Title

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bayesmh — Bayesian models using Metropolis–Hastings algorithm[+]

[+]This command includes features that are part of StataNow.

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
[+]`asymlaplaceq(`*sigma*`,` *tau*`)`	asymmetric Laplace (quantile) regression with scale *sigma* and quantile *tau*
`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

[+]These features are part of StataNow.

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 $\max\{25, \texttt{floor(burnin()/every())}\}$ 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. For the parameterization of the asymlaplaceq() likelihood, see *Methods and formulas* of [BAYES] **bayes: qreg**.

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 `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*.

`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), or linear programming estimates for `bayes: qreg`, 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 $\max\{25, \texttt{floor(burnin()/adaptation(every()))}\}$.

`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` 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

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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()` $\times$ (`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
```

mpg	Mean	Std. dev.	MCSE	Median	Equal-tailed [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

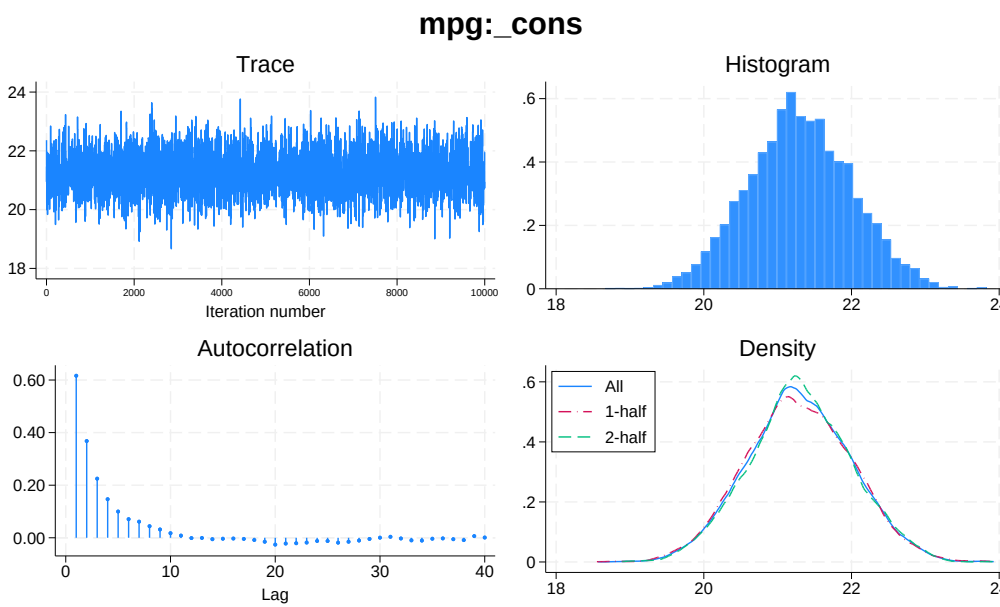
is also the sample average, so the posterior mean estimate and the MLE should be the same in this model.

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.

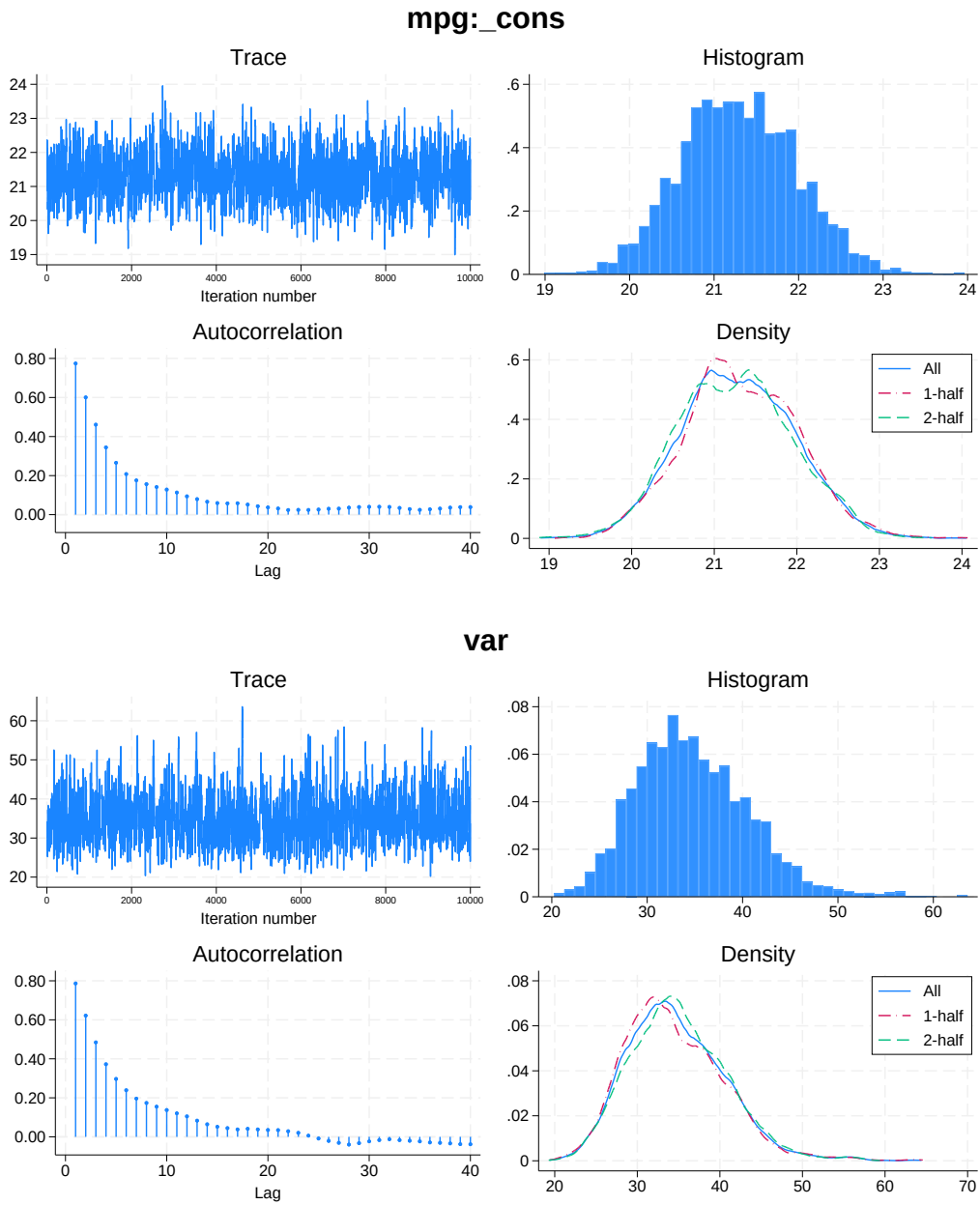
```
. set seed 14
. bayesmh mpg, likelihood(normal({var}))
> prior({mpg:_cons}, flat) prior({var}, jeffreys)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},{var})
Priors:
  {mpg:_cons} ~ 1 (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	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

◁

▷ 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
------------------------------------------------------------------------------
             |                                                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
------------------------------------------------------------------------------
```

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

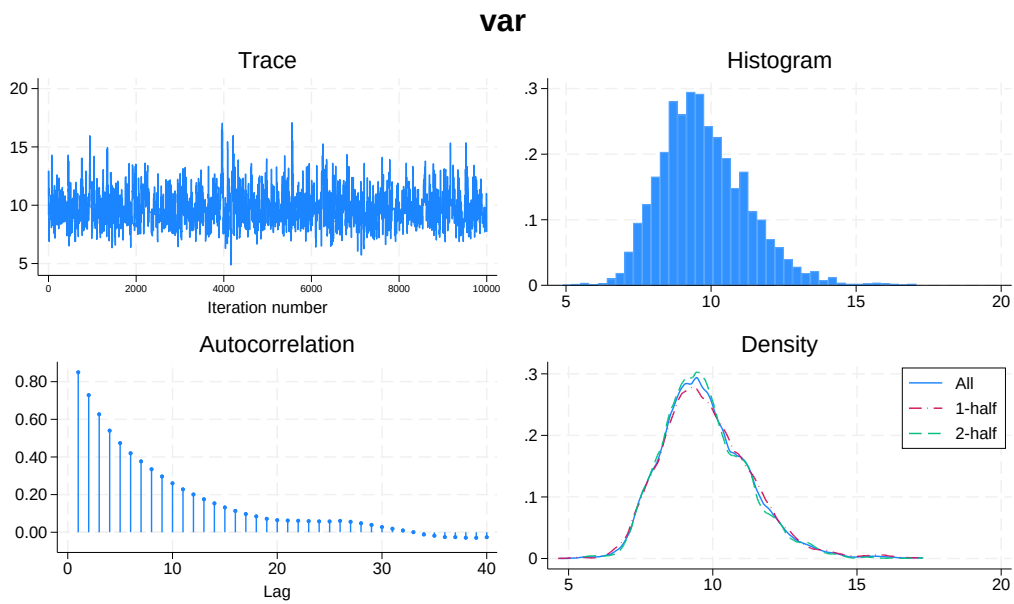
Our first simulation is performed using the default settings for the algorithm. Specifically, all three model parameters are placed in one simulation block and are updated simultaneously, as our block summary indicates.

```
. 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}
```



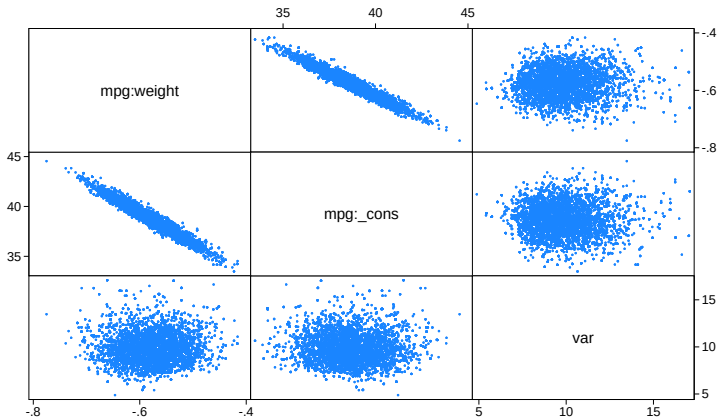
A graphical summary for the {var} parameter does not show any obvious problems. The trace plot reveals a good coverage of the domain of the marginal distribution, while the histogram and kernel density plots resemble the shape of an expected inverse-gamma distribution. The autocorrelation dies off after 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.

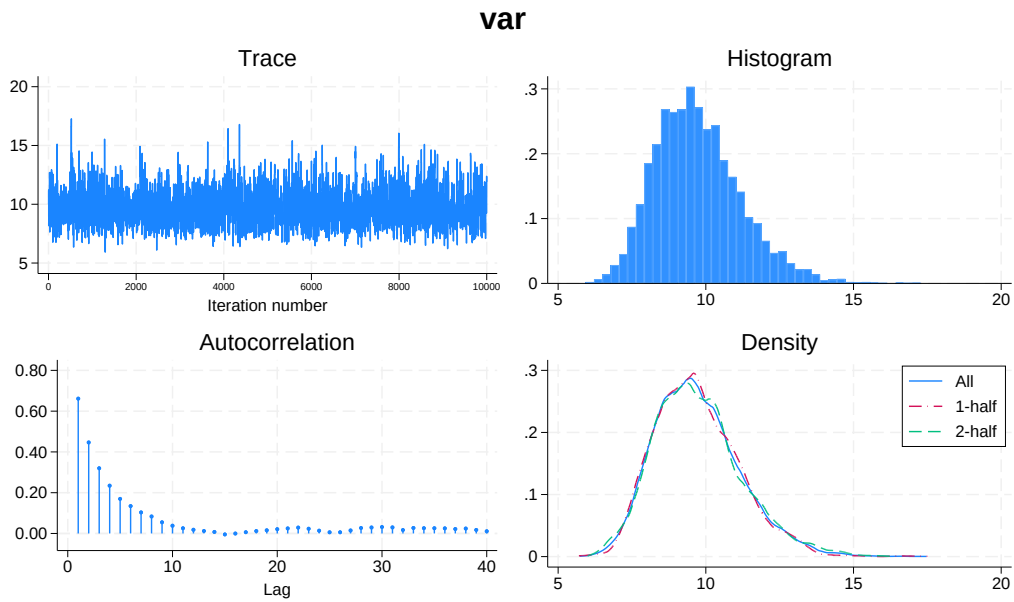
In cases like this, we can expect higher sampling efficiency if we place {var} in a separate block. We can do this by including the option `block({var})`. The other two parameters, {mpg:weight} and {mpg:_cons}, will be automatically considered as a second block.

```
. 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.

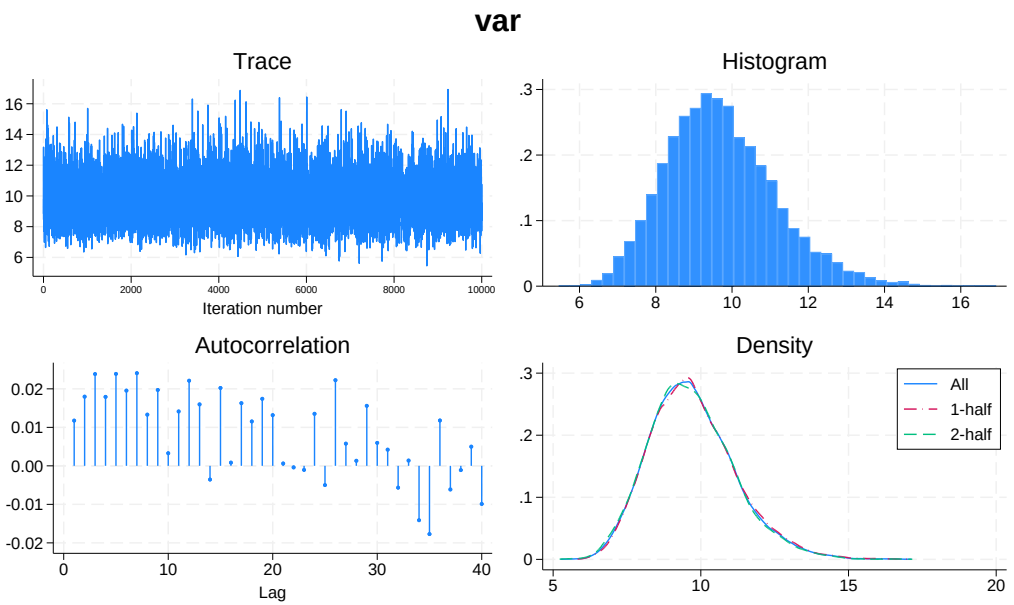
To request Gibbs sampling, we specify suboption `gibbs` within option `block()`.

```
. 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

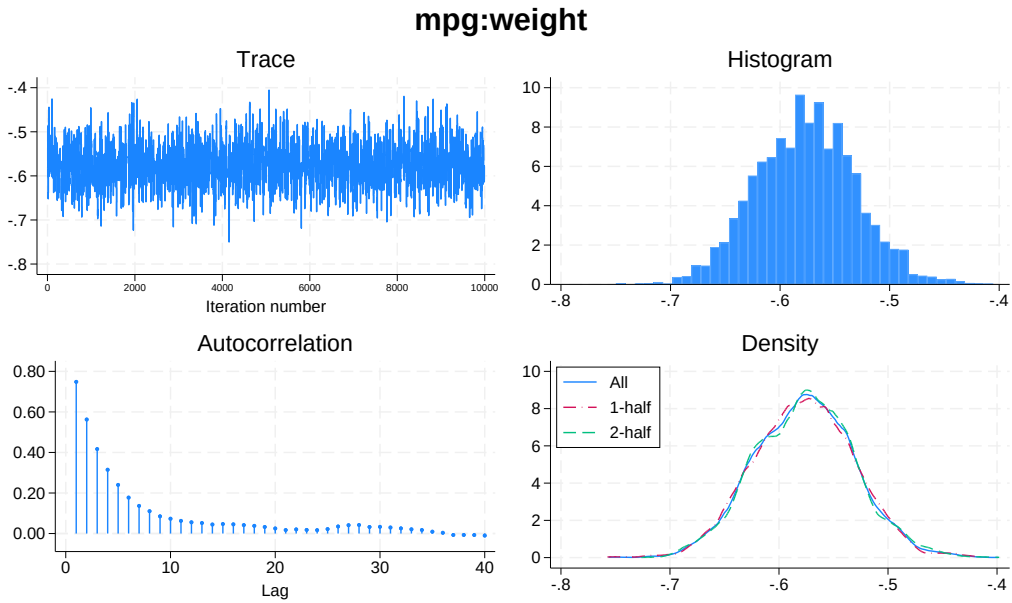
Continuing example 13, there is still room for improvement in our model in terms of sampling efficiency. The efficiency of the regression coefficients is now low relative to the variance efficiency.

```
. 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.

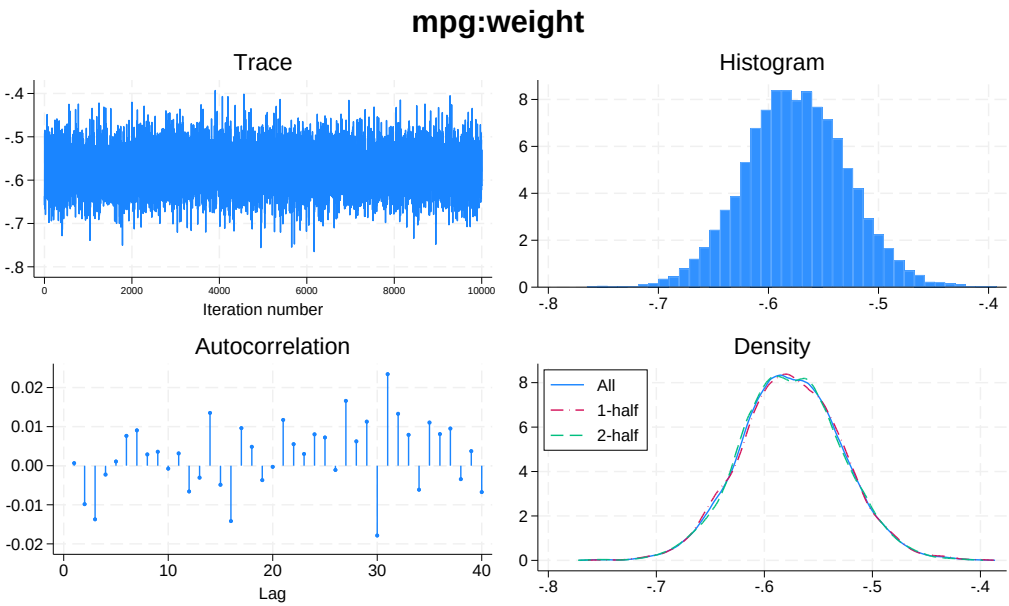
To request Gibbs sampling for the regression coefficients, we must place them in a separate block.

```
. 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.
```

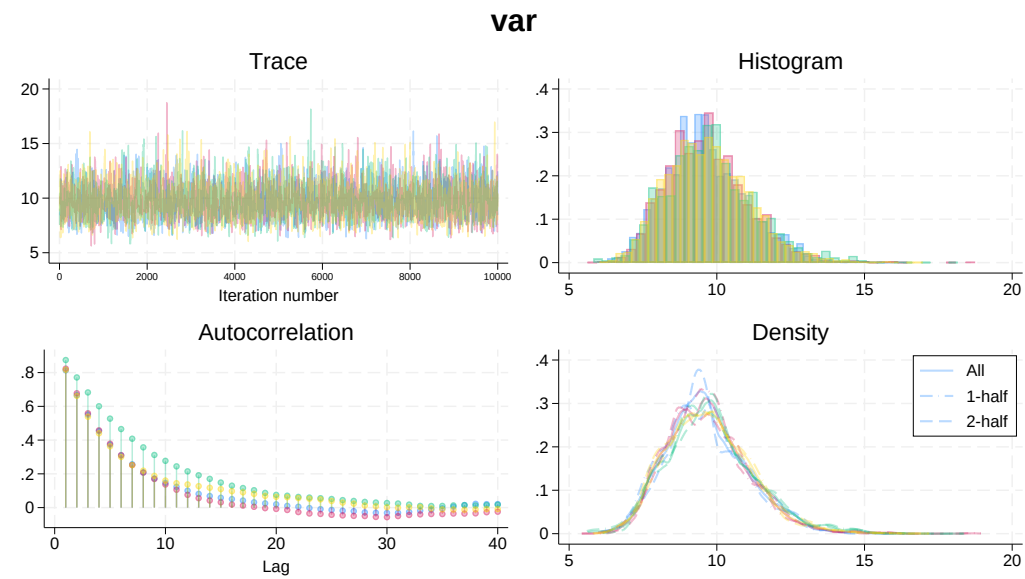
The important change in the output header of `bayesmh` with multiple chains is the presence of the maximum Gelman–Rubin convergence statistic, `Max Gelman-Rubin Rc`. This is the maximum value of the statistics across all model parameters. A convergence rule often used in practice is to declare convergence 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}`.

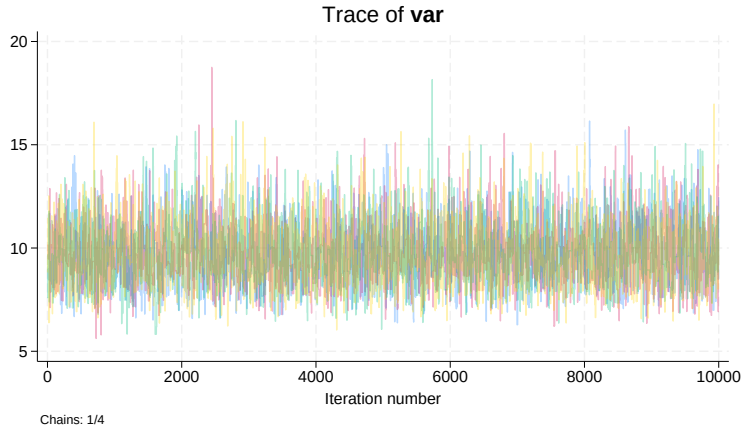
```
. bayesgraph diagnostics {var}
```



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.

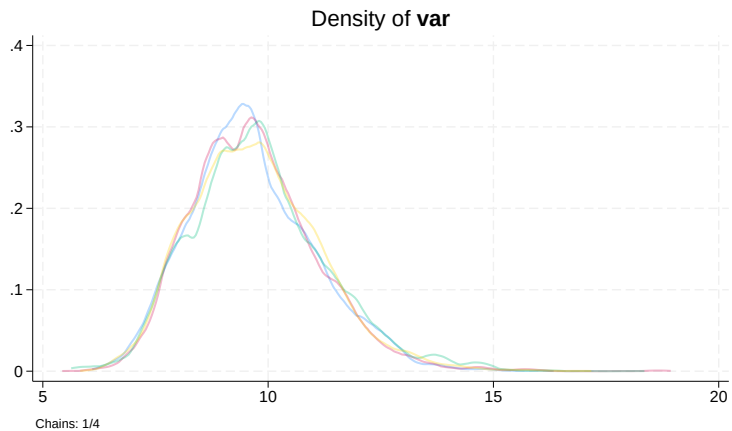
```
. bayesgraph trace {var}
```



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.

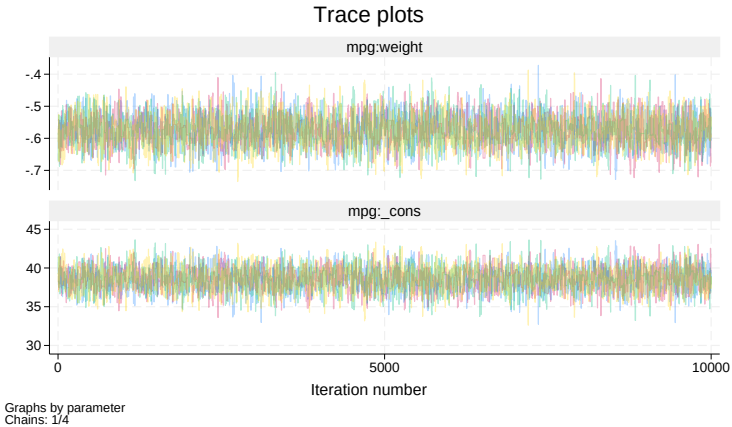
```
. bayesgraph kdensity {var}
```



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.

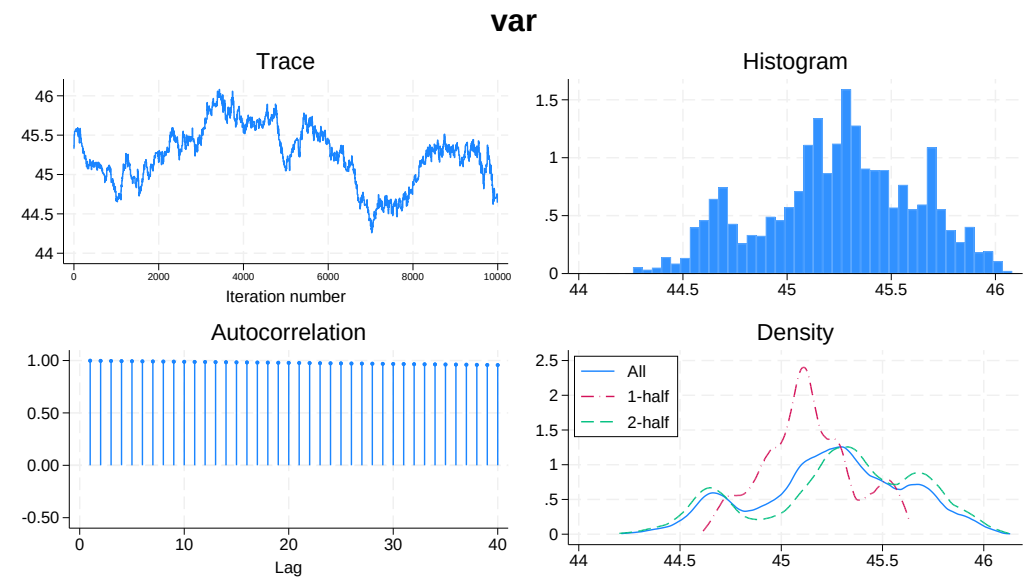
To investigate the convergence problem further visually, we inspect the trace plots of the {var} parameter from each chain.

```
. 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`.

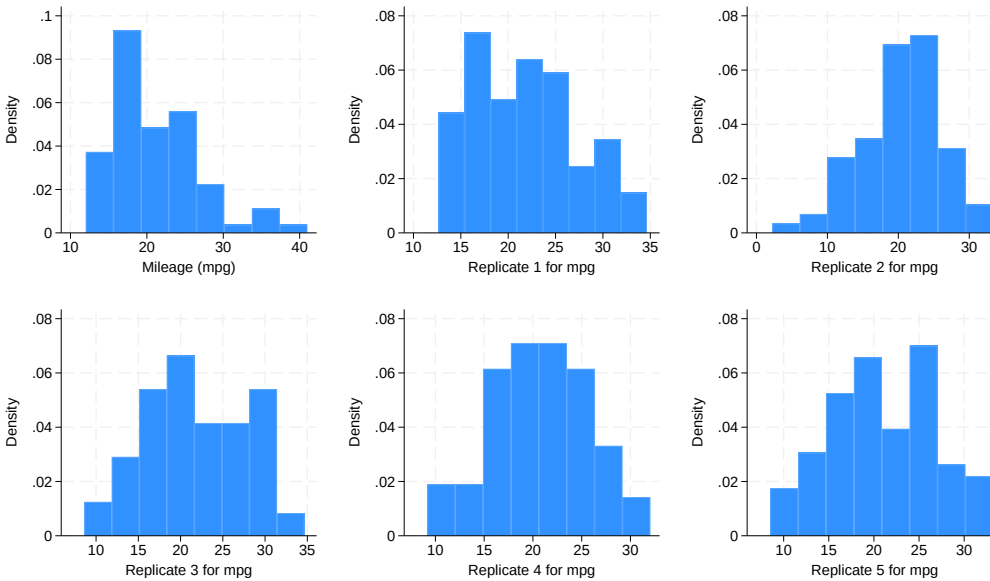
```
. quietly bayesmh mpg weight, likelihood(normal({var}))
> prior({mpg:}, normal(0,100)) prior({var}, igamma(10,10))
> saving(linregsim) rseed(16)
```

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 name	Storage type	Display format	Value 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

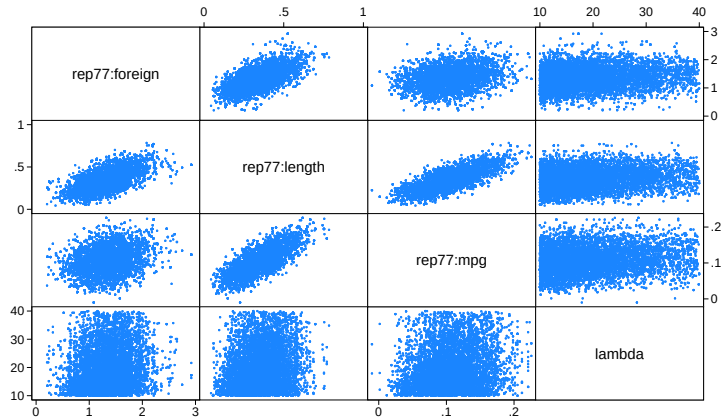
When we specify `dots` or `dots()`, `bayesmh` displays dots as simulation is performed. The burn-in and simulation iterations are displayed separately. During the adaptation period, iterations are displayed with a symbol `a` instead of a dot. This indicates the period during which the proposal distribution 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.

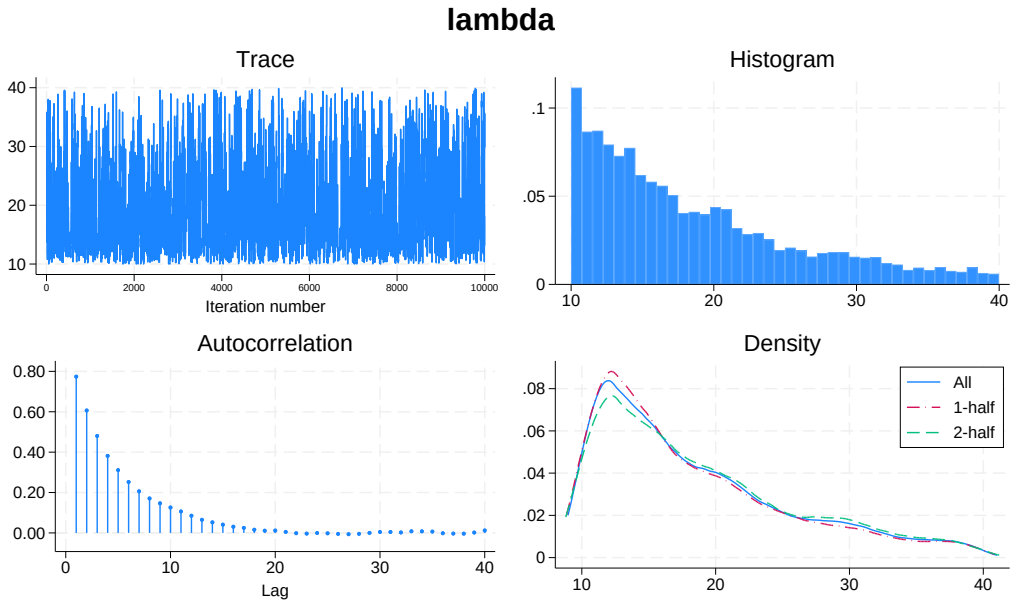
We placed the hyperparameter `{lambda}` in a separate block because we wanted to sample this nuisance parameter independently from the other model parameters. Based on the bivariate scatterplots, this parameter does appear to be independent of other model parameters a posteriori.

```
. 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.

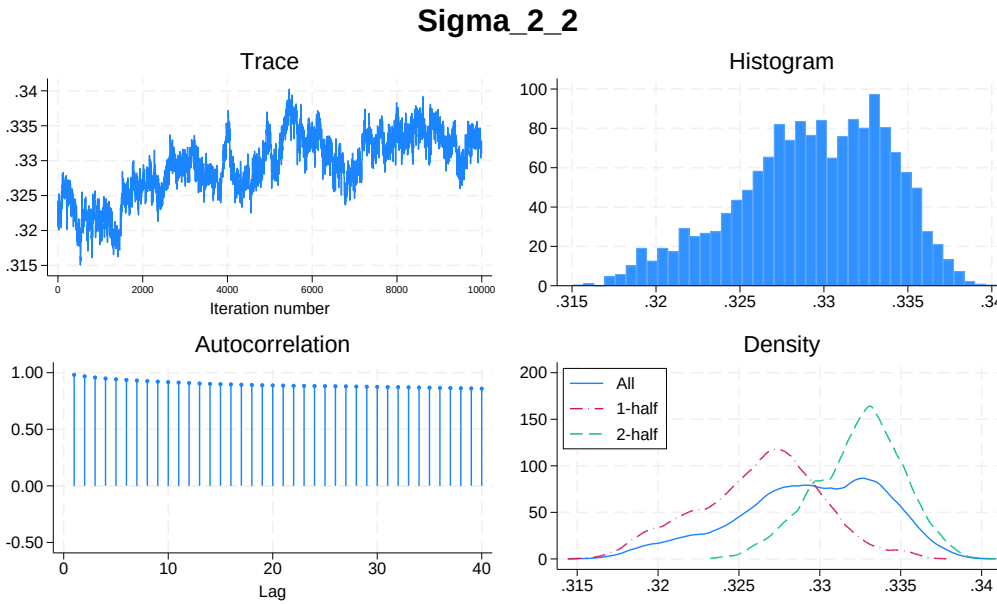
A closer inspection of the ESS table reveals very low sampling efficiencies for the elements of the covariance matrix `{Sigma}`.

```
. 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%.

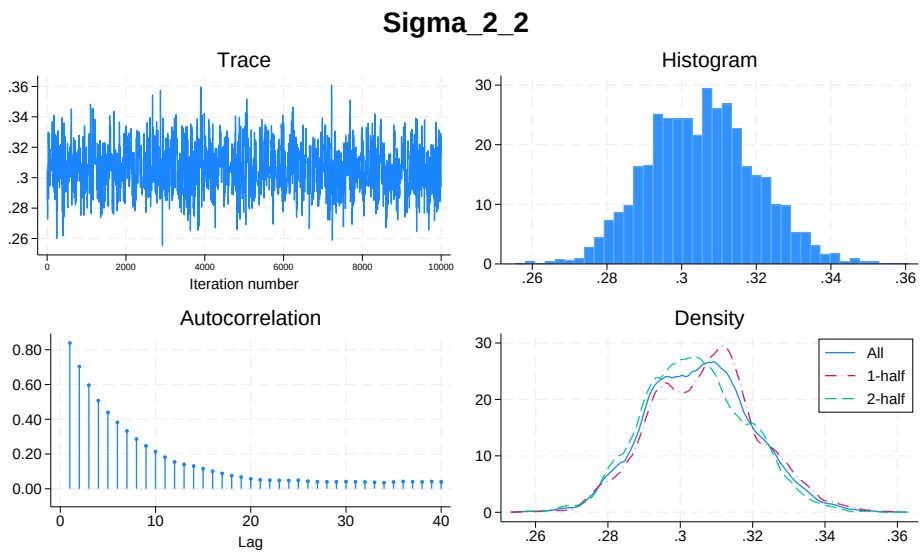
Sampling efficiencies of the elements of the covariance matrix improved substantially.

```
. 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.

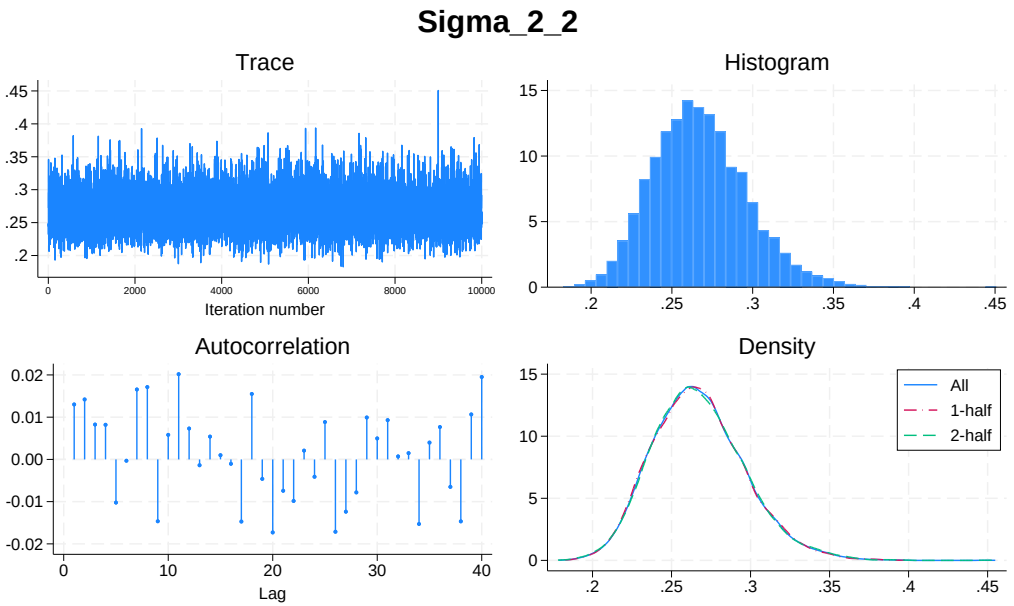
```
. set seed 14
. bayesmh (mpg) (weight) (length), likelihood(mvnormal({Sigma,m}))
> prior({mpg:_cons} {weight:_cons} {length:_cons}, normal(0,100))
> prior({Sigma,m}, iwishart(3,100,I(3)))
> block({mpg:_cons} {weight:_cons} {length:_cons})
> block({Sigma,m}, gibbs) dots
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaa.. 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
------------------------------------------------------------------------------
                                                              Equal-tailed
             |      Mean   Std. dev.     MCSE     Median  [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.

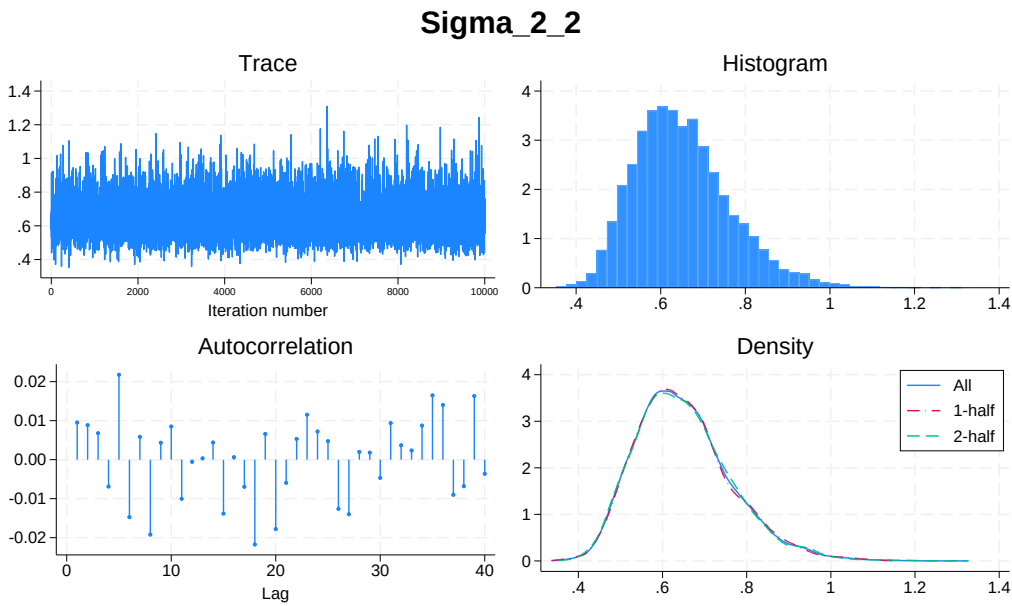
❑ Technical note: Adaptation tolerance is not met

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.

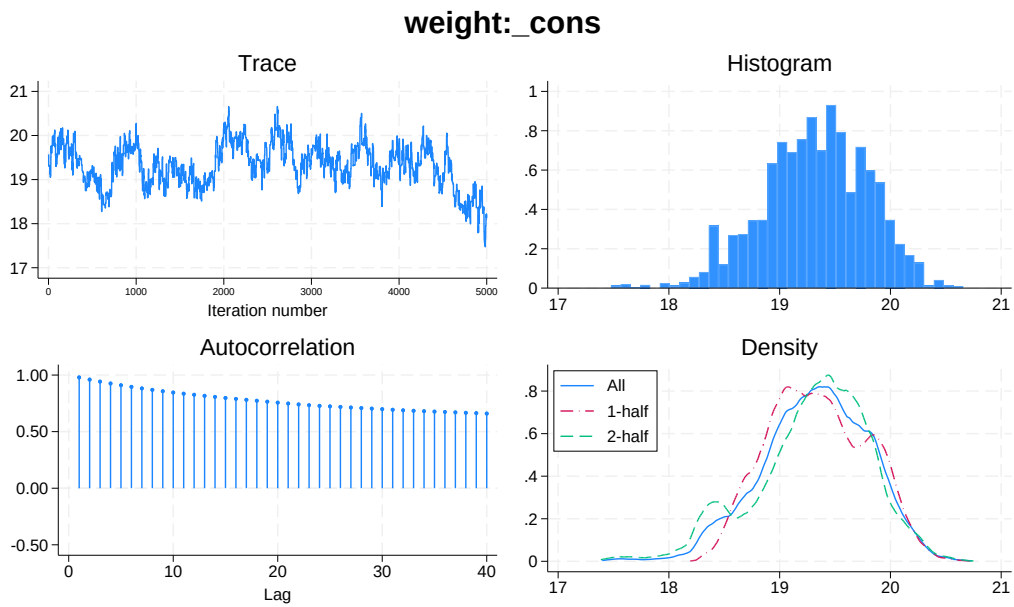
```
. bayesstats ess
Efficiency summaries      MCMC sample size =     5,000
                          Efficiency:  min =   .004996
                                       avg =   .03269
                                       max =   .05366
```

	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}`,

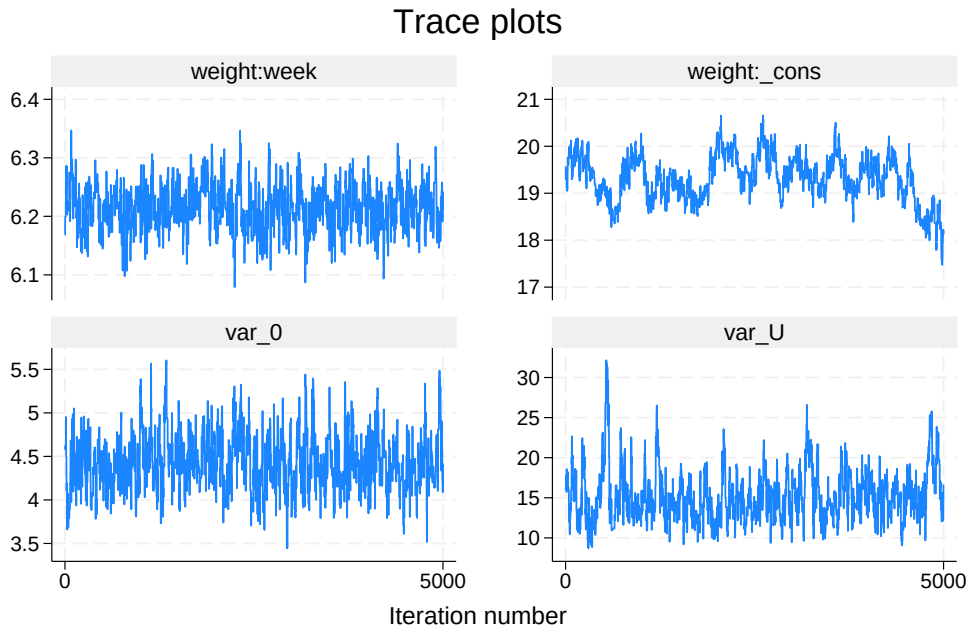
```
. bayesgraph diagnostics {weight:_cons}
```



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.

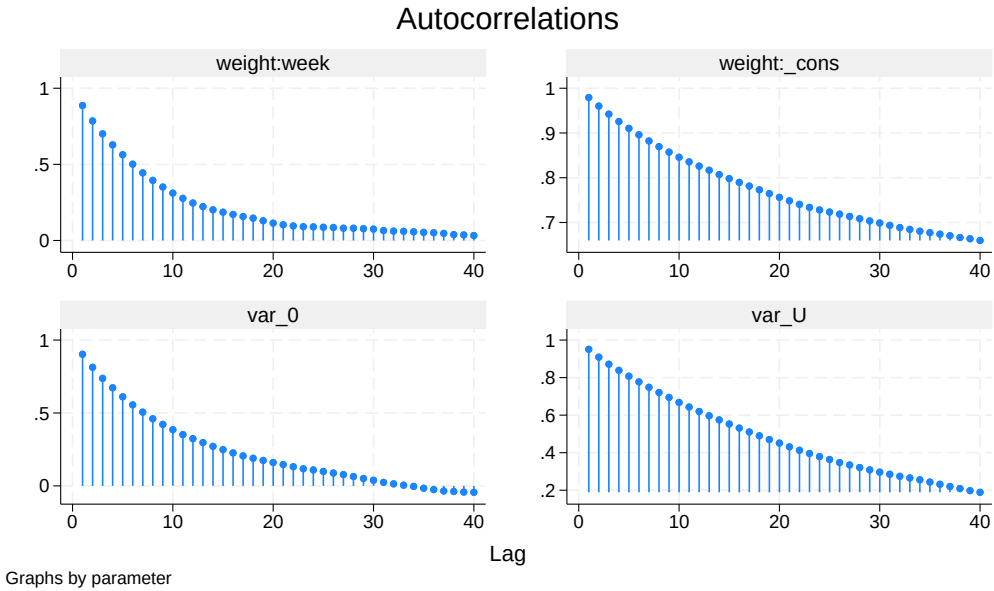
```
. bayesgraph trace _all, byparm(cols(2))
```



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

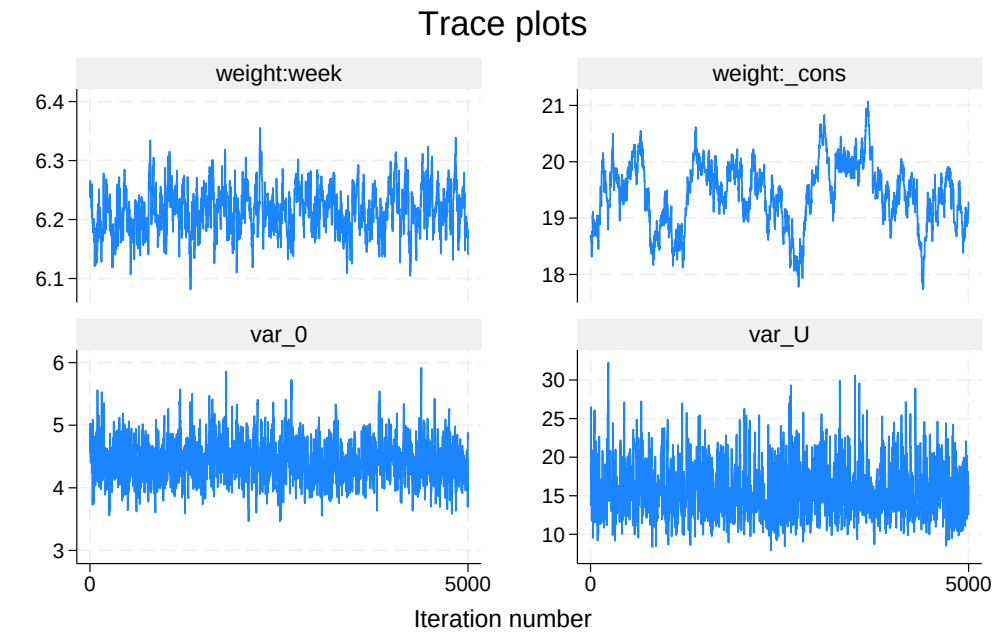
Continuing example 19, we can improve efficiency of the MH algorithm by separating model parameters into blocks to be sampled independently. We consider a separate block for each model parameter; random-effects parameters automatically share the same separate block. We also specify `nomodelsummary` to 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
------------------------------------------------------------------------------
```

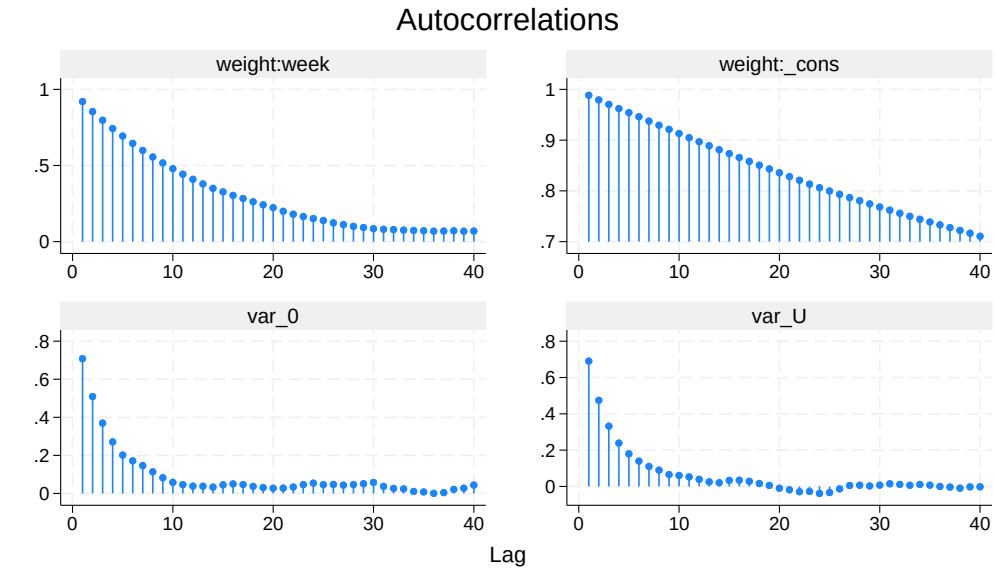
Blocking certainly improved efficiencies: the average efficiency is now 0.08, but the minimum efficiency is still low.

The trace and autocorrelation plots below have improved for variance components but not for regression coefficients.

```
. bayesgraph trace _all, byparm(cols(2))
```



```
. 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
```

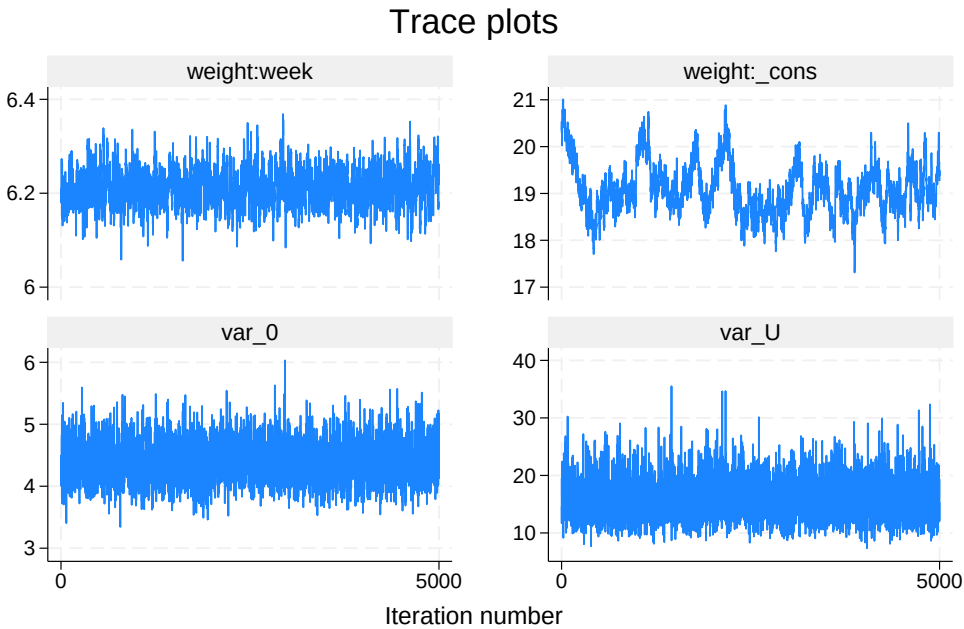
```
Bayesian normal regression                      MCMC iterations  =      7,500
Metropolis-Hastings and Gibbs sampling          Burn-in          =      2,500
                                                MCMC sample size =      5,000
                                                Number of obs    =        432
                                                Acceptance rate  =      .8455
                                                Efficiency:  min =    .007933
                                                             avg =      .3116
Log marginal-likelihood                                      max =      .6695
```

	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 efficiency increased dramatically to 0.31 but the minimum efficiency is still low.

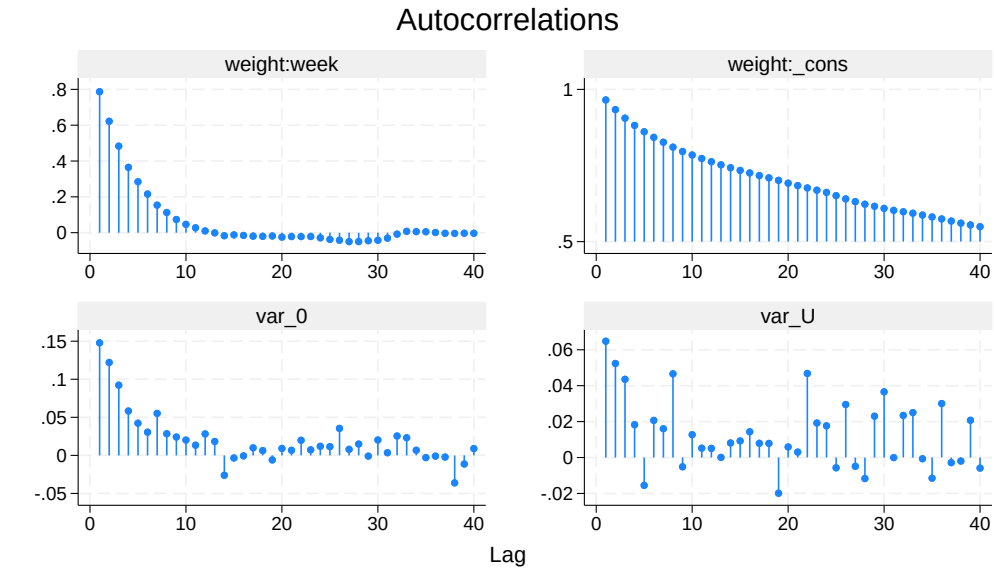
If we again inspect the diagnostic plots for main model parameters,

```
. 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.

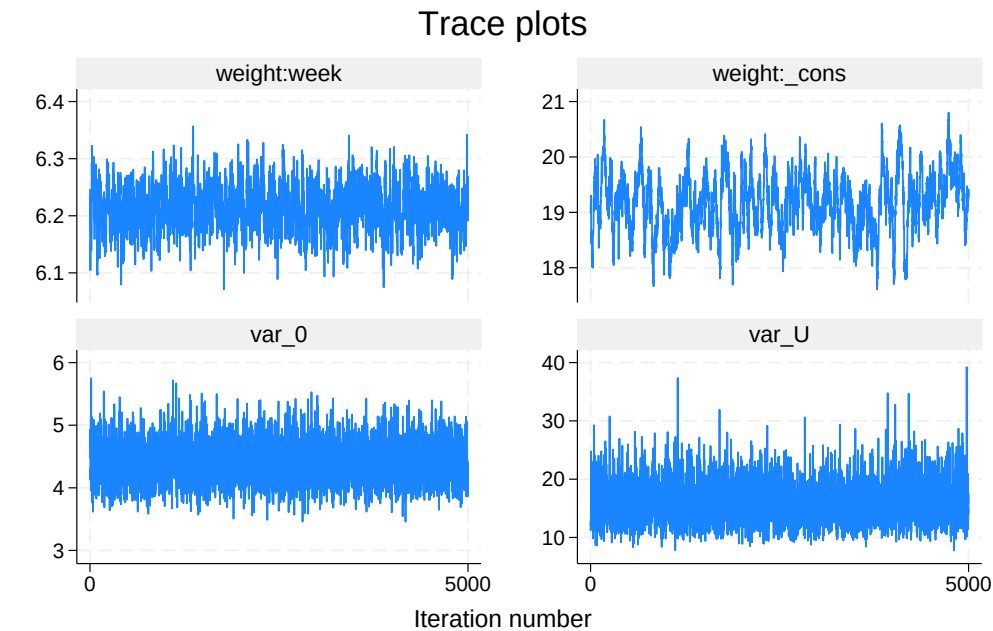
For linear multilevel models, we can further improve mixing by specifying Gibbs sampling also for random effects.

```
. 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

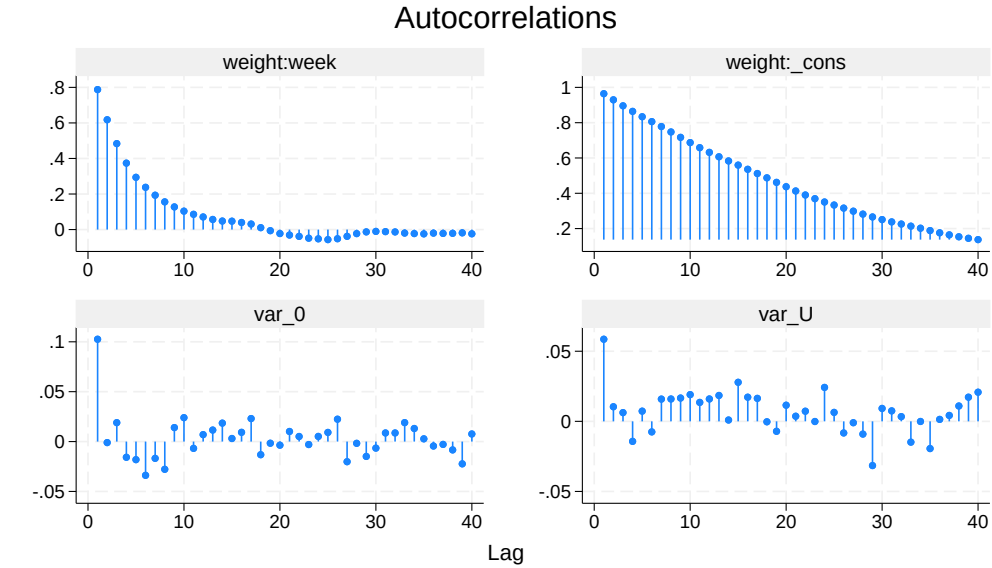
The minimum efficiency is now increased to 0.025, and the diagnostics plots for the constant term look much better:

```
. bayesgraph trace _all, byparm(cols(2))
```



Graphs by parameter

```
. 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.

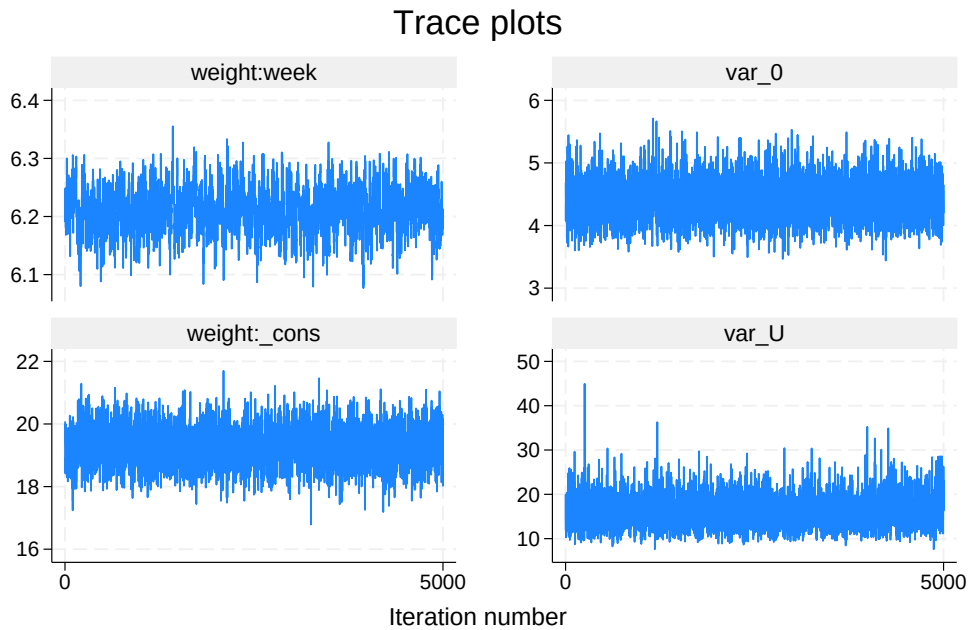
Continuing with example 21, we now fit a reparameterized model:

```
. 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.

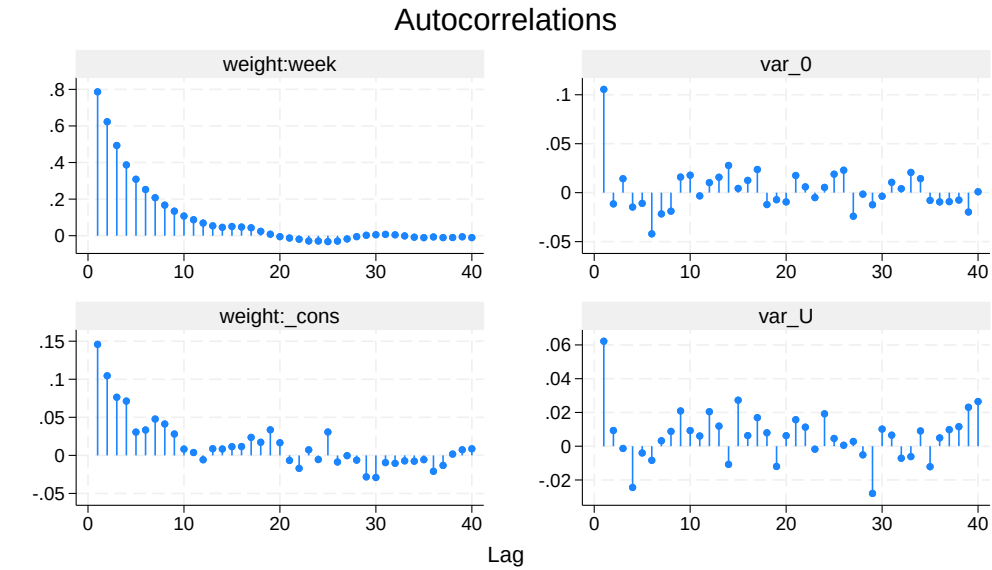
The diagnostic plots now show perfect mixing for all main model parameters:

```
. 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:

$$\texttt{weight}_{ij} = \beta_0 + \beta_1\texttt{week}_{ij} + u_{0j} + u_{1j}\texttt{week}_{ij} + \epsilon_{ij} = \tau_{0j} + \tau_{1j}\texttt{week}_{ij} + \epsilon_{ij},$$

$$\begin{aligned}
\epsilon_{ij} &\sim \text{i.i.d. } N(0, \sigma_0^2)\\
\tau_{0j} &\sim \text{i.i.d. } N(\beta_0, \sigma_{\tau_0}^2)\\
\tau_{1j} &\sim \text{i.i.d. } N(\beta_1, \sigma_{\tau_1}^2)\\
\beta_0 &\sim N(0, 100)\\
\beta_1 &\sim N(0, 100)\\
\sigma_0^2 &\sim \text{InvGamma}(0.001, 0.001)\\
\sigma_{\tau_0}^2 &\sim \text{InvGamma}(0.001, 0.001)\\
\sigma_{\tau_1}^2 &\sim \text{InvGamma}(0.001, 0.001)
\end{aligned}$$

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.

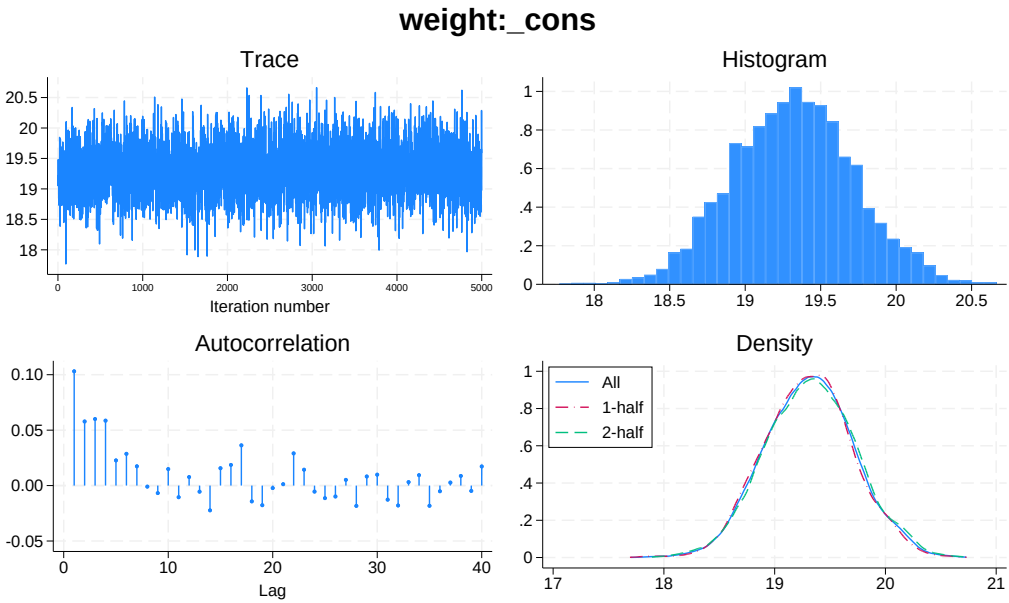
We fit our model using `bayesmh`. Following example 21, we perform blocking of parameters and use Gibbs sampling for the blocks. For brevity, we also combine the same prior specifications in one statement but use `prior()`'s `split` suboption to continue treating the parameters from the same `prior()` 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

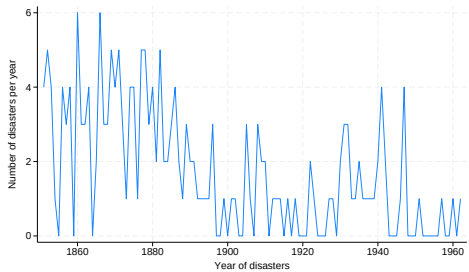
Change-point problems deal with stochastic data, usually time-series data, that undergo some abrupt change at some time point. It is of interest to localize the point of change and estimate the properties of the stochastic process before and after the change.

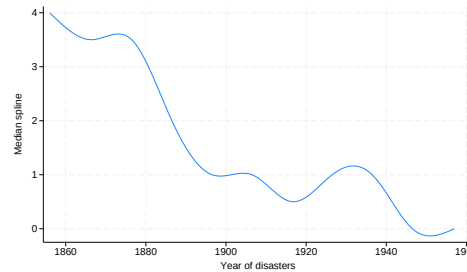
Here we analyze the British coal mining disaster data for the years 1851 to 1962 as given in table 5 in Carlin, Gelfand, and Smith (1992). The data are originally from Maguire, Pearson, and Wynn (1952) with updates from Jarrett (1979).

`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}))
```

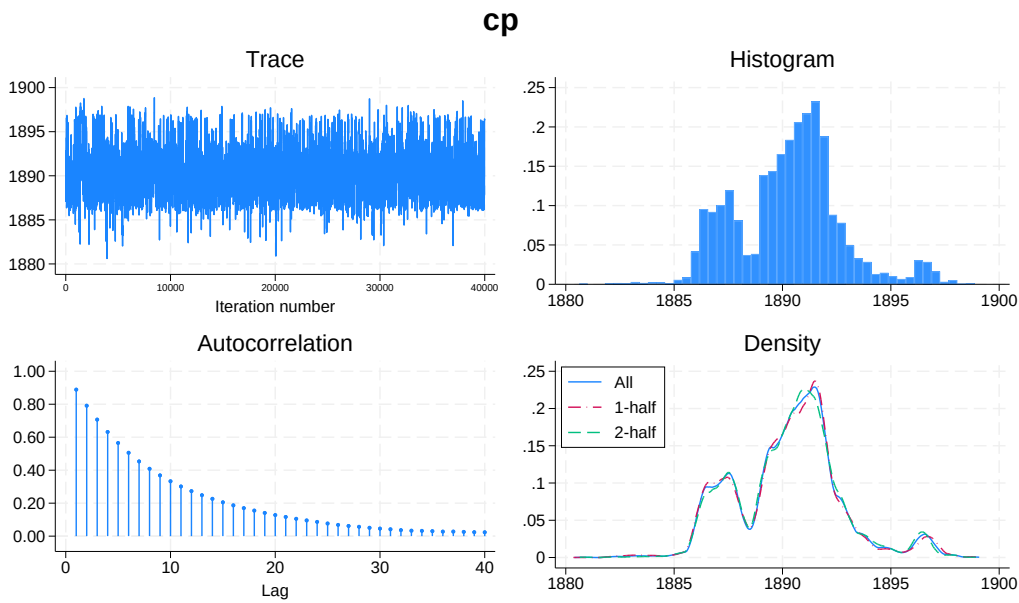
as the mean of a Poisson distribution `dpoisson()`. To ensure the feasibility of the initial state, we specify the desired initial values in option `initial()`. Because of high autocorrelation in the MCMC chain, we increase the MCMC size to achieve higher precision of our estimates. We change the default 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.

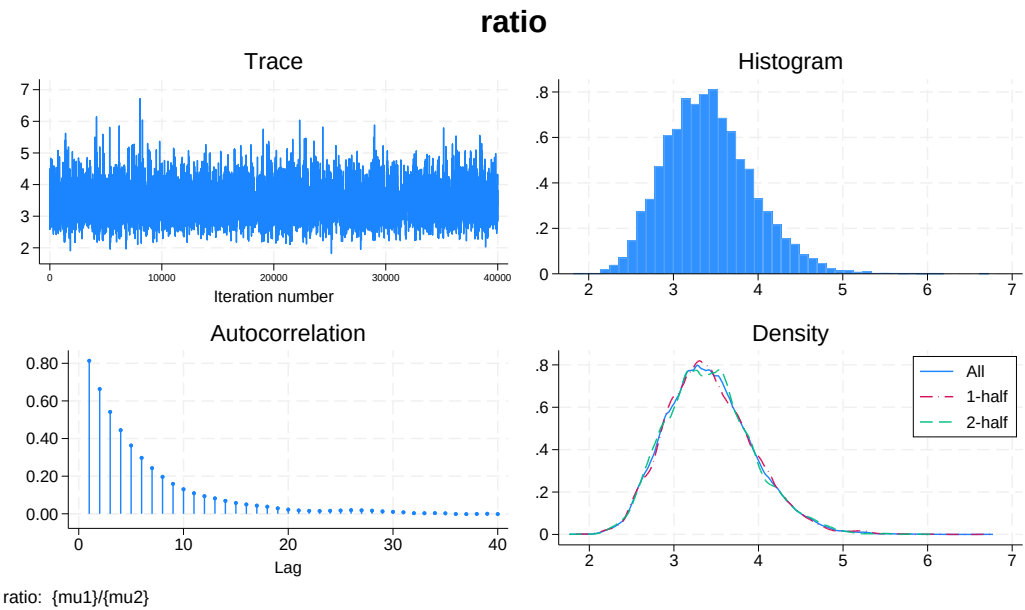
```
. bayesstats summary (ratio:{mu1}/{mu2})
Posterior summary statistics                         MCMC sample size =    40,000
       ratio : {mu1}/{mu2}
```

	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`.

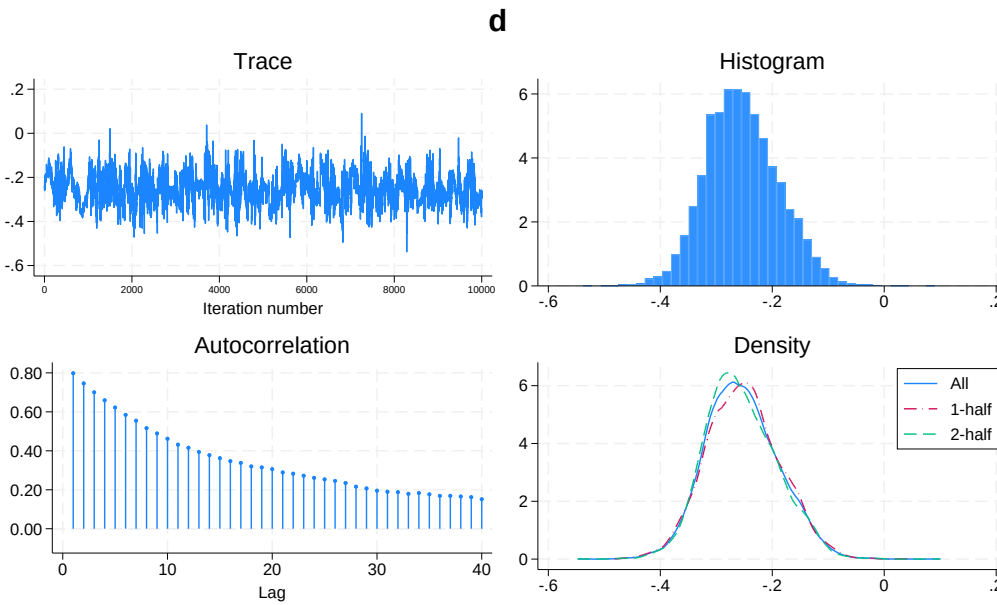
```
. bayesstats ess {d} {sig2}
Efficiency summaries     MCMC sample size =    10,000
                         Efficiency:  min =    .02206
                                      avg =    .02348
                                      max =    .02491
```

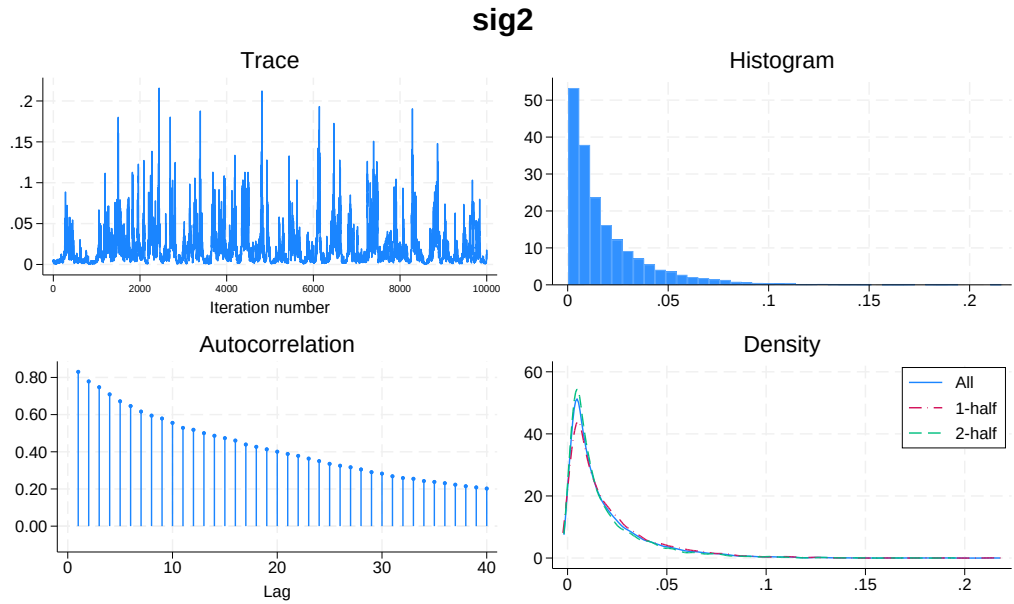
	ESS	Corr. time	Efficiency
d	249.13	40.14	0.0249
sig2	220.55	45.34	0.0221

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).

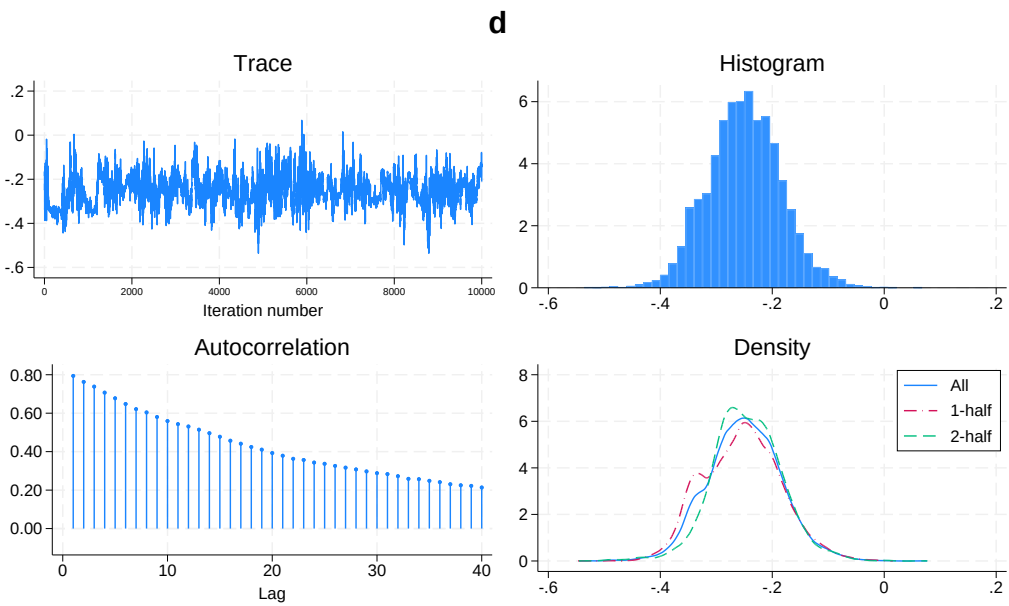
Compared with example 26, the efficiencies and other statistics for the main parameters are similar.

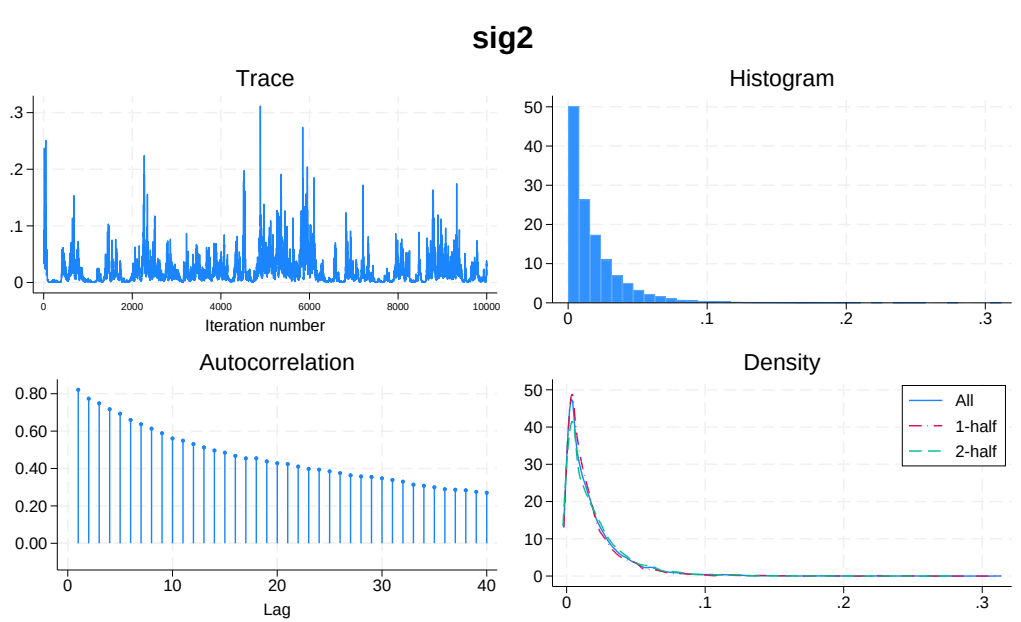
```
. bayesstats ess {d} {sig2}
Efficiency summaries     MCMC sample size =     10,000
                         Efficiency:  min =     .01025
                                      avg =     .01398
                                      max =     .01771
```

	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,

$$\texttt{lncrime}_i = \texttt{I} + i\texttt{S} + \boldsymbol{\epsilon}$$

where I and S are latent variables and $\boldsymbol{\epsilon}$ 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 $\boldsymbol{\theta}^1, \boldsymbol{\theta}^2, \ldots, \boldsymbol{\theta}^B$, 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*.

References

Andrieu, C., and É. Moulines. 2006. On the ergodicity properties of some adaptive MCMC algorithms. *Annals of Applied Probability* 16: 1462–1505. https://doi.org/10.1214/105051606000000286.

Andrieu, C., and J. Thoms. 2008. A tutorial on adaptive MCMC. *Statistics and Computing* 18: 343–373. https://doi.org/10.1007/s11222-008-9110-y.

Atchadé, Y. F., and J. S. Rosenthal. 2005. On adaptive Markov chain Monte Carlo algorithms. *Bernoulli* 11: 815–828. https://doi.org/10.3150/bj/1130077595.

Balov, N. 2016a. Bayesian binary item response theory models using bayesmh. *The Stata Blog: Not Elsewhere Classified.* http://blog.stata.com/2016/01/18/bayesian-binary-item-response-theory-models-using-bayesmh/.

——. 2016b. Fitting distributions using bayesmh. *The Stata Blog: Not Elsewhere Classified.* http://blog.stata.com/2016/03/30/fitting-distributions-using-bayesmh/.

——. 2016c. 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/.

——. 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/.

——. 2022. Bayesian threshold autoregressive models. *The Stata Blog: Not Elsewhere Classified.* https://blog.stata.com/2022/05/18/bayesian-threshold-autoregressive-models/.

Birnbaum, A. 1968. Some latent trait models and their use in inferring an examinee's ability. In *Statistical Theories of Mental Test Scores*, ed. F. M. Lord and M. R. Novick, 395–479. Reading, MA: Addison–Wesley.

Carlin, B. P., A. E. Gelfand, and A. F. M. Smith. 1992. Hierarchical Bayesian analysis of changepoint problems. *Journal of the Royal Statistical Society, Series C* 41: 389–405. https://doi.org/10.2307/2347570.

Carlin, J. B. 1992. Meta-analysis for 2×2 tables: A Bayesian approach. *Statistics in Medicine* 11: 141–158. https://doi.org/10.1002/sim.4780110202.

De Boeck, P., and M. Wilson, ed. 2004. *Explanatory Item Response Models: A Generalized Linear and Nonlinear Approach.* New York: Springer.

Diggle, P. J., P. J. Heagerty, K.-Y. Liang, and S. L. Zeger. 2002. *Analysis of Longitudinal Data.* 2nd ed. Oxford: Oxford University Press.

Gelfand, A. E., S. E. Hills, A. Racine-Poon, and A. F. M. Smith. 1990. Illustration of Bayesian inference in normal data models using Gibbs sampling. *Journal of the American Statistical Association* 85: 972–985. https://doi.org/10.2307/2289594.

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.

Gelman, A., W. R. Gilks, and G. O. Roberts. 1997. Weak convergence and optimal scaling of random walk Metropolis algorithms. *Annals of Applied Probability* 7: 110–120. https://doi.org/10.1214/aoap/1034625254.

Geweke, J. 1989. Bayesian inference in econometric models using Monte Carlo integration. *Econometrica* 57: 1317–1339. https://doi.org/10.2307/1913710.

Geyer, C. J. 2011. Introduction to Markov chain Monte Carlo. In *Handbook of Markov Chain Monte Carlo*, ed. S. P. Brooks, A. Gelman, G. L. Jones, and X.-L. Meng, 3–48. Boca Raton, FL: Chapman and Hall/CRC.

Giordani, P., and R. J. Kohn. 2010. Adaptive independent Metropolis–Hastings by fast estimation of mixtures of normals. *Journal of Computational and Graphical Statistics* 19: 243–259. https://doi.org/10.1198/jcgs.2009.07174.

Grant, R. L., B. Carpenter, D. C. Furr, and A. Gelman. 2017a. Introducing the StataStan interface for fast, complex Bayesian modeling using Stan. *Stata Journal* 17: 330–342.

——. 2017b. Fitting Bayesian item response models in Stata and Stan. *Stata Journal* 17: 343–357.

Haario, H., E. Saksman, and J. Tamminen. 2001. An adaptive Metropolis algorithm. *Bernoulli* 7: 223–242. https://doi.org/10.2307/3318737.

Hand, D. J., and M. J. Crowder. 1996. *Practical Longitudinal Data Analysis.* Boca Raton, FL: Chapman and Hall.

Hoff, P. D. 2009. *A First Course in Bayesian Statistical Methods.* New York: Springer.

Huber, C. 2016a. 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/.

——. 2016b. 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/.

Huq, N. M., and J. Cleland. 1990. *Bangladesh Fertility Survey 1989 (Main Report).* National Institute of Population Research and Training.

Jarrett, R. G. 1979. A note on the intervals between coal-mining disasters. *Biometrika* 66: 191–193. https://doi.org/10.2307/2335266.

Jeffreys, H. 1946. An invariant form for the prior probability in estimation problems. *Proceedings of the Royal Society of London, Series A* 186: 453–461. https://doi.org/10.1098/rspa.1946.0056.

Lichman, M. 2013. UCI Machine Learning Repository. http://archive.ics.uci.edu/ml.

Maas, B., W. R. Garnett, I. M. Pellock, and T. J. Comstock. 1987. A comparative bioavailability study of Carbamazepine tablets and chewable formulation. *Therapeutic Drug Monitoring* 9: 28–33. https://doi.org/10.1097/00007691-198703000-00006.

Maguire, B. A., E. S. Pearson, and A. H. A. Wynn. 1952. The time intervals between industrial accidents. *Biometrika* 39: 168–180. https://doi.org/10.2307/2332475.

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/.

Raftery, A. E. 1996. Hypothesis testing and model selection. In *Markov Chain Monte Carlo in Practice*, ed. W. R. Gilks, S. Richardson, and D. J. Spiegelhalter, 163–187. Boca Raton, FL: Chapman and Hall.

Raftery, A. E., and V. E. Akman. 1986. Bayesian analysis of a Poisson process with a change-point. *Biometrika* 73: 85–89. https://doi.org/10.2307/2336274.

Rasch, G. 1960. *Probabilistic Models for Some Intelligence and Attainment Tests.* Copenhagen: Danish Institute of Educational Research.

Roberts, G. O., and J. S. Rosenthal. 2001. Optimal scaling for various Metropolis–Hastings algorithms. *Statistical Science* 16: 351–367. https://doi.org/10.1214/ss/1015346320.

——. 2007. Coupling and ergodicity of adaptive Markov chain Monte Carlo algorithms. *Journal of Applied Probability* 44: 458–475. https://doi.org/10.1239/jap/1183667414.

——. 2009. Examples of adaptive MCMC. *Journal of Computational and Graphical Statistics* 18: 349–367. https://doi.org/10.1198/jcgs.2009.06134.

Ruppert, D., M. P. Wand, and R. J. Carroll. 2003. *Semiparametric Regression.* Cambridge: Cambridge University Press.

Thomas, A., B. O'Hara, U. Ligges, and S. Sturtz. 2006. Making BUGS Open. *R News* 6: 12–17.

Thompson, J. 2014. *Bayesian Analysis with Stata.* College Station, TX: Stata Press.

Yusuf, S., R. Simon, and S. S. Ellenberg. 1987. Proceedings of the workshop on methodological issues in overviews of randomized clinical trials, May 1986. In *Statistics in Medicine*, vol. 6.

Zellner, A. 1986. On assessing prior distributions and Bayesian regression analysis with g-prior distributions. In Vol. 6 of *Bayesian Inference and Decision Techniques: Essays in Honor of Bruno De Finetti (Studies in Bayesian Econometrics and Statistics)*, ed. P. K. Goel and A. Zellner, 233–343. Amsterdam: North-Holland.

Zellner, A., and N. S. Revankar. 1969. Generalized production functions. *Review of Economic Studies* 36: 241–250. https://doi.org/10.2307/2296840.

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