking, we adapt an example described in Gelman et al. (2014, sec. 6.3). The example analyzes the speed of light measurements from the experiment performed by Newcomb (1891). Newcomb measured the time (in nanoseconds) it takes for light to travel 7,442 meters. `splight.dta` contains 66 independent measurements of the deviance of the travel time from 24,800 nanoseconds in variable `timedev`.

```
. use https://www.stata-press.com/data/r18/splight
(Newcomb's speed of light measurements)
. describe
Contains data from https://www.stata-press.com/data/r18/splight.dta
 Observations:            66                  Newcomb's speed of light
                                                measurements
    Variables:             1                  22 Feb 2023 13:24
                                              (_dta has notes)
------------------------------------------------------------------------------
Variable      Storage   Display    Value
    name         type    format    label      Variable label
------------------------------------------------------------------------------
timedev         byte    %9.0g                 Deviation of travel time (ns)
------------------------------------------------------------------------------
Sorted by:
```

Let's look at the distribution of the data.

```
. histogram timedev
(bin=8, start=-44, width=10.5)
```



The data have several extreme observations in the left tail—the smallest observed `timedev` is -44, which is more than 6 standard deviations smaller than the sample mean.

To demonstrate posterior predictive checking, Gelman et al. (2014) intentionally used a simplified model for `timedev`, a normal model with unknown mean μ and variance σ^2, which may not be a good fit given the presence of extreme observations. The authors chose a noninformative prior for the model parameters, $(\mu, \sigma^2) \sim 1/\sigma^2$, to achieve more objective analysis.

We fit the described model using bayesmh as follows:

```
. bayesmh timedev, likelihood(normal({sig2}))
> prior({timedev:_cons}, flat) prior({sig2}, jeffreys)
> mcmcsize(1000) rseed(16) saving(splight_mcmc)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  timedev ~ normal({timedev:_cons},{sig2})
Priors:
  {timedev:_cons} ~ 1 (flat)
           {sig2} ~ jeffreys
------------------------------------------------------------------------------
Bayesian normal regression                      MCMC iterations  =      3,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =      1,000
                                                Number of obs    =         66
                                                Acceptance rate  =      .2128
                                                Efficiency:  min =       .104
                                                             avg =      .1123
Log marginal-likelihood = -249.39408                         max =      .1207
------------------------------------------------------------------------------
                                                              Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
timedev      |
       _cons |  26.40191   1.306144   .128102   26.42451   23.57925   28.71792
-------------+----------------------------------------------------------------
        sig2 |  118.8588   21.83563   1.98746   115.8515   81.03243   163.9617
------------------------------------------------------------------------------
file splight_mcmc.dta saved.
```

The described prior is modeled in bayesmh by specifying the flat prior for {timedev:_cons}, the mean parameter of the normal model, and the Jeffreys prior for variance {sig2}. We requested a small MCMC sample of only 1,000. We also specified the saving() option to save MCMC estimates of model parameters, which is required to use bayespredict or bayesreps.

bayesmh reports a 95% equal-tailed credible interval of [23.6, 28.7] for {timedev:_cons}. The true deviance of the travel time of light is known to be 33.0 nanoseconds and is outside the reported credible interval. Clearly, our model does not produce an accurate estimate for the speed of light. The question is, Can we detect the misfit without the knowledge of the true value? We explore the answers to this question in the following examples:

▷ Example 6: Goodness of fit using MCMC replicates of simulated outcomes

One way of checking goodness of fit is to compare the observed sample with the replication samples drawn from the posterior predictive distribution. Any systematic discrepancy between replicated and observed data will indicate misfit.

Let's start with visual inspection of the replicated data. We can use the bayesreps command to generate 20 MCMC replicates for the outcome timedev. Each replicate has 66 observations and is saved as a new variable in the dataset. We specify tdrep* as a variable stub for the replicate names.

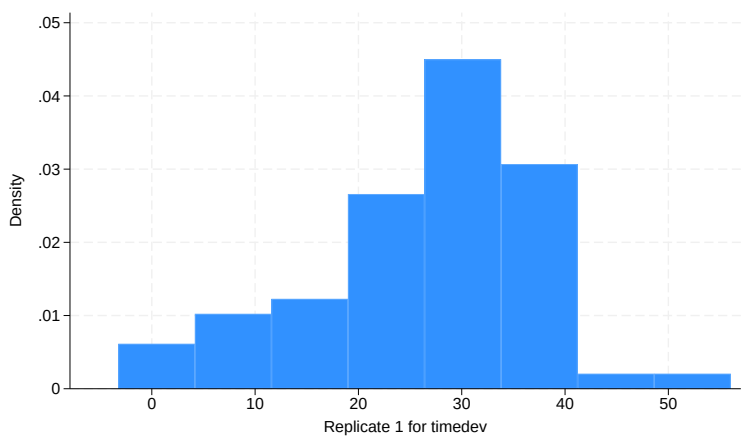
```
. bayesreps tdrep*, nreps(20) rseed(16)
Computing predictions ...
. summarize
```

Variable	Obs	Mean	Std. dev.	Min	Max
timedev	66	26.21212	10.74532	-44	40
tdrep1	66	26.10487	11.25766	-3.237112	56.03574
tdrep2	66	23.29179	11.30281	-12.58518	47.92589
tdrep3	66	26.21224	14.93573	-4.078057	61.37516
tdrep4	66	27.28245	11.60644	-2.502777	59.27184
tdrep5	66	27.74366	8.093924	5.70912	44.75622
tdrep6	66	26.15271	13.0279	-1.115488	53.42055
tdrep7	66	26.57665	10.11741	5.395408	46.71115
tdrep8	66	27.9395	12.06432	-4.903924	48.62425
tdrep9	66	25.54143	11.15095	1.560754	51.17381
tdrep10	66	28.11942	11.39326	1.364191	57.17214
tdrep11	66	24.18664	9.37403	7.49153	52.94038
tdrep12	66	25.87535	8.766691	10.5051	44.38683
tdrep13	66	27.49002	9.937486	4.89093	52.40338
tdrep14	66	26.17611	12.34034	-4.824428	51.16258
tdrep15	66	28.35187	10.58047	1.968471	50.73883
tdrep16	66	27.00237	11.44632	.7238956	52.77098
tdrep17	66	28.38859	11.1474	6.04494	63.34375
tdrep18	66	24.16652	9.289006	-.0226819	44.17939
tdrep19	66	24.9675	9.931602	6.675714	45.19432
tdrep20	66	27.69125	10.94969	1.289953	57.45961

The summary table shows that, compared with the observed data, the replicates have similar means and standard deviations but not the minimum and maximum values.

We can explore the entire distribution of a replicate. For example, we can produce the histogram for the first replicate and compare it with the earlier histogram of the observed data.

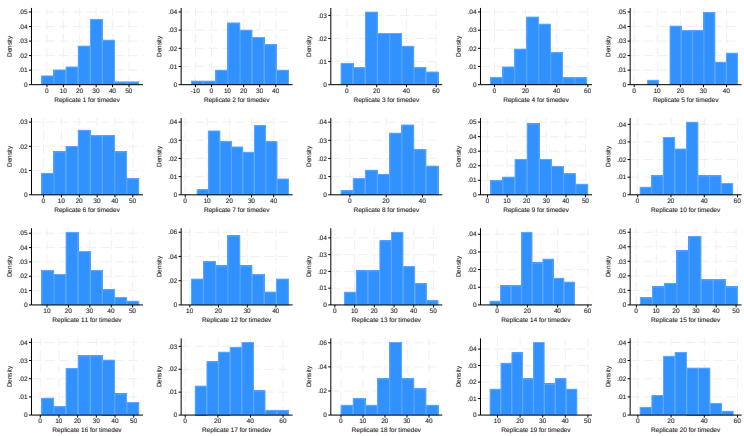
```
. histogram tdrep1
(bin=8, start=-3.237112, width=7.4091061)
```



The histograms look quite different. The replicate sample does not have the extreme negative values observed in the data.

With a few lines of code, we can produce histograms for all replicates and combine them on one graph.

```
. local histlist
. forvalues i = 1/20 {
  2.         quietly hist tdrep`i', name(hist`i') nodraw
  3.         local histlist `histlist' hist`i'
  4. }
. graph combine `histlist'
```



The histograms of all replicates look different from the observed data. The range for the replicated samples is about 0 to 50 with only a few negative values, which are smaller in magnitude than the negative values observed in the original data.

◁

▷ Example 7: Test statistics as scalar functions of simulated outcomes

Gelman et al. (2014) suggest to use the smallest observation to measure the discrepancy between the observed and replicated data. That is, to compare the smallest values in the replicated samples with Newcomb's smallest observation of −44.

In addition to simulating outcome values, as we demonstrated in example 1, we can use `bayespredict` to compute functions of simulated values that summarize the observations in a single statistic such as the minimum statistic. A function can be any Mata function that takes a column vector as an argument and returns a scalar. The result from `bayespredict` in this case is an MCMC sample of function values stored in the prediction dataset as a new variable.

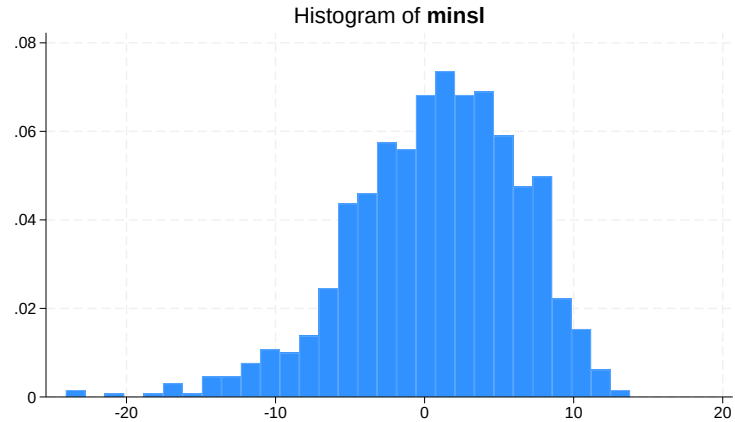
Let's use `bayespredict` to produce an MCMC sample of the smallest observations (minimums) of the replicated data. Because we are not interested in individual observations, we can request that only the smallest observation be simulated and stored by using the function specification `@min({_ysim})` with `bayespredict`.

```
. bayespredict (minsl:@min({_ysim})), saving(splight_pred) rseed(16)
Computing predictions ...
file splight_pred.dta saved.
file splight_pred.ster saved.
```

Per our specification, the command creates a new dataset, `splight_pred.dta`, that stores minimum statistics of the replicated data in the variable `minsl`. The prediction dataset has 1,000 observations, because 1,000 is the size of the MCMC sample simulated by `bayesmh`.

We can now use `{minsl}` within other Bayesian postestimation commands such as `bayesgraph` and `bayesstats summary` provided we supply the prediction dataset with the `using` specification. For example, let's draw the histogram of `{minsl}` using `bayesgraph histogram`.

```
. bayesgraph histogram {minsl} using splight_pred
```



The histogram provides the estimate of the posterior predictive distribution for the minimum statistic. The range of the histogram does not cover the observed minimum value of -44.

We can compare the posterior predictive distribution of the minimum statistic with the observed minimum value more formally by computing the posterior predictive p-value by using `bayesstats ppvalues`.

```
. bayesstats ppvalues {minsl} using splight_pred
Posterior predictive summary    MCMC sample size =      1,000
```

T	Mean	Std. dev.	E(T_obs)	P(T>=T_obs)
minsl	.8017725	5.590955	-44	1

```
Note: P(T>=T_obs) close to 0 or 1 indicates lack of fit.
```

The output table shows the posterior mean and standard deviation of `{minsl}`, the observed minimum value, -44, and the estimated posterior predictive p-value. The last is the probability that the replicated smallest value be greater or equal to the observed one. For a well-fitting model, the posterior predictive p-value should, ideally, be close to 0.5, although values between 0.05 and 0.95 are often considered acceptable in the literature (Gelman et al. 2014, 150). In our example, its estimate is essentially 1, which indicates a strong misfit of the specified normal model. Therefore, if modeling of the tails of the outcome distribution is important, we should reconsider the normal likelihood model and find a better alternative.

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Example 8: Test quantities via user-defined Stata programs

It is not sufficient to assess goodness of fit by examining just one test statistic. Different test statistics capture different aspects of the data. Which statistic to use depends on the research problem and the data characteristics you wish to account for. Generally, as pointed out by Gelman et al. (2014), for noninformative priors, sufficient statistics such as a sample mean and variance may not be good choices for checking model fit because they are typically modeled directly by the parameters of the likelihood function.

We demonstrated that our model does not model the minimum statistic well. Let's consider another aspect of `timedev`: symmetry with respect to the mean μ.

Following Gelman et al. (2014), we define the following test quantity to measure asymmetry,

$$T(\texttt{timedev}, \mu) = |\texttt{timedev}_{(61)} - \mu| - |\texttt{timedev}_{(6)} - \mu|$$

where $\texttt{timedev}_{(a)}$ defines the ath ordered value of `timedev` and $(\texttt{timedev}_{(6)}, \texttt{timedev}_{(61)})$ represents about 90% of the distribution of `timedev`.

There is no predefined computation for the above statistic, so we need to write our own. For statistics that depend only on simulated outcome values, expected values, and residuals, we can write our own Mata functions or Stata programs. Mata functions are generally faster. For statistics that directly use model parameters, writing a Stata program is our only choice. Because the calculation of $T(\texttt{timedev}, \mu)$ involves a model parameter, μ, we must write a Stata program to calculate this statistic. Let's call our program `symstatprog`.

```
program symstatprog
        version 18.0
        args symout ysim
        tempname mu
        scalar `mu' = $BAYESPR_theta[1,1]
        sort `ysim'
        scalar `symout' = abs(`ysim'[61]-`mu')-abs(`ysim'[6]-`mu')
end
```

The program has two input arguments, `symout` and `ysim`. The local macro `symout` contains the name of a temporary scalar for storing the final result. The local macro `ysim` contains the name of a temporary variable that stores the simulated outcome values of `timedev`. The global macro `$BAYESPR_theta` contains the name of a temporary matrix (row vector) that stores the current values of simulated model parameters, which are μ and σ^2 in our example. The parameters are stored in the same order they are displayed by `bayesmh`. Thus, in our example, the first element of this matrix corresponds to the mean, μ. We use the earlier definition to compute the asymmetry test quantity and store it in the scalar `` `symout' ``.

We now call `bayespredict` to use the `symstatprog` program to compute the asymmetry test quantity for each set of simulated model parameters and label the prediction results as `symstat`. We replace our previously generated prediction dataset, `splight_pred.dta`, with these new prediction results.

```
. bayespredict (symstat:@symstatprog {_ysim}), saving(splight_pred, replace)
> rseed(16)
Computing predictions ...
file splight_pred.dta saved.
file splight_pred.ster saved.
```

We can use `bayesstats ppvalues` to test the goodness of fit for $T(\texttt{timedev}, \mu)$.

```
. bayesstats ppvalues {symstat} using splight_pred
Posterior predictive summary   MCMC sample size =     1,000
```

T	Mean	Std. dev.	E(T_obs)	P(T>=T_obs)
symstat	.0953002	3.476211	3.196186	.235

```
Note: P(T>=T_obs) close to 0 or 1 indicates lack of fit.
```

The posterior predictive p-value is estimated to be 0.235 and does not suggest model misfit with respect to $T(\texttt{timedev}, \mu)$.

◁

▷ Example 9: Working with a prediction dataset

Sometimes, we may need to access the prediction results. For example, Gelman et al. (2014) provide a visual representation of the posterior predictive p-value by plotting the observed values of the asymmetry test quantity, $T(\texttt{timedev}, \mu)$, versus the replicated values, $T(\texttt{timedev}^{\text{rep}}, \mu)$. We can reproduce this graph as follows.

We start by loading the prediction dataset that contains our prediction results.

```
. use splight_pred, clear
. describe
Contains data from splight_pred.dta
 Observations:         1,000
    Variables:             5                  23 Mar 2023 15:28
```

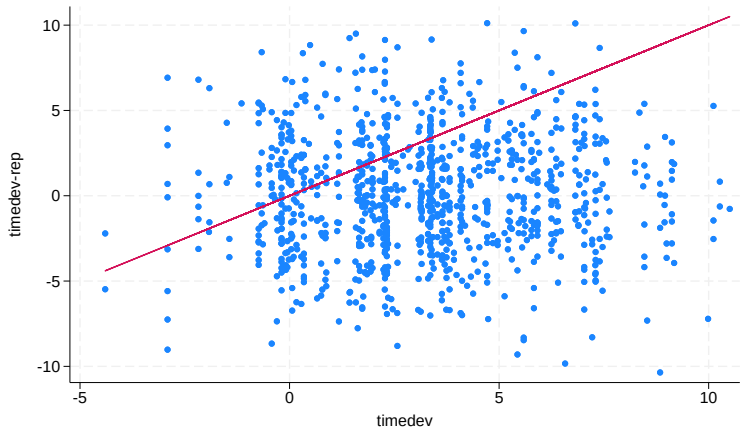
Variable name	Storage type	Display format	Value label	Variable label
_chain	int	%8.0g		Chain identifier
_index	int	%8.0g		Iteration number
symstat	double	%10.0g		symstatprog {_ysim1}
_obs_symstat	double	%10.0g		Observed symstatprog {_ysim1}
_frequency	byte	%8.0g		Frequency weight

```
Sorted by:
```

Similarly to the MCMC simulation dataset, variables `_chain` and `_index` record chain and index identifiers. Variable `symstat` contains the values for $T(\texttt{timedev}^{\text{rep}}, \mu)$, and variable `_obs_symstat` contains the values for $T(\texttt{timedev}, \mu)$. For consistency with the simulation dataset, the prediction dataset also contains the `_frequency` variable, but it is always one in the prediction dataset.

To visualize the posterior predictive p-value, we draw the scatterplot of `symstat` versus `_obs_symstat` overlaid with the diagonal line for `_obs_symstat` as the reference line.

```
. scatter symstat _obs_symstat || line _obs_symstat _obs_symstat,
> xtitle("timedev") ytitle("timedev-rep") legend(off)
```



The estimated posterior predictive p-value is the proportion of points above the diagonal line.

In conclusion, although the normal model describes well the symmetry of the observed measurements, it fails to capture some of the smaller observations. It is possible that the experimental procedure was susceptible to aberrant measurements and a different model is needed to reflect this.

Out-of-sample prediction

This section illustrates how `bayespredict` can be used as a classifier for binary outcomes.

Example 10: Out-of-sample classification using predictive posterior means

We consider `titanic800.dta`, which contains the information of 800 passengers, who were on board the ocean liner *Titanic* when it sank. The dataset is a subset from a larger dataset published by Dawson (1995).

```
. use https://www.stata-press.com/data/r18/titanic800, clear
(Titanic passenger survival (Extract))
. describe
Contains data from https://www.stata-press.com/data/r18/titanic800.dta
 Observations:           800                  Titanic passenger survival
                                                (Extract)
    Variables:             4                  22 Feb 2023 13:24
                                              (_dta has notes)
------------------------------------------------------------------------------
Variable      Storage   Display    Value
    name         type    format    label      Variable label
------------------------------------------------------------------------------
class           byte    %9.0g      class      Class
adult           byte    %9.0g      age        Adult
male            byte    %9.0g      sex        Male
survived        byte    %9.0g      survived   Survived
------------------------------------------------------------------------------
Sorted by:
```

The binary variable `survived` records whether a passenger survived (`survived` = 1) or not (`survived` = 0). Passenger characteristics include the cabin type and class membership, `class` (first, second, third, or crew); the sex, `male`; and whether the passenger was an adult or a child, `adult`.

For illustration, we consider a simple logistic regression of `survived` on the categorical predictor `class` and binary predictors `male` and `adult`.

First, we randomly split the data into training and test subsamples. We use `splitsample` ([D] **splitsample**) to generate a variable, `sample`, that assigns 50% of the data to the training subsample (`sample` = 1) and the other 50% to the test subsample (`sample` = 2).

```
. splitsample, generate(sample) rseed(12345)
```

Second, we fit a Bayesian logistic regression using the training subsample of 400 passengers. We apply a Cauchy$(0, 1)$ prior distribution for the coefficients. As a prerequisite for computing Bayesian predictions, we save the MCMC sample in `titanic_mcmc.dta`.

```
. bayesmh survived i.male i.adult ib1.class if sample==1, likelihood(logit)
> prior({survived:}, cauchy(0, 1)) saving(titanic_mcmc) rseed(16)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  survived ~ logit(xb_survived)
Prior:
  {survived:1.male 1.adult i.class _cons} ~ cauchy(0,1)                   (1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_survived.
Bayesian logistic regression                    MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =        400
                                                Acceptance rate  =      .2054
                                                Efficiency:  min =     .02887
                                                             avg =     .04189
Log marginal-likelihood = -211.35694                         max =     .05692
------------------------------------------------------------------------------
                                                              Equal-tailed
    survived |      Mean   Std. dev.      MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
        male |
        male |  -2.490095   .3330118   .019599  -2.498318   -3.13982  -1.844389
             |
       adult |
       adult |  -.5916052   .4910491   .024348  -.5666577  -1.551435   .3630116
             |
       class |
        crew |  -.6376593    .389797    .01675  -.6224151  -1.435266    .118966
      second |  -.5605325   .4214846   .017667  -.5507987  -1.423903   .2334895
       third |  -1.103689   .4064315   .021184  -1.106785  -1.923915  -.3518597
             |
       _cons |   2.386679   .6342651   .034439   2.384843   1.188944   3.692627
------------------------------------------------------------------------------
file titanic_mcmc.dta saved.
```

All coefficients are negative, which means they are associated with lower survival probabilities compared with their respective baselines. For instance, adults were less likely to survive than children, and crew members and second- and third-class passengers were less likely to survive than the first-class passengers. The male passengers on board *Titanic* were especially unfortunate—the posterior mean estimate for the coefficient on `male` is -2.5 with a 95% credible interval of $[-3.1, -1.8]$.

Let's now compute out-of-sample predictions for the test subsample of the other 400 passengers. We use `bayespredict` with the `mean` option to calculate the posterior means of the simulated outcome for these passengers and store them as a new variable, `pmean`, in the current dataset.

```
. bayespredict pmean if sample==2, mean dots(100, every(1000)) rseed(16)
Computing predictions 10000 .........1000.........2000.........3000.........
> 4000.........5000.........6000.........7000.........8000.........9000.........
> 10000 done
```

The posterior means estimate the survival probabilities of the passengers and are, in fact, the optimal predictors with respect to the mean squared error (MSE). Let's compute MSE for `pmean` to assess prediction accuracy of the model.

```
. generate err2 = (survived-pmean)^2
(400 missing values generated)
. summarize err2 if sample==2
    Variable |        Obs        Mean    Std. dev.       Min        Max
-------------+---------------------------------------------------------
        err2 |        400    .1740713    .2328064   .0187416    .741321
```

Our model achieves an MSE of 0.17, but this number is difficult to interpret on its own, without any reference models.

Let's compute the prediction accuracy of our model or how well our model predicted the outcome in the test subsample. We generate a new variable, `survived_logit`, to contain the binary outcome predicted from our Bayesian logistic model. We assign the predicted outcome to be 1 if `pmean` is greater than 0.5, and 0 otherwise. We then estimate the prediction accuracy as the proportion of matches between the observed `survived` and the predicted `survived_logit` in the test subsample.

```
. generate survived_logit = (pmean>0.5)
. generate pacc = (survived==survived_logit)
. summarize pacc if sample==2
    Variable |        Obs        Mean    Std. dev.       Min        Max
-------------+---------------------------------------------------------
        pacc |        400         .76     .427618         0          1
```

The prediction accuracy of our simple logistic model is about 0.76, which is not that high. Thus, a better prediction model should be considered for these data.

◁

One-step-ahead Bayesian forecast after Bayesian VAR

After fitting Bayesian VAR models using the `bayes: var` command, you can use `bayespredict` to compute Bayesian forecasts; see example 10 in [BAYES] **bayes: var**.

Stored results

`bayespredict` stores the following in an estimation file, *filename*`.ster`, where *filename* is specified in the `saving(`*filename*`)` option.

Scalars

`e(N)`	number of observations
`e(nchains)`	number of MCMC chains
`e(mcmcsize)`	MCMC sample size

Macros

`e(cmd)`	`bayespredict`
`e(est_cmd)`	`bayesmh`
`e(cmdline)`	command as typed
`e(est_cmdline)`	estimation command as typed
`e(predfile)`	file containing prediction results
`e(mcmcfile)`	file containing simulation results
`e(predynames)`	names of simulated outcome observations, `_ysim#_#`
`e(predfnames)`	names of specified functions and programs
`e(predrngstate#)`	random-number state for #th chain for prediction
`e(rngstate)`	random-number state for simulation (only with single chain)
`e(rngstate#)`	random-number state for #th chain for simulation (only with `nchains()`)

Methods and formulas

Methods and formulas are presented under the following headings:

Posterior predictive distribution

Recall from *Overview of Bayesian predictions* that the posterior predictive distribution of new data $\mathbf{y}^{\text{new}}$ given observed data $\mathbf{y}^{\text{obs}}$ is

$$\begin{aligned} p(\mathbf{y}^{\text{new}}|\mathbf{y}^{\text{obs}}) &= \int p(\mathbf{y}^{\text{new}}, \boldsymbol{\theta}|\mathbf{y}^{\text{obs}}) d\boldsymbol{\theta} \\ &= \int p(\mathbf{y}^{\text{new}}|\mathbf{y}^{\text{obs}}, \boldsymbol{\theta}) p(\boldsymbol{\theta}|\mathbf{y}^{\text{obs}}) d\boldsymbol{\theta} \\ &= \int p(\mathbf{y}^{\text{new}}|\boldsymbol{\theta}) p(\boldsymbol{\theta}|\mathbf{y}^{\text{obs}}) d\boldsymbol{\theta} \end{aligned} \tag{3}$$

where we used the assumption of independence between $\mathbf{y}^{\text{new}}$ and $\mathbf{y}^{\text{obs}}$ given $\boldsymbol{\theta}$ to arrive at the final expression.

Simulated outcomes, $\mathbf{y}^{\text{sim}}$, are the outcome values simulated from the posterior predictive distribution (3).

In a regression setting, posterior predictive distribution (3) also depends on the covariate data,

$$p(\mathbf{y}^{\text{new}}|\mathbf{y}^{\text{obs}}, X^{\text{new}}) = \int p(\mathbf{y}^{\text{new}}|\boldsymbol{\theta}, X^{\text{new}}) p(\boldsymbol{\theta}|\mathbf{y}^{\text{obs}}, X^{\text{obs}}) d\boldsymbol{\theta} \tag{4}$$

where X^{new} is the data matrix containing new covariate values and X^{obs} is the data matrix containing observed covariate values used to fit the model.

The concept of replicated outcomes or replicated data, $\mathbf{y}^{\text{rep}}$, arises in a regression setting when the data matrix used to generate new outcome values is the same as the observed data matrix used to fit the Bayesian model. That is,

$$p(\mathbf{y}^{\text{rep}}|\mathbf{y}^{\text{obs}}, X^{\text{obs}}) = \int p(\mathbf{y}^{\text{rep}}|\boldsymbol{\theta}, X^{\text{obs}}) p(\boldsymbol{\theta}|\mathbf{y}^{\text{obs}}, X^{\text{obs}}) d\boldsymbol{\theta} \tag{5}$$

In a regression setting, we use a general definition for the simulated outcome, $\mathbf{y}^{\text{sim}}$, as one generated either from (4) or (5).

Test quantities and test statistics are commonly used to check goodness of fit of a Bayesian model. A test quantity, $T_q(\mathbf{y}^{\text{rep}}, \boldsymbol{\theta})$, is a scalar function of replicated data $\mathbf{y}^{\text{rep}}$ and model parameters $\boldsymbol{\theta}$. A test statistic, $T_s(\mathbf{y}^{\text{rep}})$, is a scalar function that depends only on the replicated data $\mathbf{y}^{\text{rep}}$. If the model fits the data well, $T_q(\mathbf{y}^{\text{rep}}, \boldsymbol{\theta})$ should be close to $T_q(\mathbf{y}^{\text{obs}}, \boldsymbol{\theta})$, and, similarly, $T_s(\mathbf{y}^{\text{rep}})$ should be close to $T_s(\mathbf{y}^{\text{obs}})$.

MCMC sampling from posterior predictive distribution

Like the posterior distribution of model parameters, posterior predictive distributions (3), (4), and (5) usually do not have closed forms and must be approximated. In what follows, we will concentrate on the more general posterior predictive distribution $p(\mathbf{y}^{\text{new}}|\mathbf{y}^{\text{obs}}, X^{\text{new}})$, but the same principles apply to the other distributions by removing conditioning on covariate data in case of (3) and by replacing X^{new} with X^{obs} in case of (5).

The goal of Bayesian prediction is to simulate data from $p(\mathbf{y}^{\text{new}}|\mathbf{y}^{\text{obs}}, X^{\text{new}})$. Formula (4) underlies the following two-step iterative process for obtaining simulated outcomes from $p(\mathbf{y}^{\text{new}}|\mathbf{y}^{\text{obs}}, X^{\text{new}})$.

1. Draw a realization of model parameters, $\boldsymbol{\theta}^{\star}$, from their posterior distribution, $p(\boldsymbol{\theta}|\mathbf{y}^{\text{obs}}, X^{\text{obs}})$.
2. Generate $\mathbf{y}^{\text{sim}}$ from $p(\mathbf{y}^{\text{new}}|\boldsymbol{\theta}^{\star}, X^{\text{new}})$, the data distribution (likelihood) conditional on the parameters obtained in step 1.

Steps 1 and 2 are repeated to produce an MCMC sample of simulated outcomes, $(\mathbf{y}^{\text{sim},1}, \mathbf{y}^{\text{sim},2}, \ldots, \mathbf{y}^{\text{sim},\text{T}})$, where T is the MCMC sample size. We can use this sample to estimate the posterior predictive distribution.

For step 1, `bayespredict` uses the MCMC sample of model parameters as produced by the `bayesmh` command. The main computation of `bayespredict` is the simulation of the outcome values from the respective likelihood model for each set of simulated model parameters from the MCMC sample. For an outcome variable with n observations, the result of a Bayesian prediction is a dataset containing T observations and n columns.

A function of simulated values is computed as follows: $\{f(\mathbf{y}^{\text{sim},1}), f(\mathbf{y}^{\text{sim},2}), \ldots, f(\mathbf{y}^{\text{sim},\text{T}})\}$, where $f(\cdot)$ is a function that operates on a column vector and returns a scalar. The resulting prediction dataset will contain a variable with T observations.

For a test statistic $T_s(\mathbf{y}^{\text{rep}})$, the following simulated sample is produced:

$\{T_s(\mathbf{y}^{\text{rep},1}), T_s(\mathbf{y}^{\text{rep},2}), \ldots, T_s(\mathbf{y}^{\text{rep},\text{T}})\}$. For a well-fitting model, the distribution of this sample should be concentrated around $T_s(\mathbf{y}^{\text{obs}})$.

For a test quantity $T_q(\mathbf{y}^{\text{rep}}, \boldsymbol{\theta})$, the following simulated sample is produced:

$\{T_q(\mathbf{y}^{\text{rep},1}, \boldsymbol{\theta}^1), T_q(\mathbf{y}^{\text{rep},2}, \boldsymbol{\theta}^2), \ldots, T_q(\mathbf{y}^{\text{rep},\text{T}}, \boldsymbol{\theta}^T)\}$. For a well-fitting model, the distribution of this sample should be close to the distribution of $\{T_q(\mathbf{y}^{\text{obs}}, \boldsymbol{\theta}^1), T_q(\mathbf{y}^{\text{obs}}, \boldsymbol{\theta}^2), \ldots, T_q(\mathbf{y}^{\text{obs}}, \boldsymbol{\theta}^T)\}$.

Residuals and expected values

Consider simulated outcome values $\mathbf{y}_i^{\text{sim}}$ for an observation $i = 1, 2, \ldots, n$, where $\mathbf{y}_i^{\text{sim}} = (y_i^{\text{sim},1}, y_i^{\text{sim},2}, \ldots, y_i^{\text{sim},\text{T}})^T$. Let $\widehat{\boldsymbol{\mu}}_i = (\widehat{\mu}_i^1, \widehat{\mu}_i^2, \ldots, \widehat{\mu}_i^{\text{T}})^T$, where $\widehat{\mu}_i^t = E(y_i|\mathbf{x}_i, \boldsymbol{\theta}^t)$ is the estimated expected value of y_i given covariate vector $\mathbf{x}_i$ and simulated parameters $\boldsymbol{\theta}^t$, $t = 1, 2, \ldots, T$. Let $\mathbf{r}_i^{\text{sim}} = (r_i^{\text{sim},1}, r_i^{\text{sim},2}, \ldots, r_i^{\text{sim},\text{T}})^T$ be simulated residuals for an observation i.

Simulated residuals are then defined as

$$\mathbf{r}_i^{\text{sim}} = \mathbf{y}_i^{\text{sim}} - \widehat{\boldsymbol{\mu}_i}$$

Within `bayespredict`, you refer to $\mathbf{y}_i^{\text{sim}}$ as `{_ysim_`i`}`, $\mathbf{r}_i^{\text{sim}}$ as `{_resid_`i`}`, and $\widehat{\boldsymbol{\mu}_i}$ as `{_mu_`i`}`. You can also use `{_ysim}`, `{_resid}`, and `{_mu}` to refer to all observations at once. With multiple outcomes, the above specifications correspond to the first outcome variable. For the #th outcome variable, use `{_ysim#_`i`}`, `{_resid#_`i`}`, `{_mu#_`i`}`, `{_ysim#}`, `{_resid#}`, and `{_mu#}`, respectively.

Below are the definitions of $\widehat{\mu}_i^t$ for the likelihood models supported by `bayesmh`.

1. **Normal regression**: $\widehat{\mu}_i^t = \mathbf{x}_i\boldsymbol{\beta}^t$.
2. **t-regression**: $\widehat{\mu}_i^t = \mathbf{x}_i\boldsymbol{\beta}^t$.
3. **Lognormal regression**: $\widehat{\mu}_i^t = \exp(\mathbf{x}_i\boldsymbol{\beta}^t)$.
4. **Exponential regression**: $\widehat{\mu}_i^t = \exp(\mathbf{x}_i\boldsymbol{\beta}^t)$.
5. **Probit regression**: $\widehat{\mu}_i^t = \Phi(\mathbf{x}_i\boldsymbol{\beta}^t)$.
6. **Logistic regression**: $\widehat{\mu}_i^t = \text{invlogit}(\mathbf{x}_i\boldsymbol{\beta}^t)$.
7. **Binomial regression**: $\widehat{\mu}_i^t = n_{\text{trials}} \times \text{invlogit}(\mathbf{x}_i\boldsymbol{\beta}^t)$, where n_{trials} is the number of trials in binomial regression.
8. **Ordered probit regression**: `{_resid}` and `{_mu}` not supported.
9. **Ordered logistic regression**: `{_resid}` and `{_mu}` not supported.
10. **Poisson regression**: $\widehat{\mu}_i^t = \exp(\mathbf{x}_i\boldsymbol{\beta}^t)$.

Next are the definitions of $\widehat{\mu}_i^t$ for the distribution models `dexponential(`*beta*`)`, `dbernoulli(`*p*`)`, `dbinomial(`n_{trials}`,`*p*`)`, and `dpoisson(`*mu*`)`.

11. **Exponential distribution**: $\widehat{\mu}_i^t = \beta^t$.
12. **Bernoulli distribution**: $\widehat{\mu}_i^t = p^t$.
13. **Binomial distribution**: $\widehat{\mu}_i^t = n_{\text{trials}}p^t$.
14. **Poisson distribution**: $\widehat{\mu}_i^t = \mu^t$.

Typically, the expected values for the distribution models will be constant over observations unless the distribution parameters vary over the observations.

Raw residuals, $\mathbf{r}_i^{\text{sim}}$, may not always be the most appropriate for diagnostic purposes. For example, Pearson residuals are better suited for discrete outcome models such as binomial and Poisson regressions.

References

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Also see

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

[BAYES] **bayesgraph** — Graphical summaries and convergence diagnostics

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **bayesstats ess** — Effective sample sizes and related statistics

[BAYES] **bayesstats ppvalues** — Bayesian predictive p-values and other predictive summaries

[BAYES] **bayesstats summary** — Bayesian summary statistics

[BAYES] **bayestest interval** — Interval hypothesis testing

Title

set clevel — Set default credible level

Description Syntax Option Remarks and examples Also see

Description

`set clevel` specifies the default credible level for credible intervals for all Bayesian commands (see [BAYES] **Bayesian commands**) that report credible intervals. The initial value is 95, meaning 95% credible intervals.

Syntax

```
set clevel # [, permanently]
```

is any number between 10.00 and 99.99 and may be specified with at most two digits after the decimal point.

Option

`permanently` specifies that in addition to making the change right now, the `clevel` setting be remembered and become the default setting when you invoke Stata.

Remarks and examples

To change the level of credible intervals reported by a particular command, you need not reset the default credible level. All commands that report credible intervals have a `clevel(#)` option. When you do not specify the option, the credible intervals are calculated for the default level set by `set clevel` or for 95% if you have not reset `set clevel`.

▷ Example 1

We use the bayesmh command to obtain the credible interval for the mean of mpg:

```
. use https://www.stata-press.com/data/r18/auto
(1978 automobile data)
. set seed 14
. bayesmh mpg, likelihood(normal(30)) prior({mpg:_cons}, flat)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},30)
Prior:
  {mpg:_cons} ~ 1 (flat)
------------------------------------------------------------------------------

Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .4195
Log marginal-likelihood = -234.09275            Efficiency       =      .2378

------------------------------------------------------------------------------
             |                                                 Equal-tailed
         mpg |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
       _cons |   21.30364   .6429995   .013186   21.30381   20.03481    22.5555
------------------------------------------------------------------------------
```

To obtain 90% credible intervals, we would type

```
. bayesmh, clevel(90)
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},30)
Prior:
  {mpg:_cons} ~ 1 (flat)
------------------------------------------------------------------------------

Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .4195
Log marginal-likelihood = -234.09275            Efficiency       =      .2378

------------------------------------------------------------------------------
             |                                                 Equal-tailed
         mpg |      Mean   Std. dev.     MCSE     Median  [90% cred. interval]
-------------+----------------------------------------------------------------
       _cons |   21.30364   .6429995   .013186   21.30381   20.24172    22.35158
------------------------------------------------------------------------------
```

or we could type

```
. set clevel 90
. bayesmh
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},30)
Prior:
  {mpg:_cons} ~ 1 (flat)
------------------------------------------------------------------------------

Bayesian normal regression                      MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling        Burn-in          =      2,500
                                                MCMC sample size =     10,000
                                                Number of obs    =         74
                                                Acceptance rate  =      .4195
Log marginal-likelihood = -234.09275            Efficiency       =      .2378

------------------------------------------------------------------------------
             |                                                 Equal-tailed
         mpg |      Mean   Std. dev.     MCSE     Median  [90% cred. interval]
-------------+----------------------------------------------------------------
       _cons |   21.30364   .6429995   .013186   21.30381   20.24172   22.35158
------------------------------------------------------------------------------
```

If we opt for the second alternative, the next time that we fit a model, 90% credible intervals will be reported. If we wanted 95% credible intervals, we could specify `clevel(95)` on the estimation command, or we could reset the default by typing `set clevel 95`.

The current setting of `clevel()` is stored as the c-class value `c(clevel)`; see [P] **creturn**.

◁

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[R] **query** — Display system parameters

[P] **creturn** — Return c-class values

Title

bayes: betareg — Bayesian beta regression

Description

`bayes: betareg` fits a Bayesian beta regression to a fractional outcome whose values are greater than 0 and less than 1; see [BAYES] **bayes** and [R] **betareg** for details.

Quick start

Bayesian beta regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: betareg y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): betareg y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): betareg y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): betareg y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): betareg y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **betareg**.

Menu

Statistics > Fractional outcomes > Bayesian beta regression

Syntax

```
bayes [, bayesopts]: betareg depvar indepvars [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
scale(*varlist*[, noconstant])	specify independent variables for scale
link(*linkname*)	specify link function for the conditional mean; default is link(logit)
slink(*slinkname*)	specify link function for the conditional scale; default is slink(log)
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars and *varlist* may contain factor variables; see [U] **11.4.3 Factor variables**.

fweights are allowed; see [U] **11.1.6 weight**.

bayes: betareg, level() is equivalent to bayes, clevel(): betareg.

For a detailed description of *options*, see *Options* in [R] **betareg**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref*[, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} for the main regression and {scale:*varlist*} for the scale equation. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **betareg**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **betareg** — Beta regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: binreg — Bayesian generalized linear models: Extensions to the binomial family

Description

`bayes: binreg` fits a Bayesian binomial regression to a binary outcome, assuming different link functions; see [BAYES] **bayes** and [R] **binreg** for details.

Quick start

Bayesian binomial regression of `y` on `x1` and `x2`, using the default logit link and using default normal priors for regression coefficients

```
bayes: binreg y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): binreg y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): binreg y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): binreg y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): binreg y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display odds ratios instead of coefficients

```
bayes: binreg y x1 x2, or
```

Use the log link and report risk ratios

```
bayes: binreg y x1 x2, rr
```

Display coefficients instead of risk ratios

```
bayes, coefficients
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **binreg**.

Menu

Statistics > Generalized linear models > Bayesian GLM for the binomial family

Syntax

```
bayes [, bayesopts]: binreg depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
or	use logit link and report odds ratios
rr	use log link and report risk ratios
hr	use log-complement link and report health ratios
rd	use identity link and report risk differences
n(# | *varname*)	use # or *varname* for number of trials
exposure(*varname*)	include ln(*varname*) in model with coefficient constrained to 1
offset(*varname*)	include *varname* in model with coefficient constrained to 1
mu(*varname*)	use *varname* as the initial estimate for the mean of *depvar*
init(*varname*)	synonym for mu(*varname*)
Reporting	
coefficients	report nonexponentiated coefficients
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

fweights are allowed; see [U] **11.1.6 weight**.

bayes: binreg, level() is equivalent to bayes, clevel(): binreg.

For a detailed description of *options*, see *Options* in [R] **binreg**. binreg's option ml is implied with bayes: binreg.

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
* blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
* noblocking	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
coefficients	report nonexponentiated coefficients
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **binreg**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Logistic regression with perfect predictors* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **binreg** — Generalized linear models: Extensions to the binomial family

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: biprobit — Bayesian bivariate probit regression

Description

`bayes: biprobit` fits a Bayesian bivariate probit regression to two binary outcomes; see [BAYES] **bayes** and [R] **biprobit** for details.

Quick start

Bayesian bivariate probit regression of `y1` and `y2` on `x1` and `x2`, using default normal priors for regression coefficients and atanh-transformed correlation

```
bayes: biprobit y1 y2 x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): biprobit y1 y2 x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept of the dependent variable `y2`

```
bayes, prior({y2: x1 x2}, uniform(-10,10)) ///
prior({y2:_cons}, normal(0,10)): biprobit y1 y2 x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): biprobit y1 y2 x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): biprobit y1 y2 x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Bayesian seemingly unrelated bivariate probit regression using default priors

```
bayes: biprobit (y1 = x1 x2 x3) (y2 = x1 x2)
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **biprobit**.

Menu

Statistics > Binary outcomes > Bayesian regression > Bivariate probit regression

Statistics > Binary outcomes > Bayesian regression > Seemingly unrelated bivariate probit

Syntax

Bayesian bivariate probit regression

```
bayes [ , bayesopts ] : biprobit depvar1 depvar2 [indepvars] [if] [in] [weight]
    [ , options ]
```

Bayesian seemingly unrelated bivariate probit regression

```
bayes [ , bayesopts ] : biprobit equation1 equation2 [if] [in] [weight] [ , options ]
```

where $equation_1$ and $equation_2$ are specified as

```
( [eqname:] depvar [=] [indepvars] [ , noconstant offset(varname) ] )
```

options	Description
Model	
noconstant	suppress constant term
offset1(*varname*)	offset variable for first equation
offset2(*varname*)	offset variable for second equation
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar$_1$, *depvar*$_2$, *depvar*, and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

fweights are allowed; see [U] **11.1.6 weight**.

bayes: biprobit, level() is equivalent to bayes, clevel(): biprobit.

For a detailed description of *options*, see *Options* in [R] **biprobit**. Options noconstant, offset1(), and offset2() are not allowed with seemingly unrelated bivariate probit regression.

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients and atanh-transformed correlation; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results

Blocking

*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*$_1$:*indepvars*} and {*depvar*$_2$:*indepvars*} and atanh-transformed correlation {athrho}. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **biprobit**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **biprobit** — Bivariate probit regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: clogit — Bayesian conditional logistic regression

Description

`bayes: clogit` fits a Bayesian conditional logistic regression to matched case–control data; see [BAYES] **bayes** and [R] **clogit** for details.

Quick start

Bayesian conditional logistic regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: clogit y x1 x2, group(id)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): clogit y x1 x2, group(id)
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): clogit y x1 x2, group(id)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): clogit y x1 x2, group(id)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): clogit y x1 x2, group(id)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display odds ratios instead of coefficients

```
bayes: clogit y x1 x2, group(id) or
```

Display odds ratios on replay

```
bayes, or
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **clogit**.

Menu

Statistics > Binary outcomes > Bayesian regression > Conditional logistic regression

Syntax

```
bayes [, bayesopts]: clogit depvar [indepvars] [if] [in] [weight],
    group(varname) [options]
```

options	Description
Model	
* `group(`*varname*`)`	matched group variable
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
Reporting	
`or`	report odds ratios
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

*`group(`*varname*`)` is required.

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

`fweight`s are allowed; see [U] **11.1.6 weight**. `fweight`s are interpreted to apply to groups as a whole, not to individual observations. See *Use of weights* in [R] **clogit**.

`bayes: clogit, level()` is equivalent to `bayes, clevel(): clogit`.

For a detailed description of *options*, see *Options* in [R] **clogit**.

bayesopts	Description
Priors	
* `normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
Blocking	
* `blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref*`[, `*blockopts*`])`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
* `noblocking`	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
*or	report odds ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **clogit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **clogit** — Conditional (fixed-effects) logistic regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: cloglog — Bayesian complementary log–log regression

Description

`bayes: cloglog` fits a Bayesian complementary log–log regression to a binary outcome; see [BAYES] **bayes** and [R] **cloglog** for details.

Quick start

Bayesian complementary log–log regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: cloglog y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): cloglog y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): cloglog y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): cloglog y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): cloglog y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display results as exponentiated coefficients

```
bayes: cloglog y x1 x2, eform
```

Display exponentiated coefficients on replay

```
bayes, eform
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **cloglog**.

Menu

Statistics > Binary outcomes > Bayesian regression > Complementary log–log regression

Syntax

```
bayes [, bayesopts]: cloglog depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
asis	retain perfect predictor variables
Reporting	
eform	report exponentiated coefficients
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

fweights are allowed; see [U] **11.1.6 weight**.

bayes: cloglog, level() is equivalent to bayes, clevel(): cloglog.

For a detailed description of *options*, see *Options* in [R] **cloglog**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **cloglog**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Logistic regression with perfect predictors* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **cloglog** — Complementary log–log regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: dsge — Bayesian linear dynamic stochastic general equilibrium models

Description

`bayes: dsge` fits a Bayesian linear dynamic stochastic general equilibrium model to continuous multivariate time series; see [BAYES] **bayes** and [DSGE] **dsge** for details.

Quick start

Autoregressive model of order 1 with uniform prior for the autoregressive coefficient `{rho}`

```
bayes, prior({rho}, uniform(0,1)): dsge (y = z) (F.z = {rho}*z, state)
```

Save simulation results to `bdsgesim.dta`, and use a random-number seed for reproducibility

```
bayes, prior({rho}, uniform(0,1)) rseed(17) saving(bdsgesim):    ///
       dsge (y = z) (F.z = {rho}*z, state)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, and set length of burn-in period to 5,000

```
bayes, prior({rho}, uniform(0,1)) mcmcsize(20000) burnin(5000):  ///
       dsge (y = z) (F.z = {rho}*z, state)
```

Estimate an Euler equation for variable y

```
bayes, prior({rho}, uniform(0,1)) prior({sigma}, beta(5, 5)):    ///
       dsge (y = f.y - {sigma}*r) (F.r = {rho}*r, state)
```

In the above, request that a 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval.

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes**.

Menu

Statistics > Multivariate time series > Bayesian models > Linear DSGE models

Syntax

```
bayes, prior(userparams,...) [bayesopts]: dsge eqlist [if] [in] [, options]
```

options	Description
Advanced	
`lintolerance(#)`	set tolerance used for linearity check; seldom used
`level(#)`	set credible level; default is `level(95)`
`noidencheck`	do not check for parameter identification; implied
`solve`	return model solution at initial values; implied

`bayes: dsge, level()` is equivalent to `bayes, clevel(): dsge`.

For a detailed description of *options*, see *Options* in [DSGE] **dsge**.

Options `level()`, `noidencheck`, and `stable` do not appear on the dialog box.

bayesopts	Description
Priors	
* `igammaprior(# #)`	specify shape and scale of default inverse-gamma prior for standard deviations of shocks; default is `igammaprior(0.01 0.01)`
`prior(priorspec)`	prior for model parameters; this option may be repeated and is required for all user-defined parameters *userparams*
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(paramref)`	specify model parameters to be excluded from the simulation results
Blocking	
`block(paramref [, blockopts])`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
Initialization	
`initial(initspec)`	specify initial values for model parameters with a single chain
`init#(initspec)`	specify initial values for #th chain; requires `nchains()`
`initall(initspec)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
* `noisily`	display output from the estimation command during initialization

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are user-defined parameters *userparams* and standard deviations of shocks {sd(e.*exogstate*)}. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

nomleinitial is assumed. Default parameter values are set to means of priors.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [DSGE] **dsge**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**. For an introduction to and examples of Bayesian DSGEs, see [DSGE] **Intro 9** and [DSGE] **Intro 9a**.

Stored results

See *Stored results* in [BAYES] **bayes**. Also see *Stored results* in [DSGE] **dsge**.

Methods and formulas

See *Methods and formulas* in [DSGE] **dsge** and [DSGE] **Intro 9**. See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes: dsge postestimation** — Postestimation tools for bayes: dsge and bayes: dsgenl

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[DSGE] **dsge** — Linear dynamic stochastic general equilibrium models

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: dsgenl — Bayesian nonlinear dynamic stochastic general equilibrium models

Description

`bayes: dsgenl` fits a Bayesian nonlinear dynamic stochastic general equilibrium (DSGE) model to continuous multivariate time series; see [BAYES] **bayes** and [DSGE] **dsgenl** for details.

Quick start

Nonlinear DSGE model in which observed variable `y` depends on unobserved state `z`

```
bayes, prior({rho}, uniform(0,1)) prior({alpha}, beta(5,5)):  ///
       dsgenl (y = z^({alpha})) (ln(F.z) = {rho}*ln(z)),      ///
       exostate(z) observed(y)
```

Save simulation results to `bdsgenlsim.dta`, and use a random-number seed for reproducibility

```
bayes, prior({rho}, uniform(0,1)) prior({alpha}, beta(5,5)):  ///
       rseed(17) saving(bdsgenlsim):                          ///
       dsgenl (y = z^({alpha})) (ln(F.z) = {rho}*ln(z)),      ///
       exostate(z) observed(y)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, and set length of burn-in period to 5,000

```
bayes, prior({rho}, uniform(0,1)) prior({alpha}, beta(5,5)):  ///
       mcmcsize(20000) burnin(5000):                          ///
       dsgenl (y = z^({alpha})) (ln(F.z) = {rho}*ln(z)),      ///
       exostate(z) observed(y)
```

Estimate parameters of a four-equation production model. Priors for `{alpha}`, `{beta}`, and `{rho}` are given by beta distributions with means 0.3, 0.9, and 0.5, respectively

```
bayes, prior({alpha}, beta(3,7))                              ///
       prior({beta},  beta(9,1))                              ///
       prior({rho},   beta(7,7)) :                            ///
       dsgenl (1/c = {alpha}*{beta}*(1/F.c)*(F.y/F.k))        ///
              (y = z*k^({alpha})) (F.k = y - c)               ///
              (ln(F.z) = {rho}*ln(z)) ,                       ///
              exostate(z) endostate(k) observed(y) unobserved(c)
```

In the above, request that a 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval.

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes**.

Menu

Statistics > Multivariate time series > Bayesian models > Nonlinear DSGE models

Syntax

```
bayes, prior(userparams, ...) [bayesopts] : dsgenl (eqn_list) [if] [in] [, options]
```

options	Description
Model	
* `observed(`*string*`)`	list observed control variables
`unobserved(`*string*`)`	list unobserved control variables
* `exostate(`*string*`)`	list exogenous state variables
`endostate(`*string*`)`	list endogenous state variables
`linearapprox`	take a linear, rather than log-linear, approximation
`level(#)`	set credible level; default is `level(95)`
`noidencheck`	do not check for parameter identification; implied
`solve`	return model solution at initial values; implied

*`observed()` and `exostate()` are required.

`bayes: dsgenl, level()` is equivalent to `bayes, clevel(): dsgenl`.

For a detailed description of *options*, see *Options* in [DSGE] **dsgenl**.

Options `level()`, `noidencheck`, and `stable` do not appear on the dialog box.

bayesopts	Description
Priors	
* `igammaprior(# #)`	specify shape and scale of default inverse-gamma prior for standard deviations of shocks; default is `igammaprior(0.01 0.01)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated and is required for all user-defined parameters *userparams*
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
Blocking	
`block(`*paramref*`[ , `*blockopts*`])`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
Initialization	
`initial(`*initspec*`)`	specify initial values for model parameters with a single chain
`init#(`*initspec*`)`	specify initial values for #th chain; requires `nchains()`
`initall(`*initspec*`)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
* `noisily`	display output from the estimation command during initialization

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are user-defined parameters *userparams* and standard deviations of shocks {sd(e.*exogstate*)}. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

nomleinitial is assumed. Default parameter values are set to means of priors.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [DSGE] **dsgenl**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**. For an introduction to and examples of Bayesian DSGEs, see [DSGE] **Intro 9** and [DSGE] **Intro 9b**.

Stored results

See *Stored results* in [BAYES] **bayes**. Also see *Stored results* in [DSGE] **dsgenl**.

Methods and formulas

See *Methods and formulas* in [DSGE] **dsge** and [DSGE] **Intro 9**. See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes: dsge postestimation** — Postestimation tools for bayes: dsge and bayes: dsgenl

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[DSGE] **dsgenl** — Nonlinear dynamic stochastic general equilibrium models

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: dsge postestimation — Postestimation tools for bayes: dsge and bayes: dsgenl

Postestimation commands Remarks and examples Also see

Postestimation commands

The following Bayesian postestimation commands are of special interest after `bayes: dsge` and `bayes: dsgenl`:

Command	Description
`bayesirf`	Bayesian impulse–response functions

The following standard Bayesian postestimation commands are also available:

Command	Description
`bayesgraph`	graphical summaries and convergence diagnostics
`bayesstats grubin`	Gelman–Rubin convergence diagnostics
`bayesstats ess`	effective sample sizes and related statistics
`bayesstats summary`	Bayesian summary statistics for model parameters and their functions
`bayesstats ic`	Bayesian information criteria and Bayes factors
`bayestest model`	hypothesis testing using model posterior probabilities
`bayestest interval`	interval hypothesis testing
* `estimates`	cataloging estimation results

* `estimates table` and `estimates stats` are not appropriate with `bayes: var` estimation results.

Remarks and examples

See [DSGE] **Intro 9a** and [DSGE] **Intro 9b** for examples of `bayesirf` after `bayes: dsge` and `bayes: dsgenl`. Also see [BAYES] **Bayesian postestimation** for generic Bayesian postestimation tools.

Also see

[BAYES] **bayes: dsge** — Bayesian linear dynamic stochastic general equilibrium models

[BAYES] **bayes: dsgenl** — Bayesian nonlinear dynamic stochastic general equilibrium models

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

[U] 20 Estimation and postestimation commands

Title

bayes: fracreg — Bayesian fractional response regression

Description

`bayes: fracreg` fits a Bayesian fractional response regression to a fractional outcome whose values are greater than or equal to 0 and less than or equal to 1; see [BAYES] **bayes** and [R] **fracreg** for details.

Quick start

Bayesian fractional probit regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: fracreg probit y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): fracreg probit y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): fracreg probit y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): fracreg probit y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): fracreg probit y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Fit a fractional logistic regression and display results as odds ratios

```
bayes: fracreg logit y x1 x2, or
```

Display odds ratios on replay

```
bayes, or
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **fracreg**.

Menu

Statistics > Fractional outcomes > Bayesian fractional regression

Syntax

Syntax for fractional probit regression

```
bayes [ , bayesopts ] : fracreg probit depvar [ indepvars ] [ if ] [ in ] [ weight ]
    [ , options ]
```

Syntax for fractional logistic regression

```
bayes [ , bayesopts ] : fracreg logit depvar [ indepvars ] [ if ] [ in ] [ weight ]
    [ , options ]
```

Syntax for fractional heteroskedastic probit regression

```
bayes [ , bayesopts ] : fracreg probit depvar [ indepvars ] [ if ] [ in ] [ weight ],
    het(varlist[ , offset(varname_o) ]) [ options ]
```

options	Description
Model	
noconstant	suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
* het(*varlist*[, offset(*varname*$_o$)])	independent variables to model the variance and possible offset variable with fracreg probit
Reporting	
or	report odds ratios; only valid with fracreg logit
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

* het() may be used only with fracreg probit to compute fractional heteroskedastic probit regression.
indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.
depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.
fweights are allowed; see [U] **11.1.6 weight**.
bayes: fracreg, level() is equivalent to bayes, clevel(): fracreg.
For a detailed description of *options*, see *Options* in [R] **fracreg**.

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation

Simulation

nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results

Blocking

*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
*or	report odds ratio; only valid with fracreg logit
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

`search(`*search_options*`)`	control the search for feasible initial values
`corrlag(#)`	specify maximum autocorrelation lag; default varies
`corrtol(#)`	specify autocorrelation tolerance; default is `corrtol(0.01)`

*Starred options are specific to the `bayes` prefix; other options are common between `bayes` and `bayesmh`.

Options `prior()` and `block()` may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} and, if option `het()` is specified, regression coefficients {`lnsigma`:*varlist*} for the log-standard deviation equation. Use the `dryrun` option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **fracreg**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **fracreg** — Fractional response regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: glm — Bayesian generalized linear models

Description

`bayes: glm` fits a Bayesian generalized linear model to outcomes of different types such as continuous, binary, count, and so on; see [BAYES] **bayes** and [R] **glm** for details.

Quick start

Bayesian generalized linear model of `y` on `x1` and `x2`, using the Gaussian family and log link and using default normal priors for regression coefficients

```
bayes: glm y x1 x2, family(gaussian) link(log)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): glm y x1 x2, family(gaussian) link(log)
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)):  ///
glm y x1 x2, family(gaussian) link(log)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123):  ///
glm y x1 x2, family(gaussian) link(log)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500):  ///
glm y x1 x2, family(gaussian) link(log)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Fit a logit model and display results as odds ratios

```
bayes: glm z x1 x2, family(binomial) eform
```

Display odds ratios on replay

```
bayes, eform
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **glm**.

Menu

Statistics > Generalized linear models > Bayesian generalized linear models (GLM)

Syntax

```
bayes [, bayesopts]: glm depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
`family(`*familyname*`)`	distribution of *depvar*; default is `family(gaussian)`
`link(`*linkname*`)`	link function; default is canonical link for `family()` specified
Model 2	
`noconstant`	suppress constant term
`exposure(`*varname*`)`	include ln(*varname*) in model with coefficient constrained to 1
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`asis`	retain perfect predictor variables
`mu(`*varname*`)`	use *varname* as the initial estimate for the mean of *depvar*
`init(`*varname*`)`	synonym for `mu(`*varname*`)`
Reporting	
`eform`	report exponentiated coefficients
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`fweights` are allowed; see [U] **11.1.6 weight**.

`bayes: glm, level()` is equivalent to `bayes, clevel(): glm`.

For a detailed description of *options*, see *Options* in [R] **glm**.

bayesopts	Description
Priors	
* `normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
Blocking	
* `blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref*`[, `*blockopts*`])`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
* `noblocking`	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **glm**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Generalized linear model* in [BAYES] **bayes**.

`bayes: glm` does not estimate the scale parameter but uses a fixed value as provided by the `glm` command. If you want to fit a GLM and estimate the scale parameter, use `bayes: meglm` without specifying random effects.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **glm** — Generalized linear models

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: gnbreg — Bayesian generalized negative binomial regression

Description

`bayes: gnbreg` fits a Bayesian generalized negative binomial regression to a nonnegative count outcome; see [BAYES] **bayes** and [R] **nbreg** for details.

Quick start

Bayesian generalized negative binomial regression of `y` on `x1` and `x2`, using `z` to model the log-overdispersion and using default normal priors for regression coefficients and log-overdispersion parameter

```
bayes: gnbreg y x1 x2, lnalpha(z)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): gnbreg y x1 x2, lnalpha(z)
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): gnbreg y x1 x2, lnalpha(z)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): gnbreg y x1 x2, lnalpha(z)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): gnbreg y x1 x2, lnalpha(z)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display incidence-rate ratios instead of coefficients

```
bayes: gnbreg y x1 x2, lnalpha(z) irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **nbreg**.

Menu

Statistics > Count outcomes > Bayesian regression > Generalized negative binomial regression

Syntax

```
bayes [, bayesopts]: gnbreg depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
lnalpha(*varlist*)	dispersion model variables
exposure(*varname*$_e$)	include ln(*varname*$_e$) in model with coefficient constrained to 1
offset(*varname*$_o$)	include *varname*$_o$ in model with coefficient constrained to 1
Reporting	
irr	report incidence-rate ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars and *varlist* may contain factor variables; see **[U] 11.4.3 Factor variables**.

fweights are allowed; see **[U] 11.1.6 weight**.

bayes: gnbreg, level() is equivalent to bayes, clevel(): gnbreg.

For a detailed description of *options*, see *Options for gnbreg* in **[R] nbreg**.

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients and log-overdispersion parameter; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
* blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
* noblocking	do not block parameters by default

Initialization	
initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
Adaptation	
adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix
Reporting	
clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
*irr	report incidence-rate ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells
Advanced	
search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} for the main regression and {lnalpha:*varlist*} for the log-dispersion equation. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **nbreg**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **nbreg** — Negative binomial regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: heckman — Bayesian Heckman selection model

Description

`bayes: heckman` fits a Bayesian sample-selection linear regression to a partially observed continuous outcome; see [BAYES] **bayes** and [R] **heckman** for details.

Quick start

Bayesian Heckman model of `y` on `x1` and `x2`, using `z1` and `z2` to model selection and using default normal priors for regression coefficients, log-standard-deviation, and atanh-correlation

```
bayes: heckman y x1 x2, select(z1 z2)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): heckman y x1 x2, select(z1 z2)
```

Use uniform priors for the slopes and a normal prior for the intercept of the main regression

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): heckman y x1 x2, select(z1 z2)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123):, ///
heckman y x1 x2, select(z1 z2)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500):, ///
heckman y x1 x2, select(z1 z2)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **heckman**.

Menu

Statistics > Linear models and related > Bayesian regression > Heckman selection model

Syntax

```
bayes [ , bayesopts ] : heckman depvar [ indepvars ] [ if ] [ in ] [ weight ] ,
    select( [ depvar_s = ] varlist_s [ , noconstant offset(varname_o) ] ) [ options ]
```

options	Description
Model	
* `select()`	specify selection equation: dependent and independent variables; whether to have constant term and offset variable
`noconstant`	suppress constant term
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
Reporting	
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

* `select()` is required.

The full specification is `select(` [*depvar*$_s$ `=`] *varlist*$_s$ [`, noconstant offset(`*varname*$_o$`)`] `)`.

indepvars and *varlist*$_s$ may contain factor variables; see **[U] 11.4.3 Factor variables**.

depvar, *indepvars*, *varlist*$_s$, and *depvar*$_s$ may contain time-series operators; see **[U] 11.4.4 Time-series varlists**.

`fweights` are allowed; see **[U] 11.1.6 weight**.

`bayes: heckman, level()` is equivalent to `bayes, clevel(): heckman`.

For a detailed description of *options*, see *Options for Heckman selection model (ML)* and *Options for Heckman selection model (two-step)* in **[R] heckman**.

bayesopts	Description
Priors	
* `normalprior(#)`	specify standard deviation of default normal priors for regression coefficients, log-standard-deviation, and atanh-correlation; default is `normalprior(100)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
Blocking	
* `blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [`,` *blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
* `noblocking`	do not block parameters by default

Initialization	
initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
Adaptation	
adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix
Reporting	
clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells
Advanced	
search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} for the main regression and {select:*varlist_s*} for the selection equation, atanh-transformed correlation {athrho}, and log-standard deviation {lnsigma}. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **heckman**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Heckman selection model* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **heckman** — Heckman selection model

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: heckoprobit — Bayesian ordered probit model with sample selection

Description

`bayes: heckoprobit` fits a Bayesian sample-selection ordered probit regression to a partially observed ordinal outcome; see [BAYES] **bayes** and [R] **heckoprobit** for details.

Quick start

Bayesian sample-selection ordered probit regression of `y` on `x1` and `x2`, using `z1` and `z2` to model selection, and using default normal priors for regression coefficients and atanh-correlation and flat priors for cutpoints

```
bayes: heckoprobit y x1 x2, select(z1 z2)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): heckoprobit y x1 x2, select(z1 z2)
```

Use uniform priors for the slopes and a normal prior for the intercept of the main regression

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): heckoprobit y x1 x2, select(z1 z2)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123):, ///
heckoprobit y x1 x2, select(z1 z2)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500):, ///
heckoprobit y x1 x2, select(z1 z2)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **heckoprobit**.

Menu

Statistics > Ordinal outcomes > Bayesian regression > Ordered probit regression with sample selection

Syntax

```
bayes [, bayesopts]: heckoprobit depvar indepvars [if] [in] [weight],
    select([depvar_s =] varlist_s [, noconstant offset(varname_o)]) [options]
```

options	Description
Model	
* `select()`	specify selection equation: dependent and independent variables; whether to have constant term and offset variable
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
Reporting	
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

* `select()` is required.

The full specification is `select(` [*depvar*$_s$ `=`] *varlist*$_s$ [`, noconstant offset(`*varname*$_o$`)`] `)`.

indepvars and *varlist*$_s$ may contain factor variables; see **[U] 11.4.3 Factor variables**.

depvar, *indepvars*, *varlist*$_s$, and *depvar*$_s$ may contain time-series operators; see **[U] 11.4.4 Time-series varlists**.

`fweight`s are allowed; see **[U] 11.1.6 weight**.

`bayes: heckoprobit, level()` is equivalent to `bayes, clevel(): heckoprobit`.

For a detailed description of *options*, see *Options* in **[R] heckoprobit**.

bayesopts	Description
Priors	
* `normalprior(#)`	specify standard deviation of default normal priors for regression coefficients and atanh-correlation; default is `normalprior(100)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
Blocking	
* `blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [`, `*blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
* `noblocking`	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} for the main regression and {select:*varlist_s*} for the selection equation, atanh-transformed correlation {athrho}, and cutpoints {cut1}, {cut2}, and so on. Use the dryrun option to see the definitions of model parameters prior to estimation.

Flat priors, flat, are used by default for cutpoints.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **heckoprobit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Heckman selection model* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **heckoprobit** — Ordered probit model with sample selection

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: heckprobit — Bayesian probit model with sample selection

Description

`bayes: heckprobit` fits a Bayesian sample-selection probit regression to a partially observed binary outcome; see [BAYES] **bayes** and [R] **heckprobit** for details.

Quick start

Bayesian sample-selection probit regression of `y` on `x1` and `x2`, using `z1` and `z2` to model selection and using default normal priors for regression coefficients and atanh-correlation

```
bayes: heckprobit y x1 x2, select(z1 z2)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): heckprobit y x1 x2, select(z1 z2)
```

Use uniform priors for the slopes and a normal prior for the intercept of the main regression

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): heckprobit y x1 x2, select(z1 z2)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123):, ///
heckprobit y x1 x2, select(z1 z2)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500):, ///
heckprobit y x1 x2, select(z1 z2)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **heckprobit**.

Menu

Statistics > Binary outcomes > Bayesian regression > Probit model with sample selection

Syntax

```
bayes [ , bayesopts ] : heckprobit depvar indepvars [ if ] [ in ] [ weight ] ,
    select( [ depvar_s = ] varlist_s [ , noconstant offset(varname_o) ] ) [ options ]
```

options	Description
Model	
* `select()`	specify selection equation: dependent and independent variables; whether to have constant term and offset variable
`noconstant`	suppress constant term
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
Reporting	
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

*`select()` is required.

The full specification is `select(` [*depvar*$_s$ `=`] *varlist*$_s$ [`, noconstant offset(`*varname*$_o$`)`] `)`.

indepvars and *varlist*$_s$ may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *indepvars*, *varlist*$_s$, and *depvar*$_s$ may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`fweight`s are allowed; see [U] **11.1.6 weight**.

`bayes: heckprobit, level()` is equivalent to `bayes, clevel(): heckprobit`.

For a detailed description of *options*, see *Options* in [R] **heckprobit**.

bayesopts	Description
Priors	
* `normalprior(#)`	specify standard deviation of default normal priors for regression coefficients and atanh-correlation; default is `normalprior(100)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
Blocking	
* `blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [`,` *blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
* `noblocking`	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} for the main regression and {select:*varlist_s*} for the selection equation, and atanh-transformed correlation {athrho}. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **heckprobit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Heckman selection model* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **heckprobit** — Probit model with sample selection

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: hetoprobit — Bayesian heteroskedastic ordered probit regression

Description

`bayes: hetoprobit` fits a Bayesian heteroskedastic ordered probit regression to an ordinal outcome; see [BAYES] **bayes** and [R] **hetoprobit** for details.

Quick start

Bayesian heteroskedastic ordered probit regression of `y` on `x1` and `x2`, using `z1` to model the variance, and using default normal priors for regression coefficients and log-standard-deviation coefficients and flat priors for cutpoints

```
bayes: hetoprobit y x1 x2, het(z1)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): hetoprobit y x1 x2, het(z1)
```

Use uniform priors for the slopes and a normal prior for the intercept of the main regression

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): hetoprobit y x1 x2, het(z1)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123):  ///
hetoprobit y x1 x2, het(z1)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500):  ///
hetoprobit y x1 x2, het(z1)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **hetoprobit**.

Menu

Statistics > Ordinal outcomes > Bayesian regression > Heteroskedastic ordered probit regression

Syntax

```
bayes [ , bayesopts ] : hetoprobit depvar [indepvars] [if] [in] [weight] ,
    het(varlist[ , offset(varname_o) ]) [options]
```

options	Description
Model	
*`het(varlist[...])`	independent variables to model the variance and possible offset variable
`offset(varname)`	include *varname* in model with coefficient constrained to 1
Reporting	
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

*`het()` is required. The full specification is `het(`*varlist*` [ , offset(`*varname*$_o$`) ])`.
indepvars and *varlist* may contain factor variables; see **[U] 11.4.3 Factor variables**.
depvar, *indepvars*, and *varlist* may contain time-series operators; see **[U] 11.4.4 Time-series varlists**.
`fweight`s are allowed; see **[U] 11.1.6 weight**.
`bayes: hetoprobit, level()` is equivalent to `bayes, clevel(): hetoprobit`.
For a detailed description of *options*, see *Options* in **[R] hetoprobit**.

bayesopts	Description
Priors	
*`normalprior(#)`	specify standard deviation of default normal priors for regression coefficients and log-standard-deviation coefficients; default is `normalprior(100)`
`prior(priorspec)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(paramref)`	specify model parameters to be excluded from the simulation results
Blocking	
*`blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(paramref[ , blockopts ])`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
*`noblocking`	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} for the main regression and {lnsigma:*varlist*} for the log-standard-deviation equation and cutpoints {cut1}, {cut2}, and so on. Use the dryrun option to see the definitions of model parameters prior to estimation.

Flat priors, flat, are used by default for cutpoints.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **hetoprobit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **hetoprobit** — Heteroskedastic ordered probit regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: hetprobit — Bayesian heteroskedastic probit regression

Description

`bayes: hetprobit` fits a Bayesian heteroskedastic probit regression to a binary outcome; see [BAYES] **bayes** and [R] **hetprobit** for details.

Quick start

Bayesian heteroskedastic probit regression of `y` on `x1` and `x2`, using `z1` to model the variance and using default normal priors for regression coefficients and log-variance coefficients

```
bayes: hetprobit y x1 x2, het(z1)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): hetprobit y x1 x2, het(z1)
```

Use uniform priors for the slopes and a normal prior for the intercept of the main regression

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): hetprobit y x1 x2, het(z1)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): hetprobit y x1 x2, het(z1)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): hetprobit y x1 x2, het(z1)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **hetprobit**.

Menu

Statistics > Binary outcomes > Bayesian regression > Heteroskedastic probit regression

Syntax

```
bayes [, bayesopts]: hetprobit depvar [indepvars] [if] [in] [weight],
    het(varlist[, offset(varname_o)]) [options]
```

options	Description
Model	
*`het(varlist[...])`	independent variables to model the variance and possible offset variable
`noconstant`	suppress constant term
`offset(varname)`	include *varname* in model with coefficient constrained to 1
`asis`	retain perfect predictor variables
Reporting	
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

*`het()` is required. The full specification is `het(`*varlist* `[, offset(`*varname*$_o$`)])`.
indepvars and *varlist* may contain factor variables; see **[U] 11.4.3 Factor variables**.
depvar, *indepvars*, and *varlist* may contain time-series operators; see **[U] 11.4.4 Time-series varlists**.
`fweight`s are allowed; see **[U] 11.1.6 weight**.
`bayes: hetprobit, level()` is equivalent to `bayes, clevel(): hetprobit`.
For a detailed description of *options*, see *Options* in **[R] hetprobit**.

bayesopts	Description
Priors	
*`normalprior(#)`	specify standard deviation of default normal priors for regression coefficients and log-variance coefficients; default is `normalprior(100)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
Blocking	
*`blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref*`[, `*blockopts*`])`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
*`noblocking`	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} for the main regression and {lnsigma:*varlist*} for the log-variance equation. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **hetprobit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **hetprobit** — Heteroskedastic probit model

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: hetregress — Bayesian heteroskedastic linear regression

Description

`bayes: hetregress` fits a Bayesian heteroskedastic linear regression to a continuous outcome; see [BAYES] **bayes** and [R] **hetregress** for details.

Quick start

Bayesian heteroskedastic linear regression of `y` on `x1` and `x2`, using `z1` to model the variance and using default normal priors for regression coefficients and log-variance coefficients

```
bayes: hetregress y x1 x2, het(z1)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): hetregress y x1 x2, het(z1)
```

Use uniform priors for the slopes and a normal prior for the intercept of the main regression

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): hetregress y x1 x2, het(z1)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123):  ///
hetregress y x1 x2, het(z1)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500):  ///
hetregress y x1 x2, het(z1)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **hetregress**.

Menu

Statistics > Linear models and related > Bayesian regression > Heteroskedastic linear regression

Syntax

```
bayes [, bayesopts]: hetregress depvar [indepvars] [if] [in] [weight]
    [, options]
```

options	Description
Model	
`het(`*varlist*`)`	independent variables to model the variance
`noconstant`	suppress constant term
Reporting	
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

indepvars and *varlist* may contain factor variables; see **[U] 11.4.3 Factor variables**.

depvar, *indepvars*, and *varlist* may contain time-series operators; see **[U] 11.4.4 Time-series varlists**.

`fweights` are allowed; see **[U] 11.1.6 weight**.

`bayes: hetregress, level()` is equivalent to `bayes, clevel(): hetregress`.

For a detailed description of *options*, see *Options for maximum likelihood estimation* and *Options for two-step GLS estimation* in [R] **hetregress**.

bayesopts	Description
Priors	
* `normalprior(#)`	specify standard deviation of default normal priors for regression coefficients and log-variance coefficients; default is `normalprior(100)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
Blocking	
* `blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref*`[, `*blockopts*`])`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
* `noblocking`	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} for the main regression and {lnsigma2:*varlist*} for the log-variance equation. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **hetregress**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **hetregress** — Heteroskedastic linear regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: intreg — Bayesian interval regression

Description

`bayes: intreg` fits a Bayesian interval regression to a continuous, interval-measured outcome; see [BAYES] **bayes** and [R] **intreg** for details.

Quick start

Bayesian interval regression of `y_lower` and `y_upper` on `x1` and `x2`, using default normal priors for regression coefficients and log-variance

```
bayes: intreg y_lower y_upper x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): intreg y_lower y_upper x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y_lower: x1 x2}, uniform(-10,10)) ///
prior({y_lower:_cons}, normal(0,10)): intreg y_lower y_upper x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123):  ///
intreg y_lower y_upper x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500):  ///
intreg y_lower y_upper x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **intreg**.

Menu

Statistics > Linear models and related > Bayesian regression > Interval regression

Syntax

```
bayes [ , bayesopts ] : intreg depvar1 depvar2 [ indepvars ] [ if ] [ in ] [ weight ]
    [ , options ]
```

options	Description
Model	
noconstant	suppress constant term
het(*varlist* [, noconstant])	independent variables to model the variance; use noconstant to suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars and *varlist* may contain factor variables; see **[U] 11.4.3 Factor variables**.

$depvar_1$, $depvar_2$, *indepvars*, and *varlist* may contain time-series operators; see **[U] 11.4.4 Time-series varlists**.

fweights are allowed; see **[U] 11.1.6 weight**.

bayes: intreg, level() is equivalent to bayes, clevel(): intreg.

For a detailed description of *options*, see *Options* in **[R] intreg**.

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients and log-variance; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
* blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
* noblocking	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*$_1$:*indepvars*} and log-standard deviation {lnsigma} or, if option het(*varlist*) is specified, coefficients {lnsigma:*varlist*} of the log-standard-deviation equation. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **intreg**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **intreg** — Interval regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: logistic — Bayesian logistic regression, reporting odds ratios

Description

`bayes: logistic` fits a Bayesian logistic regression to a binary outcome; see [BAYES] **bayes** and [R] **logistic** for details.

Quick start

Bayesian logistic regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: logistic y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): logistic y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): logistic y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): logistic y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): logistic y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display coefficients instead of odds ratios

```
bayes: logistic y x1 x2, coef
```

Display coefficients on replay

```
bayes, coef
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **logistic**.

Menu

Statistics > Binary outcomes > Bayesian regression > Logistic regression

Syntax

```
bayes [, bayesopts]: logistic depvar indepvars [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
asis	retain perfect predictor variables
Reporting	
coef	report estimated coefficients
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

fweights are allowed; see [U] **11.1.6 weight**.

bayes: logistic, level() is equivalent to bayes, clevel(): logistic.

For a detailed description of *options*, see *Options* in [R] **logistic**.

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
* blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
* noblocking	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
*coef	report estimated coefficients
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **logistic**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Logistic regression with perfect predictors* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Reference

Balov, N. 2017. Bayesian logistic regression with Cauchy priors using the bayes prefix. *The Stata Blog: Not Elsewhere Classified*. https://blog.stata.com/2017/09/08/bayesian-logistic-regression-with-cauchy-priors-using-the-bayes-prefix/.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **logistic** — Logistic regression, reporting odds ratios

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: logit — Bayesian logistic regression, reporting coefficients

Description

`bayes: logit` fits a Bayesian logistic regression to a binary outcome; see [BAYES] **bayes** and [R] **logit** for details.

Quick start

Bayesian logistic regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: logit y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): logit y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): logit y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): logit y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): logit y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display odds ratios instead of coefficients

```
bayes: logit y x1 x2, or
```

Display odds ratios on replay

```
bayes, or
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **logit**.

Menu

Statistics > Binary outcomes > Bayesian regression > Logistic regression

Syntax

```
bayes [, bayesopts]: logit depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
asis	retain perfect predictor variables
Reporting	
or	report odds ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

fweights are allowed; see [U] **11.1.6 weight**.

bayes: logit, level() is equivalent to bayes, clevel(): logit.

For a detailed description of *options*, see *Options* in [R] **logit**.

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
* blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
* noblocking	do not block parameters by default

Initialization	
`initial(`*initspec*`)`	specify initial values for model parameters with a single chain
`init#(`*initspec*`)`	specify initial values for #th chain; requires `nchains()`
`initall(`*initspec*`)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
* `noisily`	display output from the estimation command during initialization
Adaptation	
`adaptation(`*adaptopts*`)`	control the adaptive MCMC procedure
`scale(#)`	initial multiplier for scale factor; default is `scale(2.38)`
`covariance(`*cov*`)`	initial proposal covariance; default is the identity matrix
Reporting	
`clevel(#)`	set credible interval level; default is `clevel(95)`
`hpd`	display HPD credible intervals instead of the default equal-tailed credible intervals
* `or`	report odds ratios
`eform[ (`*string*`) ]`	report exponentiated coefficients and, optionally, label as *string*
`batch(#)`	specify length of block for batch-means calculations; default is `batch(0)`
`saving(`*filename*`[ , replace ])`	save simulation results to *filename*`.dta`
`nomodelsummary`	suppress model summary
`chainsdetail`	display detailed simulation summary for each chain
`[no]dots`	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is `nodots`
`dots(#[ , every(#) ])`	display dots as simulation is performed
`[no]show(`*paramref*`)`	specify model parameters to be excluded from or included in the output
`notable`	suppress estimation table
`noheader`	suppress output header
`title(`*string*`)`	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells
Advanced	
`search(`*search_options*`)`	control the search for feasible initial values
`corrlag(#)`	specify maximum autocorrelation lag; default varies
`corrtol(#)`	specify autocorrelation tolerance; default is `corrtol(0.01)`

*Starred options are specific to the `bayes` prefix; other options are common between `bayes` and `bayesmh`.

Options `prior()` and `block()` may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}. Use the `dryrun` option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **logit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Logistic regression with perfect predictors* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Reference

Balov, N. 2017. Bayesian logistic regression with Cauchy priors using the bayes prefix. *The Stata Blog: Not Elsewhere Classified*. https://blog.stata.com/2017/09/08/bayesian-logistic-regression-with-cauchy-priors-using-the-bayes-prefix/.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **logit** — Logistic regression, reporting coefficients

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: mecloglog — Bayesian multilevel complementary log–log regression

Description

`bayes: mecloglog` fits a Bayesian multilevel complementary log–log regression to a binary outcome; see [BAYES] **bayes** and [ME] **mecloglog** for details.

Quick start

Bayesian two-level complementary log–log regression of `y` on `x1` and `x2` with random intercepts by `id` , using default normal priors for regression coefficients and default inverse-gamma prior for the variance of random intercepts

```
bayes: mecloglog y x1 x2 || id:
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): mecloglog y x1 x2 || id:
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): mecloglog y x1 x2 || id:
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): mecloglog y x1 x2 || id:
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): mecloglog y x1 x2 || id:
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display results as exponentiated coefficients

```
bayes: mecloglog y x1 x2 || id: , eform
```

Display exponentiated coefficients on replay

```
bayes, eform
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **mecloglog**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Complementary log–log regression

Syntax

```
bayes [ , bayesopts ] : mecloglog depvar fe_equation
    [ || re_equation ] [ || re_equation ... ] [ , options ]
```

where the syntax of *fe_equation* is

```
[ indepvars ] [ if ] [ in ] [ weight ] [ , fe_options ]
```

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

```
levelvar: [ varlist ] [ , re_options ]
```

for random effects among the values of a factor variable

```
levelvar: R.varname
```

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`noconstant`	suppress constant term from the fixed-effects equation
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`asis`	retain perfect predictor variables

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `exchangeable`, `identity`, and `unstructured` are supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Model	
`binomial(`*varname*`|#)`	set binomial trials if data are in binomial form
Reporting	
`eform`	report exponentiated coefficients
`notable`	suppress coefficient table
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *indepvars*, and *varlist* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`fweights` are allowed; see [U] **11.1.6 weight**.

`bayes: mecloglog, level()` is equivalent to `bayes, clevel(): mecloglog`.

For a detailed description of *options*, see *Options* in [ME] **mecloglog**.

bayesopts	Description
Priors	
*`normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
*`igammaprior(# #)`	specify shape and scale of default inverse-gamma prior for variance components; default is `igammaprior(0.01 0.01)`
*`iwishartprior(# [...])`	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
`restubs(`*restub1 restub2 ...*`)`	specify stubs for random-effects parameters for all levels
Blocking	
*`blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [`,` *blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
*`noblocking`	do not block parameters by default
Initialization	
`initial(`*initspec*`)`	specify initial values for model parameters with a single chain
`init#(`*initspec*`)`	specify initial values for #th chain; requires `nchains()`
`initall(`*initspec*`)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
*`noisily`	display output from the estimation command during initialization
Adaptation	
`adaptation(`*adaptopts*`)`	control the adaptive MCMC procedure
`scale(#)`	initial multiplier for scale factor; default is `scale(2.38)`
`covariance(`*cov*`)`	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal-likelihood
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
nomesummary	suppress multilevel-structure summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
showreffects[(*reref*)]	specify that all or a subset of random-effects parameters be included in the output
melabel	display estimation table using the same row labels as mecloglog
nogroup	suppress table summarizing groups
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *rename*s and *restub* are defined. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [ME] **mecloglog**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. For multilevel examples, see *Multilevel models* in [BAYES] **bayes**. Also see *Crossed-effects model* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[ME] **mecloglog** — Multilevel mixed-effects complementary log–log regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: meglm — Bayesian multilevel generalized linear model

Description

`bayes: meglm` fits a Bayesian multilevel generalized linear model to outcomes of different types such as continuous, binary, count, and so on; see [BAYES] **bayes** and [ME] **meglm** for details.

Quick start

Bayesian two-level generalized linear model of `y` on `x1` and `x2` with random intercepts by `id` , using the Gaussian family and log link, and using default normal priors for regression coefficients and default inverse-gamma prior for the variance of random intercepts

```
bayes: meglm y x1 x2 || id:, family(gaussian) link(log)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): meglm y x1 x2 || id:, family(gaussian) link(log)
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)):  ///
meglm y x1 x2 || id:, family(gaussian) link(log)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123):  ///
meglm y x1 x2 || id:, family(gaussian) link(log)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500):  ///
meglm y x1 x2 || id:, family(gaussian) link(log)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Fit a logit model and display results as odds ratios

```
bayes: meglm z x1 x2 || id:, family(binomial) eform
```

Display odds ratios on replay

```
bayes, eform
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **meglm**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Generalized linear model (GLM)

Syntax

```
bayes [, bayesopts] : meglm depvar fe_equation
    [|| re_equation] [|| re_equation ...] [, options]
```

where the syntax of *fe_equation* is

```
[indepvars] [if] [in] [weight] [, fe_options]
```

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

```
levelvar: [varlist] [, re_options]
```

for random effects among the values of a factor variable

```
levelvar: R.varname
```

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`noconstant`	suppress constant term from the fixed-effects equation
`exposure(`$varname_e$`)`	include $\ln(varname_e)$ in model with coefficient constrained to 1
`offset(`$varname_o$`)`	include $varname_o$ in model with coefficient constrained to 1
`asis`	retain perfect predictor variables

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `exchangeable`, `identity`, and `unstructured` are supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Model	
`family(`*family*`)`	distribution of *depvar*; default is `family(gaussian)`
`link(`*link*`)`	link function; default varies per family
Reporting	
`eform`	report exponentiated coefficients
`irr`	report incidence-rate ratios
`or`	report odds ratios
`notable`	suppress coefficient table
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *indepvars*, and *varlist* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`fweights` are allowed; see [U] **11.1.6 weight**.

`bayes: meglm, level()` is equivalent to `bayes, clevel(): meglm`.

For a detailed description of *options*, see *Options* in [ME] **meglm**.

bayesopts	Description
Priors	
* `normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
* `igammaprior(# #)`	specify shape and scale of default inverse-gamma prior for variance components; default is `igammaprior(0.01 0.01)`
* `iwishartprior(# [...])`	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
`restubs(`*restub1 restub2 ...*`)`	specify stubs for random-effects parameters for all levels
Blocking	
* `blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [, *blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
* `noblocking`	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
* noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
* irr	report incidence-rate ratios
* or	report odds ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal-likelihood
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
nomesummary	suppress multilevel-structure summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
showreffects[(*reref*)]	specify that all or a subset of random-effects parameters be included in the output
melabel	display estimation table using the same row labels as meglm
nogroup	suppress table summarizing groups
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}, parameters as described in *Additional model parameters*, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *rename*s and *restub* are defined. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [ME] **meglm**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**. For multilevel examples, see *Multilevel models* in [BAYES] **bayes**. Also see *Crossed-effects model* in [BAYES] **bayes**.

Additional model parameters

In addition to regression coefficients {*depvar*:*indepvars*}, bayes: meglm defines extra parameters that depend on the chosen family; see table 1 below.

Table 1. Additional model parameters defined by bayes: meglm

Family	Parameter	Model parameter	Default prior
Gaussian	Error variance	{e.*depvar*:sigma2}	InvGamma$(0.01, 0.01)$
Bernoulli/Binomial	None	None	None
Ordinal	Cutpoints	{cut1}, {cut2}, ...	Flat
Poisson	None	None	None
Negative binomial	Log-overdispersion	{lnalpha} (mean disp.)	$N(0, 10000)$
		{lndelta} (constant disp.)	$N(0, 10000)$
Gamma	Log-scale	{lnscale}	$N(0, 10000)$

Use the dryrun option with the bayes prefix to see the definitions of model parameters prior to estimation.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[ME] **meglm** — Multilevel mixed-effects generalized linear models

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: meintreg — Bayesian multilevel interval regression

Description

`bayes: meintreg` fits a Bayesian multilevel interval regression to a continuous, interval-measured outcome; see [BAYES] **bayes** and [ME] **meintreg** for details.

Quick start

Bayesian two-level interval regression of `y_lower` and `y_upper` on `x1` and `x2` with random intercepts by `id` , using default normal priors for regression coefficients and default inverse-gamma priors for the error variance and for the variance of random intercepts

```
bayes: meintreg y_lower y_upper x1 x2 || id:
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): meintreg y_lower y_upper x1 x2 || id:
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y_lower: x1 x2}, uniform(-10,10)) ///
prior({y_lower:_cons}, normal(0,10)):  ///
meintreg y_lower y_upper x1 x2 || id:
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123):  ///
meintreg y_lower y_upper x1 x2 || id:
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500):  ///
meintreg y_lower y_upper x1 x2 || id:
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **meintreg**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Interval regression

Syntax

```
bayes [ , bayesopts ] : meintreg depvar_lower depvar_upper fe_equation
    [ || re_equation ] [ || re_equation ... ] [ , options ]
```

where the syntax of *fe_equation* is

```
[ indepvars ] [ if ] [ in ] [ weight ] [ , fe_options ]
```

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

```
levelvar: [ varlist ] [ , re_options ]
```

for random effects among the values of a factor variable

```
levelvar: R.varname
```

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`noconstant`	suppress constant term from the fixed-effects equation
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `exchangeable`, `identity`, and `unstructured` are supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Reporting	
`notable`	suppress coefficient table
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar$_{\text{lower}}$, *depvar*$_{\text{upper}}$, *indepvars*, and *varlist* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`fweights` are allowed; see [U] **11.1.6 weight**.

`bayes: meintreg, level()` is equivalent to `bayes, clevel(): meintreg`.

For a detailed description of *options*, see *Options* in [ME] **meintreg**.

bayesopts	Description
Priors	
*`normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
*`igammaprior(# #)`	specify shape and scale of default inverse-gamma prior for variance components; default is `igammaprior(0.01 0.01)`
*`iwishartprior(# [...])`	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
`restubs(`*restub1 restub2 ...*`)`	specify stubs for random-effects parameters for all levels
Blocking	
*`blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref*`[ , `*blockopts*`])`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
*`noblocking`	do not block parameters by default
Initialization	
`initial(`*initspec*`)`	specify initial values for model parameters with a single chain
`init#(`*initspec*`)`	specify initial values for #th chain; requires `nchains()`
`initall(`*initspec*`)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
*`noisily`	display output from the estimation command during initialization
Adaptation	
`adaptation(`*adaptopts*`)`	control the adaptive MCMC procedure
`scale(#)`	initial multiplier for scale factor; default is `scale(2.38)`
`covariance(`*cov*`)`	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal-likelihood
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
nomesummary	suppress multilevel-structure summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
showreffects[(*reref*)]	specify that all or a subset of random-effects parameters be included in the output
melabel	display estimation table using the same row labels as meintreg
nogroup	suppress table summarizing groups
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*$_{\text{lower}}$:*indepvars*}, error variance {e.*depvar*$_{\text{lower}}$:sigma2}, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *rename*s and *restub* are defined. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [ME] **meintreg**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. For multilevel examples, see *Multilevel models* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[ME] **meintreg** — Multilevel mixed-effects interval regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: melogit — Bayesian multilevel logistic regression

Description

`bayes: melogit` fits a Bayesian multilevel logistic regression to a binary outcome; see [BAYES] **bayes** and [ME] **melogit** for details.

Quick start

Bayesian two-level logistic regression of `y` on `x1` and `x2` with random intercepts by `id` , using default normal priors for regression coefficients and default inverse-gamma prior for the variance of random intercepts

```
bayes: melogit y x1 x2 || id:
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): melogit y x1 x2 || id:
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): melogit y x1 x2 || id:
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): melogit y x1 x2 || id:
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): melogit y x1 x2 || id:
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display odds ratios instead of coefficients

```
bayes: melogit y x1 x2 || id: , or
```

Display odds ratios on replay

```
bayes, or
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **melogit**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Logistic regression

Syntax

```
bayes [, bayesopts]: melogit depvar fe_equation
    [|| re_equation] [|| re_equation ...] [, options]
```

where the syntax of *fe_equation* is

```
[indepvars] [if] [in] [weight] [, fe_options]
```

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

```
levelvar: [varlist] [, re_options]
```

for random effects among the values of a factor variable

```
levelvar: R.varname
```

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`noconstant`	suppress constant term from the fixed-effects equation
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`asis`	retain perfect predictor variables

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `exchangeable`, `identity`, and `unstructured` are supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Model	
`binomial(`*varname*`|#)`	set binomial trials if data are in binomial form
Reporting	
`or`	report odds ratios
`notable`	suppress coefficient table
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *indepvars*, and *varlist* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`fweights` are allowed; see [U] **11.1.6 weight**.

`bayes: melogit, level()` is equivalent to `bayes, clevel(): melogit`.

For a detailed description of *options*, see *Options* in [ME] **melogit**.

bayesopts	Description
Priors	
*`normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
*`igammaprior(# #)`	specify shape and scale of default inverse-gamma prior for variance components; default is `igammaprior(0.01 0.01)`
*`iwishartprior(# [...])`	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
`restubs(`*restub1 restub2 ...*`)`	specify stubs for random-effects parameters for all levels
Blocking	
*`blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [`,` *blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
*`noblocking`	do not block parameters by default
Initialization	
`initial(`*initspec*`)`	specify initial values for model parameters with a single chain
`init#(`*initspec*`)`	specify initial values for #th chain; requires `nchains()`
`initall(`*initspec*`)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
*`noisily`	display output from the estimation command during initialization
Adaptation	
`adaptation(`*adaptopts*`)`	control the adaptive MCMC procedure
`scale(#)`	initial multiplier for scale factor; default is `scale(2.38)`
`covariance(`*cov*`)`	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
* or	report odds ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal-likelihood
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
nomesummary	suppress multilevel-structure summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
showreffects[(*reref*)]	specify that all or a subset of random-effects parameters be included in the output
melabel	display estimation table using the same row labels as melogit
nogroup	suppress table summarizing groups
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *rename*s and *restub* are defined. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [ME] **melogit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. For multilevel examples, see *Multilevel models* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[ME] **melogit** — Multilevel mixed-effects logistic regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: menbreg — Bayesian multilevel negative binomial regression

Description

`bayes: menbreg` fits a Bayesian multilevel negative binomial regression to a nonnegative count outcome; see [BAYES] **bayes** and [ME] **menbreg** for details.

Quick start

Bayesian two-level negative binomial regression of `y` on `x1` and `x2` with random intercepts by `id`, using default normal priors for regression coefficients and log-overdispersion parameter and default inverse-gamma prior for the variance of random intercepts

```
bayes: menbreg y x1 x2 || id:
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): menbreg y x1 x2 || id:
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): menbreg y x1 x2 || id:
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): menbreg y x1 x2 || id:
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): menbreg y x1 x2 || id:
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display incidence-rate ratios instead of coefficients

```
bayes: menbreg y x1 x2 || id: , irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **menbreg**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Negative binomial regression

Syntax

```
bayes [ , bayesopts ] : menbreg depvar fe_equation
    [ || re_equation ] [ || re_equation ... ] [ , options ]
```

where the syntax of *fe_equation* is

```
[ indepvars ] [ if ] [ in ] [ weight ] [ , fe_options ]
```

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

```
levelvar: [ varlist ] [ , re_options ]
```

for random effects among the values of a factor variable

```
levelvar: R.varname
```

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`noconstant`	suppress constant term from the fixed-effects equation
`exposure(`*varname*$_e$`)`	include ln(*varname*$_e$) in model with coefficient constrained to 1
`offset(`*varname*$_o$`)`	include *varname*$_o$ in model with coefficient constrained to 1

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `exchangeable`, `identity`, and `unstructured` are supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Model	
`dispersion(`*dispersion*`)`	parameterization of the conditional overdispersion; *dispersion* may be `mean` (default) or `constant`
Reporting	
`irr`	report incidence-rate ratios
`notable`	suppress coefficient table
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *indepvars*, and *varlist* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`fweights` are allowed; see [U] **11.1.6 weight**.

`bayes: menbreg, level()` is equivalent to `bayes, clevel(): menbreg`.

For a detailed description of *options*, see *Options* in [ME] **menbreg**.

bayesopts	Description
Priors	
* `normalprior(#)`	specify standard deviation of default normal priors for regression coefficients and log-overdispersion parameter; default is `normalprior(100)`
* `igammaprior(# #)`	specify shape and scale of default inverse-gamma prior for variance components; default is `igammaprior(0.01 0.01)`
* `iwishartprior(# [...])`	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
`restubs(`*restub1 restub2 ...*`)`	specify stubs for random-effects parameters for all levels
Blocking	
* `blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [`,` *blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
* `noblocking`	do not block parameters by default
Initialization	
`initial(`*initspec*`)`	specify initial values for model parameters with a single chain
`init#(`*initspec*`)`	specify initial values for #th chain; requires `nchains()`
`initall(`*initspec*`)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
* `noisily`	display output from the estimation command during initialization
Adaptation	
`adaptation(`*adaptopts*`)`	control the adaptive MCMC procedure
`scale(#)`	initial multiplier for scale factor; default is `scale(2.38)`
`covariance(`*cov*`)`	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
*irr	report incidence-rate ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal-likelihood
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
nomesummary	suppress multilevel-structure summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
showreffects[(*reref*)]	specify that all or a subset of random-effects parameters be included in the output
melabel	display estimation table using the same row labels as menbreg
nogroup	suppress table summarizing groups
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}, log-overdispersion parameter {lnalpha} with mean dispersion or {lndelta} with constant dispersion, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *rename*s and *restub* are defined. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For

remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [ME] **menbreg**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. For multilevel examples, see *Multilevel models* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[ME] **menbreg** — Multilevel mixed-effects negative binomial regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: meologit — Bayesian multilevel ordered logistic regression

Description

`bayes: meologit` fits a Bayesian multilevel ordered logistic regression to an ordinal outcome; see [BAYES] **bayes** and [ME] **meologit** for details.

Quick start

Bayesian two-level ordered logistic regression of `y` on `x1` and `x2` with random intercepts by `id` , using default normal priors for regression coefficients, flat priors for cutpoints, and default inverse-gamma prior for the variance of random intercepts

```
bayes: meologit y x1 x2 || id:
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): meologit y x1 x2 || id:
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): meologit y x1 x2 || id:
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): meologit y x1 x2 || id:
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): meologit y x1 x2 || id:
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display odds ratios instead of coefficients

```
bayes: meologit y x1 x2 || id: , or
```

Display odds ratios on replay

```
bayes, or
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **meologit**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Ordered logistic regression

Syntax

```
bayes [, bayesopts] : meologit depvar fe_equation
    [|| re_equation] [|| re_equation ...] [, options]
```

where the syntax of *fe_equation* is

```
[indepvars] [if] [in] [weight] [, fe_options]
```

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

```
levelvar: [varlist] [, re_options]
```

for random effects among the values of a factor variable

```
levelvar: R.varname
```

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `exchangeable`, `identity`, and `unstructured` are supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Reporting	
`or`	report odds ratios
`notable`	suppress coefficient table
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *indepvars*, and *varlist* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`fweights` are allowed; see [U] **11.1.6 weight**.

`bayes: meologit, level()` is equivalent to `bayes, clevel(): meologit`.

For a detailed description of *options*, see *Options* in [ME] **meologit**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
*igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance components; default is igammaprior(0.01 0.01)
*iwishartprior(# [...])	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
restubs(*restub1 restub2 ...*)	specify stubs for random-effects parameters for all levels
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
Adaptation	
adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
* or	report coefficients as odds ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal-likelihood
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
nomesummary	suppress multilevel-structure summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
showreffects[(*reref*)]	specify that all or a subset of random-effects parameters be included in the output
melabel	display estimation table using the same row labels as meologit
nogroup	suppress table summarizing groups
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}, cutpoints {cut1}, {cut2}, and so on, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *rename*s and *restub* are defined. Use the dryrun option to see the definitions of model parameters prior to estimation.

Flat priors, flat, are used by default for cutpoints.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For

remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [ME] **meologit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. For multilevel examples, see *Multilevel models* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[ME] **meologit** — Multilevel mixed-effects ordered logistic regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: meoprobit — Bayesian multilevel ordered probit regression

Description

`bayes: meoprobit` fits a Bayesian multilevel ordered probit regression to an ordinal outcome; see [BAYES] **bayes** and [ME] **meoprobit** for details.

Quick start

Bayesian two-level ordered probit regression of `y` on `x1` and `x2` with random intercepts by `id` , using default normal priors for regression coefficients, flat priors for cutpoints, and default inverse-gamma prior for the variance of random intercepts

```
bayes: meoprobit y x1 x2 || id:
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): meoprobit y x1 x2 || id:
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): meoprobit y x1 x2 || id:
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): meoprobit y x1 x2 || id:
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): meoprobit y x1 x2 || id:
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **meoprobit**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Ordered probit regression

Syntax

```
bayes [, bayesopts]: meoprobit depvar fe_equation
    [|| re_equation] [|| re_equation ...] [, options]
```

where the syntax of *fe_equation* is

```
[indepvars] [if] [in] [weight] [, fe_options]
```

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

```
levelvar: [varlist] [, re_options]
```

for random effects among the values of a factor variable

```
levelvar: R.varname
```

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `exchangeable`, `identity`, and `unstructured` are supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Reporting	
`notable`	suppress coefficient table
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *indepvars*, and *varlist* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`fweight`s are allowed; see [U] **11.1.6 weight**.

`bayes: meoprobit, level()` is equivalent to `bayes, clevel(): meoprobit`.

For a detailed description of *options*, see *Options* in [ME] **meoprobit**.

bayesopts	Description
Priors	
*`normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
*`igammaprior(# #)`	specify shape and scale of default inverse-gamma prior for variance components; default is `igammaprior(0.01 0.01)`
*`iwishartprior(# [...])`	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
`restubs(`*restub1 restub2 ...*`)`	specify stubs for random-effects parameters for all levels
Blocking	
*`blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref*`[ , `*blockopts*`])`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
*`noblocking`	do not block parameters by default
Initialization	
`initial(`*initspec*`)`	specify initial values for model parameters with a single chain
`init#(`*initspec*`)`	specify initial values for #th chain; requires `nchains()`
`initall(`*initspec*`)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
*`noisily`	display output from the estimation command during initialization
Adaptation	
`adaptation(`*adaptopts*`)`	control the adaptive MCMC procedure
`scale(#)`	initial multiplier for scale factor; default is `scale(2.38)`
`covariance(`*cov*`)`	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal-likelihood
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
nomesummary	suppress multilevel-structure summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
showreffects[(*reref*)]	specify that all or a subset of random-effects parameters be included in the output
melabel	display estimation table using the same row labels as meoprobit
nogroup	suppress table summarizing groups
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}, cutpoints {cut1}, {cut2}, and so on, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *rename*s and *restub* are defined. Use the dryrun option to see the definitions of model parameters prior to estimation.

Flat priors, flat, are used by default for cutpoints.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [ME] **meoprobit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. For multilevel examples, see *Multilevel models* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[ME] **meoprobit** — Multilevel mixed-effects ordered probit regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: mepoisson — Bayesian multilevel Poisson regression

Description

`bayes: mepoisson` fits a Bayesian multilevel Poisson regression to a nonnegative count outcome; see [BAYES] **bayes** and [ME] **mepoisson** for details.

Quick start

Bayesian two-level Poisson regression of `y` on `x1` and `x2` with random intercepts by `id` , using default normal priors for regression coefficients and default inverse-gamma prior for the variance of random intercepts

```
bayes: mepoisson y x1 x2 || id:
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): mepoisson y x1 x2 || id:
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): mepoisson y x1 x2 || id:
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): mepoisson y x1 x2 || id:
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): mepoisson y x1 x2 || id:
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display incidence-rate ratios instead of coefficients

```
bayes: mepoisson y x1 x2 || id: , irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **mepoisson**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Poisson regression

Syntax

```
bayes [, bayesopts]: mepoisson depvar fe_equation
    [|| re_equation] [|| re_equation ...] [, options]
```

where the syntax of *fe_equation* is

```
[indepvars] [if] [in] [weight] [, fe_options]
```

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

```
levelvar: [varlist] [, re_options]
```

for random effects among the values of a factor variable

```
levelvar: R.varname
```

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`noconstant`	suppress constant term from the fixed-effects equation
`exposure(`$varname_e$`)`	include $\ln(varname_e)$ in model with coefficient constrained to 1
`offset(`$varname_o$`)`	include $varname_o$ in model with coefficient constrained to 1

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `exchangeable`, `identity`, and `unstructured` are supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Reporting	
`irr`	report incidence-rate ratios
`notable`	suppress coefficient table
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

indepvars may contain factor variables; see **[U] 11.4.3 Factor variables**.

depvar, *indepvars*, and *varlist* may contain time-series operators; see **[U] 11.4.4 Time-series varlists**.

`fweights` are allowed; see **[U] 11.1.6 weight**.

`bayes: mepoisson, level()` is equivalent to `bayes, clevel(): mepoisson`.

For a detailed description of *options*, see *Options* in **[ME] mepoisson**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
*igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance components; default is igammaprior(0.01 0.01)
*iwishartprior(# [...])	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
restubs(*restub1 restub2 ...*)	specify stubs for random-effects parameters for all levels
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
Adaptation	
adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
*irr	report incidence-rate ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal-likelihood
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
nomesummary	suppress multilevel-structure summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
showreffects[(*reref*)]	specify that all or a subset of random-effects parameters be included in the output
melabel	display estimation table using the same row labels as mepoisson
nogroup	suppress table summarizing groups
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *rename*s and *restub* are defined. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [ME] **mepoisson**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. For multilevel examples, see *Multilevel models* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[ME] **mepoisson** — Multilevel mixed-effects Poisson regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: meprobit — Bayesian multilevel probit regression

Description

`bayes: meprobit` fits a Bayesian multilevel probit regression to a binary outcome; see [BAYES] **bayes** and [ME] **meprobit** for details.

Quick start

Bayesian two-level probit regression of `y` on `x1` and `x2` with random intercepts by `id` , using default normal priors for regression coefficients and default inverse-gamma prior for the variance of random intercepts

```
bayes: meprobit y x1 x2 || id:
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): meprobit y x1 x2 || id:
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): meprobit y x1 x2 || id:
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): meprobit y x1 x2 || id:
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): meprobit y x1 x2 || id:
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **meprobit**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Probit regression

Syntax

```
bayes [, bayesopts] : meprobit depvar fe_equation
    [|| re_equation] [|| re_equation ...] [, options]
```

where the syntax of *fe_equation* is

```
[indepvars] [if] [in] [weight] [, fe_options]
```

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

```
levelvar: [varlist] [, re_options]
```

for random effects among the values of a factor variable

```
levelvar: R.varname
```

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`noconstant`	suppress constant term from the fixed-effects equation
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`asis`	retain perfect predictor variables

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `exchangeable`, `identity`, and `unstructured` are supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Model	
`binomial(`*varname* | *#*`)`	set binomial trials if data are in binomial form
Reporting	
`notable`	suppress coefficient table
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *indepvars*, and *varlist* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`fweights` are allowed; see [U] **11.1.6 weight**.

`bayes: meprobit, level()` is equivalent to `bayes, clevel(): meprobit`.

For a detailed description of *options*, see *Options* in [ME] **meprobit**.

bayesopts	Description
Priors	
*`normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
*`igammaprior(# #)`	specify shape and scale of default inverse-gamma prior for variance components; default is `igammaprior(0.01 0.01)`
*`iwishartprior(# [...])`	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
`restubs(`*restub1 restub2 ...*`)`	specify stubs for random-effects parameters for all levels
Blocking	
*`blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [`,` *blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
*`noblocking`	do not block parameters by default
Initialization	
`initial(`*initspec*`)`	specify initial values for model parameters with a single chain
`init#(`*initspec*`)`	specify initial values for #th chain; requires `nchains()`
`initall(`*initspec*`)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
*`noisily`	display output from the estimation command during initialization
Adaptation	
`adaptation(`*adaptopts*`)`	control the adaptive MCMC procedure
`scale(#)`	initial multiplier for scale factor; default is `scale(2.38)`
`covariance(`*cov*`)`	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal-likelihood
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
nomesummary	suppress multilevel-structure summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
showreffects[(*reref*)]	specify that all or a subset of random-effects parameters be included in the output
melabel	display estimation table using the same row labels as meprobit
nogroup	suppress table summarizing groups
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *rename*s and *restub* are defined. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [ME] **meprobit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. For multilevel examples, see *Multilevel models* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[ME] **meprobit** — Multilevel mixed-effects probit regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: mestreg — Bayesian multilevel parametric survival models

Description

`bayes: mestreg` fits a Bayesian multilevel parametric survival model to a survival-time outcome; see [BAYES] **bayes** and [ME] **mestreg** for details.

Quick start

Bayesian two-level Weibull survival model of `stset` survival-time outcome on `x1` and `x2` with random intercepts by `id` , using default normal priors for regression coefficients and log-ancillary parameters and default inverse-gamma prior for the variance of random intercepts

```
bayes: mestreg x1 x2 || id:, distribution(weibull)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): mestreg x1 x2 || id:, distribution(weibull)
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({_t: x1 x2}, uniform(-10,10)) ///
prior({_t:_cons}, normal(0,10)):  ///
mestreg x1 x2 || id:, distribution(weibull)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123):  ///
mestreg x1 x2 || id:, distribution(weibull)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500):  ///
mestreg x1 x2 || id:, distribution(weibull)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Use accelerated failure-time metric instead of proportional-hazards parameterization, and display time ratios instead of coefficients

```
bayes, tratio: mestreg x1 x2 || id:, distribution(weibull) time
```

Display time ratios on replay

```
bayes, tratio
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **mestreg**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Parametric survival regression

Syntax

```
bayes [ , bayesopts ] : mestreg fe_equation
    [ || re_equation ] [ || re_equation ... ], distribution(distname) [ options ]
```

where the syntax of *fe_equation* is

```
[ indepvars ] [ if ] [ in ] [ weight ] [ , fe_options ]
```

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

```
levelvar: [ varlist ] [ , re_options ]
```

for random effects among the values of a factor variable

```
levelvar: R.varname
```

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`noconstant`	suppress constant term from the fixed-effects equation
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `exchangeable`, `identity`, and `unstructured` are supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Model	
* `distribution(`*distname*`)`	specify survival distribution
`time`	use accelerated failure-time metric
Reporting	
`nohr`	do not report hazard ratios
`tratio`	report time ratios
`noshow`	do not show st setting information
`notable`	suppress coefficient table
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

*distribution(*distname*) is required.
You must stset your data before using bayes: mestreg; see [ST] stset.
indepvars may contain factor variables; see [U] 11.4.3 Factor variables.
fweights are allowed; see [U] 11.1.6 weight.
bayes: mestreg, level() is equivalent to bayes, clevel(): mestreg.
For a detailed description of *options*, see *Options* in [ME] mestreg.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients and log-ancillary parameters; default is normalprior(100)
*igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance components; default is igammaprior(0.01 0.01)
*iwishartprior(# [...])	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
restubs(*restub1 restub2 ...*)	specify stubs for random-effects parameters for all levels
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
Adaptation	
adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
*nohr	do not report hazard ratios
*tratio	report time ratios; requires option time with mestreg
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal-likelihood
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
nomesummary	suppress multilevel-structure summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
showreffects[(*reref*)]	specify that all or a subset of random-effects parameters be included in the output
melabel	display estimation table using the same row labels as mestreg
nogroup	suppress table summarizing groups
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}, ancillary parameters as described in *Ancillary model parameters*, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *rename*s and *restub* are defined. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For

remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [ME] **mestreg**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**. For multilevel examples, see *Multilevel models* in [BAYES] **bayes**.

Ancillary model parameters

In addition to regression coefficients {_t:*varlist*}, bayes: mestreg defines ancillary parameters that depend on the chosen survival model; see table 1 below. Positive ancillary parameters are transformed to be defined on the whole real line. All ancillary parameters are assigned default normal priors with zero mean and variance of 10,000.

Table 1. Ancillary model parameters defined by bayes: mestreg

Distribution	Ancillary parameters	Transformed model parameters
Exponential	None	None
Weibull	p	{ln_p}
Lognormal	σ	{lnsigma}
Loglogistic	γ	{lngamma}
Gamma	s	{lnscale}

Use the dryrun option with the bayes prefix to see the definitions of model parameters prior to estimation.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[ME] **mestreg** — Multilevel mixed-effects parametric survival models

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: metobit — Bayesian multilevel tobit regression

Description

`bayes: metobit` fits a Bayesian multilevel tobit regression to a censored continuous outcome; see [BAYES] **bayes** and [ME] **metobit** for details.

Quick start

Bayesian two-level tobit regression of `y` on `x1` and `x2` with random intercepts by `id` , using a lower censoring limit of 17, and using default normal priors for regression coefficients and default inverse-gamma priors for the error variance and for the variance of random intercepts

```
bayes: metobit y x1 x2 || id:, ll(17)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): metobit y x1 x2 || id:, ll(17)
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): metobit y x1 x2 || id:, ll(17)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123):  ///
metobit y x1 x2 || id:, ll(17)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500):  ///
metobit y x1 x2 || id:, ll(17)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **metobit**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Tobit regression

Syntax

```
bayes [, bayesopts] : metobit depvar fe_equation
    [|| re_equation] [|| re_equation ...] [, options]
```

where the syntax of *fe_equation* is

```
[indepvars] [if] [in] [weight] [, fe_options]
```

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

```
levelvar: [varlist] [, re_options]
```

for random effects among the values of a factor variable

```
levelvar: R.varname
```

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`noconstant`	suppress constant term from the fixed-effects equation
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `exchangeable`, `identity`, and `unstructured` are supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Model	
`ll(`*varname*`|#)`	left-censoring variable or limit
`ul(`*varname*`|#)`	right-censoring variable or limit
Reporting	
`notable`	suppress coefficient table
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *indepvars*, and *varlist* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`fweights` are allowed; see [U] **11.1.6 weight**.

`bayes: metobit, level()` is equivalent to `bayes, clevel(): metobit`.

For a detailed description of *options*, see *Options* in [ME] **metobit**.

bayesopts	Description
Priors	
*`normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
*`igammaprior(# #)`	specify shape and scale of default inverse-gamma prior for variance components; default is `igammaprior(0.01 0.01)`
*`iwishartprior(# [...])`	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
`restubs(`*restub1 restub2 ...*`)`	specify stubs for random-effects parameters for all levels
Blocking	
*`blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [`,` *blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
*`noblocking`	do not block parameters by default
Initialization	
`initial(`*initspec*`)`	specify initial values for model parameters with a single chain
`init#(`*initspec*`)`	specify initial values for #th chain; requires `nchains()`
`initall(`*initspec*`)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
*`noisily`	display output from the estimation command during initialization
Adaptation	
`adaptation(`*adaptopts*`)`	control the adaptive MCMC procedure
`scale(#)`	initial multiplier for scale factor; default is `scale(2.38)`
`covariance(`*cov*`)`	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal-likelihood
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
nomesummary	suppress multilevel-structure summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
showreffects[(*reref*)]	specify that all or a subset of random-effects parameters be included in the output
melabel	display estimation table using the same row labels as metobit
nogroup	suppress table summarizing groups
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}, error variance {e.*depvar*:sigma2}, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *rename*s and *restub* are defined. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [ME] **metobit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. For multilevel examples, see *Multilevel models* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[ME] **metobit** — Multilevel mixed-effects tobit regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: mixed — Bayesian multilevel linear regression

Description

`bayes: mixed` fits a Bayesian multilevel linear regression to a continuous outcome; see [BAYES] **bayes** and [ME] **mixed** for details.

Quick start

Bayesian two-level linear regression of `y` on `x1` and `x2` with random intercepts by `id` , using default normal priors for regression coefficients and default inverse-gamma priors for the error variance and for the variance of random intercepts

```
bayes: mixed y x1 x2 || id:
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): mixed y x1 x2 || id:
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): mixed y x1 x2 || id:
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): mixed y x1 x2 || id:
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): mixed y x1 x2 || id:
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **mixed**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Linear regression

Syntax

```
bayes [, bayesopts] : mixed depvar fe_equation
    [|| re_equation] [|| re_equation ...] [, options]
```

where the syntax of *fe_equation* is

```
[indepvars] [if] [in] [weight] [, fe_options]
```

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

```
levelvar: [varlist] [, re_options]
```

for random effects among the values of a factor variable

```
levelvar: R.varname
```

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`noconstant`	suppress constant term from the fixed-effects equation

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; structures `independent`, `exchangeable`, `identity`, and `unstructured` are supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Reporting	
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *indepvars*, and *varlist* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`fweight`s are allowed; see [U] **11.1.6 weight**.

`bayes: mixed, level()` is equivalent to `bayes, clevel(): mixed`.

For a detailed description of *options*, see *Options* in [ME] **mixed**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
*igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance components; default is igammaprior(0.01 0.01)
*iwishartprior(# [...])	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
restubs(*restub1 restub2 ...*)	specify stubs for random-effects parameters for all levels
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
Adaptation	
adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal-likelihood
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
nomesummary	suppress multilevel-structure summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
showreffects[(*reref*)]	specify that all or a subset of random-effects parameters be included in the output
melabel	display estimation table using the same row labels as mixed
nogroup	suppress table summarizing groups
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}, error variance {e.*depvar*:sigma2}, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *rename*s and *restub* are defined. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using adaptive Metropolis–Hastings and Gibbs algorithms, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [ME] **mixed**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. For multilevel examples, see *Multilevel models* in [BAYES] **bayes**.

By default, `bayes: mixed` uses Gibbs sampling for all model parameters except the random-effects parameters. If you specify a `prior()` distribution for which Gibbs sampling is not available, `bayes: mixed` will switch to adaptive Metropolis–Hastings sampling. In general, `bayes: mixed` will try to use a more efficient Gibbs sampling for the model parameters whenever available.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[ME] **mixed** — Multilevel mixed-effects linear regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: mlogit — Bayesian multinomial logistic regression

Description

`bayes: mlogit` fits a Bayesian multinomial logistic regression to a categorical outcome; see [BAYES] **bayes** and [R] **mlogit** for details.

Quick start

Bayesian multinomial logistic regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: mlogit y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): mlogit y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept for the category `2`

```
bayes, prior({2: x1 x2}, uniform(-10,10)) ///
prior({2:_cons}, normal(0,10)): mlogit y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): mlogit y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): mlogit y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display relative-risk ratios instead of coefficients

```
bayes: mlogit y x1 x2, rrr
```

Display relative-risk ratios on replay

```
bayes, rrr
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **mlogit**.

Menu

Statistics > Categorical outcomes > Bayesian regression >Multinomial logistic regression

Syntax

```
bayes [, bayesopts]: mlogit depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
baseoutcome(#)	value of *depvar* that will be the base outcome
Reporting	
rrr	report relative-risk ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

indepvars may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

fweights are allowed; see [U] **11.1.6 weight**.

bayes: mlogit, level() is equivalent to bayes, clevel(): mlogit.

For a detailed description of *options*, see *Options* in [R] **mlogit**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation	
adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix
Reporting	
clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
* rrr	report relative-risk ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells
Advanced	
search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*outcome*$_1$:*indepvars*}, {*outcome*$_2$:*indepvars*}, and so on, where *outcome*$_\#$'s are the values of the dependent variable or the value labels of the dependent variable if they exist. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **mlogit**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Multinomial logistic regression* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **mlogit** — Multinomial (polytomous) logistic regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: mprobit — Bayesian multinomial probit regression

Description

`bayes: mprobit` fits a Bayesian multinomial probit regression to a categorical outcome; see [BAYES] **bayes** and [R] **mprobit** for details.

Quick start

Bayesian multinomial probit regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: mprobit y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): mprobit y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept for the category `2`

```
bayes, prior({2: x1 x2}, uniform(-10,10)) ///
prior({2:_cons}, normal(0,10)): mprobit y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): mprobit y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): mprobit y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **mprobit**.

Menu

Statistics > Categorical outcomes > Bayesian regression >Multinomial probit regression

Syntax

```
bayes [, bayesopts]: mprobit depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
baseoutcome(#)	value of *depvar* that will be the base outcome
probitparam	use the probit variance parameterization
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

fweights are allowed; see [U] **11.1.6 weight**.

bayes: mprobit, level() is equivalent to bayes, clevel(): mprobit.

For a detailed description of *options*, see *Options* in [R] **mprobit**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

`adaptation(`*adaptopts*`)`	control the adaptive MCMC procedure
`scale(#)`	initial multiplier for scale factor; default is `scale(2.38)`
`covariance(`*cov*`)`	initial proposal covariance; default is the identity matrix

Reporting

`clevel(#)`	set credible interval level; default is `clevel(95)`
`hpd`	display HPD credible intervals instead of the default equal-tailed credible intervals
`eform[ (`*string*`) ]`	report exponentiated coefficients and, optionally, label as *string*
`batch(#)`	specify length of block for batch-means calculations; default is `batch(0)`
`saving(`*filename*`[ , replace ])`	save simulation results to *filename*`.dta`
`nomodelsummary`	suppress model summary
`chainsdetail`	display detailed simulation summary for each chain
`[no]dots`	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is `nodots`
`dots(#[ , every(#) ])`	display dots as simulation is performed
`[no]show(`*paramref*`)`	specify model parameters to be excluded from or included in the output
`notable`	suppress estimation table
`noheader`	suppress output header
`title(`*string*`)`	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

`search(`*search_options*`)`	control the search for feasible initial values
`corrlag(#)`	specify maximum autocorrelation lag; default varies
`corrtol(#)`	specify autocorrelation tolerance; default is `corrtol(0.01)`

*Starred options are specific to the `bayes` prefix; other options are common between `bayes` and `bayesmh`.

Options `prior()` and `block()` may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*outcome*$_1$`:`*indepvars*}, {*outcome*$_2$`:`*indepvars*}, and so on, where *outcome*$_\#$'s are the values of the dependent variable or the value labels of the dependent variable if they exist. Use the `dryrun` option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **mprobit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Multinomial logistic regression* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **mprobit** — Multinomial probit regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: mvreg — Bayesian multivariate regression

Description

`bayes: mvreg` fits a Bayesian multivariate regression to multiple continuous outcomes; see [BAYES] **bayes** and [MV] **mvreg** for details.

Quick start

Bayesian multivariate regression of `y1` and `y2` on `x1` and `x2`, using default normal priors for regression coefficients and Jeffreys prior for the covariance matrix

```
bayes: mvreg y1 y2 = x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): mvreg y1 y2 = x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept of the dependent variable `y2`

```
bayes, prior({y2: x1 x2}, uniform(-10,10)) ///
prior({y2:_cons}, normal(0,10)): mvreg y1 y2 = x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): mvreg y1 y2 = x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): mvreg y1 y2 = x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [MV] **mvreg**.

Menu

Statistics > Linear models and related > Bayesian regression > Multivariate regression

Syntax

```
bayes [ , bayesopts ] : mvreg depvars = indepvars [ if ] [ in ] [ weight ] [ , options ]
```

options	Description
Model	
noconstant	suppress constant term
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

fweights are allowed; see [U] **11.1.6 weight**.

bayes: mvreg, level() is equivalent to bayes, clevel(): mvreg.

For a detailed description of *options*, see *Options* in [MV] **mvreg**.

bayesopts	Description
Priors	
*gibbs	specify Gibbs sampling; available only with normal priors for regression coefficients and multivariate Jeffreys prior for covariance
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*$_1$:*indepvars*}, {*depvar*$_2$:*indepvars*}, and so on, and covariance matrix {Sigma,matrix}. Use the dryrun option to see the definitions of model parameters prior to estimation.

Multivariate Jeffreys prior, jeffreys(*d*), is used by default for the covariance matrix of dimension *d*.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using adaptive Metropolis–Hastings and Gibbs algorithms, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [MV] **mvreg**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[MV] **mvreg** — Multivariate regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: nbreg — Bayesian negative binomial regression

Description

`bayes: nbreg` fits a Bayesian negative binomial regression to a nonnegative count outcome; see [BAYES] **bayes** and [R] **nbreg** for details.

Quick start

Bayesian negative binomial regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients and log-overdispersion parameter

```
bayes: nbreg y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): nbreg y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): nbreg y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): nbreg y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): nbreg y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display incidence-rate ratios instead of coefficients

```
bayes: nbreg y x1 x2, irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **nbreg**.

Menu

Statistics > Count outcomes > Bayesian regression > Negative binomial regression

Syntax

```
bayes [, bayesopts]: nbreg depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
dispersion(mean)	parameterization of dispersion; the default
dispersion(constant)	constant dispersion for all observations
exposure(*varname*$_e$)	include ln(*varname*$_e$) in model with coefficient constrained to 1
offset(*varname*$_o$)	include *varname*$_o$ in model with coefficient constrained to 1
Reporting	
irr	report incidence-rate ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *indepvars*, *varname*$_e$, and *varname*$_o$ may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

fweights are allowed; see [U] **11.1.6 weight**.

bayes: nbreg, level() is equivalent to bayes, clevel(): nbreg.

For a detailed description of options, see *Options for nbreg* in [R] **nbreg**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients and log-overdispersion parameter; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
*irr	report incidence-rate ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} and log-overdispersion parameter {lnalpha} with mean dispersion or {lndelta} with constant dispersion. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **nbreg**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **nbreg** — Negative binomial regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: ologit — Bayesian ordered logistic regression

Description

`bayes: ologit` fits a Bayesian ordered logistic regression to an ordinal outcome; see [BAYES] **bayes** and [R] **ologit** for details.

Quick start

Bayesian ordered logistic regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients and flat priors for cutpoints

```
bayes: ologit y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): ologit y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): ologit y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): ologit y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): ologit y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display odds ratios instead of coefficients

```
bayes: ologit y x1 x2, or
```

Display odds ratios on replay

```
bayes, or
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **ologit**.

Menu

Statistics > Ordinal outcomes > Bayesian regression > Ordered logistic regression

Syntax

```
bayes [ , bayesopts ] : ologit depvar [indepvars] [if] [in] [weight] [ , options ]
```

options	Description
Model	
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
Reporting	
`or`	report odds ratios
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`fweights` are allowed; see [U] **11.1.6 weight**.

`bayes: ologit, level()` is equivalent to `bayes, clevel(): ologit`.

For a detailed description of *options*, see *Options* in [R] **ologit**.

bayesopts	Description
Priors	
*`normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
Blocking	
*`blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref*`[ , `*blockopts*`])`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
*`noblocking`	do not block parameters by default
Initialization	
`initial(`*initspec*`)`	specify initial values for model parameters with a single chain
`init#(`*initspec*`)`	specify initial values for #th chain; requires `nchains()`
`initall(`*initspec*`)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
*`noisily`	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
* or	report odds ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} and cutpoints {cut1}, {cut2}, and so on. Use the dryrun option to see the definitions of model parameters prior to estimation.

Flat priors, flat, are used by default for cutpoints.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **ologit**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **ologit** — Ordered logistic regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: oprobit — Bayesian ordered probit regression

Description

`bayes: oprobit` fits a Bayesian ordered probit regression to an ordinal outcome; see [BAYES] **bayes** and [R] **oprobit** for details.

Quick start

Bayesian ordered probit regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients and flat priors for cutpoints

```
bayes: oprobit y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): oprobit y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): oprobit y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): oprobit y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): oprobit y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **oprobit**.

Menu

Statistics > Ordinal outcomes > Bayesian regression > Ordered probit regression

Syntax

```
bayes [ , bayesopts ] : oprobit depvar [ indepvars ] [ if ] [ in ] [ weight ] [ , options ]
```

options	Description
Model	
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
Reporting	
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`fweights` are allowed; see [U] **11.1.6 weight**.

`bayes: oprobit, level()` is equivalent to `bayes, clevel(): oprobit`.

For a detailed description of *options*, see *Options* in [R] **oprobit**.

bayesopts	Description
Priors	
*`normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
Blocking	
*`blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref*`[ , `*blockopts*`])`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
*`noblocking`	do not block parameters by default
Initialization	
`initial(`*initspec*`)`	specify initial values for model parameters with a single chain
`init#(`*initspec*`)`	specify initial values for #th chain; requires `nchains()`
`initall(`*initspec*`)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
*`noisily`	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} and cutpoints {cut1}, {cut2}, and so on. Use the dryrun option to see the definitions of model parameters prior to estimation.

Flat priors, flat, are used by default for cutpoints.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **oprobit**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **oprobit** — Ordered probit regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: poisson — Bayesian Poisson regression

Description

`bayes: poisson` fits a Bayesian Poisson regression to a nonnegative count outcome; see [BAYES] **bayes** and [R] **poisson** for details.

Quick start

Bayesian Poisson regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: poisson y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): poisson y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): poisson y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): poisson y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): poisson y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display incidence-rate ratios instead of coefficients

```
bayes: poisson y x1 x2, irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **poisson**.

Menu

Statistics > Count outcomes > Bayesian regression > Poisson regression

Syntax

```
bayes [, bayesopts]: poisson depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
exposure(*varname*$_e$)	include ln(*varname*$_e$) in model with coefficient constrained to 1
offset(*varname*$_o$)	include *varname*$_o$ in model with coefficient constrained to 1
Reporting	
irr	report incidence-rate ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *indepvars*, *varname*$_e$, and *varname*$_o$ may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

fweights are allowed; see [U] **11.1.6 weight**.

bayes: poisson, level() is equivalent to bayes, clevel(): poisson.

For a detailed description of *options*, see *Options* in [R] **poisson**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
*irr	report incidence-rate ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **poisson**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **poisson** — Poisson regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: probit — Bayesian probit regression

Description

`bayes: probit` fits a Bayesian probit regression to a binary outcome; see [BAYES] **bayes** and [R] **probit** for details.

Quick start

Bayesian probit regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: probit y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): probit y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): probit y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): probit y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): probit y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **probit**.

Menu

Statistics > Binary outcomes > Bayesian regression > Probit regression

Syntax

```
bayes [ , bayesopts ] : probit depvar [indepvars] [if] [in] [weight] [ , options ]
```

options	Description
Model	
noconstant	suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
asis	retain perfect predictor variables
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

fweights are allowed; see [U] **11.1.6 weight**.

bayes: probit, level() is equivalent to bayes, clevel(): probit.

For a detailed description of *options*, see *Options* in [R] **probit**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **probit**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Logistic regression with perfect predictors* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **probit** — Probit regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: regress — Bayesian linear regression

Description

`bayes: regress` fits a Bayesian linear regression to a continuous outcome; see [BAYES] **bayes** and [R] **regress** for details.

Quick start

Bayesian linear regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients and default inverse-gamma prior for the variance

```
bayes: regress y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): regress y x1 x2
```

Use a shape of 1 and a scale of 2 instead of values of 0.01 for the default inverse-gamma prior

```
bayes, igammaprior(1 2): regress y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): regress y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): regress y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): regress y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **regress**.

Menu

Statistics > Linear models and related > Bayesian regression > Linear regression

Syntax

```
bayes [, bayesopts]: regress depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
Reporting	
eform(*string*)	report exponentiated coefficients and label as *string*
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

fweights are allowed; see [U] **11.1.6 weight**.

bayes: regress, level() is equivalent to bayes, clevel(): regress.

For a detailed description of *options*, see *Options* in [R] **regress**.

bayesopts	Description
Priors	
*gibbs	specify Gibbs sampling; available only with normal priors for regression coefficients and an inverse-gamma prior for variance
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
*igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance; default is igammaprior(0.01 0.01)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} and variance {sigma2}. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using adaptive Metropolis–Hastings and Gibbs algorithms, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **regress**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Linear regression: A case of informative default priors* in [BAYES] **bayes**.

Video examples

Bayesian linear regression using the bayes prefix

Bayesian linear regression using the bayes prefix: How to specify custom priors

Bayesian linear regression using the bayes prefix: Checking convergence of the MCMC chain

Bayesian linear regression using the bayes prefix: How to customize the MCMC chain

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **regress** — Linear regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

[BMA] **bmaregress** — Bayesian model averaging for linear regression

Title

bayes: streg — Bayesian parametric survival models

Description

`bayes: streg` fits a Bayesian parametric survival model to a survival-time outcome; see [BAYES] **bayes** and [ST] **streg** for details.

Quick start

Bayesian Weibull survival model of `stset` survival-time outcome on `x1` and `x2`, using default normal priors for regression coefficients and log-ancillary parameters

```
bayes: streg x1 x2, distribution(weibull)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): streg x1 x2, distribution(weibull)
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({_t: x1 x2}, uniform(-10,10)) ///
prior({_t:_cons}, normal(0,10)): streg x1 x2, distribution(weibull)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123):  ///
streg x1 x2, distribution(weibull)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500):  ///
streg x1 x2, distribution(weibull)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Use accelerated failure-time metric instead of proportional-hazards parameterization, and display time ratios instead of coefficients

```
bayes, tratio: streg x1 x2, distribution(weibull) time
```

Display time ratios on replay

```
bayes, tratio
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ST] **streg**.

Menu

Statistics > Survival analysis > Regression models > Bayesian parametric survival models

Syntax

```
bayes [ , bayesopts ] : streg [ varlist ] [ if ] [ in ] [ , options ]
```

options	Description
Model	
noconstant	suppress constant term
distribution(exponential)	exponential survival distribution
distribution(gompertz)	Gompertz survival distribution
distribution(loglogistic)	loglogistic survival distribution
distribution(llogistic)	synonym for distribution(loglogistic)
distribution(weibull)	Weibull survival distribution
distribution(lognormal)	lognormal survival distribution
distribution(lnormal)	synonym for distribution(lognormal)
distribution(ggamma)	generalized gamma survival distribution
frailty(gamma)	gamma frailty distribution
frailty(invgaussian)	inverse-Gaussian distribution
time	use accelerated failure-time metric
Model 2	
strata(*varname*)	strata ID variable
offset(*varname*)	include *varname* in model with coefficient constrained to 1
shared(*varname*)	shared frailty ID variable
ancillary(*varlist*)	use *varlist* to model the first ancillary parameter
anc2(*varlist*)	use *varlist* to model the second ancillary parameter
Reporting	
nohr	do not report hazard ratios
tratio	report time ratios
noshow	do not show st setting information
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

You must stset your data before using bayes: streg; see [ST] **stset**.
varlist may contain factor variables; see [U] **11.4.3 Factor variables**.
bayes: streg, level() is equivalent to bayes, clevel(): streg.
For a detailed description of *options*, see *Options* in [ST] **streg**.

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients and log-ancillary parameters; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation

Simulation

nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results

Blocking

*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
*nohr	do not report hazard ratios
*tratio	report time ratios; requires option time with streg
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

`search(`*search_options*`)`	control the search for feasible initial values
`corrlag(#)`	specify maximum autocorrelation lag; default varies
`corrtol(#)`	specify autocorrelation tolerance; default is `corrtol(0.01)`

*Starred options are specific to the `bayes` prefix; other options are common between `bayes` and `bayesmh`.

Options `prior()` and `block()` may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} and ancillary parameters as described in *Ancillary model parameters*. Use the `dryrun` option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [ST] **streg**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Parametric survival model* in [BAYES] **bayes**.

Ancillary model parameters

In addition to regression coefficients {`_t:`*varlist*}, `bayes: streg` defines ancillary parameters that depend on the chosen survival model; see table 1 below. Positive ancillary parameters are transformed to be defined on the whole real line. All ancillary parameters are assigned default normal priors with zero mean and variance of 10,000.

Table 1. Ancillary model parameters defined by `bayes: streg`

Distribution	Ancillary parameters	Transformed model parameters
Exponential	None	None
Weibull	p	{`ln_p`}
Gompertz	γ	{`gamma`}
Lognormal	σ	{`lnsigma`}
Loglogistic	γ	{`lngamma`}
Generalized gamma	σ, κ	{`lnsigma`}, {`kappa`}

For frailty models, when option `frailty()` or option `shared()` is specified with `streg`, `bayes: streg` also defines the log-frailty parameter {`lntheta`}.

If option `ancillary(`*varlist*`)` is specified, regression coefficients {`ln_p:`*varlist*}, {`gamma:`*varlist*}, and so on are defined for all ancillary parameters except κ. If option `anc2(`*varlist*`)` is specified, then regression coefficients {`kappa:`*varlist*} are defined for κ.

If option `strata(`*varname*`)` is specified, additional stratum-specific coefficients of the form `{`*eqname*`:#.`*varname*`}` are defined for the main regression and ancillary parameters. For example, if `drug` contains three strata, then specifying option `strata(drug)` will result in additional main regression coefficients `{_t:2.drug}` and `{_t:3.drug}` and—say, for Weibull regression—in additional parameters `{ln_p:2.drug}` and `{ln_p:3.drug}`. In the model summary with default priors, you may see these parameters labeled as `{_t:i.drug}` and `{ln_p:i.drug}`, for short.

Use the `dryrun` option with the `bayes` prefix to see the definitions of model parameters prior to estimation.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[ST] **streg** — Parametric survival models

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: tnbreg — Bayesian truncated negative binomial regression

Description

`bayes: tnbreg` fits a Bayesian truncated negative binomial regression to a positive count outcome whose values are all above the truncation point; see [BAYES] **bayes** and [R] **tnbreg** for details.

Quick start

Bayesian truncated negative binomial regression of `y` on `x1` and `x2`, using a lower truncation limit of 5 and using default normal priors for regression coefficients and log-overdispersion parameter

```
bayes: tnbreg y x1 x2, ll(5)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): tnbreg y x1 x2, ll(5)
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): tnbreg y x1 x2, ll(5)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): tnbreg y x1 x2, ll(5)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): tnbreg y x1 x2, ll(5)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display incidence-rate ratios instead of coefficients

```
bayes: tnbreg y x1 x2, ll(5) irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **tnbreg**.

Menu

Statistics > Count outcomes > Bayesian regression > Truncated negative binomial regression

Syntax

```
bayes [, bayesopts]: tnbreg depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
ll(# | *varname*)	truncation point; default value is ll(0), zero truncation
dispersion(mean)	parameterization of dispersion; the default
dispersion(constant)	constant dispersion for all observations
exposure(*varname*$_e$)	include ln(*varname*$_e$) in model with coefficient constrained to 1
offset(*varname*$_o$)	include *varname*$_o$ in model with coefficient constrained to 1
Reporting	
irr	report incidence-rate ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

fweights are allowed; see [U] **11.1.6 weight**.

bayes: tnbreg, level() is equivalent to bayes, clevel(): tnbreg.

For a detailed description of *options*, see *Options* in [R] **tnbreg**.

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients and log-overdispersion parameter; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
* blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
* noblocking	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
*irr	report incidence-rate ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} and log-overdispersion parameter {lnalpha} with mean dispersion or {lndelta} with constant dispersion. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **tnbreg**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Truncated Poisson regression* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **tnbreg** — Truncated negative binomial regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: tobit — Bayesian tobit regression

Description

`bayes: tobit` fits a Bayesian tobit regression to a censored continuous outcome; see [BAYES] **bayes** and [R] **tobit** for details.

Quick start

Bayesian tobit regression of `y` on `x1` and `x2`, using a lower censoring limit of 17 and using default normal priors for regression coefficients and default inverse-gamma prior for the variance

```
bayes: tobit y x1 x2, ll(17)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): tobit y x1 x2, ll(17)
```

Use a shape of 1 and a scale of 2 instead of values of 0.01 for the default inverse-gamma prior

```
bayes, igammaprior(1 2): tobit y x1 x2, ll(17)
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): tobit y x1 x2, ll(17)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): tobit y x1 x2, ll(17)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): tobit y x1 x2, ll(17)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **tobit**.

Menu

Statistics > Linear models and related > Bayesian regression > Tobit regression

Syntax

```
bayes [, bayesopts]: tobit depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
ll[(*varname*|#)]	left-censoring variable or limit
ul[(*varname*|#)]	right-censoring variable or limit
offset(*varname*)	include *varname* in model with coefficient constrained to 1
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

fweights are allowed; see [U] **11.1.6 weight**.

bayes: tobit, level() is equivalent to bayes, clevel(): tobit.

For a detailed description of *options*, see *Options* in [R] **tobit**.

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
* igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance; default is igammaprior(0.01 0.01)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
* blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref*[, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
* noblocking	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} and variance {sigma2}. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **tobit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **tobit** — Tobit regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: tpoisson — Bayesian truncated Poisson regression

Description

`bayes: tpoisson` fits a Bayesian truncated Poisson regression to a positive count outcome whose values are all above the truncation point; see [BAYES] **bayes** and [R] **tpoisson** for details.

Quick start

Bayesian truncated Poisson regression of `y` on `x1` and `x2`, using a lower truncation limit of 5 and using default normal priors for regression coefficients

```
bayes: tpoisson y x1 x2, ll(5)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): tpoisson y x1 x2, ll(5)
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): tpoisson y x1 x2, ll(5)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): tpoisson y x1 x2, ll(5)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): tpoisson y x1 x2, ll(5)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display incidence-rate ratios instead of coefficients

```
bayes: tpoisson y x1 x2, ll(5) irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **tpoisson**.

Menu

Statistics > Count outcomes > Bayesian regression > Truncated Poisson regression

Syntax

```
bayes [, bayesopts]: tpoisson depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
ll(# | *varname*)	lower limit for truncation; default is ll(0)
ul(# | *varname*)	upper limit for truncation
exposure(*varname*$_e$)	include ln(*varname*$_e$) in model with coefficient constrained to 1
offset(*varname*$_o$)	include *varname*$_o$ in model with coefficient constrained to 1
Reporting	
irr	report incidence-rate ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

fweights are allowed; see [U] **11.1.6 weight**.

bayes: tpoisson, level() is equivalent to bayes, clevel(): tpoisson.

For a detailed description of *options*, see *Options* in [R] **tpoisson**.

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
* blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
* noblocking	do not block parameters by default

Initialization	
`initial(`*initspec*`)`	specify initial values for model parameters with a single chain
`init#(`*initspec*`)`	specify initial values for #th chain; requires `nchains()`
`initall(`*initspec*`)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
* `noisily`	display output from the estimation command during initialization
Adaptation	
`adaptation(`*adaptopts*`)`	control the adaptive MCMC procedure
`scale(#)`	initial multiplier for scale factor; default is `scale(2.38)`
`covariance(`*cov*`)`	initial proposal covariance; default is the identity matrix
Reporting	
`clevel(#)`	set credible interval level; default is `clevel(95)`
`hpd`	display HPD credible intervals instead of the default equal-tailed credible intervals
* `irr`	report incidence-rate ratios
`eform[ (`*string*`) ]`	report exponentiated coefficients and, optionally, label as *string*
`batch(#)`	specify length of block for batch-means calculations; default is `batch(0)`
`saving(`*filename*`[ , replace ])`	save simulation results to *filename*`.dta`
`nomodelsummary`	suppress model summary
`chainsdetail`	display detailed simulation summary for each chain
`[no]dots`	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is `nodots`
`dots(#[ , every(#) ])`	display dots as simulation is performed
`[no]show(`*paramref*`)`	specify model parameters to be excluded from or included in the output
`notable`	suppress estimation table
`noheader`	suppress output header
`title(`*string*`)`	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells
Advanced	
`search(`*search_options*`)`	control the search for feasible initial values
`corrlag(#)`	specify maximum autocorrelation lag; default varies
`corrtol(#)`	specify autocorrelation tolerance; default is `corrtol(0.01)`

*Starred options are specific to the `bayes` prefix; other options are common between `bayes` and `bayesmh`.

Options `prior()` and `block()` may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}. Use the `dryrun` option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **tpoisson**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Truncated Poisson regression* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **tpoisson** — Truncated Poisson regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: truncreg — Bayesian truncated regression

Description

`bayes: truncreg` fits a Bayesian truncated linear regression to a continuous outcome; see [BAYES] **bayes** and [R] **truncreg** for details.

Quick start

Bayesian truncated linear regression of `y` on `x1` and `x2`, using a lower truncation limit of 17 and using default normal priors for regression coefficients and default inverse-gamma prior for the variance

```
bayes: truncreg y x1 x2, ll(17)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): truncreg y x1 x2, ll(17)
```

Use a shape of 1 and a scale of 2 instead of values of 0.01 for the default inverse-gamma prior

```
bayes, igammaprior(1 2): truncreg y x1 x2, ll(17)
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): truncreg y x1 x2, ll(17)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123):, ///
truncreg y x1 x2, ll(17)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500):, ///
truncreg y x1 x2, ll(17)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **truncreg**.

Menu

Statistics > Linear models and related > Bayesian regression > Truncated regression

Syntax

```
bayes [, bayesopts]: truncreg depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
ll(*varname*|#)	left-truncation variable or limit
ul(*varname*|#)	right-truncation variable or limit
offset(*varname*)	include *varname* in model with coefficient constrained to 1
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

fweights are allowed; see [U] **11.1.6 weight**.

bayes: truncreg, level() is equivalent to bayes, clevel(): truncreg.

For a detailed description of *options*, see *Options* in [R] **truncreg**.

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
* igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance; default is igammaprior(0.01 0.01)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
* blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
* noblocking	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} and variance {sigma2}. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **truncreg**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **truncreg** — Truncated regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: var — Bayesian vector autoregressive models

Description

`bayes: var` fits a Bayesian vector autoregressive (VAR) model—a multivariate time-series regression of each dependent variable on lags of itself and on lags of all the other dependent variables. `bayes: var` also fits a variant of Bayesian VAR models known as the Bayesian VARX model, which also includes exogenous variables. The command supports four classes of priors, which are specific to VAR, including the original and the conjugate Minnesota priors. See [BAYES] **bayes** and [TS] **var** for details.

Quick start

Bayesian VAR for three time series ($K = 3$) with default two lags ($p = 2$) and using the default conjugate Minnesota prior

```
bayes: var y1 y2 y3
```

Same as above, but with three lags and exogenous variable `x1` ($m = 1$)

```
bayes: var y1 y2 y3, lags(1/3) exog(x1)
```

Same as above, but with random seed for reproducibility and saving simulation results in dataset `bvarsim.dta`

```
bayes, rseed(17) saving(bvarsim): var y1 y2 y3, lags(1/3) exog(x1)
```

Customize the default conjugate Minnesota prior by changing the self-variables tightness parameter from 0.1 to 1, the lag decay from 1 to 0.5, and the exogenous-variables tightness parameter from 100 to 1

```
bayes, minnconjprior(selftight(1) lagdecay(0.5) exogtight(1)): ///
    var y1 y2 y3, lags(1/3) exog(x1)
```

Report posterior summaries only for coefficients on lag 1 and lag 3 of variable `y1` in the first equation (`y1`), on lag 2 of variable `y3` in the second equation (`y2`), and on exogenous variable `x1` in the third equation (`y3`)

```
. bayesstats summary {y1:L1.y1} {y1:L3.y1} {y2:L2.y3} {y3:x1}
```

Bayesian VAR for three time series with two lags using the original Minnesota prior with fixed AR error covariance

```
bayes, minnfixedcovprior: var y1 y2 y3
```

Same as above, but changing some of the default original Minnesota prior settings: self-variables tightness parameter from 0.1 to 0.5 and cross-variables tightness parameter from 0.5 to 0.1

```
bayes, minnfixedcovprior(selftight(0.5) crosstight(0.1)): var y1 y2 y3
```

Specify independent multivariate normal (MVN) prior for VAR coefficients and inverse-Wishart prior for error covariance

```
bayes, minniwishprior: var y1 y2 y3
```

Same as above, but specify a 3×1 zero mean vector for the MVN prior for self-variables first-lag coefficients (other coefficients are also set to 0 automatically) and a 3×3 identity scaling matrix for the inverse-Wishart prior for error covariance

```
matrix b0 = J(3,1,0)
matrix Omega0 = diag(J(3,1,1))
bayes, minniwishprior(mean(b0) scale(Omega0)): var y1 y2 y3
```

Specify independent MVN prior for coefficients and multivariate Jeffreys prior for error covariance

```
bayes, minnjeffprior: var y1 y2 y3
```

Same as above, but change the default MVN prior mean vector to a 21×1 zero mean vector and covariance matrix to a 21×21 identity matrix for all $21 = 3 \times (2 \times 3 + 1)$ coefficients

```
matrix b0 = J(21,1,0)
matrix S0 = I(21)
bayes, minniwishprior(mean(b0) cov(S0)): var y1 y2 y3
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [TS] **var**.

Menu

Statistics > Multivariate time series > Bayesian models > Vector autoregression (VAR)

Syntax

`bayes` [, *bayesopts*] `: var` *depvarlist* [*if*] [*in*] [, *options*]

options	Description
Model	
`noconstant`	suppress constant term
`lags(`*numlist*`)`	specify a list of lags for the VAR
`exog(`*varlist*`)`	specify exogenous variables
`level(#)`	set credible level; default is `level(95)`

You must `tsset` your data before using `bayes: var`; see [TS] **tsset**.

depvarlist and *varlist* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`bayes: var, level()` is equivalent to `bayes, clevel(): var`.

For a detailed description of *options*, see *Options* in [TS] **var**.

bayesopts	Description
Priors	
*`minnconjprior` [(*conjopts*)]	conjugate Minnesota prior for VAR coefficients and error covariance; the default
*`minnfixedcovprior` [(*fixcovopts*)]	original Minnesota prior with fixed error covariance
*`minniwishprior` [(*iwishopts*)]	Minnesota prior with inverse-Wishart prior for error covariance
*`minnjeffprior` [(*jeffopts*)]	Minnesota prior with multivariate Jeffreys prior for error covariance
`dryrun`	show model summary without estimation

Simulation

nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results

Blocking

blocksummary	display block summary

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are $K \times p$ outcome-specific regression coefficients for lagged outcome (dependent) variables plus a constant term unless `noconstant` is specified: {*depvar_k*:*Ldepvar_1 Ldepvar_2 ... Ldepvar_K* `_cons`}, where *Ldepvar_k* denotes a list of lags for dependent variable *depvar_k* such as the default `L1.`*depvar_k* `L2.`*depvar_k*. If `exog(`*varlist*`)` is specified, regression coefficients also include $K \times m$ outcome-specific coefficients for exogenous variables: {*depvar_k*:*varlist*}. Use the `dryrun` option to see the definitions of model parameters prior to estimation.

Only one of options `minnconjprior()`, `minnfixedcovprior()`, `minniwishprior()`, or `minnjeffprior()` may be specified.

For a detailed description of *bayesopts*, see *Options* below.

conjopts	Description
`mean(...)`	mean vector for the MVN prior
`phi(`*matname*`)`	covariance product matrix Φ_0 for the MVN prior; default is diagonal autoregressive-structure matrix
`df(#)`	degrees of freedom for the inverse-Wishart prior; default is $K + 2$
`scale(`*matname*`)`	scale matrix for the inverse-Wishart prior; default is proportional to AR estimate of error covariance
minnopts	Minnesota prior options

fixcovopts	Description
`mean(...)`	mean vector for the MVN prior
minnopts	Minnesota prior options

iwishopts	Description
`mean(...)`	mean vector for the MVN prior
`cov(`*matname*`)`	covariance matrix for the MVN prior; default is diagonal autoregressive-structure matrix
`df(#)`	degrees of freedom for the inverse-Wishart prior; default is $K + 2$
`scale(`*matname*`)`	scale matrix for the inverse-Wishart prior; default is proportional to AR estimate of error covariance
minnopts	Minnesota prior options

jeffopts	Description
`mean(...)`	mean vector for the MVN prior
`cov(`*matname*`)`	covariance matrix for the MVN prior; default is diagonal autoregressive-structure matrix
minnopts	Minnesota prior options

meanopts	Description
`mean(`*matname*`)`	mean vector for the MVN prior for all $K(Kp + 1 + m)$ coefficients; default is to use 1s for K self-variables first-lag coefficients and 0s otherwise
`mean(`m_1`,...,`m_K`)`	mean values for the MVN prior for K self-variables first-lag coefficients; all other means are assumed to be zero

minnopts	Description
selftight(#)	self-variables tightness parameter for the Minnesota prior; default is selftight(0.1)
crosstight(#)	cross-variables tightness parameter for the Minnesota priors; default is crosstight(0.5); not used with conjugate Minnesota prior
lagdecay(#)	lag decay parameter for the Minnesota prior; default is lagdecay(1)
exogtight(#)	exogenous-variables tightness parameter for the Minnesota prior; default is exogtight(100)
arcov	use separate AR models to estimate error covariance
varcov	use VAR model to estimate error covariance

Options

noconstant, lags(*numlist*), and exog(*varlist*); see [TS] **var**.

Priors

minnconjprior and minnconjprior(*conjopts*) specify that a conjugate Minnesota prior be used for VAR coefficients and error covariance. minnconjprior is the default. The prior for VAR coefficients is MVN with mean and covariance based on the original Minnesota prior. The prior for the error covariance is an inverse-Wishart distribution. See *Conjugate Minnesota prior for VAR model with unknown error covariance* in *Methods and formulas*.

conjopts are mean(*meanspec*), phi(*matname*), df(#), scale(*matname*), and *minnopts*. *meanspec* is one of $matname_{K(Kp+1+m)}$, or $matname_K$, or $m_1, \ldots, m_K$.

mean(*matname*) specifies the mean vector (as a Stata matrix) of the MVN prior distribution for all $K(Kp+1+m)$ VAR coefficients. The default is to use ones for K self-variables first-lag coefficients and zeros otherwise.

mean(m_1,...,m_K | *matname*) specifies K mean values or mean vector *matname* of length K of prior means for the self-variables first-lag coefficients. The rest are set to zero.

phi(*matname*) specifies the covariance product matrix Φ_0 (as a Stata matrix) of the MVN prior distribution for the VAR coefficients. The default is the Minnesota factor covariance, a diagonal matrix that accounts for the autoregressive structure of the VAR model; see *Methods and formulas*.

df(#) specifies the degrees of freedom of the inverse-Wishart prior distribution for the error covariance. The default is $K+2$, and this is the minimum allowed value.

scale(*matname*) specifies the scale matrix of the inverse-Wishart prior distribution for the error covariance. The default is proportional to the diagonal matrix of K AR variance estimates, one for each VAR equation; see *Methods and formulas*.

minnfixedcovprior and minnfixedcovprior(*fixcovopts*) specify that the Minnesota prior with a fixed AR (or VAR if option varcov is specified) covariance be used for VAR coefficients. This is the original Minnesota prior for Bayesian VAR models. In this model formulation, the error covariance is considered fixed, thus decreasing the number of parameters needed to be simulated and speeding up computations. See *Original Minnesota prior with known (fixed) error covariance* in *Methods and formulas*.

fixcovopts are mean(*meanspec*) and *minnopts*.

`minniwishprior` and `minniwishprior(`*iwishopts*`)` specify that the MVN prior for VAR coefficients and an inverse-Wishart prior for the error covariance be used. The priors for VAR coefficients and error covariance are independent. The default MVN prior for coefficients uses the Minnesota prior mean vector and covariance matrix. See *MVN-inverse Wishart prior* in *Methods and formulas*.

iwishopts are `mean(`*meanspec*`)`, `cov(`*matname*`)`, `df(#)`, `scale(`*matname*`)`, and *minnopts*.

`cov(`*matname*`)` specifies the covariance matrix Ω_0 (as a Stata matrix) of the MVN prior distribution for the VAR coefficients. The default is a diagonal matrix that accounts for the autoregressive structure of the VAR model; see *Methods and formulas*.

`df(#)` specifies the degrees of freedom of the inverse-Wishart prior distribution for the error covariance. The default is $K + 2$, and this is the minimum allowed value.

`scale(`*matname*`)` specifies the scale matrix of the inverse-Wishart prior distribution for the error covariance. The default is proportional to the diagonal matrix of K AR variance estimates, one for each VAR equation; see *Methods and formulas*.

`minnjeffprior` and `minnjeffprior(`*jeffopts*`)` specify that the MVN prior for VAR coefficients and the Jeffreys prior for the error covariance be used. The priors for VAR coefficients and error covariance are independent. The default MVN prior for coefficients uses the Minnesota prior mean vector and covariance matrix. See *Multivariate normal-diffuse (normal-Jeffreys) prior* in *Methods and formulas*.

jeffopts are `mean(`*meanspec*`)`, `cov(`*matname*`)`, and *minnopts*.

`cov(`*matname*`)` specifies the covariance matrix Ω_0 (as a Stata matrix) of the MVN prior distribution for the VAR coefficients. The default is a diagonal matrix that accounts for the autoregressive structure of the VAR model; see *Methods and formulas*.

minnopts are `selftight(#)`, `crosstight(#)`, `lagdecay(#)`, `exogtight(#)`, `arcov`, and `varcov`.

`selftight(#)` specifies the self-variables tightness parameter, λ_1, for the Minnesota prior. The default is `selftight(0.1)`. The smaller this value, the more concentrated the prior distribution around the prior mean for self-variables lag coefficients. See *Methods and formulas*.

`crosstight(#)` specifies the cross-variables tightness parameter, λ_2, for the Minnesota prior. The default is `crosstight(0.5)`. The smaller this value, the more concentrated the prior distribution around the prior mean for cross-variables lag coefficients. `crosstight()` is not used with the conjugate Minnesota prior. See *Methods and formulas*.

`lagdecay(#)` specifies the lag-decay parameter, λ_3, for the Minnesota prior. This is a rate of lag-decay correction to the prior standard deviation of all endogenous-variables lag coefficients. See *Methods and formulas*.

`exogtight(#)` specifies the exogenous-variables tightness parameter, λ_4, for the Minnesota prior. This is a multiplicative factor to the prior standard deviation of exogenous-variables coefficients. See *Methods and formulas*.

`arcov`, the default, specifies that the diagonal AR matrix estimate be used as an estimate of the error covariance matrix. This AR matrix has, on the diagonal, the estimates of error variances obtained from fitting a separate AR(p) model to each dependent variable. Only one of `arcov` or `varcov` may be specified.

`varcov` specifies that the VAR matrix estimate be used as an estimate of the error covariance matrix. The VAR matrix is an estimate of the error covariance obtained from fitting a VAR(p) model to the dependent variables.

`arcov` and `varcov` are used with all Minnesota priors. For the original prior with a fixed error covariance, these options specify which estimate will be used for the error covariance matrix.

For other priors, these options specify which estimate will be used for the prior scale matrix of an inverse-Wishart prior for error covariance matrix.

See descriptions of other *bayesopts* in *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For an introduction to VAR models, see [TS] **var intro**. For a general introduction to Bayesian estimation using Gibbs sampling, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [TS] **var**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**.

Remarks are presented under the following headings:

Advantages of Bayesian VAR models
Introductory examples
US macroeconomic examples

Examples are presented under the following headings:

Default Bayesian VAR model
Bayesian VAR model with original Minnesota prior
MVN priors with unrestricted error covariances
Testing Bayesian VAR stability
Explaining the Minnesota prior
Choosing the number of lags of a VAR model
Bayesian VAR(4) model estimation
IRFs
Forecasting
One-step-ahead Bayesian predictions

Advantages of Bayesian VAR models

Since their introduction by Doan, Litterman, and Sims (1984), Bayesian VAR models have gained popularity for several reasons. As Bayesian models in general, they benefit from a unified and coherent approach of Bayesian inference; see [BAYES] **Intro**. Kadiyala and Karlsson (1997), Bańbura, Giannone, and Reichlin (2008), and Dieppe, Legrand, and van Roye (2016) describe advantages of Bayesian VARs. We summarize some below.

One of the major problems with traditional VAR models is overparameterization. The number of regression parameters in a VAR model is quadratic to the number of response variables and proportional to the number of lags. This leads to many parameters being estimated even for small models and thus to loss of degrees of freedom when maximum likelihood estimation is used. Overparameterized models also produce poor forecasts. The problem of overparameterization is exacerbated when VAR models are applied to small datasets, which is common in many economic applications.

In the Bayesian framework, VAR model parameters are considered random and are controlled by prior distributions. Prior selection, viewed as a limitation of Bayesian inference in the past, is now a powerful tool for flexible analysis and not purely a source of subjective inference. For example, it is easy to shrink higher-lag regression parameters through their priors and thus reduce the effective number of lags. One such example prior is the Minnesota prior (Litterman 1980). The Minnesota prior on regression coefficients and error covariance supports a wide range of models, from oversimplified to overparameterized ones. The Bayesian out-of-sample prediction errors, which can be obtained by simulation, provide a measure for choosing between oversimplified and overparameterized models (Litterman 1984). In cases of small or low-quality data, stronger priors based on existing expert knowledge can greatly enhance otherwise potentially unreliable VAR analysis.

VAR model specification requires choosing the number of lags. Within the Bayesian approach, we can use Bayes factors to compare models using different lags and choose the best one. We can use Bayes factors also for other decision-based inference such as selecting exogenous variables.

The availability of flexible priors, reliable lag-selection criteria, and efficient sampling algorithms capable of producing precise Bayesian estimates makes Bayesian VAR inference a useful alternative to the traditional VAR analysis.

Introductory examples

▷ Example 1: Default Bayesian VAR model

Let's revisit example 1 from [TS] **var**, which replicates a case from Lütkepohl (2005, 77–78). The example models the relationships between the first differences of the natural log of investment, `dln_inv`, of income, `dln_inc`, and of consumption, `dln_cons`, registered at each quarter of the years between 1960 and 1978 in West Germany.

```
. webuse lutkepohl2
(Quarterly SA West German macro data, Bil DM, from Lutkepohl 1993 Table E.1)
. tsset
Time variable: qtr, 1960q1 to 1982q4
        Delta: 1 quarter
```

The original VAR in example 1 considers all observations before 1979, has two lags, and is fit using the `var` command.

```
. var dln_inv dln_inc dln_consump if qtr<=tq(1978q4)

Vector autoregression

Sample: 1960q4 thru 1978q4                      Number of obs     =         73
Log likelihood =    606.307                     AIC               =  -16.03581
FPE            =   2.18e-11                     HQIC              =  -15.77323
Det(Sigma_ml)  =   1.23e-11                     SBIC              =  -15.37691

Equation           Parms      RMSE     R-sq      chi2     P>chi2
------------------------------------------------------------------
dln_inv                7     .046148   0.1286   10.76961   0.0958
dln_inc                7     .011719   0.1142   9.410683   0.1518
dln_consump            7     .009445   0.2513   24.50031   0.0004
------------------------------------------------------------------
```

	Coefficient	Std. err.	z	P>|z|	[95% conf.	interval]
dln_inv						
dln_inv						
L1.	-.3196318	.1192898	-2.68	0.007	-.5534355	-.0858282
L2.	-.1605508	.118767	-1.35	0.176	-.39333	.0722283
dln_inc						
L1.	.1459851	.5188451	0.28	0.778	-.8709326	1.162903
L2.	.1146009	.508295	0.23	0.822	-.881639	1.110841
dln_consump						
L1.	.9612288	.6316557	1.52	0.128	-.2767936	2.199251
L2.	.9344001	.6324034	1.48	0.140	-.3050877	2.173888
_cons	-.0167221	.0163796	-1.02	0.307	-.0488257	.0153814
dln_inc						
dln_inv						
L1.	.0439309	.0302933	1.45	0.147	-.0154427	.1033046
L2.	.0500302	.0301605	1.66	0.097	-.0090833	.1091437
dln_inc						
L1.	-.1527311	.131759	-1.16	0.246	-.4109741	.1055118
L2.	.0191634	.1290799	0.15	0.882	-.2338285	.2721552
dln_consump						
L1.	.2884992	.1604069	1.80	0.072	-.0258926	.6028909
L2.	-.0102	.1605968	-0.06	0.949	-.3249639	.3045639
_cons	.0157672	.0041596	3.79	0.000	.0076146	.0239198
dln_consump						
dln_inv						
L1.	-.002423	.0244142	-0.10	0.921	-.050274	.045428
L2.	.0338806	.0243072	1.39	0.163	-.0137607	.0815219
dln_inc						
L1.	.2248134	.1061884	2.12	0.034	.0166879	.4329389
L2.	.3549135	.1040292	3.41	0.001	.1510199	.558807
dln_consump						
L1.	-.2639695	.1292766	-2.04	0.041	-.517347	-.010592
L2.	-.0222264	.1294296	-0.17	0.864	-.2759039	.231451
_cons	.0129258	.0033523	3.86	0.000	.0063554	.0194962

The output table reports summaries for 21 regression coefficients. But in VAR models, it is usually more instructive to analyze how shocks on a dependent variable affect other dependent variables and the variable itself over time. In this example, we focus on technical aspects of fitting Bayesian VAR models and the immediate impact on regression coefficients and covariances. Later in example 8, we demonstrate how to use more common impulse–response functions (IRFs) to interpret results.

Let us start by fitting the same VAR model using the `bayes: var` command with the default model prior—conjugate Minnesota prior for regression coefficients and error covariance. In addition to the `bayes` prefix, we specify the `rseed()` option for reproducibility and run three MCMC chains to compute a Gelman–Rubin convergence diagnostic; see *Convergence diagnostics using multiple chains*.

```
. bayes, rseed(17)  nchains(3):
> var dln_inv dln_inc dln_consump if qtr<=tq(1978q4)
Chain 1
  Burn-in ...
  Simulation ...
Chain 2
  Burn-in ...
  Simulation ...
Chain 3
  Burn-in ...
  Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
      dln_inv
      dln_inc
  dln_consump ~ mvnormal(3,xb_dln_inv,xb_dln_inc,xb_dln_consump,{Sigma,m})

Priors:
          {dln_inv:L(1 2).dln_inv}                                       (1)
          {dln_inv:L(1 2).dln_inc}                                       (1)
      {dln_inv:L(1 2).dln_consump}                                       (1)
                  {dln_inv:_cons}                                        (1)
          {dln_inc:L(1 2).dln_inv}                                       (2)
          {dln_inc:L(1 2).dln_inc}                                       (2)
      {dln_inc:L(1 2).dln_consump}                                       (2)
                  {dln_inc:_cons}                                        (2)
      {dln_consump:L(1 2).dln_inv}                                       (3)
      {dln_consump:L(1 2).dln_inc}                                       (3)
  {dln_consump:L(1 2).dln_consump}                                       (3)
              {dln_consump:_cons} ~ varconjugate(3,2,1,_b0,{Sigma,m},_Phi0)
                                    (3)
                        {Sigma,m} ~ iwishart(3,5,_Sigma0)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_dln_inv.
(2) Parameters are elements of the linear form xb_dln_inc.
(3) Parameters are elements of the linear form xb_dln_consump.
Bayesian vector autoregression               Number of chains    =          3
Gibbs sampling                               Per MCMC chain:
                                                 Iterations      =     12,500
                                                 Burn-in         =      2,500
                                                 Sample size     =     10,000
Sample: 1960q4 thru 1978q4                   Number of obs       =         73
                                             Avg acceptance rate =          1
                                             Avg efficiency: min =      .9755
                                                           avg   =       .994
                                                           max   =          1
Avg log marginal-likelihood =  483.43596     Max Gelman-Rubin Rc =          1
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
dln_inv						
dln_inv						
L1.	.4808475	.103581	.000598	.480019	.2786408	.6837882
L2.	.0068788	.0627703	.000362	.0069781	-.1167651	.1290908
dln_inc						
L1.	.1026098	.4103202	.002369	.1044135	-.7070827	.8989748
L2.	.0320344	.2434573	.001406	.032674	-.4520181	.5169279
dln_consump						
L1.	-.0181305	.4774359	.002766	-.0166627	-.9574952	.9252084
L2.	.0297566	.2885481	.001687	.0288948	-.5385765	.5989857
_cons	.0063813	.0152462	.000088	.0063497	-.0235027	.0364822
dln_inc						
dln_inv						
L1.	.0148781	.0245811	.000142	.0149684	-.033299	.0630655
L2.	.001391	.0147206	.000086	.0013496	-.0272677	.0305663
dln_inc						
L1.	.5782111	.0966633	.000564	.5787724	.3873585	.7675225
L2.	.0130696	.0576478	.000333	.0131284	-.0985297	.126328
dln_consump						
L1.	-.0315052	.1143589	.000664	-.0311991	-.2557682	.1961411
L2.	-.0193878	.0681031	.000393	-.0194134	-.1543933	.1152181
_cons	.0087345	.0036292	.000021	.0087388	.0016601	.0158279
dln_consump						
dln_inv						
L1.	-.0183338	.0216079	.000125	-.0182276	-.0610608	.0238827
L2.	.0086858	.0131225	.000076	.0087476	-.0172135	.0344555
dln_inc						
L1.	-.0283731	.0857885	.000498	-.0287275	-.1961209	.1409767
L2.	.0344015	.0508225	.000297	.0344959	-.0658067	.1335025
dln_consump						
L1.	.5452017	.1011028	.000584	.5452941	.3461853	.7423402
L2.	.0528311	.0603558	.00035	.0523857	-.0640511	.1727009
_cons	.0078026	.0032046	.000019	.0077938	.0015249	.014078
Sigma_1_1	.0039149	.0006512	3.8e-06	.0038459	.002843	.0054003
Sigma_2_1	-.0000195	.0001079	6.2e-07	-.0000193	-.0002359	.0001924
Sigma_3_1	.0001329	.000097	5.6e-07	.0001291	-.0000493	.0003346
Sigma_2_2	.000219	.0000365	2.1e-07	.0002148	.0001587	.0003014
Sigma_3_2	.0000463	.0000232	1.3e-07	.0000451	4.14e-06	.000096
Sigma_3_3	.0001703	.0000282	1.6e-07	.0001673	.0001239	.0002344

Note: Default initial values are used for multiple chains.

The simulation is performed using Gibbs sampling, which provides high sampling efficiency, 0.99 on average. The maximum Gelman–Rubin Rc statistic is a perfect 1, which suggests no convergence issues. Because of this and to speed up computation, we will use only one chain in subsequent examples.

The model summary provides description of the model. We have an MVN likelihood for the error terms. Regression coefficients are assigned a conjugate Minnesota prior, which is labeled as `varconjugate(3,2,1,_b0,{Sigma,m},_Phi0)` in the output. The arguments are the number of dependent variables (3), number of lags (2), number of exogenous variables (0) plus a constant term per equation (1), default prior mean vector (`_b0`), error covariance matrix parameter (`{Sigma,m}`), and Minnesota factor covariance (`_Phi0`), which is a function of tightness parameters that control the concentration of the prior around its mean. The conjugate Minnesota prior for the coefficients is MVN with mean vector β_0 and covariance $\Sigma \otimes \Phi_0$, where β_0 and Φ_0 are defined in *Methods and formulas*. We discuss the Minnesota prior in detail in example 5. If you are not familiar with this prior, you may want to look at this example.

Error covariance `{Sigma,m}` is assigned an inverse-Wishart prior with default degrees of freedom $\text{df} = K + 2 = 5$ and scale matrix `_Scale0`$= (\text{df} - K - 1)$`_Sigma0`=`_Sigma0`, where `_Sigma0` is the diagonal AR covariance matrix, a diagonal matrix formed by error-variance estimates from fitting a separate AR model to each dependent variable; see *VAR model specification* in *Methods and formulas*.

The table of results contains three groups of regression parameters, one for each dependent variable, just like the output from the `var` command. `bayes: var` additionally displays the estimates of the error covariance `{Sigma,m}`. The output table reports standard Bayesian posterior summaries ([BAYES] **bayesstats summary**).

The prior mean vector _b0 is 1 for the coefficients corresponding to the first own lags of dependent variables, which we also refer to as self-variables first-lag coefficients, and 0 otherwise. In the output table, these are labeled as `{dln_inv:L1.dln_inv}`, `{dln_inc:L1.dln_inc}`, and `{dln_consump:L1.dln_consump}`. As such, the prior is centered around each variable being a univariate random walk. The estimated posterior means for the coefficients reflect the strong prior assumptions in the model. For example, the estimated posterior mean of `{dln_inv:L1.dln_inv}` is 0.48 with a 95% CrI of $[0.28, 0.68]$ compared with the estimates from the `var` command of -0.32 with a 95% CI of $-0.55, -0.086$, which are quite different. Similarly, the posterior mean estimate for `{dln_inc:L1.dln_inc}` is 0.58 versus -0.15 and for `{dln_consump:L1.dln_consump}` is 0.55 versus -0.26. Continuing with the `dln_consump` equation, we see that the posterior mean estimates of cross-variable lag coefficients are small. The estimated posterior mean of the first lag of income, `{dln_consump:L1.dln_inc}`, is -0.03, and its 95% CrI includes 0. From the `var` results, `{dln_consump:L1.dln_inc}` is 0.22 and is statistically significantly different from 0 (with p-value$= 0.034$).

All three self-variables first-lag coefficients have positive posterior estimates: means, medians, and 95% CrIs. Posterior estimates of remaining coefficients are close to 0. The results suggest a strong AR impact for each dependent variable and weak cross-correlations between the variables. The `{Sigma,m}` estimates show that there is some residual correlation in the error terms unexplained by the regression coefficients. The prior thus dominates the information about regression coefficients available in the data. This can be partially explained by the relatively small sample size of only 73 observations given the number of estimated parameters.

The results from the VAR models rely on the stability assumption. Thus, it is important to test this assumption, as we demonstrate in example 4. When the assumption is satisfied, as it is for these data, you may consider specifying priors for regression coefficients that are centered around zero; for instance, using these priors for our dataset produces results that are similar to those from `var` (example 2).

◁

Example 2: Bayesian VAR model with original Minnesota prior

In early work on Bayesian VAR (Doan, Litterman, and Sims 1984 and Litterman 1986), researchers simplified the model prior by assuming a known, fixed-error covariance matrix. The covariance Σ in the MVN likelihood is replaced by an estimate $\widehat{\Sigma}$. A typical choice for $\widehat{\Sigma}$ is a diagonal matrix of variance estimates obtained by fitting a separate AR model to each dependent variable. The prior covariance for regression coefficients is then obtained from $\widehat{\Sigma}$ as described in *Original Minnesota prior with known (fixed) error covariance* in *Methods and formulas*. This prior specification is known as the original Minnesota prior. Also see example 5.

To fit a model with the original Minnesota prior, we specify the `minnfixedcovprior` option with `bayes: var`.

```
. bayes, minnfixedcovprior rseed(17):
> var dln_inv dln_inc dln_consump if qtr<=tq(1978q4)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
      dln_inv
      dln_inc
  dln_consump ~ mvnormal(3,xb_dln_inv,xb_dln_inc,xb_dln_consump,_Sigma0)
Priors:
          {dln_inv:L(1 2).dln_inv}                                        (1)
          {dln_inv:L(1 2).dln_inc}                                        (1)
      {dln_inv:L(1 2).dln_consump}                                        (1)
                  {dln_inv:_cons}                                         (1)
          {dln_inc:L(1 2).dln_inv}                                        (2)
          {dln_inc:L(1 2).dln_inc}                                        (2)
      {dln_inc:L(1 2).dln_consump}                                        (2)
                  {dln_inc:_cons}                                         (2)
      {dln_consump:L(1 2).dln_inv}                                        (3)
      {dln_consump:L(1 2).dln_inc}                                        (3)
  {dln_consump:L(1 2).dln_consump}                                        (3)
              {dln_consump:_cons} ~ minnesota(3,2,1,_b0,_Sigma0,.1,.5,1,100)
                                    (3)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_dln_inv.
(2) Parameters are elements of the linear form xb_dln_inc.
(3) Parameters are elements of the linear form xb_dln_consump.
```

```
Bayesian vector autoregression                  MCMC iterations  =     12,500
Gibbs sampling                                  Burn-in          =      2,500
                                                MCMC sample size =     10,000
Sample: 1960q4 thru 1978q4                      Number of obs    =         73
                                                Acceptance rate  =          1
                                                Efficiency:  min =       .946
                                                             avg =      .9957
Log marginal-likelihood =  478.02208                         max =          1
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
dln_inv						
dln_inv						
L1.	.4836549	.0751107	.000751	.4825203	.3359447	.6314641
L2.	.0077444	.0458064	.000458	.0070614	-.0813891	.0984996
dln_inc						
L1.	.0370079	.1779866	.00178	.0381258	-.3085588	.3854122
L2.	.0090371	.0963583	.000964	.0081537	-.1793915	.1992546
dln_consump						
L1.	-.0028656	.2124749	.002125	-.0027569	-.4232734	.410695
L2.	.0094103	.1125252	.001125	.0087853	-.210387	.2303232
_cons	.0081521	.0082618	.000082	.0080767	-.0079144	.0244083
dln_inc						
dln_inv						
L1.	.0052036	.0117865	.000118	.0051966	-.0176583	.0288828
L2.	.0003523	.0063033	.000061	.0003332	-.011977	.012503
dln_inc						
L1.	.5758156	.0761506	.000776	.5767133	.4271662	.7249808
L2.	.0120131	.0457046	.000457	.0124684	-.0785969	.1006224
dln_consump						
L1.	-.0081978	.0543999	.000537	-.0080116	-.1156294	.0990992
L2.	-.0057737	.0288414	.000288	-.0056489	-.0627868	.0500214
_cons	.0082507	.0024756	.000025	.0082296	.0035138	.0131572
dln_consump						
dln_inv						
L1.	-.0068309	.0099134	.000102	-.0067224	-.0262589	.0127061
L2.	.002545	.0052876	.000053	.0025395	-.0079491	.0129162
dln_inc						
L1.	-.0091519	.0393528	.000394	-.0091127	-.0874506	.0692072
L2.	.0101553	.0207397	.000207	.0101049	-.0305975	.0503957
dln_consump						
L1.	.5358264	.0760533	.000752	.5362025	.3870167	.6834547
L2.	.0540704	.0459402	.000459	.0538069	-.0364033	.1445824
_cons	.007971	.0022349	.000022	.0079594	.0036197	.0123659

Compared with the default conjugate Minnesota prior from example 1, the error covariance matrix `{Sigma,m}` in the likelihood is replaced with a fixed matrix `_Sigma0`, a diagonal AR covariance estimate. The regression coefficients are assigned the `minnesota(3,2,1,_b0,_Sigma0,.1,.5,1,100)` prior. Most of the prior arguments are as we described in example 1, except the covariance matrix

is now formed by _Sigma0 and tightness parameters (0.1, 0.5, 1, 100); see *Original Minnesota prior with known (fixed) error covariance*. Specifically, the default for the self-variables tightness parameter λ_1 is 0.1 (option `selftight()`), the default for the cross-variables tightness parameter λ_2 is 0.5 (option `crosstight()`), the default for the lag-decay parameter λ_3 is 1 (option `lagdecay()`), and the default for the exogenous-variables tightness parameter is 100 (option `exogtight()`).

Like the default conjugate Minnesota prior, the original Minnesota prior places the same strong prior assumptions on regression coefficients: the prior mean vector _b0 contains 1 for self-variables first-lag coefficients and 0s for all other coefficients. The strength of the shrinkage toward the prior mean _b0 is controlled mainly by the tightness parameter λ_1, which can be reset using the Minnesota prior option `selftight()`. Coefficients of exogenous variables, including the constant terms, are shrunk toward 0 but are given wide prior variance controlled by the tightness parameter λ_4 and specified in the `exogtight()` option.

As expected, the results assuming the original Minnesota prior are closer to those assuming the default conjugate Minnesota prior than to those from the `var` command. In the absence of strong information about model parameters in the data, the Minnesota prior may introduce a stronger time dependence in the results. For example, the prior mean value for `{dln_inv:L1.dln_inv}` is 1 and the posterior mean estimate is 0.48, whereas the estimate from the `var` command is -0.32. It is completely acceptable to have a negative first-lag correlation in the change of investments at quarterly level. The Minnesota prior, however, expects an increase in investments to be followed by another increase in investment in the next time period. The question of whether this is a reasonable prior expectation is an empirical question. It is thus important to understand the behavior of the default Minnesota prior and use it carefully.

To relax the time-dependence assumption of the Minnesota prior, we can change the prior mean _b0 to be a zero vector and decrease the tightness of the prior by increasing the λ_1 parameter from the default of 0.1 to 1. The prior for the self-variables first-lag coefficients thus changes from $N(1, 0.01)$ to $N(0, 1)$ and those for the cross-variables first-lag coefficients from $N(0, 0.0025)$ to $N(0, 0.25)$.

We change the defaults by specifying the respective suboptions within the `minnfixedcovprior()` option. There are several ways to specify the prior mean values. We can provide a full 1×21 vector of mean values. Or, if we want to change the default values only for self-variables first-lag coefficients, we can specify a vector of lower dimension, 1×3 in our example. The remaining coefficients will be automatically set to zeros. Alternatively, for self-variables first-lag coefficients, we can list the values directly in the `mean()` suboption, that is, `mean(0,0,0)`. We use the second approach below and specify a zero mean vector for self-variables first-lag coefficients.

```
. matrix b0 = J(1,3,0)
. bayes, minnfixedcovprior(mean(b0) selftight(1)) rseed(17):
> var dln_inv dln_inc dln_consump if qtr<=tq(1978q4)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
      dln_inv
      dln_inc
  dln_consump ~ mvnormal(3,xb_dln_inv,xb_dln_inc,xb_dln_consump,_Sigma0)
Priors:
          {dln_inv:L(1 2).dln_inv}                                        (1)
          {dln_inv:L(1 2).dln_inc}                                        (1)
      {dln_inv:L(1 2).dln_consump}                                        (1)
                  {dln_inv:_cons}                                         (1)
          {dln_inc:L(1 2).dln_inv}                                        (2)
          {dln_inc:L(1 2).dln_inc}                                        (2)
      {dln_inc:L(1 2).dln_consump}                                        (2)
                  {dln_inc:_cons}                                         (2)
      {dln_consump:L(1 2).dln_inv}                                        (3)
      {dln_consump:L(1 2).dln_inc}                                        (3)
  {dln_consump:L(1 2).dln_consump}                                        (3)
              {dln_consump:_cons} ~ minnesota(3,2,1,b0,_Sigma0,1,.5,1,100) (3)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_dln_inv.
(2) Parameters are elements of the linear form xb_dln_inc.
(3) Parameters are elements of the linear form xb_dln_consump.
Bayesian vector autoregression                  MCMC iterations  =     12,500
Gibbs sampling                                  Burn-in          =      2,500
                                                MCMC sample size =     10,000
Sample: 1960q4 thru 1978q4                      Number of obs    =         73
                                                Acceptance rate  =          1
                                                Efficiency:  min =       .946
                                                             avg =      .9946
Log marginal-likelihood =  539.71278                         max =          1
------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
dln_inv      |
  dln_inv    |
         L1. | -.2987647   .1218328   .001218   -.300605  -.5383571  -.0590116
         L2. | -.1415209   .1192125   .001192  -.1439763  -.3729553   .0926795
             |
  dln_inc    |
         L1. |  .2014271   .5068694   .005069      .2036  -.7741228   1.196341
         L2. |  .1683548   .4567907   .004512   .1662872  -.7269593   1.058442
             |
 dln_consump |
         L1. |  .8313647   .6128113   .006128   .8291778  -.3631793   2.037414
         L2. |  .6988162    .554944   .005549   .6984739  -.3870548   1.810489
             |
       _cons | -.0124058    .016376   .000161  -.0123152  -.0449067   .0197023
------------------------------------------------------------------------------
```

dln_inc						
dln_inv						
L1.	.0401237	.0307154	.000307	.0401054	-.0194542	.1018312
L2.	.0397051	.0285189	.000276	.0396625	-.0158618	.0955686
dln_inc						
L1.	-.1359873	.1350215	.001376	-.133623	-.4004453	.1259119
L2.	.0225672	.1266313	.001266	.0237303	-.2302853	.2689963
dln_consump						
L1.	.269855	.1601578	.001602	.2691198	-.0423728	.579863
L2.	-.003682	.1444577	.001445	-.001067	-.2915697	.276431
_cons	.0158543	.0041686	.000042	.0158808	.0075933	.0241443
dln_consump						
dln_inv						
L1.	-.0046515	.0259292	.000267	-.0043679	-.055467	.0464489
L2.	.0277595	.0239298	.000239	.0277642	-.0190999	.0748595
dln_inc						
L1.	.1971296	.1126233	.001126	.1963476	-.025344	.4199598
L2.	.273373	.100819	.001008	.2730468	.076632	.4698413
dln_consump						
L1.	-.2200755	.1392633	.001393	-.2176729	-.4890732	.0503819
L2.	.0383448	.1342118	.001342	.0392141	-.2271728	.2978496
_cons	.0132401	.0036414	.000036	.0132355	.0062362	.0203544

Now the posterior mean estimates of regression coefficients are similar to the estimates from the original `var` command. For example, the posterior mean estimate of `{dln_inv:L1.dln_inv}` is about -0.30 compared with `var`'s estimate of -0.32.

The original Minnesota prior always assumes no correlation between cross-equation error terms. The following two priors relax this assumption.

◁

▷ Example 3: MVN priors with unrestricted error covariances

What if we want to relax the assumption about the error covariance imposed by the original Minnesota prior? We can use a MVN-inverse-Wishart prior (option `minniwishprior`) or MVN-Jeffreys prior (option `minnjeffprior`). These priors use the same default MVN prior for the regression coefficients as the original Minnesota prior, but they assume an unrestricted error covariance and use the respective inverse-Wishart or Jeffreys prior for it.

Let's start with an MVN-inverse-Wishart prior. Continuing with example 2, we change the default prior means for the regression coefficients to be zeros by specifying zero values for the three self-variables first-lag coefficients in the `mean()` option. This specification automatically assigns zero prior means for all other coefficients. We also use the self-variables tightness parameter of 1 instead of the default 0.1 to loosen the prior variance tightness.

```
. bayes, minniwishprior(mean(0,0,0) selftight(1)) rseed(17):
> var dln_inv dln_inc dln_consump if qtr<=tq(1978q4)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
      dln_inv
      dln_inc
  dln_consump ~ mvnormal(3,xb_dln_inv,xb_dln_inc,xb_dln_consump,{Sigma,m})
Priors:
          {dln_inv:L(1 2).dln_inv}                                        (1)
          {dln_inv:L(1 2).dln_inc}                                        (1)
      {dln_inv:L(1 2).dln_consump}                                        (1)
                  {dln_inv:_cons}                                         (1)
          {dln_inc:L(1 2).dln_inv}                                        (2)
          {dln_inc:L(1 2).dln_inc}                                        (2)
      {dln_inc:L(1 2).dln_consump}                                        (2)
                  {dln_inc:_cons}                                         (2)
      {dln_consump:L(1 2).dln_inv}                                        (3)
      {dln_consump:L(1 2).dln_inc}                                        (3)
  {dln_consump:L(1 2).dln_consump}                                        (3)
              {dln_consump:_cons} ~ varmvnormal(3,2,1,(0,0,0),_Omega0)    (3)
                        {Sigma,m} ~ iwishart(3,5,_Sigma0)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_dln_inv.
(2) Parameters are elements of the linear form xb_dln_inc.
(3) Parameters are elements of the linear form xb_dln_consump.
Bayesian vector autoregression                  MCMC iterations  =     12,500
Gibbs sampling                                  Burn-in          =      2,500
                                                MCMC sample size =     10,000
Sample: 1960q4 thru 1978q4                      Number of obs    =         73
                                                Acceptance rate  =          1
                                                Efficiency:  min =      .8113
                                                             avg =      .9438
Log marginal-likelihood =  527.12015                         max =          1
------------------------------------------------------------------------------
             |                                                 Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [95% cred. interval]
-------------+----------------------------------------------------------------
dln_inv      |
     dln_inv |
         L1. |  -.2510453   .1176975   .001153  -.2528143  -.4765424  -.0235274
         L2. |  -.1063315    .116444   .001164  -.1059882  -.3344738   .1229004
             |
     dln_inc |
         L1. |   .2446635   .3498178   .003498   .2500731  -.4573745   .9259674
         L2. |    .095764    .219266   .002193   .0971031  -.3381891   .5251107
             |
 dln_consump |
         L1. |   .3645458   .3744485   .003811   .3680423  -.3646316   1.108422
         L2. |   .1400995      .2298   .002392   .1395888   -.310524   .5901507
             |
       _cons |   .0074369   .0119759   .000123   .0073878  -.0153556   .0307578
------------------------------------------------------------------------------
```

dln_inc						
dln_inv						
L1.	.046923	.0316428	.000316	.0469129	-.0145534	.1098345
L2.	.0505845	.0310234	.000319	.0506224	-.0100996	.1122741
dln_inc						
L1.	-.1526888	.1310382	.00131	-.1527139	-.4111528	.106306
L2.	-.0118679	.1209026	.001225	-.0130416	-.2506488	.2254785
dln_consump						
L1.	.2586053	.1552061	.001552	.259664	-.0444987	.5662822
L2.	-.013651	.1354632	.001407	-.0124392	-.278631	.2532518
_cons	.0170262	.0041118	.000043	.0170605	.0090405	.0250246
dln_consump						
dln_inv						
L1.	.000902	.0253473	.000253	.0008	-.0484133	.0512205
L2.	.0365412	.025467	.000261	.0366538	-.0138045	.0861043
dln_inc						
L1.	.2124569	.1058319	.001058	.2127713	.0019291	.421758
L2.	.2993713	.0940064	.000973	.2987598	.1160611	.4852742
dln_consump						
L1.	-.2757223	.1279485	.001279	-.2756011	-.5238806	-.0256011
L2.	-.0293205	.1199357	.001199	-.0295581	-.2669714	.2049208
_cons	.0146112	.003401	.000035	.0145617	.0080611	.0213525
Sigma_1_1	.0021287	.0003691	3.9e-06	.0020854	.0015264	.0029714
Sigma_2_1	.0000718	.0000664	7.3e-07	.0000693	-.0000518	.0002108
Sigma_3_1	.0001215	.0000558	6.1e-07	.0001178	.0000212	.0002401
Sigma_2_2	.0001363	.0000239	2.6e-07	.0001338	.0000971	.0001908
Sigma_3_2	.0000601	.0000153	1.7e-07	.0000588	.0000341	.0000943
Sigma_3_3	.0000892	.0000155	1.7e-07	.0000875	.0000638	.0001243

In the model summary, the regression coefficients are assigned the `varmvnormal()` prior, in which the prior covariance matrix `_Omega0` is a function of tightness parameters, the same as with the original Minnesota prior.

The inverse-Wishart prior for the error covariance matrix is controlled by the degrees of freedom and the scaling matrix. The default degrees of freedom $\text{df} = K+2 = 3+2 = 5$, and the default scale is `_Scale0`$= (\text{df} - K - 1)$`_Sigma0=_Sigma0`. The low degrees of freedom of the inverse-Wishart prior constrain the `{Sigma,m}` matrix parameter to be close to the scaling matrix `_Sigma0`.

The results are somewhat similar to those using the original Minnesota prior, but the error covariance matrix is now being estimated. Some of the covariance estimates are bounded away from zero based on their estimated CrIs, which suggests that the assumption of no correlation between the error terms imposed by the original Minnesota prior may not be appropriate for these data. Note that these results are closer to the results obtained from the `var` command.

Instead of assuming an inverse-Wishart prior for the error covariance, we can use the multivariate Jeffreys prior.

```
. bayes, minnjeffprior(mean(0,0,0) selftight(1)) rseed(17):
> var dln_inv dln_inc dln_consump if qtr<=tq(1978q4)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
      dln_inv
      dln_inc
  dln_consump ~ mvnormal(3,xb_dln_inv,xb_dln_inc,xb_dln_consump,{Sigma,m})

Priors:
          {dln_inv:L(1 2).dln_inv}                                        (1)
          {dln_inv:L(1 2).dln_inc}                                        (1)
      {dln_inv:L(1 2).dln_consump}                                        (1)
                  {dln_inv:_cons}                                         (1)
          {dln_inc:L(1 2).dln_inv}                                        (2)
          {dln_inc:L(1 2).dln_inc}                                        (2)
      {dln_inc:L(1 2).dln_consump}                                        (2)
                  {dln_inc:_cons}                                         (2)
      {dln_consump:L(1 2).dln_inv}                                        (3)
      {dln_consump:L(1 2).dln_inc}                                        (3)
  {dln_consump:L(1 2).dln_consump}                                        (3)
              {dln_consump:_cons} ~ varmvnormal(3,2,1,(0,0,0),_Omega0)    (3)
                        {Sigma,m} ~ jeffreys(3)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_dln_inv.
(2) Parameters are elements of the linear form xb_dln_inc.
(3) Parameters are elements of the linear form xb_dln_consump.

Bayesian vector autoregression                  MCMC iterations  =     12,500
Gibbs sampling                                  Burn-in          =      2,500
                                                MCMC sample size =     10,000
Sample: 1960q4 thru 1978q4                      Number of obs    =         73
                                                Acceptance rate  =          1
                                                Efficiency:  min =      .8186
                                                             avg =      .9489
Log marginal-likelihood =  535.28175                         max =          1
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
dln_inv						
dln_inv						
L1.	-.2455836	.1221811	.001236	-.2462348	-.4869383	-.0050753
L2.	-.1025647	.1181023	.001181	-.102274	-.3362211	.127451
dln_inc						
L1.	.2298239	.3566309	.003566	.2342159	-.4802715	.9178026
L2.	.0920532	.2204407	.002259	.0922503	-.332021	.5241679
dln_consump						
L1.	.3544481	.3829504	.00383	.3546005	-.4036804	1.108751
L2.	.1308923	.230888	.002307	.130488	-.3293822	.5811411
_cons	.00804	.012356	.000125	.0080513	-.0161679	.0326142

dln_inc						
dln_inv						
L1.	.0467331	.0327457	.000331	.0468285	-.0167597	.1107341
L2.	.0501114	.0318974	.000319	.050056	-.0133188	.1128243
dln_inc						
L1.	-.1506219	.1354065	.001354	-.1523624	-.4147838	.1141846
L2.	-.0144403	.1264436	.001279	-.0141583	-.2584229	.2348877
dln_consump						
L1.	.2593289	.1596995	.001637	.2588021	-.0541279	.5715087
L2.	-.0130386	.1386775	.001409	-.0140483	-.2836371	.2634825
_cons	.0170224	.004309	.000044	.0170312	.0085191	.0255192
dln_consump						
dln_inv						
L1.	.0011214	.026178	.000262	.0010064	-.0490433	.0534858
L2.	.0364058	.0259021	.000259	.036759	-.0159044	.0879265
dln_inc						
L1.	.2110716	.1078844	.001117	.2120819	-.0014118	.4214028
L2.	.2979752	.0981546	.000982	.2974221	.1032472	.4875104
dln_consump						
L1.	-.2786814	.1301325	.001329	-.2805229	-.5309565	-.0213882
L2.	-.0292443	.1226758	.001257	-.0298197	-.270218	.2118989
_cons	.014751	.0035158	.000036	.0147164	.0078041	.021617
Sigma_1_1	.0022852	.000416	4.4e-06	.0022362	.0016076	.0032668
Sigma_2_1	.000077	.0000744	8.1e-07	.0000744	-.0000643	.0002339
Sigma_3_1	.0001311	.0000621	6.8e-07	.0001268	.000018	.0002672
Sigma_2_2	.0001475	.0000269	3.0e-07	.0001445	.0001042	.0002088
Sigma_3_2	.0000659	.0000175	1.9e-07	.0000642	.0000367	.0001061
Sigma_3_3	.0000961	.0000177	1.9e-07	.0000941	.0000676	.0001365

The results are similar to the MVN-inverse-Wishart prior results. The change in the prior for the error covariance did not change its estimates much, which again confirms that the data contribution to the posterior model is weak.

◁

▷ Example 4: Testing Bayesian VAR stability

A VAR model has meaningful interpretation in terms of IRFs and forecast-error variance decompositions only if the time-series process it represents is stable. The default Minnesota prior is based on the assumption that each dependent variable follows a univariate random walk, which is an unstable process. In the absence of strong information about model parameters in the data, the posterior is shrunk more toward the prior, so it is possible that Bayesian posterior estimates may not satisfy the stability assumption even when the frequentist estimates from the VAR model do. Thus, a stability check for a Bayesian VAR is particularly important.

In a frequentist setting, VAR stability can be checked by inspecting the eigenvalues of the companion matrix using the [TS] **varstable** command. In a Bayesian setting, the companion matrix and its eigenvalues are random, so we must inspect their posterior distributions. The Bayesian command for testing stationarity, `bayesvarstable`, reports posterior summaries for the eigenvalue moduli. Stability is declared when all eigenvalues are within the unit circle with high probability.

Let us refit the Bayesian VAR model from example 1 using the default prior options. In addition, we save simulation results in `bvarsex1.dta`, which is required by `bayesvarstable`. Because we already discussed the estimation results, we rerun the command quietly.

```
. quietly bayes, rseed(17) saving(bvarex1):
> var dln_inv dln_inc dln_consump if qtr<=tq(1978q4)
```

Now we call `bayesvarstable` to check the stability condition.

```
. bayesvarstable
Eigenvalue stability condition                  Companion matrix size =     6
                                                MCMC sample size      = 10000
```

Eigenvalue modulus	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
1	.7204885	.0946585	.000947	.7185141	.5401149	.911899
2	.5959965	.1036993	.001037	.6005058	.3817847	.7834288
3	.4271097	.1243872	.001244	.4243446	.2125586	.6563634
4	.2109317	.0790968	.000791	.1972916	.0886465	.3853979
5	.1357284	.0561101	.000561	.1322702	.0390514	.254025
6	.075227	.0499245	.000499	.0688643	.0033007	.1854592

```
Pr(eigenvalues lie inside the unit circle) = 0.9975
```

The companion matrix is of dimension 6 (3 dependent variables times 2 lags), so the output table reports posterior summaries for the moduli of 6 eigenvalues. The eigenvalues are displayed in decreasing order of their moduli. The largest eigenvalue modulus has a posterior mean of 0.72 and is within the unit circle. The command also reports the posterior probability that all eigenvalues lie in the unit circle, 0.9975. The high value of this probability provides confidence that the stability condition is satisfied.

◁

US macroeconomic examples

In the next set of examples, we will use `usmacro.dta`, quarterly macroeconomic data extracted from the Federal Reserve Economic Database that spans from 1954 to 2010.

```
. use https://www.stata-press.com/data/r18/usmacro
(Federal Reserve Economic Data - St. Louis Fed)
. describe
Contains data from https://www.stata-press.com/data/r18/usmacro.dta
 Observations:           226                  Federal Reserve Economic Data -
                                                St. Louis Fed
    Variables:             4                  4 Dec 2022 12:39
```

Variable name	Storage type	Display format	Value label	Variable label
fedfunds	double	%10.0g		Federal funds rate
date	int	%tq		Date (quarters)
inflation	float	%9.0g		Annual rate of inflation
ogap	float	%9.0g		GDP gap

```
Sorted by: date
. tsset
Time variable: date, 1954q3 to 2010q4
        Delta: 1 quarter
```

Observed are three dependent variables: `fedfunds`, for federal funds rate, `inflation`, for annual rate of inflation, and `ogap`, for the GDP output gap, or the difference between actual and potential GDP. The `date` variable registers the quarterly periods.

▷ Example 5: Explaining the Minnesota prior

Consider the following simple VAR(2) model for `usmacro.dta` with dependent variables `ogap` and `inflation`:

$$\texttt{ogap} = a_{11}\texttt{L.ogap} + a_{12}\texttt{L2.ogap} + a_{21}\texttt{L.inflation} + a_{22}\texttt{L2.inflation} + a_0 + u_1$$

$$\texttt{inflation} = b_{11}\texttt{L.ogap} + b_{12}\texttt{L2.ogap} + b_{21}\texttt{L.inflation} + b_{22}\texttt{L2.inflation} + b_0 + u_2$$

In the specification of the original Minnesota prior, (u_1, u_2) is assumed to follow a bivariate normal distribution with 0 means and fixed error covariance $\mathbf{\Sigma_0} = \text{diag}(\widehat{\sigma}_1^2, \widehat{\sigma}_2^2)$, which we define later.

Consider the vector $\boldsymbol{\beta}$ of 8 endogenous regression coefficients a_{ij}'s and b_{ij}'s and 2 exogenous constant terms a_0 and b_0. Specifically, we refer to a_{11}, a_{12}, b_{21}, and b_{22} as endogenous-self-variables lag coefficients (or simply self-variables coefficients); to a_{21}, a_{22}, b_{11}, and b_{12} as endogenous-cross-variables lag coefficients (or simply cross-variables coefficients); and to a_0 and b_0 as "exogenous-variables" coefficients. We used quotes for a_0 and b_0 because, technically, these are constant terms that do not correspond to any exogenous variables. But in what follows, we will treat them as such. In the presence of exogenous variables, we would refer to their coefficients as exogenous-variables coefficients. We also refer to a_{11} and b_{21} as self-variables first-lag coefficients, also know as first own lag coefficients.

The original Minnesota prior for $\boldsymbol{\beta}$ is MVN with 10×1 mean vector $\boldsymbol{\beta}_0$ and 10×10 covariance Ω_0, where $\boldsymbol{\beta}_0$ and Ω_0 are defined in *Original Minnesota prior with known (fixed) error covariance*. $\boldsymbol{\beta}_0$ contains 1 for all self-variables first-lag coefficients and 0 for all the other coefficients. Ω_0 is a diagonal matrix in which diagonals are functions of error variance estimates from individual AR models and tightness parameters. Because the covariance matrix Ω_0 is diagonal, all regression coefficients are assumed uncorrelated a priori.

In our example, the error variance estimates are the ordinary least-squares (OLS) residual variance estimates $\widehat{\sigma}_1^2$ and $\widehat{\sigma}_2^2$ obtained from fitting separately the following two AR models,

$$\texttt{ogap} = c_1\texttt{L.ogap} + c_2\texttt{L2.ogap} + c_3 + e_1$$

$$\texttt{inflation} = d_1\texttt{L.inflation} + d_2\texttt{L2.inflation} + d_3 + e_2$$

where $e_i \sim N(0, \sigma_i^2)$ for $i = 1, 2$.

The Minnesota prior has four control (tightness) parameters: λ_1, λ_2, λ_3, and λ_4, with default values of 0.1, 0.5, 1, and 100. These parameters can be reset using the `selftight()`, `crosstight()`, `lagdecay()`, and `exogtight()` Minnesota prior options, respectively.

Below, we show the default prior distributions for all coefficients. Let l denote the current lag.

Priors for endogenous-self-variables first-lag and second-lag coefficients are

$$a_{11}, b_{21} \sim N(1,\ 0.01)$$

$$a_{12}, b_{22} \sim N(0,\ 0.0025)$$

where $\lambda_1^2/l^{2\lambda_3} = \lambda_1^2 = 0.01$ for $l = 1$ and $\lambda_1^2/l^{2\lambda_3} = 0.0025$ for $l = 2$.

Priors for endogenous-cross-variables first-lag and second-lag coefficients are

$$a_{21} \sim N(0,\ 0.0025\frac{\widehat{\sigma}_1^2}{\widehat{\sigma}_2^2})$$

$$b_{11} \sim N(0,\ 0.0025\frac{\widehat{\sigma}_2^2}{\widehat{\sigma}_1^2})$$

$$a_{22} \sim N(0,\ 0.000625\frac{\widehat{\sigma}_1^2}{\widehat{\sigma}_2^2})$$

$$b_{12} \sim N(0,\ 0.000625\frac{\widehat{\sigma}_2^2}{\widehat{\sigma}_1^2})$$

where $(\lambda_1^2\lambda_2^2)/l^{2\lambda_3} = \lambda_1^2\lambda_2^2 = 0.0025$ for $l = 1$ and $(\lambda_1^2\lambda_2^2)/l^{2\lambda_3} = 0.000625$ for $l = 2$.

Priors for exogenous constant terms are

$$a_0 \sim N(0,\ 100\widehat{\sigma}_1^2)$$

$$b_0 \sim N(0,\ 100\widehat{\sigma}_2^2)$$

where $\lambda_1^2\lambda_4^2 = 100$.

The default prior variances for the coefficients of all endogenous variables are rather small. The Minnesota prior essentially assumes that we have two independent time series each representing a univariate random walk:

$$\texttt{ogap} = \texttt{L1.ogap} + \epsilon_1$$

$$\texttt{inflation} = \texttt{L1.inflation} + \epsilon_2$$

The prior variances shrink as the lag l increases as long as λ_3 is positive. Also, cross-variables variances shrink by a factor of λ_2^2 from self-variables variances. All variances are proportional to λ_1^2. If we increase λ_1 from 0.1, the default, to 1, all variances will increase by a factor of 100.

In the specification of the conjugate Minnesota prior, (u_1, u_2) is assumed to follow a bivariate normal with 0 means and an unknown error covariance $\mathbf{\Sigma}$.

The prior for $\boldsymbol{\beta}$ is conditional on $\mathbf{\Sigma}$. The prior mean stays the same, but the prior covariance matrix Ω_0 is replaced by $\mathbf{\Sigma} \otimes \Phi_0$, where Φ_0 has a structure similar to Ω_0 but of dimension 5 instead of 10,

$$\Phi_0 = \text{diag}\left(\frac{1}{\widehat{\sigma}_1^2}0.01, \frac{1}{\widehat{\sigma}_2^2}0.01, \frac{1}{\widehat{\sigma}_1^2}0.0025, \frac{1}{\widehat{\sigma}_2^2}0.0025, 100\right)$$

where $\lambda_1^2/l^{2\lambda_3} = \lambda_1^2 = 0.01$ for $l = 1$, $\lambda_1^2/l^{2\lambda_3} = 0.0025$ for $l = 2$, and $\lambda_1^2\lambda_4^2 = 100$.

In this case, the prior assumption on $\boldsymbol{\beta}$ implies that the multivariate process consists of two dependent random walks.

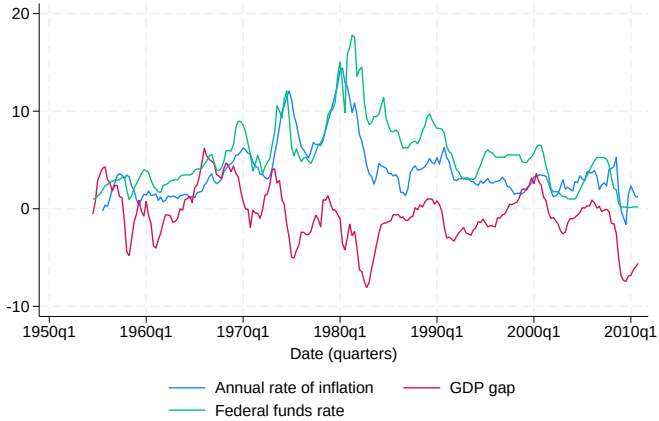
Error covariance $\mathbf{\Sigma}$ is assigned an inverse-Wishart prior with default degrees of freedom $K+2 = 4$, and the default scale matrix S_0 is a diagonal matrix formed by the AR variance estimates. The effect of this prior can be interpreted as a lack of contemporaneous correlation among the error terms.

◁

Example 6: Choosing the number of lags of a VAR model

Consider `usmacro.dta`. Let's look at time series of the three dependent variables.

```
. use https://www.stata-press.com/data/r18/usmacro
(Federal Reserve Economic Data - St. Louis Fed)
. tsline inflation ogap fedfunds
```



Time-series plots suggest a relationship between the three dependent variables that we would like to explore using a Bayesian VAR model.

Our goal is to model the dynamics of the three time series using VAR. We will use the `bayes: var` command to fit a Bayesian VAR model with the default conjugate Minnesota prior for the regression coefficients and error covariance. We will use all observations before the 1st quarter of 2004 to fit the model and leave out the later observations to test the forecasting ability of the model.

An important consideration in specifying the model is choosing the maximum number of lags. An expert in the field may have an optimal choice based on theoretical or empirical knowledge, but for us, it is not immediately clear whether we should use 2, 4, or more lags. In a classical setting, one can use the `varsoc` command to choose the maximum lag. It is not uncommon for `varsoc` to suggest too large of a lag length. For example, if we run `varsoc` on our data using up to 12 lags,

```
. varsoc inflation ogap fedfunds, maxlag(12)
Lag-order selection criteria
   Sample: 1958q3 thru 2010q4                              Number of obs = 210
```

Lag	LL	LR	df	p	FPE	AIC	HQIC	SBIC
0	-1488.6				296.509	14.2057	14.225	14.2535
1	-723.715	1529.8	9	0.000	.221616	7.00681	7.08413	7.19807
2	-689.089	69.252	9	0.000	.173634	6.76275	6.89806	7.09746*
3	-673.171	31.836	9	0.000	.162585	6.69686	6.89017	7.17502
4	-661.806	22.729	9	0.007	.159006	6.67434	6.92564	7.29595
5	-639.015	45.583	9	0.000	.139492	6.543	6.85228	7.30805
6	-619.85	38.329	9	0.000	.126698	6.44619	6.81346*	7.35469
7	-615.967	7.7663	9	0.558	.133135	6.49492	6.92019	7.54687
8	-610.886	10.161	9	0.338	.138349	6.53225	7.0155	7.72765
9	-587.182	47.409	9	0.000	.120437	6.39221	6.93345	7.73105
10	-581.902	10.559	9	0.307	.124996	6.42764	7.02688	7.90993
11	-567.442	28.921*	9	0.001	.118912*	6.37564*	7.03286	8.00137
12	-565.064	4.7562	9	0.855	.126973	6.4387	7.15392	8.20789

```
* optimal lag
Endogenous: inflation ogap fedfunds
 Exogenous: _cons
```

the AIC criterion suggests a maximum lag of 11. A VAR model with 11 lags for our data will have 102 coefficients, which is likely too many given the sample size of 190. The resulting imprecision in the estimates would lead to wide forecast intervals.

From a Bayesian viewpoint, an optimal way to solve this problem is to use Bayesian model comparison. First, we choose a reasonable set of possible lags, $1, \ldots, p_{\max}$. Then, for each lag p, we fit a Bayesian VAR(p) model. Finally, we compare the fitted models using their log-marginal likelihoods. Except the number of lags, all other model specifications, including the choice of priors, stay the same.

In this example, we consider six possible VAR models with lags ranging from 1 to 6. We specify two options with `bayes: var`: `rseed(17)`, for reproducibility, and `saving()` to save the simulation results. The latter is required by `estimates store` to store Bayesian model estimation results. We run the models quietly to suppress lengthy estimation output.

```
. quietly bayes, rseed(17) saving(bvarsim,replace):
> var inflation ogap fedfunds if date < tq(2004q1), lags(1/1)
. estimates store bvar1
. quietly bayes, rseed(17) saving(bvarsim,replace):
> var inflation ogap fedfunds if date < tq(2004q1), lags(1/2)
. estimates store bvar2
. quietly bayes, rseed(17) saving(bvarsim,replace):
> var inflation ogap fedfunds if date < tq(2004q1), lags(1/3)
. estimates store bvar3
. quietly bayes, rseed(17) saving(bvarsim,replace):
> var inflation ogap fedfunds if date < tq(2004q1), lags(1/4)
. estimates store bvar4
. quietly bayes, rseed(17) saving(bvarsim,replace):
> var inflation ogap fedfunds if date < tq(2004q1), lags(1/5)
. estimates store bvar5
. quietly bayes, rseed(17) saving(bvarsim,replace):
> var inflation ogap fedfunds if date < tq(2004q1), lags(1/6)
. estimates store bvar6
```

We compare the models using the bayestest model command. All six models are assumed equally probable a priori, as can be seen from the second column of the output table. The third column shows posterior model probabilities; the model with the highest probability is the best.

```
. bayestest model bvar1 bvar2 bvar3 bvar4 bvar5 bvar6
Bayesian model tests
```

	log(ML)	P(M)	P(M|y)
bvar1	-690.7037	0.1667	0.0000
bvar2	-680.1811	0.1667	0.0000
bvar3	-674.5212	0.1667	0.0065
bvar4	-670.3258	0.1667	0.4313
bvar5	-670.7045	0.1667	0.2953
bvar6	-670.8059	0.1667	0.2669

```
Note: Marginal likelihood (ML) is computed using
      Laplace-Metropolis approximation.
```

The model with four lags has the highest posterior probability, 0.43, and thus four is our choice for the number of lags. Incidentally or not, four lags corresponds to a period of one year.

▷ Example 7: Bayesian VAR(4) model estimation

Continuing with example 6, we proceed with Bayesian estimation of the chosen VAR(4) model. We rerun the model but this time showing the MCMC summary and output tables. The model summary is suppressed for brevity, but as we mentioned in example 6, we use the default conjugate Minnesota prior.

```
. bayes, nomodelsummary rseed(17):
> var inflation ogap fedfunds if date < tq(2004q1), lags(1/4)
Burn-in ...
Simulation ...
```

```
Bayesian vector autoregression                  MCMC iterations  =     12,500
Gibbs sampling                                  Burn-in          =      2,500
                                                MCMC sample size =     10,000
Sample: 1956q3 thru 2003q4                      Number of obs    =        190
                                                Acceptance rate  =          1
                                                Efficiency:  min =      .9322
                                                             avg =       .993
Log marginal-likelihood = -670.32584                         max =          1
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
inflation						
inflation						
L1.	1.107465	.0422849	.000423	1.106848	1.02544	1.192476
L2.	-.064825	.0417594	.000418	-.064536	-.1470882	.0176208
L3.	-.0358872	.0290815	.000291	-.0359867	-.092745	.0210088
L4.	-.0397985	.0215853	.000216	-.0397207	-.0821996	.002274
ogap						
L1.	.0646785	.0294384	.000305	.0644936	.0070243	.1229662
L2.	.0071294	.0267595	.000268	.0072498	-.0444994	.058461
L3.	-.002015	.0187035	.000192	-.0021291	-.038934	.0346847
L4.	-.0088532	.0142951	.000141	-.0089083	-.0366927	.0193774
fedfunds						
L1.	.0770026	.027543	.000275	.076643	.0237776	.1315991
L2.	-.0351476	.0243814	.000244	-.0351349	-.0831241	.0124089
L3.	-.0151671	.0173423	.000173	-.0154901	-.0487873	.0193082
L4.	-.0190271	.0134133	.000134	-.0191324	-.0456025	.0072003
_cons	.1225433	.0832813	.000833	.1225758	-.0433392	.2853939
ogap						
inflation						
L1.	-.068909	.0627925	.000628	-.0683572	-.1934463	.0524915
L2.	.0073091	.0617798	.000609	.0066414	-.1153963	.1276874
L3.	.0098226	.0437754	.000438	.0105327	-.0773841	.0942487
L4.	.0146217	.0325626	.000326	.0147658	-.0498018	.0778098
ogap						
L1.	1.030706	.0443351	.000436	1.030381	.9445329	1.117702
L2.	-.0533506	.0405626	.000406	-.0536868	-.1331328	.0269409
L3.	-.0463432	.028635	.000286	-.0468054	-.1021503	.0103083
L4.	-.0243524	.0215736	.000216	-.0246339	-.0671305	.0178628
fedfunds						
L1.	-.0080148	.0410321	.000404	-.0079538	-.0897528	.0726622
L2.	-.0513393	.0362004	.000362	-.0514847	-.1208578	.0196766
L3.	.0096443	.0264572	.000265	.0092495	-.0416928	.0618986
L4.	.0028706	.0200856	.000201	.002678	-.0362012	.0424353
_cons	.3851112	.1261445	.001261	.3836084	.1334414	.6333448

fedfunds						
inflation						
L1.	.0568126	.0719825	.00072	.0563617	-.0829406	.2008528
L2.	.0568927	.0706982	.000699	.0569514	-.0811303	.1967728
L3.	-.0026048	.0495878	.000474	-.0023296	-.1001453	.09392
L4.	-.0159998	.0369476	.000375	-.0163655	-.0877556	.0563861
ogap						
L1.	.1873653	.0495204	.000498	.1873384	.0899816	.2850046
L2.	-.0544593	.045749	.000465	-.055174	-.1438389	.035413
L3.	-.0485134	.0324919	.000335	-.048869	-.1120501	.0148947
L4.	-.0327431	.0245286	.000245	-.0324051	-.0807114	.0156984
fedfunds						
L1.	.9623752	.0472236	.000472	.9622282	.8696618	1.054146
L2.	-.0728725	.0414158	.000414	-.0731102	-.1538312	.0082934
L3.	.0146377	.0293537	.000294	.0143481	-.0419335	.072309
L4.	.0018861	.0228329	.000228	.0021041	-.0430797	.0462406
_cons	.1931161	.1433129	.001433	.1950842	-.0912408	.4717853
Sigma_1_1	.2873009	.0293728	.000297	.2853721	.2349716	.3493519
Sigma_2_1	.0281781	.0315254	.000315	.0276486	-.0345647	.0912571
Sigma_3_1	.1480748	.0372496	.000372	.1468518	.0777631	.2251876
Sigma_2_2	.6575456	.0671182	.000684	.6530136	.5395734	.8029292
Sigma_3_2	.2398338	.0559347	.000559	.238127	.1357633	.3561841
Sigma_3_3	.8371554	.0857785	.000858	.8298623	.6868505	1.024522

The Gibbs sampling used to simulate the posterior distribution has high efficiency of 99% on average and the perfect acceptance rate of 1. There is no indication of convergence problems.

There are 39 regression coefficients in the model, which would be difficult to interpret directly. The posterior estimates for the error covariance matrix `{Sigma,m}` suggest a positive correlation between `fedfunds` and `inflation` and `fedfunds` and `ogdp`; see the estimates for `{Sigma_3_1}` and `{Sigma_3_2}`.

Because we did not use the `saving()` option with `bayes: var`, the simulation results are saved in a temporary dataset. If you plan to use one of the postestimation commands such as `bayesirf` or `bayesfcast`, you need to save the simulation results to a permanent dataset. We can do this by using the `saving()` option on replay.

```
. bayes, saving(bvarex2)
note: file bvarex2.dta saved.
```

Before continuing with postestimation analysis, let's check the stability condition of the model using the `bayesvarstable` command.

```
. bayesvarstable
Eigenvalue stability condition                  Companion matrix size =    12
                                                MCMC sample size      = 10000
```

Eigenvalue modulus	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
1	.9473457	.0199198	.000199	.9481282	.9057116	.9838371
2	.9417123	.0257058	.000257	.9453142	.877582	.9811621
3	.8184194	.0716288	.000716	.8274233	.6763741	.9322606
4	.5930213	.0930861	.000931	.5836551	.4256008	.7733104
5	.4859573	.0896516	.000897	.4866775	.330644	.6554575
6	.3659255	.0417669	.000418	.3635287	.291461	.459251
7	.3499339	.0365851	.000366	.3496959	.2767796	.4214287
8	.3155561	.0383687	.000384	.3173136	.2348504	.3856269
9	.3014183	.0396995	.000397	.3038818	.2177103	.3736035
10	.2670156	.0479518	.00048	.2717858	.1582521	.3475958
11	.2361436	.0556598	.000557	.2414199	.1135724	.329785
12	.1887299	.0805818	.000806	.2036124	.0151749	.3102756

```
Pr(eigenvalues lie inside the unit circle) = 0.9977
```

The command reports that the companion matrix of our model is of size 12 (three response variables times four lags) and thus reports posterior summaries for the moduli of 12 eigenvalues. The posterior probability that all eigenvalues lie in the unit circle is estimated to be essentially 1, so the stability condition is satisfied.

◁

The main postestimation tools for interpreting VAR models are IRFs and forecasting, which we illustrate in the following examples.

▷ Example 8: IRFs

IRFs are commonly used to summarize a VAR model. IRFs measure the effect of a shock in one variable, also called an impulse variable, on a given response variable. The effect of the shock on the response variable is traced out over a predefined number of future steps. We compute a number of IRF statistics associated with our model using the `bayesirf` command, whose syntax is similar to the frequentist `irf` command. For computational details, see *Methods and formulas* of [BAYES] **bayesirf create**.

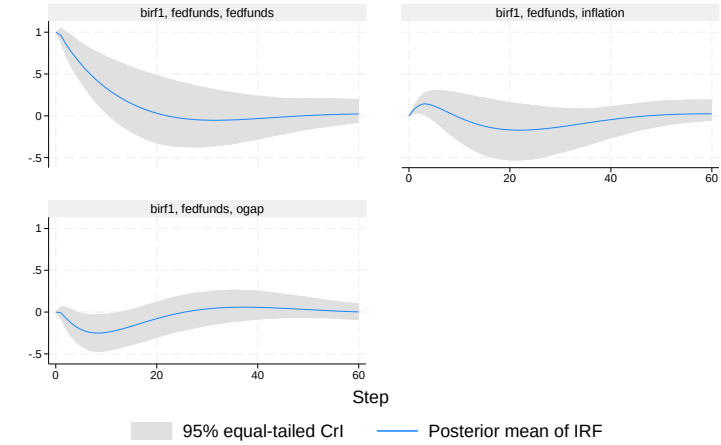
The `bayesirf create` command computes IRF results and stores them in a dataset with a special structure and with the `.irf` extension. One `.irf` dataset may contain several sets of IRF results.

Continuing with example 7, let's compute the effect of shocks for up to 15 years (60 quarter periods) into the future. We name the set of results `birf1` and save them in `birfex2.irf`.

```
. bayesirf create birf1, step(60) set(birfex2)
(file birfex2.irf created)
(file birfex2.irf now active)
(file birfex2.irf updated)
```

It is easier to visualize the effect of a shock in one response variable on all other response variables and itself by using the `bayesirf graph` command. The command draws the posterior mean estimates of IRF coefficients along with 95% CrIs. Let's inspect the effect of shock on `fedfunds`. Shocks of interests are specified using the `impulse()` option.

```
. bayesirf graph irf, impulse(fedfunds)
```



Graphs by irfname, impulse variable, and response variable

IRFs are obtained by setting the error vector in the likelihood model to (0,0,1) (1 for `fedfunds` and 0 otherwise) at step 0 and propagating this unit vector in time according to the VAR equations. For example, the response of `inflation` (second graph) starts from 0 at step 0, slightly increases during the first year, then slowly decreases during the next 4 years, and finally converges to a small positive value at the end of our 15-year period. According to the third graph, after a monetary shock from the Federal Reserve, the output gap decreases during the first two years, then slowly increases for the following eight years, and finally stabilizes at a small positive value. Notably, the shock effect on all response variables reach equilibrium after about 12 years.

We can examine IRF coefficients in more detail by listing them in a table using `bayesirf table`. For example, let's inspect how the output gap is responding to a shock in federal funds in the first two years. This particular choice is made using the `response()`, `impulse()`, and `step()` options.

```
. bayesirf table irf, response(ogap) impulse(fedfunds) step(7)
Results from birf1
```

Step	(1) irf	(1) Lower	(1) Upper
0	0	0	0
1	-.008015	-.089753	.072662
2	-.072428	-.205354	.059264
3	-.128667	-.296316	.039592
4	-.174391	-.361456	.009988
5	-.208873	-.409928	-.009742
6	-.232076	-.444489	-.021792
7	-.245563	-.466458	-.028681

```
Posterior means reported.
95% equal-tailed credible lower and upper bounds reported.
(1) irfname = birf1, impulse = fedfunds, and response = ogap.
```

The bayesirf table command reports posterior mean estimates (first column), lower 95% credible limits (second column), and upper 95% credible limits (third column). We see that a 1% increase in fedfunds leads to about a 0.01 units decrease in ogap after 1 quarter and to 0.25 units decrease in ogap after 8 quarters (2 years). That is, in the short term, an increase in federal spending increases the gap between real and potential GDP.

The regular IRF functions do not account for the fact that the shocks in different impulse variables are generally not independent. For example, in our case, shocks in federal funds and inflation are likely dependent. A better representation of the dynamics between variables is provided by the so-called orthogonalized IRFs (OIRFs), referred to as oirf in bayesirf commands. The latter depends on the preset causal ordering of the impulse variables, as specified using the order() option. The default order is the order in which the variables are listed in the bayes: var command specification.

For example, let's examine the following causal order: inflation → fedfunds → ogap. In other words, let's assume that fedfunds has no immediate effect on inflation and that ogap has no immediate effect on inflation and fedfunds.

```
. bayesirf create birf2, step(60) set(birfex2) order(inflation fedfunds ogap)
(file birfex2.irf now active)
(file birfex2.irf updated)
```

The new IRF statistics are saved as birf2 in birfex2.irf.

We can now summarize oirf statistics of ogap response to impulse in the third equation, referred to as fedfunds, corresponding to the new order we have specified.

```
. bayesirf table oirf, irf(birf2) response(ogap) impulse(fedfunds) step(7)
Results from birf2
```

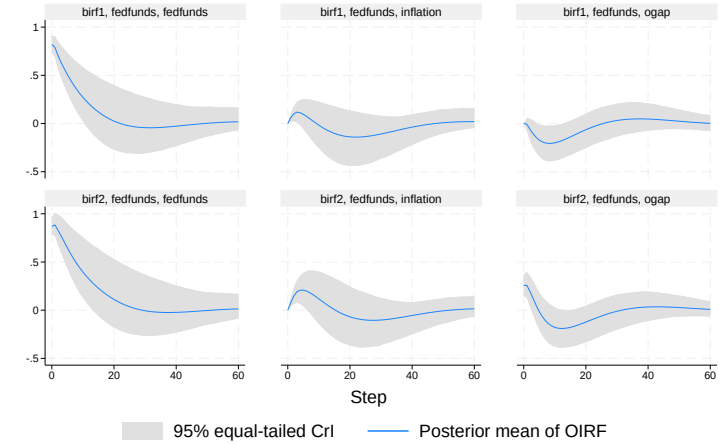
Step	(1) oirf	(1) Lower	(1) Upper
0	.257325	.148406	.370283
1	.258308	.128963	.395361
2	.195725	.041816	.35614
3	.123306	-.047116	.30244
4	.050238	-.130222	.241047
5	-.014137	-.201699	.186256
6	-.067159	-.261451	.13775
7	-.109004	-.309117	.103761

```
Posterior means reported.
95% equal-tailed credible lower and upper bounds reported.
(1) irfname = birf2, impulse = fedfunds, and response = ogap.
```

We observe notable differences between oirf and irf estimates reported above. A shock in the fedfunds equation now starts at 0.26 at step 0 and initially has little effect on closing the positive output gap, but after 4 steps (about a year), ogap becomes negative. As in the case with irf values, we see that a shock in federal funds has a negative effect on the output gap in a short term. OIRFs have the benefit of accounting for the correlation between inflation and fedfunds.

The interpretation of OIRFs very much depends on the causal order of response variables. Choosing an order can be difficult when there is no obvious choice based on expert knowledge. Next, for easier comparison, we show how to use bayesirf graph to plot the OIRFs from both birf1 and birf2, which differ only in the response variable ordering.

```
. bayesirf graph oirf, impulse(fedfunds)
```

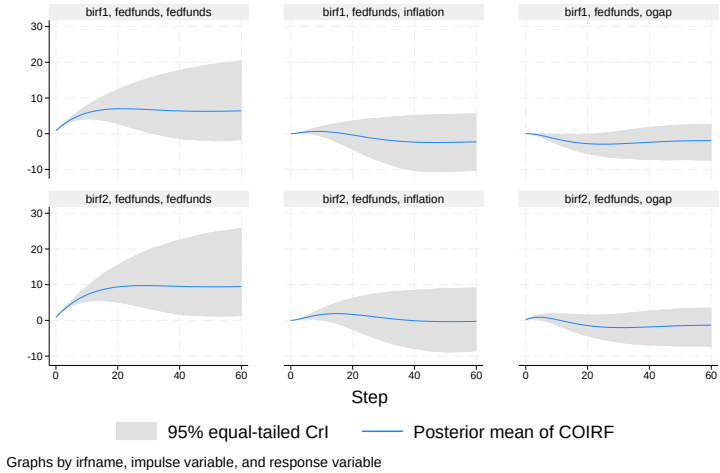


Graphs by irfname, impulse variable, and response variable

The first row shows OIRFs for the original order, `inflation` → `ogap` → `fedfunds`, and the second row shows results for the new order, `inflation` → `fedfunds` → `ogap`. As we remarked above, there are differences between the OIRF results corresponding to different orderings.

Another way to follow the dynamics in ogap is to inspect the cumulative OIRF, coirf. Cumulative IRF statistics accumulate the shock effects over time. The following graph compares the cumulative OIRFs of birf1 and birf2 to a shock in fedfunds.

```
. bayesirf graph coirf, impulse(fedfunds)
```



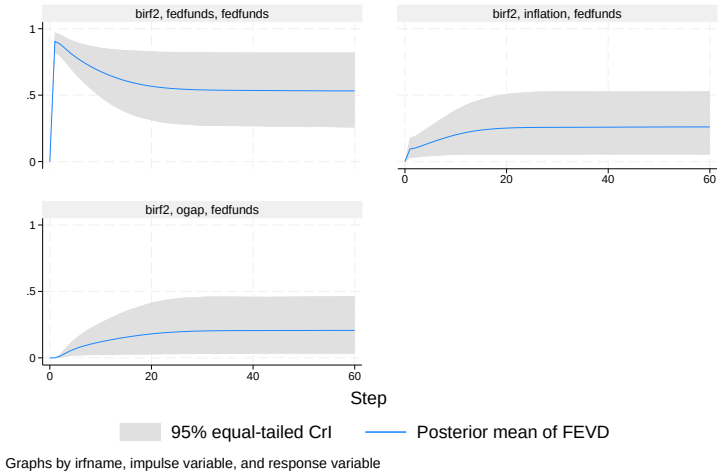
Graphs by irfname, impulse variable, and response variable

All two shock effects reach equilibrium after about 10 years. In the long term, a monetary shock reduces inflation and decreases the output gap.

Another set of IRFs that are useful for interpreting VAR models is the forecast error variance decompositions, or FEVDs. FEVDs measure the contribution, in terms of variability, of impulse variables to the forecast error in response variables. FEVDs, similar to OIRFs, depend on the causal ordering of the response variables.

For illustration, let's inspect the FEVDs of the response variable `fedfunds` for the `birf2` results corresponding to the `inflation` → `fedfunds` → `ogap` order. First, we show FEVD graphs.

```
. bayesirf graph fevd, irf(birf2) response(fedfunds)
```



Graphs by irfname, impulse variable, and response variable

In the long term, half the forecast error of `fedfunds` is contributed by `fedfunds` itself, whereas `inflation` and `ogap` contribute by a quarter each.

A table of FEVD estimates gives us more details.

```
. bayesirf table fevd, irf(birf2) response(fedfunds) step(7)
Results from birf2
```

Step	(1) fevd	(1) Lower	(1) Upper
0	0	0	0
1	.095083	.027875	.180163
2	.102093	.029869	.192633
3	.114495	.034531	.216095
4	.128495	.038329	.242878
5	.142093	.041094	.268065
6	.155334	.043475	.293326
7	.16808	.045986	.318506

Step	(2) fevd	(2) Lower	(2) Upper
0	0	0	0
1	.904917	.819837	.972125
2	.885277	.794215	.957829
3	.852453	.751346	.936377
4	.818721	.702946	.917391
5	.789353	.659076	.902321
6	.763024	.619474	.890185
7	.739026	.582641	.879954

Step	(3) fevd	(3) Lower	(3) Upper
0	0	0	0
1	0	0	0
2	.01263	.002624	.027988
3	.033052	.00823	.069683
4	.052784	.013287	.111021
5	.068554	.016546	.144177
6	.081642	.018741	.174098
7	.092895	.020159	.199897

```
Posterior means reported.
95% equal-tailed credible lower and upper bounds reported.
(1) irfname = birf2, impulse = inflation, and response = fedfunds.
(2) irfname = birf2, impulse = fedfunds, and response = fedfunds.
(3) irfname = birf2, impulse = ogap, and response = fedfunds.
```

The command output contains three tables, one for each impulse. At step 1, which corresponds to one-step-ahead predictions, FEVD posterior mean estimates are about 0.095 for `inflation`, 0.905 for `fedfunds`, and 0 for `ogap` due to the imposed order. The sum of FEVDs across impulses is 1. Most of the forecast error in `fedfunds` is because of the variability in `fedfunds` itself. At step 8, however, FEVD estimates become 0.18 for `inflation`, 0.72 for `fedfunds`, and 0.10 for `ogap`. The predominant effect of its own variability in FEVD estimates is an indirect effect of the Minnesota prior that shrinks self-variables first-lag coefficients to 1 and all others to 0.

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Example 9: Forecasting

Bayesian dynamic forecasting is a special case of Bayesian predictions that uses posterior predictive distributions conditional on time to predict a response variable at multiple steps into the future; see *Methods and formulas* of [BAYES] **bayesfcast compute**.

`bayesfcast compute` is the Bayesian counterpart of the [TS] **fcast compute** command, which is used for Bayesian forecasting after the `bayes: var` command.

Let's compute dynamic forecasts starting with the first quarter of 2004 until the end of the observed time frame, or 28 quarter periods ahead.

```
. bayesfcast compute b_, step(28) dynamic(tq(2004q1))
```

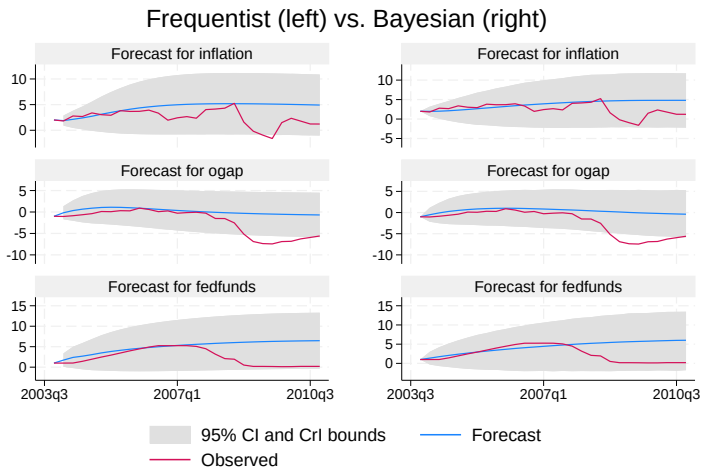
By default, `bayesfcast compute` computes and saves in the current dataset the posterior mean estimates of the predicted response variables along with the 95% credible intervals. The new variables are prefixed with `b_`.

It would be interesting to compare the Bayesian forecast results with the frequentist ones obtained by `fcast compute` after fitting the `var` command on the same model.

```
. quietly var inflation ogap fedfunds if date < tq(2004q1), lags(1/4)
. fcast compute f_, step(28) dynamic(tq(2004q1))
```

We can use the `bayesfcast graph` command to plot the observed and forecasted values along with their 95% CIs for the frequentist and 95% CrIs for the Bayesian results. Frequentist results are on the left, and Bayesian results are on the right.

```
. bayesfcast graph f_inflation b_inflation f_ogap b_ogap f_fedfunds b_fedfunds,
> observed byopts(rows(3) title("Frequentist (left) vs. Bayesian (right)"))
> legend(label(1 "95% CI and CrI bounds"))
```



In the forecast period before 2008, the Bayesian forecasts seem to fit the observed response variables slightly better. The 95% CrIs include the observed values most of the time, except for `ogap` at the second half of 2008 during the great recession. We should not expect a VAR model to forecast extreme events such as recessions.

Example 10: One-step-ahead Bayesian predictions

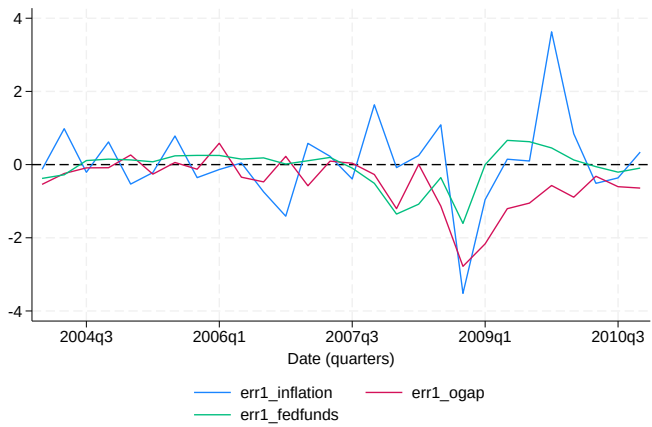
One-step-ahead Bayesian predictions are a special case of Bayesian forecasts, where current observed responses are used to make predictions for the next time period. In contrast to dynamic predictions, one-step-ahead predictions can be computed using the general postestimation command for Bayesian predictions, `bayespredict`.

For illustration, let's compute predicted posterior means for the three responses starting with the first quarter of 2004 and save the results as new variables `pr1_inflation`, `pr1_ogap`, and `pr1_fedfunds`.

```
. bayespredict pr1_inflation pr1_ogap pr1_fedfunds if date>=tq(2004q1), mean
Computing predictions ...
```

Because these are one-step-ahead predictions, we expect them to be fairly close to the observed responses, much more so than dynamic forecasts with multiple prediction steps ahead. To verify that, let's look at the prediction errors computed as the difference between the observed and predicted responses and plot them as time series.

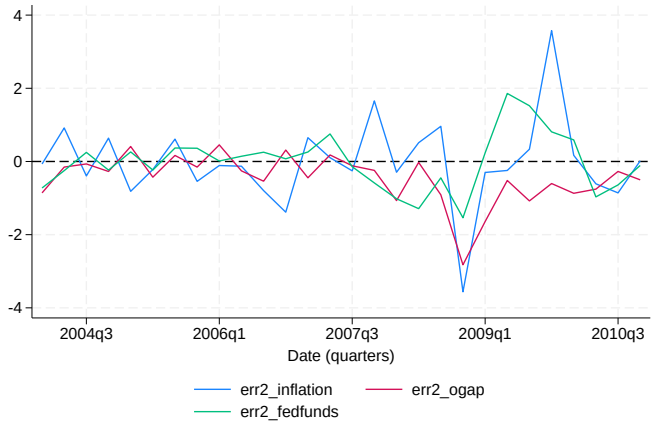
```
. generate err1_inflation = inflation - pr1_inflation
(198 missing values generated)
. generate err1_ogap = ogap - pr1_ogap
(198 missing values generated)
. generate err1_fedfunds = fedfunds - pr1_fedfunds
(198 missing values generated)
. tsline err1_inflation err1_ogap err1_fedfunds if date>=tq(2004q1), yline(0)
```



Recall that the measurement units in this example are percentage growth rates for inflation and federal funds and percentage deviation from trend for the output gap. We see that one-step-ahead predictions perform well right before the beginning of the great recession in 2008, within a margin of 1 unit; that is, prediction errors are within 1 percentage point of realized values. After that, all three errors become negative for a period of time, which means they commit overprediction, but then stabilize again at the end of 2009. The predictions for `inflation` are particularly off, overpredicting before the second quarter of 2009 and underpredicting after that until the end of 2009. A logical conclusion is that our model, fit on the data before the great recession, cannot capture the macroeconomic disruption of 2008 and 2009.

Finally, for those of you interested in comparing Bayesian and classical one-step-ahead predictions, we show the computation for the latter.

```
. quietly var inflation ogap fedfunds if date < tq(2004q1), lags(1/4)
. predict pr2_inflation, equation(inflation)
(option xb assumed; fitted values)
(8 missing values generated)
. predict pr2_ogap, equation(ogap)
(option xb assumed; fitted values)
(8 missing values generated)
. predict pr2_fedfunds, equation(fedfunds)
(option xb assumed; fitted values)
(8 missing values generated)
. generate err2_inflation = inflation - pr2_inflation
(8 missing values generated)
. generate err2_ogap = ogap - pr2_ogap
(8 missing values generated)
. generate err2_fedfunds = fedfunds - pr2_fedfunds
(8 missing values generated)
. tsline err2_inflation err2_ogap err2_fedfunds if date>=tq(2004q1), yline(0)
```



Bayesian and classical one-step-ahead predictions are similar, both failing to follow the dynamics of 2008–2009. However, Bayesian predictions for federal funds appear to be more precise.

◁

Stored results

See *Stored results* in [BAYES] **bayes**. In addition, `bayes: var` stores the following in `e()`:

Scalars

`e(tmin)`	first time period in sample
`e(tmax)`	maximum time
`e(mlag)`	highest lag in VAR
`e(selftight)`	self-variables tightness parameter in Minnesota priors
`e(crosstight)`	cross-variables tightness parameter in Minnesota priors (not with conjugate Minnesota prior)
`e(lagdecay)`	lag-decay parameter in Minnesota priors
`e(exogtight)`	exogenous-variables tightness parameter in Minnesota priors
`e(dfcov)`	degrees of freedom of inverse-Wishart prior

Macros

`e(cmdname)`	`var`
`e(prefix)`	`bayes`
`e(command)`	`var` command specification
`e(varprior)`	prior model for VAR coefficients and error covariance
`e(endog)`	names of endogenous variables
`e(exog)`	names of exogenous variables, and their lags, if specified
`e(exogvars)`	names of exogenous variables, if specified
`e(lags)`	lags in model
`e(exlags)`	lags of exogenous variables in model, if specified
`e(timevar)`	time variable specified in `tsset`
`e(tsfmt)`	format for the current time variable

Matrices

`e(exlagsm)`	matrix mapping lags to exogenous variables (with `exog()`)
`e(phi)`	covariance product matrix $\tilde{\Phi}_0$ for conjugate Minnesota prior
`e(arcov)`	AR covariance matrix (with `arcov`)
`e(varcov)`	VAR covariance matrix (with `varcov`)
`e(mvnmean)`	mean vector of MVN prior
`e(mvncov)`	covariance matrix of MVN prior (with `mvniwishprior()` or `mvnjeffprior()`)
`e(scalecov)`	scale matrix of inverse-Wishart prior

Methods and formulas

Methods and formulas are presented under the following headings:

VAR model specification
Original Minnesota prior with known (fixed) error covariance
Conjugate Minnesota prior for VAR model with unknown error covariance
MVN-inverse Wishart prior
MVN-diffuse (normal-Jeffreys) prior

VAR model specification

Let $\mathbf{y}_t$ be a $K \times 1$ vector of endogenous (dependent) variables at time t for $t = 1, \ldots, T$ and $\mathbf{x}_t$ be a $m \times 1$ vector of exogenous regressors including the constant terms.

A p-order VAR model, VAR(p), can be defined according to Lütkepohl (2005) as

$$\mathbf{y}_t = \mathbf{A}_1\mathbf{y}_{t-1} + \cdots + \mathbf{A}_p\mathbf{y}_{t-p} + \mathbf{C}\mathbf{x}_t + \mathbf{u}_t, \;\; \mathbf{u}_t \sim N(\mathbf{0}, \mathbf{\Sigma})$$

where p is the number of lags;

$\mathbf{A}_l = (a_{ij}^l)$ are $K \times K$ matrices of unknown endogenous-variables lag coefficients ($l = 1, \ldots, p$);

$\mathbf{C} = (c_{is})$ is a $K \times m$ matrix of exogenous-variables coefficients; and

$\mathbf{u}_t$ is a $K \times 1$ vector of error terms with a $K \times K$ covariance matrix $\mathbf{\Sigma}$.

A VAR(p) model can be written in a more compact form as

$$\mathbf{Y} = \mathbf{XB} + \mathbf{U}$$

where

$$\mathbf{Y} = \begin{pmatrix} \mathbf{y}_1' \\ \vdots \\ \mathbf{y}_T' \end{pmatrix}, \mathbf{X} = \begin{pmatrix} \mathbf{y}_0' \ \mathbf{y}_{-1}' \ \cdots \ \mathbf{y}_{1-p}' \ \mathbf{x}_1' \\ \vdots \\ \mathbf{y}_{T-1}' \ \mathbf{y}_{T-2}' \ \cdots \ \mathbf{y}_{T-p}' \ \mathbf{x}_T' \end{pmatrix}, \mathbf{B} = \begin{pmatrix} \mathbf{A}_1' \\ \vdots \\ \mathbf{A}_p' \\ \mathbf{C}' \end{pmatrix}, \mathbf{U} = \begin{pmatrix} \mathbf{u}_1' \\ \vdots \\ \mathbf{u}_T' \end{pmatrix}$$

$\mathbf{Y}$ is a $T \times k$ matrix, $\mathbf{X}$ is a $T \times (Kp + m)$ matrix, $\mathbf{B}$ is a $(Kp + m) \times K$ matrix of all coefficients, and $\mathbf{U}$ is a $T \times K$ matrix.

The OLS estimates of $\mathbf{B}$ and $\mathbf{\Sigma}$ are

$$\widehat{\mathbf{B}} = (\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{Y}$$

$$\widehat{\mathbf{\Sigma}}_{\text{OLS}} = \widehat{\mathbf{U}}'\widehat{\mathbf{U}}/(T - Kp - m - 1), \ \widehat{\mathbf{U}} = \mathbf{Y} - \mathbf{X}\widehat{\mathbf{B}} \tag{1}$$

Vectorizing the above matrix equation, we obtain

$$\mathbf{y} = \mathbf{X}^{\star}\boldsymbol{\beta} + \mathbf{u}$$

where $\mathbf{y} = \text{vec}(\mathbf{Y})$ is $KT \times 1$ vector, $\mathbf{X}^{\star} = I_K \otimes \mathbf{X}$ is a $KT \times K(Kp + m)$ matrix ($\otimes$ is the Kronecker product and I_K is a $K \times K$ identity matrix), $\boldsymbol{\beta} = \text{vec}(\mathbf{B})$ is a $K(Kp + m) \times 1$ vector of all coefficients, and $\mathbf{u} = \text{vec}(\mathbf{U})$ is a $KT \times 1$ error vector with a $KT \times KT$ covariance matrix $\mathbf{\Sigma}^{\star} = \mathbf{\Sigma} \otimes I_T$.

An essential component of every Bayesian VAR model is specifying a suitable prior for the vector of coefficients $\boldsymbol{\beta}$. In what follows, we will describe several commonly used priors, all based on a so-called Minnesota prior. But before we continue, let's define components that are used by all of these priors.

Consider a univariate AR(p) model for each outcome $k = 1, \ldots, K$,

$$y_{k,t} = a_1 y_{k,t-1} + \cdots + a_p y_{k,t-p} + a_0 + e_{k,t} \tag{2}$$

where $e_{k,t} \sim N(0, \sigma_k^2)$. All priors considered below use the OLS estimate, $\widehat{\sigma}_k^2$, of σ_k^2. Some of the priors also use a diagonal covariance estimate formed by K error-variance estimates from separate AR(p) models: $\widehat{\mathbf{\Sigma}}_{\text{diag}} = \text{diag}(\widehat{\sigma}_1^2, \ldots, \widehat{\sigma}_K^2)$.

Original Minnesota prior with known (fixed) error covariance

The original Bayesian VAR model with a Minnesota prior (Litterman 1980, 1986) assumes that the covariance matrix of the error vectors $\mathbf{u}_t$ is known, $\mathbf{\Sigma} = \mathbf{\Sigma}_0$; that is,

$$\mathbf{u} \sim N(\mathbf{0}, \mathbf{\Sigma}_0 \otimes I_T)$$

The original formulation (suboption `arcov` in *minnopts*) used a diagonal matrix with the estimated error variances from K separate AR models (2) on the diagonal as a covariance estimate, $\boldsymbol{\Sigma}_0 = \widehat{\boldsymbol{\Sigma}}_{\text{diag}} = \text{diag}(\widehat{\sigma}_1^2, \ldots, \widehat{\sigma}_K^2)$. Litterman thus proposed to estimate the VAR model equation by equation, rather than as a system of equations, to reduce the computational burden, which at the time was a serious problem. Another formulation (suboption `varcov` in *minnopts*) used the OLS estimate of the covariance matrix from the VAR model, $\boldsymbol{\Sigma}_0 = \widehat{\boldsymbol{\Sigma}}_{\text{OLS}}$, defined in (1).

This prior is implemented by the `minnfixedcovprior` option of `bayes: var`, but it is not the default prior. The default prior is the conjugate Minnesota prior (option `minnconjprior`) described in the next section, which uses a less restrictive prior covariance. But we describe the original Minnesota prior first because the conjugate Minnesota prior is its extension.

The Minnesota prior for coefficient vector $\boldsymbol{\beta}$ is an MVN prior,

$$\boldsymbol{\beta} \sim N(\boldsymbol{\beta}_0, \boldsymbol{\Omega}_0)$$

where a $KT \times 1$ vector $\boldsymbol{\beta}_0$ and a $KT \times KT$ matrix $\boldsymbol{\Omega}_0$ are defined in a way that accounts for the special time-series structure of the VAR(p) model, which we describe next.

The regression vector $\boldsymbol{\beta}$ is formed by the endogenous-variables lag coefficients a_{ij}^l ($l = 1, \ldots, p$ and $i, j = 1, \ldots, K$) and exogenous-variables coefficients c_{is} ($i = 1, \ldots, K$ and $s = 1, \ldots, m$). The Minnesota priors assumes that expected values for all coefficients are zero, except for the self-variables first-lag coefficients; that is,

$$E(a_{ij}^l) = \delta_{1l}\delta_{ij} \text{ and } E(c_{is}) = 0$$

where $\delta_{ij} = 1$ if $i = j$ and 0 otherwise, so the prior mean vector $\boldsymbol{\beta}_0$ is a $K(Kp + m) \times 1$ vector of 0s and 1s, with 1s corresponding to the self-variables first-lag coefficients.

The original Minnesota prior assumes that there is no correlation between the coefficients of $\boldsymbol{\beta}$. The Minnesota covariance $\boldsymbol{\Omega}_0$ is thus a diagonal matrix, its diagonal formed by the prior variances $\sigma^2_{a_{ij}^l}$ for the endogenous-variables lag coefficients and $\sigma^2_{c_{is}}$ for the exogenous-variables coefficients. The prior variances are based on the OLS estimates of error variances, $\widehat{\sigma}_k^2$'s, and are defined below.

For endogenous-self-variables lag coefficients, the prior variances are

$$\sigma^2_{a_{ii}^l} = \left(\frac{\lambda_1}{l^{\lambda_3}}\right)^2$$

For endogenous-cross-variables lag coefficients ($i \neq j$), the prior variances are

$$\sigma^2_{a_{ij}^l} = \left(\frac{\widehat{\sigma}_i^2}{\widehat{\sigma}_j^2}\right)\left(\frac{\lambda_1\lambda_2}{l^{\lambda_3}}\right)^2$$

For exogenous-variables coefficients, the prior variances are

$$\sigma^2_{c_{is}} = \widehat{\sigma}_i^2(\lambda_1\lambda_4)^2$$

In the above formulas, λ_1 controls the tightness of the prior variance for self-variables lag coefficients and can be specified in the `selftight()` suboption of the Minnesota prior options, *minnopts*; λ_2 controls the cross-variables lag coefficients spread and can be specified in the `crosstight()` suboption; λ_3 controls the lag attenuation and can be specified in the `lagdecay()` suboption (the higher the lag, the tighter the prior variances); and λ_4 controls the prior variance of the exogenous-variables coefficients and can be specified in the `exogtight()` option. Default values for these control parameters are $\lambda_1 = 0.1$, $\lambda_2 = 0.5$, $\lambda_3 = 1$, and $\lambda_4 = 100$.

The prior mean $\boldsymbol{\beta}_0$ and diagonal covariance matrix $\boldsymbol{\Omega}_0$ described above define the original Minnesota prior, which is available by specifying the `minnfixedcovprior` option with `bayes: var`. You can customize this prior by specifying the `minnfixedcovprior(`*fixcovopts*`)` option.

In the model-summary output of `bayes: var`, we refer to the defaults $\boldsymbol{\Sigma}_0$ and $\boldsymbol{\beta}_0$ as `_Sigma0` and `_b0`, respectively. $\boldsymbol{\Omega}_0$ is viewed as a function of `_Sigma0` and prior control parameters λ's.

Conjugate Minnesota prior for VAR model with unknown error covariance

Another framework of Bayesian VAR models assumes that error vectors $\mathbf{u}_t$ have an unknown covariance matrix $\boldsymbol{\Sigma}$. In this case, $\mathbf{u} \sim N(\mathbf{0}, \boldsymbol{\Sigma} \otimes I_T)$.

Karlsson (2013) proposed a prior for $\boldsymbol{\beta}$ with the prior covariance having a similar form to the covariance matrix $\boldsymbol{\Sigma}$. Specifically, the author defined the prior covariance as a product of $\boldsymbol{\Sigma}$ and another covariance matrix, $\boldsymbol{\Phi}_0$, which we refer to as a Minnesota factor covariance,

$$\boldsymbol{\beta} \sim N(\boldsymbol{\beta}_0, \boldsymbol{\Sigma} \otimes \boldsymbol{\Phi}_0)$$

The prior mean vector $\boldsymbol{\beta}_0$ is the same as in the original Minnesota prior, and $\boldsymbol{\Phi}_0$ is a fixed $(Kp+m) \times (Kp+m)$ covariance matrix as defined below.

$\boldsymbol{\Phi}_0 = \text{diag}\left(\left\{\sigma^2_{a_j^l}\right\}_{j=1,l=1}^{K,p}, \left\{\sigma^2_{c_s}\right\}_{s=1}^{m}\right)$ is set to be a diagonal matrix similar to the Minnesota covariance $\boldsymbol{\Omega}_0$ but of a lower dimension $(Kp+m) \times (Kp+m)$ compared with $KT \times KT$. The elements of $\boldsymbol{\Phi}_0$ are defined below for $l = 1, \ldots, p$, $j = 1 \ldots, K$, and $s = 1, \ldots, m$.

For endogenous-variables lag coefficients,

$$\sigma^2_{a_j^l} = \left(\frac{1}{\widehat{\sigma}^2_j}\right)\left(\frac{\lambda_1}{l^{\lambda_3}}\right)^2$$

And for exogenous-variables coefficients,

$$\sigma^2_{c_s} = (\lambda_1 \lambda_4)^2$$

In the above formulas, λ_1, λ_3, and λ_4 have the same interpretation as in the original Minnesota prior. In this formulation, λ_2 is not used because there is no distinction between the self- and cross-variables.

The covariance parameter $\boldsymbol{\Sigma}$ has an inverse-Wishart prior with a scale matrix $\mathbf{S}_0$ and degrees of freedom α_0:

$$\boldsymbol{\Sigma} \sim \text{InvWishart}(\alpha_0, \mathbf{S}_0)$$

You can specify α_0 in the `df()` suboption and $\mathbf{S}_0$ in the `scale()` suboption of the `minnconjprior()` option. The default values are $\alpha_0 = K + 2$, the minimum possible value such that the mean exists, and $\mathbf{S}_0 = (\alpha_0 - K - 1)\boldsymbol{\Sigma}_0$, where $\boldsymbol{\Sigma}_0$ is as it is defined for the original Minnesota prior. With these default values, the prior mean of $\boldsymbol{\Sigma}$ is $\boldsymbol{\Sigma}_0$.

The conjugate Minnesota prior is the default prior for `bayes: var`, and it corresponds to the `minnconjprior` option, which is implied by default. You can customize this prior by specifying the `minnconjprior(`*conjopts*`)` option.

In the model-summary output of `bayes: var`, we refer to the defaults $\boldsymbol{\Phi}_0$ as `_Phi0`, $\boldsymbol{\beta}_0$ as `_b0`, and $\mathbf{S}_0$ as `_Scale0`. With degrees of freedom $K + 2$ (default), $\mathbf{S}_0$ is displayed as `_Sigma0`.

MVN-inverse Wishart prior

You can also specify an MVN-inverse Wishart prior for the VAR coefficients and error covariance. This prior also assumes an unknown error covariance $\boldsymbol{\Sigma}$, $\mathbf{u} \sim N(0, \boldsymbol{\Sigma} \otimes I_T)$.

The regression vector $\boldsymbol{\beta}$ has an MVN prior

$$\boldsymbol{\beta} \sim N(\widetilde{\boldsymbol{\beta}}, \widetilde{\boldsymbol{\Omega}})$$

with a fixed mean vector $\widetilde{\boldsymbol{\beta}}$ and a covariance matrix $\widetilde{\boldsymbol{\Omega}}$, which can be specified independently.

The covariance parameter $\boldsymbol{\Sigma}$ has an inverse-Wishart prior with a scale matrix $\mathbf{S}_0$ and degrees of freedom α_0,

$$\boldsymbol{\Sigma} \sim \text{InvWishart}(\alpha_0, \mathbf{S}_0)$$

You can specify this prior by using the `minniwishprior(`*iwishopts*`)` option. You can specify $\widetilde{\boldsymbol{\beta}}$ using the `mean()` suboption and $\widetilde{\boldsymbol{\Omega}}$ using the `cov()` suboption. Default values for $\widetilde{\boldsymbol{\beta}}$ and $\widetilde{\boldsymbol{\Omega}}$ are the prior mean and covariance, $\boldsymbol{\beta}_0$ and $\boldsymbol{\Omega}_0$, of the original Minnesota prior.

You can specify α_0 using the `df()` suboption and $\mathbf{S}_0$ using the `scale()` suboption. The default values are $\alpha_0 = K + 2$, the minimum possible value such that the mean exists, and $\mathbf{S}_0 = (\alpha_0 - K - 1)\boldsymbol{\Sigma}_0$.

In the model-summary output of `bayes: var`, we refer to the defaults $\boldsymbol{\beta}_0$ as `_b0`, $\boldsymbol{\Omega}_0$ as `_Omega0`, and $\mathbf{S}_0$ as `_Scale0`. With degrees of freedom $K + 2$ (default), $\mathbf{S}_0$ is displayed as `_Sigma0`.

MVN-diffuse (normal-Jeffreys) prior

Instead of an inverse-Wishart prior for the covariance matrix, as in the previous section, one may consider a diffused (multivariate Jeffreys) prior. As before, $\mathbf{u} \sim N(0, \boldsymbol{\Sigma} \otimes I_T)$.

The prior for $\boldsymbol{\beta}$ is still the MVN prior, as defined in *MVN-inverse Wishart prior*,

$$\boldsymbol{\beta} \sim N(\widetilde{\boldsymbol{\beta}}, \widetilde{\boldsymbol{\Omega}})$$

with a mean vector $\widetilde{\boldsymbol{\beta}}$ and a covariance matrix $\widetilde{\boldsymbol{\Omega}}$. But the covariance matrix $\boldsymbol{\Sigma}$ has a multivariate Jeffreys prior,

$$\pi(\boldsymbol{\Sigma}) \propto |\boldsymbol{\Sigma}|^{\frac{K+1}{2}}$$

You can specify the `minnjeffprior(`*jeffopts*`)` option for this prior. You can specify $\widetilde{\boldsymbol{\beta}}$ using the `mean()` suboption and $\widetilde{\boldsymbol{\Omega}}$ using the `cov()` suboption. As with MVN-inverse Wishart prior, the default values for $\widetilde{\boldsymbol{\beta}}$ and $\widetilde{\boldsymbol{\Omega}}$ are the prior mean and covariance, $\boldsymbol{\beta}_0$ and $\boldsymbol{\Omega}_0$, of the original Minnesota prior.

In the model-summary output of `bayes: var`, we refer to the defaults $\boldsymbol{\beta}_0$ and $\boldsymbol{\Omega}_0$ as `_b0` and `_Omega0`, respectively.

Also see *Methods and formulas* in [BAYES] **bayesmh**.

References

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Also see

[BAYES] **bayes: var postestimation** — Postestimation tools for bayes: var

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[TS] **var** — Vector autoregressive models

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: var postestimation — Postestimation tools for bayes: var

Postestimation commands Also see

Postestimation commands

The following Bayesian postestimation commands are of special interest after `bayes: var`:

Command	Description
`bayesfcast`	Bayesian dynamic forecasts
`bayesirf`	Bayesian impulse–response functions
`bayesvarstable`	check stability condition of estimates

The following standard Bayesian postestimation commands are also available:

Command	Description
`bayesgraph`	graphical summaries and convergence diagnostics
`bayesstats grubin`	Gelman–Rubin convergence diagnostics
`bayesstats ess`	effective sample sizes and related statistics
`bayesstats ppvalues`	Bayesian predictive p-values
`bayesstats summary`	Bayesian summary statistics for model parameters and their functions
`bayesstats ic`	Bayesian information criteria and Bayes factors
`bayestest model`	hypothesis testing using model posterior probabilities
`bayestest interval`	interval hypothesis testing
`bayespredict`	Bayesian predictions
* `estimates`	cataloging estimation results

* `estimates table` and `estimates stats` are not appropriate with `bayes: var` estimation results.

Also see

[BAYES] **bayes: var** — Bayesian vector autoregressive models

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[TS] **var postestimation** — Postestimation tools for var

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

[U] **20 Estimation and postestimation commands**

Title

bayesvarstable — Check the stability condition of Bayesian VAR estimates

Description

`bayesvarstable` checks the eigenvalue stability condition after fitting Bayesian vector autoregression (VAR) by using `bayes: var`.

Quick start

Checking eigenvalue stability condition after `bayes: var`

```
bayesvarstable
```

Same as above, but compute 80% highest posterior density (HPD) credible intervals instead of 95% equal-tailed credible intervals

```
bayesvarstable, hpd clevel(80)
```

Menu

Statistics > Multivariate time series > Bayesian models > Check stability condition of VAR estimates

Syntax

```
bayesvarstable [ , options ]
```

options	Description
`estimates(`*estname*`)`	use previously stored results *estname*; default is to use active results
`clevel(#)`	set credible interval level; default is `clevel(95)`
`hpd`	save HPD credible intervals instead of the default equal-tailed credible intervals
`mcmcsaving(`*filename*`[ , replace ])`	save simulation results to *filename*`.dta`

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

Options

`estimates(`*estname*`)` requests that `bayesvarstable` use the previously obtained set of `bayes: var` estimates stored as *estname*. By default, `bayesvarstable` uses the active estimation results. See [R] **estimates** for information on manipulating estimation results.

`clevel(#)` specifies the credible level, as a percentage, for equal-tailed and HPD credible intervals. The default is `clevel(95)` or as set by [BAYES] **set clevel**.

`hpd` displays the HPD credible intervals instead of the default equal-tailed credible intervals.

`mcmcsaving(`*filename*`[ , replace ])` saves simulation results in *filename*`.dta`. The `replace` option specifies to overwrite *filename*`.dta` if it exists. If the `mcmcsaving()` option is not specified, simulation results are not saved.

The saved dataset has the following structure. Variable `_chain` records chain identifiers. Variable `_index` records iteration numbers. `bayesvarstable` saves only states (sets of values) that are different from one iteration to another and the frequency of each state in variable `_frequency`. As such, `_index` may not necessarily contain consecutive integers. Remember to use `_frequency` as a frequency weight if you need to obtain any summaries of this dataset. Values for modulus of each eigenvalue are saved in a separate variable in the dataset.

Remarks and examples

Stability is an important condition for VAR model interpretation; see *Remarks and examples* of [TS] **varstable**. If the stability condition of a VAR model is not met, its impulse–response functions (IRFs) and forecast-error variance decompositions do not reach equilibrium and thus do not have clear interpretation.

Lütkepohl (2005) and Hamilton (1994) show that if the modulus of each eigenvalue of the companion matrix $\mathbf{A}$ is strictly less than one, the estimated VAR is stable (see *Methods and formulas* for the definition of the matrix $\mathbf{A}$). In a Bayesian setting, we are concerned with the posterior distribution of $\mathbf{A}$ and its eigenvalues.

Following are two examples illustrating stable and unstable VAR models.

Example 1: Stable VAR model

We revisit example 1 from [TS] **varstable**. It uses `lutkepohl2.dta` of West Germany microeconomic quarterly data for the years between 1960 and 1978. The example studies the relationships between investment, `dln_inv`, income, `dln_inc`, and consumption, `dln_consump`.

```
. use https://www.stata-press.com/data/r18/lutkepohl2
. tsset
```

Using the `bayes: var` command, we fit a Bayesian VAR model with two lags on the dependent variables `dln_inv`, `dln_inc`, and `dln_consump`. Considered are observations between the second quarter of 1961 and the fourth quarter of 1978. We use the default conjugate Minnesota prior for regression coefficients and error covariance matrix.

```
. bayes, rseed(17) nomodelsummary:
> var dln_inv dln_inc dln_consump if qtr>=tq(1961q2) & qtr<=tq(1978q4)
Burn-in ...
Simulation ...
Bayesian vector autoregression                  MCMC iterations  =     12,500
Gibbs sampling                                  Burn-in          =      2,500
                                                MCMC sample size =     10,000
Sample: 1961q2 thru 1978q4                      Number of obs    =         71
                                                Acceptance rate  =          1
                                                Efficiency:  min =      .9556
                                                             avg =      .9962
Log marginal-likelihood =  467.75286                         max =          1
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
dln_inv						
dln_inv						
L1.	.4749526	.1046821	.001071	.4762824	.2706787	.6790291
L2.	.0062935	.063174	.000632	.0058376	-.1181113	.129959
dln_inc						
L1.	.1150521	.4145854	.004146	.1155755	-.7122031	.9358321
L2.	.0096558	.2461088	.002464	.0129206	-.4780951	.490937
dln_consump						
L1.	-.0693822	.4910385	.004828	-.0712677	-1.016477	.9050535
L2.	.0182113	.2919327	.002919	.0169657	-.5563898	.6010627
_cons	.0067839	.0153897	.000154	.0067986	-.0233363	.0367596

dln_inc						
dln_inv						
L1.	.0152113	.0248328	.000248	.0154024	-.0341219	.0635173
L2.	.000957	.0149204	.000147	.0010833	-.0285813	.0306545
dln_inc						
L1.	.600281	.0981275	.000981	.5997577	.4077653	.7928394
L2.	.011757	.0577031	.000577	.0123101	-.1009659	.1245041
dln_consump						
L1.	-.0331359	.1151265	.001151	-.0318916	-.2594495	.1939938
L2.	-.0266197	.0694851	.000695	-.0263958	-.1637059	.1123704
_cons	.0084678	.0036265	.000037	.0084371	.0013034	.0155666
dln_consump						
dln_inv						
L1.	-.0183312	.0220482	.00022	-.0182937	-.062597	.0243933
L2.	.0092806	.0135179	.000135	.0094044	-.0171007	.036166
dln_inc						
L1.	-.0365965	.0875614	.000876	-.0368425	-.2086565	.1364804
L2.	.0345945	.0520216	.000514	.0339648	-.0668323	.136918
dln_consump						
L1.	.5444814	.1030406	.001027	.5432019	.3416401	.7489821
L2.	.0555939	.0617942	.000618	.055126	-.063175	.1763757
_cons	.0078414	.0032597	.000033	.0078245	.001402	.0141132
Sigma_1_1	.003945	.0006693	6.4e-06	.0038783	.0028446	.0054382
Sigma_2_1	-.0000314	.0001118	1.1e-06	-.0000291	-.0002548	.0001897
Sigma_3_1	.000138	.0001007	1.0e-06	.0001355	-.0000512	.0003478
Sigma_2_2	.0002195	.0000373	3.7e-07	.0002158	.0001579	.0003039
Sigma_3_2	.0000502	.0000238	2.4e-07	.000049	6.46e-06	.0001007
Sigma_3_3	.0001743	.0000294	2.9e-07	.0001714	.0001261	.0002408

For explanation of the output of `bayes: var`, see *Remarks and examples* of [BAYES] **bayes: var**.

To use the `bayesvarstable` command, we need to save simulation results computed by `bayes: var` in a permanent dataset.

```
. bayes, saving(bvarex1)
note: file bvarex1.dta saved.
```

Now we are ready to check the stability condition for the above Bayesian model.

```
. bayesvarstable
Eigenvalue stability condition                  Companion matrix size =     6
                                                MCMC sample size      = 10000
```

Eigenvalue modulus	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
1	.7295294	.0952871	.000953	.7272906	.547312	.9209245
2	.6039037	.1045099	.001045	.6094994	.3810883	.7904044
3	.428933	.1272649	.001273	.4239249	.2113325	.6645651
4	.2126552	.0780213	.00078	.1997342	.0900884	.3846134
5	.1378018	.0565196	.000565	.1349177	.0385605	.2577174
6	.0759403	.05052	.000505	.0700686	.0035577	.1847619

```
Pr(eigenvalues lie inside the unit circle) = 0.9966
```

The VAR model has a companion matrix of size 6 (3 response variables times 2 lags). The `bayesvarstable` command thus reports posterior summaries for the moduli of 6 eigenvalues. The maximum one has a posterior mean of 0.73, less than 1. In addition to posterior means, we also see posterior standard deviations, MCMC standard errors, medians, and credible intervals.

The `bayesvarstable` command estimates the probability of unit circle inclusion for all eigenvalues to be 0.9966, or essentially 1. The stability condition is thus satisfied.

We may specify the HPD credible intervals instead of the default equal-tailed ones and change the level of the intervals. This, however, would not change the estimated probability of inclusion and the overall conclusion.

```
. bayesvarstable, hpd clevel(80)
Eigenvalue stability condition                  Companion matrix size =     6
                                                MCMC sample size      = 10000
```

Eigenvalue modulus	Mean	Std. dev.	MCSE	Median	HPD [80% cred.	interval]
1	.7295294	.0952871	.000953	.7272906	.6066106	.8490679
2	.6039037	.1045099	.001045	.6094994	.4782224	.7449145
3	.428933	.1272649	.001273	.4239249	.2656266	.6001815
4	.2126552	.0780213	.00078	.1997342	.1065876	.3036596
5	.1378018	.0565196	.000565	.1349177	.0623463	.2060198
6	.0759403	.05052	.000505	.0700686	.0000169	.1200219

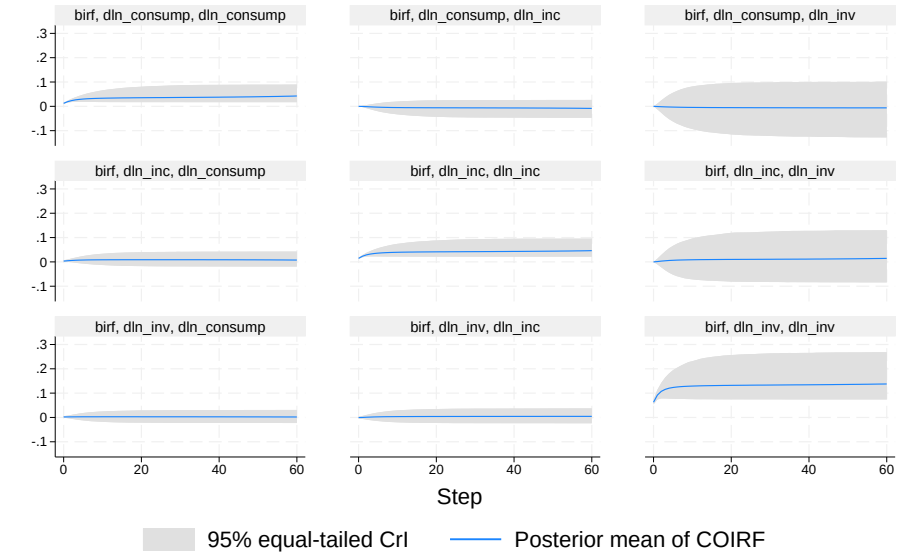
```
Pr(eigenvalues lie inside the unit circle) = 0.9966
```

As we mentioned above, a stable VAR model has IRFs that reach equilibrium in the long run. Let's verify this. We compute IRFs for 60 quarters (15 years) ahead and save them as `birf` estimates in `birfex1.irf`.

```
. bayesirf create birf, step(60) set(birfex1)
(file birfex1.irf created)
(file birfex1.irf now active)
(file birfex1.irf updated)
```

See *Remarks and examples* for details about [BAYES] **bayesirf create**. We check the long-term behavior of the cumulative orthogonalized IRFs using the `bayesirf graph` command.

```
. bayesirf graph coirf
```



Graphs by irfname, impulse variable, and response variable

In particular, we look at the cumulative shock effects of impulse variables on themselves (the graphs on the diagonal). It is clear that all shocks reach long-term equilibrium after about 2 years (all graphs converge to horizontal asymptotes). These are the types of graphs we expect to see from a stable VAR model.

◁

▷ Example 2: Unstable VAR model

In this example, we show how the specification of a strong prior may violate the stability condition of a VAR model.

We consider the same VAR model as in the previous example, but now we reduce the number of lags from 2 to 1 and strengthen the default Minnesota prior. In particular, we change the `selftight()` suboption of `minnconjprior()` from its default value of 0.1 to 0.001. This option determines the prior variance of regression coefficients; see *self-variables tightness parameter*. A value of 0.001 will shrink the regression coefficients to their prior mean values, which are 1 for self-variables first-lag coefficients and 0 otherwise. The shrinkage is thus toward a *random-walk* behavior, which is known to be unstable. Given the modest sample size of 90 observations, we expect the prior to dominate the information available in the data.

```
. bayes, minnconjprior(selftight(0.001)) rseed(17) saving(bvarex2) nomodelsummary:
> var dln_inv dln_inc dln_consump, lags(1)
Burn-in ...
Simulation ...
Bayesian vector autoregression                  MCMC iterations  =     12,500
Gibbs sampling                                  Burn-in          =      2,500
                                                MCMC sample size =     10,000
Sample: 1960q3 thru 1982q4                      Number of obs    =         90
                                                Acceptance rate  =          1
                                                Efficiency:  min =      .9779
                                                             avg =      .9988
Log marginal-likelihood =   590.1324                         max =          1
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
dln_inv						
dln_inv L1.	.9999075	.0015466	.000015	.9999005	.9968787	1.002993
dln_inc L1.	-.0001024	.0057483	.000056	-.0000905	-.0113532	.0112184
dln_consump L1.	.0000347	.0062553	.000063	.0000484	-.0122773	.0124097
_cons	-.0000218	.0050112	.00005	-4.42e-06	-.009838	.0097902
dln_inc						
dln_inv L1.	5.87e-06	.0003621	3.6e-06	6.24e-06	-.0006947	.000714
dln_inc L1.	.9999134	.0013413	.000013	.9999053	.9973009	1.002532
dln_consump L1.	-.0000275	.0014526	.000015	-.0000321	-.0028922	.0028222
_cons	-.0001133	.0011346	.000011	-.0001213	-.002378	.0021637
dln_consump						
dln_inv L1.	-7.21e-06	.0003546	3.5e-06	-8.11e-06	-.0007066	.0006912
dln_inc L1.	-.0000405	.001341	.000014	-.0000284	-.0027065	.002576
dln_consump L1.	.9998961	.0014424	.000014	.9999152	.9970457	1.002728
_cons	-.000031	.0011446	.000011	-.0000338	-.0022769	.0022331
Sigma_1_1	.004672	.0006967	7.0e-06	.0046044	.0034928	.00625
Sigma_2_1	-.0000808	.0001147	1.1e-06	-.0000799	-.0003115	.0001442
Sigma_3_1	.0002439	.0001158	1.2e-06	.00024	.0000266	.0004826
Sigma_2_2	.0002519	.0000382	3.8e-07	.0002482	.0001879	.000336
Sigma_3_2	.000067	.0000275	2.8e-07	.0000655	.0000169	.0001243
Sigma_3_3	.0002483	.0000366	3.7e-07	.0002447	.0001869	.0003288

```
file bvarex2.dta saved.
```

The posterior mean estimates of regression coefficients are very close to their prior mean values.

We use bayesvarstable to check the stability condition.

```
. bayesvarstable
Eigenvalue stability condition                  Companion matrix size =     3
                                                MCMC sample size      = 10000
```

Eigenvalue modulus	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
1	1.001409	.0012333	.000012	1.001324	.999263	1.004065
2	.9998958	.0011205	.000011	.9998891	.997711	1.002059
3	.9984138	.0012513	.000013	.998492	.9957189	1.000603

```
Pr(eigenvalues lie inside the unit circle) = 0.1194
```

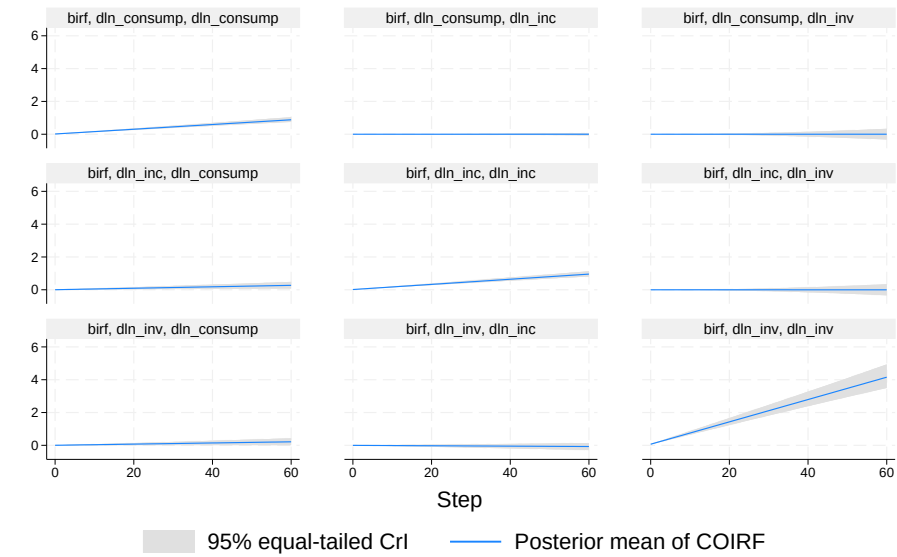
The reported probability that all three eigenvalues lie in the unit circle is only about 12% and is clearly insufficient to claim the stability of the estimates.

We can also look at IRFs for visual confirmation of the instability of the model. We compute IRFs for 60 quarters ahead and save them as birf estimates in birfex2.irf.

```
. bayesirf create birf, step(60) set(birfex2)
(file birfex2.irf created)
(file birfex2.irf now active)
(file birfex2.irf updated)
```

Then we plot the cumulative orthogonalized IRFs using bayesirf graph.

```
. bayesirf graph coirf
```



Graphs by irfname, impulse variable, and response variable

It is clear that the shocks of impulses on themselves (the graphs on the diagonal) do not reach equilibrium and continue to increase beyond the 60-quarter period. This is a typical behavior of an unstable VAR model.

This particular instability problem arises because the used prior strongly favors an unstable, random-walk model, and there is not enough information in the data to outweigh this prior. For instance, if we

specified zero prior means for all coefficients, we would not run into this problem. What constitutes a strong prior depends on the sample size and the amount of information contained in the data about model parameters. The conclusion in this example may not hold for other VAR models and datasets. We thus recommend checking the stability condition after fitting any VAR model before proceeding with postestimation analysis.

◁

Stored results

`bayesvarstable` stores the following in `r()`:

Scalars

`r(prob_incl)`	probability of unit circle inclusion of all eigenvalues
`r(mcmcsize)`	MCMC sample size
`r(compsize)`	companion matrix size

Matrices

`r(summary)`	matrix with posterior summary statistics for eigenvalues

Methods and formulas

Consider a companion matrix $\mathbf{A}$ defined in *Methods and formulas* of [TS] **varstable**. In a Bayesian setting, $\mathbf{A}$ is a random matrix with a posterior distribution that depends on the prior distribution of regression coefficients and error covariance matrix. The Bayesian computations use the MCMC sample created by the `bayes: var` command that contains draws from the posterior distribution of the regression coefficients/matrices and error covariance.

For each draw, the eigenvalue moduli of the companion matrix $\mathbf{A}^*$ that corresponds to that draw are computed and saved in an MCMC sample. Finally, the resulting MCMC samples of eigenvalue moduli are summarized, and standard Bayesian statistics such as posterior mean, medians, and credible intervals are reported.

The posterior probability of the unit circle inclusion is estimated as the proportion of MCMC observations for which all eigenvalues of $\mathbf{A}^*$'s are strictly within the unit circle.

References

Hamilton, J. D. 1994. *Time Series Analysis*. Princeton, NJ: Princeton University Press.

Lütkepohl, H. 2005. *New Introduction to Multiple Time Series Analysis*. New York: Springer.

Also see

[BAYES] **bayes: var postestimation** — Postestimation tools for bayes: var

[BAYES] **bayes: var** — Bayesian vector autoregressive models

[TS] **varstable** — Check the stability condition of VAR or SVAR estimates

Title

bayesfcast — Bayesian dynamic forecasts

Description Quick start Syntax Also see

Description

`bayesfcast` computes and graphs Bayesian dynamic forecasts of the endogenous variables after `bayes: var`. `bayesfcast` has two subcommands. `bayesfcast compute` computes the posterior means or medians of dynamic forecasts, posterior standard deviations, and credible intervals. `bayesfcast graph` graphs Bayesian predictions, credible intervals, and observed values.

Quick start

Fit a Bayesian vector autoregression model

```
bayes, saving(bvarmcmc): var y1 y2 y3
```

Compute posterior means and credible intervals of dynamic forecast for 8 steps ahead

```
bayesfcast compute bf_, step(8)
```

Graph the posterior means, credible intervals, and observed values

```
bayesfcast graph bf_y1 bf_y2 bf_y3, observed
```

Syntax

`bayesfcast` *subcommand* ... [, ...]

subcommand	Description
`compute`	obtain dynamic forecasts
`graph`	graph dynamic forecasts obtained from `bayesfcast compute`

`bayesfcast` can be used after `bayes: var`; see [BAYES] **bayes: var**.

Also see

[BAYES] **bayes: var** — Bayesian vector autoregressive models

Title

bayesfcast compute — Compute Bayesian dynamic forecasts

Description

`bayesfcast compute` produces Bayesian dynamic forecasts of the dependent variables in a model previously fit by `bayes: var`. It creates new variables for prediction results and, if necessary, extends the time frame of the dataset to contain the prediction horizon. Prediction results can be posterior means or medians, posterior standard deviations, and credible intervals.

Quick start

Posterior means stored in `b_y1`, `b_y2`, and `b_y3` as dynamic forecasts after fitting a model with `bayes: var` for dependent variables `y1`, `y2`, and `y3`

```
bayesfcast compute b_
```

Same as above, but begin forecast on the first quarter of 1979 for 10 periods ahead

```
bayesfcast compute b_, dynamic(q(1979q1)) step(10)
```

Same as above, but requesting posterior medians instead of posterior means be saved as forecasts along with 80% equal-tailed credible intervals.

```
bayesfcast compute b_, dynamic(q(1979q1)) step(10) median clevel(80)
```

Menu

Statistics > Multivariate time series > Bayesian models > VAR forecasts > Compute forecasts (required for graph)

Syntax

```
bayesfcast compute prefix [ , options ]
```

prefix is the prefix appended to the names of the dependent variables to create the names of the variables holding the dynamic forecasts.

options	Description
step(#)	set # periods to forecast; default is step(1)
dynamic(*time_constant*)	begin dynamic forecasts at *time_constant*
estimate(*estname*)	use previously stored results *estname*; default is to use active results
replace	replace existing forecast variables that have the same prefix
clevel(#)	set credible interval level; default is clevel(95)
hpd	save HPD credible intervals instead of the default equal-tailed credible intervals
median	save posterior medians instead of default posterior means and standard deviations
mcmcsaving(*filename*[, replace])	save simulation results to *filename*.dta
mcmcsaving	save simulation results to *prefix*_mcmc.dta
rseed(#)	random-number seed

bayesfcast compute can be used only after bayes: var.

You must tsset your data before using bayesfcast compute; see [TS] **tsset**.

Options

step(#), dynamic(*time_constant*), estimate(*estname*), and replace; see [TS] **fcast compute**.

clevel(#) specifies the credible level, as a percentage, for equal-tailed and HPD credible intervals. The default is clevel(95) or as set by [BAYES] **set clevel**.

hpd displays the HPD credible intervals instead of the default equal-tailed credible intervals.

median calculates and saves posterior medians instead of the posterior means and standard deviations.

mcmcsaving(*filename*[, replace]) saves simulation results in *filename*.dta. The replace option specifies to overwrite *filename*.dta if it exists. If the mcmcsaving() option is not specified, simulation results are not saved.

The saved dataset has the following structure. Variable _chain records chain identifiers. Variable _index records iteration numbers. bayesfcast saves only states (sets of values) that are different from one iteration to another and the frequency of each state in variable _frequency. As such, _index may not necessarily contain consecutive integers. Remember to use _frequency as a frequency weight if you need to obtain any summaries of this dataset. Values for each forecasted outcome are saved in a separate variable in the dataset. The variable corresponding to outcome y and time period t is named as y_t.

mcmcsaving saves the simulation results in *prefix*_mcmc.dta.

rseed(#) sets the random-number seed. This option can be used to reproduce results. With one chain, rseed(#) is equivalent to typing set seed # prior to calling the bayes prefix; see [R] **set seed**. With multiple chains, you should use rseed() for reproducibility; see *Reproducing results* in [BAYES] **bayesmh**.

Remarks and examples

Below, we show examples of dynamic forecasts after fitting Bayesian vector autoregression (VAR) models. Also see example 9 in [BAYES] **bayes: var** for another example.

▷ Example 1

We revisit example 1 from [TS] **fcast compute**. It uses `lutkepohl2.dta` of West Germany microeconomic quarterly data for the years between 1960 and 1978. The example studies the relationships between investment (`dln_inv`), income (`dln_inc`), and consumption (`dln_consump`).

```
. use https://www.stata-press.com/data/r18/lutkepohl2
. tsset
```

First, we fit a Bayesian VAR model with two lags on the dependent variables `dln_inv`, `dln_inc`, and `dln_consump` using the `bayes: var` command with default settings. The output of the command is suppressed. The subsequent `bayesfcast` command requires that the simulation results generated by `bayes: var` be saved in a permanent dataset, in our case `bfcastex1.dta`.

```
. bayes, rseed(17) nomodelsummary notable noheader:
> var dln_inv dln_inc dln_consump if qtr<tq(1979q1)
Burn-in ...
Simulation ...

. bayes, saving(bfcastex1, replace)
note: file bfcastex1.dta not found; file saved.
```

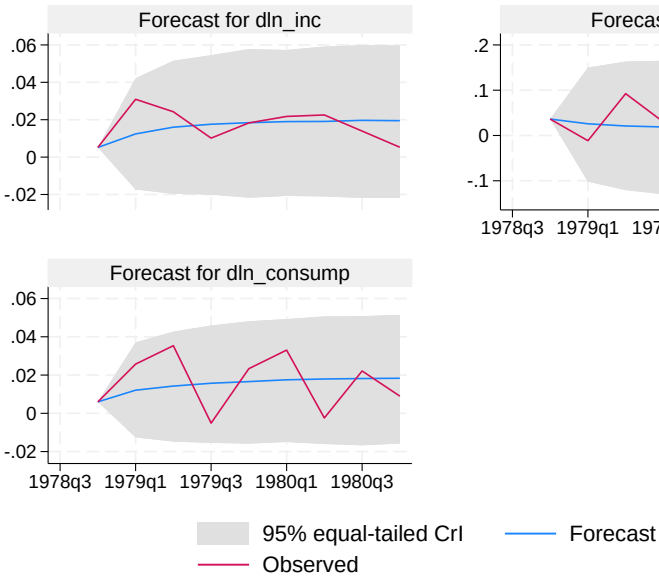
We then compute 8-step dynamic predictions for each of the three dependent variables using `bayesfcast compute`. We specify `b1_` prefix for the newly created variables.

```
. bayesfcast compute b1_, step(8)
```

The prediction results are saved in the current dataset and include posterior means, `b1_*`, posterior standard deviations, `b1_*_sd`, and 95% credible intervals, `b1_*_lb` and `b1_*_ub`. Populated are observations between `qtr = 1978q4` and `qtr = 1980q4`.

Next, using the `bayesfcast graph` command, we show the posterior mean forecasts along with the 95% credible bands.

```
. bayesfcast graph b1_dln_inc b1_dln_inv b1_dln_consump, observed
```



Compared with the original forecasts shown in example 1, the Bayesian posterior means forecasts are much smoother and closer to the stationary state. The variability of the Bayesian forecasts, as measured by the width of the 95% credible bands, tends to increase slightly with time, whereas the width of the confidence bands in the original forecasts stays the same. The Bayesian forecasts thus appear to provide more conservative predictions.

◁

▷ Example 2

Continuing with example 1, we fit a second VAR model in which the Minnesota prior on regression coefficients is more relaxed, thus giving us posterior estimates that are closer to the frequentist ones, as obtained by the `var` command.

We use the same VAR(2) model specification but specify the `selftight(1)` suboption of the `minnconjprior()` option, which controls the Minnesota prior. Again, we suppress the output of the `bayes: var` command and save the simulation results in `bfcastex2.dta`.

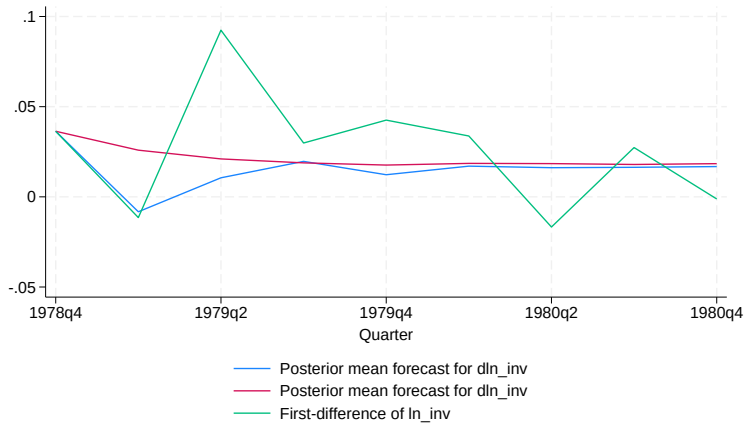
```
. bayes, minnconjprior(selftight(1)) rseed(17) nomodelsummary notable noheader:
> var dln_inc dln_consump dln_inv if qtr<tq(1979q1)
Burn-in ...
Simulation ...
. bayes, saving(bfcastex2, replace)
note: file bfcastex2.dta not found; file saved.
```

Then, we compute Bayesian forecasts based on the second model and save them in the current dataset using the `b2_` prefix for the newly created variables.

```
. bayesfcast compute b2_, step(8)
```

Finally, we plot the forecasts of the two models along with the observed values for the `dln_inv` variable (shown in green).

```
. graph twoway line b2_dln_inv b1_dln_inv dln_inv qtr
> if b2_dln_inv < ., legend(pos(6))
```



The Bayesian forecasts of the second model (shown in blue) are more rugged than those of the first model and are indeed closer to the original forecasts from example 1. Although initially the second model forecasts are closer to the observed, their precision quickly drops afterward, and the more conservative predictions of the first model appear to fare better later on. The forecasts of both models converge with each other after six time steps.

◁

Methods and formulas

Methods and formulas are presented under the following headings:

Bayesian dynamic forecasts
Dynamic forecasts after bayes: var

Bayesian dynamic forecasts

In the frequentist context, dynamic forecasts are based on one set of point estimates of the model parameter vector $\boldsymbol{\theta}$. In a Bayesian framework, instead of point estimates, an entire posterior distribution of $\boldsymbol{\theta}$ is used to compute forecasts.

Let $\mathbf{y}_t$ be a vector of outcome variables at time t. A dynamic forecast with horizon h is a realization of future observations $\mathbf{y}_{T+1}$, $\mathbf{y}_{T+2}$, …, $\mathbf{y}_{T+h}$ based on the observations up to time T: $\mathbf{y}_1$, $\mathbf{y}_2$, …, $\mathbf{y}_T$. Let $f(\mathbf{y}_{T+1:T+h}|\mathbf{y}_{1:T}, \boldsymbol{\theta})$ be the distribution of future observations conditional on the observations up to time T. Bayesian dynamic forecasts are drawn from the posterior predictive distribution

$$p(\mathbf{y}_{T+1:T+h}|\mathbf{y}_{1:T}) = \int f(\mathbf{y}_{T+1:T+h}|\mathbf{y}_{1:T}, \boldsymbol{\theta}) p(\boldsymbol{\theta}|D) d\boldsymbol{\theta}$$

where $p(\boldsymbol{\theta}|D)$ is the posterior distribution of the model with respect to some data D. For example, D may include the outcome observations $\mathbf{y}|_{1:T}$ along with observations on exogenous variables $\mathbf{X}_{1:T}$.

In practice, $f(\mathbf{y}_{T+1:T+h}|\mathbf{y}_{1:T}, \boldsymbol{\theta})$ is computed recursively using the factorization

$$f(\mathbf{y}_{T+1:T+h}|\mathbf{y}_{1:T}, \boldsymbol{\theta}) = f(\mathbf{y}_{T+1}|\mathbf{y}_{1:T}, \boldsymbol{\theta}) f(\mathbf{y}_{T+2}|\mathbf{y}_{1:T+1}, \boldsymbol{\theta}) \dots f(\mathbf{y}_{T+h}|\mathbf{y}_{1:T+h-1}, \boldsymbol{\theta})$$

After fitting a time-series model using `bayes: var`, we have a Markov chain Monte Carlo (MCMC) sample of realizations of $\boldsymbol{\theta}$ from its posterior distribution $p(\boldsymbol{\theta}|D)$. To simulate the distribution of the dynamic forecast $p(\mathbf{y}_{T+1:T+h}|\mathbf{y}_{1:T})$, we recycle this same MCMC sample.

1. For each draw $\boldsymbol{\theta}^s$ from the MCMC sample $\{\theta^1, \theta^2, \dots, \theta^M\}$, repeat the following:
   2.1. Generate $\widetilde{\mathbf{y}}^s_{T+1}$ from $f(\mathbf{y}_{T+1}|\mathbf{y}_{1:T}, \boldsymbol{\theta}^s)$.
   2.2. Generate $\widetilde{\mathbf{y}}^s_{T+2}$ from $f(\mathbf{y}_{T+2}|\mathbf{y}_{1:T}, \widetilde{\mathbf{y}}^s_{T+1}, \boldsymbol{\theta}^s)$.
   …
   2.h. Generate $\widetilde{\mathbf{y}}^s_{T+h}$ from $f(\mathbf{y}_{T+h}|\mathbf{y}_{1:T}, \widetilde{\mathbf{y}}^s_{T+1:T+h-1}, \boldsymbol{\theta}^s)$.
   3. Save the forecast draw $(\widetilde{\mathbf{y}}^s_{T+1}, \widetilde{\mathbf{y}}^s_{T+2}, \dots, \widetilde{\mathbf{y}}^s_{T+h})$.
4. Using the simulated forecast draws, compute posterior summaries such as means, medians, and credible intervals for each of the h forecast steps $\mathbf{y}_{T+1}$, …, $\mathbf{y}_{T+h}$.

The `bayesfcast compute` command saves the estimated posterior summaries computed by the above algorithm in the current dataset similar to the way the `fcast compute` command computes and saves forecast point estimates.

Dynamic forecasts after bayes: var

The method of simulating Bayesian dynamic forecasts in the special case of VAR is proposed in Karlsson (2013). It follows the steps of the above general algorithm for simulating an MCMC sample of forecasts from the posterior predictive distribution $p(\mathbf{y}_{T+1:T+h}|\mathbf{y}_{1:T})$.

Let's consider a VAR(p) model using the notation from *Methods and formulas* of [BAYES] **bayes: var**:

$$\mathbf{y}_t = \mathbf{A}_1\mathbf{y}_{t-1} + \dots + \mathbf{A}_p\mathbf{y}_{t-p} + \mathbf{C}\mathbf{x}_t + \mathbf{u}_t$$

for $t = 1, \dots, T$.

The model parameter vector $\boldsymbol{\theta}$ includes elements of $\mathbf{A}_1$, …, $\mathbf{A}_p$, $\mathbf{C}$, and error covariance matrix $\boldsymbol{\Sigma}$ of the error terms $\mathbf{u}_t$'s. For each MCMC draw of the parameters $\boldsymbol{\theta}^s$, the forecast steps 2.1 to 2.h reduce to the following,

$$\widetilde{\mathbf{y}}^s_{T+1} = \mathbf{A}^s_1\mathbf{y}_T + \mathbf{A}^s_2\mathbf{y}_{T-1}\cdots + \mathbf{A}^s_p\mathbf{y}_{T-p+1} + \mathbf{C}^s\mathbf{x}_{T+1} + \widetilde{\mathbf{u}}_{T+1}$$
$$\widetilde{\mathbf{y}}^s_{T+2} = \mathbf{A}^s_1\widetilde{\mathbf{y}}^s_{T+1} + \mathbf{A}^s_2\mathbf{y}_T + \cdots + \mathbf{A}^s_p\mathbf{y}_{T-p} + \mathbf{C}^s\mathbf{x}_{T+2} + \widetilde{\mathbf{u}}_{T+2}$$
$$\cdots$$
$$\widetilde{\mathbf{y}}^s_{T+h} = \mathbf{A}^s_1\widetilde{\mathbf{y}}^s_{T+h-1} + \mathbf{A}^s_2\widetilde{\mathbf{y}}^s_{T+h-2} + \cdots + \mathbf{C}^s\mathbf{x}_{T+h} + \widetilde{\mathbf{u}}_{T+h}$$

where $\widetilde{\mathbf{u}}_{T+1}$, …, $\widetilde{\mathbf{u}}_{T+h}$ are independent draws from $N(\mathbf{0}, \boldsymbol{\Sigma}^s)$.

Reference

Karlsson, S. 2013. Forecasting with Bayesian vector autoregression. In *Handbook of Economic Forecasting, vol. 2B*, ed. G. Elliott and A. Timmermann, 791–897. Amsterdam: North-Holland. https://doi.org/10.1016/B978-0-444-62731-5.00015-4.

Also see

[TS] **fcast compute** — Compute dynamic forecasts after var, svar, or vec

[BAYES] **bayesfcast graph** — Graphs of Bayesian dynamic forecasts

[BAYES] **bayes: var** — Bayesian vector autoregressive models

Title

bayesfcast graph — Graphs of Bayesian dynamic forecasts

Description

`bayesfcast graph` graphs Bayesian dynamic forecasts of the endogenous variables from a VAR(p) model that has already been obtained from `bayesfcast compute`; see [BAYES] **bayesfcast compute**.

Menu

Statistics > Multivariate time series > Bayesian models > VAR forecasts > Graph forecasts

Syntax

`bayesfcast graph` *varlist* [*if*] [*in*] [, *options*]

varlist contains one or more forecasted variables generated by `bayesfcast compute`.

options	Description
fcast_options	any *options* documented in [TS] **fcast graph**
`nocri`	suppress credible bands
CrI plot	
`criopts(`*area_options*`)`	affect rendition of the credible bands

`bayesfcast compute` can be used only after `bayes: var`.

The `nocri` option replaces the `noci` option on the **Main** tab of [TS] **fcast graph**.

The **CrI plot** tab replaces the **CI plot** tab of [TS] **fcast graph**.

Options

fcast_options are any of the *options* documented in [TS] **fcast graph** for the `var` command. `noci` is a synonym for `nocri`, and `ciopts()` is a synonym for `criopts()`. Synonymous options do not appear on the dialog box.

`nocri` suppresses displaying the credible bands. This option replaces the `noci` option of [TS] **fcast graph** on the **Main** tab.

CrI plot

`criopts(`*area_options*`)` affects the rendition of the credible bands for the forecasts. *area_options* are as described in [G-3] ***area_options***. `fcast`'s `ciopts()` is a synonym for `criopts()`.

The **CrI plot** tab replaces the **CI plot** tab of [TS] **fcast graph**.

Remarks and examples

See [TS] **fcast graph** for a general discussion, and see example 9 in [BAYES] **bayes: var** for an example.

Also see

[TS] **fcast graph** — Graph forecasts after fcast compute

[BAYES] **bayesfcast compute** — Compute Bayesian dynamic forecasts

[BAYES] **bayes: var** — Bayesian vector autoregressive models

Title

bayesirf — Bayesian IRFs, dynamic-multiplier functions, and FEVDs

Description Quick start Syntax Remarks and examples Also see

Description

`bayesirf` creates and manipulates Bayesian impulse–response function (IRF) files that contain estimates of the IRFs, dynamic-multiplier functions, and forecast-error variance decompositions (FEVDs) created after estimation by `bayes: var`; see [BAYES] **bayes: var**.

`bayesirf` creates and manipulates Bayesian IRF files that contain estimates of the IRFs created after estimation by `bayes: dsge` or `bayes: dsgenl`; see [BAYES] **bayes: dsge** or [BAYES] **bayes: dsgenl**.

IRFs and FEVDs are described in [TS] **irf**.

Quick start

Fit a Bayesian vector autoregression (VAR) model

```
bayes, saving(bvarmcmc): var y1 y2 y3
```

Create IRF `myirf` and IRF file `bayesirfs.irf`

```
bayesirf create myirf, set(bayesirfs)
```

Graph orthogonalized IRF for dependent variables `y1` and `y2` given a shock to `y1`

```
bayesirf graph oirf, impulse(y1) response(y1 y2)
```

Same as above, but present results in a table

```
bayesirf table oirf, impulse(y1) response(y1 y2)
```

See other `bayesirf` subcommands for additional Quick starts.

Syntax

```
bayesirf subcommand ... [ , ... ]
```

subcommand	Description
`create`	create IRF file containing IRFs, dynamic-multiplier functions, and FEVDs; [BAYES] **bayesirf create**
`set`	set the active IRF file; [TS] **irf set**
`graph`	graph results from active file; [BAYES] **bayesirf graph**
`cgraph`	combine graphs of IRFs, dynamic-multiplier functions, and FEVDs; [BAYES] **bayesirf cgraph**
`ograph`	graph overlaid IRFs, dynamic-multiplier functions, and FEVDs; [BAYES] **bayesirf ograph**
`table`	create tables of IRFs, dynamic-multiplier functions, and FEVDs from active file; [BAYES] **bayesirf table**
`ctable`	combine tables of IRFs, dynamic-multiplier functions, and FEVDs; [BAYES] **bayesirf ctable**
`describe`	describe contents of active file; [TS] **irf describe**
`add`	add results from an IRF file to the active IRF file; [TS] **irf add**
`drop`	drop IRF results from active file; [TS] **irf drop**
`rename`	rename IRF results within a file; [TS] **irf rename**

`bayesirf` can be used after `bayes: var`, `bayes: dsge` or `bayes: dsgenl`; see [BAYES] **bayes: var**, [BAYES] **bayes: dsge**, or [BAYES] **bayes: dsgenl**.

`bayesirf set`, `describe`, `add`, `drop`, and `rename` have the same syntax as their respective `irf` commands.

Remarks and examples

For examples and details about IRFs and other functions, see *Remarks and examples* in [BAYES] **bayesirf create**. Also see example 8 in [BAYES] **bayes: var**.

Also see

[TS] **irf** — Create and analyze IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayes: dsge** — Bayesian linear dynamic stochastic general equilibrium models

[BAYES] **bayes: dsgenl** — Bayesian nonlinear dynamic stochastic general equilibrium models

[BAYES] **bayes: var** — Bayesian vector autoregressive models

Title

bayesirf create — Obtain Bayesian IRFs, dynamic-multiplier functions, and FEVDs

Description

`bayesirf create` computes posterior summaries of impulse–response functions (IRFs), dynamic-multiplier functions, and forecast-error variance decompositions (FEVDs). Posterior means, medians, and credible intervals of all of these functions are referred to collectively as Bayesian IRF results and are saved in an IRF file under a specified filename. Once you have created a set of Bayesian IRF results, you can use the other `bayesirf` commands to analyze them.

Quick start

Create IRF `myirf` with 8 forecast periods in the active IRF file

```
bayesirf create myirf
```

Same as above, but save the entire Markov chain Monte Carlo (MCMC) sample of results in `myirfmcmc.dta` (required when option `clevel()` or `hpd` is specified with other `bayesirf` subcommands)

```
bayesirf create myirf, mcmcsaving(myirfmcmc)
```

Compute IRF for 12 periods and use `myirfs.irf` file for saving results

```
bayesirf create myirf, set(myirfs) step(12)
```

Same as above, but compute 80% highest posterior density (HPD) credible intervals instead of 95% equal-tailed credible intervals

```
bayesirf create myirf, set(myirfs) step(12) clevel(80) hpd
```

Note: `bayesirf` commands can be used after `bayes: var`, `bayes: dsge`, or `bayes: dsgenl`; see [BAYES] **bayes: var**, [BAYES] **bayes: dsge**, or [BAYES] **bayes: dsgenl**.

Menu

Statistics > Multivariate time series > Bayesian models > IRF and FEVD analysis

Syntax

```
bayesirf create irfname [ , options ]
```

irfname is any valid name that does not exceed 15 characters.

options	Description
Main	
`set(`*filename*`[, replace])`	make *filename* active
`replace`	replace *irfname* if it already exists
`step(#)`	set forecast horizon to #; default is `step(8)`
`order(`*varlist*`)`	specify Cholesky ordering of endogenous variables; available only after `bayes: var`
`estimates(`*estname*`)`	use previously stored results *estname*; default is to use active results
Bayesian	
`clevel(#)`	set credible interval level; default is `clevel(95)`
`equaltailed`	save equal-tailed credible intervals; the default
`hpd`	save HPD credible intervals instead of the default equal-tailed credible intervals
`mcmcsaving(`*filename*`[, replace])`	save simulation results to *filename*`.dta`
`mcmcsaving`	save simulation results to *irfname*`_mcmc.dta`

`bayesirf create` can be used only after `bayes: var`, `bayes: dsge`, and `bayes: dsgenl`.

You must `tsset` your data before using `bayes: var` or `bayes: dsge` and, hence, before using `bayesirf create`; see [TS] **tsset**.

Options

Main

`set(`*filename*`[, replace])`, `replace`, `step(#)`, `order(`*varlist*`)`, and `estimates(`*estname*`)`; see [TS] **irf create**. Option `order()` is available only after estimation using `bayes: var`.

Bayesian

`clevel(#)` specifies the credible level, as a percentage, for equal-tailed and HPD credible intervals. The default is `clevel(95)` or as set by [BAYES] **set clevel**.

`hpd` displays the HPD credible intervals instead of the default equal-tailed credible intervals.

`mcmcsaving(`*filename*`[, replace])` saves simulation results in *filename*`.dta`. The `replace` option specifies to overwrite *filename*`.dta` if it exists. If the `mcmcsaving()` option is not specified, simulation results are not saved.

The saved dataset has the following structure. Variable `_chain` records chain identifiers. Variable `_index` records iteration numbers. `bayesirf create` saves only states (sets of values) that are different from one iteration to another and the frequency of each state in variable `_frequency`. As such, `_index` may not necessarily contain consecutive integers. Remember to use `_frequency` as a frequency weight if you need to obtain any summaries of this dataset. MCMC values for each computed function *func* for each combination of an impulse $\#_1$ and response $\#_2$ variables and for

each time period t are saved in a separate variable in the dataset. These variables are named as *func*_#$_1$_#$_2$_t.

`mcmcsaving` saves the simulation results in *irfname*`_mcmc.dta`.

Remarks and examples

Please read [TS] **irf** first. An introductory example using IRFs is presented there.

`bayesirf create` estimates several types of IRFs, dynamic-multiplier functions, and FEVDs. Which estimates are saved depends on the estimation method previously used to fit the model.

	Estimation command	
Saves	`var`	`dsge`/ `dsgenl`
simple IRFs	x	x
orthogonalized IRFs	x	
dynamic multipliers	x	
cumulative IRFs	x	
cumulative orthogonalized IRFs	x	
cumulative dynamic multipliers	x	
Cholesky FEVDs	x	

`bayesirf` computes results based on the MCMC sample from the corresponding posterior distributions of IRF and other functions, which we will call the IRF MCMC sample. `bayesirf create` computes posterior means, medians, standard deviations, and, by default, 95% equal-tailed credible intervals for all functions and saves them in *irfname*`.dta`. When you later display or graph credible intervals by using, for instance, `bayesirf table` or `bayesirf graph`, the default credible intervals will be reported. If, for instance, you want to change the default level by using `clevel()` or compute HPD credible intervals by using `hpd` with those commands, you must first save the IRF MCMC sample by using `mcmcsaving()` with `bayesirf create`. For example,

```
. bayesirf create myirf, mcmcsaving(myirfmcmc)
```

You can also specify the `clevel()` or `hpd` option directly with `bayesirf create` to save the desired credible intervals in the current IRF file to be used by all `bayesirf` subcommands by default.

Remarks and examples are presented under the following headings:

IRFs after Bayesian vector autoregression (VAR) models
Technical aspects of IRF files

IRFs after Bayesian vector autoregression (VAR) models

▷ Example 1: Bayesian VAR(2) model with default prior

We revisit example 1 from the documentation of the `irf create` command. It uses the `lutkepohl2` dataset of West Germany microeconomic quarterly data for the years between 1960 and 1978. The example studies the relationships between investment, `dln_inv`, income, `dln_inc`, and consumption, `dln_consump`.

```
. use https://www.stata-press.com/data/r18/lutkepohl2
. tsset
```

Using the `bayes: var` command, we fit a Bayesian VAR model with two lags on the dependent variables `dln_inv`, `dln_inc`, and `dln_consump`.

```
. bayes, rseed(17) saving(bvarex1) nomodelsummary:
> var dln_inv dln_inc dln_consump if qtr>=tq(1961q2) & qtr<=tq(1978q4)
Burn-in ...
Simulation ...

Bayesian vector autoregression                  MCMC iterations  =     12,500
Gibbs sampling                                  Burn-in          =      2,500
                                                MCMC sample size =     10,000
```

Sample: 1961q2 thru 1978q4 — Number of obs = 71
Acceptance rate = 1
Efficiency: min = .9556
avg = .9962
Log marginal-likelihood = 467.75286 — max = 1

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
dln_inv						
dln_inv						
L1.	.4749526	.1046821	.001071	.4762824	.2706787	.6790291
L2.	.0062935	.063174	.000632	.0058376	-.1181113	.129959
dln_inc						
L1.	.1150521	.4145854	.004146	.1155755	-.7122031	.9358321
L2.	.0096558	.2461088	.002464	.0129206	-.4780951	.490937
dln_consump						
L1.	-.0693822	.4910385	.004828	-.0712677	-1.016477	.9050535
L2.	.0182113	.2919327	.002919	.0169657	-.5563898	.6010627
_cons	.0067839	.0153897	.000154	.0067986	-.0233363	.0367596
dln_inc						
dln_inv						
L1.	.0152113	.0248328	.000248	.0154024	-.0341219	.0635173
L2.	.000957	.0149204	.000147	.0010833	-.0285813	.0306545
dln_inc						
L1.	.600281	.0981275	.000981	.5997577	.4077653	.7928394
L2.	.011757	.0577031	.000577	.0123101	-.1009659	.1245041
dln_consump						
L1.	-.0331359	.1151265	.001151	-.0318916	-.2594495	.1939938
L2.	-.0266197	.0694851	.000695	-.0263958	-.1637059	.1123704
_cons	.0084678	.0036265	.000037	.0084371	.0013034	.0155666
dln_consump						
dln_inv						
L1.	-.0183312	.0220482	.00022	-.0182937	-.062597	.0243933
L2.	.0092806	.0135179	.000135	.0094044	-.0171007	.036166
dln_inc						
L1.	-.0365965	.0875614	.000876	-.0368425	-.2086565	.1364804
L2.	.0345945	.0520216	.000514	.0339648	-.0668323	.136918
dln_consump						
L1.	.5444814	.1030406	.001027	.5432019	.3416401	.7489821
L2.	.0555939	.0617942	.000618	.055126	-.063175	.1763757
_cons	.0078414	.0032597	.000033	.0078245	.001402	.0141132
Sigma_1_1	.003945	.0006693	6.4e-06	.0038783	.0028446	.0054382
Sigma_2_1	-.0000314	.0001118	1.1e-06	-.0000291	-.0002548	.0001897
Sigma_3_1	.000138	.0001007	1.0e-06	.0001355	-.0000512	.0003478
Sigma_2_2	.0002195	.0000373	3.7e-07	.0002158	.0001579	.0003039
Sigma_3_2	.0000502	.0000238	2.4e-07	.000049	6.46e-06	.0001007
Sigma_3_3	.0001743	.0000294	2.9e-07	.0001714	.0001261	.0002408

file **bvarex1.dta** saved.

There are 21 regression coefficients in the model. By default, `bayes: var` applies a conjugate Minnesota prior on regression coefficients, the effect of which may be difficult to observe directly from the output table. The IRF functions provide a more accessible interpretation of estimation results by assessing the effect of an instant change in one variable on the rest as this effect develops in time. It would be interesting to see a comparison between Bayesian and frequentist results.

Before continuing, let's check the stability condition of the model. The interpretation of IRFs assumes that this condition is satisfied.

```
. bayesvarstable
Eigenvalue stability condition                  Companion matrix size =     6
                                                MCMC sample size      = 10000
```

Eigenvalue modulus	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
1	.7295294	.0952871	.000953	.7272906	.547312	.9209245
2	.6039037	.1045099	.001045	.6094994	.3810883	.7904044
3	.428933	.1272649	.001273	.4239249	.2113325	.6645651
4	.2126552	.0780213	.00078	.1997342	.0900884	.3846134
5	.1378018	.0565196	.000565	.1349177	.0385605	.2577174
6	.0759403	.05052	.000505	.0700686	.0035577	.1847619

```
Pr(eigenvalues lie inside the unit circle) = 0.9966
```

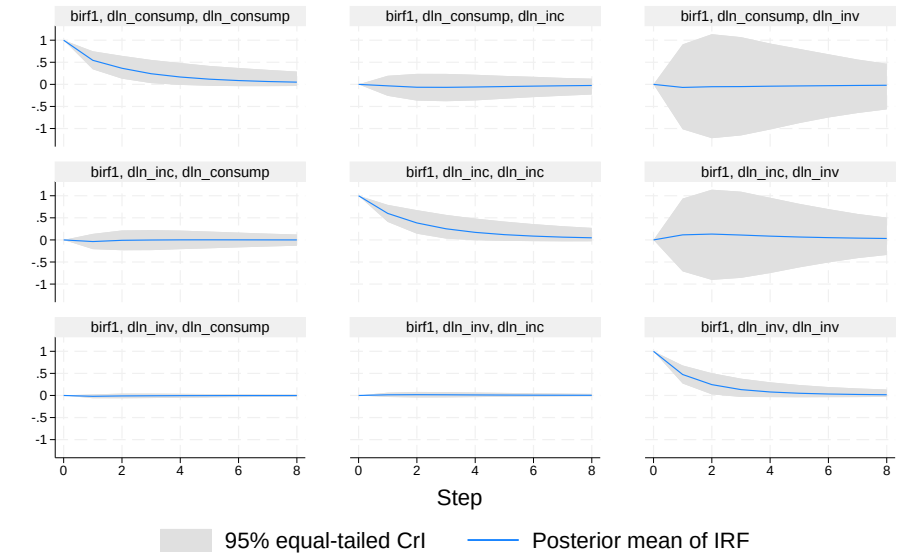
The unit circle inclusion probability for eigenvalues is essentially 1, so the stability condition is satisfied.

We continue with computing IRFs for 8 steps ahead and save the results as `birf1` in `birfex1.irf`.

```
. bayesirf create birf1, step(8) set(birfex1)
(file birfex1.irf created)
(file birfex1.irf now active)
(file birfex1.irf updated)
```

A quick way to inspect IRF estimates is by using `bayesirf graph`.

```
. bayesirf graph irf
```



Graphs by irfname, impulse variable, and response variable

There are nine IRF graphs, one for each combination of the three impulses and three responses.

Example 2: Bayesian VAR(2) model with weakly informative prior

To see the effect of priors on regression coefficients, we fit a second model in which we relax the Minnesota prior by changing the `selftight()` parameter from the default of 0.1 to 1. The effect of this change is that now the Bayesian estimates will be closer to the frequentist ones, as would be obtained from the corresponding [TS] **var** command.

```
. bayes, minnconjprior(selftight(1)) rseed(17) saving(bvarex2) nomodelsummary:
> var dln_inv dln_inc dln_consump if qtr>=tq(1961q2) & qtr<=tq(1978q4)
Burn-in ...
Simulation ...
Bayesian vector autoregression                  MCMC iterations  =     12,500
Gibbs sampling                                  Burn-in          =      2,500
                                                MCMC sample size =     10,000
```

```
Sample: 1961q2 thru 1978q4                      Number of obs    =         71
                                                Acceptance rate  =          1
                                                Efficiency:  min =      .9551
                                                             avg =      .9982
Log marginal-likelihood =  516.18125                         max =          1
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
dln_inv						
dln_inv						
L1.	-.291233	.1205245	.001233	-.2896978	-.5273294	-.0564433
L2.	-.147377	.1174619	.001175	-.1479881	-.37888	.0835443
dln_inc						
L1.	.2349793	.5412359	.005412	.2376725	-.8448062	1.296301
L2.	.0318927	.5068351	.005074	.0364385	-.9534818	1.014282
dln_consump						
L1.	.7590264	.6437021	.006356	.7512454	-.4969188	2.034697
L2.	.7816876	.6184552	.006185	.7857257	-.4503459	2.015964
_cons	-.0115762	.0166601	.000167	-.0115223	-.0447488	.0209634
dln_inc						
dln_inv						
L1.	.0437786	.031111	.000311	.0439332	-.017398	.1045939
L2.	.0455046	.0301702	.000296	.0456176	-.0144909	.1057367
dln_inc						
L1.	-.1070955	.1398919	.001399	-.1073961	-.3828335	.1651545
L2.	.0235544	.1295408	.001295	.0245432	-.2289609	.2773168
dln_consump						
L1.	.2556043	.1658887	.001659	.2566669	-.0714113	.5763302
L2.	-.0311667	.1611506	.001612	-.0307495	-.3473144	.2870275
_cons	.0158357	.004275	.000043	.0158581	.0074012	.024185
dln_consump						
dln_inv						
L1.	-.0043581	.0251223	.000251	-.0044075	-.0539712	.0445555
L2.	.0340665	.024665	.000247	.0340276	-.0140267	.082563
dln_inc						
L1.	.1833481	.1134026	.001134	.1830458	-.0411146	.4053818
L2.	.3091415	.1060541	.001049	.3090028	.1014922	.5166988
dln_consump						
L1.	-.2203787	.1344117	.001314	-.2190475	-.479903	.0415251
L2.	.0221078	.1295494	.001295	.0226184	-.228624	.2798039
_cons	.0128598	.0034698	.000035	.0128702	.0060369	.0195489
Sigma_1_1	.0020092	.0003405	3.3e-06	.0019742	.0014548	.0027654
Sigma_2_1	.0000578	.0000625	6.2e-07	.0000563	-.0000618	.0001857
Sigma_3_1	.0001097	.0000518	5.2e-07	.0001073	.0000149	.0002205
Sigma_2_2	.0001322	.0000223	2.2e-07	.0001301	.0000954	.0001828
Sigma_3_2	.0000562	.0000143	1.4e-07	.000055	.0000316	.0000877
Sigma_3_3	.000087	.0000147	1.5e-07	.0000855	.0000629	.0001202

```
file bvarex2.dta saved.
```

We compute IRFs for the second model and save them as `birf2` in the same dataset `birfex1`.

```
. bayesirf create birf2, step(8) set(birfex1)
(file birfex1.irf now active)
(file birfex1.irf updated)
```

Using the `bayesirf ctable` command, we show the posterior means of FEVDs of the impulse `dln_inc` on the response `dln_consump` along with estimates of posterior standard deviations.

```
. bayesirf ctable (birf1 dln_inc dln_consump fevd)
> (birf2 dln_inc dln_consump fevd), nocri stddev
```

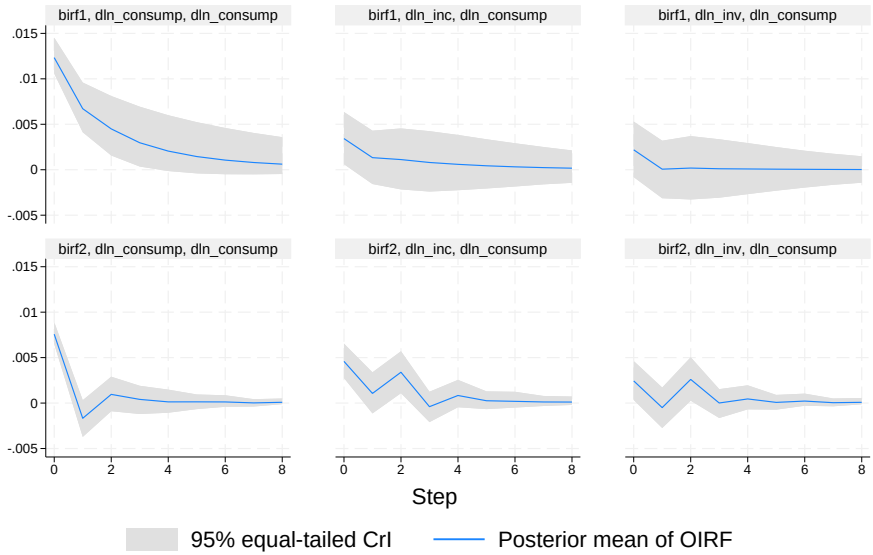
Step	(1) fevd	(1) Std. dev.	(2) fevd	(2) Std. dev.
0	0	0	0	0
1	.078122	.054559	.249063	.08115
2	.077138	.053865	.254958	.077739
3	.083944	.058845	.313267	.084101
4	.090341	.064417	.31425	.083694
5	.095177	.068994	.318057	.085284
6	.098524	.072337	.318697	.085481
7	.100779	.074699	.319035	.085732
8	.102291	.076363	.31923	.085885

```
Posterior means reported.
(1) irfname = birf1, impulse = dln_inc, and response = dln_consump.
(2) irfname = birf2, impulse = dln_inc, and response = dln_consump.
```

We notice that the FEVD estimates for the second model are much closer to those in the original example 1. In contrast, for the first model, the contribution of `dln_inc` to the variance of `dln_consump` is substantially lower, starting from 8% for step 1 and increasing only to 10% for step 8. The difference between the two models can be explained by the effect of using different priors for regression coefficients. The default conjugate Minnesota prior with the `selftight()` parameter of 0.1 shrinks the cross-variables lag coefficients to zero, thus reducing the corresponding FEVDs. For example, the posterior mean estimates of `{dln_consump:L1.dln_inc}` and `{dln_consump:L2.dln_inc}` are about 0.18 and 0.31 in the second model but only -0.04 and 0.03 in the first model.

Finally, let's examine the orthogonalized IRF (OIRF) response on `dln_consump` using the `bayesirf graph` command.

```
. bayesirf graph oirf, response(dln_consump)
```

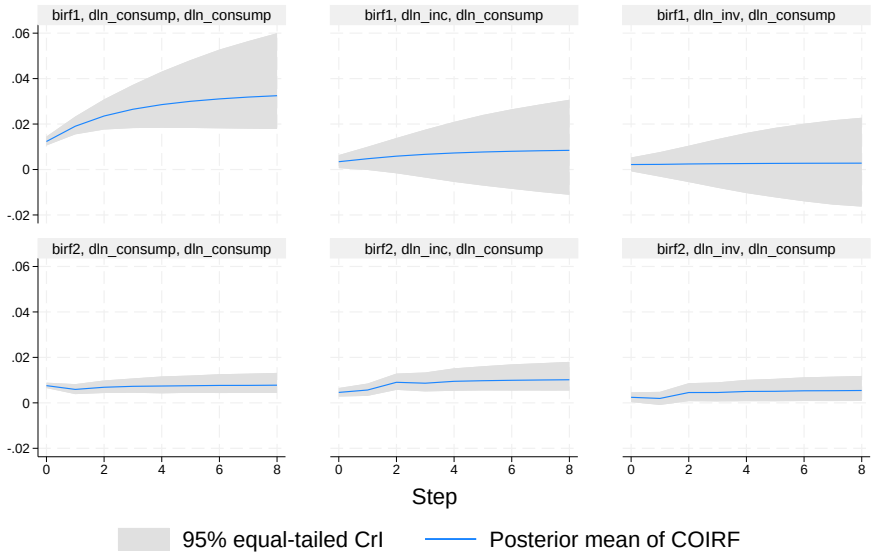


Graphs by irfname, impulse variable, and response variable

The IRF graphs confirm the differences between the two models caused by the effect of the Minnesota prior on regression coefficients. For the first model, which has stronger priors, the impulse responses on `dln_consump` are smoother and have larger uncertainty, as evident by their credible bands. For the second model, the prior effect is minimal, and the graphs have ups and downs that may be due to some seasonal trends. There are no general rules for choosing the right amount of prior strength. The choice should be based on subject matter and prior experience. We also observe that all OIRFs converge to 0 relatively fast, as we expect from a stable VAR model.

The cumulative OIRFs show equilibrium convergence clearly:

```
. bayesirf graph coirf, response(dln_consump)
```



Graphs by irfname, impulse variable, and response variable

Technical aspects of IRF files

`bayesirf create` computes posterior statistics of a series of IRFs and saves them in an IRF file. IRF files are just Stata datasets that have names ending in `.irf` instead of `.dta`. The dataset in the file has a nested panel structure.

Variable `irfname` contains the *irfname* specified by the user. Variable `impulse` records the name of the endogenous variable whose innovations are the impulse. Variable `response` records the name of the endogenous variable that is responding to the innovations. In a model with K endogenous variables, there are K^2 combinations of `impulse` and `response`. Variable `step` records the periods for which these estimates were computed.

Below is a catalog of the statistics that `bayesirf create` estimates after the `bayes: var` command and the variable names under which they are saved in the IRF file.

Posterior statistic	Name
Posterior mean of IRFs	`irf`
Posterior mean of OIRFs	`oirf`
Posterior mean of cumulative IRFs	`cirf`
Posterior mean of cumulative OIRFs	`coirf`
Posterior mean of dynamic-multiplier functions	`dm`
Posterior mean of cumulative dynamic-multiplier functions	`cdm`
Posterior mean of Cholesky forecast-error decomposition	`fevd`
Posterior standard deviation of the IRFs	`stdirf`
Posterior standard deviation of the OIRFs	`stdoirf`
Posterior standard deviation of the cumulative IRFs	`stdcirf`
Posterior standard deviation of the cumulative OIRFs	`stdcoirf`
Posterior standard deviation of dynamic-multiplier functions	`stddm`
Posterior standard deviation of cumulative dynamic-multiplier functions	`stdcdm`
Posterior standard deviation of the Cholesky forecast-error decomposition	`stdfevd`
Posterior median of the IRFs	`medirf`
Posterior median of the OIRFs	`medoirf`
Posterior median of the cumulative IRFs	`medcirf`
Posterior median of the cumulative OIRFs	`medcoirf`
Posterior median of dynamic-multiplier functions	`meddm`
Posterior median of cumulative dynamic-multiplier functions	`medcdm`
Posterior median of the Cholesky forecast-error decomposition	`medfevd`
Lower CrI of the IRFs	`irfl`
Lower CrI of the OIRFs	`oirfl`
Lower CrI of the cumulative IRFs	`cirfl`
Lower CrI of the cumulative OIRFs	`coirfl`
Lower CrI of dynamic-multiplier functions	`dml`
Lower CrI of cumulative dynamic-multiplier functions	`cdml`
Lower CrI of the Cholesky forecast-error decomposition	`fevdl`
Upper CrI of the IRFs	`irfu`
Upper Crl of the OIRFs	`oirfu`
Upper CrI of the cumulative IRFs	`cirfu`
Upper CrI of the cumulative OIRFs	`coirfu`
Upper CrI of dynamic-multiplier functions	`dmu`
Upper CrI of cumulative dynamic-multiplier functions	`cdmu`
Upper CrI of the Cholesky forecast-error decomposition	`fevdu`

In addition to the variables, information is stored in _dta characteristics. See *Technical aspects of IRF files* for the list of main characteristics. Below we list the characteristics that are specific to the bayes prefix models. For each *irfname* in _dta[irfnames], these are the additional characteristics:

Name	Contents
_dta[*irfname*_bayes]	it is bayes if *irfname* is created by bayesirf create
_dta[*irfname*_level]	level of the saved credible intervals
_dta[*irfname*_hpd]	it is hpd if HPD instead of equal-tailed CrIs are saved
_dta[*irfname*_mcmcfile]	MCMC file of simulated IRFs
_dta[*irfname*_mcmcsize]	MCMC sample size

Methods and formulas

Bayesian estimates of IRFs and other functions are obtained from their respective posterior distributions.

Let $\mathbf{\Phi_i} = (\phi_{jk,i})$ denote the impulse–response matrix after i periods; see *Methods and formulas* in [TS] **irf create** for its definition. Bayesian computation of IRFs involves estimation of the posterior distribution of each coefficient $\phi_{jk,i}$. Specifically, we recycle the MCMC sample created by the bayes: prefix command that contains draws from the posterior distribution of the model parameters such as regression coefficients and error covariance. For each draw, the IRF coefficients are computed according to the formulas in [TS] **irf create** and saved as MCMC samples, one for each coefficient. Finally, the resulting MCMC samples of IRF coefficients are summarized, and standard statistics such as posterior means, medians, and credible intervals are saved in the .irf file produced by bayesirf create.

Other functions are computed similarly; see *Methods and formulas* in [TS] **irf create** for their definitions.

Also see

[BAYES] **bayesirf** — Bayesian IRFs, dynamic-multiplier functions, and FEVDs

[TS] **irf** — Create and analyze IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayes: dsge** — Bayesian linear dynamic stochastic general equilibrium models

[BAYES] **bayes: dsgenl** — Bayesian nonlinear dynamic stochastic general equilibrium models

[BAYES] **bayes: var** — Bayesian vector autoregressive models

Title

bayesirf graph — Graphs of Bayesian IRFs, dynamic-multiplier functions, and FEVDs

Description

`bayesirf graph` graphs Bayesian impulse–response functions (IRFs), dynamic-multiplier functions, and forecast-error variance decompositions (FEVDs) over time.

Quick start

Graph IRF for dependent variables `y1` and `y2` given an unexpected shock to `y1`

```
bayesirf graph irf, impulse(y1) response(y2)
```

Same as above, but for orthogonalized shocks

```
bayesirf graph oirf, impulse(y1) response(y2)
```

Same as above, but begin the plot with the third forecast period

```
bayesirf graph oirf, impulse(y1) response(y2) lstep(3)
```

Same as above, but with a separate graph for each IRF in the current IRF file

```
bayesirf graph oirf, impulse(y1) response(y2) lstep(3) individual
```

Note: `bayesirf` commands can be used after `bayes: var`, `bayes: dsge`, or `bayes: dsgenl`; see [BAYES] **bayes: var**, [BAYES] **bayes: dsge**, or [BAYES] **bayes: dsgenl**.

Menu

Statistics > Multivariate time series > Bayesian models > IRF and FEVD analysis

Syntax

```
bayesirf graph stat [ , options ]
```

stat	Description
Main	
`irf`	IRF
`oirf`	orthogonalized IRF
`dm`	dynamic-multiplier function
`cirf`	cumulative IRF
`coirf`	cumulative orthogonalized IRF
`cdm`	cumulative dynamic-multiplier function
`fevd`	Cholesky forecast-error variance decomposition

Notes: 1. No statistic may appear more than once.
2. If credible intervals are included (the default), only two statistics may be included.
3. If credible intervals are suppressed (option `nocri`), up to four statistics may be included.
4. Only `irf` is available after `bayes: dsge` and `bayes: dsgenl`.

options	Description
irf_options	any *options* documented in [TS] **irf graph**
Bayesian	
`nocri`	suppress credible intervals
`clevel(#)`	set credible interval level; default is set by `bayesirf create`
`equaltailed`	display equal-tailed credible intervals; default is set by `bayesirf create`
`hpd`	display HPD credible intervals; default is set by `bayesirf create`
`median`	display posterior medians instead of posterior means
CrI plot	
`cri#opts(`*area_options*`)`	affect rendition of the credible interval for the # *stat*

The **CrI plot** tab replaces the **CI plot** tab of [TS] **irf graph**.

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

Options

irf_options are any of the *options* documented in [TS] **irf graph**. `level(#)` is a synonym for `clevel(#)`, `noci` is a synonym for `nocri`, and `ci#opts()` is a synonym for `cri#opts()`. Synonymous options do not appear on the dialog box.

Bayesian

`nocri` suppresses displaying the credible intervals for each statistic.

`clevel(#)`, `equaltailed`, and `hpd` affect the calculation of credible intervals. When the specified options do not correspond to the default credible intervals saved in the current IRF file by `bayesirf`

`create`, `bayesirf` will need an IRF MCMC sample to recompute the credible intervals. You can save this sample by specifying option `mcmcsaving()` with `bayesirf create`. Alternatively, if you would like to save the desired credible intervals as the default credible intervals in the current IRF file, you can specify the corresponding options directly with `bayesirf create`. See *Remarks and examples* in [BAYES] **bayesirf create**.

`clevel(#)` specifies the credible level, as a percentage, for equal-tailed and HPD credible intervals.

`equaltailed` displays the equal-tailed credible intervals. `equaltailed` may not be specified with `hpd`.

`hpd` displays the HPD credible intervals. `hpd` may not be specified with `equaltailed`.

`median` displays the posterior medians instead of the default posterior means.

CrI plot

`cri1opts(`*area_options*`)` and `cri2opts(`*area_options*`)` affect the rendition of the credible intervals for the first (`cri1opts()`) and second (`cri2opts()`) statistics in *stat*. *area_options* are as described in [G-3] ***area_options***. `irf`'s `ci#opts()` is a synonym for `cri#opts()`.

The **CrI plot** tab replaces the **CI plot** tab of [TS] **irf graph**.

Remarks and examples

See [TS] **irf graph** for a general discussion about IRF and other graphs, and see example 8 in [BAYES] **bayes: var** for an example.

Also see [BAYES] **bayesirf cgraph**, which produces combined graphs; [BAYES] **bayesirf ograph**, which produces overlaid graphs; and [BAYES] **bayesirf table**, which displays results in tabular form.

Stored results

For stored results, see *Stored results* in [TS] **irf graph**.

Also see

[TS] **irf graph** — Graphs of IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayesirf cgraph** — Combined graphs of Bayesian IRF results

[BAYES] **bayesirf ograph** — Overlaid graphs of Bayesian IRF results

[BAYES] **bayesirf create** — Obtain Bayesian IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayesirf table** — Tables of Bayesian IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayesirf** — Bayesian IRFs, dynamic-multiplier functions, and FEVDs

Title

bayesirf cgraph — Combined graphs of Bayesian IRF results

Description

`bayesirf cgraph` makes a combined graph of Bayesian impulse–response function (IRF) results. A graph is made for specified combinations of named IRF results, impulse variables, response variables, and statistics. `bayesirf cgraph` combines these graphs into one image, unless separate graphs are requested.

Quick start

Combine graphs of an orthogonalized IRF `birf` and cumulative IRF `birf` for dependent variable `y1` and `y2`.

```
bayesirf cgraph (birf y1 y2 oirf) (birf y1 y2 cirf)
```

Same as above, but with maximum steps of 4 and 80% credible interval

```
bayesirf cgraph (birf y1 y2 oirf) (birf y1 y2 cirf), ustep(4) clevel(80)
```

Note: `bayesirf` commands can be used after `bayes: var`, `bayes: dsge`, or `bayes: dsgenl`; see [BAYES] **bayes: var**, [BAYES] **bayes: dsge**, or [BAYES] **bayes: dsgenl**.

Menu

Statistics > Multivariate time series > Bayesian models > IRF and FEVD analysis

Syntax

```
bayesirf cgraph (spec1) [(spec2) ... (specN)] [, options]
```

where (*spec*$_k$) is

```
(irfname impulsevar responsevar stat [, spec_options])
```

irfname is the name of a set of IRF results in the active IRF file. *impulsevar* should be specified as an endogenous variable for all statistics except `dm` and `cdm`; for those, specify as an exogenous variable. *responsevar* is an endogenous variable name. *stat* is one or more statistics from the list below:

stat	Description
Main	
`irf`	IRF
`oirf`	orthogonalized IRF
`dm`	dynamic-multiplier function
`cirf`	cumulative IRF
`coirf`	cumulative orthogonalized IRF
`cdm`	cumulative dynamic-multiplier function
`fevd`	Cholesky forecast-error variance decomposition

Notes: 1. No statistic may appear more than once.
2. If credible intervals are included (the default), only two statistics may be included.
3. If credible intervals are suppressed (option `nocri`), up to four statistics may be included.
4. Only `irf` is available after `bayes: dsge` and `bayes: dsgenl`.

options	Description
irf_options	any *options* documented in [TS] **irf cgraph**
Bayesian	
`nocri`	suppress credible intervals
`clevel(#)`	set credible interval level; default is set by `bayesirf create`
`equaltailed`	display equal-tailed credible intervals; default is set by `bayesirf create`
`hpd`	display HPD credible intervals; default is set by `bayesirf create`
`median`	display posterior medians instead of posterior means
CrI plot	
`cri#opts(`*area_options*`)`	affect rendition of the credible interval for the # *stat*

The **CrI plot** tab replaces the **CI plot** tab of [TS] **irf cgraph**.

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

spec_options	Description
irf_spec_options	any *spec_options* documented in [TS] **irf cgraph**
Bayesian	
`nocri`	suppress credible intervals
`clevel(#)`	set credible interval level; default is set by `bayesirf create`
`equaltailed`	display equal-tailed credible intervals; default is set by `bayesirf create`
`hpd`	display HPD credible intervals; default is set by `bayesirf create`
`median`	display posterior medians instead of posterior means
CrI plot	
`cri#opts(`*area_options*`)`	affect rendition of the credible interval for the *# stat*

spec_options may be specified within a graph specification, globally, or in both. When specified in a graph specification, the *spec_options* affect only the specification in which they are used. When supplied globally, the *spec_options* affect all graph specifications. When supplied in both places, options in the graph specification take precedence.

Options

irf_options and *irf_spec_options* are any of the *options* and *spec_options*, respectively, documented in [TS] **irf cgraph**. `level(#)` is a synonym for `clevel(#)`, `noci` is a synonym for `nocri`, and `ci#opts()` is a synonym for `cri#opts()`. Synonymous options do not appear on the dialog box.

Bayesian

`nocri` suppresses displaying the credible intervals for each statistic.

`clevel(#)`, `equaltailed`, and `hpd` affect the calculation of credible intervals. When the specified options do not correspond to the default credible intervals saved in the current IRF file by `bayesirf create`, `bayesirf` will need an IRF MCMC sample to recompute the credible intervals. You can save this sample by specifying option `mcmcsaving()` with `bayesirf create`. Alternatively, if you would like to save the desired credible intervals as the default credible intervals in the current IRF file, you can specify the corresponding options directly with `bayesirf create`. See *Remarks and examples* in [BAYES] **bayesirf create**.

`clevel(#)` specifies the credible level, as a percentage, for equal-tailed and HPD credible intervals.

`equaltailed` displays the equal-tailed credible intervals. `equaltailed` may not be specified with `hpd`.

`hpd` displays the HPD credible intervals. `hpd` may not be specified with `equaltailed`.

`median` displays the posterior medians instead of the default posterior means.

CrI plot

`cri1opts(`*area_options*`)` and `cri2opts(`*area_options*`)` affect the rendition of the credible intervals for the first (`cri1opts()`) and second (`cri2opts()`) statistics in *stat*. *area_options* are as described in [G-3] ***area_options***. `irf`'s `ci#opts()` is a synonym for `cri#opts()`.

The **CrI plot** tab replaces the **CI plot** tab of [TS] **irf cgraph**.

Remarks and examples

See [TS] **irf cgraph** for a general discussion about combined IRF and other graphs.

Also see [BAYES] **bayesirf graph**, which produces individual graphs; [BAYES] **bayesirf ograph**, which produces overlaid graphs; and [BAYES] **bayesirf table**, which displays results in tabular form.

Stored results

For stored results, see *Stored results* in [TS] **irf cgraph**.

Also see

[TS] **irf cgraph** — Combined graphs of IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayesirf graph** — Graphs of Bayesian IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayesirf ograph** — Overlaid graphs of Bayesian IRF results

[BAYES] **bayesirf create** — Obtain Bayesian IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayesirf table** — Tables of Bayesian IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayesirf** — Bayesian IRFs, dynamic-multiplier functions, and FEVDs

Title

bayesirf ograph — Overlaid graphs of Bayesian IRF results

Description

`bayesirf ograph` displays plots of Bayesian impulse–response function (IRF) results on one graph (one pair of axes).

Quick start

Graph of an orthogonalized IRF `birf` overlaid on cumulative IRF `birf` for dependent variable `y1` and `y2`

```
bayesirf ograph (birf y1 y2 oirf) (birf y1 y2 cirf)
```

Note: `bayesirf` commands can be used after `bayes: var`, `bayes: dsge`, or `bayes: dsgenl`; see [BAYES] **bayes: var**, [BAYES] **bayes: dsge**, or [BAYES] **bayes: dsgenl**.

Menu

Statistics > Multivariate time series > Bayesian models > IRF and FEVD analysis

Syntax

```
bayesirf ograph (spec1) [(spec2) ... [(spec15)]] [, options]
```

where (*spec*$_k$) is

```
(irfname impulsevar responsevar stat [, spec_options]) )
```

irfname is the name of a set of IRF results in the active IRF file or "`.`", which means the first named result in the active IRF file. *impulsevar* should be specified as an endogenous variable for all statistics except `dm` and `cdm`; for those, specify as an exogenous variable. *responsevar* is an endogenous variable name. *stat* is one or more statistics from the list below:

stat	Description
Main	
`irf`	IRF
`oirf`	orthogonalized IRF
`dm`	dynamic-multiplier function
`cirf`	cumulative IRF
`coirf`	cumulative orthogonalized IRF
`cdm`	cumulative dynamic-multiplier function
`fevd`	Cholesky forecast-error variance decomposition

Note: Only `irf` is available after `bayes: dsge` and `bayes: dsgenl`.

options	Description
irf_options	any *options* documented in [TS] **irf ograph**
Bayesian	
`cri`	add credible bands to the graph
`clevel(#)`	set credible interval level; default is set by `bayesirf create`
`equaltailed`	display equal-tailed credible intervals; default is set by `bayesirf create`
`hpd`	display HPD credible intervals; default is set by `bayesirf create`
`median`	display posterior medians instead of posterior means
CrI plot	
`criopts(`*area_options*`)`	affect rendition of the credible intervals

The **CrI plot** tab replaces the **CI plot** tab of [TS] **irf ograph**.

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

spec_options	Description
irf_spec_options	any *spec_options* documented in [TS] **irf ograph**
Bayesian	
`cri`	add credible bands to the graph
`clevel(#)`	set credible interval level; default is set by `bayesirf create`
`equaltailed`	display equal-tailed credible intervals; default is set by `bayesirf create`
`hpd`	display HPD credible intervals; default is set by `bayesirf create`
`median`	display posterior medians instead of posterior means
CrI plot	
`criopts(`*area_options*`)`	affect rendition of the credible intervals

spec_options may be specified within a graph specification, globally, or in both. When specified in a graph specification, the *spec_options* affect only the specification in which they are used. When supplied globally, the *spec_options* affect all graph specifications. When supplied in both places, options in the graph specification take precedence.

Options

irf_options and *irf_spec_options* are any of the *options* and *spec_options*, respectively, documented in [TS] **irf ograph**. `level(#)` is a synonym for `clevel(#)`, `ci` is a synonym for `cri`, and `ciopts()` is a synonym for `criopts()`. Synonymous options do not appear on the dialog box.

Bayesian

`cri` displays the credible intervals for each statistic. It is implied if `hpd` or `equaltailed` is specified.

`clevel(#)`, `equaltailed`, and `hpd` affect the calculation of credible intervals. When the specified options do not correspond to the default credible intervals saved in the current IRF file by `bayesirf create`, `bayesirf` will need an IRF MCMC sample to recompute the credible intervals. You can save this sample by specifying option `mcmcsaving()` with `bayesirf create`. Alternatively, if you would like to save the desired credible intervals as the default credible intervals in the current IRF file, you can specify the corresponding options directly with `bayesirf create`. See *Remarks and examples* in [BAYES] **bayesirf create**.

`clevel(#)` specifies the credible level, as a percentage, for equal-tailed and HPD credible intervals.

`equaltailed` displays the equal-tailed credible intervals. `equaltailed` may not be specified with `hpd`.

`hpd` displays the HPD credible intervals. `hpd` may not be specified with `equaltailed`.

`median` displays the posterior medians instead of the default posterior means.

CrI plot

`criopts(`*area_options*`)` affects the rendition of the credible intervals for the plotted statistics; see [G-3] ***area_options***. `criopts()` implies `cri`. `irf`'s `ciopts()` is a synonym for `criopts()`.

The **CrI plot** tab replaces the **CI plot** tab of [TS] **irf ograph**.

Remarks and examples

See [TS] **irf ograph** for a general discussion about overlaid IRF and other graphs.

Also see [BAYES] **bayesirf graph**, which produces individual graphs; [BAYES] **bayesirf cgraph**, which produces combined graphs; and [BAYES] **bayesirf table**, which displays results in tabular form.

Stored results

For stored results, see *Stored results* in [TS] **irf ograph**.

Also see

[TS] **irf ograph** — Overlaid graphs of IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayesirf graph** — Graphs of Bayesian IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayesirf cgraph** — Combined graphs of Bayesian IRF results

[BAYES] **bayesirf table** — Tables of Bayesian IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayesirf create** — Obtain Bayesian IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayesirf** — Bayesian IRFs, dynamic-multiplier functions, and FEVDs

Title

bayesirf table — Tables of Bayesian IRFs, dynamic-multiplier functions, and FEVDs

Description

`bayesirf table` makes a table of the values of the requested Bayesian statistics at each time since impulse. Each column represents a combination of an impulse variable and a response variable for each statistic from the named impulse–response function (IRF) results.

Quick start

Table of IRFs for dependent variables `y1` and `y2` given an unexpected shock to `y1`

```
bayesirf table irf, impulse(y1) response(y2)
```

Same as above, but for orthogonalized shocks

```
bayesirf table oirf, impulse(y1) response(y2)
```

Same as above, but with 3 as the common maximum step horizon for all tables

```
bayesirf table oirf, impulse(y1) response(y2) step(3)
```

Same as above, but with a separate table for each IRF in the active IRF file

```
bayesirf table oirf, impulse(y1) response(y2) step(3) individual
```

Note: `bayesirf` commands can be used after `bayes: var`, `bayes: dsge`, or `bayes: dsgenl`; see [BAYES] **bayes: var**, [BAYES] **bayes: dsge**, or [BAYES] **bayes: dsgenl**.

Menu

Statistics > Multivariate time series > Bayesian models > IRF and FEVD analysis

Syntax

```
bayesirf table [stat] [, options]
```

stat	Description
Main	
irf	IRF
oirf	orthogonalized IRF
dm	dynamic-multiplier function
cirf	cumulative IRF
coirf	cumulative orthogonalized IRF
cdm	cumulative dynamic-multiplier function
fevd	Cholesky forecast-error variance decomposition

If *stat* is not specified, all statistics are included. You may specify more than one *stat*.
Note: Only `irf` is available after `bayes: dsge` and `bayes: dsgenl`.

options	Description
irf_options	any *options* documented in [TS] **irf table**
Bayesian	
nocri	suppress credible intervals
clevel(#)	set credible interval level; default is set by `bayesirf create`
equaltailed	display equal-tailed credible intervals; default is set by `bayesirf create`
hpd	display HPD credible intervals; default is set by `bayesirf create`
median	display posterior medians instead of posterior means
stddev	include posterior standard deviations in the tables

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

Options

irf_options are any of the *options* documented in [TS] **irf table**. `level(#)` is a synonym for `clevel(#)`, `noci` is a synonym for `nocri`, and `stderror` is a synonym for `stddev`. Synonymous options do not appear on the dialog box.

Bayesian

`nocri` suppresses displaying the credible intervals for each statistic.

`clevel(#)`, `equaltailed`, and `hpd` affect the calculation of credible intervals. When the specified options do not correspond to the default credible intervals saved in the current IRF file by `bayesirf create`, `bayesirf` will need an IRF MCMC sample to recompute the credible intervals. You can save this sample by specifying option `mcmcsaving()` with `bayesirf create`. Alternatively, if you would like to save the desired credible intervals as the default credible intervals in the current IRF file, you can specify the corresponding options directly with `bayesirf create`. See *Remarks and examples* in [BAYES] **bayesirf create**.

`clevel(#)` specifies the credible level, as a percentage, for equal-tailed and HPD credible intervals.

`equaltailed` displays the equal-tailed credible intervals. `equaltailed` may not be specified with `hpd`.

`hpd` displays the HPD credible intervals. `hpd` may not be specified with `equaltailed`.

`median` displays the posterior medians instead of the default posterior means.

`stddev` specifies that posterior standard deviations for each statistic also be included in the table.

Remarks and examples

See [TS] **irf table** for a general discussion, and see example 8 in [BAYES] **bayes: var** for an example.

Also see [TS] **irf ctable**, which produces combined tables; and [TS] **irf graph**, which displays results on a graph.

Stored results

For stored results, see *Stored results* in [TS] **irf table**.

Also see

[TS] **irf table** — Tables of IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayesirf ctable** — Combined tables of Bayesian IRF results

[BAYES] **bayesirf graph** — Graphs of Bayesian IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayesirf create** — Obtain Bayesian IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayesirf** — Bayesian IRFs, dynamic-multiplier functions, and FEVDs

Title

bayesirf ctable — Combined tables of Bayesian IRF results

Description

`bayesirf ctable` makes a table or a combined table of Bayesian impulse–response function (IRF) results. A table is made for specified combinations of named IRF results, impulse variables, response variables, and statistics. `irf ctable` combines these tables into one table, unless separate tables are requested.

`bayesirf ctable` operates on the active IRF file; see [TS] **irf set**.

Quick start

Combine tables of an orthogonalized IRF `birf` and cumulative IRF `birf` for dependent variable `y1` and `y2`

```
bayesirf ctable (birf y1 y2 oirf) (birf y1 y2 cirf)
```

Same as above, but with maximum steps of 4 and 80% credible interval

```
bayesirf ctable (birf y1 y2 oirf) (birf y1 y2 cirf), step(4) clevel(80)
```

Note: `bayesirf` commands can be used after `bayes: var`, `bayes: dsge`, or `bayes: dsgenl`; see [BAYES] **bayes: var**, [BAYES] **bayes: dsge**, or [BAYES] **bayes: dsgenl**.

Menu

Statistics > Multivariate time series > Bayesian models > IRF and FEVD analysis

Syntax

```
bayesirf ctable (spec1) [(spec2) ... [(specN)]] [, options]
```

where (*spec*$_k$) is

```
(irfname impulsevar responsevar stat [, spec_options])
```

irfname is the name of a set of IRF results in the active IRF file. *impulsevar* should be specified as an endogenous variable for all statistics except `dm` and `cdm`; for those, specify as an exogenous variable. *responsevar* is an endogenous variable name. *stat* is one or more statistics from the list below:

stat	Description
Main	
`irf`	IRF
`oirf`	orthogonalized IRF
`dm`	dynamic-multiplier function
`cirf`	cumulative IRF
`coirf`	cumulative orthogonalized IRF
`cdm`	cumulative dynamic-multiplier function
`fevd`	Cholesky forecast-error variance decomposition

Note: Only `irf` is available after `bayes: dsge` and `bayes: dsgenl`.

options	Description
irf_options	any *options* documented in [TS] **irf ctable**
Bayesian	
`nocri`	suppress credible intervals
`clevel(#)`	set credible interval level; default is set by `bayesirf create`
`equaltailed`	display equal-tailed credible intervals; default is set by `bayesirf create`
`hpd`	display HPD credible intervals; default is set by `bayesirf create`
`median`	display posterior medians instead of posterior means
`stddev`	include posterior standard deviations in the tables

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

spec_options	Description
irf_spec_options	any *spec_options* documented in [TS] **irf ctable**
Bayesian	
`nocri`	suppress credible intervals
`clevel(#)`	set credible interval level; default is set by `bayesirf create`
`equaltailed`	display equal-tailed credible intervals; default is set by `bayesirf create`
`hpd`	display HPD credible intervals; default is set by `bayesirf create`
`median`	display posterior medians instead of posterior means
`stddev`	include posterior standard deviations in the tables

spec_options may be specified within a table specification, globally, or both. When specified in a table specification, the *spec_options* affect only the specification in which they are used. When supplied globally, the *spec_options* affect all table specifications. When specified in both places, options for the table specification take precedence.

Options

irf_options and *irf_spec_options* are any of the *options* and *spec_options*, respectively, documented in [TS] **irf ctable**. `level(#)` is a synonym for `clevel(#)`, `noci` is a synonym for `nocri`, and `stderror` is a synonym for `stddev`. Synonymous options do not appear on the dialog box.

Bayesian

`nocri` suppresses displaying the credible intervals for each statistic.

`clevel(#)`, `equaltailed`, and `hpd` affect the calculation of credible intervals. When the specified options do not correspond to the default credible intervals saved in the current IRF file by `bayesirf create`, `bayesirf` will need an IRF MCMC sample to recompute the credible intervals. You can save this sample by specifying option `mcmcsaving()` with `bayesirf create`. Alternatively, if you would like to save the desired credible intervals as the default credible intervals in the current IRF file, you can specify the corresponding options directly with `bayesirf create`. See *Remarks and examples* in [BAYES] **bayesirf create**.

`clevel(#)` specifies the credible level, as a percentage, for equal-tailed and HPD credible intervals.

`equaltailed` displays the equal-tailed credible intervals. `equaltailed` may not be specified with `hpd`.

`hpd` displays the HPD credible intervals. `hpd` may not be specified with `equaltailed`.

`median` displays the posterior medians instead of the default posterior means.

`stddev` specifies that posterior standard deviations for each statistic also be included in the table.

Remarks and examples

See [TS] **irf ctable** for a general discussion, and see example 2 in [BAYES] **bayesirf create** for an example.

Also see [TS] **irf table**, which produces individual tables; and [TS] **irf graph**, which displays results on a graph.

Stored results

For stored results, see *Stored results* in [TS] **irf ctable**.

Also see

[TS] **irf ctable** — Combined tables of IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayesirf table** — Tables of Bayesian IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayesirf graph** — Graphs of Bayesian IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayesirf create** — Obtain Bayesian IRFs, dynamic-multiplier functions, and FEVDs

[BAYES] **bayesirf** — Bayesian IRFs, dynamic-multiplier functions, and FEVDs

Title

bayes: xtlogit — Bayesian random-effects logit model

Description

`bayes: xtlogit` fits a Bayesian panel-data random-effects logit model to a binary outcome; see [BAYES] **bayes** and [XT] **xtlogit** for details.

Quick start

Bayesian random-effects logit model of `y` on `x1` and `x2` with random intercepts by `id` (after `xtset`ing on panel variable `id`), using default normal priors for regression coefficients and default inverse-gamma prior for the variance of random intercepts

```
bayes: xtlogit y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): xtlogit y x1 x2
```

Use a shape of 1 and a scale of 2 instead of values of 0.01 for the default inverse-gamma prior

```
bayes, igammaprior(1 2): xtlogit y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): xtlogit y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): xtlogit y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): xtlogit y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Report odds ratios instead of regression coefficients

```
bayes, or
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [XT] **xtlogit**.

Menu

Statistics > Longitudinal/panel data > Binary outcomes > Bayesian regression > Logistic regression

Syntax

```
bayes [, bayesopts]: xtlogit depvar [indepvars] [if] [in] [, options]
```

options	Description
Model	
noconstant	suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
asis	retain perfect predictor variables
Reporting	
or	report odds ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

A panel variable must be specified; see [XT] **xtset**.

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

bayes: xtlogit, level() is equivalent to bayes, clevel(): xtlogit.

For a detailed description of options, see *Options* in [XT] **xtlogit**.

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
* igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance components; default is igammaprior(0.01 0.01)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
*or	report odds ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal-likelihood; suppressed by default
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
showreffects[(*reref*)]	specify that all or a subset of random-effects parameters be included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}, random effects {U[*panelvar*]} or simply {U}, and random-effects variance {var_U}. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [XT] **xtlogit**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Panel-data models* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**. In addition, bayes: xtlogit also stores the following results:

Macros

e(ivar)	variable denoting groups
e(redistrib)	distribution of random effects

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[XT] **xtlogit** — Fixed-effects, random-effects, and population-averaged logit models

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: xtmlogit — Bayesian random-effects multinomial logit model

Description

`bayes: xtmlogit` fits a Bayesian panel-data random-effects multinomial logit model to categorical outcomes; see [BAYES] **bayes** and [XT] **xtmlogit** for details.

Quick start

Bayesian random-effects multinomial logit model of `y` on `x1` and `x2` with random intercepts by `id` (after `xtset`ing on panel variable `id`), using default normal priors for regression coefficients and default inverse-gamma prior for the variance of random intercepts

```
bayes: xtmlogit y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): xtmlogit y x1 x2
```

Use a shape of 1 and a scale of 2 instead of values of 0.01 for the default inverse-gamma prior

```
bayes, igammaprior(1 2): xtmlogit y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): xtmlogit y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): xtmlogit y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): xtmlogit y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Bayesian random-effects multinomial logit model of `y` on `x1` and `x2`, with the second outcome as the base outcome

```
bayes: xtmlogit y x1 x2, baseoutcome(2)
```

As above, but report relative-risk ratios

```
bayes: xtmlogit y x1 x2, baseoutcome(2) rrr
```

As above, but using shared random-effects covariance between outcomes

```
bayes: xtmlogit y x1 x2, baseoutcome(2) covariance(shared) rrr
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [XT] **xtmlogit**.

Menu

Statistics > Longitudinal/panel data > Categorical outcomes > Bayesian regression > Multinomial logistic regression

Syntax

```
bayes [, bayesopts]: xtmlogit depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
`noconstant`	suppress constant term
`baseoutcome(#)`	value of *depvar* that will be the base outcome; default is the last outcome level
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; default is `covariance(independent)`
Reporting	
`rrr`	report relative-risk ratios
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

A panel variable must be specified; see [XT] **xtset**.

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`fweight`s are allowed; see [U] **11.1.6 weight**.

`bayes: xtmlogit, level()` is equivalent to `bayes, clevel(): xtmlogit`.

For a detailed description of options, see *Options* in [XT] **xtmlogit**.

bayesopts	Description
Priors	
* `normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
* `igammaprior(# #)`	specify shape and scale of default inverse-gamma prior for variance components; default is `igammaprior(0.01 0.01)`
* `iwishartprior(# [...])`	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results

Blocking

`block(`*paramref*`[ , `*blockopts*`])`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary

Initialization

`initial(`*initspec*`)`	specify initial values for model parameters with a single chain
`init#(`*initspec*`)`	specify initial values for #th chain; requires `nchains()`
`initall(`*initspec*`)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
* `noisily`	display output from the estimation command during initialization

Adaptation

`adaptation(`*adaptopts*`)`	control the adaptive MCMC procedure
`scale(#)`	initial multiplier for scale factor; default is `scale(2.38)`
`covariance(`*cov*`)`	initial proposal covariance; default is the identity matrix

Reporting

`clevel(#)`	set credible interval level; default is `clevel(95)`
`hpd`	display HPD credible intervals instead of the default equal-tailed credible intervals
* `rrr`	report relative-risk ratios
`eform[ (`*string*`) ]`	report exponentiated coefficients and, optionally, label as *string*
`remargl`	compute log marginal-likelihood; suppressed by default
`batch(#)`	specify length of block for batch-means calculations; default is `batch(0)`
`saving(`*filename*`[ , replace ])`	save simulation results to *filename*`.dta`
`nomodelsummary`	suppress model summary
`chainsdetail`	display detailed simulation summary for each chain
`[no]dots`	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is `nodots`
`dots(#[ , every(#) ])`	display dots as simulation is performed
`[no]show(`*paramref*`)`	specify model parameters to be excluded from or included in the output
`showreffects[ (`*reref*`) ]`	specify that all or a subset of random-effects parameters be included in the output
`notable`	suppress estimation table
`noheader`	suppress output header
`title(`*string*`)`	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

`search(`*search_options*`)`	control the search for feasible initial values
`corrlag(#)`	specify maximum autocorrelation lag; default varies
`corrtol(#)`	specify autocorrelation tolerance; default is `corrtol(0.01)`

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

The full specification of iwishartprior() is iwishartprior(# [matname] [, relevel(levelvar)]).

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*outcome*$_1$:*indepvars*}, {*outcome*$_2$:*indepvars*}, and so on, where *outcome*$_\#$'s are the values of the dependent variable or the value labels of the dependent variable if they exist, random effects {U#[*panelvar*]} or simply {U#}, and random-effects variances {var_U#} or, if random effects are correlated, covariance {U:Sigma,m}; see *Methods and formulas* for a full list of parameters. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [XT] **xtmlogit**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Panel-data models* in [BAYES] **bayes**.

▷ Example 1

Let's revisit example 1 from [XT] **xtmlogit**. The example uses a fictional estatus dataset to model women employment status, estatus, as a function of various socioeconomic factors such as having children under 18 years of age, hhchild; age; household income, hhincome; having significant other, hhsigno; and whether the woman is the primary breadwinner, bwinner. The employment status falls into three categories: employed, unemployed, and out of labor force.

Women are identified by the id variable, which is declared as the panel variable.

```
. use https://www.stata-press.com/data/r18/estatus
(Fictional employment status data)
. xtset id
Panel variable: id (unbalanced)
```

Let's fit a Bayesian analog of the model from example 1 of [XT] **xtmlogit**. The dataset contains 800 random effects and a total of 4,761 observations. To speed up the execution, we reduce the MCMC sample size from the default of 10,000 to 1,000, and we specify the `rseed()` option for reproducibility.

```
. bayes, rseed(17) mcmcsize(1000): xtmlogit estatus i.hhchild age hhincome
> i.hhsigno i.bwinner
note: Gibbs sampling is used for variance components.
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 1000 .........1000 done

Model summary
------------------------------------------------------------------------------
Likelihood:
  estatus ~ mlogit(xb_Out_of_labor_force,xb_Unemployed)

Priors:
  {Out_of_lab~e:1.hhchild} ~ normal(0,10000)                              (1)
        {Out_of_lab~e:age} ~ normal(0,10000)                              (1)
   {Out_of_lab~e:hhincome} ~ normal(0,10000)                              (1)
  {Out_of_lab~e:1.hhsigno} ~ normal(0,10000)                              (1)
  {Out_of_lab~e:1.bwinner} ~ normal(0,10000)                              (1)
      {Out_of_lab~e:_cons} ~ normal(0,10000)                              (1)
                  {U1[id]} ~ normal(0,{var_U1})                           (1)
    {Unemployed:1.hhchild} ~ normal(0,10000)                              (2)
          {Unemployed:age} ~ normal(0,10000)                              (2)
     {Unemployed:hhincome} ~ normal(0,10000)                              (2)
    {Unemployed:1.hhsigno} ~ normal(0,10000)                              (2)
    {Unemployed:1.bwinner} ~ normal(0,10000)                              (2)
        {Unemployed:_cons} ~ normal(0,10000)                              (2)
                  {U2[id]} ~ normal(0,{var_U2})                           (2)

Hyperprior:
  {var_U1 var_U2} ~ igamma(0.01,0.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_Out_of_labor_force.
(2) Parameters are elements of the linear form xb_Unemployed.
```

```
Bayesian RE multinomial logistic regression      MCMC iterations  =      3,500
Metropolis-Hastings and Gibbs sampling           Burn-in          =      2,500
                                                 MCMC sample size =      1,000
Group variable: id                               Number of groups =        800
                                                 Obs per group:
                                                               min =          5
                                                               avg =        6.0
                                                               max =          7
Base outcome: Employed                           Number of obs    =      4,761
                                                 Acceptance rate  =       .462
                                                 Efficiency:  min =      .0067
                                                               avg =     .02054
Log marginal-likelihood                                        max =     .03473
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
Out_of_lab~e						
hhchild						
Yes	.4577437	.0904496	.017864	.4640043	.2710479	.6218431
age	-.002879	.0055965	.001219	-.0026383	-.0130767	.0085352
hhincome	-.0042843	.0018489	.000402	-.0040465	-.0083297	-.0014658
hhsigno						
Yes	.4691271	.0889745	.017166	.4582264	.3251738	.6559253
bwinner						
Yes	-.4503803	.0732228	.01895	-.4500302	-.5924365	-.3002816
U1	1	0	0	1	1	1
_cons	-.5534515	.2478516	.060647	-.5376768	-1.010935	-.0486457
Unemployed						
hhchild						
Yes	-.0519455	.1168531	.023891	-.0398437	-.2755692	.1858482
age	.0092687	.0075203	.001441	.0091324	-.0050356	.0250353
hhincome	-.0293463	.0030542	.00118	-.0293997	-.0356738	-.0227989
hhsigno						
Yes	.0412739	.114903	.021569	.0361712	-.1694103	.2494766
bwinner						
Yes	-.1812031	.1003491	.033786	-.1773746	-.3642266	.0072658
U2	1	0	0	1	1	1
_cons	-.3242398	.3382746	.100034	-.3894121	-.9363997	.335811
var_U1	.8864246	.0884571	.01501	.8815608	.7235478	1.060998
var_U2	.7769171	.1137603	.025427	.757853	.605616	1.036373

```
Note: Default priors are used for model parameters.
Note: Adaptation tolerance is not met in at least one of the blocks.
```

Because the `Employed` outcome level is selected as the base outcome, the results are reported only for the `Out_of_labor_force` and `Unemployed` outcome levels. The posterior mean estimates for regression coefficients and variances of random effects are similar to the maximum likelihood estimates from example 1 from [XT] **xtmlogit**.

The Bayesian model introduced one set of random intercepts for each outcome level except the base outcome: `{U1[id]}` and `{U2[id]}`. By default, the random effects are assigned independent normal priors with variances `{var_U1}` and `{var_U2}`, respectively.

Following the original example, we can obtain estimates of relative-risk ratios by specifying the `rrr` option with `bayes`.

```
. bayes, rrr noheader
```

	RRR	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
Out_of_lab~e						
hhchild						
Yes	1.586934	.1424381	.028002	1.59043	1.311338	1.862358
age	.9971407	.0055807	.001215	.9973652	.9870084	1.008572
hhincome	.9957265	.0018402	.0004	.9959617	.9917049	.9985352
hhsigno						
Yes	1.605004	.1453829	.028037	1.581267	1.384271	1.926925
bwinner						
Yes	.6390981	.0469746	.012111	.6376089	.5529823	.7406096
U1	2.718282	0	0	2.718282	2.718282	2.718282
_cons	.5928508	.1479	.036194	.5841037	.3638785	.9525185
Unemployed						
hhchild						
Yes	.9559229	.1133981	.023185	.9609396	.7591399	1.204239
age	1.00934	.0075995	.001456	1.009174	.994977	1.025351
hhincome	.9710847	.0029661	.001146	.9710282	.964955	.977459
hhsigno						
Yes	1.049005	.1200204	.022401	1.036833	.8441625	1.283353
bwinner						
Yes	.8384893	.0847624	.028742	.837466	.6947338	1.007292
U2	2.718282	0	0	2.718282	2.718282	2.718282
_cons	.7657877	.2650145	.074494	.677455	.3921156	1.399075
var_U1	.8864246	.0884571	.01501	.8815608	.7235478	1.060998
var_U2	.7769171	.1137603	.025427	.757853	.605616	1.036373

The original example also estimated marginal probabilities with respect to the `hhchild` variable using the `margins` command. Below, we demonstrate Bayesian estimation of these marginal probabilities using Bayesian predictions.

First, we save the simulation results produced by `bayes: xtmlogit` to a permanent Stata dataset.

```
. bayes, saving(xtmlogitsim, replace)
note: file xtmlogitsim.dta saved.
```

We then define a Stata program, `margprob`, that calculates the marginal probabilities based on the simulated outcomes. See *User-defined Stata programs* in [BAYES] **bayespredict** for details.

```
. program margprob
  1.         version 18.0
  2.         args sum ysim
  3.         local xvar $BAYESPR_extravars
  4.         local ylabel $BAYESPR_passthruopts
  5.         gettoken ylabel xlabel : ylabel
  6.         tempvar presid
  7.         generate byte `presid' = `ysim' == `ylabel' if `xvar' == `xlabel'
  8.         summarize `presid', meanonly
  9.         scalar `sum' = r(mean)
 10. end
```

In addition to the simulated outcome ‘ysim’, the program uses the conditional variable ‘xvar’, hhchild in our example, passed as an extra variable, and two indices ‘ylabel’ and ‘xlabel’ that specify the outcome category and the conditional variable category, respectively. ‘ylabel’ takes values 1 , 2, and 3, and ‘xlabel’ takes values 0 and 1. ‘ylabel’ and ‘xlabel’ values are specified in the passthruopts() options of bayespredict. To calculate all marginal probabilities, we need to call the program for all six combinations of ylabel and xlabel.

Given the size of the dataset, calculating the Bayesian marginal probabilities using a user-defined Stata program is time consuming and will take a couple of minutes. We specify the dots option with bayespredict to monitor the simulation progress.

```
. bayespredict
> (pr1childNo :@margprob {_ysim1}, extravars(hhchild) passthruopts(1 0))
> (pr1childYes:@margprob {_ysim1}, extravars(hhchild) passthruopts(1 1))
> (pr2childNo :@margprob {_ysim1}, extravars(hhchild) passthruopts(2 0))
> (pr2childYes:@margprob {_ysim1}, extravars(hhchild) passthruopts(2 1))
> (pr3childNo :@margprob {_ysim1}, extravars(hhchild) passthruopts(3 0))
> (pr3childYes:@margprob {_ysim1}, extravars(hhchild) passthruopts(3 1)),
>         saving(xtmlogitpred, replace) rseed(17) dots

Computing predictions 1000 .........1000 done

file xtmlogitpred.dta saved.
file xtmlogitpred.ster saved.
```

The posterior predicted marginal probabilities are saved as xtmlogitpred estimation results.

Finally, we use bayesstats summary to calculate posterior estimates of the marginal probabilities.

```
. bayesstats summary {pr1childNo} {pr1childYes}
> {pr2childNo} {pr2childYes}
> {pr3childNo} {pr3childYes} using xtmlogitpred
Posterior summary statistics                     MCMC sample size =     1,000
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
pr1childNo	.3001763	.0133316	.000946	.3004053	.2745694	.3259878
pr1childYes	.3909447	.0113229	.00092	.3914604	.368676	.4133477
pr2childNo	.1615598	.0114636	.001266	.1616008	.1377913	.1843972
pr2childYes	.1368543	.0088284	.000782	.1367061	.1205597	.1546466
pr3childNo	.5382639	.0150199	.001759	.5382472	.508612	.5678825
pr3childYes	.4722009	.0114689	.001325	.4721923	.4497668	.4949767

Because we used uninformative default priors, the reported posterior mean estimates are close to the marginal probabilities calculated by the margins command.

◁

Stored results

See *Stored results* in [BAYES] **bayes**. In addition, bayes: xtmlogit also stores the following results:

Macros

e(ivar)	variable denoting groups
e(baseoutcome)	base outcome
e(redistrib)	distribution of random effects
e(covariance)	random-effects covariance structure

Methods and formulas

Bayesian random-effects multinomial logit models are based on random-effects multinomial logit models described in *Methods and formulas* of [XT] **xtmlogit**.

A multinomial logit model for a dependent variable with J outcome levels has $J-1$ equations, ignoring the baseline outcome, each having its own set of random intercepts. The equation for the #th outcome level includes a random-effects parameter `{U#[`*panelvar*`]}`, where *panelvar* is the panel variable. You can also refer to the random-effects parameters simply as `{U#}`. Random effects `{U#}`'s can be independent, shared, or correlated.

Independent `{U#}`'s, `covariance(independent)`, are assigned independent normal priors with zero means and random-effects variances `{var_U#}`'s. The default prior for `{var_U#}` is an inverse-gamma distribution with shape and scale of 0.01. You can use the `igammaprior()` options to change the default shape and scale parameters.

For a shared covariance structure, `covariance(shared)`, there is one random-effects parameter, `{U[`*panelvar*`]}`, shared between the outcome-level equations.

For an identity covariance structure, `covariance(identity)`, the random effects `{U#[`*panelvar*`]}` are different but have the same prior variance `{var_U}`.

For an exchangeable covariance structure, `covariance(exchangeable)`, `{U#[`*panelvar*`]}`'s are assigned `mvn0exchangeable(`$J-1$`, {var_U}, {rho_U})` prior. The default prior for the correlation parameter `{rho_U}` is uniform on $(-1, 1)$.

For an unstructured covariance, `covariance(unstructured)`, `{U#[`*panelvar*`]}`'s are assigned `mvn0(`$J-1$`, {U:Sigma,m})` prior. The default hyperprior for the variance–covariance matrix `{U:Sigma,m}` is inverse-Wishart with J degrees of freedom and the identity scale matrix. You can use the `iwishartprior()` option to change the default degrees of freedom and scale matrix.

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[XT] **xtmlogit** — Fixed-effects and random-effects multinomial logit models

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: xtnbreg — Bayesian random-effects negative binomial model

Description

`bayes: xtnbreg` fits a Bayesian panel-data random-effects negative binomial model to a nonnegative count outcome; see [BAYES] **bayes** and [XT] **xtnbreg** for details.

Quick start

Bayesian random-effects negative binomial model of `y` on `x1` and `x2` with random intercepts by `id` (after `xtset`ing on panel variable `id`), using default normal priors for regression coefficients and beta prior for the random effects, and Pareto prior for the shape parameters of the beta prior

```
bayes: xtnbreg y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): xtnbreg y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): xtnbreg y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): xtnbreg y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): xtnbreg y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display incidence-rate ratios instead of coefficients

```
bayes: xtnbreg y x1 x2, irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

Random-effects model with exposure variable `evar`

```
bayes: xtnbreg y x1 x2, exposure(evar)
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [XT] **xtnbreg**.

Menu

Statistics > Longitudinal/panel data > Bayesian regression > Negative binomial regression

Syntax

```
bayes [ , bayesopts ] : xtnbreg depvar [ indepvars ] [ if ] [ in ] [ , options ]
```

options	Description
Model	
noconstant	suppress constant term
exposure(*varname*$_e$)	include ln(*varname*$_e$) in model with coefficient constrained to 1
offset(*varname*$_o$)	include *varname*$_o$ in model with coefficient constrained to 1
Reporting	
irr	report incidence-rate ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

A panel variable must be specified; see [XT] **xtset**.

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *indepvars*, *varname*$_e$, and *varname*$_o$ may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

bayes: xtnbreg, level() is equivalent to bayes, clevel(): xtnbreg.

For a detailed description of options, see *Options for RE/FE models* in [XT] **xtnbreg**.

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary

Initialization	
`initial(`*initspec*`)`	specify initial values for model parameters with a single chain
`init#(`*initspec*`)`	specify initial values for #th chain; requires `nchains()`
`initall(`*initspec*`)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
* `noisily`	display output from the estimation command during initialization
Adaptation	
`adaptation(`*adaptopts*`)`	control the adaptive MCMC procedure
`scale(#)`	initial multiplier for scale factor; default is `scale(2.38)`
`covariance(`*cov*`)`	initial proposal covariance; default is the identity matrix
Reporting	
`clevel(#)`	set credible interval level; default is `clevel(95)`
`hpd`	display HPD credible intervals instead of the default equal-tailed credible intervals
* `irr`	report incidence-rate ratios
`eform[ (`*string*`) ]`	report exponentiated coefficients and, optionally, label as *string*
`remargl`	compute log marginal-likelihood; suppressed by default
`batch(#)`	specify length of block for batch-means calculations; default is `batch(0)`
`saving(`*filename*`[ , replace ])`	save simulation results to *filename*`.dta`
`nomodelsummary`	suppress model summary
`chainsdetail`	display detailed simulation summary for each chain
`[no]dots`	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is `nodots`
`dots(#[ , every(#) ])`	display dots as simulation is performed
`[no]show(`*paramref*`)`	specify model parameters to be excluded from or included in the output
`showreffects[ (`*reref*`) ]`	specify that all or a subset of random-effects parameters be included in the output
`notable`	suppress estimation table
`noheader`	suppress output header
`title(`*string*`)`	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells
Advanced	
`search(`*search_options*`)`	control the search for feasible initial values
`corrlag(#)`	specify maximum autocorrelation lag; default varies
`corrtol(#)`	specify autocorrelation tolerance; default is `corrtol(0.01)`

*Starred options are specific to the `bayes` prefix; other options are common between `bayes` and `bayesmh`.

Options `prior()` and `block()` may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}, random effects {U[*panelvar*]} or simply {U}, and shape parameters {r} and {s} for the beta prior of {U}; also see *Methods and formulas*. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [XT] **xtnbreg**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Panel-data models* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**. In addition, bayes: xtnbreg also stores the following results:

Macros

e(ivar)	variable denoting groups
e(redistrib)	distribution of random effects

Methods and formulas

Bayesian random-effects negative binomial models are based on random-effects negative binomial models described in *Methods and formulas* of [XT] **xtnbreg**.

Let y_{it} be the count for the tth observation in the ith group. We assume $y_{it} \mid \gamma_{it} \sim \text{Poisson}(\gamma_{it})$, where $\gamma_{it} \mid u_i \sim \text{gamma}\{\lambda_{it}, (1-u_i)/u_i\}$ with $\lambda_{it} = \exp(\mathbf{x}_{it}\boldsymbol{\beta} + \text{offset}_{it})$ and u_i is a dispersion-control parameter that varies randomly across groups. The likelihood of the model is thus

$$\Pr(Y_{it} = y_{it} \mid \mathbf{x}_{it}, u_i) = \frac{\Gamma(\lambda_{it} + y_{it})}{\Gamma(\lambda_{it})\Gamma(y_{it}+1)} u_i^{\lambda_{it}} (1-u_i)^{y_{it}}$$

We further assume that random-effects dispersion parameters u_i's are a priori independent and follow beta distribution with shape parameters r and s, $u_i \sim \text{Beta}(r, s)$. The hyperprior for the shape parameters is chosen so that the joint distribution of the mean $r/(r+s)$ and inverse square-root of the sample size $(r+s)$ of the beta distribution is uniform, $\{r/(r+s), (r+s)^{-0.5}\} \sim 1$; see Gelman et al. (2014, sec. 5.3). This choice leads to a diffused distribution for (r, s) with a density proportional to $(r+s)^{-2.5}$, which is a Pareto-type distribution.

bayes: xtnbreg uses the default initial value of 0.5 for the random effects u_i's.

See *Methods and formulas* in [BAYES] **bayesmh**.

Reference

Gelman, A., J. B. Carlin, H. S. Stern, D. B. Dunson, A. Vehtari, and D. B. Rubin. 2014. *Bayesian Data Analysis*. 3rd ed. Boca Raton, FL: Chapman and Hall/CRC.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[XT] **xtnbreg** — Fixed-effects, random-effects, & population-averaged negative binomial models

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: xtologit — Bayesian random-effects ordered logistic model

Description

`bayes: xtologit` fits a Bayesian panel-data random-effects ordered logistic model to an ordinal outcome; see [BAYES] **bayes** and [XT] **xtologit** for details.

Quick start

Bayesian random-effects ordered logistic model of `y` on `x1` and `x2` with random intercepts by `id` (after `xtset`ing on panel variable `id`), using default normal priors for regression coefficients and flat priors for cutpoints and default inverse-gamma prior for the variance of random intercepts

```
bayes: xtologit y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): xtologit y x1 x2
```

Use a shape of 1 and a scale of 2 instead of values of 0.01 for the default inverse-gamma prior

```
bayes, igammaprior(1 2): xtologit y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): xtologit y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): xtologit y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): xtologit y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Report odds ratios instead of regression coefficients

```
bayes, or
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [XT] **xtologit**.

Menu

Statistics > Longitudinal/panel data > Ordinal outcomes > Bayesian regression > Ordered logistic regression

Syntax

```
bayes [, bayesopts]: xtologit depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
Reporting	
`or`	report odds ratios
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

A panel variable must be specified; see [XT] **xtset**.

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`fweight`s are allowed; see [U] **11.1.6 weight**.

`bayes: xtologit, level()` is equivalent to `bayes, clevel(): xtologit`.

For a detailed description of *options*, see *Options* in [XT] **xtologit**.

bayesopts	Description
Priors	
*`normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
*`igammaprior(# #)`	specify shape and scale of default inverse-gamma prior for variance components; default is `igammaprior(0.01 0.01)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
Blocking	
`block(`*paramref*`[, `*blockopts*`])`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
Initialization	
`initial(`*initspec*`)`	specify initial values for model parameters with a single chain
`init#(`*initspec*`)`	specify initial values for #th chain; requires `nchains()`
`initall(`*initspec*`)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
*`noisily`	display output from the estimation command during initialization

Adaptation	
adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix
Reporting	
clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
* or	report odds ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal-likelihood; suppressed by default
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
showreffects[(*reref*)]	specify that all or a subset of random-effects parameters be included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells
Advanced	
search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}, cutpoints {cut1}, {cut2}, and so on, random effects {U[*panelvar*]} or simply {U}, and random-effects variance {var_U}. Use the dryrun option to see the definitions of model parameters prior to estimation.

Flat priors, flat, are used by default for cutpoints.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For

remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [XT] **xtologit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Panel-data models* in [BAYES] **bayes**. Also see example 19 in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**. In addition, `bayes: xtologit` also stores the following results:

Macros

`e(ivar)`	variable denoting groups
`e(redistrib)`	distribution of random effects

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[XT] **xtologit** — Random-effects ordered logistic models

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: xtoprobit — Bayesian random-effects ordered probit model

Description

`bayes: xtoprobit` fits a Bayesian panel-data random-effects ordered probit model to an ordinal outcome; see [BAYES] **bayes** and [XT] **xtoprobit** for details.

Quick start

Bayesian random-effects ordered probit model of `y` on `x1` and `x2` with random intercepts by `id` (after `xtset`ing on panel variable `id`), using default normal priors for regression coefficients and flat priors for cutpoints and default inverse-gamma prior for the variance of random intercepts

```
bayes: xtoprobit y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): xtoprobit y x1 x2
```

Use a shape of 1 and a scale of 2 instead of values of 0.01 for the default inverse-gamma prior

```
bayes, igammaprior(1 2): xtoprobit y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): xtoprobit y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): xtoprobit y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): xtoprobit y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [XT] **xtoprobit**.

Menu

Statistics > Longitudinal/panel data > Ordinal outcomes > Bayesian regression > Ordered probit regression

Syntax

```
bayes [ , bayesopts ] : xtoprobit depvar [indepvars] [if] [in] [weight] [ , options ]
```

options	Description
Model	
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
Reporting	
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

A panel variable must be specified; see [XT] **xtset**.

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`fweight`s are allowed; see [U] **11.1.6 weight**.

`bayes: xtoprobit, level()` is equivalent to `bayes, clevel(): xtoprobit`.

For a detailed description of *options*, see *Options* in [XT] **xtoprobit**.

bayesopts	Description
Priors	
*`normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
*`igammaprior(# #)`	specify shape and scale of default inverse-gamma prior for variance components; default is `igammaprior(0.01 0.01)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
Blocking	
`block(`*paramref*`[ , `*blockopts*`])`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
Initialization	
`initial(`*initspec*`)`	specify initial values for model parameters with a single chain
`init#(`*initspec*`)`	specify initial values for #th chain; requires `nchains()`
`initall(`*initspec*`)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
*`noisily`	display output from the estimation command during initialization

Adaptation	
adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix
Reporting	
clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal-likelihood; suppressed by default
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
showreffects[(*reref*)]	specify that all or a subset of random-effects parameters be included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells
Advanced	
search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}, cutpoints {cut1}, {cut2}, and so on, random effects {U[*panelvar*]} or simply {U}, and random-effects variance {var_U}. Use the dryrun option to see the definitions of model parameters prior to estimation.

Flat priors, flat, are used by default for cutpoints.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For

remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [XT] **xtoprobit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Panel-data models* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**. In addition, `bayes: xtoprobit` also stores the following results:

Macros

`e(ivar)`	variable denoting groups
`e(redistrib)`	distribution of random effects

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[XT] **xtoprobit** — Random-effects ordered probit models

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: xtpoisson — Bayesian random-effects Poisson model

Description

`bayes: xtpoisson` fits a Bayesian panel-data random-effects Poisson model to a nonnegative count outcome; see [BAYES] **bayes** and [XT] **xtpoisson** for details.

Quick start

Bayesian random-effects Poisson model of `y` on `x1` and `x2` with random intercepts by `id` (after `xtset`ing on panel variable `id`), using default normal priors for regression coefficients and default inverse-gamma prior for the variance of random intercepts

```
bayes: xtpoisson y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): xtpoisson y x1 x2
```

Use a shape of 1 and a scale of 2 instead of values of 0.01 for the default inverse-gamma prior

```
bayes, igammaprior(1 2): xtpoisson y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): xtpoisson y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): xtpoisson y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): xtpoisson y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Use a normal prior distribution for random effects instead of the default gamma prior

```
bayes: xtpoisson y x1 x2, normal
```

Display incidence-rate ratios instead of coefficients

```
bayes: xtpoisson y x1 x2, irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [XT] **xtpoisson**.

Menu

Statistics > Longitudinal/panel data > Count outcomes > Bayesian regression > Poisson regression

Syntax

```
bayes [ , bayesopts ] : xtpoisson depvar [indepvars] [if] [in] [ , options ]
```

options	Description
Model	
noconstant	suppress constant term
exposure(*varname*$_e$)	include ln(*varname*$_e$) in model with coefficient constrained to 1
offset(*varname*$_o$)	include *varname*$_o$ in model with coefficient constrained to 1
normal	use a normal distribution for random effects instead of gamma
Reporting	
irr	report incidence-rate ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

A panel variable must be specified; see [XT] **xtset**.

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *indepvars*, *varname*$_e$, and *varname*$_o$ may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

bayes: xtpoisson, level() is equivalent to bayes, clevel(): xtpoisson.

For a detailed description of options, see *Options* in [XT] **xtpoisson**.

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
* igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance components; default is igammaprior(0.01 0.01)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary

Initialization	
initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
Adaptation	
adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix
Reporting	
clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
*irr	report incidence-rate ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal-likelihood; suppressed by default
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
showreffects[(*reref*)]	specify that all or a subset of random-effects parameters be included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells
Advanced	
search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}, random effects {U[*panelvar*]} or simply {U}, and parameter {alpha} with the gamma prior or random-effects variance {var_U} with the normal prior; also see *Methods and formulas*. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [XT] **xtpoisson**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Panel-data models* in [BAYES] **bayes**.

▷ Example 1

Let's revisit example 1 from [XT] **xtpoisson**. The example models the number of ship accidents, accident, affected by the period of their construction and operation. The factor variables co_75_79, co_70_74, and co_65_69 mark consecutive construction periods of 5 years, and op_75_79 indicates the operating period between 1975 and 1979.

```
. use https://www.stata-press.com/data/r18/ships
. xtset
Panel variable: ship (balanced)
```

The number of accidents is modeled by a Poisson distribution with the number of months in service, service, as exposure. The ship variable identifies the individual ships and is set as the panel variable.

We use bayes: xtpoisson to fit the Bayesian analog of the model. We use the default priors for regression coefficients and random effects. The random effects are assigned an exponential gamma prior with a hyperparameter {alpha}. The latter is assigned an inverse-gamma hyperprior. To improve sampling efficiency, we double the burn-in period, burnin(5000). We also include the irr option to report incidence-rate ratios instead of regression coefficients.

```
. bayes, burnin(5000) rseed(17):
> xtpoisson accident op_75_79 co_65_69 co_70_74 co_75_79, exp(service) irr
Burn-in 5000 aaaaaaaaa1000aaaaaaaaa2000aaaaaaaaa3000aaaaaaaaa4000aaaaaaaaa5000
> done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  accident service ~ poissonreg(xb_accident)
Priors:
  {accident:op_75_79} ~ normal(0,10000)                                   (1)
  {accident:co_65_69} ~ normal(0,10000)                                   (1)
  {accident:co_70_74} ~ normal(0,10000)                                   (1)
  {accident:co_75_79} ~ normal(0,10000)                                   (1)
     {accident:_cons} ~ normal(0,10000)                                   (1)
            {U[ship]} ~ expgamma(1/{alpha},{alpha})                       (1)
Hyperprior:
  {alpha} ~ igamma(0.01,0.01)
------------------------------------------------------------------------------
```

```
(1) Parameters are elements of the linear form xb_accident.
Bayesian RE Poisson regression                  MCMC iterations  =     15,000
Random-walk Metropolis-Hastings sampling        Burn-in          =      5,000
                                                MCMC sample size =     10,000
Group variable: ship                            Number of groups =          5
                                                Obs per group:
                                                              min =          6
                                                              avg =        6.8
                                                              max =          7
                                                Number of obs    =         34
                                                Acceptance rate  =      .4103
                                                Efficiency:  min =    .004533
                                                              avg =     .02627
Log marginal-likelihood                                       max =     .06637
```

	IRR	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
accident						
op_75_79	1.482028	.1872034	.012245	1.466002	1.15391	1.885356
co_65_69	2.056534	.3147425	.012217	2.038204	1.516147	2.745889
co_70_74	2.365398	.4163733	.027752	2.31289	1.673906	3.377834
co_75_79	1.641278	.386874	.024248	1.610142	1.021594	2.514659
_cons	.0014965	.000378	.000056	.0014293	.0009432	.0024066
alpha	.182512	.149803	.012089	.1351156	.0271875	.606201

```
Note: Variable service is included in the model as the exposure.
Note: _cons estimates baseline incidence rate.
Note: Default priors are used for model parameters.
```

The posterior mean estimates for regression coefficients are similar to the maximum likelihood estimates reported in example 1. The posterior mean estimate for {alpha}, about 0.18, is greater than its maximum likelihood counterpart, 0.09, because its marginal posterior distribution is skewed.

We can use bayesstats summary to report posterior estimates for the random effects {U[ship]}.

```
. bayesstats summary {U[1/5]}
Posterior summary statistics                    MCMC sample size =     10,000
```

U[ship]	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
1	.0603	.2287246	.028578	.0650362	-.4104326	.5109287
2	-.4250167	.2156037	.035458	-.4172961	-.8843667	-.0511939
3	-.422064	.3049497	.032655	-.3893351	-1.115965	.0824852
4	-.0106956	.2549407	.026575	-.0067523	-.5325561	.4791908
5	.3031554	.2326076	.025797	.3001452	-.1498397	.7672204

Next, we would like to assess the goodness of fit of the model by using bayespredict and bayesstats ppvalues to perform posterior predictive checks. But first, we need to save the current simulation results to a permanent Stata dataset.

```
. bayes, saving(xtpoissim1)
note: file xtpoissim1.dta saved.
```

Deviance is commonly used as a goodness-of-fit statistic for generalized linear models. We define a Mata function, deviance(), that computes the deviance, which will be used by bayespredict to compute the deviance based on the simulated outcome ysim and the mean vector mu.

```
. mata:
------------------------------------------------- mata (type end to exit) -----
: real scalar deviance(real colvector ysim, real colvector mu) {
>         return (2*sum(ysim:*ln(ysim:/mu):-ysim:+mu))
> }
: end
-------------------------------------------------------------------------------
```

Next, we call `bayespredict` to compute the deviance of outcomes simulated from the posterior predictive distribution and save the results in `xtpoispred1`.

```
. bayespredict (@deviance({_ysim1},{_mu1})), rseed(17) saving(xtpoispred1)
Computing predictions ...
file xtpoispred1.dta saved.
file xtpoispred1.ster saved.
```

Now, we can compute the posterior predictive p-value of the deviance statistics using the `bayesstats ppvalues` command.

```
. bayesstats ppvalues using xtpoispred1
Posterior predictive summary      MCMC sample size =    10,000
```

T	Mean	Std. dev.	E(T_obs)	P(T>=T_obs)
_ysim1_deviance	25.02129	7.157104	39.40344	.0523

```
Note: P(T>=T_obs) close to 0 or 1 indicates lack of fit.
```

The estimated p-value is only 0.05, but in the absence of a reference model, it is difficult to decide whether this indicates a lack of fit.

◁

Stored results

See *Stored results* in [BAYES] **bayes**. In addition, `bayes: xtpoisson` also stores the following results:

Macros

`e(ivar)`	variable denoting groups
`e(redistrib)`	distribution of random effects

Methods and formulas

Bayesian random-effects Poisson models are based on random-effects Poisson models described in *Methods and formulas* of [XT] **xtpoisson**.

Let y_{it} be the count for the tth observation in the ith group. We assume $y_{it} \mid u_i, \lambda_{it} \sim \text{Poisson}\{\exp(u_i)\lambda_{it}\}$, with $\lambda_{it} = \exp(\mathbf{x}_{it}\boldsymbol{\beta} + \text{offset}_{it})$ and u_i a parameter that varies randomly across groups. In `bayes: xtpoisson`, parameters u_i's are represented by `{U[`*panelvar*`]}`, where *panelvar* is the panel variable.

By default, random effects $\exp(u_i)$ are a priori independent and have a gamma prior distribution with mean 1 and variance α. u_i's are thus assigned an exponential gamma prior with shape $1/\alpha$ and scale α. The hyperparameter α, `{alpha}` in the output of `bayes: xtpoisson`, has an inverse-gamma prior with shape and scale of 0.01.

When the `normal` option is specified with `xtpoisson`, the random effects u_i's are assigned a normal prior distribution with mean 0 and variance σ_u^2, denoted as `{var_U}` in the output of `bayes: xtpoisson`. By default, σ_u^2 is assigned an inverse-gamma prior with shape and scale of 0.01.

You can use the `igammaprior()` option to change the shape and scale of the default inverse-gamma prior. See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[XT] **xtpoisson** — Fixed-effects, random-effects, and population-averaged Poisson models

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: xtprobit — Bayesian random-effects probit model

Description

`bayes: xtprobit` fits a Bayesian panel-data random-effects probit model to a binary outcome; see [BAYES] **bayes** and [XT] **xtprobit** for details.

Quick start

Bayesian random-effects probit model of `y` on `x1` and `x2` with random intercepts by `id` (after `xtset`ing on panel variable `id`), using default normal priors for regression coefficients and default inverse-gamma prior for the variance of random intercepts

```
bayes: xtprobit y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): xtprobit y x1 x2
```

Use a shape of 1 and a scale of 2 instead of values of 0.01 for the default inverse-gamma prior

```
bayes, igammaprior(1 2): xtprobit y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): xtprobit y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): xtprobit y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): xtprobit y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [XT] **xtprobit**.

Menu

Statistics > Longitudinal/panel data > Binary outcomes > Bayesian regression > Probit regression

Syntax

```
bayes [ , bayesopts ] : xtprobit depvar [indepvars] [if] [in] [ , options ]
```

options	Description
Model	
noconstant	suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
asis	retain perfect predictor variables
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

A panel variable must be specified; see [XT] **xtset**.

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

bayes: xtprobit, level() is equivalent to bayes, clevel(): xtprobit.

For a detailed description of options, see *Options* in [XT] **xtprobit**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
*igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance components; default is igammaprior(0.01 0.01)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
Initialization	
initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation	
adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix
Reporting	
clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal-likelihood; suppressed by default
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
showreffects[(*reref*)]	specify that all or a subset of random-effects parameters be included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells
Advanced	
search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*}, random effects {U[*panelvar*]} or simply {U}, and random-effects variance {var_U}. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [XT] **xtprobit**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Panel-data models* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**. In addition, bayes: xtprobit also stores the following results:

Macros

e(ivar)	variable denoting groups
e(redistrib)	distribution of random effects

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[XT] **xtprobit** — Random-effects and population-averaged probit models

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: xtreg — Bayesian random-effects linear model

Description

`bayes: xtreg` fits a Bayesian panel-data random-effects linear regression to a continuous outcome; see [BAYES] **bayes** and [XT] **xtreg** for details.

Quick start

Bayesian random-effects linear regression of `y` on `x1` and `x2` with random intercepts by `id` (after `xtset`ing on panel variable `id`), using default normal priors for regression coefficients and default inverse-gamma priors for the error variance and for the variance of random intercepts

```
bayes: xtreg y x1 x2
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): xtreg y x1 x2
```

Use a shape of 1 and a scale of 2 instead of values of 0.01 for the default inverse-gamma prior

```
bayes, igammaprior(1 2): xtreg y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): xtreg y x1 x2
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): xtreg y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): xtreg y x1 x2
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Use Gibbs sampling for all parameters, including random effects

```
bayes, gibbs: xtreg y x1 x2
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [XT] **xtreg**.

Menu

Statistics > Longitudinal/panel data > Bayesian regression > Linear regression

Syntax

```
bayes [ , bayesopts ] : xtreg depvar [ indepvars ] [ if ] [ in ] [ , options ]
```

options	Description
Model	
noconstant	suppress constant term
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

A panel variable must be specified; see [XT] **xtset**.

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

bayes: xtreg, level() is equivalent to bayes, clevel(): xtreg.

For a detailed description of options, see *Options* in [XT] **xtreg**.

bayesopts	Description
Priors	
*gibbs	specify Gibbs sampling; available only with normal priors for regression coefficients and an inverse-gamma prior for variance
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
*igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance components; default is igammaprior(0.01 0.01)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
Initialization	
initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation	
`adaptation(`*adaptopts*`)`	control the adaptive MCMC procedure
`scale(`#`)`	initial multiplier for scale factor; default is `scale(2.38)`
`covariance(`*cov*`)`	initial proposal covariance; default is the identity matrix
Reporting	
`clevel(`#`)`	set credible interval level; default is `clevel(95)`
`hpd`	display HPD credible intervals instead of the default equal-tailed credible intervals
`eform[ (`*string*`) ]`	report exponentiated coefficients and, optionally, label as *string*
`remargl`	compute log marginal-likelihood; suppressed by default
`batch(`#`)`	specify length of block for batch-means calculations; default is `batch(0)`
`saving(`*filename*`[ , replace ])`	save simulation results to *filename*`.dta`
`nomodelsummary`	suppress model summary
`chainsdetail`	display detailed simulation summary for each chain
`[no]dots`	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is `nodots`
`dots(`#`[ , every(`#`) ])`	display dots as simulation is performed
`[no]show(`*paramref*`)`	specify model parameters to be excluded from or included in the output
`showreffects[ (`*reref*`) ]`	specify that all or a subset of random-effects parameters be included in the output
`notable`	suppress estimation table
`noheader`	suppress output header
`title(`*string*`)`	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells
Advanced	
`search(`*search_options*`)`	control the search for feasible initial values
`corrlag(`#`)`	specify maximum autocorrelation lag; default varies
`corrtol(`#`)`	specify autocorrelation tolerance; default is `corrtol(0.01)`

*Starred options are specific to the `bayes` prefix; other options are common between `bayes` and `bayesmh`.

Options `prior()` and `block()` may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*`:`*indepvars*}, error variance `{sigma2}`, random effects `{U[`*panelvar*`]}` or simply `{U}`, and random-effects variance `{var_U}`. Use the `dryrun` option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using adaptive Metropolis–Hastings and Gibbs algorithms, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [XT] **xtreg**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Panel-data models* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**. In addition, bayes: xtreg also stores the following results:

Macros

e(ivar)	variable denoting groups
e(redistrib)	distribution of random effects

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[XT] **xtreg** — Fixed-, between-, and random-effects and population-averaged linear models

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: zinb — Bayesian zero-inflated negative binomial regression

Description

`bayes: zinb` fits a Bayesian zero-inflated negative binomial regression to a nonnegative count outcome with a high fraction of zeros; see [BAYES] **bayes** and [R] **zinb** for details.

Quick start

Bayesian zero-inflated negative binomial regression of `y` on `x1` and `x2`, using `z` to model excess zeros and using default normal priors for regression coefficients and log-overdispersion parameter

```
bayes: zinb y x1 x2, inflate(z)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): zinb y x1 x2, inflate(z)
```

Use uniform priors for the slopes and a normal prior for the intercept of the main regression

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): zinb y x1 x2, inflate(z)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): zinb y x1 x2, inflate(z)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): zinb y x1 x2, inflate(z)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display incidence-rate ratios instead of coefficients

```
bayes: zinb y x1 x2, inflate(z) irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **zinb**.

Menu

Statistics > Count outcomes > Bayesian regression > Zero-inflated negative binomial regression

Syntax

```
bayes [ , bayesopts ] : zinb depvar [ indepvars ] [ if ] [ in ] [ weight ] ,
    inflate(varlist [ , offset(varname) ] | _cons) [ options ]
```

options	Description
Model	
* `inflate( )`	equation that determines whether the count is zero
`noconstant`	suppress constant term
`exposure(`$varname_e$`)`	include ln($varname_e$) in model with coefficient constrained to 1
`offset(`$varname_o$`)`	include $varname_o$ in model with coefficient constrained to 1
`probit`	use probit model to characterize excess zeros; default is logit
Reporting	
`irr`	report incidence-rate ratios
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

* `inflate(`*varlist*`[ , offset(`*varname*`) ] | _cons)` is required.

indepvars and *varlist* may contain factor variables; see **[U] 11.4.3 Factor variables**.

`fweight`s are allowed; see **[U] 11.1.6 weight**.

`bayes: zinb, level()` is equivalent to `bayes, clevel(): zinb`.

For a detailed description of *options*, see *Options* in **[R] zinb**.

bayesopts	Description
Priors	
* `normalprior(#)`	specify standard deviation of default normal priors for regression coefficients and log-overdispersion parameter; default is `normalprior(100)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
Blocking	
* `blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref*`[ , `*blockopts*`])`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
* `noblocking`	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
*irr	report incidence-rate ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} for the main regression and {inflate:*varlist*} for the inflation equation and log-overdispersion parameter {lnalpha}. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **zinb**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Zero-inflated negative binomial model* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **zinb** — Zero-inflated negative binomial regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: ziologit — Bayesian zero-inflated ordered logit regression

Description

`bayes: ziologit` fits a Bayesian zero-inflated ordered logit regression to an ordinal outcome with a high fraction of zeros; see [BAYES] **bayes** and [R] **ziologit** for details.

Quick start

Bayesian zero-inflated ordered logit regression of `y` on `x1` and `x2`, using `z` to model excess zeros and using default normal priors for regression coefficients and flat priors for cutpoints

```
bayes: ziologit y x1 x2, inflate(z)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): ziologit y x1 x2, inflate(z)
```

Use uniform priors for the slopes and a normal prior for the intercept of the main regression

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): ziologit y x1 x2, inflate(z)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123):  ///
ziologit y x1 x2, inflate(z)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500):  ///
ziologit y x1 x2, inflate(z)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display odds ratios instead of coefficients on replay

```
bayes, or
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **ziologit**.

Menu

Statistics > Ordinal outcomes > Bayesian regression > Zero-inflated ordered logit regression

Syntax

```
bayes [, bayesopts]: ziologit depvar [indepvars] [if] [in] [weight],
  inflate(varlist[, noconstant offset(varname)] | _cons) [options]
```

options	Description
Model	
*inflate( )	inflation equation that determines excess zero values
offset(*varname*)	include *varname* in model with coefficient constrained to 1
Reporting	
or	report odds ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

*inflate(*varlist*[, noconstant offset(*varname*)] | _cons) is required.

indepvars and *varlist* may contain factor variables; see [U] **11.4.3 Factor variables**.

fweights are allowed; see [U] **11.1.6 weight**.

bayes: ziologit, level() is equivalent to bayes, clevel(): ziologit.

For a detailed description of *options*, see *Options* in [R] **ziologit**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref*[, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
*or	report odds ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} for the main regression and {inflate:*varlist*} for the inflation equation and cutpoints {cut1}, {cut2}, and so on. Use the dryrun option to see the definitions of model parameters prior to estimation.

Flat priors, flat, are used by default for cutpoints.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **ziologit**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Zero-inflated negative binomial models* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **ziologit** — Zero-inflated ordered logit regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: zioprobit — Bayesian zero-inflated ordered probit regression

Description

`bayes: zioprobit` fits a Bayesian zero-inflated ordered probit regression to an ordinal outcome with a high fraction of zeros; see [BAYES] **bayes** and [R] **zioprobit** for details.

Quick start

Bayesian zero-inflated ordered probit regression of `y` on `x1` and `x2`, using `z` to model excess zeros and using default normal priors for regression coefficients and flat priors for cutpoints

```
bayes: zioprobit y x1 x2, inflate(z)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): zioprobit y x1 x2, inflate(z)
```

Use uniform priors for the slopes and a normal prior for the intercept of the main regression

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): zioprobit y x1 x2, inflate(z)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123):  ///
zioprobit y x1 x2, inflate(z)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500):  ///
zioprobit y x1 x2, inflate(z)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **zioprobit**.

Menu

Statistics > Ordinal outcomes > Bayesian regression > Zero-inflated ordered probit regression

Syntax

```
bayes [, bayesopts]: zioprobit depvar [indepvars] [if] [in] [weight],
    inflate(varlist[, noconstant offset(varname)] | _cons) [options]
```

options	Description
Model	
* `inflate()`	inflation equation that determines excess zero values
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
Reporting	
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

* `inflate(`*varlist*`[, noconstant offset(`*varname*`)] | _cons)` is required.

indepvars and *varlist* may contain factor variables; see **[U] 11.4.3 Factor variables**.

`fweights` are allowed; see **[U] 11.1.6 weight**.

`bayes: zioprobit, level()` is equivalent to `bayes, clevel(): zioprobit`.

For a detailed description of *options*, see *Options* in **[R] zioprobit**.

bayesopts	Description
Priors	
* `normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
Blocking	
* `blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref*`[, `*blockopts*`])`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
* `noblocking`	do not block parameters by default

Initialization

`initial(`*initspec*`)`	specify initial values for model parameters with a single chain
`init#(`*initspec*`)`	specify initial values for #th chain; requires `nchains()`
`initall(`*initspec*`)`	specify initial values for all chains; requires `nchains()`
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
* `noisily`	display output from the estimation command during initialization

Adaptation

`adaptation(`*adaptopts*`)`	control the adaptive MCMC procedure
`scale(#)`	initial multiplier for scale factor; default is `scale(2.38)`
`covariance(`*cov*`)`	initial proposal covariance; default is the identity matrix

Reporting

`clevel(#)`	set credible interval level; default is `clevel(95)`
`hpd`	display HPD credible intervals instead of the default equal-tailed credible intervals
`eform[ (`*string*`) ]`	report exponentiated coefficients and, optionally, label as *string*
`batch(#)`	specify length of block for batch-means calculations; default is `batch(0)`
`saving(`*filename*`[ , replace ])`	save simulation results to *filename*`.dta`
`nomodelsummary`	suppress model summary
`chainsdetail`	display detailed simulation summary for each chain
`[no]dots`	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is `nodots`
`dots(#[ , every(#) ])`	display dots as simulation is performed
`[no]show(`*paramref*`)`	specify model parameters to be excluded from or included in the output
`notable`	suppress estimation table
`noheader`	suppress output header
`title(`*string*`)`	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

`search(`*search_options*`)`	control the search for feasible initial values
`corrlag(#)`	specify maximum autocorrelation lag; default varies
`corrtol(#)`	specify autocorrelation tolerance; default is `corrtol(0.01)`

* Starred options are specific to the `bayes` prefix; other options are common between `bayes` and `bayesmh`.

Options `prior()` and `block()` may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

`collect` is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients `{`*depvar*`:`*indepvars*`}` for the main regression and `{inflate:`*varlist*`}` for the inflation equation and cutpoints `{cut1}`, `{cut2}`, and so on. Use the `dryrun` option to see the definitions of model parameters prior to estimation.

Flat priors, `flat`, are used by default for cutpoints.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **zioprobit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Zero-inflated negative binomial models* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **zioprobit** — Zero-inflated ordered probit regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Title

bayes: zip — Bayesian zero-inflated Poisson regression

Description

`bayes: zip` fits a Bayesian zero-inflated Poisson regression to a nonnegative count outcome with a high fraction of zeros; see [BAYES] **bayes** and [R] **zip** for details.

Quick start

Bayesian zero-inflated Poisson regression of `y` on `x1` and `x2`, using `z` to model excess zeros and using default normal priors for regression coefficients

```
bayes: zip y x1 x2, inflate(z)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): zip y x1 x2, inflate(z)
```

Use uniform priors for the slopes and a normal prior for the intercept of the main regression

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): zip y x1 x2, inflate(z)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): zip y x1 x2, inflate(z)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): zip y x1 x2, inflate(z)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display incidence-rate ratios instead of coefficients

```
bayes: zip y x1 x2, inflate(z) irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **zip**.

Menu

Statistics > Count outcomes > Bayesian regression > Zero-inflated Poisson regression

Syntax

```
bayes [, bayesopts]: zip depvar [indepvars] [if] [in] [weight],
    inflate(varlist[, offset(varname)] | _cons) [options]
```

options	Description
Model	
* `inflate()`	equation that determines whether the count is zero
`noconstant`	suppress constant term
`exposure(`*varname*$_e$`)`	include ln(*varname*$_e$) in model with coefficient constrained to 1
`offset(`*varname*$_o$`)`	include *varname*$_o$ in model with coefficient constrained to 1
`probit`	use probit model to characterize excess zeros; default is logit
Reporting	
`irr`	report incidence-rate ratios
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

* `inflate(`*varlist*`[, offset(`*varname*`)] | _cons)` is required.

indepvars and *varlist* may contain factor variables; see **[U] 11.4.3 Factor variables**.

`fweight`s are allowed; see **[U] 11.1.6 weight**.

`bayes: zip, level()` is equivalent to `bayes, clevel(): zip`.

For a detailed description of *options*, see *Options* in **[R] zip**.

bayesopts	Description
Priors	
* `normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`nchains(#)`	number of chains; default is to simulate one chain
`mcmcsize(#)`	MCMC sample size; default is `mcmcsize(10000)`
`burnin(#)`	burn-in period; default is `burnin(2500)`
`thinning(#)`	thinning interval; default is `thinning(1)`
`rseed(#)`	random-number seed
`exclude(`*paramref*`)`	specify model parameters to be excluded from the simulation results
Blocking	
* `blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref*`[, `*blockopts*`])`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
* `noblocking`	do not block parameters by default

Initialization

initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

Adaptation

adaptation(*adaptopts*)	control the adaptive MCMC procedure
scale(#)	initial multiplier for scale factor; default is scale(2.38)
covariance(*cov*)	initial proposal covariance; default is the identity matrix

Reporting

clevel(#)	set credible interval level; default is clevel(95)
hpd	display HPD credible intervals instead of the default equal-tailed credible intervals
*irr	report incidence-rate ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
batch(#)	specify length of block for batch-means calculations; default is batch(0)
saving(*filename*[, replace])	save simulation results to *filename*.dta
nomodelsummary	suppress model summary
chainsdetail	display detailed simulation summary for each chain
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is nodots
dots(#[, every(#)])	display dots as simulation is performed
[no]show(*paramref*)	specify model parameters to be excluded from or included in the output
notable	suppress estimation table
noheader	suppress output header
title(*string*)	display *string* as title above the table of parameter estimates
display_options	control spacing, line width, and base and empty cells

Advanced

search(*search_options*)	control the search for feasible initial values
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.

Options prior() and block() may be repeated.

priorspec and *paramref* are defined in [BAYES] **bayesmh**.

paramref may contain factor variables; see [U] **11.4.3 Factor variables**.

collect is allowed; see [U] **11.1.10 Prefix commands**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Model parameters are regression coefficients {*depvar*:*indepvars*} for the main regression and {inflate:*varlist*} for the inflation equation. Use the dryrun option to see the definitions of model parameters prior to estimation.

For a detailed description of *bayesopts*, see *Options* in [BAYES] **bayes**.

Remarks and examples

For a general introduction to Bayesian analysis, see [BAYES] **Intro**. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **zip**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Zero-inflated negative binomial model* in [BAYES] **bayes**.

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

See *Methods and formulas* in [BAYES] **bayesmh**.

Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix

[R] **zip** — Zero-inflated Poisson regression

[BAYES] **Bayesian postestimation** — Postestimation tools for bayesmh and the bayes prefix

[BAYES] **Bayesian estimation** — Bayesian estimation commands

[BAYES] **Bayesian commands** — Introduction to commands for Bayesian analysis

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**

Glossary

a posteriori. In the context of Bayesian analysis, we use a posteriori to mean "after the sample is observed". For example, a posteriori information is any information obtained after the data sample is observed. See *posterior distribution, posterior*.

a priori. In the context of Bayesian analysis, we use a priori to mean "before the sample is observed". For example, a priori information is any information obtained before the data sample is observed. In a Bayesian model, a priori information about model parameters is specified by prior distributions.

acceptance rate. In the context of the MH algorithm, acceptance rate is the fraction of the proposed samples that is accepted. The optimal acceptance rate depends on the properties of the target distribution and is not known in general. If the target distribution is normal, however, the optimal acceptance rate is known to be 0.44 for univariate distributions and 0.234 for multivariate distributions.

adaptation. In the context of the MH algorithm, adaptation refers to the process of tuning or adapting the proposal distribution to optimize the MCMC sampling. Typically, adaptation is performed periodically during the MCMC sampling. The `bayesmh` command performs adaptation every # of iterations as specified in option `adaptation(every(#))` for a maximum of `adaptation(maxiter())` iterations. In a continuous-adaptation regimes, the adaptation lasts during the entire process of the MCMC sampling. See [BAYES] **bayesmh**.

adaptation period. Adaptation period includes all MH adaptive iterations. It equals the length of the adaptation interval, as specified by `adaptation(every())`, times the maximum number of adaptations, `adaptation(maxiter())`.

adaptive iteration. In the adaptive MH algorithm, adaptive iterations are iterations during which adaptation is performed.

Akaike information criterion, AIC. Akaike information criterion (AIC) is an information-based model-selection criterion. It is given by the formula $-2 \times \log$ likelihood $+ 2k$, where k is the number of parameters. AIC favors simpler models by penalizing for the number of model parameters. It does not, however, account for the sample size. As a result, the AIC penalization diminishes as the sample size increases, as does its ability to guard against overparameterization.

batch means. Batch means are means obtained from batches of sample values of equal size. Batch means provide an alternative method for estimating MCMC standard errors (MCSE). The batch size is usually chosen to minimize the correlation between different batches of means.

Bayes factor. Bayes factor is given by the ratio of the marginal likelihoods of two models, M_1 and M_2. It is a widely used criterion for Bayesian model comparison. Bayes factor is used in calculating the posterior odds ratio of model M_1 versus M_2,

$$\frac{P(M_1|\mathbf{y})}{P(M_2|\mathbf{y})} = \frac{P(\mathbf{y}|M_1)}{P(\mathbf{y}|M_2)}\frac{P(M_1)}{P(M_2)}$$

where $P(M_i|\mathbf{y})$ is a posterior probability of model M_i, and $P(M_i)$ is a prior probability of model M_i. When the two models are equally likely, that is, when $P(M_1) = P(M_2)$, the Bayes factor equals the posterior odds ratio of the two models.

Bayes's theorem. The Bayes's theorem is a formal method for relating conditional probability statements. For two (random) events X and Y, the Bayes's theorem states that

$$P(X|Y) \propto P(Y|X)P(X)$$

that is, the probability of X conditional on Y is proportional to the probability of X and the probability of Y conditional on X. In Bayesian analysis, the Bayes's theorem is used for combining prior information about model parameters and evidence from the observed data to form the posterior distribution.

Bayesian analysis. Bayesian analysis is a statistical methodology that considers model parameters to be random quantities and estimates their posterior distribution by combining prior knowledge about parameters with the evidence from the observed data sample. Prior knowledge about parameters is described by prior distributions and evidence from the observed data is incorporated through a likelihood model. Using the Bayes's theorem, the prior distribution and the likelihood model are combined to form the posterior distribution of model parameters. The posterior distribution is then used for parameter inference, hypothesis testing, and prediction.

Bayesian estimation. Bayesian estimation consists of fitting Bayesian models and estimating their parameters based on the resulting posterior distribution. Bayesian estimation in Stata can be done using the convenient `bayes` prefix or the more general `bayesmh` command. See [BAYES] **Bayesian estimation** for details.

Bayesian estimation results. Estimation results obtained after the `bayes` prefix or the `bayesmh` command.

Bayesian hypothesis testing. Bayesian hypothesis testing computes probabilities of hypotheses conditional on the observed data. In contrast to the frequentist hypothesis testing, the Bayesian hypothesis testing computes the actual probability of a hypothesis H by using the Bayes's theorem,

$$P(H|\mathbf{y}) \propto P(\mathbf{y}|H)P(H)$$

where $\mathbf{y}$ is the observed data, $P(\mathbf{y}|H)$ is the marginal likelihood of $\mathbf{y}$ given H, and $P(H)$ is the prior probability of H. Two different hypotheses, H_1 and H_2, can be compared by simply comparing $P(H_1|\mathbf{y})$ to $P(H_2|\mathbf{y})$.

Bayesian information criterion, BIC. The Bayesian information criterion (BIC), also known as Schwarz criterion, is an information based criterion used for model selection in classical statistics. It is given by the formula $-2 \times \log$ likelihood $+ k \times \ln n$, where k is the number of parameters and n is the sample size. BIC favors simpler, in terms of complexity, models and it is more conservative than AIC.

Bayesian model checking. In Bayesian statistics, model checking refers to testing likelihood and prior model adequacy in the context of a research problem and observed data. A simple sanity check may include verifying that posterior inference produces results that are reasonable in the context of the problem. More substantive checks may include analysis of the sensitivity of Bayesian inference to changes in likelihood and prior distribution specifications. See *posterior predictive checking*.

Bayesian predictions. Bayesian predictions are samples from the posterior predictive distribution of outcome variables and functions of these samples and, optionally, model parameters. Examples of Bayesian predictions include replicated data, out-of-sample predictions, and test statistics of simulated outcomes.

blocking. In the context of the MH algorithm, blocking refers to the process of separating model parameters into different subsets or blocks to be sampled independently of each other. MH algorithm generates proposals and applies the acceptance–rejection rule sequentially for each block. It is recommended that correlated parameters are kept in one block. Separating less-correlated or independent model parameters in different blocks may improve the mixing of the MH algorithm.

burn-in period. The burn-in period is the number of iterations it takes for an MCMC sequence to reach stationarity.

central posterior interval. See *equal-tailed credible interval*.

conditional conjugacy. See *semiconjugate prior*.

conjugate prior. A prior distribution is conjugate for a family of likelihood distributions if the prior and posterior distributions belong to the same family of distributions. For example, the gamma distribution is a conjugate prior for the Poisson likelihood. Conjugacy may provide an efficient way of sampling from posterior distributions and is used in Gibbs sampling.

continuous parameters. Continuous parameters are parameters with continuous prior distributions.

credible interval. In Bayesian analysis, the credible interval of a scalar model parameter is an interval from the domain of the marginal posterior distribution of that parameter. Two types of credible intervals are typically used in practice: equal-tailed credible intervals and HPD credible intervals.

credible level. The credible level is a probability level between 0% and 100% used for calculating credible intervals in Bayesian analysis. For example, a 95% credible interval for a scalar parameter is an interval the parameter belongs to with the probability of 95%.

cross-variable. A cross-variable is a Stata term to refer to the dependent variable used as a lagged regressor in the VAR model in an outcome equation that is not its own. For instance, in a VAR model with two dependent variables (`y1` and `y2`) and two lags,

$$\texttt{y1} = a_{11}\texttt{L.y1} + a_{12}\texttt{L2.y1} + a_{21}\texttt{L.y2} + a_{22}\texttt{L2.y2} + a_0 + u_1$$

$$\texttt{y2} = b_{11}\texttt{L.y1} + b_{12}\texttt{L2.y1} + b_{21}\texttt{L.y2} + b_{22}\texttt{L2.y2} + b_0 + u_2$$

`y2` is the cross-variable in the first outcome equation (`y1`), and `y1` is the cross-variable in the second outcome equation (`y2`). Note that `y1` and `y2` are self-variables in the first and second equations, respectively. Cross-variables are always endogenous variables. We also often refer to the coefficients of cross-variables as cross-variables first-lag coefficients (a_{21} and b_{11}), cross-variables second-lag coefficients (a_{22} and b_{12}), and so on. See [BAYES] **bayes: var**.

cross-variables first-lag coefficients. Regression coefficients in a VAR model that correspond to first lags ([U] **11.4.4 Time-series varlists**) of cross-variables. See [BAYES] **bayes: var**.

cross-variables tightness parameter. A cross-variables tightness parameter is a parameter, λ_2, that controls the tightness of the Minnesota prior distribution by controlling the prior variance for the cross-variables coefficients. It is specified in the Minnesota prior option `crosstight()`. See *Methods and formulas* of [BAYES] **bayes: var** for details.

cusum plot, CUSUM plot. The cusum (CUSUM) plot of an MCMC sample is a plot of cumulative sums of the differences between sample values and their overall mean against the iteration number. Cusum plots are useful graphical summaries for detecting early drifts in MCMC samples.

deviance information criterion, DIC. The deviance information criterion (DIC) is an information based criterion used for Bayesian model selection. It is an analog of AIC and is given by the formula $D(\overline{\theta}) + 2 \times p_D$, where $D(\overline{\theta})$ is the deviance at the sample mean and p_D is the effective complexity, a quantity equivalent to the number of parameters in the model. Models with smaller DIC are preferred.

diminishing adaptation. Diminishing adaptation of the adaptive algorithm is the type of adaptation in which the amount of adaptation decreases with the size of the MCMC chain.

discrete parameters. Discrete parameters are parameters with discrete prior distributions.

effective sample size, ESS. Effective sample size (ESS) is the MCMC sample size T adjusted for the autocorrelation in the sample. It represents the number of independent observations in an MCMC sample. ESS is used instead of T in calculating MCSE. Small ESS relative to T indicates high autocorrelation and consequently poor mixing of the chain.

efficiency. In the context of MCMC, efficiency is a term used for assessing the mixing quality of an MCMC procedure. Efficient MCMC algorithms are able to explore posterior domains in less time (using fewer iterations). Efficiency is typically quantified by the sample autocorrelation and effective sample size. An MCMC procedure that generates samples with low autocorrelation and consequently high ESS is more efficient.

endogenous variable. In the context of VAR, an endogenous variable is a dependent variable included in the model as a regressor with a lag operator; see **[U] 11.4.4 Time-series varlists**. Also see *endogenous variable* in [TS] **Glossary** for a general definition.

equal-tailed credible interval. An equal-tailed credible interval is a credible interval defined in such a way that both tails of the marginal posterior distribution have the same probability. A $\{100 \times (1-\alpha)\}\%$ equal-tailed credible interval is defined by the $\alpha/2$th and $\{(1-\alpha)/2\}$th quantiles of the marginal posterior distribution.

exogenous variable. In the context of VAR, an exogenous variable is an independent variable (regressor) included in the model. Also see *exogenous variable* in [TS] **Glossary** for a general definition.

exogenous-variables tightness parameter. An exogenous-variables tightness parameter is a parameter, λ_4, that controls the tightness of the Minnesota prior distribution by controlling the prior variance for the exogenous-variables coefficients. It is specified in the Minnesota prior option `exogtight()`. See *Methods and formulas* of [BAYES] **bayes: var** for details.

feasible initial value. An initial-value vector is feasible if it corresponds to a state with a positive posterior probability.

fixed effects. See *fixed-effects parameters*.

fixed-effects parameters. In the Bayesian context, the term "fixed effects" or "fixed-effects parameters" is a misnomer, because all model parameters are inherently random. We use this term in the context of Bayesian multilevel models to refer to regression model parameters and to distinguish them from the random-effects parameters. You can think of fixed-effects parameters as parameters modeling population averaged or marginal relationship of the response and the variables of interest.

frequentist analysis. Frequentist analysis is a form of statistical analysis where model parameters are considered to be unknown but fixed constants and the observed data are viewed as a repeatable random sample. Inference is based on the sampling distribution of the data.

full conditionals. A full conditional is the probability distribution of a random variate conditioned on all other random variates in a joint probability model. Full conditional distributions are used in Gibbs sampling.

full Gibbs sampling. See *Gibbs sampling, Gibbs sampler*.

Gelman–Rubin convergence diagnostic, Gelman–Rubin convergence statistic. Gelman–Rubin convergence diagnostic assesses MCMC convergence by analyzing differences between multiple Markov chains. The convergence is assessed by comparing the estimated between-chains and within-chain variances for each model parameter. Large differences between these variances indicate nonconvergence. See [BAYES] **bayesstats grubin**.

Gibbs sampling, Gibbs sampler. Gibbs sampling is an MCMC method, according to which each random variable from a joint probability model is sampled according to its full conditional distribution.

highest posterior density credible interval, HPD credible interval. The highest posterior density (HPD) credible interval is a type of a credible interval with the highest marginal posterior density. An HPD interval has the shortest width among all other credible intervals. For some multimodal marginal distributions, HPD may not exists. See *highest posterior density region, HPD region*.

highest posterior density region, HPD region. The highest posterior density (HPD) region for model parameters has the highest marginal posterior probability among all domain regions. Unlike an HPD credible interval, an HPD region always exist.

hybrid MH sampling, hybrid MH sampler. A hybrid MH sampler is an MCMC method in which some blocks of parameters are updated using the MH algorithms and other blocks are updated using Gibbs sampling.

hyperparameter. In Bayesian analysis, hyperparameter is a parameter of a prior distribution, in contrast to a model parameter.

hyperprior. In Bayesian analysis, hyperprior is a prior distribution of hyperparameters. See *hyperparameter*.

improper prior. A prior is said to be improper if it does not integrate to a finite number. Uniform distributions over unbounded intervals are improper. Improper priors may still yield proper posterior distributions. When using improper priors, however, one has to make sure that the resulting posterior distribution is proper for Bayesian inference to be invalid.

independent a posteriori. Parameters are considered independent a posteriori if their marginal posterior distributions are independent; that is, their joint posterior distribution is the product of their individual marginal posterior distributions.

independent a priori. Parameters are considered independent a priori if their prior distributions are independent; that is, their joint prior distribution is the product of their individual marginal prior distributions.

informative prior. An informative prior is a prior distribution that has substantial influence on the posterior distribution.

in-sample predictions. See *replicated outcome*.

interval hypothesis testing. Interval hypothesis testing performs interval hypothesis tests for model parameters and functions of model parameters.

interval test. In Bayesian analysis, an interval test applied to a scalar model parameter calculates the marginal posterior probability for the parameter to belong to the specified interval.

Jeffreys prior. The Jeffreys prior of a vector of model parameters $\boldsymbol{\theta}$ is proportional to the square root of the determinant of its Fisher information matrix $I(\boldsymbol{\theta})$. Jeffreys priors are locally uniform and, by definition, agree with the likelihood function. Jeffreys priors are considered noninformative priors that have minimal impact on the posterior distribution.

lag coefficient. In the context of time-series regression analysis, a lag coefficient is a regression coefficient that corresponds to a variable included in the regression model with a lag operator; see **[U] 11.4.4 Time-series varlists**.

lag-decay parameter. A lag-decay parameter is a parameter, λ_3, that controls the tightness of the Minnesota prior distribution by controlling the prior variance as a function of a lag for all endogenous-variables coefficients. It is specified in the Minnesota prior option `lagdecay()`. See *Methods and formulas* of [BAYES] **bayes: var** for details.

marginal distribution. In Bayesian context, a distribution of the data after integrating out parameters from the joint distribution of the parameters and the data.

marginal likelihood. In the context of Bayesian model comparison, a marginalized over model parameters $\boldsymbol{\theta}$ likelihood of data $\mathbf{y}$ for a given model M, $P(\mathbf{y}|M) = m(\mathbf{y}) = \int P(\mathbf{y}|\boldsymbol{\theta}, M)P(\boldsymbol{\theta}|M)d\boldsymbol{\theta}$. Also see *Bayes factor*.

marginal posterior distribution. In Bayesian context, a marginal posterior distribution is a distribution resulting from integrating out all but one parameter from the joint posterior distribution.

Markov chain. Markov chain is a random process that generates sequences of random vectors (or states) and satisfies the Markov property: the next state depends only on the current state and not on any of the previous states. MCMC is the most common methodology for simulating Markov chains.

matrix model parameter. A matrix model parameter is any model parameter that is a matrix. Matrix elements, however, are viewed as scalar model parameters.

Matrix model parameters are defined and referred to within the `bayesmh` command as {*param*,`matrix`} or {*eqname*:*param*,`matrix`} with the equation name *eqname*. For example, {`Sigma, matrix`} and {`Scale:Omega, matrix`} are matrix model parameters. Individual matrix elements cannot be referred to within the `bayesmh` command, but they can be referred within postestimation commands accepting parameters. For example, to refer to the individual elements of the defined above, say, 2×2 matrices, use {`Sigma_1_1`}, {`Sigma_2_1`}, {`Sigma_1_2`}, {`Sigma_2_2`} and {`Scale:Omega_1_1`}, {`Scale:Omega_2_1`}, {`Scale:Omega_1_2`}, {`Scale:Omega_2_2`}, respectively. See [BAYES] **bayesmh**.

matrix parameter. See *matrix model parameter*.

MCMC, Markov chain Monte Carlo. MCMC is a class of simulation-based methods for generating samples from probability distributions. Any MCMC algorithm simulates a Markov chain with a target distribution as its stationary or equilibrium distribution. The precision of MCMC algorithms increases with the number of iterations. The lack of a stopping rule and convergence rule, however, makes it difficult to determine for how long to run MCMC. The time needed to converge to the target distribution within a prespecified error is referred to as mixing time. Better MCMC algorithms have faster mixing times. Some of the popular MCMC algorithms are random-walk Metropolis, Metropolis–Hastings, and Gibbs sampling.

MCMC replicates. An MCMC sample of simulated outcomes.

MCMC sample. An MCMC sample is obtained from MCMC sampling. An MCMC sample approximates a target distribution and is used for summarizing this distribution.

MCMC sample size. MCMC sample size is the size of the MCMC sample. It is specified in `bayesmh`'s option `mcmcsize()`; see [BAYES] **bayesmh**.

MCMC sampling, MCMC sampler. MCMC sampling is an MCMC algorithm that generates samples from a target probability distribution.

MCMC standard error, MCSE MCSE is the standard error of the posterior mean estimate. It is defined as the standard deviation divided by the square root of ESS. MCSEs are analogs of standard errors in frequentist statistics and measure the accuracy of the simulated MCMC sample.

Metropolis–Hastings (MH) sampling, MH sampler. A Metropolis–Hastings (MH) sampler is an MCMC method for simulating probability distributions. According to this method, at each step of the Markov chain, a new proposal state is generated from the current state according to a prespecified proposal distribution. Based on the current and new state, an acceptance probability is calculated and then used to accept or reject the proposed state. Important characteristics of MH sampling is the acceptance rate and mixing time. The MH algorithm is very general and can be applied to an arbitrary target distribution. However, its efficiency is limited, in terms of mixing time, and decreases as the dimension of the target distribution increases. Gibbs sampling, when available, can provide much more efficient sampling than MH sampling.

Minnesota prior. In Bayesian VAR models, Minnesota priors are used as priors for regression coefficients. A Minnesota prior is a multivariate normal distribution with a special mean vector and covariance matrix. The mean vector contains all zeroes except the values corresponding to self-variables first-lag coefficients, which are set to 1. The covariance matrix can be fixed or can be a product of a fixed matrix and a matrix model parameter as in the case of a conjugate Minnesota

prior. The Minnesota prior assumes that, a priori, each univariate time series in the model is a random walk.

Minnesota factor covariance. In Bayesian VAR models with a conjugate Minnesota prior, the factor covariance matrix is used to form the covariance of the multivariate normal prior for regression coefficients. The latter is defined as the Kronecker product of the unknown covariance matrix of error terms with the Minnesota factor covariance.

mixing of Markov chain. Mixing refers to the rate at which a Markov chain traverses the parameter space. It is a property of the Markov chain that is different from convergence. Poor mixing indicates a slow rate at which the chain explores the stationary distribution and will require more iterations to provide inference at a given precision. Poor (slow) mixing is typically a result of high correlation between model parameters or of weakly-defined model specifications.

model hypothesis testing. Model hypothesis testing tests hypotheses about models by computing model posterior probabilities.

model parameter. A model parameter refers to any (random) parameter in a Bayesian model. Model parameters can be scalars or matrices. Examples of model parameters as defined in `bayesmh` are `{mu}`, `{scale:s}`, `{Sigma,matrix}`, and `{Scale:Omega,matrix}`. See [BAYES] **bayesmh** and, specifically, *Declaring model parameters* and *Referring to model parameters* in that entry. Also see *Different ways of specifying model parameters* in [BAYES] **Bayesian postestimation**.

model posterior probability. Model posterior probability is probability of a model M computed conditional on the observed data $\mathbf{y}$,

$$P(M|\mathbf{y}) = P(M)P(\mathbf{y}|M) = P(M)m(\mathbf{y})$$

where $P(M)$ is the prior probability of a model M and $m(\mathbf{y})$ is the marginal likelihood under model M.

noninformative prior. A noninformative prior is a prior with negligible influence on the posterior distribution. See, for example, *Jeffreys prior*.

objective prior. See *noninformative prior*.

one-at-a-time MCMC sampling. A one-at-a-time MCMC sample is an MCMC sampling procedure in which random variables are sampled individually, one at a time. For example, in Gibbs sampling, individual variates are sampled one at a time, conditionally on the most recent values of the rest of the variates.

out-of-sample predictions. Predictions of future observations; see *simulated outcome*.

overdispersed initial value. An overdispersed initial value is obtained from a distribution that is overdispersed or has larger variability relative to the true marginal posterior distribution. Overdispersed initial values are used with multiple Markov chains for diagnosing MCMC convergence. Also see *Specifying initial values* in [BAYES] **bayesmh**.

posterior distribution, posterior. A posterior distribution is a probability distribution of model parameters conditional on observed data. The posterior distribution is determined by the likelihood of the parameters and their prior distribution. For a parameter vector $\boldsymbol{\theta}$ and data $\mathbf{y}$, the posterior distribution is given by

$$P(\boldsymbol{\theta}|\mathbf{y}) = \frac{P(\boldsymbol{\theta})P(\mathbf{y}|\boldsymbol{\theta})}{P(\mathbf{y})}$$

where $P(\boldsymbol{\theta})$ is the prior distribution, $P(\mathbf{y}|\boldsymbol{\theta})$ is the model likelihood, and $P(\mathbf{y})$ is the marginal distribution for $\mathbf{y}$. Bayesian inference is based on a posterior distribution.

posterior independence. See *independent a posteriori*.

posterior interval. See *credible interval*.

posterior odds. Posterior odds for $\boldsymbol{\theta}_1$ compared with $\boldsymbol{\theta}_2$ is the ratio of posterior density evaluated at $\boldsymbol{\theta}_1$ and $\boldsymbol{\theta}_2$ under a given model,

$$\frac{p(\boldsymbol{\theta}_1|\mathbf{y})}{p(\boldsymbol{\theta}_2|\mathbf{y})} = \frac{p(\boldsymbol{\theta}_1)}{p(\boldsymbol{\theta}_2)} \frac{p(\mathbf{y}|\boldsymbol{\theta}_1)}{p(\mathbf{y}|\boldsymbol{\theta}_2)}$$

In other words, posterior odds are prior odds times the likelihood ratio.

posterior predictive checking. Posterior predictive checking is a methodology for assessing goodness of fit of a Bayesian model using replicated data simulated from the posterior predictive distribution of the model. For example, graphical diagnostics of the replicated residuals may be used to check the distributional assumptions of the model error terms. A more formal and systematic approach uses test quantities and test statistics to measure discrepancies between replicated data and observed data. Test statistics such as a mean, minimum, and maximum can be used to compare different aspects of the observed data distribution with those of the replicated-data distribution. Posterior predictive p-values, also called Bayesian p-values, computed for test quantities and test statistics are used to quantify the discrepancy between the observed and replicated data. Also see *Bayesian model checking*.

posterior predictive distribution. Posterior predictive distribution is a distribution of unobserved (future) data conditional on observed data. Posterior predictive distribution is derived by marginalizing the likelihood function with respect to the posterior distribution of model parameters.

posterior predictive p-value. Posterior predictive p-value, also called a Bayesian p-value, is the probability that a test quantity (or statistic) computed for the replicated data is greater or equal to the test quantity computed for the observed data. Posterior predictive p-values are used in posterior predictive checking. p-values less than 0.05 or greater than 0.95 typically indicate model misfit (Gelman et al. 2014).

predictive distribution. See *prior predictive distribution* and *posterior predictive distribution*.

predictive inference. In Bayesian statistics, predictive inference is inference about unobserved (future) data conditionally on past data and prior knowledge of model parameters. Predictive inference is based on prior predictive or posterior predictive distribution of model parameters.

predictive outcome. Predictive outcome $\widetilde{y}$ is a value or a set of values simulated from a posterior predictive distribution $p(\widetilde{y}|y)$ of a Bayesian model (Gelman et al. 2014). In contrast with replicated outcome, predictive outcomes may use the values of independent variables that are different from those used to fit the model. Also see *simulated outcome*.

prior distribution, prior. In Bayesian statistics, prior distributions are probability distributions of model parameters formed based on some a priori knowledge about parameters. Prior distributions are independent of the observed data.

prior independence. See *independent a priori*.

prior odds. Prior odds for $\boldsymbol{\theta}_1$ compared with $\boldsymbol{\theta}_2$ is the ratio of prior density evaluated at $\boldsymbol{\theta}_1$ and $\boldsymbol{\theta}_2$ under a given model, $p(\boldsymbol{\theta}_1)/p(\boldsymbol{\theta}_2)$. Also see *posterior odds*.

prior predictive distribution. Prior predictive distribution is a distribution of unobserved (future) data derived by marginalizing the likelihood function with respect to the prior distribution of model parameters. Also see *marginal distribution*.

prior tightness. A prior tightness is controlled by a tightness parameter, which is typically a multiplier for the prior variance. The smaller the value of this parameter, the smaller the prior variance, and the "tighter" (more highly concentrated) the prior around the prior mean. See [BAYES] **bayes: var**.

probability of unit circle inclusion. In the context of Bayesian VAR, this is a posterior probability that all moduli of eigenvalues of a companion matrix lie within the unit circle. The higher this probability, the more likely the stability condition is met for the considered Bayesian VAR model.

proposal distribution. In the context of the MH algorithm, a proposal distribution is used for defining the transition steps of the Markov chain. In the standard random-walk Metropolis algorithm, the proposal distribution is a multivariate normal distribution with zero mean and adaptable covariance matrix.

pseudoconvergence. A Markov chain may appear to converge when in fact it did not. We refer to this phenomenon as pseudoconvergence. Pseudoconvergence is typically caused by multimodality of the stationary distribution, in which case the chain may fail to traverse the weakly connected regions of the distribution space. A common way to detect pseudoconvergence is to run multiple chains using different starting values and to verify that all of the chain converge to the same target distribution.

random effects. See *random-effects parameters*.

random-effects linear form. A linear form representing a random-effects variable that can be used in substitutable expressions.

random-effects parameters. In the context of Bayesian multilevel models, random-effects parameters are parameters associated with a random-effects variable. Random-effects parameters are assumed to be conditionally independent across levels of the random-effects variable given all other model parameters. Often, random-effects parameters are assumed to be normally distributed with a zero mean and an unknown variance–covariance matrix.

random-effects variable. A variable identifying the group structure for the random effects at a specific level of hierarchy.

reference prior. See *noninformative prior*.

replicated data. Replicated data, $\mathbf{y}^{\text{rep}}$, are data that could be observed if the experiment that produced the observed data, $\mathbf{y}^{\text{obs}}$, were replicated using the same model and the same values of independent variables that generated $\mathbf{y}^{\text{obs}}$. See Gelman et al. (2014, 145), [BAYES] **bayespredict**, and [BAYES] **bayesstats ppvalues**.

replicated outcome. Replicated outcome is a special case of a simulated outcome that is generated using the same values of independent variables as those used to fit the model. Also see *replicated data*.

scalar model parameter. A scalar model parameter is any model parameter that is a scalar. For example, `{mean}` and `{hape:alpha}` are scalar parameters, as declared by the `bayesmh` command. Elements of matrix model parameters are viewed as scalar model parameters. For example, for a 2×2 matrix parameter `{Sigma,matrix}`, individual elements `{Sigma_1_1}`, `{Sigma_2_1}`, `{Sigma_1_2}`, and `{Sigma_2_2}` are scalar parameters. If a matrix parameter contains a label, the label should be included in the specification of individual elements as well. See [BAYES] **bayesmh**.

scalar parameter. See *scalar model parameter*.

self-variable. A self-variable is a Stata term to refer to the dependent variable used as a lagged regressor in the VAR model in its own outcome equation. For instance, in a VAR model with two dependent variables (`y1` and `y2`) and two lags,

$$\texttt{y1} = a_{11}\texttt{L.y1} + a_{12}\texttt{L2.y1} + a_{21}\texttt{L.y2} + a_{22}\texttt{L2.y2} + a_0 + u_1$$

$$\texttt{y2} = b_{11}\texttt{L.y1} + b_{12}\texttt{L2.y1} + b_{21}\texttt{L.y2} + b_{22}\texttt{L2.y2} + b_0 + u_2$$

`y1` is the self-variable in the first outcome equation (`y1`), and `y2` is the self-variable in the second outcome equation (`y2`). Note that `y2` and `y1` are cross-variables in the first and second equations, respectively. Self-variables are always endogenous variables. We also often refer to the coefficients of self-variables as self-variables first-lag coefficients (a_{11} and b_{21}), self-variables second-lag coefficients (a_{12} and b_{22}), and so on. See [BAYES] **bayes: var**.

self-variables first-lag coefficients. Self-variables first-lag coefficients are regression coefficients in a VAR model that correspond to first lags ([U] **11.4.4 Time-series varlists**) of self-variables. See [BAYES] **bayes: var**.

self-variables tightness parameter. A self-variables tightness parameter is a parameter, λ_1, that controls the tightness of the Minnesota prior distribution by controlling the prior variance for the self-variables coefficients. It is specified in the Minnesota prior option `selftight()`. See *Methods and formulas* of [BAYES] **bayes: var** for details.

semiconjugate prior. A prior distribution is semiconjugate for a family of likelihood distributions if the prior and (full) conditional posterior distributions belong to the same family of distributions. For semiconjugacy to hold, parameters must typically be independent a priori; that is, their joint prior distribution must be the product of the individual marginal prior distributions. For example, the normal prior distribution for a mean parameter of a normal data distribution with an unknown variance (which is assumed to be independent of the mean a priori) is a semiconjugate prior. Semiconjugacy may provide an efficient way of sampling from posterior distributions and is used in Gibbs sampling.

simulated outcome. In Bayesian predictive inference, simulated outcomes are samples from the posterior predictive distribution. In the context of `bayespredict`, we define a simulated outcome as a $T \times n$ matrix of new outcome values simulated from the posterior predictive distribution, $p(\tilde{\mathbf{y}}|\mathbf{y})$, for a particular outcome variable $\mathbf{y}$, where T is the MCMC sample size and n is the number of observations.

stationary distribution. Stationary distribution of a stochastic process is a joint distribution that does not change over time. In the context of MCMC, stationary distribution is the target probability distribution to which the Markov chain converges. When MCMC is used for simulating a Bayesian model, the stationary distribution is the target joint posterior distribution of model parameters.

subjective prior. See *informative prior*.

subsampling the chain. See *thinning*.

sufficient statistic. Sufficient statistic for a parameter of a parametric likelihood model is any function of the sample that contains all the information about the model parameter.

test quantity. In Bayesian predictive inference, test quantity is any function of a simulated outcome, $\mathbf{y}^{\text{sim}}$, and model parameters $\boldsymbol{\theta}$. It is estimated by sampling from the joint posterior distribution $p(\mathbf{y}^{\text{sim}}, \boldsymbol{\theta})$. A test quantity that depends only on $\mathbf{y}^{\text{sim}}$ is called a test statistic. Test quantities are used in posterior predictive checking to assess model fit.

test statistic. A special case of a test quantity that depends only on the data.

thinning. Thinning is a way of reducing autocorrelation in the MCMC sample by subsampling the MCMC chain every prespecified number of iterations determined by the thinning interval. For example, the thinning interval of 1 corresponds to using the entire MCMC sample; the thinning interval of 2 corresponds to using every other sample value; and the thinning interval of 3 corresponds to using values from iterations 1, 4, 7, 10, and so on. Thinning should be applied with caution when used to reduce autocorrelation because it may not always be the most appropriate way of improving the precision of estimates.

tightness. See *prior tightness*.

tightness parameter. A tightness parameter is a parameter, typically a multiplier for the prior variance, that controls the tightness of the prior. The smaller the value of this parameter, the smaller the prior variance, and the "tighter" (more highly concentrated) the prior around the prior mean. See *self-variables tightness parameter*, *cross-variables tightness parameter*, *lad-decay parameter*, and *exogenous-variables tightness parameter*. Also see *Methods and formula* in [BAYES] **bayes: var**.

vague prior. See *noninformative prior*.

valid initial state. See *feasible initial value*.

vanishing adaptation. See *diminishing adaptation*.

VAR, vector autoregression. See *VAR* in [TS] **Glossary**.

Zellner's g-prior. Zellner's g-prior is a form of a weakly informative prior for the regression coefficients in a linear model. It accounts for the correlation between the predictor variables and controls the impact of the prior of the regression coefficients on the posterior with parameter g. For example, $g = 1$ means that prior weight is 50% and $g \to \infty$ means diffuse prior.

Reference

Gelman, A., J. B. Carlin, H. S. Stern, D. B. Dunson, A. Vehtari, and D. B. Rubin. 2014. *Bayesian Data Analysis*. 3rd ed. Boca Raton, FL: Chapman and Hall/CRC.

Subject and author index

See the combined subject index and the combined author index in the *Stata Index*.