

bayes: tpoisson — Bayesian truncated Poisson regression

[Description](#)[Remarks and examples](#)[Quick start](#)[Stored results](#)[Menu](#)[Methods and formulas](#)[Syntax](#)[Also see](#)

Description

`bayes: tpoisson` fits a Bayesian truncated Poisson regression to a positive count outcome whose values are all above the truncation point; see [\[BAYES\] bayes](#) and [\[R\] tpoisson](#) for details.

Quick start

Bayesian truncated Poisson regression of `y` on `x1` and `x2`, using a lower truncation limit of 5 and using default normal priors for regression coefficients

```
bayes: tpoisson y x1 x2, ll(5)
```

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

```
bayes, normalprior(10): tpoisson y x1 x2, ll(5)
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): tpoisson y x1 x2, ll(5)
```

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

```
bayes, saving(simdata) rseed(123): tpoisson y x1 x2, ll(5)
```

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

```
bayes, mcmcsize(20000) burnin(5000) dots(500): tpoisson y x1 x2, ll(5)
```

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

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

Display incidence-rate ratios instead of coefficients

```
bayes: tpoisson y x1 x2, ll(5) irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

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

Menu

Statistics > Count outcomes > Bayesian regression > Truncated Poisson regression

Syntax

```
bayes [ , bayesopts ] : tpoisson deivar [indepvars] [if] [in] [weight] [ , options ]
```

| <i>options</i> | Description |
|----------------|-------------|
|----------------|-------------|

Model

| | |
|---|--|
| <code>noconstant</code> | suppress constant term |
| <code>ll(# <i>varname</i>)</code> | lower limit for truncation; default is <code>ll(0)</code> |
| <code>ul(# <i>varname</i>)</code> | upper limit for truncation |
| <code>exposure(<i>varname</i>_e)</code> | include $\ln(\text{varname}_e)$ in model with coefficient constrained to 1 |
| <code>offset(<i>varname</i>_o)</code> | include <i>varname</i> _o in model with coefficient constrained to 1 |

Reporting

| | |
|------------------------------|---|
| <code>irr</code> | report incidence-rate ratios |
| <code>display_options</code> | control spacing, line width, and base and empty cells |
| <code>level(#)</code> | set credible level; default is <code>level(95)</code> |

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

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

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

`bayes: tpoisson`, `level()` is equivalent to `bayes, clevel(): tpoisson`.

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

| <i>bayesopts</i> | Description |
|------------------|-------------|
|------------------|-------------|

Priors

| | |
|--------------------------------------|---|
| <code>*normalprior(#)</code> | specify standard deviation of default normal priors for regression coefficients; default is <code>normalprior(100)</code> |
| <code>prior(<i>priorspec</i>)</code> | prior for model parameters; this option may be repeated |
| <code>dryrun</code> | show model summary without estimation |

Simulation

| | |
|---------------------------------------|---|
| <code>nchains(#)</code> | number of chains; default is to simulate one chain |
| <code>mcmcsize(#)</code> | MCMC sample size; default is <code>mcmcsize(10000)</code> |
| <code>burnin(#)</code> | burn-in period; default is <code>burnin(2500)</code> |
| <code>thinning(#)</code> | thinning interval; default is <code>thinning(1)</code> |
| <code>rseed(#)</code> | random-number seed |
| <code>exclude(<i>paramref</i>)</code> | specify model parameters to be excluded from the simulation results |

Blocking

| | |
|--|--|
| <code>*blocksize(#)</code> | maximum block size; default is <code>blocksize(50)</code> |
| <code>block(<i>paramref</i> [, <i>blockopts</i>])</code> | specify a block of model parameters; this option may be repeated |
| <code>blocksummary</code> | display block summary |
| <code>*noblocking</code> | 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>initrandom</code> | specify random initial values |
| <code>initsummary</code> | display initial values used for simulation |
| * <code>noisily</code> | display output from the estimation command during initialization |

Adaptation

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

Reporting

| | |
|--|---|
| <code>clevel(#)</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>irr</code> | report incidence-rate ratios |
| <code>eform[(<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>saving(<i>filename</i>[, <i>replace</i>])</code> | save simulation results to <i>filename.dta</i> |
| <code>nomodelsummary</code> | suppress model summary |
| <code>chainsdetail</code> | display detailed simulation summary for each chain |
| <code>[no]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>[no]show(<i>paramref</i>)</code> | specify model parameters to be excluded from or included in the output |
| <code>notable</code> | suppress estimation table |
| <code>noheader</code> | suppress output header |
| <code>title(<i>string</i>)</code> | display <i>string</i> as title above the table of parameter estimates |
| <code>display_options</code> | control spacing, line width, and base and empty cells |

Advanced

| | |
|--|--|
| <code>search(<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 `{devar:indepvars}`. Use the `dryrun` option to see the definitions of model parameters prior to estimation.

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

Remarks and examples

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

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

Stored results

See *Stored results* in [BAYES] **bayes**.

Methods and formulas

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

Also see

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

[R] **tpoisson** — Truncated Poisson regression

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

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

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

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

[BAYES] **Glossary**

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