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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 x_1 and x_2 , 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 devar [indepvars] [if] [in] [weight] [ , options ]
```

<i>options</i>	Description
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Model

<code>noconstant</code>	suppress constant term
<code>ll(# <i>varname</i>)</code>	lower limit for truncation; default is ll(0)
<code>ul(# <i>varname</i>)</code>	upper limit for truncation
<code>exposure(<i>varname</i>_e)</code>	include ln(<i>varname</i> _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 level(95)

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

devar 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
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Priors

* <code>normalprior(#)</code>	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
<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 mcmcsize(10000)
<code>burnin(#)</code>	burn-in period; default is burnin(2500)
<code>thinning(#)</code>	thinning interval; default is thinning(1)
<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 blocksize(50)
<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>initial(<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 `{depvar:indepvars}`. Use the `dryrun` option to see the definitions of model parameters prior to estimation.

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

Remarks and examples

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

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

Stored results

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

Methods and formulas

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

Also see

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

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

[BAYES] **Bayesian postestimation** — Postestimation tools after Bayesian estimation

[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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