# Title

bayes: truncreg — Bayesian truncated regression

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#### Syntax Also see

# Description

bayes: truncreg fits a Bayesian truncated linear regression to a continuous outcome; see [BAYES] bayes and [R] truncreg for details.

# Quick start

- Bayesian truncated linear regression of y on x1 and x2, using a lower truncation limit of 17 and using default normal priors for regression coefficients and default inverse-gamma prior for the variance bayes: truncreg y x1 x2, ll(17)
- Use a standard deviation of 10 instead of 100 for the default normal priors bayes, normalprior(10): truncreg y x1 x2, ll(17)
- Use a shape of 1 and a scale of 2 instead of values of 0.01 for the default inverse-gamma prior bayes, igammaprior(1 2): truncreg y x1 x2, ll(17)
- Use uniform priors for the slopes and a normal prior for the intercept bayes, prior({y: x1 x2}, uniform(-10,10)) /// prior({y:\_cons}, normal(0,10)): truncreg y x1 x2, ll(17)
- Save simulation results to simdata.dta, and use a random-number seed for reproducibility bayes, saving(simdata) rseed(123):, /// truncreg y x1 x2, ll(17)
- Specify 20,000 Markov chain Monte Carlo (MCMC) samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations bayes, mcmcsize(20000) burnin(5000) dots(500):, /// truncreg y x1 x2, ll(17)
- In the above, request that the 90% highest posterior density (HPD) credible interval be displayed instead of the default 95% equal-tailed credible interval bayes, clevel(90) hpd

Also see Quick start in [BAYES] bayes and Quick start in [R] truncreg.

## Menu

Statistics > Linear models and related > Bayesian regression > Truncated regression

# **Syntax**

<u>blocksumm</u>ary

\* noblocking

| options   | Description  |  |
|---|--|--|
| Model   |  |  |
| <u>nocons</u> tant  | suppress constant term   |  |
| ll( <i>varname</i>   #)   | left-truncation variable or limit  |  |
| ul( <i>varname</i>   #)   | right-truncation variable or limit   |  |
| <u>off</u> set( <i>varname</i> )  | include varname in model with coefficient constrained to 1   |  |
| Reporting   |  |  |
| display_options   | control spacing, line width, and base and empty cells  |  |
| <u>l</u> evel(#)  | set credible level; default is level(95)   |  |
|   | is equivalent to bayes, clevel(): truncreg.<br>options, see Options in [R] truncreg.<br>Description  |  |
| pavesopis   | Description  |  |
|   |  |  |
| Priors  |  |  |
| Priors  | specify standard deviation of default normal priors for regression   |  |
| Priors  | specify standard deviation of default normal priors for regression<br>coefficients; default is normalprior(100)<br>specify shape and scale of default inverse-gamma prior for  |  |
| Priors<br>formalprior(#)<br>figammaprior(# #)   | <pre>specify standard deviation of default normal priors for regression<br/>coefficients; default is normalprior(100)<br/>specify shape and scale of default inverse-gamma prior for<br/>variance; default is igammaprior(0.01 0.01)</pre>   |  |
| Priors * normalprior(#) * igammaprior(# #) prior(priorspec)   | <pre>specify standard deviation of default normal priors for regression<br/>coefficients; default is normalprior(100)<br/>specify shape and scale of default inverse-gamma prior for<br/>variance; default is igammaprior(0.01 0.01)<br/>prior for model parameters; this option may be repeated</pre>   |  |
| Priors<br><u>normalpr</u> ior(#)<br><u>igammapr</u> ior(# #)<br>prior( <i>priorspec</i> )<br>dryrun   | <pre>specify standard deviation of default normal priors for regression<br/>coefficients; default is normalprior(100)<br/>specify shape and scale of default inverse-gamma prior for<br/>variance; default is igammaprior(0.01 0.01)</pre>   |  |
| Priors<br>normalprior(#)<br>igammaprior(# #)<br>prior( <i>priorspec</i> )<br>dryrun<br>Simulation   | <pre>specify standard deviation of default normal priors for regression<br/>coefficients; default is normalprior(100)<br/>specify shape and scale of default inverse-gamma prior for<br/>variance; default is igammaprior(0.01 0.01)<br/>prior for model parameters; this option may be repeated<br/>show model summary without estimation</pre>   |  |
| Priors<br>normalprior(#)<br>igammaprior(# #)<br>prior(priorspec)<br>dryrun<br>Simulation<br>nchains(#)  | <pre>specify standard deviation of default normal priors for regression<br/>coefficients; default is normalprior(100)<br/>specify shape and scale of default inverse-gamma prior for<br/>variance; default is igammaprior(0.01 0.01)<br/>prior for model parameters; this option may be repeated<br/>show model summary without estimation<br/>number of chains; default is to simulate one chain</pre>  |  |
| Priors<br>normalprior(#)<br>igammaprior(# #)<br>prior(priorspec)<br>dryrun<br>Simulation<br>nchains(#)<br><u>mcmcs</u> ize(#)   | <pre>specify standard deviation of default normal priors for regression<br/>coefficients; default is normalprior(100)<br/>specify shape and scale of default inverse-gamma prior for<br/>variance; default is igammaprior(0.01 0.01)<br/>prior for model parameters; this option may be repeated<br/>show model summary without estimation<br/>number of chains; default is to simulate one chain<br/>MCMC sample size; default is mcmcsize(10000)</pre>   |  |
| Priors<br>normalprior(#)<br>figammaprior(# #)<br>prior(priorspec)<br>dryrun<br>Simulation<br>nchains(#)<br><u>mcmcsize(#)</u><br><u>burn</u> in(#)  | <pre>specify standard deviation of default normal priors for regression<br/>coefficients; default is normalprior(100)<br/>specify shape and scale of default inverse-gamma prior for<br/>variance; default is igammaprior(0.01 0.01)<br/>prior for model parameters; this option may be repeated<br/>show model summary without estimation<br/>number of chains; default is to simulate one chain<br/>MCMC sample size; default is mcmcsize(10000)<br/>burn-in period; default is burnin(2500)</pre>   |  |
| Priors<br>fnormalprior(#)<br>figammaprior(# #)<br>prior(priorspec)<br>dryrun<br>Simulation<br>nchains(#)<br><u>mcmcs</u> ize(#)<br><u>burn</u> in(#)<br><u>thin</u> ning(#)   | <pre>specify standard deviation of default normal priors for regression<br/>coefficients; default is normalprior(100)<br/>specify shape and scale of default inverse-gamma prior for<br/>variance; default is igammaprior(0.01 0.01)<br/>prior for model parameters; this option may be repeated<br/>show model summary without estimation<br/>number of chains; default is to simulate one chain<br/>MCMC sample size; default is mcmcsize(10000)<br/>burn-in period; default is burnin(2500)<br/>thinning interval; default is thinning(1)</pre>   |  |
| Priors<br>* normalprior(#)<br>* igammaprior(# #)<br>prior(priorspec)<br>dryrun<br>Simulation<br>nchains(#)<br>mcmcsize(#)<br>burnin(#)<br>thinning(#)<br>rseed(#)   | <pre>specify standard deviation of default normal priors for regression<br/>coefficients; default is normalprior(100)<br/>specify shape and scale of default inverse-gamma prior for<br/>variance; default is igammaprior(0.01 0.01)<br/>prior for model parameters; this option may be repeated<br/>show model summary without estimation<br/>number of chains; default is to simulate one chain<br/>MCMC sample size; default is mcmcsize(10000)<br/>burn-in period; default is burnin(2500)<br/>thinning interval; default is thinning(1)<br/>random-number seed</pre>  |  |
| Priors<br>* normalprior(#)<br>* <u>igammapr</u> ior(# #)<br>prior( <i>priorspec</i> )<br>dryrun<br>Simulation<br>nchains(#)<br><u>mcmcs</u> ize(#)<br><u>burn</u> in(#)<br><u>thin</u> ning(#)                                    | <pre>specify standard deviation of default normal priors for regression<br/>coefficients; default is normalprior(100)<br/>specify shape and scale of default inverse-gamma prior for<br/>variance; default is igammaprior(0.01 0.01)<br/>prior for model parameters; this option may be repeated<br/>show model summary without estimation<br/>number of chains; default is to simulate one chain<br/>MCMC sample size; default is mcmcsize(10000)<br/>burn-in period; default is burnin(2500)<br/>thinning interval; default is thinning(1)<br/>random-number seed</pre>  |  |
| Priors<br>* normalprior(#)<br>* igammaprior(# #)<br>prior(priorspec)<br>dryrun<br>Simulation<br>nchains(#)<br><u>mcmcsize(#)</u><br><u>burn</u> in(#)<br><u>thin</u> ning(#)<br>rseed(#)<br><u>excl</u> ude(paramref)<br>Blocking | <pre>specify standard deviation of default normal priors for regression<br/>coefficients; default is normalprior(100)<br/>specify shape and scale of default inverse-gamma prior for<br/>variance; default is igammaprior(0.01 0.01)<br/>prior for model parameters; this option may be repeated<br/>show model summary without estimation<br/>number of chains; default is to simulate one chain<br/>MCMC sample size; default is mcmcsize(10000)<br/>burn-in period; default is burnin(2500)<br/>thinning interval; default is thinning(1)<br/>random-number seed<br/>specify model parameters to be excluded from the simulation resu</pre> |  |
| Priors<br>* normalprior(#)<br>* igammaprior(# #)<br>prior(priorspec)<br>dryrun<br>Simulation<br>nchains(#)<br>mcmcsize(#)<br>burnin(#)<br>thinning(#)<br>rseed(#)<br>exclude(paramref)<br>Blocking<br>* blocksize(#)              | <pre>specify standard deviation of default normal priors for regression<br/>coefficients; default is normalprior(100)<br/>specify shape and scale of default inverse-gamma prior for<br/>variance; default is igammaprior(0.01 0.01)<br/>prior for model parameters; this option may be repeated<br/>show model summary without estimation<br/>number of chains; default is to simulate one chain<br/>MCMC sample size; default is mcmcsize(10000)<br/>burn-in period; default is burnin(2500)<br/>thinning interval; default is thinning(1)</pre>   |  |

display block summary

do not block parameters by default

| Initialization                         |   |
|--|---|
| <pre>initial(initspec)</pre>           | specify initial values for model parameters with a single chain   |
| <pre>init#(initspec)</pre>             | specify initial values for #th chain; requires nchains()  |
| initall( <i>initspec</i> )             | specify initial values for all chains; requires nchains()   |
| nomleinitial                           | suppress the use of maximum likelihood estimates as starting values   |
| initrandom                             | specify random initial values   |
| <u>initsumm</u> ary                    | display initial values used for simulation  |
| * <u>noi</u> sily                      | display output from the estimation command during initialization  |
| Adaptation                             |   |
| adaptation( <i>adaptopts</i> )         | control the adaptive MCMC procedure   |
| <u>sc</u> ale(#)                       | initial multiplier for scale factor; default is scale(2.38)   |
| <pre>covariance(cov)</pre>             | initial proposal covariance; default is the identity matrix   |
| Reporting                              |   |
| <u>clev</u> el(#)                      | set credible interval level; default is clevel(95)  |
| hpd                                    | display HPD credible intervals instead of the default equal-tailed credible intervals                                 |
| <u>ef</u> orm ( <i>string</i> )        | report exponentiated coefficients and, optionally, label as string  |
| batch(#)                               | <pre>specify length of block for batch-means calculations;<br/>default is batch(0)</pre>                              |
| <pre>saving(filename[, replace])</pre> | save simulation results to <i>filename</i> .dta   |
| nomodelsummary                         | suppress model summary  |
| chainsdetail                           | display detailed simulation summary for each chain  |
| [no]dots                               | suppress dots or display dots every 100 iterations and iteration<br>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<br>the output   |
| <u>notab</u> le                        | suppress estimation table   |
| <u>nohead</u> er                       | suppress output header  |
| <pre>title(string)</pre>               | display string as title above the table of parameter estimates  |
| display_options                        | control spacing, line width, and base and empty cells   |
| Advanced                               |   |
| <pre>search(search_options)</pre>      | control the search for feasible initial values  |
| corrlag(#)                             | specify maximum autocorrelation lag; default varies   |
| corrtol(#)                             | specify autocorrelation tolerance; default is corrtol(0.01)   |
|  |   |

\*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh. Options prior() and block() may be repeated.

priorspec and paramref are defined in [BAYES] bayesmh.

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

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

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

Model parameters are regression coefficients {depvar:indepvars} and variance {sigma2}. Use the dryrun option to see the definitions of model parameters prior to estimation.

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

### **Remarks and examples**

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

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] bayes.

### Stored results

See Stored results in [BAYES] bayes.

### Methods and formulas

See Methods and formulas in [BAYES] bayesmh.

#### Also see

[BAYES] **bayes** — Bayesian regression models using the bayes prefix<sup>+</sup>

[R] truncreg — Truncated regression

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

[BAYES] Bayesian estimation — Bayesian estimation commands

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

[BAYES] Intro — Introduction to Bayesian analysis

[BAYES] Glossary

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