

**bayes: hetprobit** — Bayesian heteroskedastic probit regression

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## Description

`bayes: hetprobit` fits a Bayesian heteroskedastic probit regression to a binary outcome; see [\[BAYES\] bayes](#) and [\[R\] hetprobit](#) for details.

## Quick start

Bayesian heteroskedastic probit regression of  $y$  on  $x_1$  and  $x_2$ , using  $z_1$  to model the variance and using default normal priors for regression coefficients and log-variance coefficients

```
bayes: hetprobit y x1 x2, het(z1)
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): hetprobit y x1 x2, het(z1)
```

Use uniform priors for the slopes and a normal prior for the intercept of the main regression

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): hetprobit y x1 x2, het(z1)
```

Save simulation results to `simdata.dta`, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): hetprobit y x1 x2, het(z1)
```

Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): hetprobit y x1 x2, het(z1)
```

In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Also see [Quick start](#) in [\[BAYES\] bayes](#) and [Quick start](#) in [\[R\] hetprobit](#).

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## Syntax

```
bayes [ , bayesopts ] : hetprobit depvar [indepvars] [if] [in] [weight] ,
  het(varlist [ , offset(varnameo) ] ) [options]
```

<i>options</i>	Description
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Model	
* <b>het</b> ( <i>varlist</i> [...])	independent variables to model the variance and possible offset variable
<b>noconstant</b>	suppress constant term
<b>offset</b> ( <i>varname</i> )	include <i>varname</i> in model with coefficient constrained to 1
<b>asis</b>	retain perfect predictor variables
Reporting	
<b>display_options</b>	control spacing, line width, and base and empty cells
<b>level</b> (#)	set credible level; default is level(95)

\***het**() is required. The full specification is **het**(*varlist* [ , offset(*varname<sub>o</sub>*) ] ).

*indepvars* and *varlist* may contain factor variables; see [U] 11.4.3 **Factor variables**.

*depvar*, *indepvars*, and *varlist* may contain time-series operators; see [U] 11.4.4 **Time-series varlists**.

*fweights* are allowed; see [U] 11.1.6 **weight**.

**bayes: hetprobit**, **level**() is equivalent to **bayes, clevel**(): **hetprobit**.

For a detailed description of *options*, see *Options* in [R] **hetprobit**.

<i>bayesopts</i>	Description
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Priors	
* <b>normalprior</b> (#)	specify standard deviation of default normal priors for regression coefficients and log-variance coefficients; default is <b>normalprior</b> (100)
<b>prior</b> ( <i>priorspec</i> )	prior for model parameters; this option may be repeated
<b>dryrun</b>	show model summary without estimation
Simulation	
<b>nchains</b> (#)	number of chains; default is to simulate one chain
<b>mcmcsize</b> (#)	MCMC sample size; default is <b>mcmcsize</b> (10000)
<b>burnin</b> (#)	burn-in period; default is <b>burnin</b> (2500)
<b>thinning</b> (#)	thinning interval; default is <b>thinning</b> (1)
<b>rseed</b> (#)	random-number seed
<b>exclude</b> ( <i>paramref</i> )	specify model parameters to be excluded from the simulation results
Blocking	
* <b>blocksize</b> (#)	maximum block size; default is <b>blocksize</b> (50)
<b>block</b> ( <i>paramref</i> [ , <i>blockopts</i> ] )	specify a block of model parameters; this option may be repeated
<b>blocksummary</b>	display block summary
* <b>noblocking</b>	do not block parameters by default

Initialization

<code><u>initial</u>(<i>initspec</i>)</code>	specify initial values for model parameters with a single chain
<code>init#(<i>initspec</i>)</code>	specify initial values for #th chain; requires <code>nchains()</code>
<code>initall(<i>initspec</i>)</code>	specify initial values for all chains; requires <code>nchains()</code>
<code>nomleinitial</code>	suppress the use of maximum likelihood estimates as starting values
<code><u>initrandom</u></code>	specify random initial values
<code><u>initsummary</u></code>	display initial values used for simulation
* <code>noisily</code>	display output from the estimation command during initialization

Adaptation

<code><u>adaptation</u>(<i>adaptopts</i>)</code>	control the adaptive MCMC procedure
<code><u>scale</u>(#)</code>	initial multiplier for scale factor; default is <code>scale(2.38)</code>
<code><u>covariance</u>(<i>cov</i>)</code>	initial proposal covariance; default is the identity matrix

Reporting

<code><u>clevel</u>(#)</code>	set credible interval level; default is <code>clevel(95)</code>
<code>hpd</code>	display HPD credible intervals instead of the default equal-tailed credible intervals
<code><u>eform</u>[ (<i>string</i>) ]</code>	report exponentiated coefficients and, optionally, label as <i>string</i>
<code>batch(#)</code>	specify length of block for batch-means calculations; default is <code>batch(0)</code>
<code><u>saving</u>(<i>filename</i>[ , <i>replace</i> ])</code>	save simulation results to <i>filename.dta</i>
<code><u>nomodelsummary</u></code>	suppress model summary
<code>chainsdetail</code>	display detailed simulation summary for each chain
<code>[ <i>no</i> ]dots</code>	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is <code>nodots</code>
<code>dots(#[ , <i>every</i>(#) ])</code>	display dots as simulation is performed
<code>[ <i>no</i> ]show(<i>paramref</i>)</code>	specify model parameters to be excluded from or included in the output
<code><u>notable</u></code>	suppress estimation table
<code><u>noheader</u></code>	suppress output header
<code>title(<i>string</i>)</code>	display <i>string</i> as title above the table of parameter estimates
<code><u>display_options</u></code>	control spacing, line width, and base and empty cells

Advanced

<code><u>search</u>(<i>search_options</i>)</code>	control the search for feasible initial values
<code>corrlag(#)</code>	specify maximum autocorrelation lag; default varies
<code>corrtol(#)</code>	specify autocorrelation tolerance; default is <code>corrtol(0.01)</code>

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

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

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

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

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

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

Model parameters are regression coefficients `{depvar: indepvars}` for the main regression and `{lnsigma: varlist}` for the log-variance equation. Use the `dryrun` option to see the definitions of model parameters prior to estimation.

For a detailed description of `bayesopts`, see `Options` in [BAYES] `bayes`.

## Remarks and examples

For a general introduction to Bayesian analysis, see [\[BAYES\] Intro](#). For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [\[BAYES\] bayesmh](#). For remarks and examples specific to the `bayes` prefix, see [\[BAYES\] bayes](#). For details about the estimation command, see [\[R\] hetprobit](#).

For a simple example of the `bayes` prefix, see *Introductory example* in [\[BAYES\] bayes](#).

## Stored results

See *Stored results* in [\[BAYES\] bayes](#).

## Methods and formulas

See *Methods and formulas* in [\[BAYES\] bayesmh](#).

## Also see

[\[BAYES\] bayes](#) — Bayesian regression models using the `bayes` prefix

[\[R\] hetprobit](#) — Heteroskedastic probit model

[\[BAYES\] Bayesian postestimation](#) — Postestimation tools for `bayesmh` and the `bayes` prefix

[\[BAYES\] Bayesian estimation](#) — Bayesian estimation commands

[\[BAYES\] Bayesian commands](#) — Introduction to commands for Bayesian analysis

[\[BAYES\] Intro](#) — Introduction to Bayesian analysis

[\[BAYES\] Glossary](#)