STATA BAYESIAN ANALYSIS REFERENCE MANUAL

RELEASE 15

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Contents

Cross-referencing the documentation

When reading this manual, you will find references to other Stata manuals. For example,

[U] **26 Overview of Stata estimation commands**
[R] **regress**
[D] **reshape**

The first example is a reference to chapter 26, *Overview of Stata estimation commands*, in the *User's Guide*; the second is a reference to the `regress` entry in the *Base Reference Manual*; and the third is a reference to the `reshape` entry in the *Data Management Reference Manual*.

All the manuals in the Stata Documentation have a shorthand notation:

[GSM]	*Getting Started with Stata for Mac*
[GSU]	*Getting Started with Stata for Unix*
[GSW]	*Getting Started with Stata for Windows*
[U]	*Stata User's Guide*
[R]	*Stata Base Reference Manual*
[BAYES]	*Stata Bayesian Analysis Reference Manual*
[D]	*Stata Data Management Reference Manual*
[ERM]	*Stata Extended Regression Models Reference Manual*
[FMM]	*Stata Finite Mixture Models Reference Manual*
[FN]	*Stata Functions Reference Manual*
[G]	*Stata Graphics Reference Manual*
[IRT]	*Stata Item Response Theory Reference Manual*
[DSGE]	*Stata Linearized Dynamic Stochastic General Equilibrium Reference Manual*
[XT]	*Stata Longitudinal-Data/Panel-Data Reference Manual*
[ME]	*Stata Multilevel Mixed-Effects Reference Manual*
[MI]	*Stata Multiple-Imputation Reference Manual*
[MV]	*Stata Multivariate Statistics Reference Manual*
[PSS]	*Stata Power and Sample-Size Reference Manual*
[P]	*Stata Programming Reference Manual*
[SP]	*Stata Spatial Autoregressive Models Reference Manual*
[SEM]	*Stata Structural Equation Modeling Reference Manual*
[SVY]	*Stata Survey Data Reference Manual*
[ST]	*Stata Survival Analysis Reference Manual*
[TS]	*Stata Time-Series Reference Manual*
[TE]	*Stata Treatment-Effects Reference Manual: Potential Outcomes/Counterfactual Outcomes*
[I]	*Stata Glossary and Index*
[M]	*Mata Reference Manual*

Title

intro — Introduction to Bayesian analysis

Description Remarks and examples References Also see

Description

This entry provides a software-free introduction to Bayesian analysis. See [BAYES] **bayesian commands** for an overview of the software for performing Bayesian analysis and for an overview example.

Remarks and examples

Remarks are presented under the following headings:

The first five sections provide a general introduction to Bayesian analysis. The remaining sections provide a more technical discussion of the concepts of Bayesian analysis.

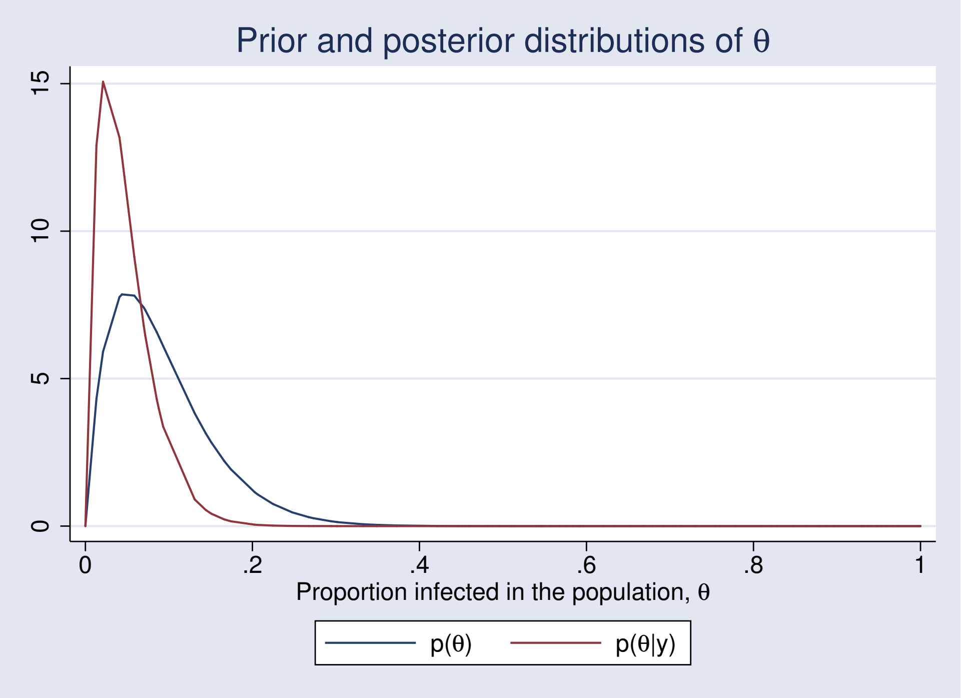
What is Bayesian analysis?

Bayesian analysis is a statistical analysis that answers research questions about unknown parameters of statistical models by using probability statements. Bayesian analysis rests on the assumption that all model parameters are random quantities and thus can incorporate prior knowledge. This assumption is in sharp contrast with the more traditional, also called frequentist, statistical inference where all parameters are considered unknown but fixed quantities. Bayesian analysis follows a simple rule of probability, the Bayes rule, which provides a formalism for combining prior information with evidence from the data at hand. The Bayes rule is used to form the so called posterior distribution of model parameters. The posterior distribution results from updating the prior knowledge about model parameters with evidence from the observed data. Bayesian analysis uses the posterior distribution to form various summaries for the model parameters including point estimates such as posterior means, medians, percentiles, and interval estimates such as credible intervals. Moreover, all statistical tests about model parameters can be expressed as probability statements based on the estimated posterior distribution.

As a quick introduction to Bayesian analysis, we use an example, described in Hoff (2009, 3), of estimating the prevalence of a rare infectious disease in a small city. A small random sample of 20 subjects from the city will be checked for infection. The parameter of interest $\theta \in [0,1]$ is the fraction of infected individuals in the city. Outcome y records the number of infected individuals in the sample. A reasonable sampling model for y is a binomial model: $y|\theta \sim \text{Binomial}(20,\theta)$. Based on the studies from other comparable cities, the infection rate ranged between 0.05 and 0.20, with an average prevalence of 0.10. To use this information, we must conduct Bayesian analysis. This information can be incorporated into a Bayesian model with a prior distribution for θ, which assigns a large probability between 0.05 and 0.20, with the expected value of θ close to 0.10. One potential prior that satisfies this condition is a $\text{Beta}(2,20)$ prior with the expected value of $2/(2+20) = 0.09$. So, let's assume this prior for the infection rate θ, that is, $\theta \sim \text{Beta}(2,20)$. We sample individuals and observe none who have an infection, that is, $y = 0$. This value is not that uncommon for a small sample and a rare disease. For example, for a true rate $\theta = 0.05$, the probability of observing 0 infections in a sample of 20 individuals is about 36% according to the binomial distribution. So, our Bayesian model can be defined as follows:

$$
\begin{aligned}
y|\theta &\sim \text{Binomial}(20,\theta) \\
\theta &\sim \text{Beta}(2,20)
\end{aligned}
$$

For this Bayesian model, we can actually compute the posterior distribution of $\theta|y$, which is $\theta|y \sim \text{Beta}(2+0, 20+20-0) = \text{Beta}(2,40)$. The prior and posterior distributions of θ are depicted below.



The posterior density (shown in red) is more peaked and shifted to the left compared with the prior distribution (shown in blue). The posterior distribution combined the prior information about θ with the information from the data, from which $y = 0$ provided evidence for a low value of θ and shifted the prior density to the left to form the posterior density. Based on this posterior distribution, the posterior mean estimate of θ is $2/(2 + 40) = 0.048$ and the posterior probability that, for example, $\theta < 0.10$ is about 93%.

If we compute a standard frequentist estimate of a population proportion θ as a fraction of the infected subjects in the sample, $\overline{y} = y/n$, we will obtain 0 with the corresponding 95% confidence interval $(\overline{y} - 1.96\sqrt{\overline{y}\,(1-\overline{y})/n}, \overline{y} + 1.96\sqrt{\overline{y}\,(1-\overline{y})/n})$ reducing to 0 as well. It may be difficult to convince a health policy maker that the prevalence of the disease in that city is indeed 0, given the small sample size and the prior information available from comparable cities about a nonzero prevalence of this disease.

We used a beta prior distribution in this example, but we could have chosen another prior distribution that supports our prior knowledge. For the final analysis, it is important to consider a range of different prior distributions and investigate the sensitivity of the results to the chosen priors.

For more details about this example, see Hoff (2009). Also see *Beta-binomial model* in [BAYES] **bayesmh** for how to fit this model using `bayesmh`.

Bayesian versus frequentist analysis, or why Bayesian analysis?

Why use Bayesian analysis? Perhaps a better question is when to use Bayesian analysis and when to use frequentist analysis. The answer to this question mainly lies in your research problem. You should choose an analysis that answers your specific research questions. For example, if you are interested in estimating the probability that the parameter of interest belongs to some prespecified interval, you will need the Bayesian framework, because this probability cannot be estimated within the frequentist framework. If you are interested in a repeated-sampling inference about your parameter, the frequentist framework provides that.

Bayesian and frequentist approaches have very different philosophies about what is considered fixed and, therefore, have very different interpretations of the results. The Bayesian approach assumes that the observed data sample is fixed and that model parameters are random. The posterior distribution of parameters is estimated based on the observed data and the prior distribution of parameters and is used for inference. The frequentist approach assumes that the observed data are a repeatable random sample and that parameters are unknown but fixed and constant across the repeated samples. The inference is based on the sampling distribution of the data or of the data characteristics (statistics). In other words, Bayesian analysis answers questions based on the distribution of parameters conditional on the observed sample, whereas frequentist analysis answers questions based on the distribution of statistics obtained from repeated hypothetical samples, which would be generated by the same process that produced the observed sample given that parameters are unknown but fixed. Frequentist analysis consequently requires that the process that generated the observed data is repeatable. This assumption may not always be feasible. For example, in meta-analysis, where the observed sample represents the collected studies of interest, one may argue that the collection of studies is a one-time experiment.

Frequentist analysis is entirely data-driven and strongly depends on whether or not the data assumptions required by the model are met. On the other hand, Bayesian analysis provides a more robust estimation approach by using not only the data at hand but also some existing information or knowledge about model parameters.

In frequentist statistics, estimators are used to approximate the true values of the unknown parameters, whereas Bayesian statistics provides an entire distribution of the parameters. In our example of a prevalence of an infectious disease from *What is Bayesian analysis?*, frequentist analysis produced one point estimate for the prevalence, whereas Bayesian analysis estimated the entire posterior distribution of the prevalence based on a given sample.

Frequentist inference is based on the sampling distributions of estimators of parameters and provides parameter point estimates and their standard errors as well as confidence intervals. The exact sampling distributions are rarely known and are often approximated by a large-sample normal distribution. Bayesian inference is based on the posterior distribution of the parameters and provides summaries of this distribution including posterior means and their MCMC standard errors (MCSE) as well as credible intervals. Although exact posterior distributions are known only in a number of cases, general posterior distributions can be estimated via, for example, Markov chain Monte Carlo (MCMC) sampling without any large-sample approximation.

Frequentist confidence intervals do not have straightforward probabilistic interpretations as do Bayesian credible intervals. For example, the interpretation of a 95% confidence interval is that if we repeat the same experiment many times and compute confidence intervals for each experiment, then 95% of those intervals will contain the true value of the parameter. For any given confidence interval, the probability that the true value is in that interval is either zero or one, and we do not know which. We may only infer that any given confidence interval provides a plausible range for the true value of the parameter. A 95% Bayesian credible interval, on the other hand, provides a range for a parameter such that the probability that the parameter lies in that range is 95%.

Frequentist hypothesis testing is based on a deterministic decision using a prespecified significance level of whether to accept or reject the null hypothesis based on the observed data, assuming that the null hypothesis is actually true. The decision is based on a p-value computed from the observed data. The interpretation of the p-value is that if we repeat the same experiment and use the same testing procedure many times, then given our null hypothesis is true, we will observe the result (test statistic) as extreme or more extreme than the one observed in the sample $(100 \times p\text{-value})\%$ of the times. The p-value cannot be interpreted as a probability of the null hypothesis, which is a common misinterpretation. In fact, it answers the question of how likely are our data given that the null hypothesis is true, and not how likely is the null hypothesis given our data. The latter question can be answered by Bayesian hypothesis testing, where we can compute the probability of any hypothesis of interest.

How to do Bayesian analysis

Bayesian analysis starts with the specification of a posterior model. The posterior model describes the probability distribution of all model parameters conditional on the observed data and some prior knowledge. The posterior distribution has two components: a likelihood, which includes information about model parameters based on the observed data, and a prior, which includes prior information (before observing the data) about model parameters. The likelihood and prior models are combined using the Bayes rule to produce the posterior distribution:

$$\text{Posterior} \propto \text{Likelihood} \times \text{Prior}$$

If the posterior distribution can be derived in a closed form, we may proceed directly to the inference stage of Bayesian analysis. Unfortunately, except for some special models, the posterior distribution is rarely available explicitly and needs to be estimated via simulations. MCMC sampling can be used to simulate potentially very complex posterior models with an arbitrary level of precision. MCMC methods for simulating Bayesian models are often demanding in terms of specifying an efficient sampling algorithm and verifying the convergence of the algorithm to the desired posterior distribution.

Inference is the next step of Bayesian analysis. If MCMC sampling is used for approximating the posterior distribution, the convergence of MCMC must be established before proceeding to inference. Point and interval estimators are either derived from the theoretical posterior distribution or estimated from a sample simulated from the posterior distribution. Many Bayesian estimators, such as posterior mean and posterior standard deviation, involve integration. If the integration cannot be performed analytically to obtain a closed-form solution, sampling techniques such as Monte Carlo integration and MCMC and numerical integration are commonly used.

Bayesian hypothesis testing can take two forms, which we refer to as interval-hypothesis testing and model-hypothesis testing. In an interval-hypothesis testing, the probability that a parameter or a set of parameters belongs to a particular interval or intervals is computed. In model hypothesis testing, the probability of a Bayesian model of interest given the observed data is computed.

Model comparison is another common step of Bayesian analysis. The Bayesian framework provides a systematic and consistent approach to model comparison using the notion of posterior odds and related to them Bayes factors. See [BAYES] **bayesstats ic** for details.

Finally, prediction of some future unobserved data may also be of interest in Bayesian analysis. The prediction of a new data point is performed conditional on the observed data using the so-called posterior predictive distribution, which involves integrating out all parameters from the model with respect to their posterior distribution. Again, Monte Carlo integration is often the only feasible option for obtaining predictions. Prediction can also be helpful in estimating the goodness of fit of a model.

Advantages and disadvantages of Bayesian analysis

Bayesian analysis is a powerful analytical tool for statistical modeling, interpretation of results, and prediction of data. It can be used when there are no standard frequentist methods available or the existing frequentist methods fail. However, one should be aware of both the advantages and disadvantages of Bayesian analysis before applying it to a specific problem.

The universality of the Bayesian approach is probably its main methodological advantage to the traditional frequentist approach. Bayesian inference is based on a single rule of probability, the Bayes rule, which is applied to all parametric models. This makes the Bayesian approach universal and greatly facilitates its application and interpretation. The frequentist approach, however, relies on a variety of estimation methods designed for specific statistical problems and models. Often, inferential methods designed for one class of problems cannot be applied to another class of models.

In Bayesian analysis, we can use previous information, either belief or experimental evidence, in a data model to acquire more balanced results for a particular problem. For example, incorporating prior information can mitigate the effect of a small sample size. Importantly, the use of the prior evidence is achieved in a theoretically sound and principled way.

By using the knowledge of the entire posterior distribution of model parameters, Bayesian inference is far more comprehensive and flexible than the traditional inference.

Bayesian inference is exact, in the sense that estimation and prediction are based on the posterior distribution. The latter is either known analytically or can be estimated numerically with an arbitrary precision. In contrast, many frequentist estimation procedures such as maximum likelihood rely on the assumption of asymptotic normality for inference.

Bayesian inference provides a straightforward and more intuitive interpretation of the results in terms of probabilities. For example, credible intervals are interpreted as intervals to which parameters belong with a certain probability, unlike the less straightforward repeated-sampling interpretation of the confidence intervals.

Bayesian models satisfy the likelihood principle (Berger and Wolpert 1988) that the information in a sample is fully represented by the likelihood function. This principle requires that if the likelihood function of one model is proportional to the likelihood function of another model, then inferences from the two models should give the same results. Some researchers argue that frequentist methods that depend on the experimental design may violate the likelihood principle.

Finally, as we briefly mentioned earlier, the estimation precision in Bayesian analysis is not limited by the sample size—Bayesian simulation methods may provide an arbitrary degree of precision.

Despite the conceptual and methodological advantages of the Bayesian approach, its application in practice is still considered controversial sometimes. There are two main reasons for this—the presumed subjectivity in specifying prior information and the computational challenges in implementing Bayesian methods. Along with the objectivity that comes from the data, the Bayesian approach uses potentially subjective prior distribution. That is, different individuals may specify different prior distributions. Proponents of frequentist statistics argue that for this reason, Bayesian methods lack objectivity and should be avoided. Indeed, there are settings such as clinical trial cases when the researchers want to minimize a potential bias coming from preexisting beliefs and achieve more objective conclusions. Even in such cases, however, a balanced and reliable Bayesian approach is possible. The trend in using noninformative priors in Bayesian models is an attempt to address the issue of subjectivity. On the other hand, some Bayesian proponents argue that the classical methods of statistical inference have built-in subjectivity such as a choice for a sampling procedure, whereas the subjectivity is made explicit in Bayesian analysis.

Building a reliable Bayesian model requires extensive experience from the researchers, which leads to the second difficulty in Bayesian analysis—setting up a Bayesian model and performing analysis is a demanding and involving task. This is true, however, to an extent for any statistical modeling procedure.

Lastly, one of the main disadvantages of Bayesian analysis is the computational cost. As a rule, Bayesian analysis involves intractable integrals that can only be computed using intensive numerical methods. Most of these methods such as MCMC are stochastic by nature and do not comply with the natural expectation from a user of obtaining deterministic results. Using simulation methods does not compromise the discussed advantages of Bayesian approach, but unquestionably adds to the complexity of its application in practice.

For more discussion about advantages and disadvantages of Bayesian analysis, see, for example, Thompson (2012), Bernardo and Smith (2000), and Berger and Wolpert (1988).

Brief background and literature review

The principles of Bayesian analysis date back to the work of Thomas Bayes, who was a Presbyterian minister in Tunbridge Wells and Pierre Laplace, a French mathematician, astronomer, and physicist in the 18th century. Bayesian analysis started as a simple intuitive rule, named after Bayes, for updating beliefs on account of some evidence. For the next 200 years, however, Bayes's rule was just an obscure idea. Along with the rapid development of the standard or frequentist statistics in 20th century, Bayesian methodology was also developing, although with less attention and at a slower pace. One of the obstacles for the progress of Bayesian ideas has been the lasting opinion among mainstream statisticians of it being subjective. Another more-tangible problem for adopting Bayesian models in practice has been the lack of adequate computational resources. Nowadays, Bayesian statistics is widely accepted by researchers and practitioners as a valuable and feasible alternative.

Bayesian analysis proliferates in diverse areas including industry and government, but its application in sciences and engineering is particularly visible. Bayesian statistical inference is used in econometrics (Poirier [1995]; Chernozhukov and Hong [2003]; Kim, Shephard, and Chib [1998], Zellner [1997]); education (Johnson 1997); epidemiology (Greenland 1998); engineering (Godsill and Rayner 1998); genetics (Iversen, Parmigiani, and Berry 1999); social sciences (Pollard 1986); hydrology (Parent et al. 1998); quality management (Rios Insua 1990); atmospheric sciences (Berliner et al. 1999); and law (DeGroot, Fienberg, and Kadane 1986), to name a few.

The subject of general statistics has been greatly influenced by the development of Bayesian ideas. Bayesian methodologies are now present in biostatistics (Carlin and Louis [2000]; Berry and Stangl [1996]); generalized linear models (Dey, Ghosh, and Mallick 2000); hierarchical modeling (Hobert 2000); statistical design (Chaloner and Verdinelli 1995); classification and discrimination (Neal [1996]; Neal [1999]); graphical models (Pearl 1998); nonparametric estimation (Müller and Vidakovic [1999]; Dey, Müller, and Sinha [1998]); survival analysis (Barlow, Clarotti, and Spizzichino 1993); sequential analysis (Carlin, Kadane, and Gelfand 1998); predictive inference (Aitchison and Dunsmore 1975); spatial statistics (Wolpert and Ickstadt [1998]; Besag and Higdon [1999]); testing and model selection (Kass and Raftery [1995]; Berger and Pericchi [1996]; Berger [2006]); and time series (Pole, West, and Harrison [1994]; West and Harrison [1997]).

Recent advances in computing allowed practitioners to perform Bayesian analysis using simulations. The simulation tools came from outside the statistics field—Metropolis et al. (1953) developed what is now known as a random-walk Metropolis algorithm to solve problems in statistical physics. Another landmark discovery was the Gibbs sampling algorithm (Geman and Geman 1984), initially used in image processing, which showed that exact sampling from a complex and otherwise intractable probability distribution is possible. These ideas were the seeds that led to the development of Markov chain Monte Carlo (MCMC)—a class of iterative simulation methods proved to be indispensable tools for Bayesian computations. Starting from the early 1990s, MCMC-based techniques slowly emerged in the mainstream statistical practice. More powerful and specialized methods appeared, such as perfect sampling (Propp and Wilson 1996), reversible-jump MCMC (Green 1995) for traversing variable dimension state spaces, and particle systems (Gordon, Salmond, and Smith 1993). Consequent widespread application of MCMC was imminent (Berger 2000) and influenced various specialized fields. For example, Gelman and Rubin (1992) investigated MCMC for the purpose of exploring posterior distributions; Geweke (1999) surveyed simulation methods for Bayesian inference in econometrics; Kim, Shephard, and Chib (1998) used MCMC simulations to fit stochastic volatility models; Carlin, Kadane, and Gelfand (1998) implemented Monte Carlo methods for identifying optimal strategies in clinical trials; Chib and Greenberg (1995) provided Bayesian formulation of a number of important econometrics models; and Chernozhukov and Hong (2003) reviewed some econometrics models involving Laplace-type estimators from an MCMC perspective. For more comprehensive exposition of MCMC, see, for example, Robert and Casella (2004); Tanner (1996); Gamerman and Lopes (2006); Chen, Shao, and Ibrahim (2000); and Brooks et al. (2011).

Bayesian statistics

Posterior distribution

To formulate the principles of Bayesian statistics, we start with a simple case when one is concerned with the interaction of two random variables, $\mathbf{A}$ and $\mathbf{B}$. Let $p(\cdot)$ denote either a probability mass function or a density, depending on whether the variables are discrete or continuous. The rule of conditional probability,

$$p(\mathbf{A}|\mathbf{B}) = \frac{p(\mathbf{A},\mathbf{B})}{p(\mathbf{B})}$$

can be used to derive the so-called Bayes's rule:

$$p(\mathbf{B}|\mathbf{A}) = \frac{p(\mathbf{A}|\mathbf{B})p(\mathbf{B})}{p(\mathbf{A})} \tag{1}$$

This rule also holds in the more general case when $\mathbf{A}$ and $\mathbf{B}$ are random vectors.

In a typical statistical problem, we have a data vector $\mathbf{y}$, which is assumed to be a sample from a probability model with an unknown parameter vector $\boldsymbol{\theta}$. We represent this model using the likelihood function $L(\boldsymbol{\theta};\mathbf{y}) = f(\mathbf{y};\boldsymbol{\theta}) = \prod_{i=1}^{n} f(y_i|\boldsymbol{\theta})$, where $f(y_i|\boldsymbol{\theta})$ denotes the probability density function of y_i given $\boldsymbol{\theta}$. We want to infer some properties of $\boldsymbol{\theta}$ based on the data $\mathbf{y}$. In Bayesian statistics, model parameters $\boldsymbol{\theta}$ is a random vector. We assume that $\boldsymbol{\theta}$ has a probability distribution $p(\boldsymbol{\theta}) = \pi(\boldsymbol{\theta})$, which is referred to as a prior distribution. Because both $\mathbf{y}$ and $\boldsymbol{\theta}$ are random, we can apply Bayes's rule (1) to derive the posterior distribution of $\boldsymbol{\theta}$ given data $\mathbf{y}$,

$$p(\boldsymbol{\theta}|\mathbf{y}) = \frac{p(\mathbf{y}|\boldsymbol{\theta})p(\boldsymbol{\theta})}{p(\mathbf{y})} = \frac{f(\mathbf{y};\boldsymbol{\theta})\pi(\boldsymbol{\theta})}{m(\mathbf{y})} \tag{2}$$

where $m(\mathbf{y}) \equiv p(\mathbf{y})$, known as the marginal distribution of $\mathbf{y}$, is defined by

$$m(\mathbf{y}) = \int f(\mathbf{y};\boldsymbol{\theta})\pi(\boldsymbol{\theta})d\boldsymbol{\theta} \tag{3}$$

The marginal distribution $m(\mathbf{y})$ in (3) does not depend on the parameter of interest $\boldsymbol{\theta}$, and we can, therefore, reduce (2) to

$$p(\boldsymbol{\theta}|\mathbf{y}) \propto L(\boldsymbol{\theta};\mathbf{y})\pi(\boldsymbol{\theta}) \tag{4}$$

Equation (4) is fundamental in Bayesian analysis and states that the posterior distribution of model parameters is proportional to their likelihood and prior probability distributions. We will often use (4) in the computationally more-convenient log-scale form

$$\ln\{p(\boldsymbol{\theta}|\mathbf{y})\} = l(\boldsymbol{\theta};\mathbf{y}) + \ln\{\pi(\boldsymbol{\theta})\} - c \tag{5}$$

where $l(\cdot;\cdot)$ denotes the log likelihood of the model. Depending on the analytical procedure involving the log-posterior $\ln\{p(\boldsymbol{\theta}|\mathbf{y})\}$, the actual value of the constant $c = \ln\{m(\mathbf{y})\}$ may or may not be relevant. For valid statistical analysis, however, we will always assume that c is finite.

Selecting priors

In Bayesian analysis, we seek a balance between prior information in a form of expert knowledge or belief and evidence from data at hand. Achieving the right balance is one of the difficulties in Bayesian modeling and inference. In general, we should not allow the prior information to overwhelm the evidence from the data, especially when we have a large data sample. A famous theoretical result, the Bernstein–von Mises theorem, states that in large data samples, the posterior distribution is independent of the prior distribution and, therefore, Bayesian and likelihood-based inferences should yield essentially the same results. On the other hand, we need a strong enough prior to support weak evidence that usually comes from insufficient data. It is always good practice to perform sensitivity analysis to check the dependence of the results on the choice of a prior.

The flexibility of choosing the prior freely is one of the main controversial issues associated with Bayesian analysis and the reason why some practitioners view the latter as subjective. It is also the reason why the Bayesian practice, especially in the early days, was dominated by noninformative priors. Noninformative priors, also called flat or vague priors, assign equal probabilities to all possible states of the parameter space with the aim of rectifying the subjectivity problem. One of the disadvantages of flat priors is that they are often improper; that is, they do not specify a legitimate probability distribution. For example, a uniform prior for a continuous parameter over an unbounded domain does not integrate to a finite number. However, this is not necessarily a problem because the corresponding posterior distribution may still be proper. Although Bayesian inference based on improper priors is possible, this is equivalent to discarding the terms $\log\pi(\boldsymbol{\theta})$ and c in (5), which nullifies the benefit of Bayesian analysis because it reduces the latter to an inference based only on the likelihood. This is why there is a strong objection to the practice of noninformative priors. In recent years, an increasing number of researchers have advocated the use of sound informative priors, for example, Thompson (2014). For example, using informative priors is mandatory in areas such as genetics, where prior distributions have a physical basis and reflect scientific knowledge.

Another convenient preference for priors is to use conjugate priors. Their choice is desirable from technical and computational standpoints but may not necessarily provide a realistic representation of the model parameters. Because of the limited arsenal of conjugate priors, an inclination to overuse them severely limits the flexibility of Bayesian modeling.

Point and interval estimation

In Bayesian statistics, inference about parameters $\boldsymbol{\theta}$ is based on the posterior distribution $p(\boldsymbol{\theta}|\mathbf{y})$ and various ways of summarizing this distribution. Point and interval estimates can be used to summarize this distribution.

Commonly used point estimators are the posterior mean,

$$E(\boldsymbol{\theta}|\mathbf{y}) = \int \boldsymbol{\theta} p(\boldsymbol{\theta}|\mathbf{y}) d\boldsymbol{\theta}$$

and the posterior median, $q_{0.5}(\boldsymbol{\theta})$, which is the 0.5 quantile of the posterior; that is,

$$P\{\boldsymbol{\theta} \le q_{0.5}(\boldsymbol{\theta}|\mathbf{y})\} = 0.5$$

Another point estimator is the posterior mode, which is the value of $\boldsymbol{\theta}$ that maximizes $p(\boldsymbol{\theta}|\mathbf{y})$.

Interval estimation is performed by constructing so-called credible intervals (CRIs). CRIs are special cases of credible regions. Let $1-\alpha \in (0,1)$ be some predefined credible level. Then, an $\{(1-\alpha)\times 100\}\%$ credible set R of θ is such that

$$\text{Pr}(\theta \in R|\mathbf{y}) = \int_R p(\theta|\mathbf{y}) d\theta = 1-\alpha$$

We consider two types of CRIs. The first one is based on quantiles. The second one is the highest posterior density (HPD) interval.

An $\{(1-\alpha)\times 100\}\%$ quantile-based, or also known as an equal-tailed CRI, is defined as $(q_{\alpha/2}, q_{1-\alpha/2})$, where q_a denotes the ath quantile of the posterior distribution. A commonly reported equal-tailed CRI is $(q_{0.025}, q_{0.975})$.

HPD interval is defined as an $\{(1-\alpha)\times 100\}\%$ CRI of the shortest width. As its name implies, this interval corresponds to the region of the posterior density with the highest concentration. For a unimodal posterior distribution, HPD is unique, but for a multimodal distribution it may not be unique. Computational approaches for calculating HPD are described in Chen and Shao (1999) and Eberly and Casella (2003).

Comparing Bayesian models

Model comparison is another important aspect of Bayesian statistics. We are often interested in comparing two or more plausible models for our data.

Let's assume that we have models M_j parameterized by vectors $\boldsymbol{\theta}_j$, $j = 1, \dots, r$. We may have varying degree of belief in each of these models given by prior probabilities $p(M_j)$, such that $\sum_{j=1}^{r} p(M_j) = 1$. By applying Bayes's rule, we find the posterior model probabilities

$$p(M_j|\mathbf{y}) = \frac{p(\mathbf{y}|M_j)p(M_j)}{p(\mathbf{y})}$$

where $p(\mathbf{y}|M_j) = m_j(y)$ is the marginal likelihood of M_j with respect to $\mathbf{y}$. Because of the difficulty in calculating $p(\mathbf{y})$, it is a common practice to compare two models, say, M_j and M_k, using the posterior odds ratio

$$\mathrm{PO}_{jk} = \frac{p(M_j|\mathbf{y})}{p(M_k|\mathbf{y})} = \frac{p(\mathbf{y}|M_j)p(M_j)}{p(\mathbf{y}|M_k)p(M_k)}$$

If all models are equally plausible, that is, $p(M_j) = 1/r$, the posterior odds ratio reduces to the so-called Bayes factors (BF) (Jeffreys 1935),

$$\mathrm{BF}_{jk} = \frac{p(\mathbf{y}|M_j)}{p(\mathbf{y}|M_k)} = \frac{m_j(\mathbf{y})}{m_k(\mathbf{y})}$$

which are simply ratios of marginal likelihoods.

Jeffreys (1961) recommended an interpretation of BF_{jk} based on half-units of the log scale. The following table provides some rules of thumb:

$\log_{10}(\mathrm{BF}_{jk})$	BF_{jk}	Evidence against M_k
0 to 1/2	1 to 3.2	Bare mention
1/2 to 1	3.2 to 10	Substantial
1 to 2	10 to 100	Strong
>2	>100	Decisive

The Schwarz criterion BIC (Schwarz 1978) is an approximation of BF in case of arbitrary but proper priors. Kass and Raftery (1995) and Berger (2006) provide a detailed exposition of Bayes factors, their calculation, and their role in model building and testing.

Posterior prediction

Prediction is another essential part of statistical analysis. In Bayesian statistics, prediction is performed using the posterior distribution. The probability of observing some future data $\mathbf{y}^*$ given the observed one can be obtained by the marginalization of

$$p(\mathbf{y}^*|\mathbf{y}) = \int p(\mathbf{y}^*|\mathbf{y}, \boldsymbol{\theta})p(\boldsymbol{\theta}|\mathbf{y})d\boldsymbol{\theta}$$

which, assuming that $\mathbf{y}^*$ is independent of $\mathbf{y}$, can be simplified to

$$p(\mathbf{y}^*|\mathbf{y}) = \int p(\mathbf{y}^*|\boldsymbol{\theta})p(\boldsymbol{\theta}|\mathbf{y})d\boldsymbol{\theta} \tag{6}$$

Equation (6) is called a posterior predictive distribution and is used for Bayesian prediction.

Bayesian computation

An unavoidable difficulty in performing Bayesian analysis is the need to compute integrals such as those expressing marginal distributions and posterior moments. The integrals involved in Bayesian inference are of the form $E\{g(\boldsymbol{\theta})\} = \int g(\boldsymbol{\theta})p(\boldsymbol{\theta}|\mathbf{y})d\boldsymbol{\theta}$ for some function $g(\cdot)$ of the random vector $\boldsymbol{\theta}$. With the exception of a few cases for which analytical integration is possible, the integration is performed via simulations.

Given a sample from the posterior distribution, we can use Monte Carlo integration to approximate the integrals. Let $\boldsymbol{\theta}_1$, $\boldsymbol{\theta}_2$, ..., $\boldsymbol{\theta}_T$ be an independent sample from $p(\boldsymbol{\theta}|\mathbf{y})$.

The original integral of interest $E\{g(\boldsymbol{\theta})\}$ can be approximated by

$$\widehat{g} = \frac{1}{T}\sum_{t=1}^{T} g(\boldsymbol{\theta}_t)$$

Moreover, if g is a scalar function, under some mild conditions, the central limit theorem holds

$$\widehat{g} \approx N\left[E\{g(\boldsymbol{\theta})\}, \sigma^2/T\right]$$

where $\sigma^2 = \mathrm{Cov}\{g(\boldsymbol{\theta}_i)\}$ can be approximated by the sample variance $\sum_{t=1}^{T}\{g(\boldsymbol{\theta}_t) - \widehat{g}\}^2/T$. If the sample is not independent, then $\widehat{g}$ still approximates $E\{g(\boldsymbol{\theta})\}$ but the variance σ^2 is given by

$$\sigma^2 = \mathrm{Var}\{g(\boldsymbol{\theta}_t)\} + 2\sum_{k=1}^{\infty}\mathrm{Cov}\{g(\boldsymbol{\theta}_t), g(\boldsymbol{\theta}_{t+k})\} \tag{7}$$

and needs to be approximated. Moreover, the conditions needed for the central limit theorem to hold involve the convergence rate of the chain and can be difficult to check in practice (Tierney 1994).

The Monte Carlo integration method solves the problem of Bayesian computation of computing a posterior distribution by sampling from that posterior distribution. The latter has been an important problem in computational statistics and a focus of intense research. Rejection sampling techniques serve as basic tools for generating samples from a general probability distribution (von Neumann 1951). They are based on the idea that samples from the target distribution can be obtained from another, easy-to-sample distribution according to some acceptance–rejection rule for the samples from this distribution. It was soon recognized, however, that the acceptance–rejection methods did not scale well with the increase of dimensions, a problem known as the "curse of dimensionality", essentially reducing the acceptance probability to zero. An alternative solution was to use the Markov chains to generate sequences of correlated sample points from the domain of the target distribution and keeping a reasonable rate of acceptance. It was not long before Markov chain Monte Carlo methods were accepted as effective tools for approximate sampling from general posterior distributions (Tanner and Wong 1987).

Markov chain Monte Carlo methods

Every MCMC method is designed to generate values from a transition kernel such that the draws from that kernel converge to a prespecified target distribution. It simulates a Markov chain with the target distribution as the stationary or equilibrium distribution of the chain. By definition, a Markov chain is any sequence of values or states from the domain of the target distribution, such that each value depends on its immediate predecessor only. For a well-designed MCMC, the longer the chain, the closer the samples to the stationary distribution. MCMC methods differ substantially in their simulation efficiency and computational complexity.

The Metropolis algorithm proposed in Metropolis and Ulam (1949) and Metropolis et al. (1953) appears to be the earliest version of MCMC. The algorithm generates a sequence of states, each obtained from the previous one, according to a Gaussian proposal distribution centered at that state. Hastings (1970) described a more-general version of the algorithm, now known as a Metropolis–Hastings (MH) algorithm, which allows any distribution to be used as a proposal distribution. Below we review the general MH algorithm and some of its special cases.

Metropolis–Hastings algorithm

Here we present the MH algorithm for sampling from a posterior distribution in a general formulation. It requires the specification of a proposal probability distribution $q(\cdot)$ and a starting state $\boldsymbol{\theta}_0$ within the domain of the posterior, that is, $p(\boldsymbol{\theta}_0|\mathbf{y}) > 0$. The algorithm generates a Markov chain $\{\boldsymbol{\theta}_t\}_{t=0}^{T-1}$ such that at each step t 1) a proposal state $\boldsymbol{\theta}_*$ is generated conditional on the current state, and 2) $\boldsymbol{\theta}_*$ is accepted or rejected according to the suitably defined acceptance probability.

For $t = 1, \ldots, T-1$:

1. Generate a proposal state: $\boldsymbol{\theta}_* \sim q(\cdot|\boldsymbol{\theta}_{t-1})$.
2. Calculate the acceptance probability $\alpha(\boldsymbol{\theta}_*|\boldsymbol{\theta}_{t-1}) = \min\{r(\boldsymbol{\theta}_*|\boldsymbol{\theta}_{t-1}), 1\}$, where

$$r(\boldsymbol{\theta}_*|\boldsymbol{\theta}_{t-1}) = \frac{p(\boldsymbol{\theta}_*|\mathbf{y})q(\boldsymbol{\theta}_{t-1}|\boldsymbol{\theta}_*)}{p(\boldsymbol{\theta}_{t-1}|\mathbf{y})q(\boldsymbol{\theta}_*|\boldsymbol{\theta}_{t-1})}$$

3. Draw $u \sim \text{Uniform}(0, 1)$.
4. Set $\boldsymbol{\theta}_t = \boldsymbol{\theta}_*$ if $u < \alpha(\boldsymbol{\theta}_*|\boldsymbol{\theta}_{t-1})$, and $\boldsymbol{\theta}_t = \boldsymbol{\theta}_{t-1}$ otherwise.

We refer to the iteration steps 1 through 4 as an MH update. By design, any Markov chain simulated using this MH algorithm is guaranteed to have $p(\boldsymbol{\theta}|\mathbf{y})$ as its stationary distribution.

Two important criteria measuring the efficiency of MCMC are the acceptance rate of the chain and the degree of autocorrelation in the generated sample. When the acceptance rate is close to 0, then most of the proposals are rejected, which means that the chain failed to explore regions of appreciable posterior probability. The other extreme is when the acceptance probability is close to 1, in which case the chain stays in a small region and fails to explore the whole posterior domain. An efficient MCMC has an acceptance rate that is neither too small nor too large and also has small autocorrelation. Gelman, Gilks, and Roberts (1997) showed that in the case of a multivariate posterior and proposal distributions, an acceptance rate of 0.234 is asymptotically optimal and, in the case of a univariate posterior, the optimal value is 0.45.

A special case of MH employs a Metropolis update with $q(\cdot)$ being a symmetric distribution. Then, the acceptance ratio reduces to a ratio of posterior probabilities,

$$r(\boldsymbol{\theta}_*|\boldsymbol{\theta}_{t-1}) = \frac{p(\boldsymbol{\theta}_*|\mathbf{y})}{p(\boldsymbol{\theta}_{t-1}|\mathbf{y})}$$

The symmetric Gaussian distribution is a common choice for a proposal distribution $q(\cdot)$, and this is the one used in the original Metropolis algorithm.

Another important MCMC method that can be viewed as a special case of MH is Gibbs sampling (Gelfand et al. 1990), where the updates are the full conditional distributions of each parameter given the rest of the parameters. Gibbs updates are always accepted. If $\boldsymbol{\theta} = (\theta^1, \dots, \theta^d)$ and, for $j = 1 \dots, d$, q_j is the conditional distribution of θ^j given the rest $\boldsymbol{\theta}^{\{-j\}}$, then the Gibbs algorithm is the following. For $t = 1, \dots, T-1$ and for $j = 1, \dots, d$: $\theta^j_t \sim q_j(\cdot|\boldsymbol{\theta}^{\{-j\}}_{t-1})$. This step is referred to as a Gibbs update.

All MCMC methods share some limitations and potential problems. First, any simulated chain is influenced by its starting values, especially for short MCMC runs. It is required that the starting point has a positive posterior probability, but even when this condition is satisfied, if we start somewhere in a remote tail of the target distribution, it may take many iterations to reach a region of appreciable probability. Second, because there is no obvious stopping criterion, it is not easy to decide for how long to run the MCMC algorithm to achieve convergence to the target distribution. Third, the observations in MCMC samples are strongly dependent and this must be taken into account in any subsequent statistical inference. For example, the errors associated with the Monte Carlo integration should be calculated according to (7), which accounts for autocorrelation.

Adaptive random-walk Metropolis–Hastings

The choice of a proposal distribution $q(\cdot)$ in the MH algorithm is crucial for the mixing properties of the resulting Markov chain. The problem of determining an optimal proposal for a particular target posterior distribution is difficult and is still being researched actively. All proposed solutions are based on some form of an adaptation of the proposal distribution as the Markov chain progresses, which is carefully designed to preserve the ergodicity of the chain, that is, its tendency to converge to the target distribution. These methods are known as adaptive MCMC methods (Haario, Saksman, and Tamminen [2001]; Giordani and Kohn [2010]; and Roberts and Rosenthal [2009]).

The majority of adaptive MCMC methods are random-walk MH algorithms with updates of the form: $\boldsymbol{\theta}_* = \boldsymbol{\theta}_{t-1} + Z_t$, where Z_t follows some symmetric distribution. Specifically, we consider a Gaussian random-walk MH algorithm with $Z_t \sim N(0, \rho^2\Sigma)$, where ρ is a scalar controlling the scale of random jumps for generating updates and Σ is a d-dimensional covariance matrix. One of the first important results regarding adaptation is from Gelman, Gilks, and Roberts (1997), where the authors derive the optimal scaling factor $\rho = 2.38/\sqrt{d}$ and note that the optimal Σ is the true covariance matrix of the target distribution.

Haario, Saksman, and Tamminen (2001) proposes Σ to be estimated by the empirical covariance matrix plus a small diagonal matrix $\epsilon \times I_d$ to prevent zero covariance matrices. Alternatively, Roberts and Rosenthal (2009) proposed a mixture of the two covariance matrices,

$$\Sigma_t = \beta\widehat{\Sigma} + (1-\beta)\Sigma_0$$

for some fixed covariance matrix Σ_0 and $\beta \in [0, 1]$.

Because the proposal distribution of an adaptive MH algorithm changes at each step, the ergodicity of the chain is not necessarily preserved. However, under certain assumptions about the adaptation procedure, the ergodicity does hold; see Roberts and Rosenthal (2007), Andrieu and Moulines (2006), Atchadé and Rosenthal (2005), and Giordani and Kohn (2010) for details.

Blocking of parameters

In the original MH algorithm, the update steps of generating proposals and applying the acceptance–rejection rule are performed for all model parameters simultaneously. For high-dimensional models, this may result in a poor mixing—the Markov chain may stay in the tails of the posterior distribution for long periods of time and traverse the posterior domain very slowly. Suboptimal mixing is manifested by either very high or very low acceptance rates. Adaptive MH algorithms are also prone to this problem, especially when model parameters have very different scales. An effective solution to this problem is called *blocking*—model parameters are separated into two or more subsets or blocks and MH updates are applied to each block separately in the order that the blocks are specified.

Let's separate a vector of parameters into B blocks: $\boldsymbol{\theta} = \{\boldsymbol{\theta}^1, \dots, \boldsymbol{\theta}^B\}$. The version of the Gaussian random-walk MH algorithm with blocking is as follows.

Let T_0 be the number of burn-in iterations, T be the number of MCMC samples, and $\rho_b^2\Sigma^b$, $b = 1, \dots, B$, be block-specific proposal covariance matrices. Let $\boldsymbol{\theta}_0$ be the starting point within the domain of the posterior, that is, $p(\boldsymbol{\theta}_0|\mathbf{y}) > 0$.

1. At iteration t, let $\boldsymbol{\theta}_t = \boldsymbol{\theta}_{t-1}$.

2. For a block of parameters $\boldsymbol{\theta}_t^b$:

   2.1. Let $\boldsymbol{\theta}_* = \boldsymbol{\theta}_t$. Generate a proposal for the bth block: $\boldsymbol{\theta}_*^b = \boldsymbol{\theta}_{t-1}^b + \epsilon$, where $\epsilon \sim N(0, \rho_b^2\Sigma^b)$.

   2.2. Calculate the acceptance ratio,

   $$r(\boldsymbol{\theta}_*|\boldsymbol{\theta}_t) = \frac{p(\boldsymbol{\theta}_*|\mathbf{y})}{p(\boldsymbol{\theta}_t|\mathbf{y})}$$

   where $\theta_* = (\boldsymbol{\theta}_t^1, \boldsymbol{\theta}_t^2, \dots, \boldsymbol{\theta}_t^{b-1}, \boldsymbol{\theta}_*^b, \boldsymbol{\theta}_t^{b+1}, \dots, \boldsymbol{\theta}_t^B)$.

   2.3. Draw $u \sim \text{Uniform}(0, 1)$.

   2.4. Let $\boldsymbol{\theta}_t^b = \boldsymbol{\theta}_*^b$ if $u < \min\{r(\boldsymbol{\theta}_*|\boldsymbol{\theta}_t), 1\}$.

3. Repeat step 2 for $b = 1, \dots, B$.

4. Repeat steps 1 through 3 for $t = 1, \dots, T + T_0 - 1$.

5. The final sequence is $\{\boldsymbol{\theta}_t\}_{t=T_0}^{T+T_0-1}$.

Blocking may not always improve efficiency. For example, separating all parameters in individual blocks (the so-called one-at-a-time update regime) can lead to slow mixing when some parameters are highly correlated. A Markov chain may explore the posterior domain very slowly if highly correlated parameters are updated independently. There are no theoretical results about optimal blocking, so you will need to use your judgment when determining the best set of blocks for your model. As a rule, parameters that are expected to be highly correlated are specified in one block. This will generally improve mixing of the chain unless the proposal correlation matrix does not capture the actual correlation structure of the block. For example, if there are two parameters in the block that have very different scales, adaptive MH algorithms that use the identity matrix for the initial proposal covariance may take a long time to approximate the optimal proposal correlation matrix. The user should, therefore, consider not only the probabilistic relationship between the parameters in the model, but also their scales to determine an optimal set of blocks.

Metropolis–Hastings with Gibbs updates

The original Gibbs sampler updates each model parameter one at a time according to its full conditional distribution. We have already noted that Gibbs is a special case of the MH algorithm. Some of the advantages of Gibbs sampling include its high efficiency, because all proposals are automatically accepted, and that it does not require any additional tuning for proposal distributions in MH algorithms. Unfortunately, for most posterior distributions in practice, the full conditionals are either not available or are very difficult to sample from. It may be the case, however, that for some model parameters or groups of parameters, the full conditionals are available and are easy to generate samples from. This is done in a hybrid MH algorithm, which implements Gibbs updates for only some blocks of parameters. A hybrid MH algorithm combines Gaussian random-walk updates with Gibbs updates to improve the mixing of the chain.

The MH algorithm with blocking allows different samplers to be used for updating different blocks. If there is a group of model parameters with a conjugate prior (or semiconjugate prior), we can place this group of parameters in a separate block and use Gibbs sampling for it. This can greatly improve the overall sampling efficiency of the algorithm.

For example, suppose that the data are normally distributed with a known mean μ and that we specify an inverse-gamma prior for σ^2 with shape α and scale β, which are some fixed constants.

$$y \sim N(\mu, \sigma^2), \quad \sigma^2 \sim \text{InvGamma}(\alpha,\ \beta)$$

The full conditional distribution for σ^2 in this case is also an inverse-gamma distribution, but with different shape and scale parameters,

$$\sigma^2 \sim \text{InvGamma}\left\{\widetilde{\alpha} = \alpha + \frac{n}{2},\ \widetilde{\beta} = \beta + \frac{1}{2}\sum_{i=1}^{n}(y_i - \mu)^2\right\}$$

where n is the data sample size. So, an inverse-gamma prior for the variance is a conjugate prior in this model. We can thus place σ^2 in a separate block and set up a Gibbs sampling for it using the above full conditional distribution.

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

Convergence diagnostics of MCMC

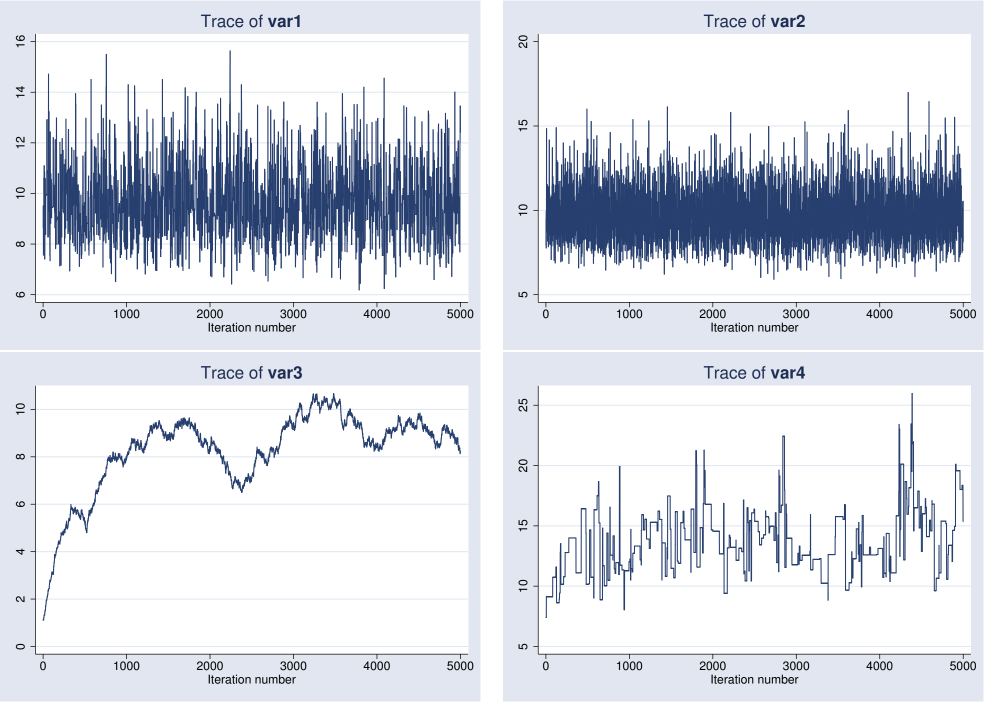
Checking convergence of MCMC is an essential step in any MCMC simulation. Bayesian inference based on an MCMC sample is valid only if the Markov chain has converged and the sample is drawn from the desired posterior distribution. It is important that we verify the convergence for all model parameters and not only for a subset of parameters of interest. One difficulty with assessing convergence of MCMC is that there is no 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.

The most extensive review of the methods for assessing convergence is Cowles and Carlin (1996). Other discussions about monitoring convergence can be found in Gelman et al. (2014) and Brooks et al. (2011).

There are at least two general approaches for detecting convergence issues. The first one is to inspect the mixing and time trends within the chains of individual parameters. The second one is to examine the mixing and time trends of multiple chains for each parameter. The lack of convergence in a Markov chain can be especially difficult to detect in a case of pseudoconvergence, which often occurs with multimodal posterior distributions. Pseudoconvergence occurs when the chain appears to have converged but it actually explored only a portion of the domain of a posterior distribution. To check for pseudoconvergence, Gelman and Rubin (1992) recommend running multiple chains from different starting states and comparing them.

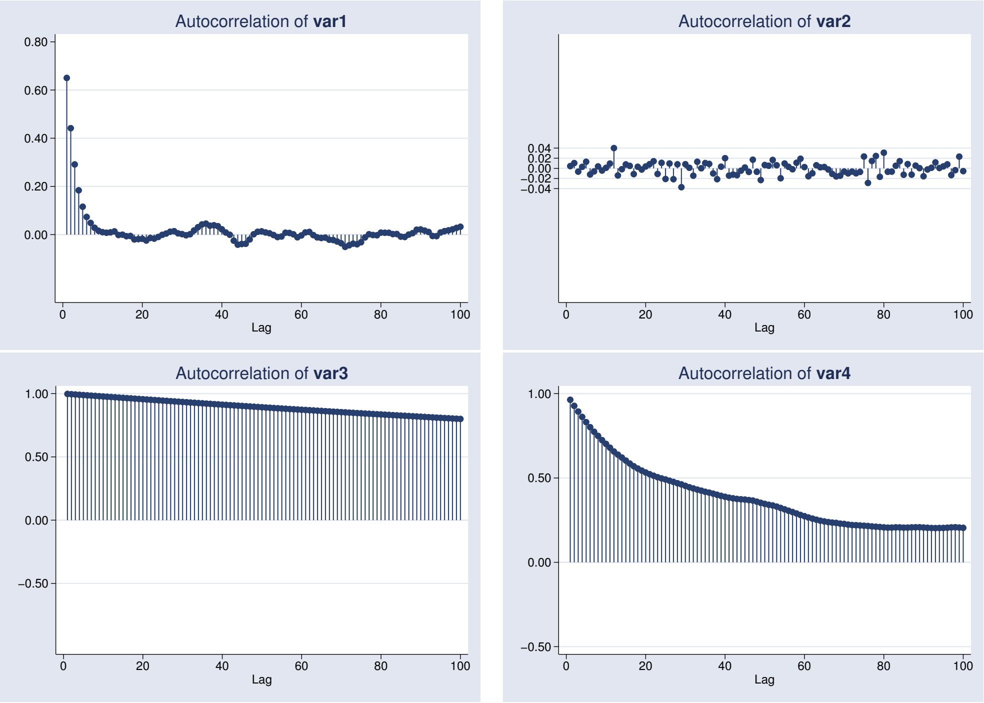
Trace plots are the most accessible convergence diagnostics and are easy to inspect visually. The trace plot of a parameter plots the simulated values for this parameter versus the iteration number. The trace plot of a well-mixing parameter should traverse the posterior domain rapidly and should have nearly constant mean and variance.

In the next figure, we show examples of trace plots for four parameters: `var1`, `var2`, `var3`, and `var4`. The first two parameters, `var1` and `var2`, have well-mixing chains, and the other two have poorly mixing chains. The chain for the parameter `var1` has a moderate acceptance rate, about 35%, and efficiency between 10% and 20%. This is a typical result for a Gaussian random-walk MH algorithm that has achieved convergence. The trace plot of `var2` in the top right panel shows almost perfect mixing—this is a typical example of Gibbs sampling with an acceptance rate close to 1 and efficiency above 95%. Although both chains traverse their marginal posterior domains, the right one does it more rapidly. On the downside, more efficient MCMC algorithms such as Gibbs sampling are usually associated with a higher computational cost.

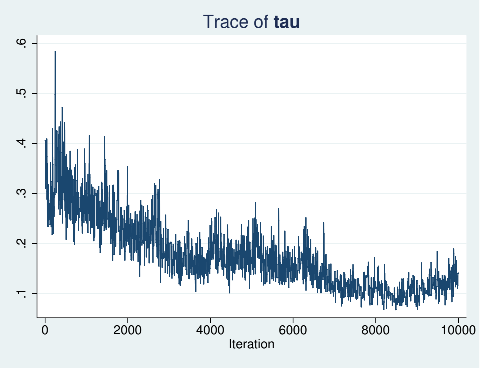


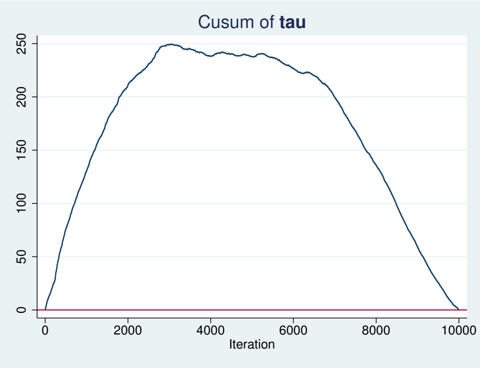
The bottom two trace plots illustrate cases of bad mixing and a lack of convergence. On the left, the chain for `var3` exhibits high acceptance rate but poor coverage of the posterior domain manifested by random drifting in isolated regions. This chain was produced by a Gaussian random-walk MH algorithm with a proposal distribution with a very small variance. On the right, the chain for the parameter `var4` has a very low acceptance rate, below 3%, because the used proposal distribution had a very large variance. In both cases, the chains do not converge; the simulation results do not represent the posterior distribution and should thus be discarded.

As we stated before, samples simulated using MCMC methods are correlated. The smaller the correlation, the more efficient the sampling process. Most of the MH algorithms typically generate highly correlated draws, whereas the Gibbs algorithm typically generates less-correlated draws. Below we show autocorrelation plots for the same four parameters using the same MCMC samples. The autocorrelation of `var1`, the one that comes from a well-mixing MH chain, becomes negligible fairly quickly, after about 10 lags. On the other hand, the autocorrelation of `var2` simulated using Gibbs sampling is essentially negligible for all positive lags. In the case of a poor mixing because of a small proposal variance (parameter `var3`), we observe very high positive correlation for at least 100 lags. The autocorrelation of `var4` is high but is lower than that of `var3`.

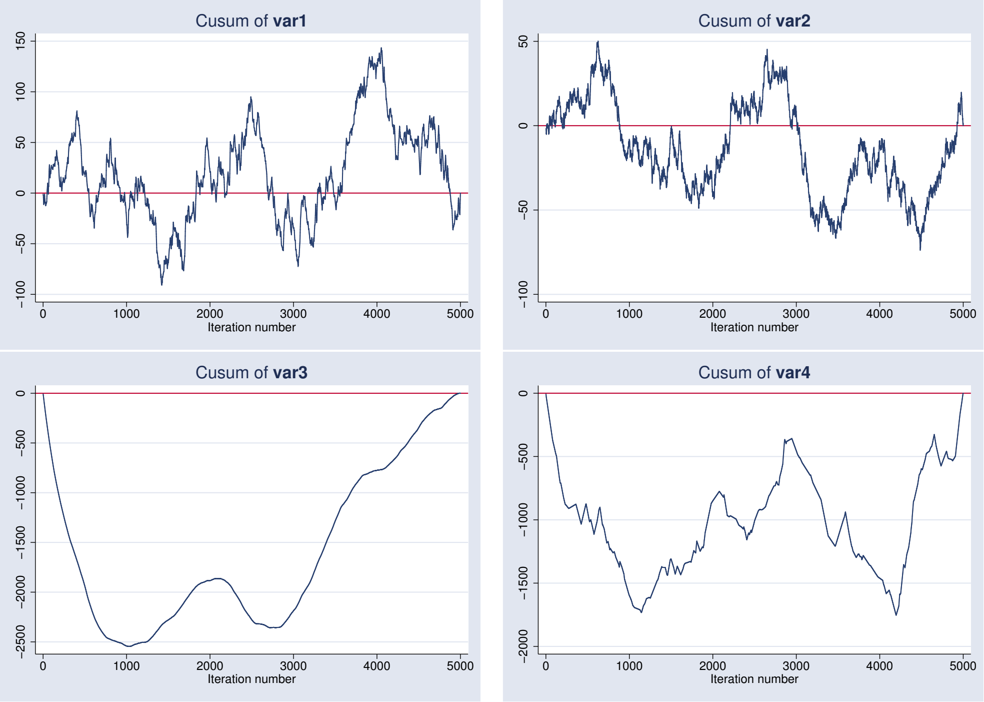


Yu and Mykland (1998) proposed a graphical procedure for assessing the convergence of individual parameters based on cumulative sums, also known as a cusum plot. By definition, any cusum plot starts at 0 and ends at 0. Cusum plots are useful for detecting drifts in the chain. For a chain without trend, the cusum plot should cross the x axis. For example, early drifts may indicate dependence on starting values. If we detect an early drift, we should discard an initial part of the chain and run it longer. Below, we show the trace plot of a poorly mixing parameter `tau` and its corresponding cusum plot on the right. There is an apparent positive drift for approximately the first half of the chain followed by the drift in the negative direction. As a result, the cusum plot has a distinctive mountain-like shape and never crosses the x axis.





Cusum plots can be also used for assessing how fast the chain is mixing. The slower the mixing of the chain, the smoother the cusum plots. Conversely, the faster the mixing of the chain, the more jagged the cusum plots. Below, we demonstrate the cusum plots for the four variables considered previously. We can clearly see the contrast between the jagged lines of the fast mixing parameters `var1` and `var2` and the very smooth cusum line of the poorly mixing parameter `var3`.



Besides graphical convergence diagnostics, there are some formal convergence tests (Geweke [1992]; Gelman and Rubin [1992]; Heidelberger and Welch [1983]; Raftery and Lewis [1992]; Zellner and Min [1995]).

Summary

Bayesian analysis is a statistical procedure that answers research questions by expressing uncertainty about unknown parameters using probabilities. Bayesian inference is based on the posterior distribution of model parameters conditional on the observed data. The posterior distribution is composed of a likelihood distribution of the data and the prior distribution of the model parameters. The likelihood model is specified in the same way it is specified with any standard likelihood-based analysis. The prior distribution is constructed based on the prior (before observing the data) scientific knowledge and results from previous studies. Sensitivity analysis is typically performed to evaluate the influence of different competing priors on the results.

Many posterior distributions do not have a closed form and must be simulated using MCMC methods such as MH methods or the Gibbs method or sometimes their combination. The convergence of MCMC must be verified before any inference can be made.

Marginal posterior distributions of the parameters are used for inference. These are summarized using point estimators such as posterior mean and median and interval estimators such as equal-tailed credible intervals and highest posterior density intervals. Credible intervals have an intuitive interpretation as fixed ranges to which a parameter is known to belong with a prespecified probability. Hypothesis testing provides a way to assign an actual probability to any hypothesis of interest. A number of criteria are available for comparing models of interest. Predictions are also available based on the posterior predictive distribution.

Bayesian analysis provides many advantages over the standard frequentist analysis, such as an ability to incorporate prior information in the analysis, higher robustness to sparse data, more-comprehensive inference based on the knowledge of the entire posterior distribution, and more intuitive and direct interpretations of results by using probability statements about parameters.

Video examples

Introduction to Bayesian analysis, part 1: The basic concepts

Introduction to Bayesian analysis, part 2: MCMC and the Metropolis–Hastings algorithm

Thomas Bayes (1701(?)–1761) was a Presbyterian minister with an interest in calculus, geometry, and probability theory. He was born in Hertfordshire, England. The son of a Nonconformist minister, Bayes was banned from English universities and so studied at Edinburgh University before becoming a clergyman himself. Only two works are attributed to Bayes during his lifetime, both published anonymously. He was admitted to the Royal Society in 1742 and never published thereafter.

The paper that gives us "Bayes's Theorem" was published posthumously by Richard Price. The theorem has become an important concept for frequentist and Bayesian statisticians alike. However, the paper indicates that Bayes considered the theorem as relatively unimportant. His main interest appears to have been that probabilities were not fixed but instead followed some distribution. The notion, now foundational to Bayesian statistics, was largely ignored at the time.

Whether Bayes's theorem is appropriately named is the subject of much debate. Price acknowledged that he had written the paper based on information he found in Bayes's notebook, yet he never said how much he added beyond the introduction. Some scholars have also questioned whether Bayes's notes represent original work or are the result of correspondence with other mathematicians of the time.

Andrey Markov (1856–1922) was a Russian mathematician who made many contributions to mathematics and statistics. He was born in Ryazan, Russia. In primary school, he was known as a poor student in all areas except mathematics. Markov attended St. Petersburg University, where he studied under Pafnuty Chebyshev and later joined the physicomathematical faculty. He was a member of the Russian Academy of the Sciences.

Markov's first interest was in calculus. He did not start his work in probability theory until 1883 when Chebyshev left the university and Markov took over his teaching duties. A large and influential body of work followed, including applications of the weak law of large numbers and what are now known as Markov processes and Markov chains. His work on processes and chains would later influence the development of a variety of disciplines such as biology, chemistry, economics, physics, and statistics.

Known in the Russian press as the "militant academician" for his frequent written protests about the czarist government's interference in academic affairs, Markov spent much of his adult life at odds with Russian authorities. In 1908, he resigned from his teaching position in response to a government requirement that professors report on students' efforts to organize protests in the wake of the student riots earlier that year. He did not resume his university teaching duties until 1917, after the Russian Revolution. His trouble with Russian authorities also extended to the Russian Orthodox Church. In 1912, he was excommunicated at his own request in protest over the Church's excommunication of Leo Tolstoy.

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Also see

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

[BAYES] **Glossary**

Title

bayesian commands — Introduction to commands for Bayesian analysis

Description Remarks and examples Acknowledgments References
Also see

Description

This entry describes commands to perform Bayesian analysis. Bayesian analysis is a statistical procedure that answers research questions by expressing uncertainty about unknown parameters using probabilities. It is based on the fundamental assumption that not only the outcome of interest but also all the unknown parameters in a statistical model are essentially random and are subject to prior beliefs.

Estimation

`bayesian estimation`	Bayesian estimation commands
`bayes`	Bayesian regression models using the `bayes` prefix
`bayesmh`	Bayesian models using MH
`bayesmh evaluators`	User-defined Bayesian models using MH

Convergence tests and graphical summaries

`bayesgraph`	Graphical summaries

Postestimation statistics

`bayesstats ess`	Effective sample sizes and related statistics
`bayesstats summary`	Bayesian summary statistics
`bayesstats ic`	Bayesian information criteria and Bayes factors

Hypothesis testing

`bayestest model`	Hypothesis testing using model posterior probabilities
`bayestest interval`	Interval hypothesis testing

Remarks and examples

This entry describes commands to perform Bayesian analysis. See [BAYES] **intro** for an introduction to the topic of Bayesian analysis.

Bayesian estimation in Stata can be as easy as prefixing your estimation command with the `bayes` prefix ([BAYES] **bayes**). For example, if your estimation command is a linear regression of `y` on `x`

```
. regress y x
```

then Bayesian estimates for this model can be obtained by typing

```
. bayes: regress y x
```

See [BAYES] **bayesian estimation** for a list of estimation commands that work with the `bayes` prefix.

In addition to the bayes prefix, there is a general-purpose Bayesian estimation command—the bayesmh command ([BAYES] **bayesmh**). bayesmh fits a variety of Bayesian models including multiple-equation linear and nonlinear models and, like the bayes prefix, estimates parameters using an adaptive MH Markov chain Monte Carlo (MCMC) method. You can choose from a variety of supported Bayesian models by specifying the likelihood() and prior() options. Or you can program your own Bayesian models by supplying a program evaluator for the posterior distributions of model parameters in the evaluator() option; see [BAYES] **bayesmh evaluators** for details.

After estimation, you can use bayesgraph to check convergence of MCMC visually. You can also use bayesstats ess to compute effective sample sizes and related statistics for model parameters and functions of model parameters to assess the efficiency of the sampling algorithm and autocorrelation in the obtained MCMC sample. Balov (2016) shows how to compute the Gelman–Rubin convergence statistic using multiple chains. Once convergence is established, you can use bayesstats summary to obtain Bayesian summaries such as posterior means and standard deviations of model parameters and functions of model parameters and bayesstats ic to compute Bayesian information criteria and Bayes factors for models. You can use bayestest model to test hypotheses by comparing posterior probabilities of models. You can also use bayestest interval to test interval hypotheses about parameters and functions of parameters.

Below we provide an overview example demonstrating the Bayesian suite of commands. In this entry, we mainly concentrate on the general command, bayesmh. For examples of using the simpler bayes prefix, see example 10 and *Remarks and examples* in [BAYES] **bayes**. Also, for more examples of bayesmh, see *Remarks and examples* in [BAYES] **bayesmh**.

Overview example

Consider an example from Kuehl (2000, 551) about the effects of exercise on oxygen uptake. The research objective is to compare the impact of the two exercise programs—12 weeks of step aerobic training and 12 weeks of outdoor running on flat terrain—on maximal oxygen uptake. Twelve healthy men were randomly assigned to one of the two groups, the “aerobic” group or the “running” group. Their changes in maximal ventilation (liters/minute) of oxygen for the 12-week period were recorded.

oxygen.dta contains 12 observations of changes in maximal ventilation of oxygen, recorded in variable change, from two groups, recorded in variable group. Additionally, ages of subjects are recorded in variable age, and an interaction between age and group is stored in variable interaction.

```
. use http://www.stata-press.com/data/r15/oxygen
(Oxygen Uptake Data)

. describe

Contains data from http://www.stata-press.com/data/r15/oxygen.dta
  obs:            12                          Oxygen Uptake Data
 vars:             4                          20 Jan 2016 15:56
 size:            84                          (_dta has notes)
───────────────────────────────────────────────────────────────────────────────
              storage   display    value
variable name   type    format     label      variable label
───────────────────────────────────────────────────────────────────────────────
change          float   %9.0g                 Change in maximal oxygen uptake
                                                (liters/minute)
group           byte    %8.0g      grouplab   Exercise group (0: Running, 1:
                                                Aerobic)
age             byte    %8.0g                 Age (years)
ageXgr          byte    %9.0g                 Interaction between age and group
───────────────────────────────────────────────────────────────────────────────
Sorted by:
```

Kuehl (2000) uses analysis of covariance to analyze these data. We use linear regression instead,

$$\texttt{change} = \beta_0 + \beta_{\rm group}\texttt{group} + \beta_{\rm age}\texttt{age} + \epsilon$$

where ϵ is a random error with zero mean and variance σ^2. Also see Hoff (2009) for Bayesian analysis of these data.

Examples are presented under the following headings:

Example 1: OLS
Example 2: Bayesian normal linear regression with noninformative prior
Example 3: Bayesian linear regression with informative prior
Example 4: Bayesian normal linear regression with multivariate prior
Example 5: Checking convergence
Example 6: Postestimation summaries
Example 7: Model comparison
Example 8: Hypothesis testing
Example 9: Erasing simulation datasets
Example 10: Bayesian linear regression using the bayes prefix

▷ Example 1: OLS

Let's fit OLS regression to our data first.

```
. regress change group age
      Source |       SS           df       MS      Number of obs   =        12
-------------+----------------------------------   F(2, 9)         =     41.42
       Model |  647.874893         2  323.937446   Prob > F        =    0.0000
    Residual |   70.388768         9  7.82097423   R-squared       =    0.9020
-------------+----------------------------------   Adj R-squared   =    0.8802
       Total |  718.263661        11  65.2966964   Root MSE        =    2.7966

------------------------------------------------------------------------------
      change |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       group |   5.442621   1.796453     3.03   0.014     1.378763    9.506479
         age |   1.885892    .295335     6.39   0.000     1.217798    2.553986
       _cons |   -46.4565   6.936531    -6.70   0.000    -62.14803   -30.76498
------------------------------------------------------------------------------
```

From the table, both `group` and `age` are significant predictors of the outcome in this model.

For example, we reject the hypothesis of H_0: $\beta_{\rm group} = 0$ at a 5% level based on the p-value of 0.014. The actual interpretation of the reported p-value is that if we repeat the same experiment and use the same testing procedure many times, then given our null hypothesis of no effect of group, we will observe the result (test statistic) as extreme or more extreme than the one observed in this sample (`t` $= 3.03$) only 1.4% of the times. The p-value cannot be interpreted as a probability of the null hypothesis, which is a common misinterpretation. In fact, it answers the question of how likely our data are, given that the null hypothesis is true, and not how likely the null hypothesis is, given our data. The latter question can be answered using Bayesian hypothesis testing, which we demonstrate in example 8.

Confidence intervals are popular alternatives to p-values that eliminate some of the p-value shortcomings. For example, the 95% confidence interval for the coefficient for `group` is [1.38, 9.51] and does not contain the value of 0, so we consider `group` to be a significant predictor of `change`. The interpretation of a 95% confidence interval is that if we repeat the same experiment many times and compute confidence intervals for each experiment, then 95% of those intervals will contain the true value of the parameter. Thus we cannot conclude that the true coefficient for `group` lies between 1.38 and 9.51 with a probability of 0.95—a common misinterpretation of a confidence interval. This probability is either 0 or 1, and we do not know which for any particular confidence interval. All we know is that [1.38, 9.51] is a plausible range for the true value of the coefficient for group. Intervals that can actually be interpreted as probabilistic ranges for a parameter of interest may be constructed within the Bayesian paradigm; see example 8.

◁

▷ Example 2: Bayesian normal linear regression with noninformative prior

In example 1, we stated that frequentist methods cannot provide probabilistic summaries for the parameters of interest. This is because in frequentist statistics, parameters are viewed as unknown but fixed quantities. The only random quantity in a frequentist model is an outcome of interest. Bayesian statistics, on the other hand, in addition to the outcome of interest, also treats all model parameters as random quantities. This is what sets Bayesian statistics apart from frequentist statistics and enables one to make probability statements about the likely values of parameters and to assign probabilities to hypotheses of interest.

Bayesian statistics focuses on the estimation of various aspects of the posterior distribution of a parameter of interest, an initial or a prior distribution that has been updated with information about a parameter contained in the observed data. A posterior distribution is thus described by the prior distribution of a parameter and the likelihood function of the data given the parameter.

Let's now fit a Bayesian linear regression to oxygen.dta. To fit a Bayesian parametric model, we need to specify the likelihood function or the distribution of the data and prior distributions for all model parameters. Our Bayesian linear model has four parameters: three regression coefficients and the variance of the data. We assume a normal distribution for our outcome, change, and start with a noninformative Jeffreys prior for the parameters. Under the Jeffreys prior, the joint prior distribution of the coefficients and the variance is proportional to the inverse of the variance.

We can write our model as follows,

$$\begin{aligned}\texttt{change} &\sim N(X\boldsymbol{\beta}, \sigma^2)\\ (\boldsymbol{\beta}, \sigma^2) &\sim \frac{1}{\sigma^2}\end{aligned}$$

where X is our design matrix, and $\boldsymbol{\beta} = (\beta_0, \beta_{\text{group}}, \beta_{\text{age}})'$, which is a vector of coefficients.

We use the bayesmh command to fit our Bayesian model. Let's consider the specification of the model first.

```
bayesmh change group age, likelihood(normal({var}))    ///
     prior({change:}, flat) prior({var}, jeffreys)
```

The specification of the regression function in bayesmh is the same as in any other Stata regression command—the name of the dependent variable follows the command, and the covariates of interest are specified next. Likelihood or outcome distribution is specified in the likelihood() option, and prior distributions are specified in the prior() options, which are repeated options.

All model parameters must be specified in curly braces, {}. bayesmh automatically creates parameters associated with the regression function—regression coefficients—but it is your responsibility to define the remaining model parameters. In our example, the only parameter we need to define is the variance parameter, which we define as {var}. The three regression coefficients {change:group}, {change:age}, and {change:_cons} are automatically created by bayesmh.

The last step is to specify the likelihood and the prior distributions. bayesmh provides several different built-in distributions for the likelihood and priors. If a certain distribution is not available or you have a particularly complicated Bayesian model, you may consider writing your own evaluator for the posterior distribution; see [BAYES] **bayesmh evaluators** for details. In our example, we specify distribution normal({var}) in option likelihood() to request the likelihood function of the normal model with the variance parameter {var}. This specification together with the regression specification defines the likelihood model for our outcome change. We assign the flat prior, a prior with a density of 1, to all regression coefficients with prior({change:}, flat), where {change:} is a shortcut for referring to all parameters with equation name change, our regression coefficients. Finally, we specify prior jeffreys for the variance parameter {var} to request the density $1/\sigma^2$.

Let's now run our command. bayesmh uses MCMC sampling, specifically, an adaptive random-walk MH MCMC method, to estimate marginal posterior distributions of parameters. Because bayesmh is using an MCMC method, which is stochastic, we must specify a random-number seed for reproducibility of our results. For consistency and simplicity, we use the same random seed of 14 in all of our examples throughout the manual.

```
. set seed 14

. bayesmh change group age, likelihood(normal({var}))
> prior({change:}, flat) prior({var}, jeffreys)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ normal(xb_change,{var})

Priors:
  {change:group age _cons} ~ 1 (flat)                                      (1)
                     {var} ~ jeffreys
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.

Bayesian normal regression                       MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         12
                                                 Acceptance rate  =      .1371
                                                 Efficiency:  min =     .02687
                                                              avg =     .03765
Log marginal likelihood = -24.703776                          max =     .05724

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
change       |
       group |  5.429677   2.007889   .083928   5.533821   1.157584   9.249262
         age |    1.8873   .3514983   .019534   1.887856   1.184714   2.567883
       _cons | -46.49866    8.32077   .450432   -46.8483  -62.48236  -30.22105
-------------+----------------------------------------------------------------
         var |  10.27946   5.541467   .338079   9.023905   3.980325   25.43771
------------------------------------------------------------------------------
```

First, bayesmh provides a summary for the specified model. It is particularly useful for complicated models with many parameters and hyperparameters. In fact, we recommend that you first specify the dryrun option, which provides only the summary of the model without estimation, to verify the specification of your model and then proceed with estimation. You can then use the nomodelsummary option during estimation to suppress the model summary, which may be rather long.

Next, `bayesmh` provides a header with various model summaries on the right-hand side. It reports the total number of MCMC iterations, 12,500, including the default 2,500 burn-in iterations, which are discarded from the analysis MCMC sample, and the number of iterations retained in the MCMC sample, or MCMC sample size, which is 10,000 by default. These default values should be viewed as initial estimates and further adjusted for the problem at hand to ensure convergence of the MCMC; see example 5.

An acceptance rate and a summary of the parameter-specific efficiencies are also part of the output header. An acceptance rate specifies the proportion of proposed parameter values that was accepted by the algorithm. An acceptance rate of 0.14 in our example means that 14% out of 10,000 proposal parameter values were accepted by the algorithm. For the MH algorithm, this number rarely exceeds 50% and is typically below 30%. A low acceptance rate (for example, below 10%) may indicate convergence problems. In our example, the acceptance rate is a bit low, so we may need to investigate this further. In general, MH tends to have lower efficiencies compared with other MCMC methods. For example, efficiencies of 10% and higher are considered good. Efficiencies below 1% may be a source of concern. The efficiencies are somewhat low in our example, so we may consider tuning our MCMC sampler; see *Improving efficiency of the MH algorithm—blocking of parameters*.

Finally, `bayesmh` reports a table with a summary of the results. The `Mean` column reports the estimates of posterior means, which are means of the marginal posterior distributions of the parameters. The posterior mean estimates are pretty close to the OLS estimates obtained in example 1. This is expected, provided MCMC converged, because we used a noninformative prior. That is, we did not provide any additional information about parameters beyond that contained in the data.

The next column reports estimates of posterior standard deviations, which are standard deviations of the marginal posterior distribution. These values describe the variability in the posterior distribution of the parameter and are comparable to our OLS standard errors.

The precision of the posterior mean estimates is described by their Monte Carlo standard errors. These numbers should be small, relative to the scales of the parameters. Increasing the MCMC sample size should decrease these numbers.

The `Median` column provides estimates of the median of the posterior distribution and can be used to assess the symmetries of the posterior distribution. At a quick glance, the estimates of posterior means and medians are pretty close for the regression coefficients, so we suspect that their posterior distributions may be symmetric.

The last two columns provide credible intervals for the parameters. Unlike confidence intervals, as discussed in example 1, these intervals have a straightforward probabilistic interpretation. For example, the probability that the coefficient for `group` is between 1.16 and 9.25 is about 0.95. The lower bound of the interval is greater than 0, so we conclude that there is an effect of the exercise program on the change in oxygen uptake. We can also use Bayesian hypothesis testing to test effects of parameters; see example 8.

Before any interpretation of the results, however, it is important to verify the convergence of MCMC; see example 5.

See example 10 for how to fit Bayesian linear regression more easily using the `bayes` prefix.

◁

▷ Example 3: Bayesian linear regression with informative prior

In example 2, we considered a noninformative prior for the model parameters. The strength (as well as the weakness) of Bayesian modeling is specifying an informative prior distribution, which may improve results. The strength is that if we have reliable prior knowledge about the distribution of a parameter, incorporating this in our model will improve results and potentially make certain analysis that would not be possible to perform in the frequentist domain feasible. The weakness is that a strong incorrect prior may lead to results that are not supported by the observed data. As with any modeling task, Bayesian or frequentist, a substantive research of the process generating the data and its parameters will be necessary for you to find appropriate models.

Let's consider an informative conjugate prior distribution for our normal regression model.

$$(\boldsymbol{\beta}|\sigma^2) \sim \text{i.i.d. } N(0, \sigma^2)$$
$$\sigma^2 \sim \text{InvGamma}(2.5, 2.5)$$

Here, for simplicity, all coefficients are assumed to be independently and identically distributed as normal with zero mean and variance σ^2, and the variance parameter is distributed according to the above inverse gamma distribution. In practice, a better prior would be to allow each parameter to have a different variance, at least for parameters with different scales.

Let's fit this model using `bayesmh`. Following the model above, we specify the `normal(0,{var})` prior for the coefficients and the `igamma(2.5,2.5)` prior for the variance.

```
. set seed 14

. bayesmh change group age, likelihood(normal({var}))
> prior({change:}, normal(0, {var}))
> prior({var}, igamma(2.5, 2.5))
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ normal(xb_change,{var})

Priors:
  {change:group age _cons} ~ normal(0,{var})                               (1)
                     {var} ~ igamma(2.5,2.5)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.

Bayesian normal regression                       MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         12
                                                 Acceptance rate  =      .1984
                                                 Efficiency:  min =     .03732
                                                              avg =     .04997
Log marginal likelihood = -49.744054                          max =     .06264

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
change       |
       group |  6.510807   2.812828   .129931    6.50829   .9605561   12.23164
         age |  .2710499   .2167863   .009413   .2657002  -.1556194   .7173697
       _cons | -6.838302   4.780343   .191005  -6.683556  -16.53356   2.495631
-------------+----------------------------------------------------------------
         var |  28.83438   10.53573   .545382   26.81462   14.75695    54.1965
------------------------------------------------------------------------------
```

The results from this model are substantially different from the results we obtained in example 2. Considering that we used this simple prior for demonstration purposes only and did not use any external information about model parameters based on prior studies, we would be reluctant to trust the results from this model.

◁

▷ Example 4: Bayesian normal linear regression with multivariate prior

Continuing with informative priors, we will consider Zellner's g-prior (Zellner 1986), which is one of the more commonly used priors for the regression coefficients in a normal linear regression. Hoff (2009) provides more details about this example, and he includes the interaction between age and group as in example 7. Here we concentrate on demonstrating how to fit our model using `bayesmh`.

The mathematical formulation of the priors is the following,

$$
\begin{aligned}
(\boldsymbol{\beta}|\sigma^2) &\sim \text{MVN}(0, g\sigma^2(X'X)^{-1}) \\
\sigma^2 &\sim \text{InvGamma}(\nu_0/2, \nu_0\sigma_0^2/2)
\end{aligned}
$$

where g reflects prior sample size, ν_0 is the prior degrees of freedom for the inverse gamma distribution, and σ_0^2 is the prior variance for the inverse gamma distribution. This prior incorporates dependencies between coefficients. We use values of the parameters similar to those in Hoff (2009): $g = 12$, $\nu_0 = 1$, and $\sigma_0^2 = 8$.

`bayesmh` provides the `zellnersg0()` prior to accommodate the above prior. The first argument is the dimension of the distribution, which is 3 in our example, the second argument is the prior degrees of freedom, which is 12 in our example, and the last argument is the variance parameter, which is `{var}` in our example. The mean is assumed to be a zero vector of the corresponding dimension. (You can use `zellnersg()` if you want to specify a nonzero mean vector; see [BAYES] **bayesmh**.)

```
. set seed 14

. bayesmh change group age, likelihood(normal({var}))
> prior({change:}, zellnersg0(3,12,{var}))
> prior({var}, igamma(0.5, 4))
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ normal(xb_change,{var})

Priors:
  {change:group age _cons} ~ zellnersg(3,12,0,{var})                       (1)
                     {var} ~ igamma(0.5,4)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.

Bayesian normal regression                       MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         12
                                                 Acceptance rate  =     .06169
                                                 Efficiency:  min =      .0165
                                                              avg =     .02018
Log marginal likelihood = -35.356501                          max =     .02159

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
change       |
       group |  4.988881   2.260571   .153837   4.919351   .7793098   9.775568
         age |  1.713159   .3545698   .024216   1.695671   1.053206   2.458556
       _cons | -42.31891   8.239571   .565879  -41.45385  -59.30145  -27.83421
-------------+----------------------------------------------------------------
         var |  12.29575   6.570879   .511475    10.3609   5.636195   30.93576
------------------------------------------------------------------------------
```

These results are more in agreement with results from example 2 than with results of example 3, but our acceptance rate and efficiencies are low and require further investigation.

◁

❑ Technical note

We can reproduce what `zellnersg0()` does above manually. First, we must compute $(X'X)^{-1}$. We can use Stata's matrix functions to do that.

```
. matrix accum xTx = group age
(obs=12)

. matrix S = syminv(xTx)
```

We now specify the desired multivariate normal prior for the coefficients, `mvnormal0(3,12*{var}*S)`. The first argument of `mvnormal0()` specifies the dimension of the distribution, and the second argument specifies the variance–covariance matrix. A mean of zero is assumed for all dimensions. One interesting feature of this specification is that the variance–covariance matrix is specified as a function of `{var}`.

```
. set seed 14

. bayesmh change group age, likelihood(normal({var}))
> prior({change:}, mvnormal0(3,12*{var}*S))
> prior({var}, igamma(0.5, 4))
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ normal(xb_change,{var})

Priors:
  {change:group age _cons} ~ mvnormal(3,0,0,0,12*{var}*S)                  (1)
                     {var} ~ igamma(0.5,4)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.

Bayesian normal regression                       MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         12
                                                 Acceptance rate  =     .06169
                                                 Efficiency:  min =      .0165
                                                              avg =     .02018
Log marginal likelihood = -35.356501                          max =     .02159

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
change       |
       group |  4.988881   2.260571   .153837   4.919351   .7793098   9.775568
         age |  1.713159   .3545698   .024216   1.695671   1.053206   2.458556
       _cons | -42.31891   8.239571   .565879  -41.45385  -59.30145  -27.83421
-------------+----------------------------------------------------------------
         var |  12.29575   6.570879   .511475    10.3609   5.636195   30.93576
------------------------------------------------------------------------------
```

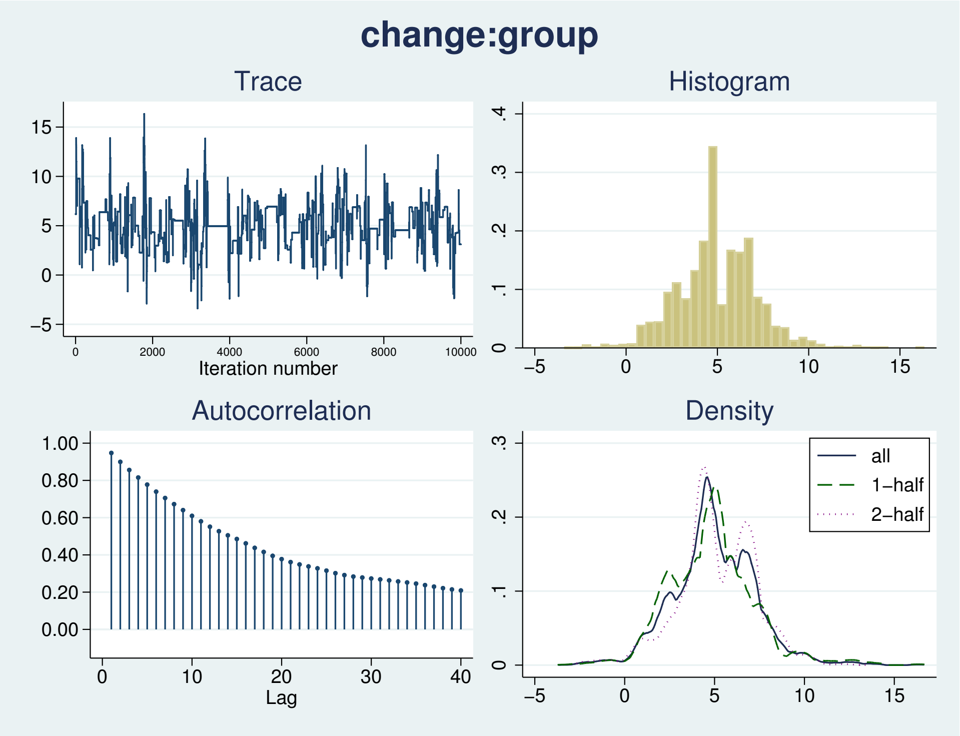
❑

▷ Example 5: Checking convergence

We can use the bayesgraph command to visually check convergence of MCMC of parameter estimates. bayesgraph provides a variety of graphs. For several commonly used visual diagnostics displayed in a compact form, use bayesgraph diagnostics.

For example, we can look at graphical diagnostics for the coefficient for group.

```
. bayesgraph diagnostics {change:group}
```



The displayed diagnostics include a trace plot, an autocorrelation plot, a histogram, and a kernel density estimate overlaid with densities estimated using the first and the second halves of the MCMC sample. Both the trace plot and the autocorrelation plot demonstrate high autocorrelation. The shape of the histogram is not unimodal. We definitely have some convergence issues in this example.

Similarly, we can look at diagnostics for other model parameters. To see all graphs at once, type

```
bayesgraph diagnostics _all
```

Other useful summaries are effective sample sizes and statistics related to them. These can be obtained by using the bayesstats ess command.

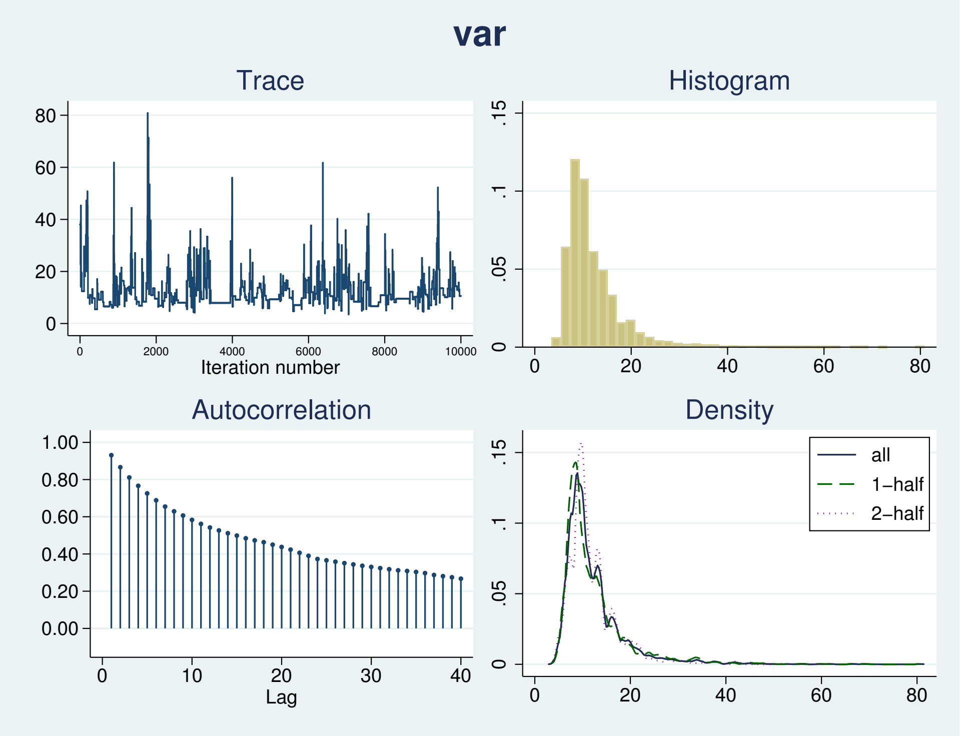
```
. bayesstats ess
Efficiency summaries    MCMC sample size =     10,000
─────────────────────────────────────────────────────
             │        ESS   Corr. time    Efficiency
─────────────┼───────────────────────────────────────
change       │
       group │     215.93        46.31        0.0216
         age │     214.39        46.64        0.0214
       _cons │     212.01        47.17        0.0212
─────────────┼───────────────────────────────────────
         var │     165.04        60.59        0.0165
─────────────────────────────────────────────────────
```

The closer ESS estimates are to the MCMC sample size, the less correlated the MCMC sample is, and the more precise our estimates of parameters are. Do not expect to see values close to the MCMC sample size with the MH algorithm, but values below 1% of the MCMC sample size are certainly red flags. In our example, ESS for {var} is somewhat low, so we may need to look into improving its sampling efficiency. For example, blocking on {var} should improve the efficiency for the variance; see *Improving efficiency of the MH algorithm—blocking of parameters*. It is usually a good idea to sample regression coefficients and the variance in two separate blocks.

Correlation times may be viewed as estimates of autocorrelation lags in the MCMC samples. For example, correlation times of the coefficients range between 46 and 47, and the correlation time for the variance parameter is higher, 61. Consequently, the efficiency for the variance is lower than for the regression coefficients. More investigation of the MCMC for {var} is needed.

Indeed, the MCMC for the variance has very poor mixing and very high autocorrelation.

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



One remedy is to update the variance parameter separately from the regression coefficients by putting the variance parameter in a separate block; see *Improving efficiency of the MH algorithm—blocking of parameters* for details about this procedure. In `bayesmh`, this can be done by specifying the `block()` option.

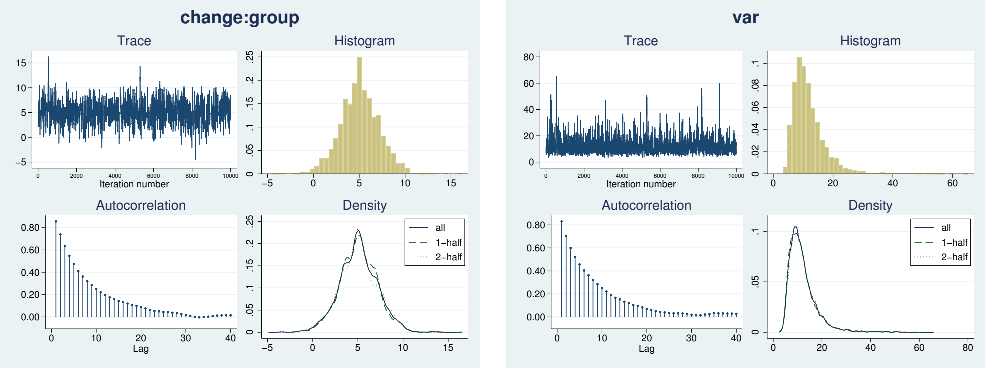
```
. set seed 14

. bayesmh change group age, likelihood(normal({var}))
> prior({change:}, zellnersg0(3,12,{var}))
> prior({var}, igamma(0.5, 4)) block({var})
> saving(agegroup_simdata)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ normal(xb_change,{var})

Priors:
  {change:group age _cons} ~ zellnersg(3,12,0,{var})                       (1)
                     {var} ~ igamma(0.5,4)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.

Bayesian normal regression                       MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         12
                                                 Acceptance rate  =      .3232
                                                 Efficiency:  min =     .06694
                                                              avg =      .1056
Log marginal likelihood = -35.460606                          max =      .1443

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
change       |
       group |  5.080653   2.110911   .080507   5.039834   .8564619   9.399672
         age |  1.748516   .3347172   .008875   1.753897   1.128348   2.400989
       _cons | -43.12425   7.865979   .207051   -43.2883  -58.64107  -27.79122
-------------+----------------------------------------------------------------
         var |  12.09916   5.971454   .230798   10.67555   5.375774   27.32451
------------------------------------------------------------------------------
file agegroup_simdata.dta saved

. estimates store agegroup
```

Our acceptance rate and efficiencies are now higher.

In this example, we also used `estimates store agegroup` to store current estimation results as `agegroup` for future use. To use `estimates store` after `bayesmh`, we had to specify the `saving()` option with `bayesmh` to save the `bayesmh` simulation results to a permanent Stata dataset; see *Storing estimation results after Bayesian estimation*.

The MCMC chains are now mixing much better. We may consider increasing the default MCMC sample size to achieve even lower autocorrelation.

```
. bayesgraph diagnostics {change:group} {var}
```



Multiple chains are often used to diagnose the convergence of MCMC; see *Graphical diagnostics using multiple chains* in [BAYES] **bayesmh**. Also see *Convergence of MCMC* in [BAYES] **bayesmh** for more information.

◁

▷ Example 6: Postestimation summaries

We can use the bayesstats summary command to compute postestimation summaries for model parameters and functions of model parameters. For example, we can compute an estimate of the standardized coefficient for change, which is $\widehat{\beta}_{\text{group}} \times \sigma_x/\sigma_y$, where σ_x and σ_y are sample standard deviations of group and change, respectively.

We use summarize (see [R] **summarize**) to compute sample standard deviations and store them in respective scalars.

```
. summarize group
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
       group |         12          .5     .522233          0          1
. scalar sd_x = r(sd)
. summarize change
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
      change |         12    2.469167    8.080637     -10.74      17.05
. scalar sd_y = r(sd)
```

The standardized coefficient is an expression of the model parameter {change:group}, so we specify it in parentheses.

```
. bayesstats summary (group_std:{change:group}*sd_x/sd_y)
Posterior summary statistics                      MCMC sample size =    10,000
   group_std : {change:group}*sd_x/sd_y
-------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+-----------------------------------------------------------------
   group_std |  .3283509   .1364233   .005203   .3257128   .0553512   .6074792
-------------------------------------------------------------------------------
```

The posterior mean estimate of the standardized `group` coefficient is 0.33 with a 95% credible interval of [0.055, 0.61].

◁

▷ Example 7: Model comparison

As we can with frequentist analysis, we can use various information criteria to compare different models. There is great flexibility in which model can be compared: you can compare models with different distributions for the outcome, you can compare models with different priors, you can compare models with different forms for the regression function, and more. The only requirement is that the same data are used to fit the models. Comparisons using Bayes factors additionally require that parameters be sampled from the complete posterior distribution, which includes the normalizing constant.

Let's compare our reduced model with the full model including an interaction term. We again use a multivariate Zellners-g prior for the coefficients and an inverse gamma prior for the variance. We use the same values as in example 4 for prior parameters. (We use the interaction variable in this example for notational simplicity. We could have used the factor-variable notation `c.age#i.group` to include this interaction directly in our model; see **[U] 11.4.3 Factor variables**.)

```
. set seed 14
. bayesmh change group age ageXgr, likelihood(normal({var}))
> prior({change:}, zellnersg0(4,12,{var}))
> prior({var}, igamma(0.5, 4)) block({var})
> saving(full_simdata)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ normal(xb_change,{var})
Priors:
  {change:group age ageXgr _cons} ~ zellnersg(4,12,0,{var})                (1)
                            {var} ~ igamma(0.5,4)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.
Bayesian normal regression                       MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         12
                                                 Acceptance rate  =      .3113
                                                 Efficiency:  min =      .0562
                                                              avg =     .06425
Log marginal likelihood = -36.738363                          max =     .08478
------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
change       |
       group |  11.94079   16.74992   .706542   12.13983  -22.31056   45.11963
         age |  1.939266   .5802772   .023359   1.938756   .7998007   3.091072
      ageXgr | -.2838718   .6985226   .028732   -.285647  -1.671354   1.159183
       _cons | -47.57742    13.4779    .55275  -47.44761  -74.64672  -20.78989
-------------+----------------------------------------------------------------
         var |  11.72886    5.08428   .174612   10.68098   5.302265   24.89543
------------------------------------------------------------------------------
file full_simdata.dta saved
. estimates store full
```

We can use the bayesstats ic command to compare the models. We list the names of the corresponding estimation results following the command name.

```
. bayesstats ic full agegroup
Bayesian information criteria

                 |       DIC     log(ML)     log(BF)
-----------------+-------------------------------------
            full |  65.03326   -36.73836           .
        agegroup |   63.5884   -35.46061    1.277756
-------------------------------------------------------
Note: Marginal likelihood (ML) is computed
      using Laplace-Metropolis approximation.
```

The smaller that DIC is and the larger that log(ML) is, the better. The model without interaction, agegroup, is preferred according to these statistics. The log Bayes-factor for the agegroup model relative to the full model is 1.28. Kass and Raftery (1995) provide a table of values for Bayes factors; see, for example, *Bayes factors* in [BAYES] **bayesstats ic**. According to their scale, because 2 × 1.28 = 2.56 is greater than 2 (slightly), there is some mild evidence that model agegroup is better than model full.

◁

▷ Example 8: Hypothesis testing

Continuing with example 7, we can compute the actual probability associated with each of the models. We can use the bayestest model command to do this.

Similar to bayesstats ic, this command requires the names of estimation results corresponding to the models of interest.

```
. bayestest model full agegroup
Bayesian model tests

                 |   log(ML)        P(M)      P(M|y)
-----------------+-------------------------------------
            full |  -36.7384      0.5000      0.2179
        agegroup |  -35.4606      0.5000      0.7821
-------------------------------------------------------
Note: Marginal likelihood (ML) is computed using
      Laplace-Metropolis approximation.
```

Under the assumption that both models are equally probable a priori, the model without interaction, agegroup, has the probability of 0.78, whereas the full model has the probability of only 0.22. Despite the drastic disparity in the probabilities, according to the results from example 7, model agegroup is only slightly preferable to model full. To have stronger evidence against full, we would expect to see higher probabilities (above 0.9) for agegroup.

We may be interested in testing an interval hypothesis about the parameter of interest. For example, for a model without interaction, let's compute the probability that the coefficient for group is between 4 and 8. We use estimates restore (see [R] **estimates store**) to load the results of the agegroup model back into memory.

```
. estimates restore agegroup
(results agegroup are active now)

. bayestest interval {change:group}, lower(4) upper(8)

Interval tests     MCMC sample size =    10,000

       prob1 : 4 < {change:group} < 8

              |      Mean    Std. Dev.       MCSE
--------------+-----------------------------------
        prob1 |     .6159      0.48641   .0155788
--------------------------------------------------
```

The estimated probability or, technically, its posterior mean estimate is 0.62 with a standard deviation of 0.49 and Monte Carlo standard errors of 0.016.

◁

▷ Example 9: Erasing simulation datasets

After you are done with your analysis, remember to erase any simulation datasets that you created using bayesmh and no longer need. If you want to save your estimation results to disk for future reference, use estimates save; see [R] **estimates save**.

We are done with our analysis, and we do not need the datasets for future reference, so we remove both simulation files we created using bayesmh.

```
. erase agegroup_simdata.dta

. erase full_simdata.dta
```

◁

▷ Example 10: Bayesian linear regression using the bayes prefix

Recall our OLS regression from example 1. There is a more convenient way to obtain Bayesian estimates for this regression than using the bayesmh command as in previous examples. Because regress is one of the estimation commands that supports the bayes prefix ([BAYES] **bayesian estimation**), we can simply type

```
. set seed 14

. bayes: regress change group age
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ regress(xb_change,{sigma2})

Priors:
  {change:group age _cons} ~ normal(0,10000)                              (1)
                  {sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.

Bayesian linear regression                       MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         12
                                                 Acceptance rate  =       .283
                                                 Efficiency:  min =     .02715
                                                              avg =     .05779
Log marginal likelihood = -45.562124                          max =      .0692

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
change       |
       group |  5.425311   2.111038   .080252   5.368975   1.104434   9.425197
         age |  1.885651   .3255098   .012472   1.887263   1.244666   2.517292
       _cons | -46.47537   7.632058   .295505  -46.73244  -60.39245   -30.5054
-------------+----------------------------------------------------------------
      sigma2 |  10.28431   7.614468   .462105   8.412747   3.595971   31.47161
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

With the bayes prefix command, the likelihood is determined automatically by the specified estimation command—regress in our example. The bayes prefix also provides the default prior specifications for model parameters, displaying this information as a note at the bottom of the output table; see *Default priors* in [BAYES] **bayes**. Model summary provides details about the used default priors. For linear regression, the regression coefficients are assigned independent normal priors with zero mean and variance of 10,000, and the variance is assigned an inverse-gamma prior with the same shape and scale parameters of 0.01.

The default priors are provided for convenience and are chosen to be fairly uninformative for models with moderately scaled parameters. However, they are not guaranteed to be uninformative for all models and datasets; see *Linear regression: A case of informative default priors* in [BAYES] **bayes**. You should choose priors carefully based on your research and model of interest.

As with bayesmh, the default MCMC method is an adaptive MH, but we can specify the gibbs option to request Gibbs sampling.

```
. set seed 14

. bayes, gibbs: regress change group age
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ normal(xb_change,{sigma2})

Priors:
  {change:group age _cons} ~ normal(0,10000)                               (1)
                  {sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.

Bayesian linear regression                       MCMC iterations  =     12,500
Gibbs sampling                                   Burn-in          =      2,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         12
                                                 Acceptance rate  =          1
                                                 Efficiency:  min =       .556
                                                              avg =       .889
Log marginal likelihood =  -45.83666                          max =          1

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
change       |
       group |  5.452439   2.062795   .020628   5.460372   1.360104   9.512987
         age |  1.875606    .330127   .003301   1.877129   1.228647   2.543129
       _cons | -46.21334   7.746862   .077469  -46.18291  -61.82541  -31.09702
-------------+----------------------------------------------------------------
      sigma2 |  9.929756   5.899176   .079113   8.426173   3.731261   24.76194
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

As expected, we obtain higher efficiency when using the Gibbs sampling. However, the gibbs option is available only with bayes: regress and bayes: mvreg and only for certain prior distributions.

We can easily change the default priors by specifying the prior() option, as with bayesmh. For example, we can reproduce bayesmh's results from example 4 but with the bayes prefix.

```
. set seed 14

. bayes, prior({change:}, zellnersg0(3,12,{sigma2}))
> prior({sigma2}, igamma(0.5, 4)): regress change group age
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ regress(xb_change,{sigma2})

Priors:
  {change:group age _cons} ~ zellnersg(3,12,0,{sigma2})                    (1)
                  {sigma2} ~ igamma(0.5,4)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.

Bayesian linear regression                       MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         12
                                                 Acceptance rate  =      .2838
                                                 Efficiency:  min =     .06423
                                                              avg =     .07951
Log marginal likelihood = -35.448029                          max =     .09277

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
change       |
       group |  4.944955   2.184113    .086181   5.052278   .7065487    9.35098
         age |  1.747984   .3390581    .011132   1.747477   1.045677   2.416091
       _cons | -43.09605   7.904334    .263186  -43.01961  -58.57942  -27.11278
-------------+----------------------------------------------------------------
      sigma2 |  12.17932    5.87997    .220888   10.72651   5.511202    28.1211
------------------------------------------------------------------------------
```

The results are similar to those from example 4 using bayesmh but not identical. By default, bayes: regress automatically splits the regression coefficients and the variance into two separate blocks, whereas bayesmh treats all parameters as one block; see *Improving efficiency of the MH algorithm—blocking of parameters* in [BAYES] **bayesmh** for details about blocking.

To match the results exactly, you can either specify the `block({var})` option with `bayesmh` in example 4 or specify the `noblocking` option to request no default blocking with the `bayes` prefix.

```
. set seed 14

. bayes, prior({change:}, zellnersg0(3,12,{sigma2}))
> prior({sigma2}, igamma(0.5, 4)) noblocking: regress change group age
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  change ~ regress(xb_change,{sigma2})

Priors:
  {change:group age _cons} ~ zellnersg(3,12,0,{sigma2})                    (1)
                  {sigma2} ~ igamma(0.5,4)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_change.

Bayesian linear regression                       MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         12
                                                 Acceptance rate  =     .06169
                                                 Efficiency:  min =      .0165
                                                              avg =     .02018
Log marginal likelihood = -35.356501                          max =     .02159

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
change       |
       group |  4.988881   2.260571   .153837   4.919351   .7793098   9.775568
         age |  1.713159   .3545698   .024216   1.695671   1.053206   2.458556
       _cons | -42.31891   8.239571   .565879  -41.45385  -59.30145  -27.83421
-------------+----------------------------------------------------------------
      sigma2 |  12.29575   6.570879   .511475    10.3609   5.636195   30.93576
------------------------------------------------------------------------------
```

See [BAYES] **bayes** for more details.

◁

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Also see

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

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

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

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

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

[BAYES] **Glossary**

Title

bayesian estimation — Bayesian estimation commands

Description   Video examples   Also see

Description

Bayesian estimation in Stata is similar to standard estimation—simply prefix the estimation commands with `bayes:` (see [BAYES] **bayes**). You can also refer to [BAYES] **bayesmh** and [BAYES] **bayesmh evaluators** for fitting more general Bayesian models.

The following estimation commands support the `bayes` prefix.

Command	Entry	Description
Linear regression models		
`regress`	[BAYES] **bayes: regress**	Linear regression
`hetregress`	[BAYES] **bayes: hetregress**	Heteroskedastic linear regression
`tobit`	[BAYES] **bayes: tobit**	Tobit regression
`intreg`	[BAYES] **bayes: intreg**	Interval regression
`truncreg`	[BAYES] **bayes: truncreg**	Truncated regression
`mvreg`	[BAYES] **bayes: mvreg**	Multivariate regression
Binary-response regression models		
`logistic`	[BAYES] **bayes: logistic**	Logistic regression, reporting odds ratios
`logit`	[BAYES] **bayes: logit**	Logistic regression, reporting coefficients
`probit`	[BAYES] **bayes: probit**	Probit regression
`cloglog`	[BAYES] **bayes: cloglog**	Complementary log-log regression
`hetprobit`	[BAYES] **bayes: hetprobit**	Heteroskedastic probit regression
`binreg`	[BAYES] **bayes: binreg**	GLM for the binomial family
`biprobit`	[BAYES] **bayes: biprobit**	Bivariate probit regression
Ordinal-response regression models		
`ologit`	[BAYES] **bayes: ologit**	Ordered logistic regression
`oprobit`	[BAYES] **bayes: oprobit**	Ordered probit regression
`zioprobit`	[BAYES] **bayes: zioprobit**	Zero-inflated ordered probit regression
Categorical-response regression models		
`mlogit`	[BAYES] **bayes: mlogit**	Multinomial (polytomous) logistic regression
`mprobit`	[BAYES] **bayes: mprobit**	Multinomial probit regression
`clogit`	[BAYES] **bayes: clogit**	Conditional logistic regression
Count-response regression models		
`poisson`	[BAYES] **bayes: poisson**	Poisson regression
`nbreg`	[BAYES] **bayes: nbreg**	Negative binomial regression
`gnbreg`	[BAYES] **bayes: gnbreg**	Generalized negative binomial regression
`tpoisson`	[BAYES] **bayes: tpoisson**	Truncated Poisson regression
`tnbreg`	[BAYES] **bayes: tnbreg**	Truncated negative binomial regression
`zip`	[BAYES] **bayes: zip**	Zero-inflated Poisson regression
`zinb`	[BAYES] **bayes: zinb**	Zero-inflated negative binomial regression

Generalized linear models		
`glm`	[BAYES] **bayes: glm**	Generalized linear models
Fractional-response regression models		
`fracreg`	[BAYES] **bayes: fracreg**	Fractional response regression
`betareg`	[BAYES] **bayes: betareg**	Beta regression
Survival regression models		
`streg`	[BAYES] **bayes: streg**	Parametric survival models
Sample-selection regression models		
`heckman`	[BAYES] **bayes: heckman**	Heckman selection model
`heckprobit`	[BAYES] **bayes: heckprobit**	Probit regression with sample selection
`heckoprobit`	[BAYES] **bayes: heckoprobit**	Ordered probit model with sample selection
Multilevel regression models		
`mixed`	[BAYES] **bayes: mixed**	Multilevel linear regression
`metobit`	[BAYES] **bayes: metobit**	Multilevel tobit regression
`meintreg`	[BAYES] **bayes: meintreg**	Multilevel interval regression
`melogit`	[BAYES] **bayes: melogit**	Multilevel logistic regression
`meprobit`	[BAYES] **bayes: meprobit**	Multilevel probit regression
`mecloglog`	[BAYES] **bayes: mecloglog**	Multilevel complementary log-log regression
`meologit`	[BAYES] **bayes: meologit**	Multilevel ordered logistic regression
`meoprobit`	[BAYES] **bayes: meoprobit**	Multilevel ordered probit regression
`mepoisson`	[BAYES] **bayes: mepoisson**	Multilevel Poisson regression
`menbreg`	[BAYES] **bayes: menbreg**	Multilevel negative binomial regression
`meglm`	[BAYES] **bayes: meglm**	Multilevel generalized linear model
`mestreg`	[BAYES] **bayes: mestreg**	Multilevel parametric survival regression

Video examples

Introduction to Bayesian analysis, part 1: The basic concepts

Introduction to Bayesian analysis, part 2: MCMC and the Metropolis–Hastings algorithm

Also see

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

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

[BAYES] **bayesmh evaluators** — User-defined evaluators with bayesmh

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

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

[BAYES] **Glossary**

Title

bayes — Bayesian regression models using the bayes prefix

Description	Quick start	Menu	Syntax
Options	Remarks and examples	Stored results	Methods and formulas
Also see			

Description

The bayes prefix fits Bayesian regression models. It provides Bayesian support for many likelihood-based estimation commands. The bayes prefix uses default or user-supplied priors for model parameters and estimates parameters using MCMC by drawing simulation samples from the corresponding posterior model. Also see [BAYES] **bayesmh** and [BAYES] **bayesmh evaluators** for fitting more general Bayesian models.

Quick start

Bayesian linear regression of y on x, using default normal priors for the regression coefficients and an inverse-gamma prior for the variance

```
bayes: regress y x
```

As above, but use a standard deviation of 10 instead of 100 for the default normal priors and shape of 2 and scale of 1 instead of values of 0.01 for the default inverse-gamma prior

```
bayes, normalprior(10) igammaprior(2 1): regress y x
```

Bayesian logistic regression of y on x1 and x2, showing model summary without performing estimation

```
bayes, dryrun: logit y x1 x2
```

As above, but estimate model parameters and use uniform priors for all regression coefficients

```
bayes, prior({y: x1 x2 _cons}, uniform(-10,10)): logit y x1 x2
```

As above, but use a shortcut notation to refer to all regression coefficients

```
bayes, prior({y:}, uniform(-10,10)): logit y x1 x2
```

As above, but report odds ratios and 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)) or: logit y x1 x2
```

Report odds ratios for the logit model on replay

```
bayes, or
```

Bayesian ordered logit regression of y on x1 and x2, saving simulation results to simdata.dta and using a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): ologit y x1 x2 x3
```

Bayesian multinomial regression of y on x1 and x2, specifying 20,000 MCMC samples, setting length of the burn-in period to 5,000, and requesting that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): mlogit y x1 x2
```

Bayesian Poisson regression of y on x1 and x2, putting regression slopes in separate blocks and showing block summary

```
bayes, block({y:x1}) block({y:x2}) blocksummary: poisson y x1 x2
```

Bayesian multivariate regression of y1 and y2 on x1, x2, and x3, using Gibbs sampling and requesting 90% HPD credible interval instead of the default 95% equal-tailed credible interval

```
bayes, gibbs clevel(90) hpd: mvreg y1 y2 = x1 x2 x3
```

As above, but use mvreg's option level() instead of bayes's option clevel()

```
bayes, gibbs hpd: mvreg y1 y2 = x1 x2 x3, level(90)
```

Suppress estimates of the covariance matrix from the output

```
bayes, noshow(Sigma, matrix)
```

Bayesian Weibull regression of stset survival-time outcome on x1 and x2, specifying starting values of 1 for {y:x1} and of 2 for {y:x2}

```
bayes, initial({y:x1} 1 {y:x2} 2): streg x1 x2, distribution(weibull)
```

Bayesian two-level linear regression of y on x1 and x2 with random intercepts by id

```
bayes: mixed y x1 x2 || id:
```

Menu

Statistics > Bayesian analysis > Regression models > *estimation_command*

Syntax

bayes [, *bayesopts*] : *estimation_command* [, *estopts*]

estimation_command is a likelihood-based estimation command, and *estopts* are command-specific estimation options; see [BAYES] **bayesian estimation** for a list of supported commands, and see the command-specific entries for the supported estimation options, *estopts*.

bayesopts	Description
Priors	
*gibbs	specify Gibbs sampling; available only with regress or mvreg for certain prior combinations
normalprior(#*)	specify standard deviation of default normal priors for regression coefficients and other real scalar parameters; default is normalprior(100)
igammaprior(# #*)	specify shape and scale of default inverse-gamma prior for variances; default is igammaprior(0.01 0.01)
iwishartprior(#* [*...*])	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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
restubs(*restub1 restub2 ...*)	specify stubs for random-effects parameters for all levels; allowed only with multilevel models
Blocking	
blocksize(#*)	maximum block size; default is blocksize(50)
block(*paramref*[, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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_option	display coefficient table in exponentiated form
`remargl`	compute log marginal likelihood
`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
`nomesummary`	suppress multilevel-structure summary; allowed only with multilevel models
[`no`]`dots`	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is command-specific
`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; allowed only with multilevel commands
`melabel`	display estimation table using the same row labels as *estimation_command*; allowed only with multilevel commands
`nogroup`	suppress table summarizing groups; allowed only with multilevel models
`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)`

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

The full specification of `iwishartprior()` is `iwishartprior(`*#* [*matname*] [`, relevel(`*levelvar*`)`]`)`.

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

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

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

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

Options

Priors

`gibbs` specifies that Gibbs sampling be used to simulate model parameters instead of the default adaptive Metropolis–Hastings sampling. This option is allowed only with the `regress` and `mvreg` estimation commands. It is available only with certain prior combinations such as normal prior for regression coefficients and an inverse-gamma prior for the variance. Specifying the `gibbs` option is equivalent to specifying `block()`'s `gibbs` suboption for all default blocks of parameters. If you use the `block()` option to define your own blocks of parameters, the `gibbs` option will have no effect on those blocks, and an MH algorithm will be used to update parameters in those blocks unless you also specify `block()`'s `gibbs` suboption.

`normalprior(`*#*`)` specifies the standard deviation of the default normal priors. The default is `normalprior(100)`. The normal priors are used for scalar parameters defined on the whole real line; see *Default priors* for details.

`igammaprior(`*# #*`)` specifies the shape and scale parameters of the default inverse-gamma priors. The default is `igammaprior(0.01 0.01)`. The inverse-gamma priors are used for positive scalar parameters such as a variance; see *Default priors* for details. Instead of a number #, you can specify a missing value (`.`) to refer to the default value of 0.01.

`iwishartprior(`*#* [*matname*] [, `relevel(`*levelvar*`)`]`)` specifies the degrees of freedom and, optionally, the scale matrix *matname* of the default inverse-Wishart priors used for unstructured covariances of random effects with multilevel models. The degrees of freedom # is a positive real scalar with the default value of $d+1$, where d is the number of random-effects terms at the level of hierarchy *levelvar*. Instead of a number #, you can specify a missing value (`.`) to refer to the default value. Matrix name *matname* is the name of a positive-definite Stata matrix with the default of $I(d)$, the identity matrix of dimension d. If `relevel(`*levelvar*`)` is omitted, the specified parameters are used for inverse-Wishart priors for all levels with unstructured random-effects covariances. Otherwise, they are used only for the prior for the specified level *levelvar*. See *Default priors* for details.

`prior(`*priorspec*`)` specifies a prior distribution for model parameters. This option may be repeated. A prior may be specified for any of the model parameters, except the random-effects parameters in multilevel models. Model parameters with the same prior specifications are placed in a separate block. Model parameters that are not included in prior specifications are assigned default priors; see *Default priors* for details. 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* in [BAYES] **bayesmh**.

All `prior()` distributions are allowed, but they are not guaranteed to correspond to proper posterior distributions for all likelihood models. You need to think carefully about the model you are building and evaluate its convergence thoroughly.

`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.

Simulation

`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()` $+$ $\big($`mcmcsize()` $-\ 1\big) \times$ `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. Also see *Burn-in period and MCMC sample size* in [BAYES] **bayesmh**.

`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. The burn-in period may need to be larger for multilevel models because these models introduce high-dimensional random-effects parameters and thus require longer adaptation period. Also see *Burn-in period and MCMC sample size* in [BAYES] **bayesmh** and *Convergence of MCMC* in [BAYES] **bayesmh**.

`thinning(`*#*`)` specifies the thinning interval. Only simulated values from every $(1+k\times\#)$th iteration for $k=0,1,2,\dots$ 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.

`rseed(`*#*`)` sets the random-number seed. This option can be used to reproduce results. `rseed(`*#*`)` is equivalent to typing `set seed` *#* prior to calling the `bayes` prefix; see [R] **set seed** and *Reproducing results* in [BAYES] **bayesmh**.

`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.

`restubs(`*restub1 restub2* ...`)` specifies the stubs for the names of random-effects parameters. You must specify stubs for all levels—one stub per level. This option overrides the default random-effects stubs. See *Likelihood model* for details about the default names of random-effects parameters.

Blocking

`blocksize(`*#*`)` specifies the maximum block size for the model parameters; default is `blocksize(50)`. This option does not apply to random-effects parameters. Each group of random-effects parameters is placed in one block, regardless of the number of random-effects parameters in that group.

`block(`*paramref* [, *blockopts*]`)` specifies a group of model parameters for the blocked MH algorithm. By default, model parameters, except the random-effects parameters, are sampled as independent blocks of 50 parameters or of the size specified in option `blocksize()`. Regression coefficients from different equations are placed in separate blocks. Auxiliary parameters such as variances and correlations are sampled as individual separate blocks, whereas the cutpoint parameters of the ordinal-outcome regressions are sampled as one separate block. With multilevel models, each group of random-effects parameters is placed in a separate block, and the `block()` option is not allowed with random-effects parameters. 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* in [BAYES] **bayesmh**.

blockopts include `gibbs`, `split`, `scale()`, `covariance()`, and `adaptation()`.

`gibbs` specifies to use Gibbs sampling to update parameters in the block. This option is allowed only for hyperparameters and only for specific combinations of prior and hyperprior distributions; see *Gibbs sampling for some likelihood-prior and prior-hyperprior configurations* in [BAYES] **bayesmh**. For more information, see *Gibbs and hybrid MH sampling* in [BAYES] **bayesmh**. `gibbs` may not be combined with `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.

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.

noblocking requests that no default blocking is applied to model parameters. By default, model parameters are sampled as independent blocks of 50 parameters or of the size specified in option blocksize(). For multilevel models, this option has no effect on random-effects parameters; blocking is always applied to them.

Initialization

initial(*initspec*) specifies initial values for the model parameters to be used in the simulation. 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

```
bayes, 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* in [BAYES] **bayesmh**. For example, to initialize all regression coefficients from equations y1 and y2 to zero, you can type

```
bayes, initial({y1:} {y2:} 0) : ...
```

The general specification of *initspec* is

paramref # [*paramref* # [...]]

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* in [BAYES] **bayesmh** for details.

nomleinitial suppresses using maximum likelihood estimates (MLEs) starting values for model parameters. By default, when no initial values are specified, MLE values from *estimation_command* are used as initial values. For multilevel commands, MLE estimates are used only for regression coefficients. Random effects are assigned zero values, and random-effects variances and covariances are initialized with ones and zeros, respectively. 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`, `density()`, `logdensity()`, and `jeffreys()` priors; you must provide fixed initial values for such parameters. This option cannot be combined with `nomleinitial`.

`initsummary` specifies that the initial values used for simulation be displayed.

`noisily` specifies that the output from the estimation command be shown during initialization. The estimation command is executed once to set up the model and calculate initial values for model parameters.

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* in [BAYES] **bayesmh** 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$\{25,$`floor(burnin()/adaptation(every()))`$\}$.

`maxiter()` is usually chosen to be no greater than (`mcmcsize()` + `burnin()`)/ `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 specifies the display of HPD credible intervals instead of the default equal-tailed credible intervals.

eform_option causes the coefficient table to be displayed in exponentiated form; see [R] ***eform_option***. The estimation command determines which *eform_option* is allowed (eform(*string*) and eform are always allowed).

remargl specifies to compute the log marginal likelihood for multilevel models. It is not reported by default for multilevel models. Bayesian 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 multilevel models, the log marginal likelihood is not reported by default. For multilevel 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, batch standard deviation, and MCSE using batch means. The default is batch(0), which means no batch calculations. When batch() is not specified, MCSE is computed using effective sample sizes instead of batch means. Option 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, the bayes prefix saves simulation results in a temporary file for later access by postestimation commands.

This temporary file will be overridden every time the bayes prefix 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. Variance _index records iteration numbers. The bayes prefix 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 the bayes prefix. 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,

```
. bayes, 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, the bayes prefix 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.

nomesummary suppresses the summary about the multilevel structure of the model. This summary is reported by default for multilevel commands.

nodots, dots, and dots(#) specify to suppress or display dots during simulation. 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). dots is the default with multilevel commands, and nodots is the default with other commands.

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 with multilevel models) 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 commands 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 first $\#_{\text{matsize}} - \#_{\text{npar}}$ random-effects parameters, where $\#_{\text{matsize}}$ is the maximum number of variables as determined by matsize (see [R] **matsize**) and $\#_{\text{npar}}$ is the number of other model parameters displayed. If you want to obtain MCMC summaries and display other random-effects parameters, you can use the show() option or use bayesstats summary (see [BAYES] **bayesstats summary**).

melabel specifies that the bayes prefix use the same row labels as *estimation_command* in the estimation table. This option is allowed only with multilevel commands. It is useful to match the estimation table output of bayes: *mecmd* with that of *mecmd*. This option implies nomesummary and nomodelsummary.

nogroup suppresses the display of group summary information (number of groups, average group size, minimum, and maximum) from the output header. This option is for use with multilevel commands.

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, 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

Remarks and examples are presented under the following headings:

For a general introduction to Bayesian analysis, see [BAYES] **intro**. For a general introduction to Bayesian estimation using adaptive MH and Gibbs algorithms, see [BAYES] **bayesmh**. See [BAYES] **bayesian estimation** for a list of supported estimation commands. For a quick overview example of all Bayesian commands, see *Overview example* in [BAYES] **bayesian commands**.

Using the bayes prefix

The `bayes` prefix provides Bayesian estimation for many likelihood-based regression models. Simply prefix your estimation command with `bayes` to get Bayesian estimates—`bayes:` *estimation_command*; see [BAYES] **bayesian estimation** for a list of supported commands. Also see [BAYES] **bayesmh** for other Bayesian models.

Similarly to the `bayesmh` command, the `bayes` prefix sets up a Bayesian posterior model, uses MCMC to simulate parameters of this model, and summarizes and reports results. The process of specifying a Bayesian model is similar to that described in *Setting up a posterior model* in [BAYES] **bayesmh**, except the likelihood model is now determined by the specified *estimation_command* and default priors are used for model parameters. The `bayes` prefix and the `bayesmh` command share the same methodology of MCMC simulation and the same summarization and reporting of simulation results; see [BAYES] **bayesmh** for details. In the following sections, we provide information specific to the `bayes` prefix.

Likelihood model

With the `bayes` prefix, the likelihood component of the Bayesian model is determined by the prefixed estimation command, and all posterior model parameters are defined by the likelihood model. For example, the parameters of the model

```
. bayes: streg age smoking, distribution(lognormal)
```

are the regression coefficients and auxiliary parameters you see when you fit

```
. streg age smoking, distribution(lognormal)
```

All estimation commands have regression coefficients as their model parameters. Some commands have additional parameters such as variances and correlation coefficients.

The bayes prefix typically uses the likelihood parameterization and the naming convention of the estimation command to define model parameters, but there are exceptions. For example, the truncreg command uses the standard deviation parameter {sigma} to parameterize the likelihood, whereas bayes: truncreg uses the variance parameter {sigma2}.

Most model parameters are scalar parameters supported on the whole real line such as regression coefficients, log-transformed positive parameters, and atanh-transformed correlation coefficients. For example, positive scalar parameters are the variance parameters in bayes: regress, bayes: tobit, and bayes: truncreg, and matrix parameters are the covariance matrix {Sigma, matrix} in bayes: mvreg and covariances of random effects in multilevel commands such as bayes: meglm.

The names of model parameters are provided in the model summary displayed by the bayes prefix. Knowing these names is useful when specifying the prior distributions, although the bayes prefix does provide default priors; see *Default priors*. You can use the dryrun option with the bayes prefix to see the names of model parameters prior to the estimation. In general, the names of regression coefficients are formed as {*depvar*:*indepvar*}, where *depvar* is the name of the specified dependent variable and *indepvar* is the name of an independent variable. There are exceptions such as bayes: streg, for which *depvar* is replaced with _t. Variance parameters are named {sigma2}, log-variance parameters are named {lnsigma2}, atanh-transformed correlation parameters are named {athrho}, and the covariance matrix of bayes: mvreg is named {Sigma, matrix} (or {Sigma, m} for short).

For multilevel models such as bayes: meglm, in addition to regression coefficients and variance components, the bayes prefix also estimates random-effects parameters. This is different from the corresponding frequentist commands, such as meglm, in which random effects are integrated out and thus are not among the final model parameters. (They can be predicted after estimation.) As such, the bayes prefix has its own naming convention for model parameters of multilevel commands. Before moving on, you should be familiar with the syntax of the multilevel commands; see, for example, *Syntax* in [ME] **meglm**.

The regression coefficients are labeled as usual, {*depvar*:*indepvar*}. Random-effects parameters are labeled as outlined in tables 1 and 2. You can change the default names by specifying the restubs() option. The common syntax of {*rename*} is {*restub#*}, where *restub* is a capital letter, U for the level specified first, or a sequence of capital letters that is unique to each random-effects level, and # refers to the group of random effects at that level: 0 for random intercepts, 1 for random coefficients associated with the variable specified first in the random-effects equation, 2 for random coefficients associated with the variable specified second, and so on. The full syntax of {*rename*}, {*fullrename*}, is {*restub#*[*levelvar*]}, where *levelvar* is the variable identifying the level of hierarchy and is often omitted from the specification for brevity. Random effects at the observation level or crossed effects, specified as _all: R.*varname* with multilevel commands, are labeled as {U0}, {V0}, {W0}, and so on. Random effects at nesting levels, or nested effects, are labeled using a sequence of capital letters starting with the letter corresponding to the top level. For example, the multilevel model

```
. bayes: melogit y x1 x2 || id1: x1 x2 || id2: x1 || id3:
```

will have random-effects parameters {U0}, {U1}, and {U2} to represent, respectively, random intercepts, random coefficients for x1, and random coefficients for x2 at the id1 level; parameters {UU0} and {UU1} for random intercepts and random coefficients for x1 at the id2 level; and random intercepts {UUU0} at the id3 level. See *Multilevel models* for more examples. Also see *Different ways of specifying model parameters* for how to refer to individual random effects during postestimation.

Table 1. Random effects at nesting levels of hierarchy (nested effects)

Hierarchy	Random effects	{*rename*}
lev1	Random intercepts	{U0}
	Random coefficients	{U1}, {U2}, etc.
lev1>*lev2*	Random intercepts	{UU0}
	Random coefficients	{UU1}, {UU2}, etc.
lev1>*lev2*>*lev3*	Random intercepts	{UUU0}
	Random coefficients	{UUU1}, {UUU2}, etc.
...		

Table 2. Random effects at the observation level, _all (crossed effects)

Hierarchy	Random effects	{*rename*}
lev1	Random intercepts	{U0}
lev2	Random intercepts	{V0}
lev3	Random intercepts	{W0}
...		

Variance components for independent random effects are labeled as {*rename*:sigma2}. In the above example, there are six variance components: {U0:sigma2}, {U1:sigma2}, {U2:sigma2}, {UU0:sigma2}, {UU1:sigma2}, and {UUU0:sigma2}.

Covariance matrices of correlated random effects are labeled as {*restub*:Sigma,matrix} (or {*restub*:Sigma,m} for short), where *restub* is the letter stub corresponding to the level at which random effects are defined. For example, if we specify an unstructured covariance for the random effects at the id1 and id2 levels (with cov(un) short for covariance(unstructured))

```
. bayes: melogit y x1 x2 || id1: x1 x2, cov(un) || id2: x1, cov(un) || id3:
```

we will have two covariance matrix parameters, a 3×3 covariance {U:Sigma,m} at the id1 level and a 2×2 covariance {UU:Sigma,m} at the id2 level, and the variance component {UUU0:sigma2} at the id3 level.

For Gaussian multilevel models such as bayes: mixed, the error variance component is labeled as {e.*depvar*:sigma2}.

Also see command-specific entries for the naming convention of additional parameters such as cutpoints with ordinal models or overdispersion parameters with negative binomial models.

Default priors

For convenience, the bayes prefix provides default priors for model parameters. The priors are chosen to be general across models and are fairly uninformative for a typical combination of a likelihood model and dataset. However, the default priors may not always be appropriate. You should always inspect their soundness and, if needed, override the prior specification for some or all model parameters using the prior() option.

All scalar parameters supported on the whole real line, such as regression coefficients and log-transformed positive parameters, are assigned a normal distribution with zero mean and variance σ^2_{prior}, $N(0, \sigma^2_{\text{prior}})$, where σ_{prior} is given by the normalprior() option. The default value for

σ_{prior} is 100, and thus the default priors for these parameters are $N(0, 10000)$. These priors are fairly uninformative for parameters of moderate size but may become informative for large-scale parameters. See the *Linear regression: A case of informative default priors* example below.

All positive scalar parameters, such as the variance parameters in `bayes: regress` and `bayes: tobit`, are assigned an inverse-gamma prior with shape parameter α and scale parameter β, InvGamma(α, β). The default values for α and β are 0.01, and thus the default prior for these parameters is InvGamma$(0.01, 0.01)$.

All cutpoint parameters of ordinal-outcome models, such as `bayes: ologit` and `bayes: oprobit` are assigned flat priors, improper uniform priors with a constant density of 1, equivalent to specifying the `flat` prior option. The reason for this choice is that the cutpoint parameters are sensitive to the range of the outcome variables, which is usually unknown a priori.

For multilevel models with `independent` and `identity` random-effects covariance structures, variances of random effects are assigned inverse-gamma priors, InvGamma$(0.01, 0.01)$. For `unstructured` random-effects covariances, covariance matrix parameters are assigned fairly uninformative inverse-Wishart priors, InvWishart$(d + 1, I(d))$, where d is the dimension of the random-effects covariance matrix and $I(d)$ is the identity matrix of dimension d. Setting the degrees-of-freedom parameter of the inverse-Wishart prior to $d + 1$ is equivalent to specifying uniform on $(-1, 1)$ distributions for the individual correlation parameters.

The model summary displayed by the `bayes` prefix describes the chosen default priors, which you can see prior to estimation if you specify `bayes`'s `dryrun` option. You can use the `prior()` option repeatedly to override the default prior specifications for some or all model parameters.

Initial values

By default, the `bayes` prefix uses the ML estimates from the prefixed estimation command as initial values for all scalar model parameters.

For example, the specification

```
. bayes: logit y x
```

will use the ML estimates from

```
. logit y x
```

as default initial values for the regression coefficients.

You can override the default initial values by using the `initial()` option; see *Specifying initial values* in [BAYES] **bayesmh**.

If the `nomleinitial` option is specified, instead of using the estimates from the prefixed command, all scalar model parameters are initialized with zeros, except for the variance parameters, which are initialized with ones.

The covariance matrix parameter `{Sigma, matrix}` of `bayes: mvreg` is always initialized with the identity matrix.

For multilevel models, regression coefficients are initialized using the ML estimates from the corresponding model without random effects, variances of random effects are initialized with ones, covariances of random effects are initialized with zeros, and random effects themselves are initialized with zeros.

Command-specific options

Not all command-specific options, that is, options specified with the estimation command, are applicable within the Bayesian framework. One example is the group of maximum-likelihood optimization options such as `technique()` and `gradient`. For a list of supported options, refer to the entry specific to each command; see [BAYES] **bayesian estimation** for a list of commands.

Some of the command-specific reporting options, such as *eform_option* and display options, can be specified either with *estimation_command* or with the `bayes` prefix. For example, to obtain estimates of odds ratios instead of coefficients after the logit model, you can specify the `or` option with the command

```
. bayes: logit y x, or
```

or with the `bayes` prefix

```
. bayes, or: logit y x
```

You can also specify this option on replay with the `bayes` prefix

```
. bayes: logit y x
. bayes, or
```

Introductory example

We start with a simple linear regression model applied to `womenwage.dta`, which contains income data for a sample of working women.

```
. use http://www.stata-press.com/data/r15/womenwage
(Wages of women)
```

Suppose we want to regress women's yearly income, represented by the `wage` variable, on their age, represented by the `age` variable. We can fit this model using the `regress` command.

```
. regress wage age

      Source |       SS           df       MS      Number of obs   =       488
-------------+----------------------------------   F(1, 486)       =     43.53
       Model |  3939.49247         1  3939.49247   Prob > F        =    0.0000
    Residual |  43984.4891       486   90.503064   R-squared       =    0.0822
-------------+----------------------------------   Adj R-squared   =    0.0803
       Total |  47923.9816       487   98.406533   Root MSE        =    9.5133

------------------------------------------------------------------------------
        wage |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |    .399348   .0605289     6.60   0.000     .2804173    .5182787
       _cons |   6.033077   1.791497     3.37   0.001     2.513041    9.553112
------------------------------------------------------------------------------
```

▷ Example 1: Bayesian simple linear regression

We can fit a corresponding Bayesian regression model by simply adding `bayes:` in front of the `regress` command. Because the `bayes` prefix is simulation based, we set a random-number seed to get reproducible results.

```
. set seed 15

. bayes: regress wage age
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  wage ~ regress(xb_wage,{sigma2})

Priors:
  {wage:age _cons} ~ normal(0,10000)                                       (1)
          {sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_wage.

Bayesian linear regression                       MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =        488
                                                 Acceptance rate  =      .3739
                                                 Efficiency:  min =      .1411
                                                              avg =      .1766
Log marginal likelihood = -1810.1432                          max =      .2271

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
wage         |
         age |  .4008591   .0595579   .001586   .4005088   .2798807   .5183574
       _cons |  5.969069   1.737247   .043218   5.997571    2.60753   9.396475
-------------+----------------------------------------------------------------
      sigma2 |  90.76252   5.891887   .123626   90.43802   79.71145   102.8558
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

The Bayesian model has two regression coefficient parameters, `{wage:age}` and `{wage:_cons}`, and a positive scalar parameter, `{sigma2}`, representing the variance of the error term. The model summary shows the default priors used for the model parameters: `normal(0, 10000)` for the regression coefficients and `igamma(0.01, 0.01)` for the variance parameter. The default priors are provided for convenience and should be used with caution. These priors are fairly uninformative in this example, but this may not always be the case; see the example in *Linear regression: A case of informative default priors*.

The first two columns of the `bayes` prefix's estimation table report the posterior means and standard deviations of the model parameters. We observe that for the regression coefficients `{wage:age}` and `{wage:_cons}`, the posterior means and standard deviations are very similar to the least-square estimates and their standard errors as reported by the `regress` command. The posterior mean estimate for `{sigma2}`, 90.76, is close to the residual mean squared estimate, 90.50, listed in the ANOVA table of the `regress` command. The estimation table of the `bayes` prefix also reports Monte Carlo standard errors (MCSEs), medians, and equal-tailed credible intervals.

The Bayesian estimates are stochastic in nature and, by default, are based on an MCMC sample of size 10,000. It is important to verify that the MCMC simulation has converged; otherwise, the Bayesian estimates cannot be trusted. The simulation efficiencies reported in the header of the estimation table can serve as useful initial indicators of convergence problems. The minimum efficiency in our example is about 0.14, and the average efficiency is about 0.17. These numbers are typical for the MH sampling algorithm used by `bayes` and do not indicate convergence problems; see *Convergence of MCMC* in [BAYES] **bayesmh** for more rigorous convergence diagnostics.

◁

▷ Example 2: Predictions

There are several postestimation commands available after the `bayes` prefix; see [BAYES] **bayesian postestimation**. Among them is the `bayesstats summary` command, which we can use to compute simple predictions. Suppose that we want to predict the expected wage of a 40-year-old woman conditional on the above fitted posterior model. Based on our model, this expected wage corresponds to the linear combination $\{\texttt{wage}:\texttt{\_cons}\} + \{\texttt{wage}:\texttt{age}\} \times 40$. We name this expression `wage40` and supply it to the `bayesstats summary` command.

```
. bayesstats summary (wage40: {wage:_cons} + {wage:age}*40)

Posterior summary statistics                      MCMC sample size =    10,000

      wage40 : {wage:_cons} + {wage:age}*40

--------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+------------------------------------------------------------------
      wage40 |  22.00343      .81679   .024045  21.99231   20.39435    23.6718
--------------------------------------------------------------------------------
```

The posterior mean estimate for the expected wage is about 22 with a 95% credible interval between 20.39 and 23.67.

◁

▷ Example 3: Gibbs sampling

The `bayes` prefix uses adaptive MH as its default sampling algorithm. However, in the special case of linear regression, a more efficient Gibbs sampling is available. We can request Gibbs sampling by specifying the `gibbs` option.

```
. set seed 15

. bayes, gibbs: regress wage age
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  wage ~ normal(xb_wage,{sigma2})

Priors:
  {wage:age _cons} ~ normal(0,10000)                                      (1)
          {sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_wage.

Bayesian linear regression                       MCMC iterations  =     12,500
Gibbs sampling                                   Burn-in          =      2,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =        488
                                                 Acceptance rate  =          1
                                                 Efficiency:  min =          1
                                                              avg =          1
Log marginal likelihood =  -1810.087                          max =          1

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
wage         |
         age |  .3999669   .0611328   .000611   .4005838   .2787908    .518693
       _cons |  6.012074   1.804246   .018042   6.000808   2.488816   9.549921
-------------+----------------------------------------------------------------
      sigma2 |  90.84221   5.939535   .059395   90.54834    79.8132   103.0164
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

The posterior summary results obtained by Gibbs sampling and MH sampling are very close except for the MCSEs. The Gibbs sampler reports substantially lower MCSEs than the default sampler because of its higher efficiency. In fact, in this example, the Gibbs sampler achieves the highest possible efficiency of 1.

◁

Linear regression: A case of informative default priors

Our example in *Introductory example* used the default priors, which were fairly uninformative for those data and that model. This may not always be true. Consider a linear regression model using the familiar `auto.dta`. Let us regress the response variable `price` on the covariate `length` and factor variable `foreign`.

```
. use http://www.stata-press.com/data/r15/auto, clear
(1978 Automobile Data)

. regress price length i.foreign

      Source |       SS           df       MS      Number of obs   =        74
-------------+----------------------------------   F(2, 71)        =     16.35
       Model |  200288930         2   100144465   Prob > F        =    0.0000
    Residual |  434776467        71  6123612.21   R-squared       =    0.3154
-------------+----------------------------------   Adj R-squared   =    0.2961
       Total |  635065396        73  8699525.97   Root MSE        =    2474.6

------------------------------------------------------------------------------
       price |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      length |   90.21239   15.83368     5.70   0.000     58.64092    121.7839
             |
     foreign |
    Foreign  |   2801.143    766.117     3.66   0.000     1273.549    4328.737
       _cons |  -11621.35   3124.436    -3.72   0.000     -17851.3   -5391.401
------------------------------------------------------------------------------
```

▷ Example 4: Default priors

We first fit a Bayesian regression model using the bayes prefix with default priors. Because the range of the outcome variable price is at least an order of magnitude larger than the range of the predictor variables length and foreign, we anticipate that some of the model parameters may have large scale, and longer adaptation may be necessary for the MCMC algorithm to reach optimal sampling for these parameters. We allow for longer adaptation by increasing the burn-in period from the default value of 2,500 to 5,000.

```
. set seed 15

. bayes, burnin(5000): regress price length i.foreign
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  price ~ regress(xb_price,{sigma2})

Priors:
  {price:length 1.foreign _cons} ~ normal(0,10000)                         (1)
                        {sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_price.
```

```
Bayesian linear 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  =      .3272
                                                 Efficiency:  min =     .05887
                                                              avg =      .1093
Log marginal likelihood = -699.23257                          max =      .1958

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
price        |
      length |  33.03301    1.80186   .060848   33.07952   29.36325   36.41022
             |
     foreign |
    Foreign  |  32.77011   98.97104   4.07922    34.3237  -164.1978   222.0855
       _cons | -8.063175   102.9479   3.34161  -9.110308  -205.9497   196.9341
-------------+----------------------------------------------------------------
      sigma2 |   7538628    1297955   29334.9    7414320    5379756   1.04e+07
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

The posterior mean estimates of the regression coefficients are smaller (in absolute value) than the corresponding estimates from the `regress` command, because the default prior for the coefficients, `normal(0, 10000)`, is informative and has a strong shrinkage effect. For example, the least-square estimate of the constant term from `regress` is about −11,621, and its scale is much larger than the default prior standard deviation of 100. As a result, the default prior shrinks the estimate of the constant toward 0 and, specifically, to −8.06.

You should be aware that the default priors are provided for convenience and are not guaranteed to be uninformative in all cases. They are designed to have little effect on model parameters, the maximum likelihood estimates of which are of moderate size, say, less than 100 in absolute value. For large-scale parameters, as in this example, the default priors can become informative.

◁

▷ Example 5: Flat priors

Continuing with example 4, we can override the default priors using the `prior()` option. We can, for example, apply the completely uninformative `flat` prior, a prior with the density of 1, for the coefficient parameters.

```
. set seed 15

. bayes, prior({price:}, flat) burnin(5000): regress price length i.foreign
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  price ~ regress(xb_price,{sigma2})

Priors:
  {price:length 1.foreign _cons} ~ 1 (flat)                                (1)
                        {sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_price.
```

```
Bayesian linear 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  =      .3404
                                                 Efficiency:  min =     .07704
                                                              avg =      .1086
Log marginal likelihood = -669.62603                          max =      .1898

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
price        |
      length |  89.51576   16.27187   .586237   89.60969   57.96996   122.7961
             |
     foreign |
    Foreign  |  2795.683   770.6359   26.0589   2787.139   1305.773   4298.785
       _cons | -11478.83   3202.027   113.271  -11504.65  -17845.87  -5244.189
-------------+----------------------------------------------------------------
      sigma2 |   6270294    1089331   25002.1    6147758    4504695    8803268
------------------------------------------------------------------------------
Note: Default priors are used for some model parameters.
```

The posterior mean estimates for the coefficient parameters are now close to the least-square estimates from `regress`. For example, the posterior mean estimate for `{price:_cons}` is about −11,479, whereas the least-square estimate is −11,621.

However, the `flat` priors should be used with caution. Flat priors are improper and may result in improper posterior distributions for which Bayesian inference cannot be carried out. You should thus choose the priors carefully, accounting for the properties of the likelihood model.

◁

▷ Example 6: Zellner's *g*-prior

A type of prior specific to the normal linear regression model is Zellner's *g*-prior. We can apply it to our example using the `zellnersg0()` prior. For this prior, we need to specify the dimension of the prior, which is the number of regression coefficients (3), a degree of freedom (50) and the variance parameter of the error term in the regression model, `{sigma2}`; the mean parameter is assumed to be 0 by `zellnersg0()`. See example 9 in [BAYES] **bayesmh** for more details about Zellner's *g*-prior.

```
. set seed 15
. bayes, prior({price:}, zellnersg0(3, 50, {sigma2})) burnin(5000):
> regress price length i.foreign
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  price ~ regress(xb_price,{sigma2})
Priors:
  {price:length 1.foreign _cons} ~ zellnersg(3,50,0,{sigma2})             (1)
                        {sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_price.
```

```
Bayesian linear 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  =      .3019
                                                 Efficiency:  min =     .06402
                                                              avg =       .105
Log marginal likelihood = -697.84862                          max =      .1944

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
price        |
      length |  87.53039   16.24762   .569888   87.72965    55.5177   119.9915
             |
     foreign |
    Foreign  |  2759.267    794.043   31.3829   2793.241   1096.567   4202.283
       _cons | -11223.95   3211.553    113.34  -11308.39  -17534.25  -4898.139
-------------+----------------------------------------------------------------
      sigma2 |   6845242    1159035   26286.9    6716739    4978729    9521252
------------------------------------------------------------------------------
Note: Default priors are used for some model parameters.
```

We see that using this Zellner's *g*-prior has little effect on the coefficient parameters, and the simulated posterior mean estimates are close to the least-square estimates from `regress`.

◁

Logistic regression with perfect predictors

Let's revisit the example in *Logistic regression model: A case of nonidentifiable parameters* of [BAYES] **bayesmh**. The example uses `heartswitz.dta` to model the binary outcome `disease`, the presence of a heart disease, using the predictor variables `restecg`, `isfbs`, `age`, and `male`. The dataset is a sample from Switzerland.

```
. use http://www.stata-press.com/data/r15/heartswitz, clear
(Subset of Switzerland heart disease data from UCI Machine Learning Repository)
```

▷ Example 7: Perfect prediction

The logistic regression model for these data is

```
. logit disease restecg isfbs age male
```
 (*output omitted*)

To fit a Bayesian logistic regression, we prefix the `logit` command with `bayes`. We also specify the `noisily` option to show the estimation output of the `logit` command, which is run by the `bayes` prefix to set up the model and compute starting values for the parameters.

```
. set seed 15
. bayes, noisily: logit disease restecg isfbs age male
note: restecg != 0 predicts success perfectly
      restecg dropped and 17 obs not used
note: isfbs != 0 predicts success perfectly
      isfbs dropped and 3 obs not used
note: male != 1 predicts success perfectly
      male dropped 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 |      Coef.   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
------------------------------------------------------------------------------
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  disease ~ logit(xb_disease)
Prior:
  {disease:age _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    =         26
                                                 Acceptance rate  =      .2337
                                                 Efficiency:  min =      .1076
                                                              avg =      .1113
Log marginal likelihood = -14.795726                          max =       .115

------------------------------------------------------------------------------
             |                                                Equal-tailed
     disease |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
     restecg |  (omitted)
       isfbs |  (omitted)
         age | -.0405907   .1650514   .004868  -.0328198  -.4005246   .2592641
        male |  (omitted)
       _cons |  6.616447   9.516872   .290075   5.491008  -8.852858   28.99392
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

As evident from the output of the logit command, the covariates restecg, isfbs, and male are dropped because of perfect prediction. Although these predictors cannot be identified using the likelihood alone, they can be identified, potentially, in a posterior model with an informative prior. The default prior normal(0, 10000), used by the bayes prefix for the regression coefficients, is not informative enough to resolve the perfect prediction, and we must override it with a more informative prior.

◁

▷ Example 8: Informative prior

In the example in *Logistic regression model: A case of nonidentifiable parameters* of [BAYES] **bayesmh**, we use information from another similar dataset, `hearthungary.dta`, to come up with informative priors for the regression coefficients. We use the same priors with the `bayes` prefix. We specify the `asis` option with the `logit` command to prevent dropping the perfect predictors from the model. We also specify the `nomleinitial` option to prevent the `bayes` prefix from trying to obtain ML estimates to use as starting values; reliable ML estimates cannot be provided by the `logit` command when the perfect predictors are retained.

```
. set seed 15
. bayes, prior({disease:restecg age}, normal(0,10))
> prior({disease:isfbs male}, normal(1,10))
> prior({disease:_cons}, normal(-4,10)) nomleinitial:
> logit disease restecg isfbs age male, asis
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  =      .2121
                                                 Efficiency:  min =     .01885
                                                              avg =     .04328
Log marginal likelihood = -11.006071                          max =     .06184

------------------------------------------------------------------------------
             |                                                Equal-tailed
     disease |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
     restecg |  1.965122   2.315475   .115615   1.655961  -2.029873   6.789415
       isfbs |  1.708631   2.726071   .113734   1.607439  -3.306837   7.334592
         age |  .1258811   .0707431   .003621   .1245266  -.0016807   .2719748
        male |  .2671381   2.237349   .162967   .3318061  -4.106425   4.609955
       _cons | -2.441911   2.750613   .110611  -2.538183  -7.596747   3.185172
------------------------------------------------------------------------------
```

For this posterior model with informative priors, we successfully estimate all regression parameters in the logistic regression model.

The informative prior in this example is based on information from an independent dataset, `hearthungary.dta`, which is a sample of observations on the same heart condition and predictor attributes as `heartswitz.dta` but sampled from Hungary's population. Borrowing information from independent datasets to construct informative priors is justified only when the datasets are compatible with the currently analyzed data.

◁

Multinomial logistic regression

Consider the health insurance dataset, sysdsn1.dta, to model the insurance outcome, insure, which takes the values Indemnity, Prepaid, and Uninsure, using the predictor variables age, male, nonwhite, and site. This model is considered in more detail in example 4 in [R] **mlogit**.

```
. use http://www.stata-press.com/data/r15/sysdsn1, clear
(Health insurance data)
```

First, we use the mlogit command to fit the model

```
. mlogit insure age male nonwhite i.site, nolog

Multinomial logistic regression                 Number of obs     =        615
                                                LR chi2(10)       =      42.99
                                                Prob > chi2       =     0.0000
Log likelihood = -534.36165                     Pseudo R2         =     0.0387

------------------------------------------------------------------------------
      insure |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
Indemnity    |  (base outcome)
-------------+----------------------------------------------------------------
Prepaid      |
         age |   -.011745   .0061946    -1.90   0.058    -.0238862    .0003962
        male |   .5616934   .2027465     2.77   0.006     .1643175    .9590693
    nonwhite |   .9747768   .2363213     4.12   0.000     .5115955    1.437958
             |
        site |
          2  |   .1130359   .2101903     0.54   0.591    -.2989296    .5250013
          3  |  -.5879879   .2279351    -2.58   0.010    -1.034733   -.1412433
             |
       _cons |   .2697127   .3284422     0.82   0.412    -.3740222    .9134476
-------------+----------------------------------------------------------------
Uninsure     |
         age |  -.0077961   .0114418    -0.68   0.496    -.0302217    .0146294
        male |   .4518496   .3674867     1.23   0.219     -.268411     1.17211
    nonwhite |   .2170589   .4256361     0.51   0.610    -.6171725     1.05129
             |
        site |
          2  |  -1.211563   .4705127    -2.57   0.010    -2.133751   -.2893747
          3  |  -.2078123   .3662926    -0.57   0.570    -.9257327     .510108
             |
       _cons |  -1.286943   .5923219    -2.17   0.030    -2.447872   -.1260134
------------------------------------------------------------------------------
```

Next, we use the bayes prefix to perform Bayesian estimation of the same multinomial logistic regression model.

```
. set seed 15

. bayes: mlogit insure age male nonwhite i.site
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  Prepaid Uninsure ~ mlogit(xb_Prepaid,xb_Uninsure)

Priors:
   {Prepaid:age male nonwhite i.site _cons} ~ normal(0,10000)             (1)
  {Uninsure:age male nonwhite i.site _cons} ~ normal(0,10000)             (2)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_Prepaid.
(2) Parameters are elements of the linear form xb_Uninsure.
```

```
Bayesian multinomial logistic regression         MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
Base outcome: Indemnity                          Number of obs    =        615
                                                 Acceptance rate  =      .2442
                                                 Efficiency:  min =     .01992
                                                              avg =     .03086
Log marginal likelihood = -614.49286                          max =     .05659

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
Prepaid      |
         age | -.0125521    .006247   .000396  -.0125871   -.024602  -.0005809
        male |  .5462718   .2086422   .012818   .5573004   .1263754   .9271802
    nonwhite |  .9796293   .2275709   .015746   .9737777     .53642   1.401076
             |
        site |
          2  |   .098451    .214039   .012887   .0994476  -.3172914   .5260208
          3  | -.6043961   .2348319   .011596  -.6072807  -1.045069  -.1323191
             |
       _cons |  .3183984   .3309283   .021325   .3219128  -.3423583    .956505
-------------+----------------------------------------------------------------
Uninsure     |
         age |  -.008377   .0118479   .000581  -.0082922  -.0323571   .0140366
        male |  .4687524   .3537416    .02376   .4748359  -.2495656   1.147333
    nonwhite |  .1755361     .42708   .022566    .198253  -.7214481    .938098
             |
        site |
          2  | -1.298562   .4746333   .033628   -1.27997  -2.258622  -.4149035
          3  | -.2057122   .3533365   .020695  -.2009649   -.904768   .4924401
             |
       _cons | -1.305083   .5830491    .02451  -1.296332  -2.463954  -.1758435
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

For this model and these data, the default prior specification of the bayes prefix is fairly uninformative and, as a result, the posterior mean estimates for the parameters are close to the ML estimates obtained with mlogit.

We can report posterior summaries for the relative-risk ratios instead of the regression coefficients. This is equivalent to applying an exponential transformation, $\exp(b)$, to the simulated values of each of the regression coefficients, b, and then summarizing them. We can obtain relative-risk ratio summaries by replaying the bayes command with the rrr option specified. We use the already available simulation results from the last estimation and do not refit the model. We could have also specified the rrr option during the estimation.

```
. bayes, rrr

Model summary
------------------------------------------------------------------------------
Likelihood:
  Prepaid Uninsure ~ mlogit(xb_Prepaid,xb_Uninsure)

Priors:
   {Prepaid:age male nonwhite i.site _cons} ~ normal(0,10000)              (1)
  {Uninsure:age male nonwhite i.site _cons} ~ normal(0,10000)              (2)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_Prepaid.
(2) Parameters are elements of the linear form xb_Uninsure.
```

```
Bayesian multinomial logistic regression         MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
Base outcome: Indemnity                          Number of obs    =        615
                                                 Acceptance rate  =      .2442
                                                 Efficiency:  min =     .02149
                                                              avg =     .03181
Log marginal likelihood = -614.49286                          max =     .06007

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |        RRR   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
Prepaid      |
         age |  .9875456   .0061686   .000391   .9874918   .9756982   .9994192
        male |  1.764212   .3634348   .022268   1.745953   1.134708   2.527372
    nonwhite |  2.732931   .6240495   .042568   2.647929   1.709875   4.059566
             |
        site |
          2  |  1.129077   .2450092   .015242   1.104561   .7281185   1.692189
          3  |  .5617084   .1338774    .00665   .5448304   .3516675   .8760614
             |
       _cons |  1.451983   .4904589   .029972   1.379764   .7100938    2.60259
-------------+----------------------------------------------------------------
Uninsure     |
         age |  .9917276   .0117452   .000575    .991742   .9681608   1.014136
        male |  1.699605   .6045513   .040763    1.60775   .7791391   3.149782
    nonwhite |  1.301138   .5448086   .027742   1.219271   .4860479   2.555117
             |
        site |
          2  |  .3045686   .1461615   .009698   .2780457   .1044944   .6604046
          3  |  .8663719   .3155926    .01806   .8179411   .4046357   1.636304
             |
       _cons |  .3203309   .1976203   .008063   .2735332   .0850978   .8387492
------------------------------------------------------------------------------
Note: _cons estimates baseline relative risk for each outcome.
Note: Default priors are used for model parameters.
```

Generalized linear model

Consider the insecticide experiment dataset, `beetle.dta`, to model the number of beetles killed, `r`, on the number of subjected beetles, `n`; the type of beetles, `beetle`; and the log-dose of insecticide, `ldose`. More details can be found in example 2 of [R] **glm**.

```
. use http://www.stata-press.com/data/r15/beetle, clear
```

Consider a generalized linear model with a binomial family and a complementary log-log link function for these data.

```
. glm r i.beetle ldose, family(binomial n) link(cloglog) nolog

Generalized linear models                         No. of obs      =         24
Optimization     : ML                             Residual df     =         20
                                                  Scale parameter =          1
Deviance         =  73.76505595                   (1/df) Deviance =   3.688253
Pearson          =   71.8901173                   (1/df) Pearson  =   3.594506

Variance function: V(u) = u*(1-u/n)               [Binomial]
Link function    : g(u) = ln(-ln(1-u/n))          [Complementary log-log]

                                                  AIC             =    6.74547
Log likelihood   = -76.94564525                   BIC             =   10.20398

------------------------------------------------------------------------------
             |                 OIM
           r |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      beetle |
   Red flour |  -.0910396   .1076132    -0.85   0.398    -.3019576    .1198783
    Mealworm |  -1.836058   .1307125   -14.05   0.000     -2.09225   -1.579867
             |
       ldose |   19.41558   .9954265    19.50   0.000     17.46458    21.36658
       _cons |  -34.84602    1.79333   -19.43   0.000    -38.36089   -31.33116
------------------------------------------------------------------------------
```

To fit a Bayesian generalized linear model with default priors, we type

```
. set seed 15

. bayes: glm r i.beetle ldose, family(binomial n) link(cloglog)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  r ~ glm(xb_r)

Prior:
  {r:i.beetle ldose _cons} ~ normal(0,10000)                                (1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_r.

Bayesian generalized linear models               MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
Family : binomial n                              Number of obs    =         24
Link   : complementary log-log                   Scale parameter  =          1
                                                 Acceptance rate  =      .2003
                                                 Efficiency:  min =     .03414
                                                              avg =     .05094
Log marginal likelihood =  -102.9776                          max =     .08012

------------------------------------------------------------------------------
             |                                                Equal-tailed
           r |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
      beetle |
   Red flour | -.0903569    .106067   .004527  -.093614  -.2964984    .112506
    Mealworm | -1.843952    .130297   .004603 -1.848374  -2.091816  -1.594582
             |
       ldose |  19.52814   .9997765   .054106  19.52709    17.6146    21.6217
       _cons | -35.04832   1.800461   .096777  -35.0574  -38.81427  -31.61378
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

The posterior mean estimates of the regression parameters are not that different from the ML estimates obtained with glm.

If desired, we can request highest posterior density intervals be reported instead of default equal-tailed credible intervals by specifying the hpd option. We can also change the credible-interval level; for example, to request 90% credible intervals, we specify the clevel(90) option. We also could specify these options during estimation.

```
. bayes, clevel(90) hpd
Model summary
------------------------------------------------------------------------------
Likelihood:
  r ~ glm(xb_r)

Prior:
  {r:i.beetle ldose _cons} ~ normal(0,10000)                               (1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_r.

Bayesian generalized linear models               MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
Family : binomial n                              Number of obs    =         24
Link   : complementary log-log                   Scale parameter  =          1
                                                 Acceptance rate  =      .2003
                                                 Efficiency:  min =     .03414
                                                              avg =     .05094
Log marginal likelihood =  -102.9776                          max =     .08012

------------------------------------------------------------------------------
             |                                                HPD
           r |      Mean   Std. Dev.     MCSE     Median  [90% Cred. Interval]
-------------+----------------------------------------------------------------
      beetle |
   Red flour | -.0903569    .106067   .004527  -.093614  -.2444412   .1020305
    Mealworm | -1.843952    .130297   .004603 -1.848374   -2.03979  -1.620806
             |
       ldose |  19.52814   .9997765   .054106  19.52709   17.86148   21.16389
       _cons | -35.04832   1.800461   .096777  -35.0574  -37.96057  -32.00411
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

Truncated Poisson regression

The semiconductor manufacturing dataset, probe.dta, contains observational data of failure rates, failure, of silicon wafers with width, width, and depth, depth, tested at four different probes, probe. A wafer is rejected if more than 10 failures are detected. See example 2 in [R] **tpoisson**.

```
. use http://www.stata-press.com/data/r15/probe, clear
```

We fit a truncated Poisson regression model with a truncation point of 10. We suppress the constant regression term from the likelihood equation using the noconstant option to retain all four probe levels by including ibn.probe in the list of covariates, which declares probe to be a factor variable with no base level.

```
. tpoisson failures ibn.probe depth width, noconstant ll(10) nolog

Truncated Poisson regression
Limits:   lower =          10                    Number of obs     =         88
          upper =        +inf                    Wald chi2(6)      =   11340.50
Log likelihood = -239.35746                      Prob > chi2       =     0.0000

------------------------------------------------------------------------------
    failures |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       probe |
          1  |   2.714025   .0752617    36.06   0.000     2.566515    2.861536
          2  |   2.602722   .0692732    37.57   0.000     2.466949    2.738495
          3  |   2.725459   .0721299    37.79   0.000     2.584087    2.866831
          4  |   3.139437   .0377137    83.24   0.000     3.065519    3.213354
             |
       depth |  -.0005034   .0033375    -0.15   0.880    -.0070447     .006038
       width |   .0330225    .015573     2.12   0.034     .0025001     .063545
------------------------------------------------------------------------------
```

▷ Example 9: Default priors

We first apply the bayes prefix with default priors to perform Bayesian estimation of the model. The estimation takes a little longer, so we specify the dots option to see the progress.

```
. set seed 15

. bayes, dots: tpoisson failures ibn.probe depth width, noconstant ll(10)
Burn-in 2500 aaaaaaaaa1000.........2000..... done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done

Model summary
------------------------------------------------------------------------------
Likelihood:
  failures ~ tpoisson(xb_failures)

Prior:
  {failures:i.probe depth width} ~ normal(0,10000)                         (1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_failures.

Bayesian truncated Poisson regression             MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling          Burn-in          =      2,500
                                                  MCMC sample size =     10,000
Limits: lower =          10                       Number of obs    =         88
        upper =        +inf                       Acceptance rate  =      .1383
                                                  Efficiency:  min =    .004447
                                                               avg =     .01322
Log marginal likelihood = -288.22663                           max =     .04082

------------------------------------------------------------------------------
             |                                                Equal-tailed
    failures |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
       probe |
          1  |  2.689072   .0696122   .008596   2.688881   2.557394   2.833737
          2  |  2.581567   .0644141    .00966   2.588534   2.436973   2.701187
          3  |  2.712054   .0695932   .006415   2.717959    2.55837   2.844429
          4  |   3.13308   .0397521   .004592   3.133433   3.055979   3.208954
             |
       depth |  -.000404   .0033313   .000165   -.000504  -.0067928   .0061168
       width |   .036127   .0165308   .001821   .0360637    .001239    .067552
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
Note: There is a high autocorrelation after 500 lags.
```

With the default prior specification, the posterior mean estimates for the regression parameters are similar to the ML estimates obtained with the tpoisson command. However, the bayes prefix issues a high autocorrelation warning note and reports a minimum efficiency of only 0.004. The posterior model with default priors seems to be somewhat challenging for the MH sampler. We could allow for longer burn-in and increase the MCMC sample size to improve the MCMC convergence and increase the estimation precision. Instead, we will provide an alternative prior specification that will increase the model flexibility and improve its fit to the data.

◁

▷ Example 10: Hyperpriors

We now assume that the four probe coefficients, {failures:ibn.probe}, have a normal prior distribution with mean parameter {probe_mean} and a variance of 10,000. It is reasonable to assume that all four probes have positive failure rates and that {probe_mean} is a positive hyperparameter. We decide to assign {probe_mean} a gamma(2, 1) hyperprior, which is a distribution with a positive domain and a mean of 2. We use this prior for the purpose of illustration; this prior is not informative for this model and these data. We initialize {probe_mean} with 1 to give it a starting value compatible with its hyperprior.

```
. set seed 15
. bayes, prior({failures:ibn.probe}, normal({probe_mean}, 10000))
> prior({probe_mean}, gamma(2, 1)) initial({probe_mean} 1) dots:
> tpoisson failures ibn.probe depth width, noconstant ll(10)
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  failures ~ tpoisson(xb_failures)
Priors:
      {failures:i.probe} ~ normal({probe_mean},10000)                      (1)
  {failures:depth width} ~ normal(0,10000)                                 (1)
Hyperprior:
  {probe_mean} ~ gamma(2,1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_failures.
```

```
Bayesian truncated Poisson regression            MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
Limits: lower =          10                      Number of obs    =         88
        upper =        +inf                      Acceptance rate  =       .304
                                                 Efficiency:  min =     .04208
                                                              avg =      .0775
Log marginal likelihood = -287.91504                          max =       .127

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
failures     |
       probe |
          1  |  2.703599   .0770656   .003757   2.704613   2.551404   2.848774
          2  |  2.592738   .0711972   .002796   2.594628   2.446274   2.728821
          3  |  2.716223   .0755001   .003549   2.719622   2.568376   2.863064
          4  |  3.137069   .0388127   .001317   3.136773   3.062074   3.211616
             |
       depth |  -.000461   .0033562   .000109  -.0004457  -.0067607   .0062698
       width |  .0337508   .0152654   .000532   .0337798    .003008   .0622191
-------------+----------------------------------------------------------------
  probe_mean |  2.051072   1.462867   .041051    1.71286   .2211973   5.809428
------------------------------------------------------------------------------
Note: Default priors are used for some model parameters.
```

The MCMC simulation achieves an average efficiency of about 8% with no indication of convergence problems. Not only are the posterior mean estimates for the regression parameters similar to the ML estimates, but the MCMC standard errors are much lower than those achieved by the previous model with default priors. By introducing the hyperparameter `{probe_mean}`, we have improved the goodness of fit of the model.

◁

Zero-inflated negative binomial model

In this example, we consider a Bayesian model using zero-inflated negative binomial likelihood. We revisit example 1 in [R] **zinb**, which models the number of fish caught by visitors to a national park. The probability that a particular visitor fished is assumed to depend on the variables `child` and `camper`, which are supplied as covariates to the `inflate()` option of `zinb`.

```
. use http://www.stata-press.com/data/r15/fish, clear
. zinb count persons livebait, inflate(child camper) nolog
Zero-inflated negative binomial regression      Number of obs     =        250
                                                Nonzero obs       =        108
                                                Zero obs          =        142

Inflation model = logit                         LR chi2(2)        =      82.23
Log likelihood  = -401.5478                     Prob > chi2       =     0.0000

------------------------------------------------------------------------------
       count |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
count        |
     persons |   .9742984   .1034938     9.41   0.000     .7714543    1.177142
    livebait |   1.557523   .4124424     3.78   0.000     .7491503    2.365895
       _cons |  -2.730064    .476953    -5.72   0.000    -3.664874   -1.795253
-------------+----------------------------------------------------------------
inflate      |
       child |   3.185999   .7468551     4.27   0.000      1.72219    4.649808
      camper |  -2.020951    .872054    -2.32   0.020    -3.730146   -.3117567
       _cons |  -2.695385   .8929071    -3.02   0.003     -4.44545   -.9453189
-------------+----------------------------------------------------------------
    /lnalpha |   .5110429   .1816816     2.81   0.005     .1549535    .8671323
-------------+----------------------------------------------------------------
       alpha |   1.667029   .3028685                      1.167604    2.380076
------------------------------------------------------------------------------
```

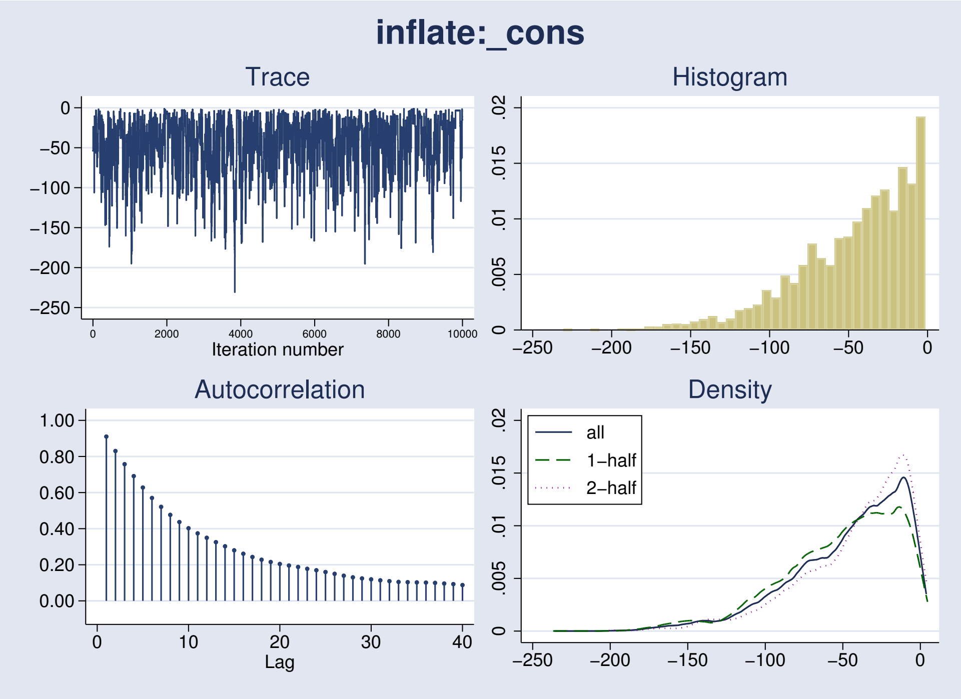
Let’s fit a Bayesian model with default normal prior distributions.

```
. set seed 15
. bayes, dots: zinb count persons livebait, inflate(child camper)
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  count ~ zinb(xb_count,xb_inflate,{lnalpha})
Priors:
  {count:persons livebait _cons} ~ normal(0,10000)                         (1)
    {inflate:child camper _cons} ~ normal(0,10000)                         (2)
                       {lnalpha} ~ normal(0,10000)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_count.
(2) Parameters are elements of the linear form xb_inflate.
```

```
Bayesian zero-inflated negative binomial model   MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
Inflation model: logit                           Number of obs    =        250
                                                 Acceptance rate  =      .3084
                                                 Efficiency:  min =     .03716
                                                              avg =      .0791
Log marginal likelihood = -438.47876                          max =      .1613

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
count        |
     persons |  .9851217   .1084239   .003601    .985452   .7641609   1.203561
    livebait |  1.536074   .4083865   .013509   1.515838    .753823     2.3539
       _cons | -2.805915   .4700702   .014974  -2.795244   -3.73847   -1.89491
-------------+----------------------------------------------------------------
inflate      |
       child |  46.95902   36.33974   1.87977   38.77997   3.612863   138.3652
      camper |   -46.123   36.34857   1.88567  -37.66796  -137.4568  -2.544566
       _cons | -46.62439   36.36232   1.88355   -38.5171  -137.5522  -3.272469
-------------+----------------------------------------------------------------
     lnalpha |  .7055935   .1591234   .003962   .7048862   .3959316   1.025356
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

The posterior mean estimates for the main regression coefficients {count:persons}, {count:livebait}, and {count:_cons} are relatively close to the ML estimates from the zinb command, but the inflation coefficients, {inflate:child}, {inflate:camper}, and {inflate:_cons}, are quite different. For example, zinb estimates {inflate:_cons} are about −2.7, whereas the corresponding posterior mean estimate is about −46.6. To explain this large discrepancy, we draw the diagnostic plot of {inflate:_cons}.

```
. bayesgraph diagnostic {inflate:_cons}
```



The marginal posterior distribution of {inflate:_cons} is highly skewed to the left, and it is apparent that its posterior mean is much smaller than its posterior mode. In large samples, under proper noninformative priors, the posterior mode estimator and the ML estimator are equivalent. Therefore, it is not surprising that the posterior mean of {inflate:_cons} is much smaller than its ML estimate. We can obtain a rough estimate of the posterior mode in this example.

First, we need to save the simulation results in a dataset, say, sim_zinb.dta. You can do this during estimation or on replay by specifying the saving() option with the bayes prefix.

```
. bayes, saving(sim_zinb)
note: file sim_zinb.dta saved
```

Next, we load the dataset and identify the variable that represents the parameter {inflate:_cons}.

```
. use sim_zinb, clear

. describe

Contains data from sim_zinb.dta
  obs:         6,874
 vars:            11                          8 Feb 2017 13:27
 size:       604,912
-------------------------------------------------------------------------------
              storage   display    value
variable name   type    format     label      variable label
-------------------------------------------------------------------------------
_index          double  %10.0g
_loglikelihood  double  %10.0g
_logposterior   double  %10.0g
eq1_p1          double  %10.0g
eq1_p2          double  %10.0g
eq1_p3          double  %10.0g
eq2_p1          double  %10.0g
eq2_p2          double  %10.0g
eq2_p3          double  %10.0g
eq0_p1          double  %10.0g
_frequency      double  %10.0g
-------------------------------------------------------------------------------
Sorted by:
```

Because {inflate:_cons} is the third parameter in the second equation, its corresponding simulation variable is eq2_p3.

Finally, we use the egen's mode() function to generate a constant variable, mode, which contains the mode estimate for {inflate:_cons}.

```
. egen mode = mode(eq2_p3)

. display mode[1]
-3.417458
```

The mode estimate for {inflate:_cons} is about −3.42, and it is indeed much closer to the ML estimate of −2.70 than its posterior mean estimate.

The inflation parameter α in the likelihood of the zero-inflated negative binomial model is log-transformed, and it is represented by {lnalpha} in our posterior model. To summarize the simulation result for α directly, we can use the bayesstats summary command to exponentiate {lnalpha}.

```
. bayesstats summary (alpha: exp({lnalpha}))

Posterior summary statistics                      MCMC sample size =    10,000

       alpha : exp({lnalpha})

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
       alpha |  2.050889   .3292052   .008191   2.023616   1.485768   2.788087
------------------------------------------------------------------------------
```

Parametric survival model

Consider example 7 in [ST] **streg**, which analyzes the effect of a hip-protection device, age, and sex on the risk of hip fractures in patients. The survival dataset is hip3.dta with time to event variable time1 and failure variable fracture. The data are already stset.

```
. use http://www.stata-press.com/data/r15/hip3, clear
(hip fracture study)

. stset
-> stset time1, id(id) failure(fracture) time0(time0)

                id:  id
     failure event:  fracture != 0 & fracture < .
obs. time interval:  (time0, time1]
 exit on or before:  failure

------------------------------------------------------------------------------
        206  total observations
          0  exclusions
------------------------------------------------------------------------------
        206  observations remaining, representing
        148  subjects
         37  failures in single-failure-per-subject data
      1,703  total analysis time at risk and under observation
                                                at risk from t =         0
                                     earliest observed entry t =         0
                                          last observed exit t =        39
```

It is assumed that the hazard curves for men and women have different shapes. We use the `streg` command to fit a model with Weibull survival distribution and the ancillary variable `male` to account for the difference between men and women.

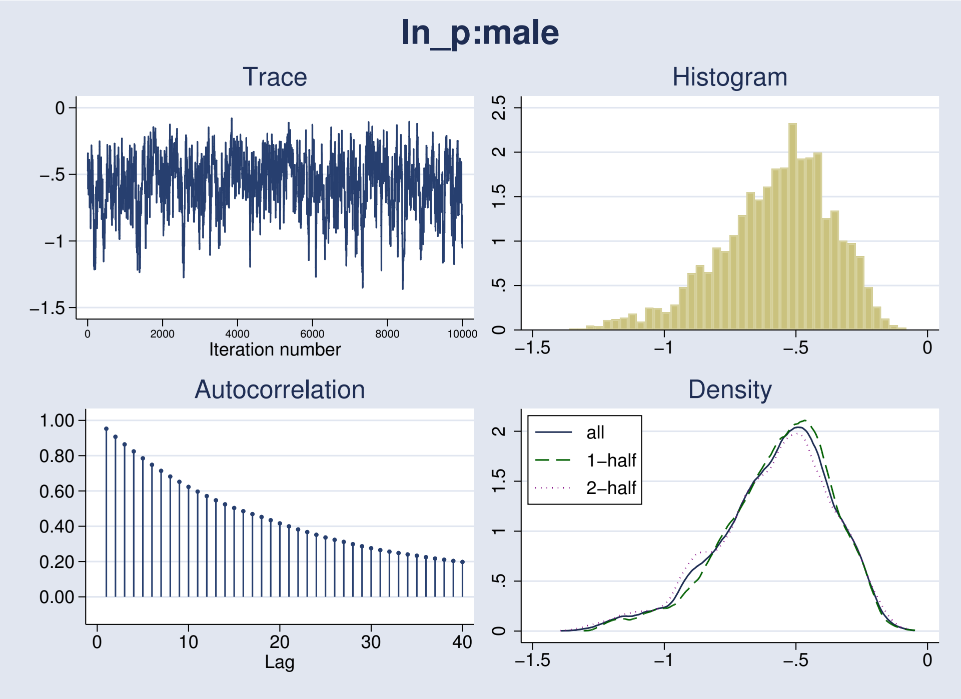
```
. streg protect age, distribution(weibull) ancillary(male) nolog

         failure _d:  fracture
   analysis time _t:  time1
                 id:  id

Weibull PH regression

No. of subjects =          148                  Number of obs    =        206
No. of failures =           37
Time at risk    =         1703
                                                LR chi2(2)       =      39.80
Log likelihood  =   -69.323532                  Prob > chi2      =     0.0000

------------------------------------------------------------------------------
          _t |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
_t           |
     protect |  -2.130058   .3567005    -5.97   0.000    -2.829178   -1.430938
         age |   .0939131   .0341107     2.75   0.006     .0270573    .1607689
       _cons |  -10.17575   2.551821    -3.99   0.000    -15.17722   -5.174269
-------------+----------------------------------------------------------------
ln_p         |
        male |  -.4887189    .185608    -2.63   0.008    -.8525039   -.1249339
       _cons |   .4540139   .1157915     3.92   0.000     .2270667    .6809611
------------------------------------------------------------------------------
```

We then perform Bayesian analysis of the same model using the `bayes` prefix. We apply more conservative normal priors, `normal(0, 100)`, by specifying the `normalprior(10)` option. To allow for longer adaptation of the MCMC sampler, we increase the burn-in period to 5,000, `burnin(5000)`.

```
. set seed 15

. bayes, normalprior(10) burnin(5000) dots:
> streg protect age, distribution(weibull) ancillary(male)

         failure _d:  fracture
   analysis time _t:  time1
                 id:  id
Burn-in 5000 aaaaaaaaa1000aaaaaaaaa2000aaaaaaaaa3000aaaaaaaaa4000aaaaaaaaa5000
> done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done

Model summary
------------------------------------------------------------------------------
Likelihood:
  _t ~ streg_weibull(xb__t,xb_ln_p)

Priors:
  {_t:protect age _cons} ~ normal(0,100)                                   (1)
       {ln_p:male _cons} ~ normal(0,100)                                   (2)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb__t.
(2) Parameters are elements of the linear form xb_ln_p.

Bayesian Weibull PH regression                   MCMC iterations  =     15,000
Random-walk Metropolis-Hastings sampling         Burn-in          =      5,000
                                                 MCMC sample size =     10,000
No. of subjects =        148                     Number of obs    =        206
No. of failures =         37
No. at risk     =       1703
                                                 Acceptance rate  =      .3418
                                                 Efficiency:  min =        .01
                                                              avg =     .03421
Log marginal likelihood = -91.348814                          max =     .05481

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
_t           |
     protect | -2.114715   .3486032   .017409  -2.105721  -2.818483   -1.46224
         age |  .0859305   .0328396   .001403   .0862394   .0210016   .1518009
       _cons |  -9.57056   2.457818   .117851  -9.551418  -14.49808   -4.78585
-------------+----------------------------------------------------------------
ln_p         |
        male | -.5753907   .2139477   .014224  -.5468488   -1.07102  -.2317242
       _cons |  .4290642     .11786   .011786   .4242712    .203933   .6548229
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

The posterior mean estimates for the regression parameters `{_t:protect}`, `{_t:age}`, and `{_t:_cons}` are close to the estimates reported by the `streg` command. However, the estimate for `{ln_p:male}` is somewhat different. If we inspect the diagnostic plot for `{ln_p:male}`, we will see that the reason for this is the asymmetrical shape of its marginal posterior distribution.

```
. bayesgraph diagnostic {ln_p:male}
```



As evident from the density plot, the posterior distribution of `{ln_p:male}` is skewed to the left, so the posterior mean estimate, −0.58, is expected to be smaller than the ML estimate, −0.49, given that we used fairly uninformative priors; see *Zero-inflated negative binomial model* for the comparison of posterior mean, posterior mode, and ML estimates for highly skewed posterior distributions.

Heckman selection model

▷ Example 11

A representative example of a Heckman selection model is provided by `wagenwk.dta`, which contains observations on the income of women who choose to work. See example 1 in [R] **heckman**.

```
. use http://www.stata-press.com/data/r15/womenwk, clear
```

The women's income (`wage`) is assumed to depend on their education (`educ`) and their age (`age`). In addition, the selection decision, or the choice of a woman to work, is assumed to depend on their marital status (`married`), number of children (`children`), education, and age. We fit this selection model using the `heckman` command.

```
. heckman wage educ age, select(married children educ age) nolog

Heckman selection model                         Number of obs     =      2,000
(regression model with sample selection)              Selected    =      1,343
                                                      Nonselected =        657

                                                Wald chi2(2)      =     508.44
Log likelihood = -5178.304                      Prob > chi2       =     0.0000

------------------------------------------------------------------------------
        wage |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
wage         |
   education |   .9899537   .0532565    18.59   0.000     .8855729    1.094334
         age |   .2131294   .0206031    10.34   0.000     .1727481    .2535108
       _cons |   .4857752   1.077037     0.45   0.652    -1.625179     2.59673
-------------+----------------------------------------------------------------
select       |
     married |   .4451721   .0673954     6.61   0.000     .3130794    .5772647
    children |   .4387068   .0277828    15.79   0.000     .3842534    .4931601
   education |   .0557318   .0107349     5.19   0.000     .0346917    .0767718
         age |   .0365098   .0041533     8.79   0.000     .0283694    .0446502
       _cons |  -2.491015   .1893402   -13.16   0.000    -2.862115   -2.119915
-------------+----------------------------------------------------------------
     /athrho |   .8742086   .1014225     8.62   0.000     .6754241    1.072993
    /lnsigma |   1.792559    .027598    64.95   0.000     1.738468     1.84665
-------------+----------------------------------------------------------------
         rho |   .7035061   .0512264                      .5885365    .7905862
       sigma |   6.004797   .1657202                       5.68862    6.338548
      lambda |   4.224412   .3992265                      3.441942    5.006881
------------------------------------------------------------------------------
LR test of indep. eqns. (rho = 0):   chi2(1) =    61.20   Prob > chi2 = 0.0000
```

We then apply the bayes prefix to perform Bayesian estimation of the Heckman selection model.

```
. set seed 15

. bayes, dots: heckman wage educ age, select(married children educ age)
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done

Model summary
------------------------------------------------------------------------------
Likelihood:
  wage ~ heckman(xb_wage,xb_select,{athrho} {lnsigma})

Priors:
                     {wage:education age _cons} ~ normal(0,10000)          (1)
  {select:married children education age _cons} ~ normal(0,10000)          (2)
                               {athrho lnsigma} ~ normal(0,10000)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_wage.
(2) Parameters are elements of the linear form xb_select.
```

```
Bayesian Heckman selection model                 MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =      2,000
                                                       Selected   =      1,343
                                                       Nonselected =       657
                                                 Acceptance rate  =      .3484
                                                 Efficiency:  min =     .02314
                                                              avg =     .03657
Log marginal likelihood = -5260.2024                          max =     .05013

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
wage         |
   education |  .9919131    .051865   .002609   .9931531   .8884407   1.090137
         age |  .2131372   .0209631   .001071   .2132548   .1720535   .2550835
       _cons |  .4696264   1.089225     .0716   .4406188  -1.612032    2.65116
-------------+----------------------------------------------------------------
select       |
     married |  .4461775   .0681721   .003045   .4456493   .3178532   .5785857
    children |  .4401305   .0255465   .001156   .4402145   .3911135   .4903804
   education |  .0559983   .0104231   .000484   .0556755   .0360289    .076662
         age |  .0364752   .0042497   .000248   .0362858   .0280584   .0449843
       _cons | -2.494424     .18976   .011327  -2.498414  -2.861266  -2.114334
-------------+----------------------------------------------------------------
      athrho |   .868392    .099374   .005961   .8699977   .6785641   1.062718
     lnsigma |  1.793428   .0269513   .001457   1.793226   1.740569   1.846779
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

The posterior mean estimates for the Bayesian model with default normal priors are similar to the ML estimates obtained with the `heckman` command.

We can calculate posterior summaries for the correlation parameter, ρ, and the standard error, σ, in their natural scale by inverse-transforming the model parameters `{athrho}` and `{lnsigma}` using the `bayesstats summary` command. We also include posterior summaries for the selectivity effect $\lambda = \rho\sigma$.

```
. bayesstats summary (rho:1-2/(exp(2*{athrho})+1))
> (sigma:exp({lnsigma}))
> (lambda:exp({lnsigma})*(1-2/(exp(2*{athrho})+1)))

Posterior summary statistics                      MCMC sample size =    10,000

         rho : 1-2/(exp(2*{athrho})+1)
       sigma : exp({lnsigma})
      lambda : exp({lnsigma})*(1-2/(exp(2*{athrho})+1))

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
         rho |  .6970522   .0510145   .003071    .701373   .5905851   .7867018
       sigma |  6.012205   .1621422   .008761   6.008807   5.700587   6.339366
      lambda |  4.196646   .3937209   .024351   4.212609   3.411479   4.946325
------------------------------------------------------------------------------
```

Again, the posterior mean estimates of ρ, σ, and λ agree with the ML estimates reported by `heckman`.

◁

Multilevel models

The bayes prefix supports several multilevel commands such as mixed and meglm; see [BAYES] **bayesian estimation**. Multilevel models introduce effects at different levels of hierarchy such as hospital effects and doctor-nested-within-hospital effects, which are often high-dimensional. These effects are commonly referred to as random effects in frequentist models. Bayesian multilevel models estimate random effects together with other model parameters. In contrast, frequentist multilevel models integrate random effects out, but provide ways to predict them after estimation, conditional on other estimated model parameters. Thus, in addition to regression coefficients and variance components (variances and covariances of random effects), Bayesian multilevel models include random effects themselves as model parameters. With a slight abuse of the terminology, we will sometimes refer to regression coefficients as fixed effects, keeping in mind that they are still random quantities from a Bayesian perspective.

Multilevel models are more difficult to simulate from because of the existence of high-dimensional random-effects parameters. They typically require longer burn-in periods to achieve convergence and larger MCMC sample sizes to obtain precise estimates of random effects and variance components.

Prior specification is particularly important for multilevel models. Using noninformative priors for all model parameters will likely result in nonconvergence or high autocorrelation of the MCMC sample, especially with small datasets. The default priors provided by the bayes prefix are chosen to be fairly uninformative, which may often lead to low simulation efficiencies for model parameters and, especially, for variance components; see *Default priors*. So, do not be surprised to see high autocorrelation with default priors, and be prepared to investigate various prior specifications during your analysis. For example, you may need to use the iwishartprior() option to increase the degrees of freedom and to specify a different scale matrix of the inverse-Wishart prior distribution used for the covariance matrices of random effects.

To change the default priors, you will need to know the names of the model parameters. See *Likelihood model* to learn how the bayes prefix labels the parameters. You can specify your own name stubs for the groups of random-effects parameters using the restubs() option. After simulation, see *Different ways of specifying model parameters* for how to refer to individual random effects to evaluate MCMC convergence or to obtain their MCMC summaries.

By default, the bayes prefix does not compute or display MCMC summaries of individual random effects to conserve computation time and space. You can specify the showreffects() or show() option to compute and display them for chosen groups of random effects. You cannot compute or display more random effects than the current value of set matsize minus other parameters in your model. You can also compute MCMC summaries of random effects after simulation by using [BAYES] **bayesstats summary**.

Also, the bayes prefix does not compute the log marginal likelihood by default for multilevel models. The computation involves the inverse of the determinant of the sample covariance matrix of all parameters and loses accuracy as the number of parameters grows. For high-dimensional models such as multilevel models, the computation 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 multilevel models, the log marginal likelihood is not computed by default. For multilevel models containing a small number of random effects, you can use the remargl option to compute and display it.

Two-level models

Consider example 1 from [ME] **mixed** that analyzed the weight gain of 48 pigs over 9 successive weeks. Detailed Bayesian analysis of these data using `bayesmh` are presented in *Panel-data and multilevel models* in [BAYES] **bayesmh**. Here, we use `bayes: mixed` to fit Bayesian two-level random-intercept and random-coefficient models to these data.

```
. use http://www.stata-press.com/data/r15/pig
(Longitudinal analysis of pig weights)
```

▷ Example 12: Random-intercept model, using option melabel

We first consider a simple random-intercept model of dependent variable `weight` on covariate `week` with variable `id` identifying pigs. The random-intercept model assumes that all pigs share a common growth rate but have different initial weight.

For comparison purposes, we first use the `mixed` command to fit this model by maximum likelihood.

```
. 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 |      Coef.   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   3.124226      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
```

To fit a Bayesian analog of this model, we simply prefix the mixed command with bayes. We also specify the melabel option with bayes to label model parameters in the output table as mixed does.

```
. set seed 15

. bayes, melabel: mixed weight week || id:
note: Gibbs sampling is used for regression coefficients and variance
      components
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done

Bayesian multilevel regression                   MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling           Burn-in          =      2,500
                                                 MCMC sample size =     10,000
Group variable: id                               Number of groups =         48

                                                 Obs per group:
                                                              min =          9
                                                              avg =        9.0
                                                              max =          9

                                                 Number of obs    =        432
                                                 Acceptance rate  =      .8112
                                                 Efficiency:  min =    .007005
                                                              avg =      .5064
Log marginal likelihood                                       max =          1

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
weight       |
        week |  6.209734   .0390718   .000391   6.209354   6.133233   6.285611
       _cons |  19.46511   .6239712    .07455   19.48275    18.2534   20.67396
-------------+----------------------------------------------------------------
id           |
   var(_cons)|   15.7247   3.436893   .049048   15.26104   10.31182   23.60471
-------------+----------------------------------------------------------------
var(Residual)|  4.411155   .3193582   .004397   4.396044   3.834341   5.080979
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

The estimates of posterior means and posterior standard deviations are similar to the ML estimates and standard errors from mixed. The results are also close to those from bayesmh in example 23 in [BAYES] **bayesmh**.

The average efficiency of the simulation is about 51% and there is no indication of any immediate convergence problems, but we should investigate convergence more thoroughly; see, for example, example 5 in [BAYES] **bayesian commands** and, more generally, *Convergence of MCMC* in [BAYES] **bayesmh**.

Because Bayesian multilevel models are generally slower than other commands, the bayes prefix displays dots by default with multilevel commands. You can specify the nodots option to suppress them.

Also, as we described in *Multilevel models*, the log marginal likelihood is not computed for multilevel models by default because of the high dimensionality of the models. This is also described in the help file that appears when you click on Log marginal likelihood in the output header in the Results window. For models with a small number of random effects, you can specify the remargl option to compute the log marginal likelihood.

An important note about `bayes: mixed` is the default simulation method. Most `bayes` prefix commands use an adaptive MH algorithm to sample model parameters. The high-dimensional nature of multilevel models greatly decreases the simulation efficiency of this algorithm. For Gaussian multilevel models, such as `bayes: mixed`, model parameters can be sampled using a more efficient, albeit slower, Gibbs algorithm under certain prior distributions. The default priors used for regression coefficients and variance components allow the `bayes` prefix to use Gibbs sampling for these parameters with the `mixed` command. If you change the prior distributions or the default blocking structure for some parameters, Gibbs sampling may not be available for those parameters and an adaptive MH sampling will be used instead.

◁

▷ Example 13: Random-intercept model, default output

When we specified the `melabel` option with `bayes` in example 12, we intentionally suppressed some of the essential output from `bayes: mixed`. Here is what we would have seen had we not specified `melabel`.

```
. bayes
Multilevel structure
──────────────────────────────────────────────────────────────────────────────
id
    {U0}: random intercepts
──────────────────────────────────────────────────────────────────────────────
Model summary
──────────────────────────────────────────────────────────────────────────────
Likelihood:
  weight ~ normal(xb_weight,{e.weight:sigma2})
Priors:
  {weight:week _cons} ~ normal(0,10000)                                    (1)
                 {U0} ~ normal(0,{U0:sigma2})                              (1)
    {e.weight:sigma2} ~ igamma(.01,.01)
Hyperprior:
  {U0:sigma2} ~ igamma(.01,.01)
──────────────────────────────────────────────────────────────────────────────
(1) Parameters are elements of the linear form xb_weight.
```

```
Bayesian multilevel regression                   MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling           Burn-in          =      2,500
                                                 MCMC sample size =     10,000
Group variable: id                               Number of groups =         48

                                                 Obs per group:
                                                              min =          9
                                                              avg =        9.0
                                                              max =          9

                                                 Number of obs    =        432
                                                 Acceptance rate  =      .8112
                                                 Efficiency:  min =    .007005
                                                              avg =      .5064
Log marginal likelihood                                       max =          1

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
weight       |
        week |  6.209734   .0390718   .000391   6.209354   6.133233   6.285611
       _cons |  19.46511   .6239712    .07455   19.48275    18.2534   20.67396
-------------+----------------------------------------------------------------
id           |
   U0:sigma2 |   15.7247   3.436893   .049048   15.26104   10.31182   23.60471
-------------+----------------------------------------------------------------
e.weight     |
      sigma2 |  4.411155   .3193582   .004397   4.396044   3.834341   5.080979
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

Let's go over the default output in detail, starting with the model summary. For multilevel models, in addition to the model summary, which describes the likelihood model and prior distributions, the `bayes` prefix displays information about the multilevel structure of the model.

```
Multilevel structure
------------------------------------------------------------------------------
id
    {U0}: random intercepts
------------------------------------------------------------------------------
```

Our multilevel model has one set of random effects, labeled as `U0`, which represent random intercepts at the `id` level. Recall that in Bayesian models, random effects are not integrated out but estimated together with other model parameters. So, `{U0}`, or using its full name `{U0[id]}`, represent random-effects parameters in our model. See *Likelihood model* to learn about the default naming convention for random-effects parameters.

According to the model summary below, the likelihood of the model is a normal linear regression with the linear predictor containing regression parameters {weight:week} and {weight:_cons} and random-effects parameters {U0}, and with the error variance labeled as {e.weight:sigma2}. Regression coefficients {weight:week} and {weight:_cons} have default normal priors with zero means and variances of 10,000. The random intercepts {U0} are normally distributed with mean zero and variance {U0:sigma2}. The variance components, error variance {e.weight:sigma2}, and random-intercept variance {U0:sigma2} have default inverse-gamma priors, InvGamma(0.01, 0.01). The random-intercept variance is a hyperparameter in our model.

```
Model summary
------------------------------------------------------------------------------
Likelihood:
  weight ~ normal(xb_weight,{e.weight:sigma2})

Priors:
  {weight:week _cons} ~ normal(0,10000)                                    (1)
                 {U0} ~ normal(0,{U0:sigma2})                              (1)
    {e.weight:sigma2} ~ igamma(.01,.01)

Hyperprior:
  {U0:sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_weight.
```

The default output table of bayes: mixed uses the names of model parameters as they are defined by the bayes prefix.

```
------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
weight       |
        week |  6.209734   .0390718   .000391   6.209354   6.133233   6.285611
       _cons |  19.46511   .6239712    .07455   19.48275    18.2534   20.67396
-------------+----------------------------------------------------------------
id           |
   U0:sigma2 |   15.7247   3.436893   .049048   15.26104   10.31182   23.60471
-------------+----------------------------------------------------------------
e.weight     |
      sigma2 |  4.411155   .3193582   .004397   4.396044   3.834341   5.080979
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

Becoming familiar with the native parameter names of the bayes prefix is important for prior specification and for later postestimation. The melabel option is provided for easier comparison of the results between the bayes prefix and the corresponding frequentist multilevel command.

◁

▷ Example 14: Displaying random effects

By default, the bayes prefix does not compute or display MCMC summaries for the random-effects parameters to conserve space and computational time. You can specify the showreffects option to display all random effects or the showreffects() or show() option to display specific random effects. For example, continuing example 13, we can display the random-effects estimates for the first five pigs as follows.

```
. bayes, show({U0[1/5]}) noheader

------------------------------------------------------------------------------
             |                                                Equal-tailed
      U0[id] |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
           1 | -1.778442   .8873077   .074832  -1.761984  -3.542545    .0062218
           2 |  .7831408   .8775376   .071421   .7961802  -.9547035    2.491798
           3 | -2.052634   .9038672   .072325  -2.061559  -3.822966   -.3246834
           4 | -1.891103    .878177   .075611  -1.858056  -3.642227   -.1028766
           5 | -3.316584   .8894319   .074946  -3.320502    -5.0469   -1.568927
------------------------------------------------------------------------------
```

These posterior mean estimates of random-effects parameters should be comparable with those predicted by `predict, reffects` after `mixed`. Posterior standard deviations, however, will generally be larger than the corresponding standard errors of random effects predicted after `mixed`, because the latter do not incorporate the uncertainty about the estimated model parameters.

You can also use [BAYES] **bayesstats summary** to obtain MCMC summaries of random-effects parameters after estimation:

```
. bayesstats summary {U0[1/5]}
  (output omitted)
```

If you decide to use the `showreffects` option to display all random-effects parameters, beware of the increased computation time for models with many random effects. Then, the `bayes` prefix will compute and display the MCMC summaries for only the first M random-effects parameters, where M is the maximum number of variables as determined by `matsize` minus the other model parameters. You can specify the `show()` option with `bayes` or use `bayesstats summary` to obtain results for other random-effects parameters.

◁

▷ Example 15: Random-coefficient model

Continuing example 13, let's consider a random-coefficient model that allows the growth rate to vary among pigs.

Following `mixed`'s specification, we include the random slope for `week` at the `id` level by specifying the `week` variable in the random-effects equation.

```
. set seed 15
. bayes: mixed weight week || id: week
note: Gibbs sampling is used for regression coefficients and variance
      components
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done
Multilevel structure
------------------------------------------------------------------------------
id
    {U0}: random intercepts
    {U1}: random coefficients for week
------------------------------------------------------------------------------

Model summary
------------------------------------------------------------------------------
Likelihood:
  weight ~ normal(xb_weight,{e.weight:sigma2})

Priors:
  {weight:week _cons} ~ normal(0,10000)                                    (1)
               {U0} ~ normal(0,{U0:sigma2})                                (1)
               {U1} ~ normal(0,{U1:sigma2})                                (1)
    {e.weight:sigma2} ~ igamma(.01,.01)

Hyperpriors:
  {U0:sigma2} ~ igamma(.01,.01)
  {U1:sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_weight.

Bayesian multilevel regression                   MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling           Burn-in          =      2,500
                                                 MCMC sample size =     10,000
Group variable: id                               Number of groups =         48

                                                 Obs per group:
                                                              min =          9
                                                              avg =        9.0
                                                              max =          9

                                                 Number of obs    =        432
                                                 Acceptance rate  =      .7473
                                                 Efficiency:  min =    .003057
                                                              avg =     .07487
Log marginal likelihood                                       max =      .1503

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
weight       |
        week |  6.233977   .0801192    .01449   6.237648    6.05268   6.387741
       _cons |  19.44135   .3426786   .044377   19.44532   18.76211   20.11843
-------------+----------------------------------------------------------------
id           |
   U0:sigma2 |  7.055525   1.649394   .050935   6.844225   4.466329   10.91587
   U1:sigma2 |  .3941786   .0901945   .002717   .3825387   .2526756   .6044887
-------------+----------------------------------------------------------------
e.weight     |
      sigma2 |  1.613775   .1261213   .003254   1.609296   1.386427   1.880891
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
Note: There is a high autocorrelation after 500 lags.
```

In addition to random intercepts {U0}, we now have random coefficients for week, labeled as {U1}, with the corresponding variance parameter {U1:sigma2}. Compared with the random-intercept model, by capturing the variability of slopes on week, we reduced the estimates of the error variance and the random-intercept variance.

The average simulation efficiency decreased to only 7%, and we now see a note about a high autocorrelation after 500 lags. We can use, for example, bayesgraph diagnostics to verify that the high autocorrelation in this example is not an indication of nonconvergence but rather of a slow mixing of our MCMC sample. If we use bayesstats ess, we will see that the coefficient on weight and the constant term have the lowest efficiency, which suggests that these parameters are likely to be correlated with some of the random-effects estimates. If we want to reduce the autocorrelation and improve precision of the estimates for these parameters, we can increase the MCMC sample size by specifying the mcmcsize() option or thin the MCMC chain by specifying the thinning() option.

◁

▷ Example 16: Random-coefficient model, unstructured covariance

In example 15, we assumed independence between random intercepts {U0} and random slopes on week, {U1}. We relax this assumption here by specifying an unstructured covariance matrix.

Before we proceed with estimation, let's review our model summary first by specifying the dryrun option.

```
. bayes, dryrun: mixed weight week || id: week, covariance(unstructured)
Multilevel structure
------------------------------------------------------------------------------
id
    {U0}: random intercepts
    {U1}: random coefficients for week
------------------------------------------------------------------------------

Model summary
------------------------------------------------------------------------------
Likelihood:
  weight ~ normal(xb_weight,{e.weight:sigma2})

Priors:
  {weight:week _cons} ~ normal(0,10000)                                    (1)
             {U0}{U1} ~ mvnormal(2,{U:Sigma,m})                            (1)
    {e.weight:sigma2} ~ igamma(.01,.01)

Hyperprior:
  {U:Sigma,m} ~ iwishart(2,3,I(2))
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_weight.
```

The prior distributions for random effects {U0} and {U1} are no longer independent. Instead, they have a joint prior—a bivariate normal distribution with covariance matrix parameter {U:Sigma,m}, which is short for {U:Sigma,matrix}. The random-effects stub U is used to label the covariance matrix. The covariance matrix {U:Sigma,m} is assigned a fairly uninformative inverse-Wishart prior with three degrees of freedom and an identity scale matrix; see *Default priors* for details.

Let’s now fit the model but suppress the model summary for brevity.

```
. set seed 15

. bayes, nomodelsummary: mixed weight week || id: week, covariance(unstructured)
note: Gibbs sampling is used for regression coefficients and variance
      components
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done

Multilevel structure
------------------------------------------------------------------------------
id
    {U0}: random intercepts
    {U1}: random coefficients for week
------------------------------------------------------------------------------

Bayesian multilevel regression                   MCMC iterations  =     12,500
Metropolis-Hastings and Gibbs sampling           Burn-in          =      2,500
                                                 MCMC sample size =     10,000
Group variable: id                               Number of groups =         48

                                                 Obs per group:
                                                              min =          9
                                                              avg =        9.0
                                                              max =          9

                                                 Number of obs    =        432
                                                 Acceptance rate  =      .7009
                                                 Efficiency:  min =    .003683
                                                              avg =     .07461
Log marginal likelihood                                       max =      .1602

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
weight       |
        week |  6.207086   .0878022   .014469   6.204974   6.041093   6.384891
       _cons |  19.39551   .4077822   .050353   19.40187   18.53869    20.1993
-------------+----------------------------------------------------------------
id           |
 U:Sigma_1_1 |  6.872161   1.627769   .061568   6.673481   4.282284   10.62194
 U:Sigma_2_1 | -.0866373   .2702822   .009861  -.0796118   -.645439   .4341423
 U:Sigma_2_2 |   .399525   .0904532   .002488   .3885861   .2575883   .6104775
-------------+----------------------------------------------------------------
e.weight     |
      sigma2 |  1.611889   .1263131   .003155   1.605368   1.381651   1.872563
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
Note: There is a high autocorrelation after 500 lags.
```

◁

The 95% credible interval for the covariance between {U0} and {U1}, labeled as {U:Sigma_2_1} in the output, is $[-.65, .43]$, which suggests independence between {U0} and {U1}.

Crossed-effects model

Let’s revisit example 4 from [ME] **meglm**, which analyzes salamander cross-breeding data. Two populations of salamanders are considered: whiteside males and females (variables wsm and wsf) and roughbutt males and females (variables rbm and rbf). Male and female identifiers are recorded in the male and female variables. The outcome binary variable y indicates breeding success or failure.

In example 4 of [ME] **meglm**, we fit a crossed-effects logistic regression for successful mating, in which the effects of `male` and `female` were crossed. For the purpose of illustration, we will fit a crossed-effects probit regression here using `meglm` with the probit link.

```
. use http://www.stata-press.com/data/r15/salamander

. meglm y wsm##wsf || _all: R.male || female:, family(bernoulli) link(probit)
note: crossed random-effects model specified; option intmethod(laplace)
implied
  (iteration log omitted)
Mixed-effects GLM                               Number of obs     =        360
Family:                 Bernoulli
Link:                      probit

--------------------------------------------------------------
                |     No. of       Observations per Group
 Group Variable |     Groups    Minimum    Average    Maximum
----------------+---------------------------------------------
           _all |          1        360      360.0        360
         female |         60          6        6.0          6
--------------------------------------------------------------

Integration method:     laplace
                                                Wald chi2(3)      =      41.50
Log likelihood = -208.11182                     Prob > chi2       =     0.0000
------------------------------------------------------------------------------
           y |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       1.wsm |  -.4121977   .2735675    -1.51   0.132    -.9483802    .1239847
       1.wsf |  -1.720323   .3223052    -5.34   0.000     -2.35203   -1.088617
             |
     wsm#wsf |
        1 1  |   2.121115   .3611665     5.87   0.000     1.413242    2.828989
             |
       _cons |   .5950942   .2350714     2.53   0.011     .1343628    1.055826
-------------+----------------------------------------------------------------
_all>male    |
   var(_cons)|   .3867491   .1789793                       .156139      .95796
-------------+----------------------------------------------------------------
female       |
   var(_cons)|   .4464111   .1976024                      .1874794    1.062959
------------------------------------------------------------------------------
LR test vs. probit model: chi2(2) = 29.35                 Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

To fit the corresponding Bayesian model, we prefix the above command with `bayes:`.

```
. set seed 15

. bayes: meglm y wsm##wsf || _all: R.male || female:, family(bernoulli)
> link(probit)
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done

Multilevel structure
------------------------------------------------------------------------------
male
    {U0}: random intercepts
female
    {V0}: random intercepts
------------------------------------------------------------------------------
```

```
Model summary
------------------------------------------------------------------------------
Likelihood:
  y ~ meglm(xb_y)

Priors:
  {y:1.wsm 1.wsf 1.wsm#1.wsf _cons} ~ normal(0,10000)                      (1)
                               {U0} ~ normal(0,{U0:sigma2})                (1)
                               {V0} ~ normal(0,{V0:sigma2})                (1)

Hyperpriors:
  {U0:sigma2} ~ igamma(.01,.01)
  {V0:sigma2} ~ igamma(.01,.01)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_y.

Bayesian multilevel GLM                          MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000

--------------------------------------------------------------
                |     No. of       Observations per Group
 Group Variable |     Groups    Minimum    Average    Maximum
----------------+---------------------------------------------
           _all |          1        360      360.0        360
         female |         60          6        6.0          6
--------------------------------------------------------------

Family : Bernoulli                               Number of obs    =        360
Link   : probit                                  Acceptance rate  =      .3223
                                                 Efficiency:  min =    .008356
                                                              avg =     .02043
Log marginal likelihood                                       max =     .02773

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
y            |
       1.wsm |  -.411886     .28122   .016889  -.4158334  -.9645049    .156521
       1.wsf | -1.722195   .3329918   .023312  -1.713574  -2.381169  -1.094443
             |
     wsm#wsf |
        1 1  |  2.110366   .3671998   .022643    2.09234   1.443113   2.831923
             |
       _cons |  .5858733   .2512646   .015407   .5906893   .0812177   1.077352
-------------+----------------------------------------------------------------
male         |
   U0:sigma2 |  .4291858   .2195246   .024015   .3876708   .1347684   .9648611
-------------+----------------------------------------------------------------
female       |
   V0:sigma2 |  .4928416   .2189307   .019043   .4576824   .1648551   1.003193
------------------------------------------------------------------------------
Note: Default priors are used for model parameters.
```

The variance components for male and female, {U0:sigma2} and {V0:sigma2}, are slightly higher than the corresponding ML estimates, but the regression coefficients are similar.

Video examples

Introduction to Bayesian analysis, part 1: The basic concepts

Introduction to Bayesian analysis, part 2: MCMC and the Metropolis–Hastings algorithm

A prefix for Bayesian regression in Stata

Bayesian linear regression using the bayes prefix: How to specify custom priors

Stored results

In addition to the results stored by `bayesmh`, the `bayes` prefix stores the following in `e()`:

Scalars	
`e(priorsigma)`	standard deviation of default normal priors
`e(priorshape)`	shape of default inverse-gamma priors
`e(priorscale)`	scale of default inverse-gamma priors
`e(blocksize)`	maximum size for blocks of model parameters
Macros	
`e(prefix)`	`bayes`
`e(cmdname)`	command name from *estimation_command*
`e(cmd)`	same as `e(cmdname)`
`e(command)`	estimation command line

Methods and formulas

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

Also see

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

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

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

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

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

[BAYES] **Glossary**

Title

bayesmh — Bayesian models using Metropolis–Hastings algorithm

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, and multiple-equations linear models. 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})
```

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))
```

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
```

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
```

As above, and set the random-number seed for reproducibility

```
set seed 1234
bayesmh y2 x1, likelihood(logit) prior({y2:}, normal(0,100))
```

Same as above

```
bayesmh y2 x1, likelihood(logit) prior({y2:}, normal(0,100))  ///
     rseed(1234)
```

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)))
```

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)))
```

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-equation 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 group variable gr and zero-mean normal prior with variance parameter {var} for the random-intercept parameters

```
bayesmh y1 x1, likelihood(logit) reffects(gr)            ///
     prior({y1:i.gr}, normal(0, {var}))                  ///
     prior({y1: x1 _cons}, flat) prior({var}, jeffreys)
```

Menu

Statistics > Bayesian analysis > General estimation and regression

Syntax

Univariate linear models

bayesmh *depvar* [*indepvars*] [*if*] [*in*] [*weight*],
    likelihood(*modelspec*) prior(*priorspec*) [reffects(*varname*) *options*]

Multivariate linear models

Multivariate normal linear regression with common regressors

bayesmh *depvars* = [*indepvars*] [*if*] [*in*] [*weight*],
    likelihood(mvnormal(...)) prior(*priorspec*) [*options*]

Multivariate normal regression with outcome-specific regressors

bayesmh ([*eqname1*:]*depvar1* [*indepvars1*])
    ([*eqname2*:]*depvar2* [*indepvars2*]) [...] [*if*] [*in*] [*weight*],
    likelihood(mvnormal(...)) prior(*priorspec*) [*options*]

Multiple-equation linear models

bayesmh (*eqspec*) [(*eqspec*)] [...] [*if*] [*in*] [*weight*], prior(*priorspec*) [*options*]

Nonlinear models

Univariate nonlinear regression

bayesmh *depvar* = (*subexpr*) [*if*] [*in*] [*weight*],
    likelihood(*modelspec*) prior(*priorspec*) [*options*]

Multivariate normal nonlinear regression

bayesmh (*depvars1* = (*subexpr1*))
    (*depvars2* = (*subexpr2*)) [...] [*if*] [*in*] [*weight*],
    likelihood(mvnormal(...)) 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*]

The syntax of *eqspec* is

varspec [*if*] [*in*] [*weight*], `likelihood(`*modelspec*`)` [`noconstant`]

The syntax of *varspec* is one of the following:

for single outcome

[*eqname*`:`]*depvar* [*indepvars*]

for multiple outcomes with common regressors

depvars `=` [*indepvars*]

for multiple outcomes with outcome-specific regressors

`(`[*eqname1*`:`]*depvar1* [*indepvars1*]`)` `(`[*eqname2*`:`]*depvar2* [*indepvars2*]`)` [`...`]

The syntax of *deqspec* is

[*eqname*`:`] *depvar* [*if*] [*in*] [*weight*], `likelihood(`*distribution*`)`

subexpr, *subexpr1*, *subexpr2*, and so on are substitutable expressions; see *Substitutable expressions* for details.

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
`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
`llf(`*subexpr*`)`	substitutable expression for observation-level log-likelihood function

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*. See *Specifying arguments of likelihood models and prior distributions*.

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`

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*, 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*

where the simplest specification of *paramref* is

paramspec [*paramspec* [...]]

Also see *Referring to model parameters* for other specifications.

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}`.

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*
`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()`
`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*}
`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*
`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*. See *Specifying arguments of likelihood models and prior distributions*.

f is a nonnegative number, *#*; an expression, *expr*; or a substitutable expression, *subexpr*.

logf is a number, *#*; an expression, *expr*; or a substitutable expression, *subexpr*.

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	
`redefine(`*label*`:i.`*varname*`)`	specify a random-effects linear form; this option may be repeated
`xbdefine(`*label*`:`*varlist*`)`	specify a linear form
Simulation	
`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*`)`	initial values for model parameters
`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*
`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
[`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()`, `redefine()`, and `block()` can be repeated.

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

With multiple-equations specifications, a local *if* specified within an equation is applied together with the global *if* specified with the command.

Only `fweight`s are allowed; see **[U] 11.1.6 weight**.

With multiple-equations specifications, local weights or (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, `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; see *Declaring model parameters* and *Specifying arguments of likelihood models and prior distributions*.

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; 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* is offset() and exposure().

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.

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.

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

reffects(*varname*) specifies a random-effects variable, a variable identifying the group structure for the random effects, with univariate linear models. This option is useful for fitting two-level random-intercept models. A random-effects variable is treated as a factor variable with no base level. As such, you can refer to random-effects parameters or, simply, random effects associated with *varname* using a conventional factor-variable notation. For example, you can use {*depvar*:i.*varname*} to refer to all random-effects parameters of *varname*. These parameters must be included in a single prior statement, usually a normal distribution with variance specified by an additional parameter. The random-effects parameters are assumed to be conditionally independent across levels of *varname* given all other model parameters. The random-effects parameters are automatically grouped in one block and are thus not allowed in the block() option. See example 23.

redefine(*label*:i.*varname*) specifies a random-effects linear form that can be used in substitutable expressions. You can use {*label*:} to refer to the linear form in substitutable expressions. You can specify {*label*:i.*varname*} to refer to all random-effects parameters associated with *varname*. The random-effects parameters are automatically grouped in one block and are thus not allowed in the block() option. This option is useful for fitting multilevel models and can be repeated. See example 29.

`xbdefine(`*label*`:`*varlist*`)` specifies a linear form of the variables in *varlist* that can be used in substitutable expressions. You can use the specification `{`*label*`:}` to refer to the linear form in substitutable expressions. For any *varname* in *varlist*, you can use `{`*label*`:`*varname*`}` to refer to the corresponding parameter. This option is useful with nonlinear specifications when the linear form contains many variables and provides more efficient computation in such cases.

Simulation

`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()` $+$ $\big($`mcmcsize()` $- 1\big) \times$ `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. 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. 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.

`rseed(`*#*`)` sets the random-number seed. This option can be used to reproduce results. `rseed(`*#*`)` is equivalent to typing `set seed` *#* prior to calling `bayesmh`; see [R] **set seed** and *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*. 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.

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 is useful for fitting hierarchical or multilevel models. See example 25 for details.

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. 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 # [*paramref* # [...]]

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.

`nomleinitial` suppresses using maximum likelihood estimates (MLEs) starting values for model parameters. 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`, `density()`, `logdensity()`, and `jeffreys()` priors; you must provide fixed initial values for such parameters. This option cannot be combined with `nomleinitial`.

`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 $(\texttt{mcmcsize()} + \texttt{burnin()})/$ `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 specifies the display of 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.

batch(*#*) specifies the length of the block for calculating batch means, batch standard deviation, and MCSE using batch means. The default is batch(0), which means no batch calculations. When batch() is not specified, MCSE is computed using effective sample sizes instead of batch means. Option 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. Variance _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.

nodots, dots, and dots(*#*) specify to suppress or display dots during simulation. 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 when reffects() is specified) 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 option reffects() 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 introduced by reffects() 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 first $\#_{\mathrm{matsize}} - \#_{\mathrm{npar}}$ random-effects parameters, where $\#_{\mathrm{matsize}}$ is the maximum number of variables as determined by matsize (see [R] **matsize**) and $\#_{\mathrm{npar}}$ is the number of other model parameters displayed. If you want to obtain MCMC summaries and display other random-effects parameters, you can use the show() option or use bayesstats summary (see [BAYES] **bayesstats summary**).

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

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-equation 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 the multiple-equation 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 also 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. 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 can 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()`.

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. 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})) ...
```

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**.

For example, factor variables are useful for constructing multilevel Bayesian models. Suppose that variable id defines the second level of hierarchy in a two-level random-effects model. We can fit a Bayesian random-intercept model as follows:

```
. bayesmh y x i.id, likelihood(normal({var})) prior({y:i.id}, normal(0,{tau})) ...
```

Here we used {y:i.id} in the prior specification to refer to all levels of id.

Similarly, we can add a random coefficient for a continuous covariate x by typing

```
. bayesmh y c.x##i.id, likelihood(normal({var}))
>                      prior({y:i.id}, normal(0,{tau1}))
>                      prior({y:c.x#i.id}, normal(0,{tau2})) ...
```

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}
```

You cannot refer to both 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 *exp*. Matrix arguments of the distributions may be specified as a matrix or as a matrix expression *exp*. Both types of arguments may be specified as a parameter (see *Declaring model parameters*) or as a substitutable expression, *subexp* (see *Substitutable expressions*). All distribution arguments, except 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.

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)))
```

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 `set seed #` prior to calling `bayesmh` (see [R] **set seed**) or you can specify the seed in `bayesmh`'s option `rseed()`. For simplicity and consistency, we use `set seed 14` in all of our examples throughout the documentation.

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`.

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() × (mcmcsize() − 1) + 1 iterations, excluding burn-in iterations, to obtain MCMC sample of size mcmcsize().

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.

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:

$$\texttt{y} = \texttt{\{a\}} + \texttt{\{b\}} \times \texttt{x} + \epsilon,\ \epsilon \sim N(0, \texttt{\{var\}})$$

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.

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, 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*.

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.

There are two different ways to specify initial values of model parameters in bayesmh. 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 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) ...
```

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 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 addition to fixed initial values, you may request random initial values for all model parameters by specifying the initrandom option. Random initial values are generated from the prior distributions of the parameters, except for parameters that are assigned flat, density(), logdensity(), or jeffreys() prior distributions. For such parameters, you must specify fixed initial values, or bayesmh will issue an error. See *Graphical diagnostics using multiple chains* for an example.

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.

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.

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.

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, 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 *Graphical 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**, and [BAYES] **bayesstats ess**.

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 analysis, part 1: The basic concepts

Introduction to Bayesian analysis, 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 http://www.stata-press.com/data/r15/auto
(1978 Automobile Data)

. describe mpg weight length

              storage   display    value
variable 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

------------------------------------------------------------------------------
             |                                                Equal-tailed
         mpg |      Mean   Std. Dev.     MCSE     Median  [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**.

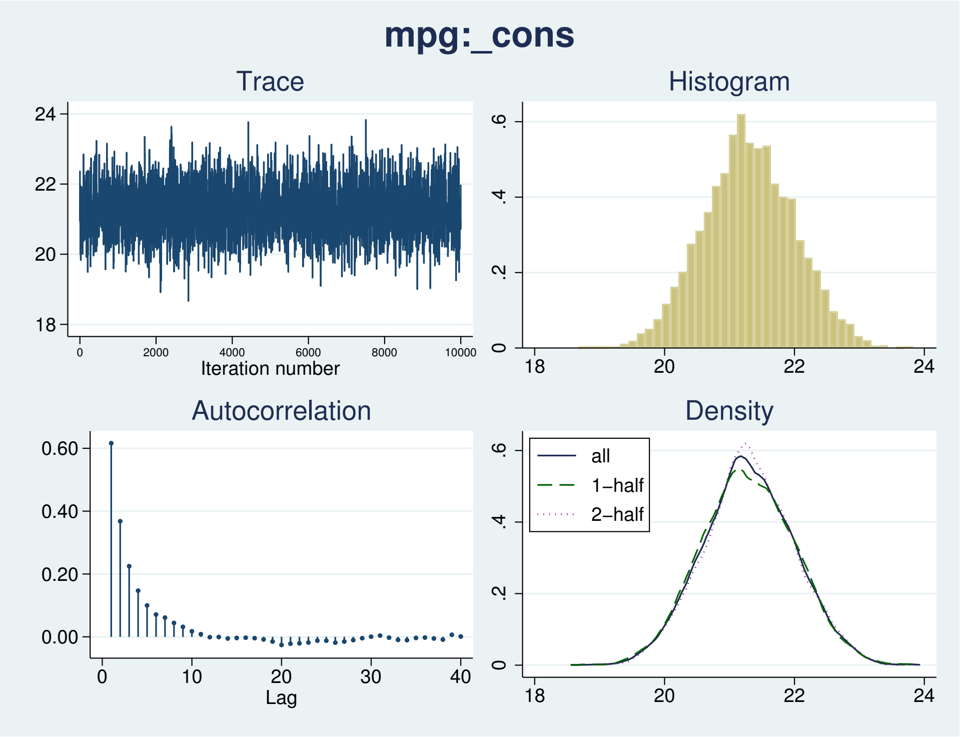
Because we used a completely noninformative prior, our results should be the same as frequentist results. In this Bayesian model, the posterior distribution of the constant parameter is known to be normal with a mean equal to the sample average. In the frequentist domain, the MLE of the constant is also 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 *Graphical 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.

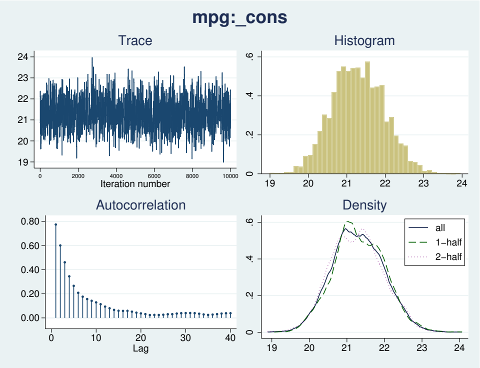
```
. set seed 14

. 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
------------------------------------------------------------------------------
```

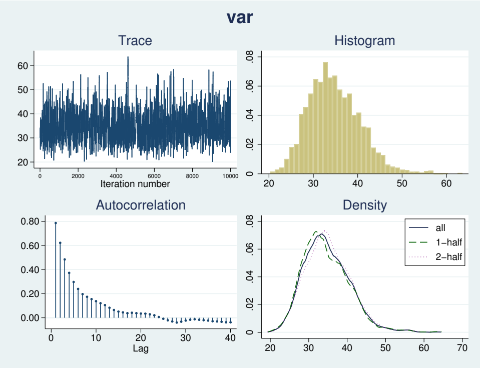
Because we used a noninformative prior, our results should be similar to the frequentist results apart from simulation uncertainty. Compared with example 1, the average efficiency of the MH algorithm decreased to 10%, as is expected with more parameters, but is still considered a good efficiency for 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.

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

$$\mu|\sigma^2 \sim N(\mu_0, \sigma^2)$$
$$\sigma^2 \sim \text{InvGamma}(\nu_0/2, \nu_0\sigma_0^2/2)$$

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 http://www.stata-press.com/data/r15/auto

. 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

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [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 │      Coef.   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}`,

$$\beta_{\text{weight}}|\sigma^2 \sim N(\mu_{\text{weight}}, \sigma^2)$$
$$\beta_{\text{cons}}|\sigma^2 \sim N(\mu_{\text{cons}}, \sigma^2)$$
$$\sigma^2 \sim \text{InvGamma}(\nu_0/2, \nu_0\sigma_0^2/2)$$

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
-------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [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.

◁

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

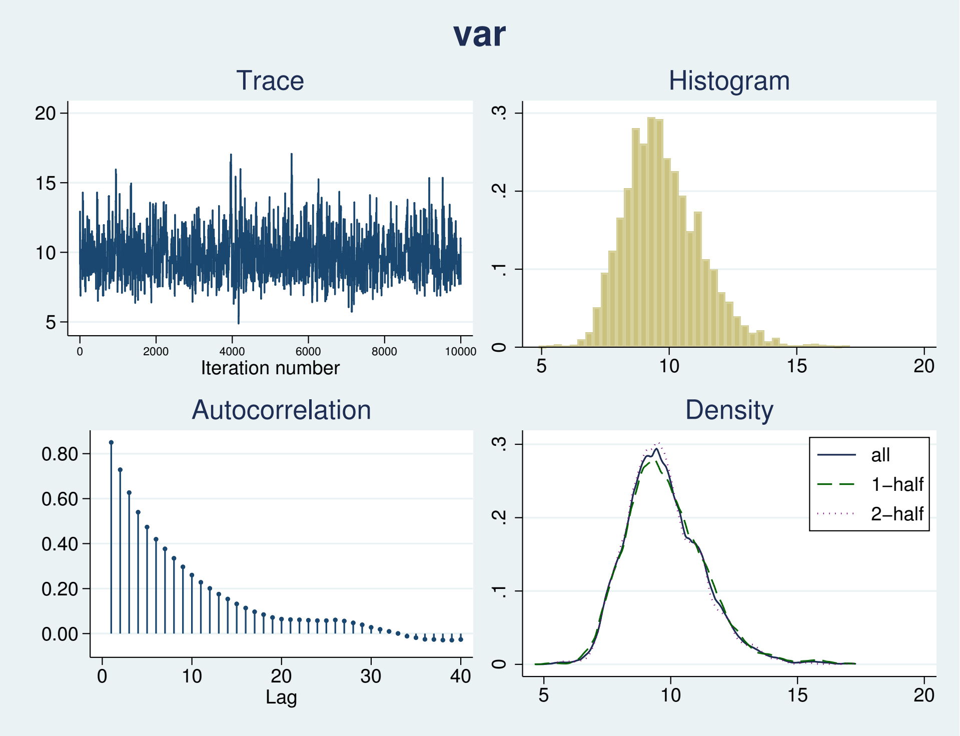
Our first simulation is performed using the default settings for the algorithm. Specifically, all three model parameters are placed in one simulation block and are updated simultaneously, as our block summary indicates.

```
. 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}
```



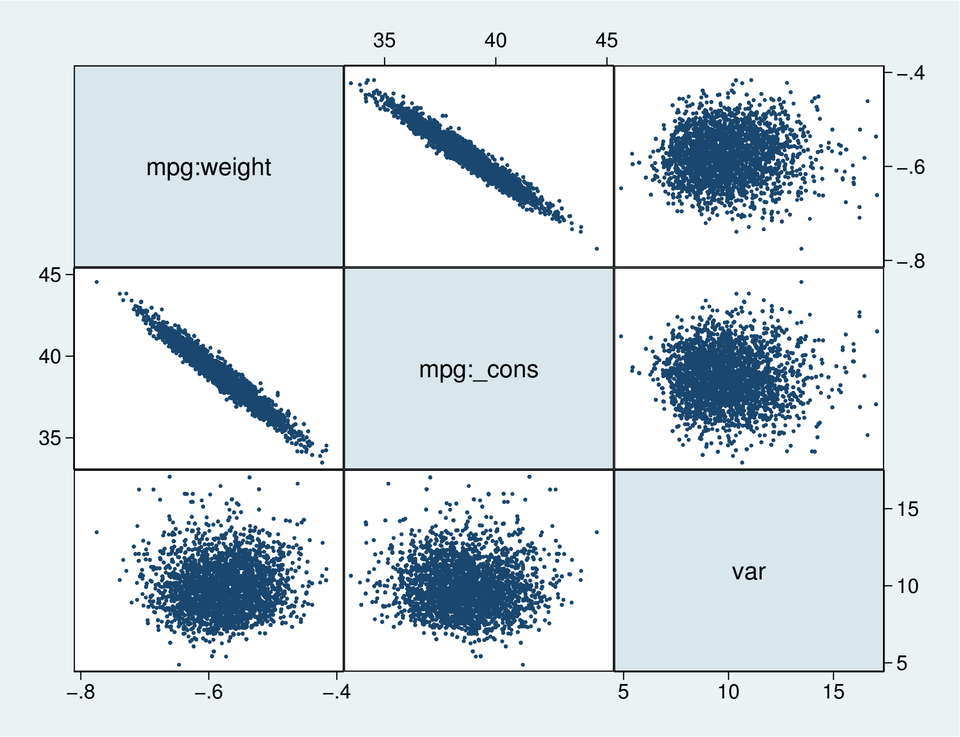
A graphical summary for the `{var}` parameter does not show any obvious problems. The trace plot reveals a good coverage of the domain of the marginal distribution, while the histogram and kernel density plots resemble the shape of an expected inverse-gamma distribution. The autocorrelation dies off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

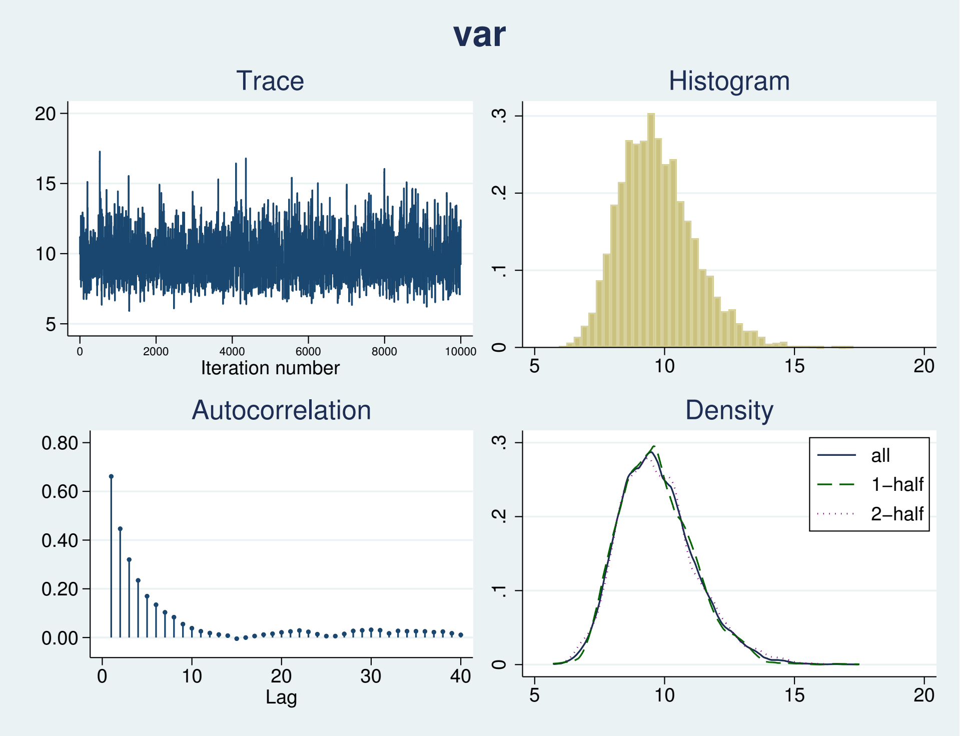
In cases like this, we can expect higher sampling efficiency if we place {var} in a separate block. We can do this by including the option block({var}). The other two parameters, {mpg:weight} and {mpg:_cons}, will be automatically considered as a second block.

```
. 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.

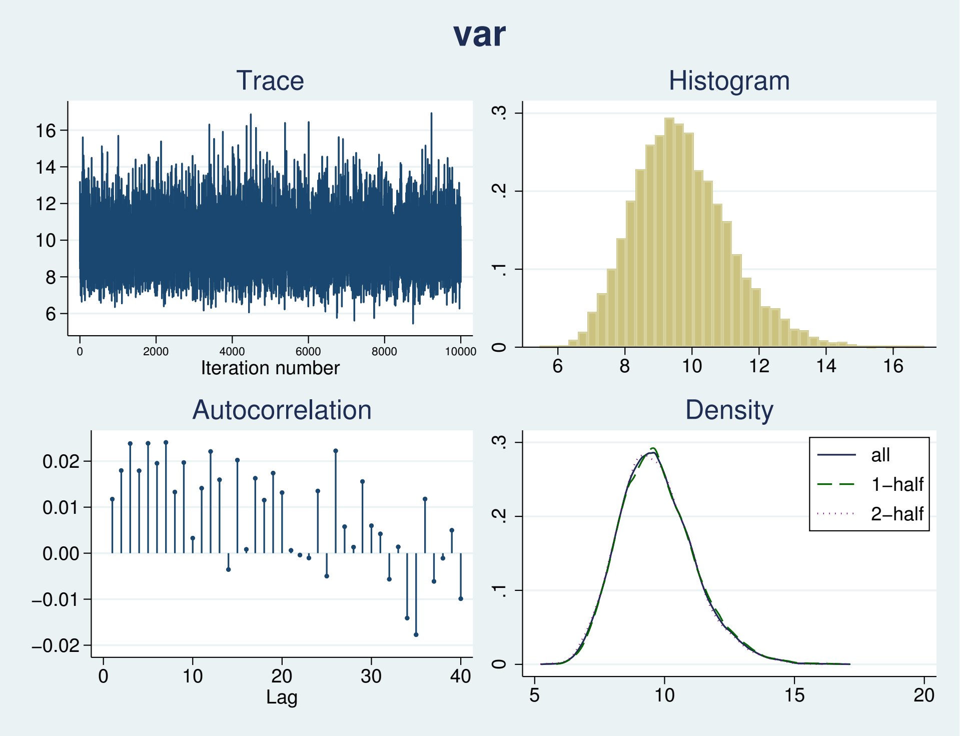
To request Gibbs sampling, we specify suboption gibbs within option block().

```
. 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}
```



◁

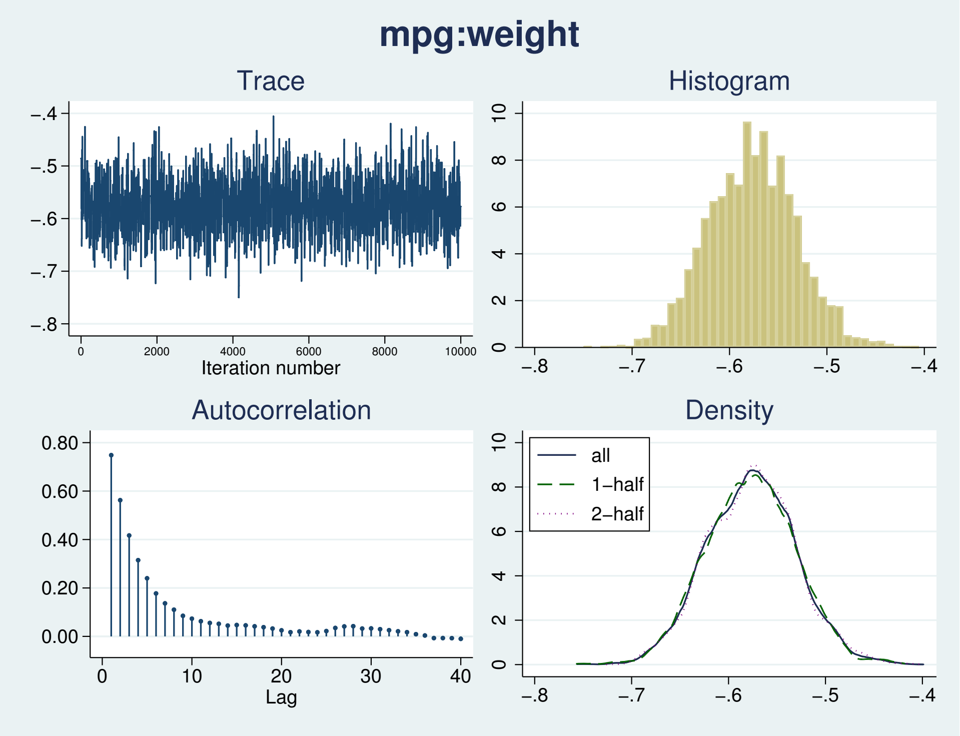
▷ Example 14: Fourth simulation run—full Gibbs sampling

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

                          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.

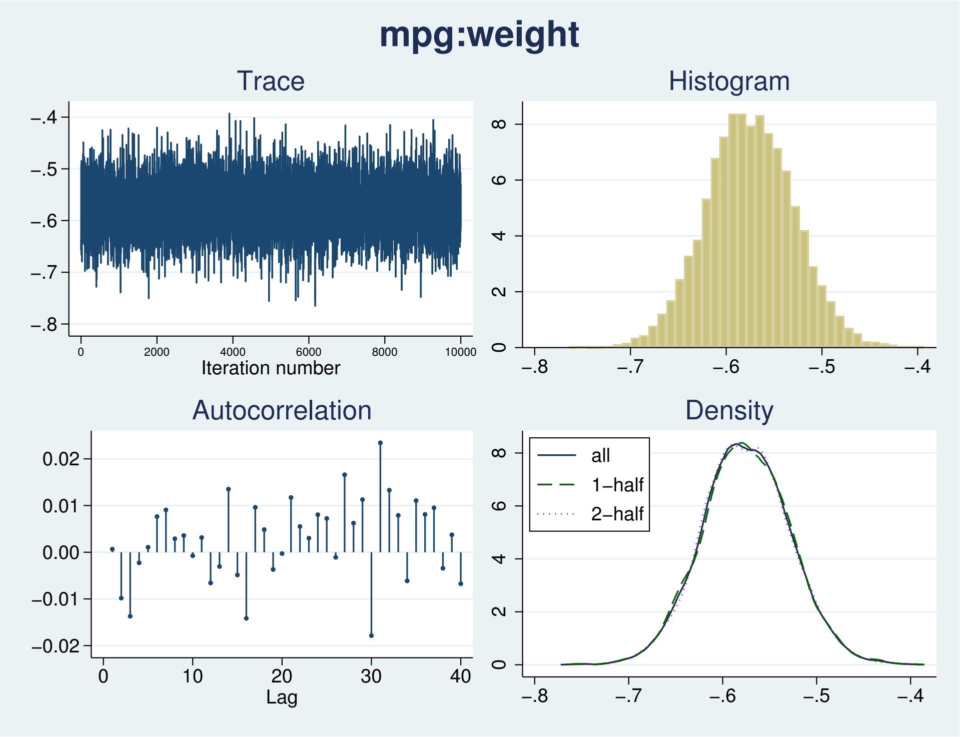
To request Gibbs sampling for the regression coefficients, we must place them in a separate block.

```
. 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 )
```

◁

Graphical 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; see, for example, chapter 11.4 in Gelman et al. (2014). In this section, we show how one can perform multiple simulation runs using bayesmh and visually compare the results using trace plots.

We use a Bayesian multiple linear regression model from example 11. For brevity, we simulate only two MCMC chains, but the approach can be easily extended to more than two chains. It is essential for the two chains to have different initial values dispersed over the range of model parameter values. With bayesmh, you can provide fixed initial values by using the initial() option or when declaring parameters in the likelihood() option, or you can request random initial values by specifying the initrandom option.

We simulate two samples of size 5,000 and save the simulation results as `sim1.dta` and `sim2.dta`. Below we show the `bayesmh` specifications and the estimation results.

```
. set seed 14

. bayesmh mpg weight, likelihood(normal({var}))
> prior({mpg:}, normal(0,100)) prior({var}, igamma(10,10))
> mcmcsize(5000) nomodelsummary initrandom saving(sim1)
Burn-in ...
Simulation ...

Bayesian normal regression                       MCMC iterations  =      7,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =      5,000
                                                 Number of obs    =         74
                                                 Acceptance rate  =      .2597
                                                 Efficiency:  min =     .06487
                                                              avg =     .07218
Log marginal likelihood = -226.83819                          max =     .07653

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
      weight | -.5779557   .0436132   .002422  -.5769825  -.6645717  -.4929187
       _cons |  38.66309   1.379251   .070509   38.61303   36.02204   41.29802
-------------+----------------------------------------------------------------
         var |  9.813336   1.439047   .074239   9.698644   7.313202   13.01305
------------------------------------------------------------------------------

file sim1.dta saved

. bayesmh mpg weight, likelihood(normal({var}))
> prior({mpg:}, normal(0,100)) prior({var}, igamma(10,10))
> mcmcsize(5000) nomodelsummary initrandom saving(sim2)
Burn-in ...
Simulation ...

Bayesian normal regression                       MCMC iterations  =      7,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =      5,000
                                                 Number of obs    =         74
                                                 Acceptance rate  =        .24
                                                 Efficiency:  min =     .09555
                                                              avg =     .09985
Log marginal likelihood = -226.83719                          max =      .1048

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
      weight | -.5733346   .0462179   .002019  -.5763298  -.6637416  -.4810475
       _cons |  38.56422   1.426843   .065279   38.62277   35.72788   41.38445
-------------+----------------------------------------------------------------
         var |   9.60628   1.361131   .061125    9.47494    7.28224   12.59361
------------------------------------------------------------------------------

file sim2.dta saved
```

The average simulation efficiency of both runs is above 7% and seems adequate. There is no indication of convergence problems. Nevertheless, inspecting the trace plots can provide additional reassurance. In particular, by comparing the trace plots of a model parameter based on different simulation sequences, we can detect convergence irregularities and assess the overlap of the simulated marginal distributions for this parameter. If the MCMC chains have converged, we should not observe substantial differences between the trace plots or between the sampled marginal distributions.

To draw overlaid trace plots, we need to combine the two simulation datasets in one dataset in the long form. We load the first simulation dataset and append the second simulation dataset to the first one. We also generate an indicator variable chain. The variable chain equals 0 for the records of the first chain and 1 for the records of the second chain.

```
. clear
. use sim1
. append using sim2, generate(chain)
```

In example 11, we rescaled variable weight of the auto dataset and thus modified the data in memory. We used the clear option when we loaded the sim1 dataset to replace the data in memory, even though the current data have not been saved to disk.

To avoid duplicates, we save the simulation results in a compressed form, recording unique values and their frequencies. We need to expand the dataset and create a unique iteration number for each chain. In the original simulation datasets, the index and duplicates are stored in the _index and _frequency variables, respectively. We expand the combined dataset using the _frequency variable and sort it by using chain and _index. Then, we generate the variable iter to index the records in the two chains.

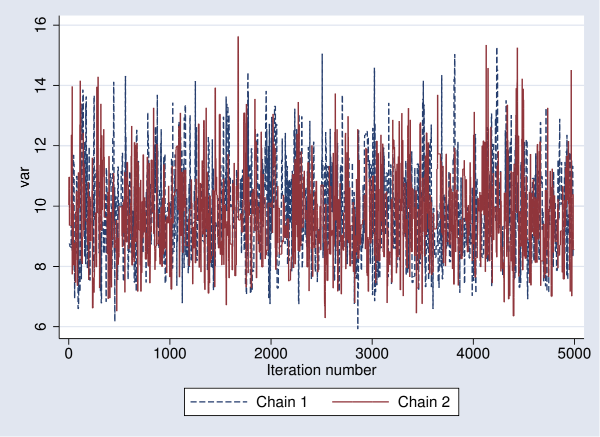
```
. expand _frequency
(7,500 observations created)
. sort chain _index
. by chain: generate iter = _n
```

Finally, we relabel the variables of interest to match the model parameter names. The scalar model parameter names are stored in e(scparams), and their corresponding variable names in the simulation dataset are stored in e(postvars).

```
. display e(scparams)
mpg:weight mpg:_cons var
. display e(postvars)
eq1_p1 eq1_p2 eq0_p1
. label variable eq1_p1 "mpg:weight"
. label variable eq1_p2 "mpg:_cons"
. label variable eq0_p1 "var"
. label variable iter "Iteration number"
```

We are now ready to draw the trace plots of the model parameters. For example, we can overlay the two trace plots of the {var} parameter as follows. We use the xtset command to declare the data to be panel data identified by the chain variable and specify iter as a time variable. We then draw the trace plots using the time-series plotting command tsline.

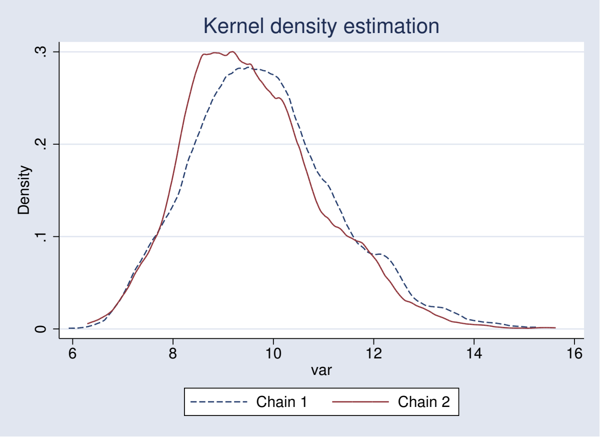
```
. xtset chain iter
       panel variable:  chain (strongly balanced)
        time variable:  iter, 1 to 5000
                delta:  1 unit
. twoway (tsline eq0_p1 if chain==0, lpattern(-))
>        (tsline eq0_p1 if chain==1, lpattern(l)),
>        legend(label(1 "Chain 1") label(2 "Chain 2"))
```



The two trace plots of {var} look similar and seem to cover approximately the same marginal posterior domain. However, the variability in the first chain does seem slightly greater, which is also evident from the reported standard deviations of {var}, 1.44 in the first run and 1.36 in the second. The estimated posterior means of {var} are somewhat different, 9.81 and 9.61, which suggests that we should either run longer MCMC simulations or improve the sampling efficiency, as we demonstrated in example 12, example 13, and example 14.

Overlaid density plots using kdensity provide another aspect of comparing multiple simulation sequences.

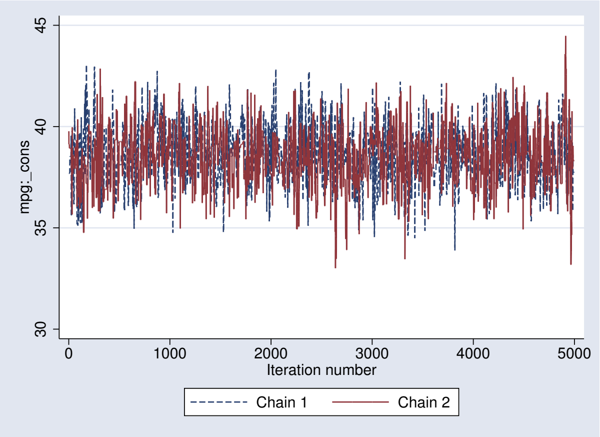
```
. twoway (kdensity eq0_p1 if chain==0, lpattern(-))
>        (kdensity eq0_p1 if chain==1, lpattern(l)),
>        legend(label(1 "Chain 1") label(2 "Chain 2"))
>        xtitle("var") ytitle("Density") title("Kernel density estimation")
```



The overlaid kdensity plots of {var} based on the two simulated chains clearly show that although the domains of the simulated marginal distributions overlap, there are also noticeable differences in the distribution of mass, which thus confirms the need for longer MCMC runs.

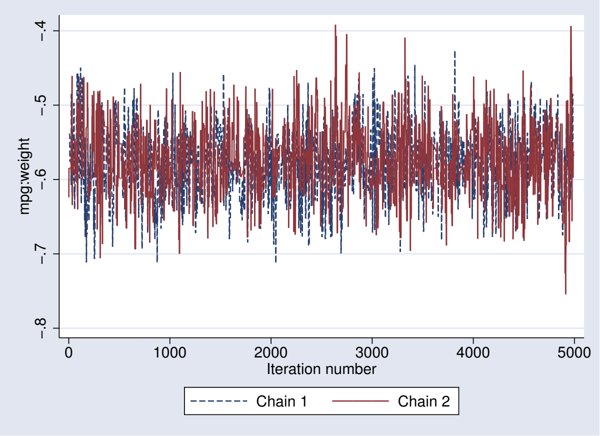
Similarly, we can draw the overlaid trace plots for parameter {mpg:_cons}.

```
. twoway (tsline eq1_p2 if chain==0, lpattern(-))
>        (tsline eq1_p2 if chain==1, lpattern(l)),
>        legend(label(1 "Chain 1") label(2 "Chain 2"))
```



The overlaid trace plots of the {mpg:_cons} parameter do not show any substantial differences or any convergence problems. However, increasing the MCMC sample sizes will further diminish the difference between the estimated posterior means of {mpg:_cons}, 38.66 and 38.56. Now, let's draw the overlaid plots for {mpg:weight}.

```
. twoway (tsline eq1_p1 if chain==0, lpattern(-))
>        (tsline eq1_p1 if chain==1, lpattern(l)),
>        legend(label(1 "Chain 1") label(2 "Chain 2"))
```



Again the overlaid trace plots of the {mpg:weight} parameter do not show any substantial differences or any convergence problems.

See Balov (2016c) for how to compute the Gelman–Rubin convergence statistic using multiple chains.

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 http://www.stata-press.com/data/r15/heartswitz, clear
(Subset of Switzerland heart disease data from UCI Machine Learning Repository)

. describe

Contains data from http://www.stata-press.com/data/r15/heartswitz.dta
  obs:           123                          Subset of Switzerland heart
                                                disease data from UCI Machine
                                                Learning Repository
 vars:             6                          5 Feb 2016 16:55
 size:           738                          (_dta has notes)
--------------------------------------------------------------------------------
              storage   display    value
variable name   type    format     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 dropped and 17 obs not used

note: isfbs != 0 predicts success perfectly
      isfbs dropped and 3 obs not used

note: male != 1 predicts success perfectly
      male dropped 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 |      Coef.   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 $N(0, 1\mathrm{e}4)$ 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

------------------------------------------------------------------------------
             |                                                Equal-tailed
     disease |      Mean   Std. Dev.     MCSE     Median  [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 http://www.stata-press.com/data/r15/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 http://www.stata-press.com/data/r15/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

──────────────────────────────────────────────────────────────────────────────
             │                                                Equal-tailed
     disease │      Mean   Std. Dev.     MCSE     Median  [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 http://www.stata-press.com/data/r15/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

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [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
------------------------------------------------------------------------------
```

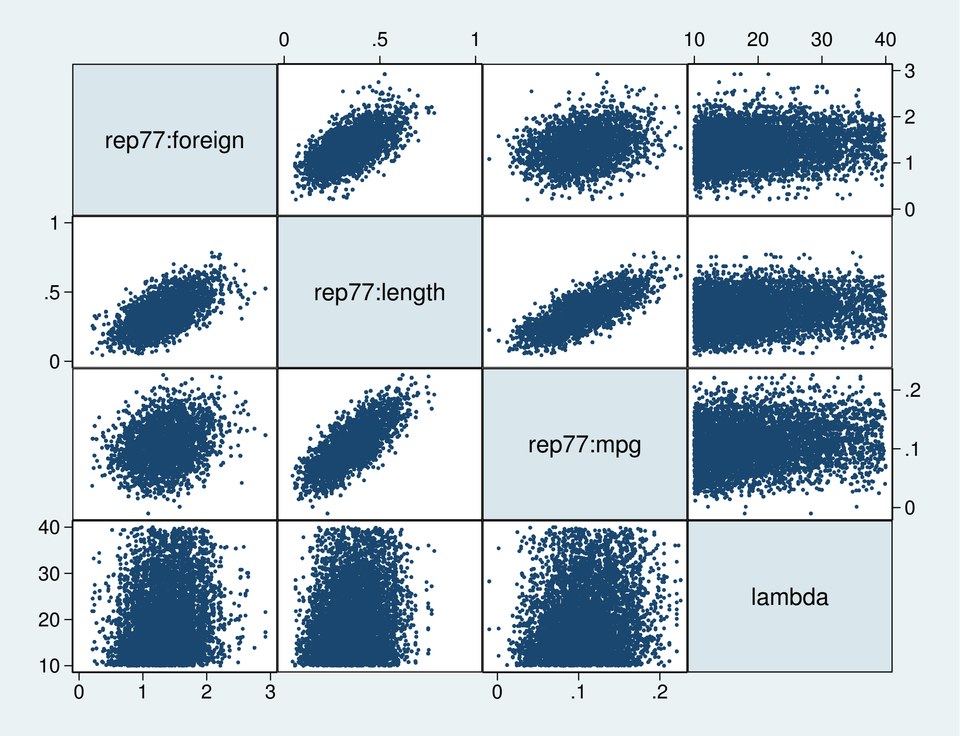
When we specify `dots` or `dots()`, `bayesmh` displays dots as simulation is performed. The burn-in and simulation iterations are displayed separately. During the adaptation period, iterations are displayed with a symbol `a` instead of a dot. This indicates the period during which the proposal distribution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

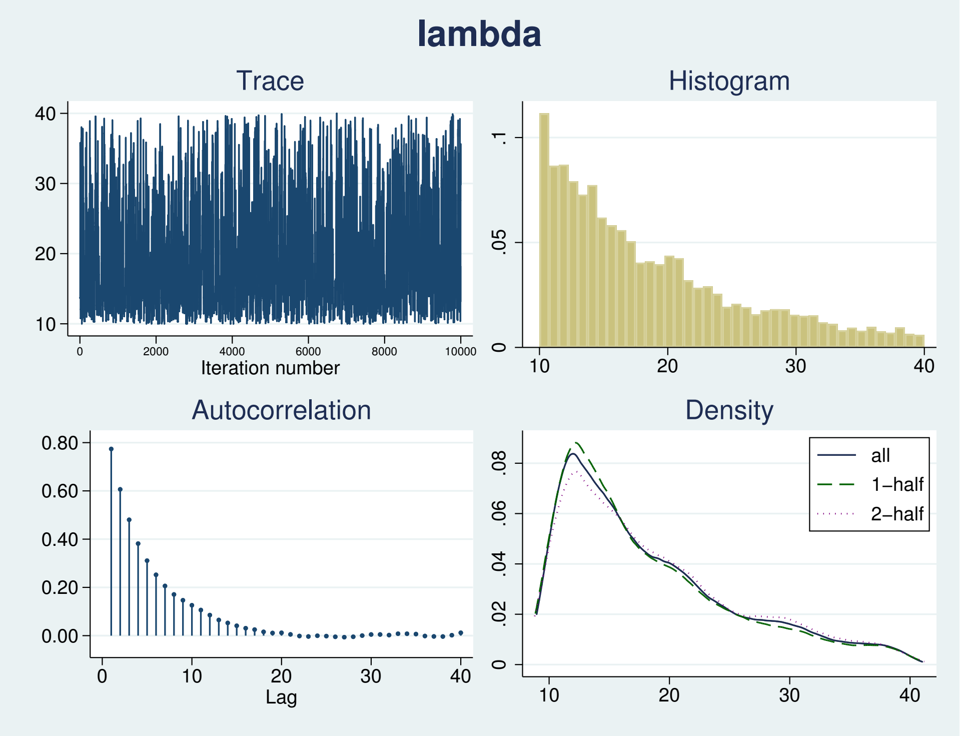
We placed the hyperparameter {lambda} in a separate block because we wanted to sample this nuisance parameter independently from the other model parameters. Based on the bivariate scatterplots, this parameter does appear to be independent of other model parameters a posteriori.

```
. 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 $\text{Beta}(2,20)$ prior. For this model, the posterior distribution of θ is known to be $\text{Beta}(2,40)$.

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 http://www.stata-press.com/data/r15/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.
```

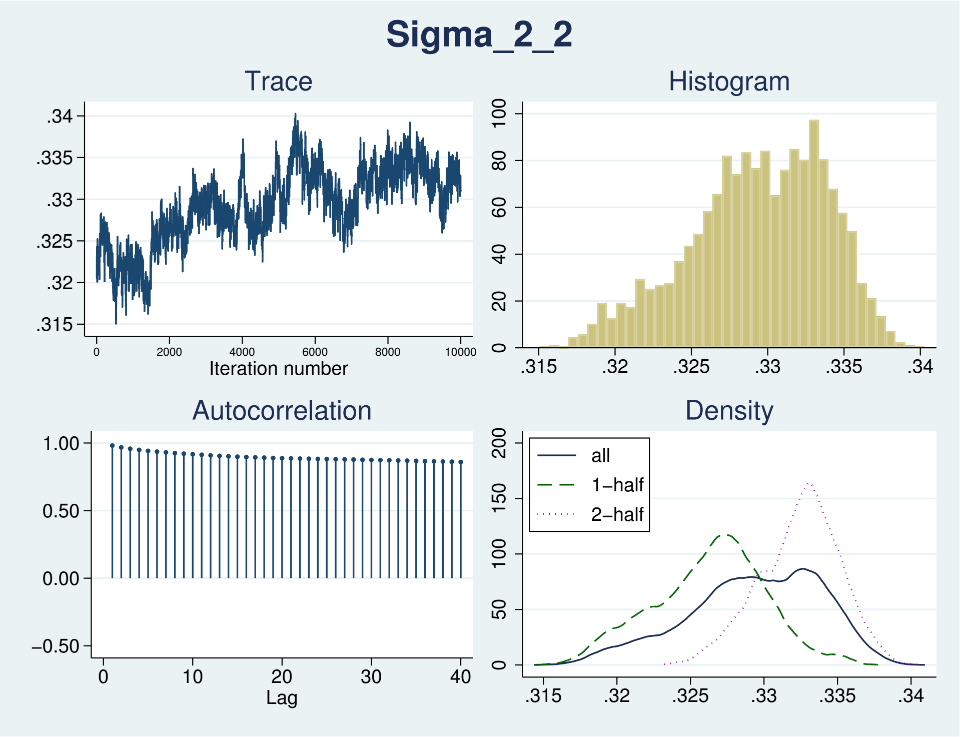
In this first run, we do not achieve good mixing of the MCMC chain. bayesmh issues a note about significant autocorrelation of the simulated parameters.

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

------------------------------------------------------
             |        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
```



What we see here is 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

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [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
------------------------------------------------------------------------------
```

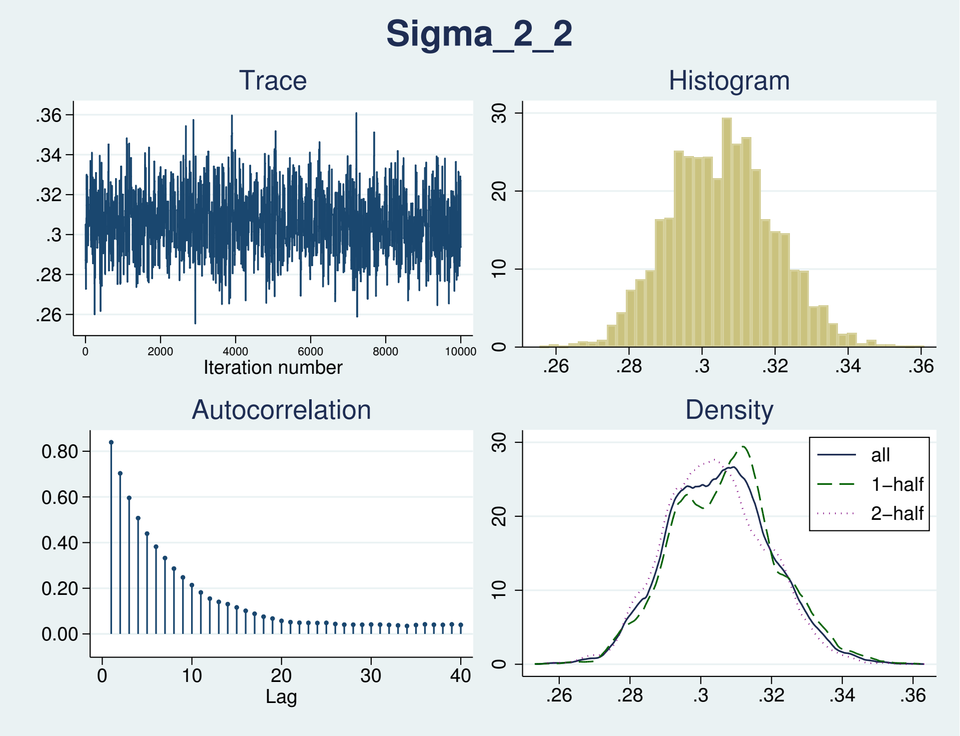
There is no note about high autocorrelation, and the average efficiency increases slightly from 4% to 5%.

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

```
. bayesstats ess
Efficiency summaries    MCMC sample size =    10,000

                    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

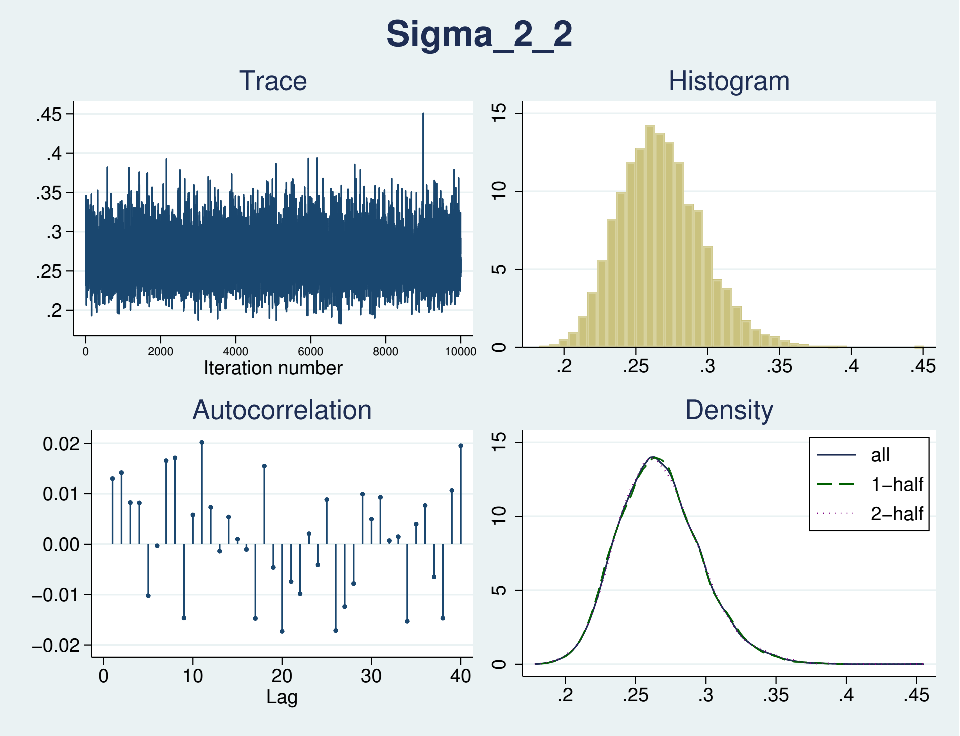
Continuing example 15, the convergence of the chain can be greatly improved if we use Gibbs sampling for the covariance matrix parameter. For a multivariate normal model, inverse Wishart is a conjugate prior, or more precisely semiconjugate prior, for the covariance matrix and thus Gibbs sampling is 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

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [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 6% and the average efficiency from 5% to 66%. 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.

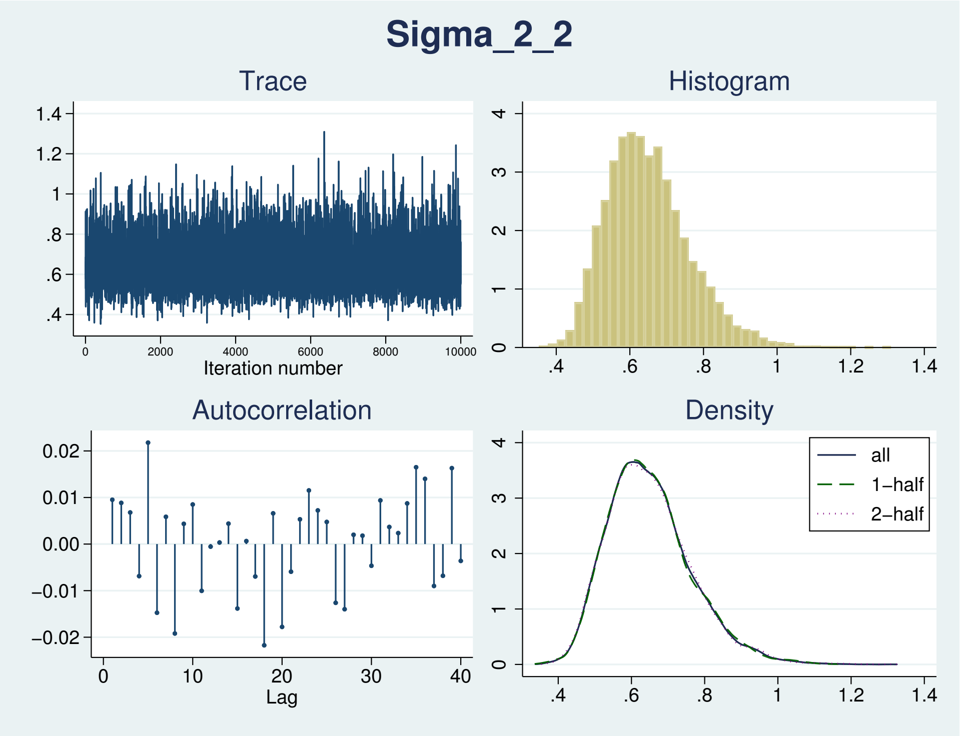
❏ Technical note: Adaptation tolerance is not met

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

Although the MH algorithm underlying bayesmh is not optimal for fitting Bayesian multilevel models, you can use it to fit some multilevel models that do not have too many random effects. Below we consider two-level random-intercept and random-coefficients models. A two-level random-effects model is also known as a panel-data model.

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, $j = 1, \dots, 48$, and the counter $i = 1, \dots, 9$ identifies the weeks.

We first use mixed to fit this model by using maximum likelihood for comparison purposes; see [ME] **mixed**.

```
. use http://www.stata-press.com/data/r15/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 |      Coef.   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   3.124226      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:

$$\texttt{weight}_{ij} = \beta_0 + \beta_1\texttt{week}_{ij} + u_j + \epsilon_{ij} = \beta_1\texttt{week}_{ij} + \tau_j + \epsilon_{ij},$$

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

The model has four main parameters of interest: regression coefficients β_0 and β_1 and variance components σ_0^2 and σ_{id}^2. β_0 is actually a hyperparameter in this example, because it is the mean parameter of the prior distribution for random effects τ_j. The pig random effects τ_j are considered nuisance parameters. We use normal priors for the regression coefficients and group levels identified by the id variable 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 by adding factor levels of the id variable to the regression by using the factor-variable specification i.id. This specification, by default, will omit one of the id categories as a base category. In our Bayesian model, we need to keep all categories of id, so we use fvset to declare no base for the id variable.

```
. fvset base none id
```

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:1.id}, {weight:2.id}, ..., {weight:48.id} for random effects. We do not include a constant in our regression function because it is modeled as a mean of random effects in their prior. So, we need to define the three remaining model parameters manually; we will use {weight:_cons} for the mean of random effects, {var_id} for the variance of random effects, and {var_0} for the error variance.

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.

```
. set seed 14
. bayesmh weight week i.id, likelihood(normal({var_0})) noconstant
>         prior({weight:i.id},  normal({weight:_cons},{var_id}))
>         prior({weight:_cons}, normal(0, 100))
>         prior({weight:week},  normal(0, 100))
>         prior({var_0},        igamma(0.001, 0.001))
>         prior({var_id},       igamma(0.001, 0.001))
>         mcmcsize(5000) dots
Burn-in 2500 aaaaaaaa.1000.........2000..... done
Simulation 5000 .........1000.........2000.........3000.........4000.........
> 5000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  weight ~ normal(xb_weight,{var_0})
Priors:
   {weight:i.id} ~ normal({weight:_cons},{var_id})                          (1)
   {weight:week} ~ normal(0,100)                                            (1)
         {var_0} ~ igamma(0.001,0.001)
  {weight:_cons} ~ normal(0,100)
Hyperprior:
  {var_id} ~ 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  =      .2382
                                                 Efficiency:  min =     .00136
                                                              avg =    .004915
Log marginal likelihood = -1483.9819                          max =     .03084
------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
weight       |
        week |  6.263434   .0264724   .002955   6.262433   6.214032    6.31423
             |
          id |
          1  |  16.24666   .2357628   .058097    16.2599   15.78635   16.67799
          2  |  24.06862   .3243331    .06509   24.07464   23.37339   24.67859
  (output omitted)
         47  |  29.73823   .3734104    .07144   29.71473   29.04301   30.48604
         48  |  20.82722   .4258745   .160651   20.78619   20.13018   21.71069
-------------+----------------------------------------------------------------
       var_0 |  9.218097   .5679745   .174024   9.181747   8.218479   10.38655
-------------+----------------------------------------------------------------
weight       |
       _cons |  13.59053   .3519081   .028341   13.62244   12.88323   14.25594
-------------+----------------------------------------------------------------
      var_id |  12.49858   .3116721   .050076   12.50611    11.9335   13.12018
------------------------------------------------------------------------------
Note: There is a high autocorrelation after 500 lags.
```

bayesmh reports the presence of a high correlation after 500 lags. This and the low average efficiency of 0.005 may indicate problems with MCMC convergence for some of the parameters.

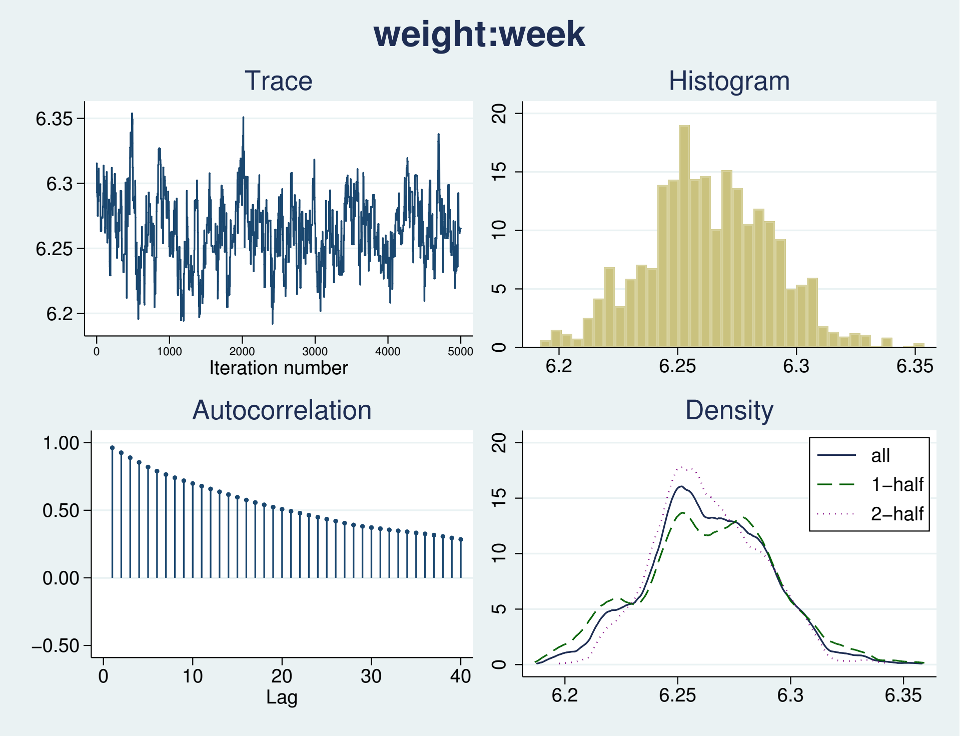
For convenience, we use `bayesstats summary` to show posterior summaries for parameters of interest only. Alternatively, you can specify the `noshow(i.id)` option with `bayesmh` to suppress the summaries for factor levels.

```
. bayesstats summary {weight:week _cons} {var_0} {var_id}

Posterior summary statistics                      MCMC sample size =     5,000

                                                               Equal-tailed
                    Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]

weight
        week    6.263434   .0264724   .002955   6.262433   6.214032    6.31423
       _cons    13.59053   .3519081   .028341   13.62244   12.88323   14.25594

       var_0    9.218097   .5679745   .174024   9.181747   8.218479   10.38655
      var_id    12.49858   .3116721   .050076   12.50611    11.9335   13.12018
```

The posterior mean estimates for `{weight:week}` and `{weight:_cons}` are 6.26 and 13.59, respectively. The estimate for the residual variance `{var_0}` is 9.22 with the standard deviation of 0.57, and the estimate of the group-effect variance `{var_id}` is 12.5 with the standard deviation of 0.31.

Because of the low efficiencies, we should be suspicious of these results. If we look at diagnostic plots for, for example, `{weight:week}`,

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



we see that the trace plot exhibits some trend and does not show good mixing and that the autocorrelation is relatively high after at least lag 40. Our MCMC does not seem to converge and thus we cannot trust the obtained results.

◁

▷ 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 with random-effects parameters sharing the same block. We also specify `nomodelsummary` to suppress the model summary and `notable` to suppress the table output of `bayesmh`.

```
. set seed 14

. bayesmh weight week i.id, likelihood(normal({var_0})) noconstant
> prior({weight:i.id}, normal({weight:_cons},{var_id}))
> prior({weight:_cons},normal(0, 100))
> prior({weight:week}, normal(0, 100))
> prior({var_0}, igamma(0.001, 0.001))
> prior({var_id}, igamma(0.001, 0.001))
> block({var_0})
> block({var_id})
> block({weight:i.id})
> block({weight:week})
> block({weight:_cons})
> burnin(3000) mcmcsize(5000) dots notable nomodelsummary
Burn-in 3000 aaaaaaaaa1000aaaaaaaaa2000aaaaaaaaa3000 done
Simulation 5000 .........1000.........2000.........3000.........4000.........
> 5000 done

Bayesian normal regression                       MCMC iterations  =      8,000
Random-walk Metropolis-Hastings sampling         Burn-in          =      3,000
                                                 MCMC sample size =      5,000
                                                 Number of obs    =        432
                                                 Acceptance rate  =      .4194
                                                 Efficiency:  min =    .001727
                                                              avg =     .01731
Log marginal likelihood = -1204.9586                          max =      .2403
```

Blocking certainly improved efficiencies: the average efficiency is now 0.017, but we still have a note about high autocorrelation.

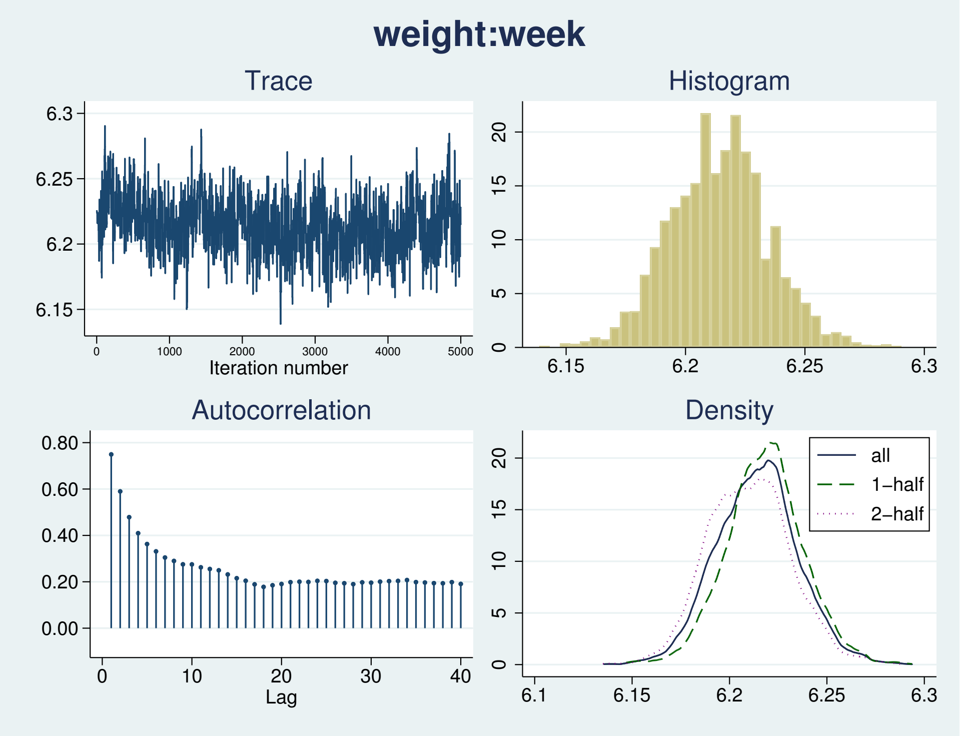
We use `bayesstats summary` below to report summaries of only model parameters of interest.

```
. bayesstats summary {weight:week _cons} {var_0} {var_id}

Posterior summary statistics                      MCMC sample size =     5,000

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
weight       |
        week |  6.214099    .020815   .002059   6.214429   6.174678   6.255888
       _cons |  19.28371    .552023   .015925   19.28177    18.2078   20.35016
-------------+----------------------------------------------------------------
       var_0 |  4.183143   .2908152   .009833   4.167876   3.669035   4.828092
      var_id |  15.53468   3.251813   .112054   15.16295   10.46451   23.19296
------------------------------------------------------------------------------
```

Here our estimates of variance components change noticeably: `{var_0}` is 4.18 and `{var_id}` is 15.53.

The diagnostic plots for {weight:week} are much better, but the mixing of MCMC is still not great.

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



◁

▷ Example 21: Third simulation—Gibbs sampling

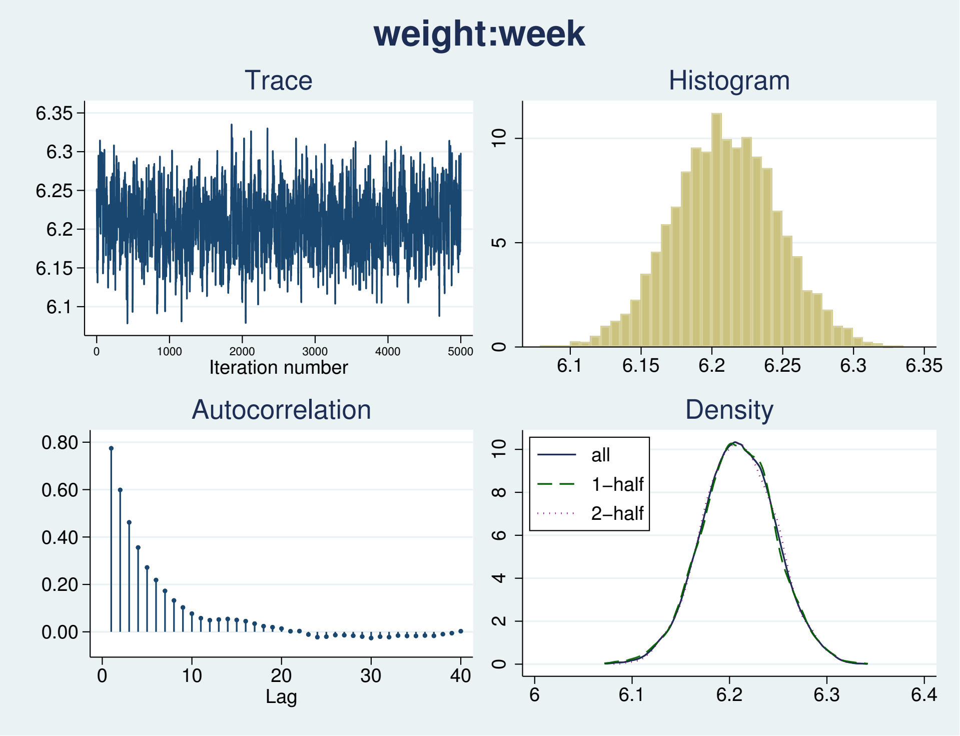
The most efficient MCMC procedure for our Bayesian model is Gibbs sampling, which can be set up as follows. To request a Gibbs sampling for a block of model parameters, we must first define them in a separate prior() statement and then put them in a separate block() with the gibbs suboption.

```
. set seed 14
. bayesmh weight week i.id, likelihood(normal({var_0})) noconstant
> prior({weight:i.id}, normal({weight:_cons},{var_id}))
> prior({weight:_cons},normal(0, 100))
> prior({weight:week}, normal(0, 100))
> prior({var_0}, igamma(0.001, 0.001))
> prior({var_id}, igamma(0.001, 0.001))
> block({var_0}, gibbs) block({var_id}, gibbs)
> block({weight:i.id}, gibbs) block({weight:week}, gibbs)
> block({weight:_cons},gibbs) mcmcsize(5000) dots notable 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 =       .123
                                                              avg =      .6764
Log marginal likelihood = -1051.4228                          max =       .857
```

There is no note about high autocorrelation in this run. The average efficiency increased dramatically to 0.68. It appears that our MCMC has now converged.

If we again inspect the diagnostic plots of, for example, {weight:week}, we will now see a very good mixing.

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



We again use bayesstats summary to see posterior summaries of the model parameters of interest.

```
. bayesstats summary {weight:week _cons} {var_0} {var_id}
Posterior summary statistics                      MCMC sample size =     5,000

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
weight       |
        week |  6.209425   .0373593   .001507   6.209439   6.135128   6.282676
       _cons |  19.29971   .6097913   .012916    19.2999   18.11953   20.47267
-------------+----------------------------------------------------------------
       var_0 |  4.414173   .3194018   .004992   4.396302   3.828712   5.099535
      var_id |  15.85026    3.45786   .052824   15.44261   10.34387    23.6678
------------------------------------------------------------------------------
```

With Gibbs sampling, our estimates change only slightly. For example, the estimates of variance components are 4.41 for {var_0:_cons} and 15.85 for {var_id}.

All estimates are very close to the MLEs obtained earlier with the mixed command.

◁

▷ 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, *Mixed-effects logistic regression* below.

In the absence of Gibbs sampling for random effects, block()'s suboption split provides the next most efficient 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 {weight:i.id}.

```
. set seed 14

. bayesmh weight week i.id, likelihood(normal({var_0})) noconstant
> prior({weight:i.id},  normal({weight:_cons},{var_id}))
> prior({weight:_cons}, normal(0, 100))
> prior({weight:week},  normal(0, 100))
> prior({var_0},        igamma(0.001, 0.001))
> prior({var_id},       igamma(0.001, 0.001))
> block({weight:_cons}, gibbs) block({weight:week}, gibbs)
> block({var_0}, gibbs) block({var_id}, gibbs)
> block({weight:i.id}, split)
> mcmcsize(5000) dots notable 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  =      .4823
                                                 Efficiency:  min =     .04123
                                                              avg =      .1773
Log marginal likelihood = -1050.2963                          max =      .7524
```

We use bayesstats summary to see posterior summaries of the model parameters of interest.

```
. bayesstats summary {weight:week _cons} {var_0} {var_id}

Posterior summary statistics                      MCMC sample size =     5,000

                                                             Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
weight       |
        week |  6.206316   .0399631   .002783   6.206429   6.127974    6.28349
       _cons |  19.31371   .6125276   .019648   19.31878   18.08646   20.52478
-------------+----------------------------------------------------------------
       var_0 |    4.4213   .3205769   .006464   4.407209   3.825247   5.085138
      var_id |  15.74962   3.448178   .056218   15.32605   10.25279   23.57063
------------------------------------------------------------------------------
```

The estimated posterior means are close to those obtained with the full Gibbs sampler in example 21, although the estimated MCMC standard errors are slightly higher. For example, the MCSE of {var_0} rises from 0.0050 to 0.0065, or about 30%.

The average sampling efficiency, 18%, is not as high as with the full Gibbs sampling in example 21 but is still high enough for reliable estimation. The caveat with using the split option for sampling the random-effects parameters is a significant decrease in speed. When speed is an issue or when the number of random-effects parameters is large, the reffects() option may be a better alternative; see example 23.

◁

▷ Example 23: Fifth simulation—using the reffects() option

The reffects() option supported by bayesmh can be used for specifying the two-level random-intercept model considered in this series of examples. It allows for faster MCMC sampling of the parameters associated with a random-effects variable compared with block()'s suboption split (see example 22).

We modify the syntax from example 22 as follows. We exclude i.id from the list of independent variables and add the reffects(id) option. We also omit the block({weight:i.id}, split) option because the blocking of the {weight:i.id} parameters is handled implicitly by the reffects() option.

```
. set seed 14

. bayesmh weight week, reffects(id) likelihood(normal({var_0})) noconstant
> prior({weight:i.id},  normal({weight:_cons},{var_id}))
> prior({weight:_cons}, normal(0, 100))
> prior({weight:week},  normal(0, 100))
> prior({var_0},        igamma(0.001, 0.001))
> prior({var_id},       igamma(0.001, 0.001))
> block({weight:_cons}, gibbs) block({weight:week}, gibbs)
> block({var_0}, gibbs) block({var_id}, gibbs)
> mcmcsize(5000) dots
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 5000 .........1000.........2000.........3000.........4000.........
> 5000 done

Model summary
------------------------------------------------------------------------------
Likelihood:
  weight ~ normal(xb_weight,{var_0})

Priors:
   {weight:i.id} ~ normal({weight:_cons},{var_id})                         (1)
   {weight:week} ~ normal(0,100)                                           (1)
         {var_0} ~ igamma(0.001,0.001)
  {weight:_cons} ~ normal(0,100)

Hyperprior:
  {var_id} ~ igamma(0.001,0.001)
------------------------------------------------------------------------------
(1) Parameters are elements 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  =      .8475
                                                 Efficiency:  min =     .03221
                                                              avg =      .3708
Log marginal likelihood = -1050.8235                          max =        .77

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
weight       |
        week |  6.209593    .040908   .003224   6.210008   6.127663   6.288345
-------------+----------------------------------------------------------------
       var_0 |  4.412871   .3171205   .006625   4.406072   3.834571   5.067036
-------------+----------------------------------------------------------------
weight       |
       _cons |  19.29717    .634793    .01903   19.28847    18.0127   20.53934
-------------+----------------------------------------------------------------
      var_id |  15.89952   3.549986   .057213   15.46713   10.36942   24.02605
------------------------------------------------------------------------------
```

Our estimates of the variance components do not change noticeably from those in examples 21 and 22: `{var_0}` is 4.41 and `{var_id}` is 15.90.

Although the average efficiency, 0.37, of the displayed parameters is lower than the corresponding efficiency of the full Gibbs sampler in example 21, the application of the `reffects()` option results in consuming about 35% less memory during simulation and a 25% improvement in speed. The real benefit of the `reffects()` option, however, becomes apparent for models with many random-effects levels and models for which full Gibbs samplers are not available; see *Mixed-effects logistic regression* below.

When we use option `reffects()`, `bayesmh` suppresses the estimates of random-effects parameters from the output. You can use the `showreffects()` or `show()` option to display them.

◁

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 $j = 1, \dots, 48$ and $i = 1, \dots, 9$.

▷ 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 http://www.stata-press.com/data/r15/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 |      Coef.   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:

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

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

The model has five main parameters of interest: regression coefficients β_0 and β_1 and variance components σ_0^2, σ_{id}^2, and σ_{week}^2. β_0 and β_1 are hyperparameters because they are specified as mean parameters of the prior distributions for random effects τ_{0j} and τ_{1j}, respectively. Random effects τ_{0j} and τ_{1j} are considered nuisance parameters. We again use normal priors for the regression coefficients and group levels identified by the id variable and their interactions with week 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 example 21, we add factor levels of the id variable to the regression by using the factor-variable specification i.id. We include random coefficients on week as i.id#c.week. By default, the specification will omit one of the id categories as a base category. In our Bayesian model, we need to keep all categories of id:

```
. fvset base none id
```

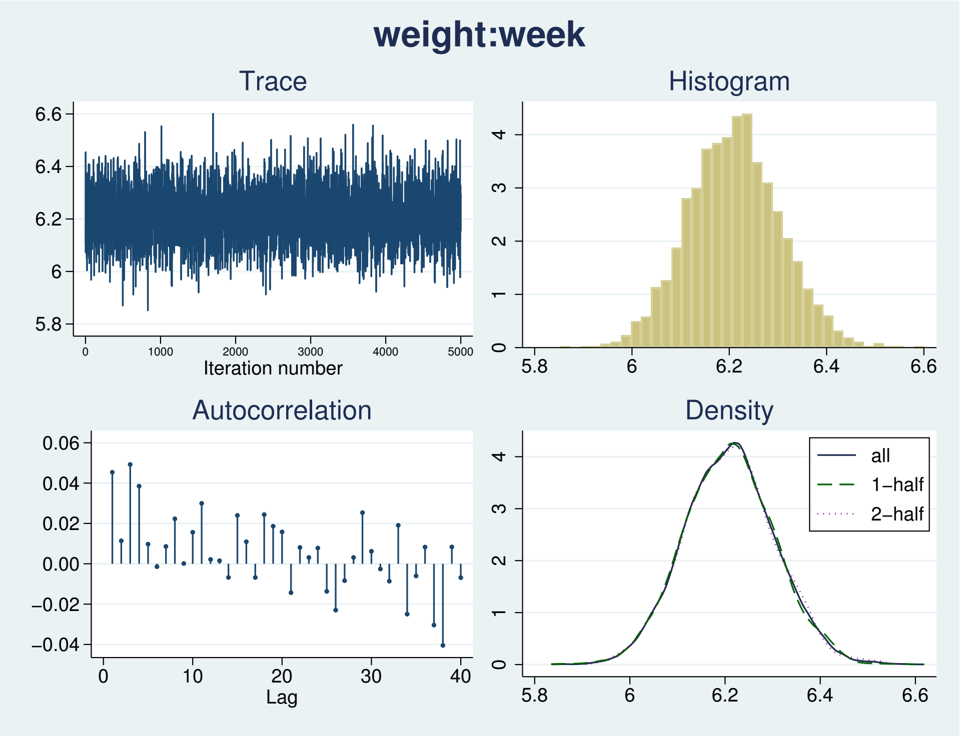
We fit our model using bayesmh. Following example 21, we perform blocking of parameters and use Gibbs sampling for the blocks. (We could have used the reffects() option as in example 23 to include random intercepts, but we want to use Gibbs sampling in this example; thus we use the factor-variable specification instead.)

```
. set seed 14
. bayesmh weight i.id i.id#c.week, likelihood(normal({var_0})) noconstant
> prior({weight:i.id}, normal({weight:_cons},{var_id}))
> prior({weight:i.id#c.week}, normal({weight:week},{var_week}))
> prior({weight:_cons}, normal(0, 100))
> prior({weight:week}, normal(0, 100))
> prior({var_0}, igamma(0.001, 0.001))
> prior({var_id}, igamma(0.001, 0.001))
> prior({var_week}, igamma(0.001, 0.001))
> block({var_0}, gibbs)
> block({var_id}, gibbs)
> block({var_week}, gibbs)
> block({weight:i.id}, gibbs)
> block({weight:i.id#c.week}, gibbs)
> block({weight:week}, gibbs)
> block({weight:_cons}, gibbs)
> mcmcsize(5000) dots notable
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 5000 .........1000.........2000.........3000.........4000.........
> 5000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  weight ~ normal(xb_weight,{var_0})
Priors:
         {weight:i.id} ~ normal({weight:_cons},{var_id})                    (1)
  {weight:i.id#c.week} ~ normal({weight:week},{var_week})                  (1)
               {var_0} ~ igamma(0.001,0.001)
   {weight:_cons week} ~ normal(0,100)
Hyperprior:
  {var_id var_week} ~ 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 =     .08386
                                                              avg =      .1582
Log marginal likelihood = -929.94517                          max =      .7758
```

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.

Let's look at diagnostic plots. We show only diagnostic plots for the mean of random coefficients on `week`, 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:week}
```



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_0} {var_id} {var_week}
Posterior summary statistics                      MCMC sample size =     5,000

                                                                Equal-tailed
                    Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]

weight
        week    6.210054   .0948751   .001523   6.210372   6.029255   6.398015
       _cons    19.32719   .4096827   .007805   19.32701   18.53177   20.14601

       var_0    1.607193   .1224062   .002371   1.600899   1.384723   1.863646
      var_id    7.253204   1.705803   .038343   7.034003   4.566251   11.32263
    var_week    .3940417   .0886511   .001723   .3822614   .2545719    .607737
```

◁

▷ 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.

```
. set seed 14
. 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 |      Coef.   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:

$$(\tau_{0j}, \tau_{1j}) \sim \text{i.i.d. MVN}(\beta_0, \beta_1, \Sigma)$$
$$\Sigma \sim \text{InvWishart}\{3, I(2)\}$$

$$\Sigma = \begin{bmatrix} \sigma^2_{\text{id}} & \sigma^2_{12} \\ \sigma^2_{21} & \sigma^2_{\text{week}} \end{bmatrix}$$

The elements σ^2_{id} and σ^2_{week} of Σ represent the variances of τ_{0j}'s and τ_{1j}'s, respectively, while σ_{21} is the covariance between them. We apply weakly informative inverse-Wishart prior with degree of freedom 3 and identity scale matrix.

Gibbs sampling is not available in `bayesmh` with unstructured covariance for the random effects. We thus replace `gibbs` with `reffects` in the corresponding `block()` option. This is possible because τ_{0j}'s are conditionally independent given τ_{1j}'s and vice versa. Using `block()`'s suboption `reffects` results in a more efficient sampling.

```
. set seed 14
. bayesmh weight i.id i.id#c.week, likelihood(normal({var_0})) noconstant
> prior({weight:i.id i.id#c.week},
>     mvnormal(2, {weight:_cons}, {weight:week}, {Sigma,m}))
> prior({weight:week _cons}, normal(0, 1e2))
> prior({var_0}, igamma(0.001,0.001))
> prior({Sigma,m}, iwishart(2,3,I(2)))
> block({var_0}, gibbs) block({Sigma,m}, gibbs)
> block({weight:_cons}) block({weight:week})
> block({weight:i.id}, reffects)
> block({weight:i.id#c.week}, reffects)
> noshow({weight:i.id i.id#c.week})
> mcmcsize(5000) dots
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 5000 .........1000.........2000.........3000.........4000.........
> 5000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  weight ~ normal(xb_weight,{var_0})
Priors:
  {weight:i.id i.id#c.week} ~ mvnormal(2,{weight:_cons},{weight:week},{Sigma,m
                              }) (1)
                    {var_0} ~ igamma(0.001,0.001)
        {weight:week _cons} ~ normal(0,1e2)
Hyperprior:
  {Sigma,m} ~ iwishart(2,3,I(2))
------------------------------------------------------------------------------
(1) Parameters are elements 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  =      .5581
                                                 Efficiency:  min =     .07112
                                                              avg =      .1423
Log marginal likelihood = -926.22043                          max =      .2238
------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
       var_0 |  1.607509   .1249066    .00435   1.601815    1.38134   1.860937
-------------+----------------------------------------------------------------
weight       |
       _cons |  19.36808   .4017089   .021302   19.36764   18.52137   20.15876
        week |  6.201477   .0952501   .003317   6.199532   6.014793   6.389815
-------------+----------------------------------------------------------------
   Sigma_1_1 |  6.850707   1.632765    .07773    6.60346   4.345719   10.66529
   Sigma_2_1 | -.0854197   .2652103   .010005  -.0803053  -.6326388   .4431884
   Sigma_2_2 |   .400556   .0903881   .002702   .3889624    .260342   .6140122
------------------------------------------------------------------------------
```

The average sampling efficiency is about 14% 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 σ^2_{id}, σ_{21}, and σ^2_{week} are 6.85, -0.85, and 0.40, respectively, from `bayesmh` and 6.82, -0.98, and 0.37, respectively, from `mixed`.

◁

Mixed-effects 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 child* 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 use the reffects() option to specify the random-effects variable district. The corresponding random-effects parameters {c_use:i.district} are assigned a zero-mean normal prior distribution with variance {district:var}. A relatively weak normal(0,100) prior is applied to the fixed-effects parameters {c_use:urban}, {c_use:age}, {c_use:child*}, and {c_use:_cons}. The variance parameter {district:var} is assigned a noninformative igamma(0.01,0.01) prior, and a Gibbs sampler is used for it.

```
. use http://www.stata-press.com/data/r15/bangladesh
(Bangladesh Fertility Survey, 1989)

. set seed 14

. bayesmh c_use urban age child*, likelihood(logit) reffects(district)
> prior({c_use:i.district}, normal(0,{district:var}))
> prior({c_use:urban age child* _cons}, normal(0, 100))
> prior({district:var}, igamma(0.01,0.01))
> block({district:var}, gibbs) dots
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:i.district} ~ normal(0,{district:var})  (1)
  {c_use:urban age child1 child2 child3 _cons} ~ normal(0,100)            (1)
                               {district:var} ~ 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  =      .4913
                                             Efficiency:  min =     .01728
                                                          avg =     .02523
Log marginal likelihood = -1240.2644                      max =     .04155

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
c_use        |
       urban |  .7252685   .1260246   .009454   .7216279   .4789413   .9849255
         age | -.0259076   .0076429   .000529  -.0259236   -.040793  -.0101205
      child1 |  1.104812   .1540978   .008963   1.104046   .8012581   1.410451
      child2 |  1.352477   .1890995   .014387   1.345373   .9832535   1.712931
      child3 |  1.343504   .1793496   .012102   1.343257   .9941767   1.697041
       _cons | -1.687957   .1420537   .008543  -1.683849  -1.964436  -1.405009
-------------+----------------------------------------------------------------
district     |
         var |  .2380246   .0857548   .004207   .2269953   .1034288   .4357797
------------------------------------------------------------------------------
```

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 {district:var}, 0.24, is slightly larger than the corresponding estimate of 0.22 from melogit.

This model has a fairly large number of parameters, 67, and the logistic likelihood does not allow for efficient Gibbs sampling of regression parameters. If we do not use the reffects() option of bayesmh (or block()'s suboption split with {c_use:i.district}) and resort to the standard MH algorithm, we may have problems drawing a well-mixed MCMC sample.

For comparison, we show a standard bayesmh specification in which the {c_use:i.district} parameters are placed in a separate block without using the reffects() option. Statistically, the two model specifications are the same because they define one and the same posterior distribution. However, they use different MCMC sampling procedures. We are not interested in the estimates of random effects in this example, so we exclude the random-effects parameters {c_use:i.district} from the output table.

```
. set seed 14

. bayesmh c_use urban age child* ibn.district, likelihood(logit)
> prior({c_use:i.district}, normal(0,{district:var}))
> prior({c_use:urban age child* _cons}, normal(0, 100))
> prior({district:var}, igamma(0.01,0.01))
> block({district:var}, gibbs)
> block({c_use:i.district}) noshow({c_use:i.district}) dots
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:i.district} ~ normal(0,{district:var})  (1)
  {c_use:urban age child1 child2 child3 _cons} ~ normal(0,100)             (1)
                                {district:var} ~ 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  =        .53
                                                 Efficiency:  min =    .007367
                                                              avg =      .0255
Log marginal likelihood = -1362.0681                          max =     .04817

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
c_use        |
       urban |  .6929174    .119883   .013968   .6906259   .4664536   .9199054
         age | -.0280929   .0080467   .000375  -.0280689  -.0440295  -.0126579
      child1 |  1.158416   .1697389   .011534   1.155004    .839977   1.490753
      child2 |  1.442235   .1769685   .008064   1.439614    1.09767   1.796089
      child3 |  1.447863   .1928966   .012707   1.448637   1.065645   1.836695
       _cons | -2.348392     .14138   .010016  -2.350597  -2.621669  -2.069296
-------------+----------------------------------------------------------------
district     |
         var |  .7490145   .1557382   .014079   .7299348   .5026288   1.110885
------------------------------------------------------------------------------
Note: There is a high autocorrelation after 500 lags.
```

In this second run, we observe that the minimal sampling efficiency is less than 1% and that the MCMC convergence is questionable. For example, the reported MCMC standard error for `{district:var}` is about 0.014, or three times higher than the corresponding error of 0.004 in the previous run. The results from this last run are not trustworthy.

Bayesian analysis of change-point problem

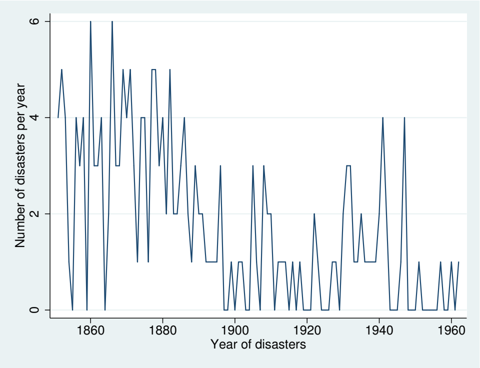
Change-point problems deal with stochastic data, usually time-series data, which undergoes some abrupt change at some time point. It is of interest to localize the point of change and estimate the properties of the stochastic process before and after the change.

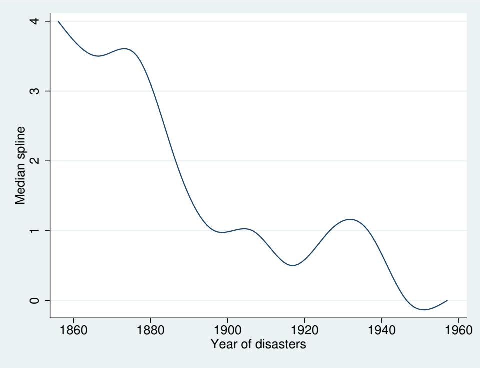
Here we analyze the British coal mining disaster data for the years 1851 to 1962 as given in table 5 in Carlin, Gelfand, and Smith (1992). The data are originally from Maguire, Pearson, and Wynn (1952) with updates from Jarrett (1979).

`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 http://www.stata-press.com/data/r15/coal
(British coal-mining disaster data, 1851-1962)
. describe
Contains data from http://www.stata-press.com/data/r15/coal.dta
  obs:           112                          British coal-mining disaster
                                                data, 1851-1962
 vars:             3                          5 Feb 2016 18:03
 size:           560                          (_dta has notes)
-------------------------------------------------------------------------------
              storage   display    value
variable 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}))
```

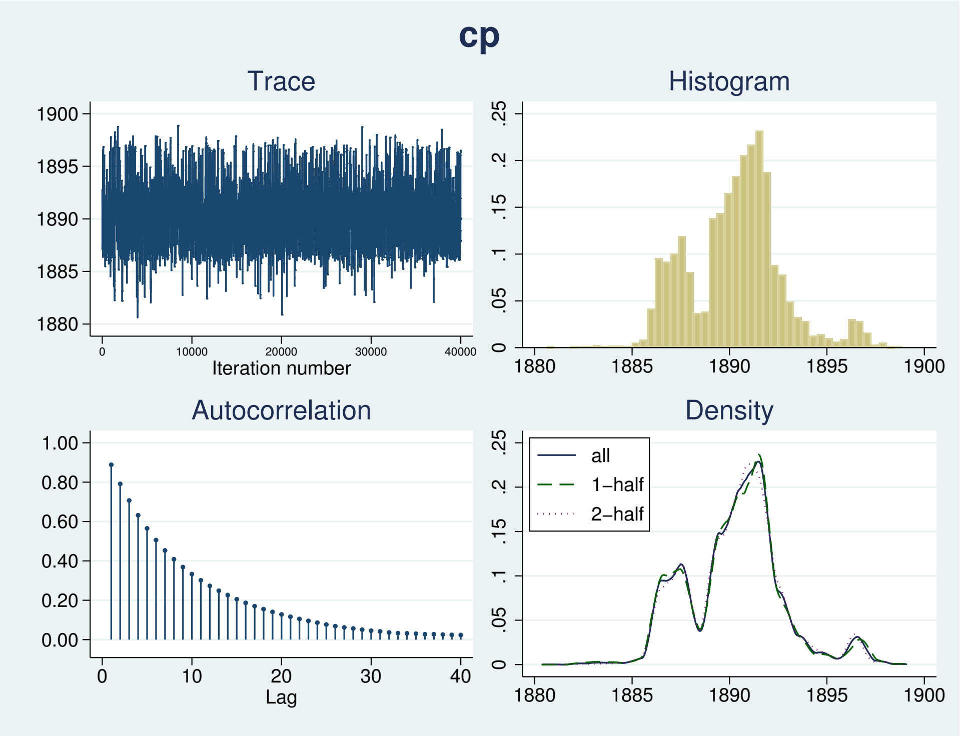
as the mean of a Poisson distribution dpoisson(). To ensure the feasibility of the initial state, we specify the desired initial values in option initial(). Because of high autocorrelation in the MCMC chain, we increase the MCMC size to achieve higher precision of our estimates. We change the default title to the title specific to our analysis. To monitor the progress of simulation, we request that bayesmh displays 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 two 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.

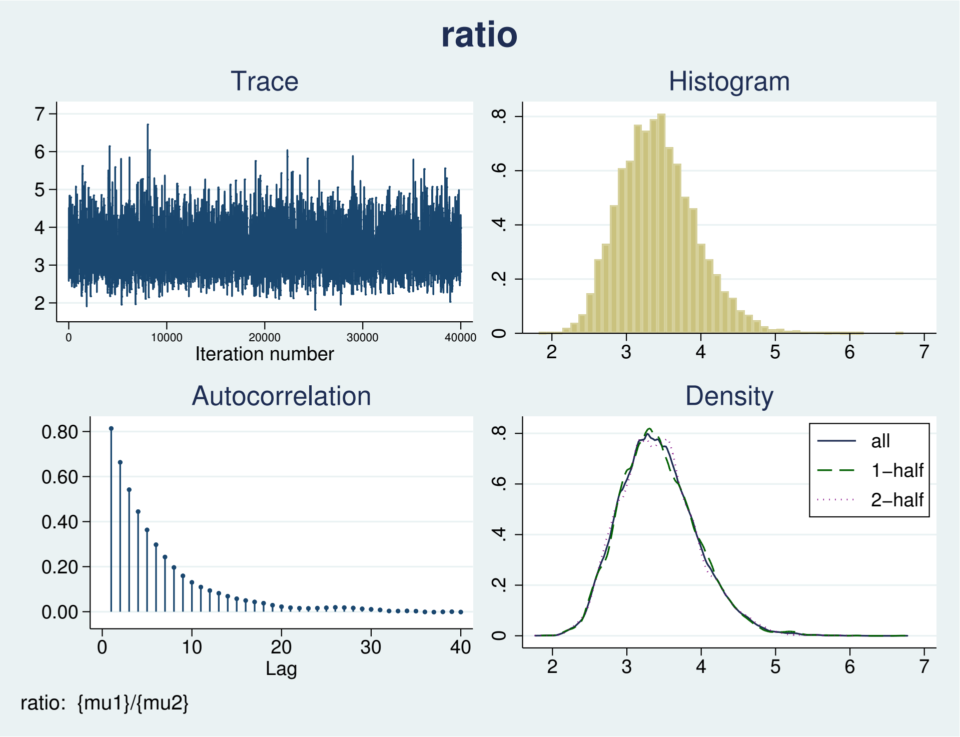
We may be interested in estimating the ratio between the two means. We can use `bayesstats summary` to estimate this ratio.

```
. bayesstats summary (ratio:{mu1}/{mu2})

Posterior summary statistics                      MCMC sample size =    40,000

      ratio : {mu1}/{mu2}

--------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [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 http://www.stata-press.com/data/r15/bioequiv
(Bioequivalent study of Carbamazepine tablets)

. describe

Contains data from http://www.stata-press.com/data/r15/bioequiv.dta
  obs:            20                          Bioequivalent study of
                                                Carbamazepine tablets
 vars:             5                          5 Feb 2016 23:45
 size:           160                          (_dta has notes)
--------------------------------------------------------------------------------
              storage   display    value
variable 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
```

Before fitting bayesmh, we request no base category for the id variable.

```
. fvset base none id
```

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 use noninformative priors for parameters and separate parameters in blocks. To improve convergence, we increase our adaptation and burn-in periods. (The command may take some time to produce results, so we specify the dots() option.)

```
. set seed 14

. bayesmh y = ({mu}+(-1)^(treat-1)*{phi}/2+(-1)^(period-1)*{pi}/2+{y:i.id, nocons}),
> likelihood(normal({var}))
> prior({y:i.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({y:i.id}, split)
> block({tau}, gibbs) block({var}, gibbs)
> adaptation(every(200) maxiter(50)) burnin(10000) dots(250, every(2500))
Burn-in 10000 aaaaaaaaa2500aaaaaaaaa5000aaaaaaaaa7500aaaaaaaaa10000 done
Simulation 10000 .........2500.........5000.........7500.........10000 done

Model summary
------------------------------------------------------------------------------
Likelihood:
  y ~ normal(<expr1>,{var})

Priors:
          {var} ~ igamma(0.001,0.001)
  {mu phi pi} ~ normal(0,1e6)
      {y:i.id} ~ normal(0,{tau})

Hyperprior:
  {tau} ~ igamma(0.001,0.001)

Expression:
  expr1 : {mu}+(-1)^(treat-1)*{phi}/2+(-1)^(period-1)*{pi}/2+{y:i.id, nocons}
------------------------------------------------------------------------------
```

```
Bayesian normal regression                       MCMC iterations  =     20,000
Metropolis-Hastings and Gibbs sampling           Burn-in          =     10,000
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         20
                                                 Acceptance rate  =      .5131
                                                 Efficiency:  min =     .01345
                                                              avg =     .02821
Log marginal likelihood = -25.692825                          max =     .04365

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
y            |
          id |
           1 |  .0668345   .0834954   .005428   .0645855  -.0879197   .2407731
           2 |  .1217473   .0895501   .005941   .1190309   -.037415    .308847
           3 |  .0561551   .0812912   .005154   .0525818  -.0971676   .2344846
           4 |  .0619807   .0827296   .005294   .0564789  -.0923602   .2365587
           5 |  .1701813     .09874   .006345   .1685315  -.0149722   .3676389
           6 | -.1640241   .0917804   .005572  -.1690176  -.3443967   .0135562
           7 | -.1191101   .0864379   .005291  -.1168358  -.2894083   .0400566
           8 | -.0590061   .0803792   .004595  -.0572132  -.2217439   .0908653
           9 | -.0779055   .0814977    .00481  -.0769495  -.2428321   .0816219
          10 |  -.014813   .0788845    .00452  -.0138628  -.1750312   .1463467
-------------+----------------------------------------------------------------
          mu |   1.43231   .0579197   .004993   1.434814   1.305574   1.545945
         phi | -.0093502    .050824    .00257  -.0104379  -.1039488   .1010855
          pi | -.1815055   .0542115   .003107  -.1821367  -.2963565  -.0702212
         var |  .0134664   .0087676   .000482   .0109334   .0042003   .0370388
         tau |  .0228884    .020285   .000971   .0182243   .0015547   .0725889
------------------------------------------------------------------------------
```

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

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
          mu |   1.43231   .0579197   .004993   1.434814   1.305574   1.545945
         phi | -.0093502    .050824    .00257  -.0104379  -.1039488   .1010855
          pi | -.1815055   .0542115   .003107  -.1821367  -.2963565  -.0702212
         tau |  .0228884    .020285   .000971   .0182243   .0015547   .0725889
         var |  .0134664   .0087676   .000482   .0109334   .0042003   .0370388
       theta |  .9919787   .0507755   .002569   .9896164   .9012714   1.106371
       equiv |     .9982   .0423903   .000892          1          1          1
------------------------------------------------------------------------------
```

We obtain an estimate of 0.998 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).

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 http://www.stata-press.com/data/r15/betablockers_wide
(Beta-blockers data in wide form)

. describe

Contains data from http://www.stata-press.com/data/r15/betablockers_wide.dta
  obs:            22                          Beta-blockers data in wide form
 vars:             7                          5 Feb 2016 19:02
 size:           550                          (_dta has notes)
───────────────────────────────────────────────────────────────────────────────
              storage   display    value
variable 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.

$$d \sim N(0, 1000)$$
$$\sigma^2 \sim \text{InvGamma}(0.001, 0.001)$$

In our data, random effects d_i is represented by a factor variable `i.study`. We use all levels of `study` in our analysis, so we use `fvset` to request no base level for this variable.

```
. fvset base none study
```

We specify `normal()` likelihood with `bayesmh` and request observation-specific variances by specifying variable `var` as `normal()`'s variance argument. 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}`. We also increase the burn-in period to 3,000 iterations and request more frequent adaptation by specifying the `adaptation(every(10))` option. The command will take a little longer to run, so we request that a dot be displayed every 500 iterations and an iteration number be displayed every 2,500 iterations to monitor the progress of the simulation.

```
. set seed 14
. bayesmh D i.study, likelihood(normal(var)) noconstant
> prior({D:i.study}, normal({d},{sig2}))
> prior({d}, normal(0,1000))
> prior({sig2}, igamma(0.001,0.001))
> block({D:i.study}, split)
> block({sig2}, gibbs)
> block({d}, gibbs)
> burnin(3000) adaptation(every(10)) dots(500, every(2500))
Burn-in 3000 aaaa2500a done
Simulation 10000 ....2500....5000....7500....10000 done
Model summary
------------------------------------------------------------------------------
Likelihood:
  D ~ normal(xb_D,var)
Prior:
  {D:i.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  =     13,000
Metropolis-Hastings and Gibbs sampling           Burn-in          =      3,000
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         22
                                                 Acceptance rate  =      .5315
                                                 Efficiency:  min =     .01845
                                                              avg =     .04462
Log marginal likelihood =   14.38145                          max =     .06842

-------------------------------------------------------------------------------
             |                                                Equal-tailed
             |       Mean   Std. Dev.      MCSE     Median  [95% Cred. Interval]
-------------+-----------------------------------------------------------------
D            |
       study |
           1 |  -.2357346   .1380931   .005394  -.2396019  -.5018659   .0564967
           2 |  -.2701697    .135307   .006741  -.2585033  -.5760455  -.0174336
           3 |  -.2538771   .1376569   .005263  -.2495234  -.5436489   .0222503
           4 |   -.246526     .08904   .003506  -.2483908  -.4212739  -.0643877
           5 |  -.1969971     .12748   .006635  -.2072718  -.4149274   .1014951
           6 |  -.2527047   .1339466    .00647  -.2526702  -.5224128   .0229356
           7 |  -.3377723   .1100308   .006646  -.3283355  -.5829385  -.1548902
           8 |  -.2054826   .1130796   .005594  -.2121369  -.4051584   .0546629
           9 |  -.2666327   .1215781   .005263  -.2630645  -.5206763  -.0297599
          10 |  -.2803866   .0841634   .003593  -.2771339  -.4590086  -.1252279
          11 |  -.2354098   .1049351   .004449   -.237795  -.4360951  -.0191799
          12 |   -.202938   .1178808   .005967   -.209884  -.4105608   .0725293
          13 |  -.2714193   .1288598   .006394   -.263365   -.564746   -.023963
          14 |  -.1273999   .1468804   .009997  -.1553146  -.3495763   .2172828
          15 |  -.2518538   .1249082   .005184  -.2502685  -.5090334  -.0021013
          16 |  -.2245814   .1210757   .004998   -.231592  -.4488306   .0415657
          17 |  -.2043954   .1357651   .007347  -.2164064  -.4321717   .1044344
          18 |  -.2153688   .1423256   .006983   -.222428  -.4718119   .0991941
          19 |  -.2242526   .1360964   .006098  -.2300817  -.4938685    .075416
          20 |  -.2428998   .1151988   .005403  -.2424417  -.4723024  -.0126589
          21 |  -.2972177   .1281401   .006041  -.2862546  -.5946982  -.0770212
          22 |  -.2979427   .1266137    .00575  -.2885006  -.5953839  -.0816952
-------------+-----------------------------------------------------------------
           d |  -.2429052   .0611413   .004501  -.2426092  -.3623229  -.1261924
        sig2 |   .0166923    .020771   .001488   .0095773   .0007359   .0753652
-------------------------------------------------------------------------------
```

Our posterior mean estimates d and sig2 of mean d and variance σ^2 are -0.24 and 0.017, 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.

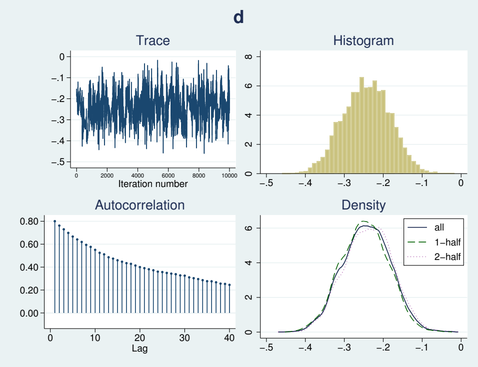
We can obtain the efficiencies for the main parameters by using bayesstats ess.

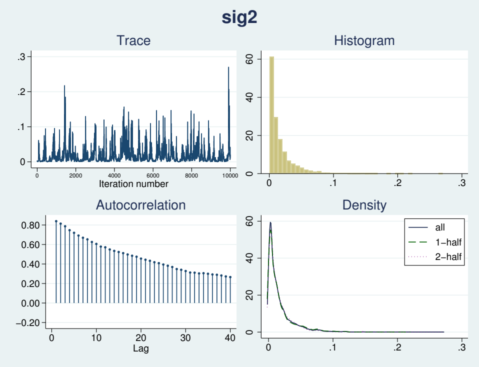
```
. bayesstats ess {d} {sig2}

Efficiency summaries    MCMC sample size =     10,000

------------------------------------------------------
             |         ESS   Corr. time    Efficiency
-------------+----------------------------------------
           d |      184.49        54.20        0.0184
        sig2 |      194.88        51.31        0.0195
------------------------------------------------------
```

The efficiencies are acceptable, but based on the correlation times, the autocorrelation becomes small only after lag 50 or so. The precision of the mean and variance estimates is comparable to those based on 184 independent observations for the mean and 195 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

$$\begin{aligned} \text{logit}(p_i) &= \mu_i + (T_i == 1) \times d_i \\ y_i &\sim \text{Binomial}(p_i, n_i) \\ d_i &\sim \text{i.i.d. } N(d, \sigma^2) \end{aligned}$$

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.

$$\begin{aligned} \mu_i &\sim 1 \\ d &\sim N(0, 1000) \\ \sigma^2 &\sim \text{InvGamma}(0.001, 0.001) \end{aligned}$$

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 http://www.stata-press.com/data/r15/betablockers_long
(Beta-blockers data in long form)

. describe

Contains data from http://www.stata-press.com/data/r15/betablockers_long.dta
  obs:            44                          Beta-blockers data in long form
 vars:             4                          5 Feb 2016 19:02
 size:           264                          (_dta has notes)
--------------------------------------------------------------------------------
              storage   display    value
variable 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.

To relate to the notation of our model, we create variable `mu` to contain identifiers for each study. We also request that no base is set for our factor variables `mu` and `study`.

```
. generate mu = study

. fvset base none mu study
```

We use a `binomial()` likelihood model for the number of `deaths`. We split all parameters into separate blocks and request Gibbs sampling for `sig2` to improve efficiency of the algorithm.

```
. set seed 14

. bayesmh deaths i.mu 1.treat#i.study, likelihood(binomial(total)) noconstant
> prior({deaths:i.mu}, flat)
> prior({deaths:1.treat#i.study}, normal({d},{sig2}))
> prior({d}, normal(0,1000)) prior({sig2}, igamma(0.001,0.001))
> block({deaths:1.treat#i.study}, split)
> block({deaths:i.mu}, split) block({d}, gibbs)
> block({sig2}, gibbs) dots(500, every(2500))
Burn-in 2500 aaaa2500 done
Simulation 10000 ....2500....5000....7500....10000 done

Model summary
------------------------------------------------------------------------------
Likelihood:
  deaths ~ binlogit(xb_deaths,total)

Priors:
             {deaths:i.mu} ~ 1 (flat)                                        (1)
  {deaths:i.treat#i.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_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  =      .4633
                                                 Efficiency:  min =     .01479
                                                              avg =       .092
Log marginal likelihood =  -126.8754                          max =       .228

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
deaths       |
          mu |
           1 | -2.445566   .4440859   .009774  -2.428504  -3.386517  -1.650575
           2 | -2.192517   .2372503   .005622  -2.189225   -2.67948  -1.751515
           3 | -2.130301   .2682139   .006193  -2.123122  -2.677923  -1.615621
           4 | -2.397429   .0783732   .002298  -2.396564   -2.55513  -2.244307
           5 | -2.406291    .160123   .004778  -2.402657  -2.731128  -2.103221
           6 | -2.235409   .3563328   .008201  -2.219613   -2.97514  -1.597156
           7 | -1.719358   .0814695   .003238  -1.720512  -1.877615  -1.558778
           8 | -2.112285   .1181128   .004557  -2.108343  -2.350633  -1.894469
           9 | -1.966916   .1456821    .00391   -1.96278  -2.266818  -1.697274
          10 | -2.246224   .0716096   .002504  -2.245524   -2.39558  -2.106513
          11 | -2.315093   .1137358   .003641  -2.314937  -2.545779  -2.097822
          12 | -1.466143   .1226934   .003342  -1.464731  -1.710775   -1.23385
          13 | -2.999446    .207893   .004396  -2.992656  -3.419645  -2.599853
          14 | -2.726241   .1262413   .006217  -2.718875  -2.992452  -2.488097
          15 | -1.358942   .1558862   .003801    -1.3591  -1.672494  -1.054848
          16 | -1.488891   .1430423   .003957  -1.488181  -1.772535  -1.220204
          17 | -2.000612    .189858   .006088  -1.989813  -2.394403  -1.647906
          18 | -2.970916   .2881977   .006512   -2.94776   -3.59226  -2.445288
          19 | -3.431928   .3386751   .007093  -3.410703  -4.129594  -2.813783
          20 | -1.487005   .1371778   .003604  -1.484245  -1.765015  -1.216753
          21 | -2.138858   .1373135   .004474  -2.135716  -2.409188  -1.871238
          22 | -2.923794   .1379264   .003928  -2.922266  -3.201064  -2.659156
```

```
             |
 treat#study |
       1  1  |  -.2332275   .1389226   .005131  -.2365335  -.5125546   .0643276
       1  2  |  -.2754821   .1376714   .005278  -.2639067  -.5865606  -.0155825
       1  3  |  -.2521373   .1376143   .005031  -.2448604  -.5515139   .0168471
       1  4  |  -.2441378   .0893076   .003315  -.2450735  -.4238717  -.0567493
       1  5  |  -.1922897   .1322661   .006521  -.2075691  -.4254067   .1204152
       1  6  |  -.2519257   .1398246   .005351  -.2490731  -.5571537   .0413351
       1  7  |  -.3394292   .1060879   .007038  -.3293058    -.57003  -.1592483
       1  8  |  -.2061079   .1133207   .005757  -.2172042   -.405318   .0483414
       1  9  |  -.2681616   .1191742    .00505  -.2642165  -.5293988  -.0371976
       1 10  |  -.2833565   .0857065   .003746   -.277193  -.4662505  -.1285165
       1 11  |  -.2347279   .1053374   .004244   -.238179  -.4488999  -.0093842
       1 12  |  -.1985932   .1140053   .005216  -.2092791  -.4048572   .0621012
       1 13  |  -.2661801   .1313768   .005161  -.2591945  -.5575894  -.0043227
       1 14  |  -.1199702   .1435854   .011808  -.1454409   -.345002   .2252269
       1 15  |  -.2528203   .1187262   .004596  -.2474198  -.5094695  -.0194982
       1 16  |  -.2250511   .1216752   .004596  -.2312945  -.4584372   .0489469
       1 17  |  -.2032452   .1313935   .006245  -.2141859  -.4449455   .1008652
       1 18  |    -.21541   .1365779   .005847  -.2247174  -.4765884   .0898225
       1 19  |  -.2256096   .1423711   .005804  -.2297091   -.519874   .0853728
       1 20  |  -.2384292    .116139   .004978  -.2397589  -.4725188   .0082366
       1 21  |  -.3012616   .1250729   .007103  -.2866182  -.5961708  -.0823887
       1 22  |    -.29952   .1259856   .006557  -.2836829  -.6027407  -.0829247
-------------+-----------------------------------------------------------------
           d |  -.2422989   .0600407   .004175   -.243193  -.3624938  -.1209386
        sig2 |   .0170769   .0196724   .001529   .0104745   .0007195    .070371
-------------------------------------------------------------------------------
Note: Adaptation tolerance is not met in at least one of the blocks.
```

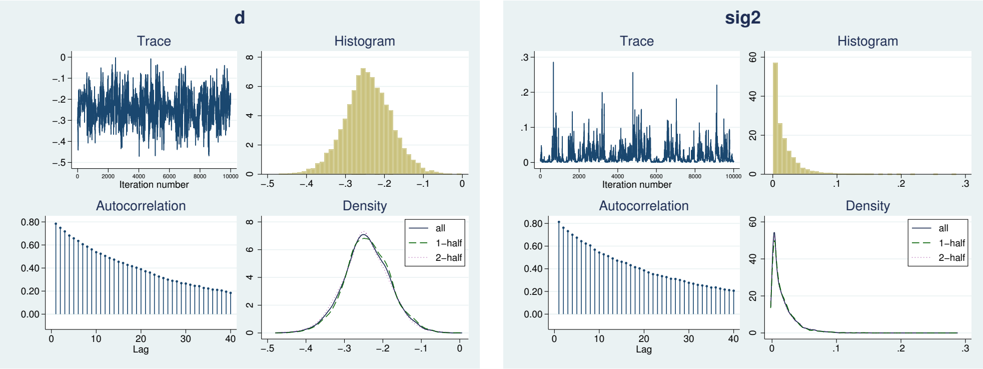
This model has 22 more parameters than the model in example 26. The posterior mean estimates d and sig2 of mean d and variance σ^2 are -0.24 and 0.017, respectively, with posterior standard deviations of 0.06 and 0.02. The estimates of the mean and variance are again close to the ones reported by Carlin (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

-------------+---------------------------------------
             |        ESS   Corr. time    Efficiency
-------------+---------------------------------------
           d |     206.78        48.36        0.0207
        sig2 |     165.58        60.39        0.0166
-----------------------------------------------------
```

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, which 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 http://www.stata-press.com/data/r15/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, item as an independent factor variable, and id as a random-effects variable. We suppress the base levels of item and id and use the noconstant option in the likelihood specification. The random-effects parameters {y:i.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 {y:i.item} [$\widetilde{b}_i$'s in model (1)] are applied ad hoc informative normal(0,10) priors. Because there are many random-effects parameters {y:i.id}, we exclude them from the simulation results and the output table by specifying the exclude() option.

```
. fvset base none id item

. set seed 14

. bayesmh y i.item, noconstant reffects(id) likelihood(logit)
> prior({y:i.id}, normal(0, {var}))
> prior({y:i.item}, normal(0, 10))
> prior({var}, igamma(0.01,0.01))
> block({var}) block({y:i.item}, reffects) exclude({y:i.id}) dots
Burn-in 2500 aaaaaaaaa1000.........2000..... done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done

Model summary
------------------------------------------------------------------------------
Likelihood:
  y ~ logit(xb_y)

Priors:
    {y:i.id} ~ normal(0,{var})                                             (1)
  {y:i.item} ~ normal(0,10)                                                (1)

Hyperprior:
  {var} ~ igamma(0.01,0.01)
------------------------------------------------------------------------------
(1) Parameters are elements 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  =      .3031
                                                 Efficiency:  min =     .02233
                                                              avg =     .09591
Log marginal likelihood =          .                          max =      .1139

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
y            |
        item |
          1  |  .6015542   .0820766    .00258   .6053092    .438748   .7659896
          2  |  .1025364   .0832577    .00262   .1027404  -.0551544   .2644014
          3  |  1.547352   .0985834   .003041   1.548773   1.352163   1.737668
          4  | -.2704933    .081763   .002509   -.269603  -.4330444  -.1116137
          5  | -1.410691   .0947962   .002899   -1.41001   -1.60001  -1.232148
          6  | -.5911439   .0837508   .002742  -.5907655   -.756948  -.4301115
          7  | -1.128951   .0906917    .00292  -1.125747   -1.31619  -.9531386
          8  |  2.060501   .1102492   .003284   2.059005   1.851561   2.277273
          9  |  1.015636   .0875144   .002593   1.015847   .8486233   1.190524
-------------+----------------------------------------------------------------
         var |   .726955    .079031   .005289   .7234471    .576551   .8930412
------------------------------------------------------------------------------
```

In the simulation summary, `bayesmh` reports a modest average efficiency of about 10% with no indications for convergence problems. The log marginal likelihood is reported as missing because we used the `exclude()` option. The Laplace–Metropolis approximation of the log marginal likelihood requires that simulation results be available for all model parameters, including random-effects parameters.

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 `{y:i.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:-{y:1bn.item}/sqrt({var}))
>                    (diff2:-{y:2.item}/sqrt({var}))
>                    (diff3:-{y:3.item}/sqrt({var}))
>                    (diff4:-{y:4.item}/sqrt({var}))
>                    (diff5:-{y:5.item}/sqrt({var}))
>                    (diff6:-{y:6.item}/sqrt({var}))
>                    (diff7:-{y:7.item}/sqrt({var}))
>                    (diff8:-{y:8.item}/sqrt({var}))
>                    (diff9:-{y:9.item}/sqrt({var})), nolegend
Posterior summary statistics                      MCMC sample size =    10,000

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
       discr |  .8513548   .0463711   .003113   .8505569   .7593095   .9450085
       diff1 | -.7082469   .1011861   .003508  -.7061776  -.9055634  -.5127043
       diff2 | -.1208126   .0983803   .003111  -.1213543  -.3106128    .066497
       diff3 | -1.821986   .1412775   .005966  -1.817721  -2.107488  -1.558985
       diff4 |  .3184996   .0975893   .003082   .3153589   .1316555   .5159253
       diff5 |   1.66113   .1341472   .005662   1.658582   1.414426   1.931525
       diff6 |   .696008   .1030643   .003547   .6927263   .4945615   .9064106
       diff7 |  1.329158   .1199949   .004557   1.325713   1.112063   1.582109
       diff8 | -2.426495   .1725481    .00809   -2.41446  -2.779606  -2.115298
       diff9 | -1.195812   .1148938   .004121   -1.19502  -1.429396  -.9759188
------------------------------------------------------------------------------
```

We observe that the reported posterior means for the common discrimination and question difficulties are close to those obtained with `irt 1pl`. For example, the estimated posterior mean for the discrimination is about 0.851, whereas the one reported by `irt 1pl` is 0.852, which is within the limits of the MCMC standard error of 0.003.

◁

In this example, we fit the Rasch model using the `reffects()` option and used 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, which precludes the use of the `reffects()` option, 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:}*({subj:}-{diff:})), likelihood(logit)     ///
        redefine(discr:i.item)                                  ///
        redefine(diff:i.item)                                   ///
        redefine(subj:i.id)                                     ///
        prior({subj:i.id},    normal(0, 1))                     ///
        prior({discr:i.item}, lognormal({mua}, {vara}))         ///
        prior({diff:i.item},  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:i.item}*({subj:i.id}-{diff:i.item})). Given the large number of subjects, it may be computationally prohibitive to use this substitutable expression. A more computationally efficient way is to use the redefine() option to specify the random effects associated with item discrimination, item difficulty, and student ability. For example, redefine(subj:i.id) introduces subject random-effects parameters, one for each subject, and represents the parameters θ_j's. Similarly, we use redefine(discr:i.item) and redefine(diff:i.item) to introduce the item-specific discrimination and difficulty parameters a_i's and b_i's, respectively. The probability of success is then modeled using the expression ({discr:}({subj:}-{diff:})).

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 zeros result in an invalid initial state. We have many random-effects parameters {subj:i.id}, so we exclude them from the simulation results and the output table by specifying the exclude() option.

```
. fvset base none id item

. set seed 14

. bayesmh y = ({discr:}*({subj:}-{diff:})), likelihood(logit)
> redefine(discr:i.item) redefine(diff:i.item) redefine(subj:i.id)
> prior({subj:i.id}, normal(0, 1))
> prior({discr:i.item}, lognormal({mua}, {vara}))
> prior({diff:i.item}, normal({mub}, {varb}))
> prior({vara varb}, gamma(1, 1)) prior({mua mub}, normal(0, 1))
> block({vara varb mua mub}, split) init({discr:i.item} 1 {diff:i.item} 1)
> exclude({subj:i.id}) showreffects({discr:i.item} {diff:i.item}) dots
Burn-in 2500 aaaaaaaaa1000aaaaaaaaa2000aaaaa done
Simulation 10000 .........1000.........2000.........3000.........4000.........
> 5000.........6000.........7000.........8000.........9000.........10000 done

Model summary
------------------------------------------------------------------------------
Likelihood:
  y ~ logit(xb_discr*(xb_subj-xb_diff))

Priors:
  {discr:i.item} ~ lognormal({mua},{vara})                                 (1)
   {diff:i.item} ~ normal({mub},{varb})                                    (2)
     {subj:i.id} ~ normal(0,1)                                             (3)

Hyperpriors:
  {vara varb} ~ gamma(1,1)
    {mua mub} ~ normal(0,1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_discr.
(2) Parameters are elements of the linear form xb_diff.
(3) Parameters are elements of the linear form xb_subj.
```

```
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  =      .3657
                                                 Efficiency:  min =     .01027
                                                              avg =     .04499
Log marginal likelihood =          .                          max =      .1762

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
discr        |
        item |
          1  |  1.498385   .2400297   .017729   1.475542   1.077856   2.016152
          2  |   .666128   .1119997   .005344   .6649249   .4541802    .886375
          3  |  .9383295   .1477952    .01186   .9204028   .6765889   1.266951
          4  |  .7994094   .1238608   .005473   .7962891   .5688815   1.059357
          5  |  .9051624   .1482122   .011637   .9043871   .6396924   1.205136
          6  |   .958388    .142267   .009086   .9504636   .7001779   1.252891
          7  |  .4792205   .0899554   .008877   .4741658   .3261732   .6680243
          8  |  1.297704    .221223   .017263   1.295304   .8673528   1.758576
          9  |  .6670617   .1104876   .009091   .6625288   .4666832   .8896693
-------------+----------------------------------------------------------------
diff         |
        item |
          1  | -.4989148   .0830179   .005137  -.4993581  -.6742972  -.3519269
          2  | -.1502021   .1239443   .003577  -.1458722  -.4059771   .0751602
          3  | -1.710592   .2234976   .016935  -1.692729  -2.214283  -1.328619
          4  |  .3466566    .114595   .004388   .3434778   .1346476   .5714364
          5  |  1.605012   .2387544   .018704    1.57642   1.229628   2.138817
          6  |  .6442216   .1147523   .006181   .6396185   .4391379   .8736935
          7  |  2.190372   .4265088   .041367   2.130899   1.530794   3.148253
          8  | -1.830477   .2345021   .019047  -1.795231  -2.420293   -1.46107
          9  | -1.472878   .2480988    .01968  -1.446161  -2.045008  -1.072642
-------------+----------------------------------------------------------------
         mua |  -.157914   .1768629   .004552  -.1556469  -.5143239    .188628
        vara |  .2516064   .1808929   .007705   .1996404   .0597163   .7334286
         mub |  -.078763   .4360087   .010388  -.0791598   -.945727   .7879737
        varb |  1.953467   .8047981   .029965   1.806903   .8319104   3.947983
------------------------------------------------------------------------------
```

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 not much different from the MLE estimates obtained with the irt 2pl command; see example 1 in [IRT] **irt 2pl**.

◁

Stored results

bayesmh stores the following in e():

Scalars

e(N)	number of observations
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(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(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)	deviation 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#_arate_last)	#th block AR from the last adaptive iteration
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
`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
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 $T_{\text{total}} = T_0 + (T-1) \times$ `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 $t = 1, \dots, T_{\text{total}}$, 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 $\boldsymbol{\theta}^1$, $\boldsymbol{\theta}^2$, ..., $\boldsymbol{\theta}^B$, 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 the `initial()` option. By default, 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 fixed initial values for all model parameters for which random initial values cannot be generated.

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

$$\rho_k = \rho_{k-1} e^{\beta_k \left\{ \Phi^{-1}(\mathrm{AR}_k/2) - \Phi^{-1}(\mathrm{TAR}/2) \right\}} \tag{2}$$

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 $\max\{0.1353, 1/n_{\mathrm{maxbins}}\}$, 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,

$$\Pr(\eta_1,\dots,\eta_m,\boldsymbol{\theta}|Y) = \pi(\boldsymbol{\theta})\left\{\prod_{j=1}^{m}\pi(\eta_j|\boldsymbol{\theta})\prod_{i=1}^{n_j}\Pr(y_{ij}|\eta_j,\boldsymbol{\theta})\right\}$$

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 specifies the `reffects()` option. 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: $\boldsymbol{\theta}^b_* \sim F_b(\boldsymbol{\theta}^b|\boldsymbol{\theta}^1_*,\dots,\boldsymbol{\theta}^{b-1}_*,\boldsymbol{\theta}^{b+1}_*,\dots,\boldsymbol{\theta}^B_*,\mathbf{y})$

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 $\mathbf{y} = (y_1,y_2,\dots,y_n)'$ be a data sample of size n. For multivariate data, $Y = (\mathbf{y}_1,\mathbf{y}_2,\dots,\mathbf{y}_n)' = \{y_{ij}\}_{i,j=1}^{n,d}$ 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,

$$\begin{aligned} y_i|\theta^b,\sigma^2 &\sim N(\theta^b,\sigma^2),\ i=1,2,\dots,n \\ \theta^b &\sim N(\mu_0,\tau_0^2) \\ \theta^b|\sigma^2,\mathbf{y} &\sim F_b = N(\mu_n,\tau_n^2) \end{aligned}$$

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 $X = (\mathbf{x}_1', \mathbf{x}_2', \dots, \mathbf{x}_n')'$ and with a variance σ^2; regression coefficients and variance are independent a priori,

$$\begin{aligned} y_i|\boldsymbol{\theta}^b, \sigma^2 &\sim N(\mathbf{x}_i'\boldsymbol{\beta}, \sigma^2),\ i = 1, 2, \dots, n \\ \theta_k^b &\sim \text{i.i.d. } N(\beta_0, \tau_0^2),\ k = 1, 2, \dots, p_1 \\ \boldsymbol{\theta}^b|\sigma^2, \mathbf{y} &\sim F_b = \text{MVN}(\boldsymbol{\mu}_n, \Lambda_n) \end{aligned}$$

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 $X_b = (\mathbf{x}_{1b}', \mathbf{x}_{2b}', \dots, \mathbf{x}_{nb}')'$ 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,

$$\begin{aligned} y_i|\mu, \theta^b &\sim N(\mu, \theta^b),\ i = 1, 2, \dots, n \\ \theta^b &\sim \text{InvGamma}(\alpha, \beta) \\ \theta^b|\mu, \mathbf{y} &\sim F_b = \text{InvGamma}(\alpha + n/2, \beta + \sum_{i=1}^n (y_i - \mu)^2/2) \end{aligned}$$

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,

$$\begin{aligned} \mathbf{y}_i|\boldsymbol{\theta}^b, \Sigma &\sim \text{MVN}(\boldsymbol{\theta}^b, \Sigma),\ i = 1, 2, \dots, n \\ \boldsymbol{\theta}^b &\sim \text{MVN}(\boldsymbol{\mu}_0, \Lambda_0) \\ \boldsymbol{\theta}^b|\Sigma, Y &\sim F_b = \text{MVN}(\boldsymbol{\mu}_n, \Lambda_n) \end{aligned}$$

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.

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,

$$\begin{aligned}\theta|\theta_h^b,\sigma_h^2 &\sim N(\theta_h^b,\sigma_h^2)\\ \theta_h^b &\sim N(\mu_0,\tau_0^2)\\ \theta_h^b|\sigma_h^2,\theta &\sim F_b = N(\mu_1,\tau_1^2)\end{aligned}$$

where μ_0 and τ_0^2 are the prior mean and prior variance of a normal hyperprior distribution for θ_h^b and

$$\begin{aligned}\mu_1 &= \left(\mu_0\tau_0^{-2}+\theta\sigma_h^{-2}\right)\tau_1^2\\ \tau_1^2 &= (\tau_0^{-2}+\sigma_h^{-2})^{-1}\end{aligned}$$

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,

$$\begin{aligned}\theta|\mu_h,\theta_h^b &\sim N(\mu_h,\theta_h^b)\\ \theta_h^b &\sim \text{InvGamma}(\alpha,\beta)\\ \theta_h^b|\mu_h,\theta &\sim F_b = \text{InvGamma}(\alpha+0.5,\beta+(\theta-\mu)^2/2)\end{aligned}$$

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.

Nicholas Constantine Metropolis (1915–1999) was born in Chicago, where he received BSc and PhD degrees in physics at the University of Chicago. He oscillated through his career between posts there and at what later became the Los Alamos National Laboratory in New Mexico. Metropolis is best known for his contributions to Monte Carlo methods, algorithms based on repeated random sampling. He was the first author on an outstanding paper about a Monte Carlo algorithm (Metropolis et al. 1953), with Arianna W. Rosenbluth, Marshall N. Rosenbluth (1927–2003), Augusta H. Teller (1909–2000), and Edward Teller (1908–2003). However, the relative contributions of these authors have been much disputed, and general and specific credit for the method should also be given to others, including John von Neumann (1903–1957), Stanisław M. Ulam (1909–1984), and Enrico Fermi (1901–1954). According to Google Scholar, Metropolis et al. (1953) has been cited over 28,000 times.

Wilfred Keith Hastings (1930–2016) was born in Toronto, Ontario. He received BA, MA, and PhD degrees in applied mathematics and statistics from the University of Toronto; his doctoral thesis was on invariant fiducial distributions. Hastings worked as a consultant in computer applications for a Toronto firm, at the University of Canterbury in New Zealand, and at Bell Labs in New Jersey before returning from 1966 to 1971 to his alma mater. In this period, he wrote a famous paper (Hastings 1970) generalizing the work of Metropolis et al. (1953) to produce what is now often called the Metropolis–Hastings algorithm. It is the most common Markov chain Monte Carlo method, widely used throughout statistical science to sample from high-dimensional distributions. According to Google Scholar, Hastings (1970) has been cited over 8,000 times. Hastings worked at the University of Victoria in British Columbia from 1971 to 1992, when he retired.

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*.

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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**

Title

bayesmh evaluators — User-defined evaluators with bayesmh

Description　Syntax　Options　Remarks and examples
Stored results　Also see

Description

`bayesmh` provides two options, `evaluator()` and `llevaluator()`, that facilitate user-defined evaluators for fitting general Bayesian regression models. `bayesmh, evaluator()` accommodates log-posterior evaluators. `bayesmh, llevaluator()` accommodates log-likelihood evaluators, which are combined with built-in prior distributions to form the desired posterior density. For a catalog of built-in likelihood models and prior distributions, see [BAYES] **bayesmh**.

Syntax

Single-equation models

User-defined log-posterior evaluator

`bayesmh` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] `,` `evaluator(`*evalspec*`)` [*options*]

User-defined log-likelihood evaluator

`bayesmh` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] `,` `llevaluator(`*evalspec*`)`
　`prior(`*priorspec*`)` [*options*]

Multiple-equations models

User-defined log-posterior evaluator

`bayesmh (`*eqspecp*`)` [`(`*eqspecp*`)` [...]] [*if*] [*in*] [*weight*] `,` `evaluator(`*evalspec*`)`
　[*options*]

User-defined log-likelihood evaluator

`bayesmh (`*eqspecll*`)` [`(`*eqspecll*`)` [...]] [*if*] [*in*] [*weight*] `,` `prior(`*priorspec*`)`
　[*options*]

The syntax of *eqspecp* is

varspec [, noconstant]

The syntax of *eqspecll* for built-in likelihood models is

varspec, likelihood(*modelspec*) [noconstant]

The syntax of *eqspecll* for user-defined log-likelihood evaluators is

varspec, llevaluator(*evalspec*) [noconstant]

The syntax of *varspec* is one of the following:

for single outcome

[*eqname*:] *depvar* [*indepvars*]

for multiple outcomes with common regressors

depvars = [*indepvars*]

for multiple outcomes with outcome-specific regressors

([*eqname1*:] *depvar1* [*indepvars1*]) ([*eqname2*:] *depvar2* [*indepvars2*]) [...]

The syntax of *evalspec* is

progname, parameters(*paramlist*) [extravars(*varlist*) passthruopts(*string*)]

where *progname* is the name of a Stata program that you write to evaluate the log-posterior density or the log-likelihood function (see Program evaluators), and *paramlist* is a list of model parameters:

paramdef [*paramdef* [...]]

The syntax of *paramdef* is

{ [*eqname*:] *param* [*param* [...]] [, matrix] }

where the parameter label *eqname* and parameter names *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=#} in the above to specify an initial value. For example, you can specify {var=1}, {mean=1.267}, or {shape:alpha=3}. You can specify the multiple parameters with same equation as {eq:p1 p2 p3} or {eq: S1 S2, matrix}. Also see *Declaring model parameters* in [BAYES] **bayesmh**.

options	Description
*evaluator(*evalspec*)	specify log-posterior evaluator; may not be combined with llevaluator() and prior()
*llevaluator(*evalspec*)	specify log-likelihood evaluator; requires prior() and may not be combined with evaluator()
*prior(*priorspec*)	prior for model parameters; required with log-likelihood evaluator and may be repeated
likelihood(*modelspec*)	distribution for the likelihood model; allowed within an equation of a multiple-equations model only
noconstant	suppress constant term; not allowed with ordered models specified in likelihood() with multiple-equations models
bayesmhopts	any options of [BAYES] **bayesmh** except likelihood() and prior()

*Option evaluator() is required for log-posterior evaluators, and options llevaluator() and prior() are required for log-likelihood evaluators. With log-likelihood evaluators, prior() must be specified for all model parameters and can be repeated.

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

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

Options

evaluator(*evalspec*) specifies the name and the attributes of the log-posterior evaluator; see *Program evaluators* for details. This option may not be combined with llevaluator() or likelihood().

llevaluator(*evalspec*) specifies the name and the attributes of the log-likelihood evaluator; see *Program evaluators* for details. This option may not be combined with evaluator() or likelihood() and requires the prior() option.

prior(*priorspec*); see [BAYES] **bayesmh**.

likelihood(*modelspec*); see [BAYES] **bayesmh**. This option is allowed within an equation of a multiple-equations model only.

noconstant; see [BAYES] **bayesmh**.

bayesmhopts specify any *options* of [BAYES] **bayesmh**, except likelihood() and prior().

Remarks and examples

Remarks are presented under the following headings:

Program evaluators

If your likelihood model or prior distributions are particularly complex and cannot be represented by one of the predefined sets of distributions or by substitutable expressions provided with `bayesmh`, you can program these functions by writing your own evaluator program.

Evaluator programs can be used for programming the full posterior density by specifying the `evaluator()` option or only the likelihood portion of your Bayesian model by specifying the `llevaluator()` option. For likelihood evaluators, `prior()` option(s) must be specified for all model parameters. Your program is expected to calculate and return an overall log-posterior or a log-likelihood density value.

It is allowed for the return values to match the log density up to an additive constant, in which case, however, some of the reported statistics such as DIC and log marginal-likelihood may not be applicable.

Your program evaluator *progname* must be a Stata program; see **[U] 18 Programming Stata**. The program must follow the style below.

```
program  progname
    args lnden xb1 [xb2 ...] [ modelparams]
    ... computations ...
    scalar ‘lnden’ = ...
end
```

Here `lnden` contains the name of a temporary scalar to be filled in with an overall log-posterior or log-likelihood value;

`xb#` contains the name of a temporary variable containing the linear predictor from the #th equation; and

modelparams is a list of names of scalars or matrices to contain the values of model parameters specified in suboption `parameters()` of `evaluator()` or `llevaluator()`. For matrix parameters, the specified names will contain the names of temporary matrices containing current values. For scalar parameters, these are the names of temporary scalars containing current values. The order in which names are listed should correspond to the order in which model parameters are specified in `parameters()`.

Also see *Global macros* for a list of global macros available to the program evaluator.

After you write a program evaluator, you specify its name in the option `evaluator()` for log-posterior evaluators,

```
. bayesmh ..., evaluator(progname, evalopts)
```

or option `llevaluator()` for log-likelihood evaluators,

```
. bayesmh ..., llevaluator(progname, evalopts)
```

Evaluator options *evalopts* include `parameters()`, `extravars()`, and `passthruopts()`.

`parameters(`*paramlist*`)` specifies model parameters. Model parameters can be scalars or matrices. Each parameter must be specified in curly braces `{}`. Multiple parameters with the same equation names may be specified within one set of `{}`.

For example,

```
parameters({mu} {var:sig2} {S,matrix} {cov:Sigma, matrix} {prob:p1 p2})
```

specifies a scalar parameter with name `mu` without an equation label, a scalar parameter with name `sig2` and label `var`, a matrix parameter with name `S`, a matrix parameter with name `Sigma` and label `cov`, and two scalar parameters `{prob:p1}` and `{prob:p2}`.

`extravars(`*varlist*`)` specifies any variables in addition to dependent and independent variables that you may need in your program evaluator. Examples of such variables are offset variables, exposure variables for count-data models, and failure or censoring indicators for survival-time models. See *Cox proportional hazards regression* for an example.

`passthruopts(`*string*`)` specifies a list of options you may want to pass to your program evaluator. For example, these options may contain fixed values of model parameters and hyperparameters. See *Multivariate normal regression model* for an example.

`bayesmh` automatically creates parameters for regression coefficients: `{`*depname*`:`*varname*`}` for every *varname* in *indepvars*, and a constant parameter `{`*depname*`:_cons}` unless `noconstant` is specified. These parameters are used to form linear predictors used by the program evaluator. If you need to access values of the parameters in the evaluator, you can use `$MH_b`; see the log-posterior evaluator in *Cox proportional hazards regression* for an example. With multiple dependent variables, regression coefficients are defined for each dependent variable.

Simple linear regression model

Suppose that we want to fit a Bayesian normal regression where we program the posterior distribution ourselves. The `normaljeffreys` program below computes the log-posterior density for the normal linear regression with flat priors for the coefficients and the Jeffreys prior for the variance parameter.

```
. program normaljeffreys
  1.         version 15.1
  2.         args lnp xb var
  3.         /* compute log likelihood */
.        tempname sd
  4.         scalar ‘sd’ = sqrt(‘var’)
  5.         tempvar lnfj
  6.         quietly generate double ‘lnfj’=lnnormalden($MH_y,‘xb’,‘sd’)
>                                              if $MH_touse
  7.         quietly summarize ‘lnfj’, meanonly
  8.         if r(N) < $MH_n {
  9.                 scalar ‘lnp’ = .
 10.                 exit
 11.         }
 12.         tempname lnf
 13.         scalar ‘lnf’ = r(sum)
 14.         /* compute log prior */
.        tempname lnprior
 15.         scalar ‘lnprior’ = -2*ln(‘sd’)
 16.         /* compute log posterior */
.        scalar ‘lnp’ = ‘lnf’ + ‘lnprior’
 17. end
```

The program accepts three parameters: a temporary name `‘lnp’` of a scalar to contain the log-posterior value, a temporary name `‘xb’` of the variable that contains the linear predictor, and a temporary name `‘var’` of a scalar that contains the values of the variance parameter.

The first part of the program calculates the overall log likelihood of the normal regression. The second part of the program calculates the log of prior distributions of the parameters. Because the coefficients have flat prior distributions with densities of 1, their log is 0 and does not contribute to the overall prior. The only contribution is from the Jeffreys prior $\ln(1/\sigma^2) = -2\ln(\sigma)$ for the variance σ^2. The third and final part of the program computes the values of the posterior density as the sum of the overall log likelihood and the log of the prior.

The substantial portion of this program is the computation of the overall log likelihood. The global macro `$MH_y` contains the name of the dependent variable, `$MH_touse` contains a temporary marker variable identifying observations to be used in computations, and $MH_n contains the total number of observations in the sample identified by the $MH_touse variable.

We used the built-in function lnnormalden() to compute observation-specific log likelihood and used summarize to obtain the overall value. Whenever a temporary variable is needed for calculations, such as ‘lnfj’ in our program, it is important to create it of type double to ensure the highest precision of the results. It is also important to perform computations using only the relevant subset of observations as identified by the marker variable stored in $MH_touse. This variable contains the value of 1 for observations to be used in the computations and 0 for the remaining observations. Missing values in used variables, if, and in affect this variable. After we compute the log-likelihood value, we should verify that the number of nonmissing observation-specific contributions to the log likelihood equals $MH_n. If it does not, the log-posterior value (or log-likelihood value in a log-likelihood evaluator) must be set to missing.

We can now specify the normaljeffreys evaluator in the evaluator() option of bayesmh. In addition to the regression coefficients, we have one extra parameter, the variance of the normal distribution, which we must specify in the parameters() suboption of evaluator().

We use auto.dta to illustrate the command. We specify a simple regression of mpg on rescaled weight.

```
. use http://www.stata-press.com/data/r15/auto
(1978 Automobile Data)

. quietly replace weight = weight/100

. set seed 14

. bayesmh mpg weight, evaluator(normaljeffreys, parameters({var}))
Burn-in ...
note: invalid initial state
Simulation ...

Model summary
------------------------------------------------------------------------------
Posterior:
  mpg ~ normaljeffreys(xb_mpg,{var})
------------------------------------------------------------------------------

Bayesian 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  =      .1433
                                                 Efficiency:  min =     .06246
                                                              avg =     .06669
Log marginal likelihood =   -198.247                          max =     .07091

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
      weight | -.6052218    .053604   .002075  -.6062666  -.7121237  -.4992178
       _cons |  39.56782   1.658124   .066344   39.54211   36.35645   42.89876
-------------+----------------------------------------------------------------
         var |  12.19046   2.008871   .075442   12.03002   8.831172   17.07787
------------------------------------------------------------------------------
```

The output of bayesmh with user-defined evaluators is the same as the output of bayesmh with built-in distributions, except the title and the model summary. The generic title Bayesian regression is used for all evaluators, but you can change it by specifying the title() option. The model summary provides the name of the posterior evaluator.

Following the command line, there is a note about invalid initial state. For program evaluators, `bayesmh` initializes all parameters with zeros, except for positive parameters used in prior specifications, which are initialized with ones. This may not be sensible for all parameters, such as the variance parameter in our example. We may consider using, for example, OLS estimates as initial values of the parameters.

```
. 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 |      Coef.   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
------------------------------------------------------------------------------

. display e(rmse)^2
11.825962
```

We specify initial values in the `initial()` option.

```
. set seed 14

. bayesmh mpg weight, evaluator(normaljeffreys, parameters({var}))
> initial({mpg:weight} -0.6 {mpg:_cons} 39 {var} 11.83)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Posterior:
  mpg ~ normaljeffreys(xb_mpg,{var})
------------------------------------------------------------------------------

Bayesian 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  =      .1668
                                                 Efficiency:  min =     .04114
                                                              avg =     .04811
Log marginal likelihood = -198.14302                          max =     .05938

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
      weight | -.6025616    .0540995   .002667  -.6038729  -.7115221  -.5005915
       _cons |  39.50491    1.677906   .080156   39.45537    36.2433   43.14319
-------------+----------------------------------------------------------------
         var |  12.26586    2.117858   .086915   12.05298   8.827655   17.10703
------------------------------------------------------------------------------
```

We can compare our results with `bayesmh` that uses a built-in normal likelihood and flat and Jeffreys priors. To match the results, we must use the same initial values, because `bayesmh` has a different initialization logic for built-in distributions.

```
. set seed 14
. bayesmh mpg weight, likelihood(normal({var}))
> prior({mpg:}, flat) prior({var}, jeffreys)
> initial({mpg:weight} -0.6 {mpg:_cons} 39 {var} 11.83)
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  =      .1668
                                                 Efficiency:  min =     .04114
                                                              avg =     .04811
Log marginal likelihood = -198.14302                          max =     .05938

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
      weight | -.6025616   .0540995   .002667  -.6038729  -.7115221  -.5005915
       _cons |  39.50491   1.677906   .080156   39.45537    36.2433   43.14319
-------------+----------------------------------------------------------------
         var |  12.26586   2.117858   .086915   12.05298   8.827655   17.10703
------------------------------------------------------------------------------
```

If your Bayesian model uses prior distributions that are supported by bayesmh but the likelihood model is not supported, you can write only the likelihood evaluator and use built-in prior distributions.

For example, we extract the portion of the normaljeffreys program computing the overall log likelihood into a separate program and call it normalreg.

```
. program normalreg
  1.         version 15.1
  2.         args lnf xb var
  3.                                                    /* compute log likelihood */
.         tempname sd
  4.         scalar `sd' = sqrt(`var')
  5.         tempvar lnfj
  6.         quietly generate double `lnfj' = lnnormalden($MH_y,`xb',`sd')
>                                               if $MH_touse
  7.         quietly summarize `lnfj', meanonly
  8.         if r(N) < $MH_n {
  9.             scalar `lnf' = .
 10.             exit
 11.         }
 12.         scalar `lnf' = r(sum)
 13. end
```

We can now specify this program in the llevaluator() option and use prior() options to specify built-in flat priors for the coefficients and the Jeffreys prior for the variance.

```
. set seed 14

. bayesmh mpg weight, llevaluator(normalreg, parameters({var}))
> prior({mpg:}, flat) prior({var}, jeffreys)
> initial({mpg:weight} -0.6 {mpg:_cons} 39 {var} 11.83)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normalreg(xb_mpg,{var})

Priors:
  {mpg:weight _cons} ~ 1 (flat)                                            (1)
               {var} ~ jeffreys
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.

Bayesian 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  =      .1668
                                                 Efficiency:  min =     .04114
                                                              avg =     .04811
Log marginal likelihood = -198.14302                          max =     .05938

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
      weight | -.6025616   .0540995   .002667  -.6038729  -.7115221  -.5005915
       _cons |  39.50491   1.677906   .080156   39.45537    36.2433   43.14319
-------------+----------------------------------------------------------------
         var |  12.26586   2.117858   .086915   12.05298   8.827655   17.10703
------------------------------------------------------------------------------
```

We obtain the same results as earlier.

Logistic regression model

Some models, such as logistic regression, do not have any additional parameters except regression coefficients. Here we show how to use a program evaluator for fitting a Bayesian logistic regression model.

We start by creating a program for computing the log likelihood.

```
. program logitll
  1.         version 15.1
  2.         args lnf xb
  3.         tempvar lnfj
  4.         quietly generate ‘lnfj’ = ln(invlogit( ‘xb’))
>                                       if $MH_y == 1 & $MH_touse
  5.         quietly replace ‘lnfj’  = ln(invlogit(-‘xb’))
>                                       if $MH_y == 0 & $MH_touse
  6.         quietly summarize ‘lnfj’, meanonly
  7.         if r(N) < $MH_n {
  8.             scalar ‘lnf’ = .
  9.             exit
 10.         }
 11.         scalar ‘lnf’ = r(sum)
 12. end
```

The structure of our log-likelihood evaluator is similar to the one described in *Simple linear regression model*, except we have no extra parameters.

We continue with `auto.dta` and regress `foreign` on `mpg`. For simplicity, we assume a flat prior for the coefficients and use `bayesmh, llevaluator()` to fit this model.

```
. use http://www.stata-press.com/data/r15/auto, clear
(1978 Automobile Data)

. set seed 14

. bayesmh foreign mpg, llevaluator(logitll) prior({foreign:}, flat)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  foreign ~ logitll(xb_foreign)

Prior:
  {foreign:mpg _cons} ~ 1 (flat)                                           (1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_foreign.

Bayesian 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  =      .2216
                                                 Efficiency:  min =     .09293
                                                              avg =     .09989
Log marginal likelihood = -41.626028                          max =      .1068

------------------------------------------------------------------------------
             |                                                Equal-tailed
     foreign |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
         mpg |    .16716   .0545771    .00167   .1644019   .0669937   .2790017
       _cons | -4.560637   1.261675   .041387  -4.503921  -7.107851  -2.207665
------------------------------------------------------------------------------
```

The results from the program-evaluator version match the results from bayesmh with a built-in logistic model.

```
. set seed 14

. bayesmh foreign mpg, likelihood(logit) prior({foreign:}, flat)
> initial({foreign:} 0)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  foreign ~ logit(xb_foreign)

Prior:
  {foreign:mpg _cons} ~ 1 (flat)                                           (1)
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_foreign.

Bayesian logistic 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  =      .2216
                                                 Efficiency:  min =     .09293
                                                              avg =     .09989
Log marginal likelihood = -41.626029                          max =      .1068

------------------------------------------------------------------------------
             |                                                Equal-tailed
     foreign |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
         mpg |    .16716   .0545771    .00167   .1644019   .0669937   .2790017
       _cons | -4.560636   1.261675   .041387  -4.503921   -7.10785  -2.207665
------------------------------------------------------------------------------
```

Because we assumed a flat prior with the density of 1, the log prior is 0, so the log-posterior evaluator for this model is the same as the log-likelihood evaluator.

```
. set seed 14

. bayesmh foreign mpg, evaluator(logitll)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Posterior:
  foreign ~ logitll(xb_foreign)
------------------------------------------------------------------------------

Bayesian 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  =      .2216
                                                 Efficiency:  min =     .09293
                                                              avg =     .09989
Log marginal likelihood = -41.626028                          max =      .1068

------------------------------------------------------------------------------
             |                                                Equal-tailed
     foreign |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
         mpg |    .16716   .0545771    .00167   .1644019   .0669937   .2790017
       _cons | -4.560637   1.261675   .041387  -4.503921  -7.107851  -2.207665
------------------------------------------------------------------------------
```

Multivariate normal regression model

Here we demonstrate how to write a program evaluator for a multivariate response. We consider a bivariate normal regression, and we again start with a log-likelihood evaluator. In this example, we also use Mata to speed up our computations.

```
. program mvnregll
  1.          version 15.1
  2.          args lnf xb1 xb2
  3.          tempvar diff1 diff2
  4.          quietly generate double ‘diff1’ = $MH_y1 - ‘xb1’ if $MH_touse
  5.          quietly generate double ‘diff2’ = $MH_y2 - ‘xb2’ if $MH_touse
  6.          local d $MH_yn
  7.          local n $MH_n
  8.          mata: st_numscalar("‘lnf’", mvnll_mata(‘d’,‘n’,"‘diff1’","‘diff2’"))
  9. end

.
. mata:
------------------------------------------------- mata (type end to exit) ------
: real scalar mvnll_mata(real scalar d, n, string scalar sdiff1, sdiff2)
> {
>         real matrix Diff
>         real scalar trace, lnf
>         real matrix Sigma
>
>         Sigma = st_matrix(st_global("MH_m1"))
>         st_view(Diff=.,.,(sdiff1,sdiff2),st_global("MH_touse"))
>
>         /* compute log likelihood */
>         trace = trace(cross(cross(Diff’,invsym(Sigma))’,Diff’))
>         lnf = -0.5*n*(d*ln(2*pi())+ln(det(Sigma)))-0.5*trace
>
>         return(lnf)
> }
: end
--------------------------------------------------------------------------------
```

The `mvnregll` program has three arguments: a scalar to store the log-likelihood values and two temporary variables containing linear predictors corresponding to each of the two dependent variables. It creates deviations `‘diff1’` and `‘diff2’` and passes them, along with other parameters, to the Mata function `mvnll_mata()` to compute the bivariate normal log-likelihood value.

The extra parameter in this model is a covariance matrix of a bivariate response. In *Simple linear regression model*, we specified an extra parameter, variance, which was a scalar, as an additional argument of the evaluator. This is not allowed with matrix parameters. They should be accessed via globals `$MH_m1`, `$MH_m2`, and so on for each matrix model parameters in the order they are specified in option `parameters()`. In our example, we have only one matrix and we access it via `$MH_m1`. `$MH_m1` contains the temporary name of a matrix containing the current value of the covariance matrix parameter.

To demonstrate, we again use `auto.dta`. We rescale the variables to be used in our example to stabilize the results.

```
. use http://www.stata-press.com/data/r15/auto
(1978 Automobile Data)

. replace weight = weight/100
variable weight was int now float
(74 real changes made)

. replace length = length/10
variable length was int now float
(74 real changes made)
```

We fit a bivariate normal regression of `mpg` and `weight` on `length`. We specify the extra covariance parameter as a matrix model parameter `{Sigma,m}` in suboption `parameters()` of `llevaluator()`. We specify flat priors for the coefficients and an inverse-Wishart prior for the covariance matrix.

```
. set seed 14

. bayesmh mpg weight = length, llevaluator(mvnregll, parameters({Sigma,m}))
> prior({mpg:} {weight:}, flat)
> prior({Sigma,m}, iwishart(2,12,I(2))) mcmcsize(1000)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg weight ~ mvnregll(xb_mpg,xb_weight,{Sigma,m})

Priors:
     {mpg:length _cons} ~ 1 (flat)                                         (1)
  {weight:length _cons} ~ 1 (flat)                                         (2)
              {Sigma,m} ~ iwishart(2,12,I(2))
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
(2) Parameters are elements of the linear form xb_weight.

Bayesian regression                              MCMC iterations  =      3,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =      1,000
                                                 Number of obs    =         74
                                                 Acceptance rate  =      .1728
                                                 Efficiency:  min =     .02882
                                                              avg =     .05012
Log marginal likelihood = -415.01504                          max =      .1275

-------------+----------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean  Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
      length | -2.040162   .2009062   .037423  -2.045437  -2.369287  -1.676332
       _cons |   59.6706   3.816341   .705609   59.63619   52.54652   65.84583
-------------+----------------------------------------------------------------
weight       |
      length |   3.31773   .1461644   .026319   3.316183   3.008416   3.598753
       _cons | -32.19877    2.79005   .484962   -32.4154  -37.72904  -26.09976
-------------+----------------------------------------------------------------
   Sigma_1_1 |  11.49666   1.682975   .149035    11.3523   8.691888   14.92026
   Sigma_2_1 |  -2.33596   1.046729   .153957  -2.238129  -4.414118  -.6414916
   Sigma_2_2 |  5.830413   .9051206   .121931   5.630011   4.383648   8.000739
-------------+----------------------------------------------------------------
```

To reduce computation time, we used a smaller MCMC sample size of 1,000 in our example. In your analysis, you should always verify whether a smaller MCMC sample size results in precise enough estimates before using it for final results.

We can check our results against bayesmh using the built-in multivariate normal regression after adjusting the initial values.

```
. set seed 14
. bayesmh mpg weight = length, likelihood(mvnormal({Sigma,m}))
> prior({mpg:} {weight:}, flat)
> prior({Sigma,m}, iwishart(2,12,I(2)))
> mcmcsize(1000) initial({mpg:} {weight:} 0)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg weight ~ mvnormal(2,xb_mpg,xb_weight,{Sigma,m})
Priors:
     {mpg:length _cons} ~ 1 (flat)                                        (1)
  {weight:length _cons} ~ 1 (flat)                                        (2)
              {Sigma,m} ~ iwishart(2,12,I(2))
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
(2) Parameters are elements of the linear form xb_weight.
Bayesian multivariate normal regression          MCMC iterations  =      3,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =      1,000
                                                 Number of obs    =         74
                                                 Acceptance rate  =      .1728
                                                 Efficiency:  min =     .02882
                                                              avg =     .05012
Log marginal likelihood = -415.01504                          max =      .1275
------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
      length | -2.040162   .2009062   .037423  -2.045437  -2.369287  -1.676332
       _cons |   59.6706   3.816341   .705609   59.63619   52.54652   65.84583
-------------+----------------------------------------------------------------
weight       |
      length |   3.31773   .1461644   .026319   3.316183   3.008416   3.598753
       _cons | -32.19877    2.79005   .484962   -32.4154  -37.72904  -26.09976
-------------+----------------------------------------------------------------
   Sigma_1_1 |  11.49666   1.682975   .149035    11.3523   8.691888   14.92026
   Sigma_2_1 |  -2.33596   1.046729   .153957  -2.238129  -4.414118  -.6414916
   Sigma_2_2 |  5.830413   .9051206   .121931   5.630011   4.383648   8.000739
------------------------------------------------------------------------------
```

We obtain the same results.

Similarly, we can define the log-posterior evaluator. We already have the log-likelihood evaluator, which we can reuse in our log-posterior evaluator. The only additional portion is to compute the log of the inverse-Wishart prior density for the covariance parameter.

```
. program mvniWishart
  1.         version 15.1
  2.         args lnp xb1 xb2
  3.         tempvar diff1 diff2
  4.         quietly generate double ‘diff1’ = $MH_y1 - ‘xb1’ if $MH_touse
  5.         quietly generate double ‘diff2’ = $MH_y2 - ‘xb2’ if $MH_touse
  6.         local d $MH_yn
  7.         local n $MH_n
  8.         mata:
>              st_numscalar("‘lnp’", mvniWish_mata(‘d’,‘n’,"‘diff1’","‘diff2’"))
  9. end

.
. mata:
------------------------------------------------- mata (type end to exit) -----
: real scalar mvniWish_mata(real scalar d, n, string scalar sdiff1, sdiff2)
> {
>         real scalar lnf, lnprior
>         real matrix Sigma
>
>         /* compute log likelihood */
>         lnf = mvnll_mata(d,n,sdiff1,sdiff2)
>         /* compute log of inverse-Wishart prior for Sigma */
>         Sigma = st_matrix(st_global("MH_m1"))
>         lnprior = lniwishartden(12,I(2),Sigma)
>         return(lnf + lnprior)
> }

: end
-------------------------------------------------------------------------------
```

The results of the log-posterior evaluator match our earlier results.

```
. set seed 14

. bayesmh mpg weight = length, evaluator(mvniWishart, parameters({Sigma,m}))
> mcmcsize(1000)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Posterior:
  mpg weight ~ mvniWishart(xb_mpg,xb_weight,{Sigma,m})
------------------------------------------------------------------------------

Bayesian regression                              MCMC iterations  =      3,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =      1,000
                                                 Number of obs    =         74
                                                 Acceptance rate  =      .1728
                                                 Efficiency:  min =     .02882
                                                              avg =     .05012
Log marginal likelihood = -415.01504                          max =      .1275

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
      length | -2.040162   .2009062   .037423  -2.045437  -2.369287  -1.676332
       _cons |   59.6706   3.816341   .705609   59.63619   52.54652   65.84583
-------------+----------------------------------------------------------------
weight       |
      length |   3.31773   .1461644   .026319   3.316183   3.008416   3.598753
       _cons | -32.19877    2.79005   .484962   -32.4154  -37.72904  -26.09976
-------------+----------------------------------------------------------------
   Sigma_1_1 |  11.49666   1.682975   .149035    11.3523   8.691888   14.92026
   Sigma_2_1 |  -2.33596   1.046729   .153957  -2.238129  -4.414118  -.6414916
   Sigma_2_2 |  5.830413   .9051206   .121931   5.630011   4.383648   8.000739
------------------------------------------------------------------------------
```

Sometimes, it may be useful to be able to pass options to our evaluators. For example, we used the identity I(2) matrix as a scale matrix of the inverse Wishart distribution. Suppose that we want to check the sensitivity of our results to other choices of the scale matrix. We can pass the name of a matrix we want to use in an option. In our example, we use the vmatrix() option to pass the name of the scale matrix. We later specify this option within suboption passthruopts() of the evaluator() option. The options passed this way are stored in the $MH_passthruopts global macro.

```
. program mvniWishartV
  1.          version 15.1
  2.          args lnp xb1 xb2
  3.          tempvar diff1 diff2
  4.          quietly generate double `diff1' = $MH_y1 - `xb1' if $MH_touse
  5.          quietly generate double `diff2' = $MH_y2 - `xb2' if $MH_touse
  6.          local d $MH_yn
  7.          local n $MH_n
  8.          local 0 , $MH_passthruopts
  9.          syntax, vmatrix(string)
 10.          mata: st_numscalar("`lnp'",
>                mvniWishV_mata(`d',`n',"`diff1'","`diff2'","`vmatrix'"))
 11. end
```

```
. mata:
------------------------------------------------- mata (type end to exit) ----
: real scalar mvniWishV_mata(real scalar d, n, string scalar sdiff1, sdiff2,
> vmat)
> {
>         real scalar lnf, lnprior
>         real matrix Sigma
>
>         /* compute log likelihood */
>         lnf = mvnll_mata(d,n,sdiff1,sdiff2)
>         /* compute log of inverse-Wishart prior for Sigma */
>         Sigma = st_matrix(st_global("MH_m1"))
>         lnprior = lniwishartden(12,st_matrix(vmat),Sigma)
>         return(lnf + lnprior)
> }
: end
-------------------------------------------------------------------------------
```

We now define the scale matrix V (as the identity matrix to match our previous results) and specify vmatrix(V) in suboption passthruopts() of evaluator().

```
. set seed 14
. matrix V = I(2)
. bayesmh mpg weight = length,
> evaluator(mvniWishartV, parameters({Sigma,m}) passthruopts(vmatrix(V)))
> mcmcsize(1000)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Posterior:
  mpg weight ~ mvniWishartV(xb_mpg,xb_weight,{Sigma,m})
------------------------------------------------------------------------------

Bayesian regression                              MCMC iterations  =      3,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =      1,000
                                                 Number of obs    =         74
                                                 Acceptance rate  =      .1728
                                                 Efficiency:  min =     .02882
                                                              avg =     .05012
Log marginal likelihood = -415.01504                          max =      .1275

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
      length | -2.040162   .2009062   .037423  -2.045437  -2.369287  -1.676332
       _cons |   59.6706   3.816341   .705609   59.63619   52.54652   65.84583
-------------+----------------------------------------------------------------
weight       |
      length |   3.31773   .1461644   .026319   3.316183   3.008416   3.598753
       _cons | -32.19877    2.79005   .484962   -32.4154  -37.72904  -26.09976
-------------+----------------------------------------------------------------
   Sigma_1_1 |  11.49666   1.682975   .149035    11.3523   8.691888   14.92026
   Sigma_2_1 |  -2.33596   1.046729   .153957  -2.238129  -4.414118  -.6414916
   Sigma_2_2 |  5.830413   .9051206   .121931   5.630011   4.383648   8.000739
------------------------------------------------------------------------------
```

The results are the same as before.

Cox proportional hazards regression

Some evaluators may require additional variables, apart from the dependent and independent variables, for computation. For example, in a Cox proportional hazards model such variable is a failure or censoring indicator. The `coxphll` program below computes partial log likelihood for the Cox proportional hazards regression. The failure indicator will be passed to the evaluator as an extra variable in suboption `extravars()` of option `llevaluator()` or option `evaluator()` and can be accessed from the global macro `$MH_extravars`.

```
. program coxphll
             version 15.1
             args lnf xb
             tempvar negt
             quietly generate double ‘negt’ = -$MH_y1
             local d "$MH_extravars"
             sort $MH_touse ‘negt’ ‘d’
             tempvar B A sumd last L
             local byby "by $MH_touse ‘negt’ ‘d’"
             quietly {
                    gen double ‘B’ = sum(exp(‘xb’)) if $MH_touse
                    ‘byby’: gen double ‘A’ = cond(_n==_N, sum(‘xb’), .)
>                                                if ‘d’==1 & $MH_touse
                    ‘byby’: gen ‘sumd’ = cond(_n==_N, sum(‘d’), .) if $MH_touse
                    ‘byby’: gen byte ‘last’ = (_n==_N & ‘d’ == 1) if $MH_touse
                    gen double ‘L’ = ‘A’ - ‘sumd’*ln(‘B’) if ‘last’ & $MH_touse
                    quietly count if $MH_touse & ‘last’
                    local n = r(N)
                    summarize ‘L’ if ‘last’ & $MH_touse, meanonly
             }
             if r(N) < ‘n’ {
                 scalar ‘lnf’ = .
                 exit
             }
             scalar ‘lnf’ = r(sum)
     end
```

We demonstrate the command using the survival-time `cancer` dataset. The survival-time variable is `studytime` and the failure indicator is `died`. The regressor of interest in this model is `age`. We use a fairly noninformative normal prior with a zero mean and a variance of 100 for the regression coefficient of `age`. (The constant in the Cox proportional hazards model is not likelihood-identifiable, so we omit it from this model with a noninformative prior.)

```
. use http://www.stata-press.com/data/r15/cancer, clear
(Patient Survival in Drug Trial)

. gsort -studytime died

. set seed 14

. bayesmh studytime age, llevaluator(coxphll, extravars(died))
> prior({studytime:}, normal(0,100)) noconstant mcmcsize(1000)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  studytime ~ coxphll(xb_studytime)

Prior:
  {studytime:age} ~ normal(0,100)                                          (1)
------------------------------------------------------------------------------
(1) Parameter is an element of the linear form xb_studytime.
```

```
Bayesian regression                              MCMC iterations  =      3,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =      1,000
                                                 Number of obs    =         48
                                                 Acceptance rate  =      .4066
Log marginal likelihood = -103.04797             Efficiency       =      .3568

                                                             Equal-tailed
   studytime        Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]

         age     .076705   .0330669   .001751    .077936   .0099328   .1454275
```

We specified the failure indicator `died` in suboption `extravars()` of `llevaluator()`. We again used a smaller value for the MCMC sample size only to reduce computation time.

For the log-posterior evaluator, we add the log of the normal prior of the `age` coefficient to the log-likelihood value to obtain the final log-posterior value. We did not need to specify the loop in the log-prior computation in this example, but we did this to be general, in case more than one regressor is included in the model.

```
. program coxphnormal
  1.          version 15.1
  2.          args lnp xb
.         /* compute log likelihood */
.         tempname lnf
  3.          scalar ‘lnf’ = .
  4.          quietly coxphll ‘lnf’ ‘xb’
.         /* compute log priors of regression coefficients */
.         tempname lnprior
  5.          scalar ‘lnprior’ = 0
  6.          forvalues i = 1/$MH_bn {
  7.              scalar ‘lnprior’ = ‘lnprior’ + lnnormalden($MH_b[1,‘i’], 10)
  8.          }
  9.          /* compute log posterior */
.         scalar ‘lnp’ = ‘lnf’ + ‘lnprior’
 10. end
```

As expected, we obtain the same results as previously.

```
. set seed 14

. bayesmh studytime age, evaluator(coxphnormal, extravars(died))
> noconstant mcmcsize(1000)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Posterior:
  studytime ~ coxphnormal(xb_studytime)
------------------------------------------------------------------------------

Bayesian regression                              MCMC iterations  =      3,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =      1,000
                                                 Number of obs    =         48
                                                 Acceptance rate  =      .4066
Log marginal likelihood = -103.04797             Efficiency       =      .3568

                                                             Equal-tailed
   studytime        Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]

         age     .076705   .0330669   .001751    .077936   .0099328   .1454275
```

Global macros

Global macros	Description
`$MH_n`	number of observations
`$MH_yn`	number of dependent variables
`$MH_touse`	variable containing 1 for the observations to be used; 0 otherwise
`$MH_w`	variable containing weight associated with the observations
`$MH_extravars`	*varlist* specified in `extravars()`
`$MH_passthruopts`	options specified in `passthruopts()`
One outcome	
`$MH_y1`	name of the dependent variable
`$MH_x1`	name of the first independent variable
`$MH_x2`	name of the second independent variable
. . .	
`$MH_xn`	number of independent variables
`$MH_xb`	name of a temporary variable containing the linear combination
Multiple outcomes	
`$MH_y1`	name of the first dependent variable
`$MH_y2`	name of the second dependent variable
. . .	
`$MH_y1x1`	name of the first independent variable modeling `y1`
`$MH_y1x2`	name of the second independent variable modeling `y1`
. . .	
`$MH_y1xn`	number of independent variables modeling `y1`
`$MH_y1xb`	name of a temporary variable containing the linear combination modeling `y1`
`$MH_y2x1`	name of the first independent variable modeling `y2`
`$MH_y2x2`	name of the second independent variable modeling `y2`
. . .	
`$MH_y2xn`	number of independent variables modeling `y2`
`$MH_y2xb`	name of a temporary variable containing the linear combination modeling `y2`
. . .	
Scalar and matrix parameters	
`$MH_b`	name of a temporary vector of coefficients; stripes are properly named after the name of the coefficients
`$MH_bn`	number of coefficients
`$MH_p`	name of a temporary vector of additional scalar model parameters, if any; stripes are properly named
`$MH_pn`	number of additional scalar model parameters
`$MH_m1`	name of a temporary matrix of the first matrix parameter, if any
`$MH_m2`	name of a temporary matrix of the second matrix parameter, if any
. . .	
`$MH_mn`	number of matrix model parameters

Stored results

In addition to the results stored by `bayesmh`, `bayesmh, evaluator()` and `bayesmh, llevaluator()` store the following in `e()`:

Macros	
`e(evaluator)`	program evaluator (one equation)
`e(evaluator#)`	program evaluator for the #th equation
`e(evalparams)`	evaluator parameters (one equation)
`e(evalparams#)`	evaluator parameters for the #th equation
`e(extravars)`	extra variables (one equation)
`e(extravars#)`	extra variables for the #th equation
`e(passthruopts)`	pass-through options (one equation)
`e(passthruopts#)`	pass-through options for the #th equation

Also see

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

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

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

[BAYES] **Glossary**

Title

bayesian postestimation — Postestimation tools for bayesmh and the bayes prefix

Postestimation commands   Remarks and examples   Also see

Postestimation commands

The following Bayesian postestimation commands are available after the `bayesmh` command ([BAYES] **bayesmh**) and the `bayes` prefix ([BAYES] **bayes**):

Command	Description
`bayesgraph`	graphical summaries and convergence diagnostics
`bayesstats ess`	effective sample sizes and related statistics
`bayesstats summary`	Bayesian summary statistics for model parameters and their functions
`bayesstats ic`	Bayesian information criteria and Bayes factors
`bayestest model`	hypothesis testing using model posterior probabilities
`bayestest interval`	interval hypothesis testing
* `estimates`	cataloging estimation results

* `estimates table` and `estimates stats` are not appropriate with `bayesmh` and `bayes:` estimation results.

Remarks and examples

Remarks are presented under the following headings:

Different ways of specifying model parameters
Specifying functions of model parameters
Storing estimation results after Bayesian estimation

After estimation, you can use `bayesgraph` to check convergence of MCMC visually. Once convergence is established, you can use `bayesstats summary` to obtain Bayesian summaries such as posterior means and standard deviations of model parameters and functions of model parameters; `bayesstats ess` to compute effective sample sizes and related statistics for model parameters and functions of model parameters; and `bayesstats ic` to compute Bayesian information criteria and Bayes factors for model parameters and their functions. You can use `bayestest model` to test hypotheses by comparing posterior probabilities of models. You can also use `bayestest interval` to test interval hypotheses about parameters and functions of parameters.

For an overview example of postestimation commands, see *Overview example* in [BAYES] **bayesian commands**.

Different ways of specifying model parameters

Many Bayesian postestimation commands such as `bayesstats summary` and `bayesgraph` allow you to specify model parameters for which you want to see the results. To see results for all parameters, simply type a postestimation command without arguments after estimation using `bayesmh` or the `bayes` prefix, for example,

```
. bayesstats summary
```

or you could type

```
. bayesstats summary _all
```

To manually list all model parameters, type

```
. bayesstats summary {param1} {param2} ...
```

or

```
. bayesstats summary {param1 param2} ...
```

The only exception is the bayesgraph command when there is more than one model parameter. In that case, bayesgraph requires that you either specify _all to request all model parameters or specify the model parameters of interest.

You can refer to a single model parameter in the same way you define parameters in, say, the bayesmh command. For example, for a parameter with name param and no equation name, you can use {param}. For a parameter with name param and equation name eqname, you can use its full name {eqname:name}, where the equation name and the parameter name are separated with a colon. With postestimation commands, you can also omit the equation name when referring to the parameter with an equation name.

In the presence of more than one model parameter, you have several ways for referring to multiple parameters at once. If parameters have the same equation name, you can refer to all the parameters with that equation name as follows.

Suppose that you have three parameters with the same equation name eqname. Then the specification

```
. bayesstats summary {eqname:param1} {eqname:param2} {eqname:param3}
```

is the same as the specification

```
. bayesstats summary {eqname:}
```

or the specification

```
. bayesstats summary {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 use only param1 and param2, we could type

```
. bayesstats summary {eqname:param1 param2}
```

There is also a convenient way to refer to the parameters with the same name but different equation names. For example, typing

```
. bayesstats summary {eqname1:param} {eqname2:param}
```

is the same as simply typing

```
. bayesstats summary {param}
```

You can mix and match all the specifications above in one call to a postestimation command. You can also specify expressions of model parameters; see *Specifying functions of model parameters* for details.

Note that if param refers to a matrix model parameter, then the results will be provided for all elements of the matrix. For example, if param is the name of a 2×2 matrix, then typing

```
. bayesstats summary {param}
```

implies the following:

```
. bayesstats summary {param_1_1} {param_1_2} {param_2_1} {param_2_2}
```

For multilevel models, there are various ways, *reref*, in which you can refer to individual random-effects parameters. Suppose that your model has random intercepts at the id level, which are labeled as {U0[id]} or {U0} for short. To refer to all random intercepts, you can use {U0}, {U0[.]}, and {U0[id]}. To refer to specific random intercepts, you can use {U0[#]}, where # refers to the #th element of the random-effects vector, or use {U0[#.id]}, where # refers to the #th level of the id variable. You can also refer to a subset *numlist* of random intercepts by using {U0[*numlist*]} or {U0[(*numlist*).id]}. For nested random effects, for example, {UU0[id1>id2]}, you can refer to all random effects as {UU0} or {UU0[.,.]} and to subsets of random effects as {UU0[*numlist*,*numlist*]} or {UU0[(*numlist*).id1,(*numlist*).id2]}.

Specifying functions of model parameters

You can use Bayesian postestimation commands to obtain results for functions or expressions of model parameters. Each expression must be specified in parentheses. An expression can be any Stata expression, but it may not include matrix model parameters. However, you may include individual elements of matrix model parameters. You may provide labels for your expressions.

For example, we can obtain results for the exponentiated parameter {param} as follows:

```
. bayesstats summary (exp({param}))
```

Note that we specified the expression in parentheses.

We can include a label, say, myexp, in the above by typing

```
. bayesstats summary (myexp: exp({param}))
```

We can specify multiple expressions by typing

```
. bayesstats summary (myexp: exp({param}) (sd: sqrt({var})))
```

If param is a matrix, we can specify expressions, including its elements, but not the matrix itself in the following:

```
. bayesstats summary (exp({param_1_1})) (exp({param_1_2})) ...
```

Storing estimation results after Bayesian estimation

The bayesmh command and the bayes prefix store various e() results such as scalars, macros, and matrices in memory like any other estimation command. Unlike other estimation commands, these commands also save the resulting simulation dataset containing MCMC samples of parameters to disk. Many Bayesian postestimation commands such as bayesstats summary and bayesstats ess require access to this file. If you do not specify the saving() option with bayesmh or the bayes prefix, the commands save simulation results in a temporary Stata dataset. This file is being replaced with the new simulation results each time bayesmh or the bayes prefix is run. To save your simulation results, you must specify the saving() option with bayesmh or the bayes prefix, in which case your simulation results are saved to the specified file in the specified location and will not be overridden by the next call to these commands.

You can specify the saving() option during estimation by typing

```
. bayesmh ..., likelihood() prior() ... saving()
```

or

```
. bayes, saving(): ...
```

or on replay by typing

```
. bayesmh, saving()
```

or

```
. bayes, saving()
```

As you can with other estimation commands, you can use `estimates store` to store Bayesian estimation results in memory and `estimates save` to save them to disk, but you must first use the `saving()` option with `bayesmh` or the `bayes` prefix to save simulation data in a permanent dataset. For example, type

```
. bayesmh ..., likelihood() prior() ... saving(bmh_simdata)
. estimates store model1
```

or, after `bayesmh` estimation, type

```
. bayesmh, saving(bmh_simdata)
. estimates store model1
```

Once you create a permanent dataset, it is your responsibility to erase it after it is no longer needed. `estimates drop` and `estimates clear` will drop estimation results only from memory; they will not erase the simulation files you saved.

```
. estimates drop model1
. erase bmh_simdata.dta
```

See [R] **estimates** for more information about commands managing estimation results. `estimates table` and `estimates stats` are not appropriate after `bayesmh` and the `bayes` prefix.

Also see

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

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

[BAYES] **bayesmh evaluators** — User-defined evaluators with bayesmh

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

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

[BAYES] **Glossary**

[U] **20 Estimation and postestimation commands**

Title

bayesgraph — Graphical summaries and convergence diagnostics

Description

`bayesgraph` provides graphical summaries and convergence diagnostics for simulated posterior distributions (MCMC samples) of model parameters and functions of model parameters obtained after Bayesian estimation. Graphical summaries include trace plots, autocorrelation plots, and various distributional plots.

Quick start

Trace plot, histogram, autocorrelation plot, and density plot for parameter {p}

```
bayesgraph diagnostics {p}
```

Add plots for parameter {y:x1}

```
bayesgraph diagnostics {p} {y:x1}
```

As above, but for all model parameters

```
bayesgraph diagnostics _all
```

As above, but for a function of model parameters {y:x1} and {p}

```
bayesgraph diagnostics ({y:x1}/{p})
```

Specify a blue trace plot line for all plots

```
bayesgraph diagnostics {p} {y:x1} {y:x2}, traceopts(lcolor(blue))
```

Specify a blue trace plot line only for the second trace plot

```
bayesgraph diagnostics {p} {y:x1} {y:x2}, trace2opts(lcolor(blue))
```

Trace plots for all parameters in a single graph

```
bayesgraph trace _all, byparm
```

Cumulative sum plot for parameter {p}

```
bayesgraph cusum {p}
```

Scatterplot matrix for parameters {p} and {y:x1}

```
bayesgraph matrix {p} {y:x1}
```

Autocorrelation plots for elements 1,1 and 2,1 of matrix parameter {S}

```
bayesgraph ac {S_1_1} {S_2_1}
```

Diagnostic plots for all parameters in the model and pause at least 3 seconds before displaying the next graph

```
bayesgraph diagnostics _all, sleep(3)
```

As above, but pause until the user presses any key

```
bayesgraph diagnostics _all, wait
```

As above, but close the current Graph window when the next graph is displayed

```
bayesgraph diagnostics _all, close
```

Menu

Statistics > Bayesian analysis > Graphical summaries

Syntax

Graphical summaries and convergence diagnostics for a single parameter

`bayesgraph` *graph* *scalar_param* [, *singleopts*]

Graphical summaries and convergence diagnostics for multiple parameters

`bayesgraph` *graph* *spec* [*spec* ...] [, *multiopts*]

`bayesgraph matrix` *spec* *spec* [*spec* ...] [, *singleopts*]

Graphical summaries and convergence diagnostics for all parameters

`bayesgraph` *graph* `_all` [, *multiopts* `showreffects`[`(`*reref*`)`]]

graph	Description
`diagnostics`	multiple diagnostics in compact form
`trace`	trace plots
`ac`	autocorrelation plots
`histogram`	histograms
`kdensity`	density plots
`cusum`	cumulative sum plots
`matrix`	scatterplot matrix

`bayesgraph matrix` requires at least two parameters.

scalar_param is a scalar model parameter specified as `{param}` or `{eqname:param}` or an expression *exprspec* of scalar model parameters. Matrix model parameters are not allowed, but you may refer to their individual elements.

exprspec is an optionally labeled expression of model parameters specified in parentheses:

(\[*exprlabel*:\]*expr*)

exprlabel is a valid Stata name, and *expr* is a scalar expression that may not contain matrix model parameters. See *Specifying functions of model parameters* in [BAYES] **bayesian postestimation** for examples.

spec is either *scalar_param* or *exprspec*.

singleopts	Description
Options	
skip(*#*)	skip every # observations from the MCMC sample; default is skip(0)
name(*name*, ...)	specify name of graph
saving(*filename*, ...)	save graph in file
graphopts	graph-specific options

multiopts	Description
Options	
byparm[(*grbyparmopts*)]	specify the display of plots on one graph; default is separate graph for each plot; not allowed with graphs diagnostics and matrix or with option combine()
combine[(*grcombineopts*)]	specify the display of plots on one graph; recommended when the number of parameters is large; not allowed with graphs diagnostics and matrix or with option byparm()
sleep(*#*)	pause for # seconds between multiple graphs; default is sleep(0)
wait	pause until the —more— condition is cleared
[no]close	(do not) close Graph windows when the next graph is displayed with multiple graphs; default is noclose
skip(*#*)	skip every # observations from the MCMC sample; default is skip(0)
name(*namespec*, ...)	specify names of graphs
saving(*filespec*, ...)	save graphs in files
graphopts(*graphopts*)	control the look of all graphs; not allowed with byparm()
graph[#]opts(*graphopts*)	control the look of #th graph; not allowed with byparm()
graphopts	equivalent to graphopts(*graphopts*); only one may be specified

graphopts	Description
diagnosticsopts	options for bayesgraph diagnostics
tslineopts	options for bayesgraph trace and bayesgraph cusum
acopts	options for bayesgraph ac
histopts	options for bayesgraph histogram
kdensityopts	options for bayesgraph kdensity
grmatrixopts	options for bayesgraph matrix

diagnosticsopts	Description
traceopts(*tslineopts*)	affect rendition of all trace plots
trace[#]opts(*tslineopts*)	affect rendition of #th trace plot
acopts(*acopts*)	affect rendition of all autocorrelation plots
ac[#]opts(*acopts*)	affect rendition of #th autocorrelation plot
histopts(*histopts*)	affect rendition of all histogram plots
hist[#]opts(*histopts*)	affect rendition of #th histogram plot
kdensopts(*kdensityopts*)	affect rendition of all density plots
kdens[#]opts(*kdensityopts*)	affect rendition of #th density plot
grcombineopts	any option documented in [G-2] **graph combine**

acopts	Description
ci	plot autocorrelations with confidence intervals; not allowed with byparm()
acopts	any options other than generate() documented for the ac command in [TS] **corrgram**

kdensityopts	Description
kdensopts	options for the overall kernel density plot
show(*showspec*)	show first-half density, second-half density, or both; default is both
kdensfirst(*kdens1opts*)	affect rendition of the first-half density plot
kdenssecond(*kdens2opts*)	affect rendition of the second-half density plot

Options

Options

byparm[(*grbyparmopts*)] specifies the display of all plots of parameters as subgraphs on one graph. By default, a separate graph is produced for each plot when multiple parameters are specified. This option is not allowed with bayesgraph diagnostics or bayesgraph matrix and may not be combined with option combine(). When many parameters or expressions are specified, this option may fail because of memory constraints. In that case, you may use option combine() instead.

grbyparmopts is any of the suboptions of by() documented in [G-3] ***by_option***.

byparm() allows y scales to differ for all graph types and forces x scales to be the same only for bayesgraph trace and bayesgraph cusum. Use noyrescale within byparm() to specify a common y axis, and use xrescale or noxrescale to change the default behavior for the x axis.

byparm() with bayesgraph trace and bayesgraph cusum defaults to displaying multiple plots in one column to accommodate the x axis with many iterations. Use norowcoldefault within byparm() to switch back to the default behavior of options rows() and cols() of the [G-3] ***by_option***.

combine[(*grcombineopts*)] specifies the display of all plots of parameters as subgraphs on one graph and is an alternative to byparm() with a large number of parameters. By default, a separate graph is produced for each plot when multiple parameters are specified. This option is not allowed with `bayesgraph diagnostics` or `bayesgraph matrix` and may not be combined with option `byparm()`. It can be used in cases where a large number of parameters or expressions are specified and the `byparm()` option would cause an error because of memory constraints.

grcombineopts is any of the options documented in [G-2] **graph combine**.

`sleep(`*#*`)` specifies pausing for # seconds before producing the next graph. This option is allowed only when multiple parameters are specified. This option may not be combined with `wait`, `combine()`, or `byparm()`.

`wait` causes `bayesgraph` to display `—more—` and pause until any key is pressed before producing the next graph. This option is allowed when multiple parameters are specified. This option may not be combined with `sleep()`, `combine()`, or `byparm()`. `wait` temporarily ignores the global setting that is specified using `set more off`.

[`no`]`close` specifies that, for multiple graphs, the Graph window be closed when the next graph is displayed. The default is `noclose` or to not close any Graph windows.

`skip(`*#*`)` specifies that every # observations from the MCMC sample not be used for computation. The default is `skip(0)` or to use all observations in the MCMC sample. Option `skip()` can be used to subsample or thin the chain. `skip(`*#*`)` is equivalent to a thinning interval of #+1. For example, if you specify `skip(1)`, corresponding to the thinning interval of 2, the command will skip every other observation in the sample and will use only observations 1, 3, 5, and so on in the computation. If you specify `skip(2)`, corresponding to the thinning interval of 3, the command will skip every 2 observations in the sample and will use only observations 1, 4, 7, and so on in the computation. `skip()` does not thin the chain in the sense of physically removing observations from the sample, as is done by, for example, `bayesmh`'s `thinning()` option. It only discards selected observations from the computation and leaves the original sample unmodified.

`name(`*namespec*[`, replace`]`)` specifies the name of the graph or multiple graphs. See [G-3] ***name_option*** for a single graph. If multiple graphs are produced, then the argument of `name()` is either a list of names or a *stub*, in which case graphs are named *stub*`1`, *stub*`2`, and so on. With multiple graphs, if `name()` is not specified and neither `sleep()` nor `wait` is specified, `name(Graph__`*#*`, replace)` is assumed, and thus the produced graphs may be replaced by subsequent `bayesgraph` commands.

The `replace` suboption causes existing graphs with the specified name or names to be replaced.

`saving(`*filespec*[`, replace`]`)` specifies the filename or filenames to use to save the graph or multiple graphs to disk. See [G-3] ***saving_option*** for a single graph. If multiple graphs are produced, then the argument of `saving()` is either a list of filenames or a *stub*, in which case graphs are saved with filenames *stub*`1`, *stub*`2`, and so on.

The `replace` suboption specifies that the file (or files) may be replaced if it already exists.

`showreffects` and `showreffects(`*reref*`)` are for use after multilevel models, and they specify that the results for all or a list *reref* of random-effects parameters be provided in addition to other model parameters. By default, all random-effects parameters are excluded from the results to conserve computation time.

`graphopts(`*graphopts*`)` and `graph`[*#*]`opts(`*graphopts*`)` affect the rendition of graphs. `graphopts()` affects the rendition of all graphs but may be overridden for specific graphs by using the `graph#opts()` option. The options specified within `graph#opts()` are specific for each type of graph.

The two specifications

```
bayesgraph ..., graphopts(graphopts)
```

and

```
    bayesgraph ..., graphopts
```

are equivalent, but you may specify one or the other.

These options are not allowed with `byparm()` and when only one parameter is specified.

graphopts specifies options specific to each graph type.

diagnosticsopts specifies options for use with `bayesgraph diagnostics`. See the corresponding table in the syntax diagram for a list of options.

tslineopts specifies options for use with `bayesgraph trace` and `bayesgraph cusum`. See the options of [TS] **tsline** except `by()`.

acopts specifies options for use with `bayesgraph ac`.

`ci` requests that the graph of autocorrelations with confidence intervals be plotted. By default, confidence intervals are not plotted. This option is not allowed with `byparm()`.

acopts specifies any options except `generate()` of the `ac` command in [TS] **corrgram**.

histopts specifies options for use with `bayesgraph histogram`. See options of [R] **histogram** except `by()`.

kdensityopts specifies options for use with `bayesgraph kdensity`.

kdensopts specifies options for the overall kernel density plot. See the options documented in [R] **kdensity** except `generate()` and `at()`.

`show(`*showspec*`)` specifies which kernel density curves to plot. *showspec* is one of `both`, `first`, `second`, or `none`. `show(both)`, the default, overlays both the first-half density curve and the second-half density curve with the overall kernel density curve. If `show(first)` is specified, only the first-half density curve, obtained from the first half of an MCMC sample, is plotted. If `show(second)` is specified, only the second-half density curve, obtained from the second half of an MCMC sample, is plotted. If `show(none)` is specified, only the overall kernel density curve is shown.

`kdensfirst(`*kdens1opts*`)` specifies options of [G-2] **graph twoway kdensity** except `by()` to affect rendition of the first-half kernel density plot.

`kdenssecond(`*kdens2opts*`)` specifies options of [G-2] **graph twoway kdensity** except `by()` to affect rendition of the second-half kernel density plot.

grmatrixopts specifies options for use with `bayesgraph matrix`. See the options of [G-2] **graph matrix** except `by()`.

Remarks and examples

Remarks are presented under the following headings:

Using bayesgraph

bayesgraph requires specifying at least one parameter with all graph types except matrix, which requires at least two parameters. To request graphs for all parameters, use _all.

When multiple graphs are produced, they are automatically stored in memory with names Graph__# and will all appear on the screen. After you are done reviewing the graphs, you can type

```
. graph close Graph__*
```

to close these graphs or type

```
. graph drop Graph__*
```

to close the graphs and drop them from memory.

If you would like to see only one graph at a time, you can specify option close to close the Graph window when the next graph is displayed. You can also use option sleep() or option wait to pause between the subsequent graphs. The sleep(#) option causes each graph to pause for # seconds. The wait option causes bayesgraph to wait until a key is pressed before producing the next graph.

You can combine separate graphs into one by specifying one of byparm() or combine(). These options are not allowed with diagnostics or matrix graphs. The byparm() option produces more compact graphs, but it may not be feasible with many parameters or expressions and large sizes of MCMC samples.

With multiple graphs, you can control the look of each individual graph with graph#opts(). Options common to all graphs may be specified in graphopts() or passed directly to the command as with single graphs.

Examples

We demonstrate the bayesgraph command using an example of Bayesian normal linear regression applied to auto.dta. We model the mpg variable using a normal distribution with unknown mean and variance. Our Bayesian model thus has two parameters, {mpg:_cons} and {var}, for which we need to specify prior distributions. We consider fairly noninformative prior distributions for these parameters: $N(0, 1000)$ for the constant and inverse gamma with shape and scale of 0.1 for the variance. Because the specified prior distributions are independent and semiconjugate relative to the normal data distribution, we can use Gibbs sampling for both parameters instead of the default MH sampling. To illustrate, we will use Gibbs sampling for the variance and MH sampling (default) for the mean.

We use bayesmh to fit our model.

```
. use http://www.stata-press.com/data/r15/auto
(1978 Automobile Data)

. set seed 14

. bayesmh mpg, likelihood(normal({var}))
> prior({mpg:_cons}, normal(0,1000))
> prior({var}, igamma(0.1,0.1)) block({var}, gibbs)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},{var})

Priors:
  {mpg:_cons} ~ normal(0,1000)
        {var} ~ igamma(0.1,0.1)
------------------------------------------------------------------------------

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  =      .7133
                                                 Efficiency:  min =      .2331
                                                              avg =      .6166
Log marginal likelihood =  -242.1155                          max =          1

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |  21.29231   .6648867   .013771   21.29419   19.94367   22.56746
-------------+----------------------------------------------------------------
         var |   34.2805   5.844213   .058442    33.6464   24.65882    47.5822
------------------------------------------------------------------------------
```

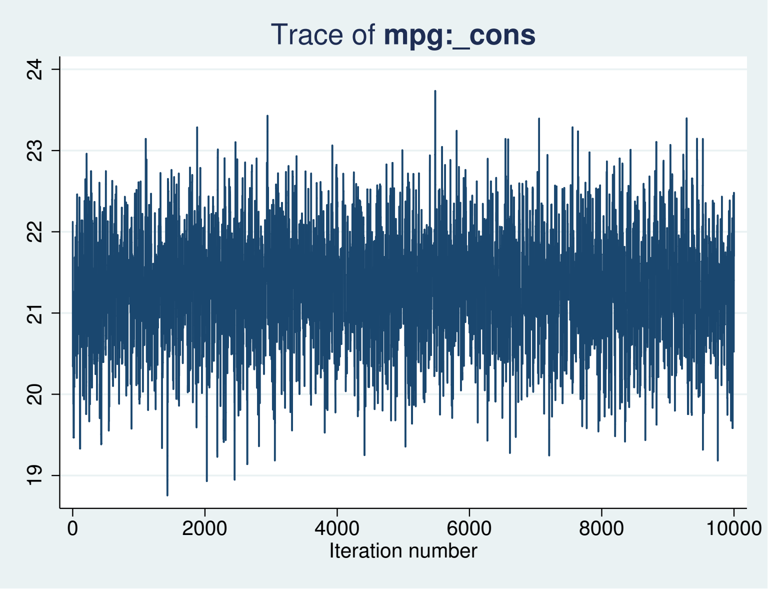
The MCMC simulation has a fairly high efficiency for the MH algorithm of 23% for the mean and an efficiency of 1 for the variance because of the Gibbs sampling. The output suggests no convergence problems. However, it is important to verify this and to also inspect various other graphical summaries of the parameters. This example demonstrates graphical summaries for a well-mixing MCMC chain that has converged and that generates samples from the posterior distribution of the model. For examples of poor-mixing MCMC chains, see *Convergence diagnostics in* MCMC in [BAYES] **intro**.

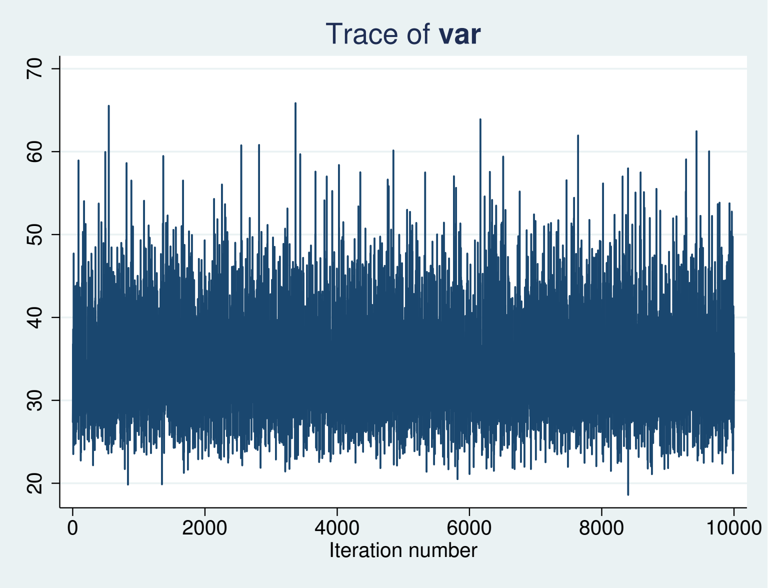
Trace plots

We start with trace plots, which plot the values of the simulated parameters against the iteration number and connect consecutive values with a line. For a well-mixing parameter, the range of the parameter is traversed rapidly by the MCMC chain, which makes the drawn lines look almost vertical and dense. Sparseness and trends in the trace plot of a parameter suggest convergence problems.

Let's use bayesgraph trace to obtain trace plots for {mpg:_cons} and {var}. We specify _all to request both plots at once.

```
. bayesgraph trace _all
```

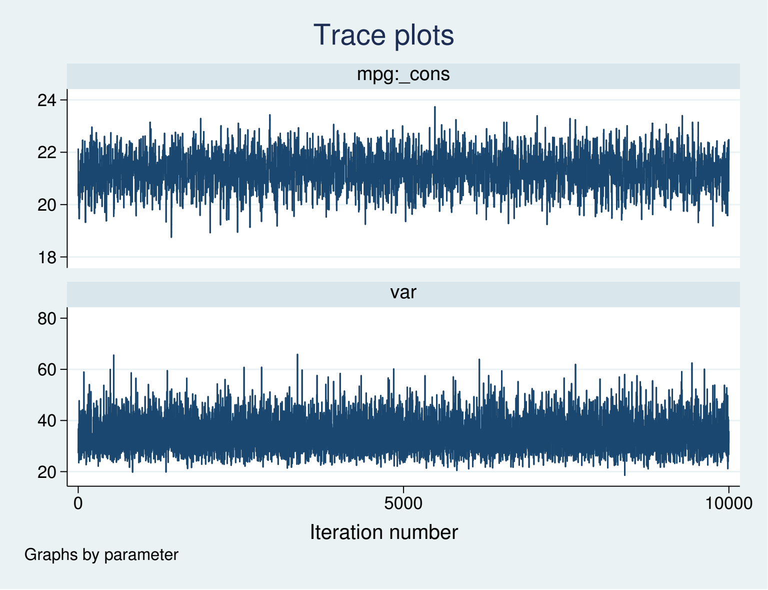




The mean parameter mixes very well and the variance parameter mixes perfectly.

Alternatively, we can use the byparm() option to plot results on one graph.

```
. bayesgraph trace _all, byparm
```



bayesgraph trace (as well as bayesgraph cusum) with option byparm() displays multiple plots in one column to accommodate an x axis with many iterations. You can specify byparm(norowcoldefault) to switch to the default behavior of options rows() and cols() documented in [G-3] *by_option*.

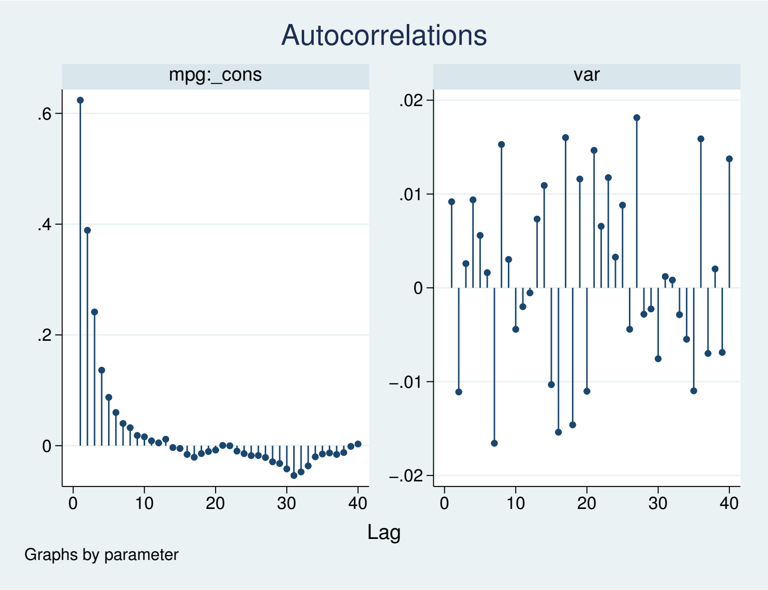
Autocorrelation plots

The second graphical summary we demonstrate is an autocorrelation plot. This plot shows the degree of autocorrelation in an MCMC sample for a range of lags, starting from lag 0. At lag 0, the plotted value corresponds to the sample variance of MCMC.

Autocorrelation is usually present in any MCMC sample. Typically, autocorrelation starts from some positive value for lag 0 and decreases toward 0 as the lag index increases. For a well-mixing MCMC chain, autocorrelation dies off fairly rapidly.

For example, autocorrelation for {mpg:_cons} becomes negligible after about lag 8 and is basically nonexistent for {var}.

```
. bayesgraph ac _all, byparm
```



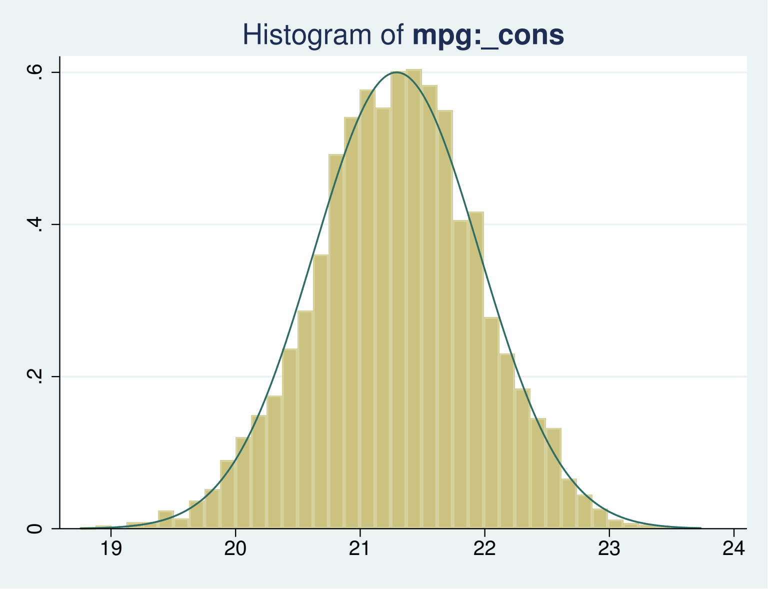
Autocorrelation lags are approximated by correlation times of parameters as reported by the `bayesstats ess` command; see [BAYES] **bayesstats ess** for details. Autocorrelation lags are also used to determine the batch size for the batch-means estimator of the MCMC standard errors; see [BAYES] **bayesstats summary**.

Histogram plots

Graphical posterior summaries such as histograms and kernel density estimates provide useful additions to the various numerical statistics (see [BAYES] **bayesstats summary**) for summarizing MCMC output. It is always a good practice to inspect the histogram and kernel density estimates of the marginal posterior distributions of parameters to ensure that these empirical distributions behave as expected. These plots can be used to compare the empirical posterior and the specified prior distributions to visualize the impact of the data.

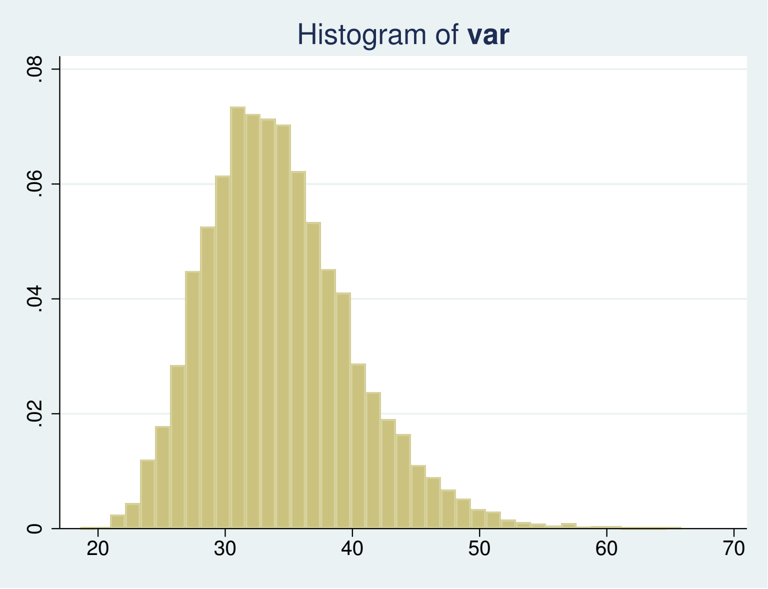
A histogram depicts the general shape of the marginal posterior distribution of a model parameter. Let's look at histograms of our parameters.

```
. bayesgraph histogram {mpg:_cons}, normal
```



The distribution of {mpg:_cons} is in good agreement with the normal distribution. This is not surprising, because the specified conjugate normal prior implies that the marginal posterior for {mpg:_cons} is a normal distribution. The unimodal histogram is also another confirmation that we have obtained a good simulation of the marginal posterior distribution of {mpg:_cons}.

```
. bayesgraph histogram {var}
```



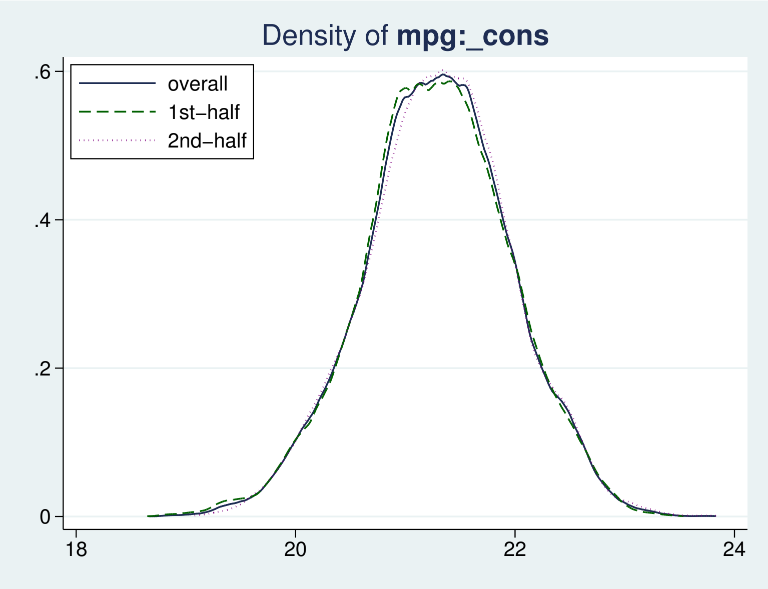
The histogram for {var} is also unimodal but is slightly skewed to the right. This is also in agreement with the specified prior because the marginal posterior for the variance is inverse gamma for the specified model.

Kernel density plots

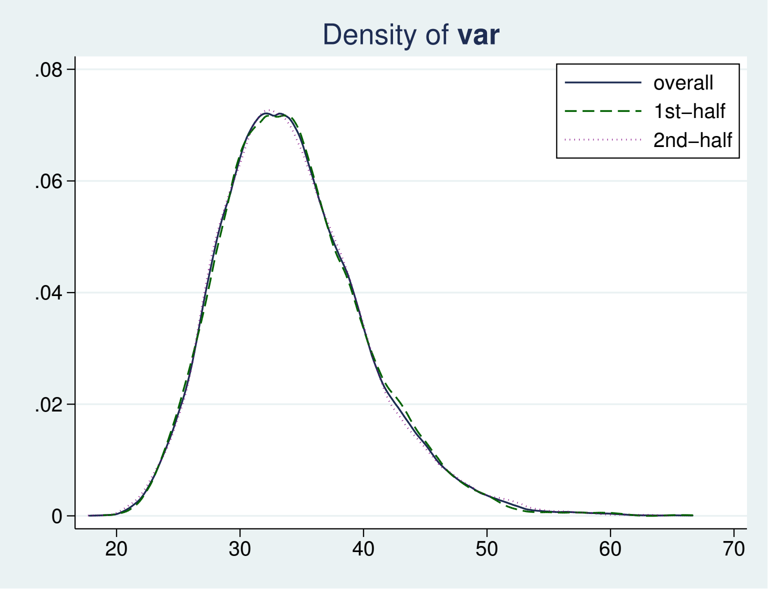
Kernel density plots provide alternative visualizations of the simulated marginal posterior distributions. They may be viewed as smoothed histograms. By default, the `bayesgraph kdensity` command shows three density curves: an overall density of the entire MCMC sample, the first-half density obtained using the first half of the MCMC sample, and the second-half density obtained using the second half of the MCMC sample. If the chain has converged and mixes well, we expect these three density curves to be close to each other. Large discrepancies between the first-half curve and the second-half curve suggest convergence problems.

Let's look at kernel density plots for our two parameters.

```
. bayesgraph kdensity {mpg:_cons}
```



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



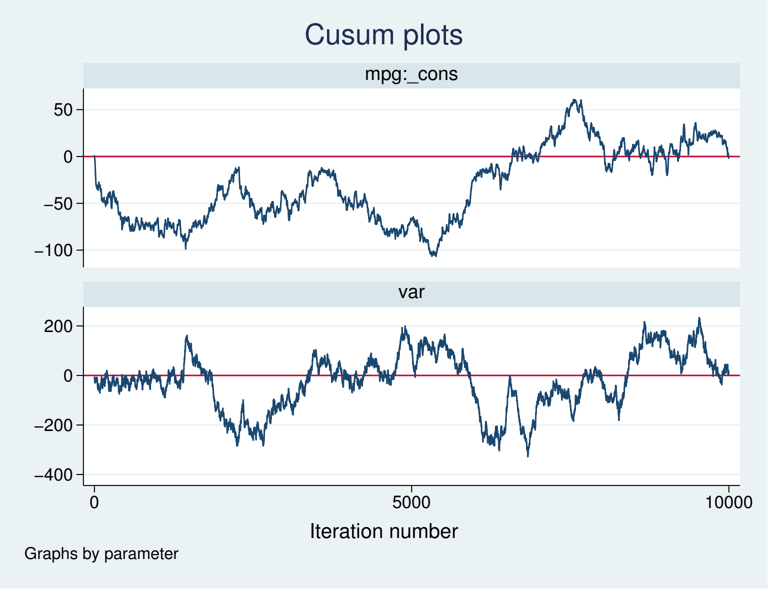
Kernel density plots for `{mpg:_cons}` and `{var}` are similar in shape to the histograms' plots from the previous section. All three density curves are close to each other for both parameters.

Cumulative sum plots

Cumulative sum (cusum) plots are useful graphical summaries for detecting persistent trends in MCMC chains. All cusum plots start and end at 0 and may or may not cross the x axis. There is great variability in the looks of cusum plots, which make them difficult to interpret sometimes. Typically, if the cusum line never crosses the x axis, this may indicate a problem. See, for example, *Convergence diagnostics of* MCMC in [BAYES] **intro** for a cusum plot demonstrating convergence problems.

By inspecting a cusum plot, we may detect an early drift in the simulated sample because of an insufficient burn-in period. In cases of pronounced persistent trends, the cusum curve may stay either in the positive or in the negative y plane. For a well-mixing parameter, the cusum curve typically crosses the x axis several times. This is the case for the cusum plots of `{mpg:_cons}` and `{var}`.

```
. bayesgraph cusum _all, byparm
```



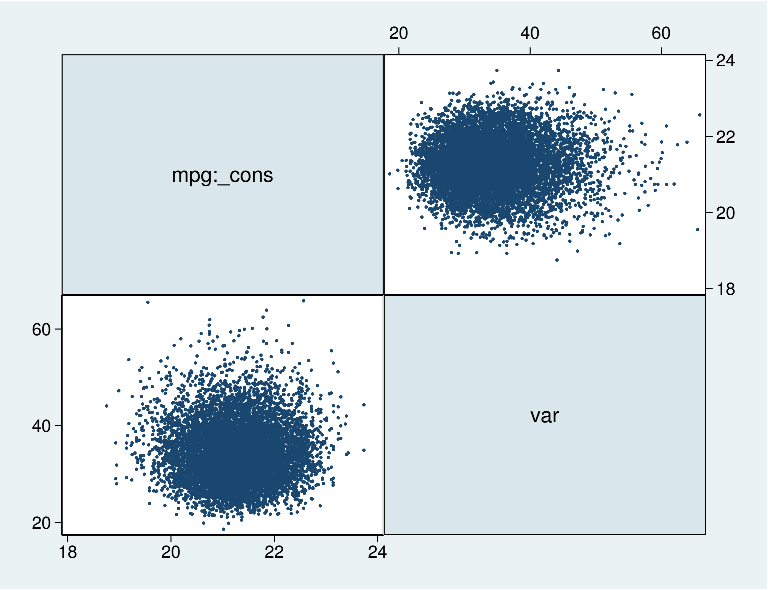
Bivariate scatterplots

The `bayesgraph matrix` command draws bivariate scatterplots of model parameters based on MCMC samples. A bivariate scatterplot represents a joint sample posterior distribution for pairs of parameters. It may reveal correlation between parameters and characterize a general shape of a multivariate posterior distribution. For example, bivariate scatterplots are useful for detecting multimodal posterior distributions.

Typically, scatterplots depict clouds of points. Sparseness and irregularities in the scatterplots can be strong indications of nonconvergence of an MCMC. For a well-mixing chain, the scatterplots have an ellipsoidal form with an increasing concentration around the posterior mode.

This scatterplot of {mpg:_cons} and {var} is an example of a well-behaved scatterplot.

```
. bayesgraph matrix {mpg:_cons} {var}
```

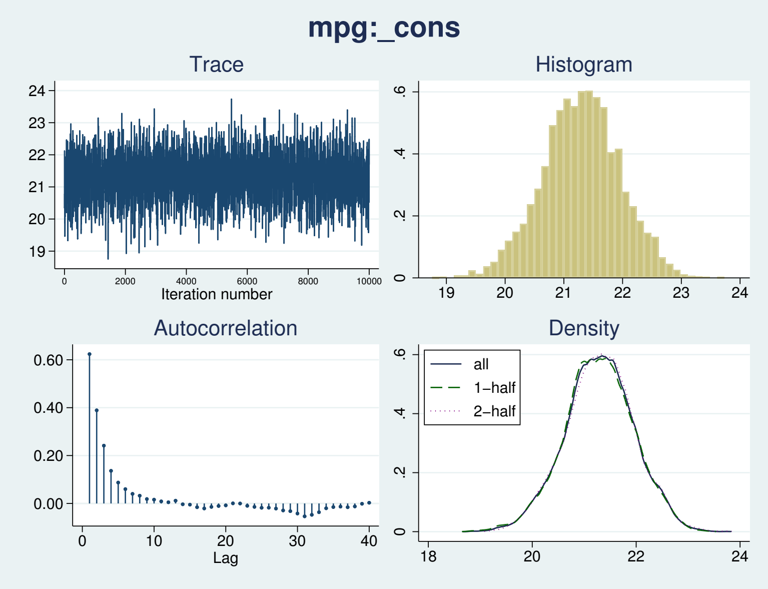


Diagnostic plots

Finally, we demonstrate the bayesgraph diagnostics command, which combines the trace, histogram, autocorrelation, and kernel density plots compactly on one graph. We already discussed the individual plots in the previous sections. Diagnostic plots are convenient for inspecting the overall behavior of a particular model parameter. We recommend that diagnostic plots for all parameters be inspected routinely as a part of the convergence-checking process.

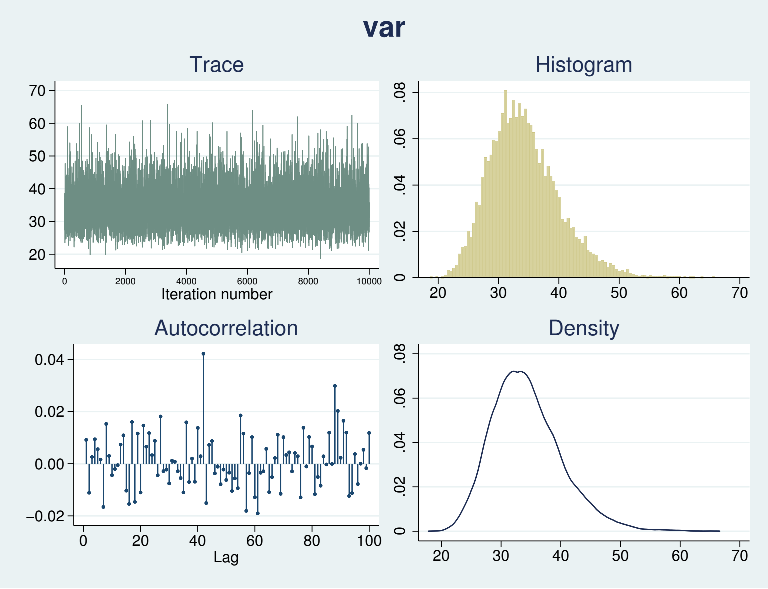
Let's obtain the diagnostic plot for {mpg:_cons}.

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



In the diagnostics plot for {var}, let's also demonstrate the use of several options of the depicted plots.

```
. bayesgraph diagnostics {var}, traceopts(lwidth(0.2) lcolor(teal))
> acopts(lag(100)) histopts(bin(100)) kdensopts(show(none))
```

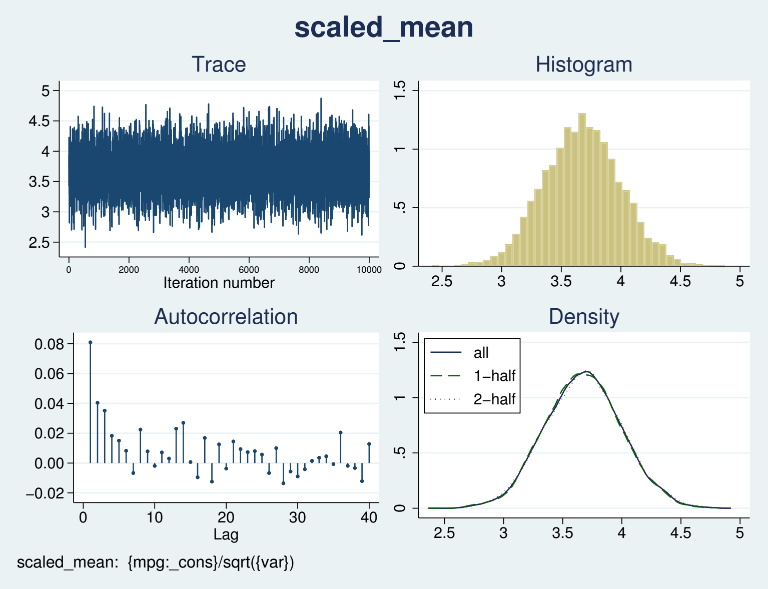


In the above, we changed the width and color of the trace line, the maximum lag for calculating the autocorrelation, the number of bins for the histogram, and requested that the two subsample kernel densities not be shown on the kernel density plot.

Functions of model parameters

All `bayesgraph` subcommands can provide graphical summaries of functions of model parameters. Below we apply `bayesgraph diagnostics` to the expression `{mpg:_cons}/sqrt({var})`, which we label as `scaled_mean`.

```
. bayesgraph diagnostics (scaled_mean: {mpg:_cons}/sqrt({var}))
```



If you detect convergence problems in a function of parameters, you must inspect every parameter used in the expression individually. In fact, we recommend that you inspect all model parameters before you proceed with any postestimation analysis.

Methods and formulas

Let θ be a scalar model parameter and $\{\theta_t\}_{t=1}^{T}$ be an MCMC sample of size T drawn from the marginal posterior distribution of θ.

The trace plot of θ plots θ_t against t with connecting lines for $t = 1, \ldots, T$.

The autocorrelation plot of θ shows the autocorrelation in the $\{\theta_t\}_{t=1}^{T}$ sample for lags from 0 to the `lag(#)` option of the `ac` command.

The histogram and kernel density plots of θ are drawn using the `histogram` and `kdensity` commands.

Yu and Mykland (1998) proposed a graphical procedure for assessing the convergence of individual parameters based on cumulative sums, also known as a cusum plot. The cusum plot for θ plots S_t against t for $t = 1, \ldots, T$ and connects the successive points. S_t is the cumulative sum at time t:

$$S_t = \sum_{k=1}^{t}(\theta_k - \widehat{\theta}), \quad \widehat{\theta} = \frac{1}{T}\sum_{k=1}^{T}\theta_k$$

and $S_0 = 0$.

The scatterplot of two model parameters θ^1 and θ^2 plots points (θ_t^1, θ_t^2) for $t = 1, \dots, T$.

References

Huber, C. 2016. 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/.

Yu, B., and P. Mykland. 1998. Looking at Markov samplers through cusum path plots: A simple diagnostic idea. *Statistics and Computing* 8: 275–286.

Also see

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

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

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

[BAYES] **bayesstats ess** — Effective sample sizes and related statistics

[BAYES] **bayesstats summary** — Bayesian summary statistics

[G-2] **graph matrix** — Matrix graphs

[G-2] **graph twoway kdensity** — Kernel density plots

[R] **histogram** — Histograms for continuous and categorical variables

[R] **kdensity** — Univariate kernel density estimation

[TS] **corrgram** — Tabulate and graph autocorrelations

[TS] **tsline** — Plot time-series data

Title

bayesstats — Bayesian statistics after Bayesian estimation

Description Reference Also see

Description

The following subcommands are available with `bayesstats` after `bayesmh`:

Command	Description
`bayesstats ess`	effective sample sizes and related statistics
`bayesstats summary`	Bayesian summary statistics for model parameters and their functions
`bayesstats ic`	Bayesian information criteria and Bayes factors

Reference

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/.

Also see

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

[BAYES] **bayesstats ess** — Effective sample sizes and related statistics

[BAYES] **bayesstats summary** — Bayesian summary statistics

[BAYES] **bayesstats ic** — Bayesian information criteria and Bayes factors

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

Title

bayesstats ess — Effective sample sizes and related statistics

Description

`bayesstats ess` calculates effective sample sizes (ESS), correlation times, and efficiencies for model parameters and functions of model parameters using current Bayesian estimation results.

Quick start

Effective sample sizes for all model parameters after a Bayesian regression model

```
bayesstats ess
```

As above, but only for model parameters `{y:x1}` and `{var}`

```
bayesstats ess {y:x1} {var}
```

As above, but skip every 5 observations from the full MCMC sample

```
bayesstats ess  {y:x1} {var}, skip(5)
```

Effective sample sizes for functions of scalar model parameters

```
bayesstats ess ({y:x1}-{y:_cons}) (sd:sqrt({var}))
```

As above, and include `{y:x1}` and `{var}`

```
bayesstats ess {y:x1} {var} ({y:x1}-{y:_cons}) (sd:sqrt({var}))
```

Menu

Statistics > Bayesian analysis > Effective sample sizes

Syntax

Statistics for all model parameters

`bayesstats ess` [, *options* `showreffects`[(*reref*)]]

`bayesstats ess _all` [, *options* `showreffects`[(*reref*)]]

Statistics for selected model parameters

`bayesstats ess` *paramspec* [, *options*]

Statistics for functions of model parameters

`bayesstats ess` *exprspec* [, *options*]

Full syntax

`bayesstats ess` *spec* [*spec* ...] [, *options*]

paramspec can be one of the following:

{*eqname*:*param*} refers to a parameter *param* with equation name *eqname*;

{*eqname*:} refers to all model parameters with equation name *eqname*;

{*eqname*:*paramlist*} refers to parameters with names in *paramlist* and with equation name *eqname*; or

{*param*} refers to all parameters named *param* from all equations.

In the above, *param* can refer to a matrix name, in which case it will imply all elements of this matrix. See *Different ways of specifying model parameters* in [BAYES] **bayesian postestimation** for examples.

exprspec is an optionally labeled expression of model parameters specified in parentheses:

([*exprlabel*:] *expr*)

exprlabel is a valid Stata name, and *expr* is a scalar expression that may not contain matrix model parameters. See *Specifying functions of model parameters* in [BAYES] **bayesian postestimation** for examples.

spec is one of *paramspec* or *exprspec*.

options	Description
Main	
`skip(#)`	skip every # observations from the MCMC sample; default is `skip(0)`
`nolegend`	suppress table legend
display_options	control spacing, line width, and base and empty cells
Advanced	
`corrlag(#)`	specify maximum autocorrelation lag; default varies
`corrtol(#)`	specify autocorrelation tolerance; default is `corrtol(0.01)`

Options

Main

`skip(#)` specifies that every # observations from the MCMC sample not be used for computation. The default is `skip(0)` or to use all observations in the MCMC sample. Option `skip()` can be used to subsample or thin the chain. `skip(#)` is equivalent to a thinning interval of #+1. For example, if you specify `skip(1)`, corresponding to the thinning interval of 2, the command will skip every other observation in the sample and will use only observations 1, 3, 5, and so on in the computation. If you specify `skip(2)`, corresponding to the thinning interval of 3, the command will skip every 2 observations in the sample and will use only observations 1, 4, 7, and so on in the computation. `skip()` does not thin the chain in the sense of physically removing observations from the sample, as is done by, for example, `bayesmh`'s `thinning()` option. It only discards selected observations from the computation and leaves the original sample unmodified.

`nolegend` suppresses the display of the table legend. The table legend identifies the rows of the table with the expressions they represent.

`showreffects` and `showreffects(`*reref*`)` are for use after multilevel models, and they specify that the results for all or a list *reref* of random-effects parameters be provided in addition to other model parameters. By default, all random-effects parameters are excluded from the results to conserve computation time.

display_options: `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `nofvlabel`, `fvwrap(#)`, `fvwrapon(`*style*`)`, and `nolstretch`; see [R] **estimation options**.

Advanced

`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()`.

`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.

Remarks and examples

Remarks are presented under the following headings:

Effective sample size and MCMC sampling efficiency
Using bayesstats ess

Effective sample size and MCMC sampling efficiency

It is well known that for a random sample of T independent subjects, the standard error of the sample mean estimator is proportional to $1/\sqrt{T}$. In Bayesian inference, it is of interest to estimate the standard error of the posterior mean estimator. The posterior mean of a parameter of interest is typically estimated as a sample mean from an MCMC sample obtained from the marginal posterior distribution of the parameter of interest. Observations from an MCMC sample are not independent and are usually positively correlated, which must be taken into account when computing the standard error. Thus the standard error of the posterior mean estimator is proportional to $1/\sqrt{\text{ESS}}$, where ESS is the effective sample size for the parameter of interest. Typically, ESS is less than T, the total number of observations in the MCMC sample. We can thus interpret the posterior mean estimate as a sample mean estimate from an independent sample of size ESS. In other words, the effective sample size is an estimate of the number of independent observations that the MCMC chain represents. We say that MCMC samples with higher ESS are more efficient.

Effective sample size is directly related to the convergence properties of an MCMC sample—very low ESS relative to T suggests nonconvergence. In the extreme case of a perfectly correlated MCMC observation, ESS is 1. It is thus a standard practice to assess the quality of an MCMC sample by inspecting ESS values for all involved model parameters. Note, however, that high ESS values are not generally sufficient for declaring convergence of MCMC because pseudoconvergence, which may occur when MCMC does not explore the entire distribution, may also lead to high ESS values.

Using bayesstats ess

`bayesstats ess` reports effective sample sizes, correlation times, and efficiencies for model parameters and their functions using the current Bayesian estimation results. When typed without arguments, the command displays results for all model parameters. Alternatively, you can specify a subset of model parameters following the command name; see *Different ways of specifying model parameters* in [BAYES] **bayesian postestimation**. You can also obtain results for scalar functions of model parameters; see *Specifying functions of model parameters* in [BAYES] **bayesian postestimation**.

Consider our analysis of `auto.dta` from example 4 in [BAYES] **bayesmh** using the mean-only normal model for `mpg` with a noninformative prior.

```
. use http://www.stata-press.com/data/r15/auto
(1978 Automobile Data)

. 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
------------------------------------------------------------------------------
```

▷ Example 1: Effective sample sizes for all parameters

To compute effective sample sizes and other related statistics for all model parameters, we type `bayesstats ess` without arguments after the `bayesmh` command.

```
. bayesstats ess
Efficiency summaries    MCMC sample size =    10,000

                           ESS   Corr. time    Efficiency

mpg
         _cons          971.82        10.29        0.0972

           var         1070.99         9.34        0.1071
```

The closer the ESS estimates are to the MCMC sample size, the better. Also, the lower the correlation times are and the higher the efficiencies are, the better. ESS estimates can be interpreted as follows. In a sample of 10,000 MCMC observations, we have only about 972 independent observations to obtain estimates for `{mpg:_cons}` and only about 1,071 independent observations to obtain estimates for `{var}`. Correlation times are reciprocal of efficiencies. You can interpret them as an estimated lag after which autocorrelation in an MCMC sample is small. In our example, the estimated lag is roughly 10 for both parameters. In general, efficiencies above 10% are considered good for the MH algorithm. In our example, they are about 12% for both parameters.

Alternatively, we could have listed all parameters manually:

```
. bayesstats ess {mpg:_cons} {var}
  (output omitted )
```

◁

▷ Example 2: Effective sample sizes for functions of model parameters

Similarly to other Bayesian postestimation commands, `bayesstats ess` accepts expressions to compute results for functions of model parameters. For example, we can use expression `(sd:sqrt({var}))` with a label, `sd`, to compute effective sample sizes for the standard deviation of `mpg` in addition to the variance.

```
. bayesstats ess (sd:sqrt({var})) {var}
Efficiency summaries    MCMC sample size =    10,000
          sd : sqrt({var})

                           ESS   Corr. time    Efficiency

            sd         1093.85         9.14        0.1094
           var         1070.99         9.34        0.1071
```

ESS and efficiency are higher for the standard deviation than for the variance, which means that we need slightly more iterations to estimate `{var}` with the same precision as `sd`.

If we wanted, we could have suppressed the `sd` legend in the output above by specifying the `nolegend` option.

◁

Stored results

`bayesstats ess` stores the following in `r()`:

Scalars	
`r(skip)`	number of MCMC observations to skip in the computation; every `r(skip)` observations are skipped
`r(corrlag)`	maximum autocorrelation lag
`r(corrtol)`	autocorrelation tolerance
Macros	
`r(expr_#)`	#th expression
`r(names)`	names of model parameters and expressions
`r(exprnames)`	expression labels
Matrices	
`r(ess)`	matrix with effective sample sizes, correlation times, and efficiencies for parameters in `r(names)`

Methods and formulas

Let θ be a scalar model parameter and $\{\theta_t\}_{t=1}^{T}$ be an MCMC sample of size T drawn from the marginal posterior distribution of θ. The effective sample size of the MCMC sample of θ is given by

$$\text{ESS} = T/(1 + 2 \sum_{k=1}^{\text{max\_lags}} \rho_k)$$

where $\rho_k = \gamma_k/\gamma_0$ is the lag-k autocorrelation of the MCMC sample, and max_lags is the maximum number less than or equal to ρ_{lag} such that for all $k = 1, \ldots, \text{max\_lags}$, $|\rho_k| > \rho_{\text{tol}}$, where ρ_{lag} and ρ_{tol} are specified in options `corrlag()` and `corrtol()` with the respective default values of 500 and 0.01.

The lag-k autocorrelation is $\rho_k = \gamma_k/\gamma_0$, where

$$\gamma_k = \frac{1}{T} \sum_{t=1}^{T-k} (\theta_t - \widehat{\theta})(\theta_{t+k} - \widehat{\theta})$$

is the empirical autocovariance of lag k, and γ_0 simplifies to the sample variance. $\widehat{\theta}$ is the posterior mean estimator.

Correlation time is defined as T/ESS, and efficiency is defined as the reciprocal of the correlation time, ESS/T. Because ESS is between 0 and T, inclusively, the efficiency is always between 0 and 1.

Also see

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

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

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

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

[BAYES] **bayesstats summary** — Bayesian summary statistics

Title

bayesstats ic — Bayesian information criteria and Bayes factors

Description	Quick start	Menu	Syntax
Options	Remarks and examples	Stored results	Methods and formulas
References	Also see		

Description

`bayesstats ic` calculates and reports model-selection statistics, including the deviance information criterion (DIC), log marginal-likelihood, and Bayes factors (BFs), using current Bayesian estimation results. BFs can be displayed in the original metric or in the log metric. The command also provides two different methods to approximate marginal likelihood.

Quick start

Information criteria for previously saved estimation results `A` and `B` with `A` used as the base model by default

```
bayesstats ic A B
```

As above, but use `B` as the base model instead of `A`

```
bayesstats ic A B, basemodel(B)
```

Report BFs instead of the default log BFs

```
bayesstats ic A B, bayesfactor
```

Menu

Statistics > Bayesian analysis > Information criteria

Syntax

```
bayesstats ic [namelist] [, options]
```

namelist is a name, a list of names, `_all`, or `*`. A name may be `.`, meaning the current (active) estimates. `_all` and `*` mean the same thing.

options	Description
Main	
`basemodel(`*name*`)`	specify a base or reference model; default is the first-listed model
`bayesfactor`	report BFs instead of the default log BFs
`diconly`	report only DIC
Advanced	
`marglmethod(`*method*`)`	specify marginal-likelihood approximation method; default is to use Laplace–Metropolis approximation, `lmetropolis`; rarely used

method	Description
`lmetropolis`	Laplace–Metropolis approximation; the default
`hmean`	harmonic-mean approximation

Options

Main

`basemodel(`*name*`)` specifies the name of the model to be used as a base or reference model when computing BFs. By default, the first-listed model is used as a base model.

`bayesfactor` specifies that BFs be reported instead of the default log BFs.

`diconly` specifies that only DIC be reported in the table and that the log marginal likelihood and Bayes factors be omitted from the table. Options `basemodel()`, `basefactor`, and `marglmethod()` have no effect when the `diconly` option is specified.

Advanced

`marglmethod(`*method*`)` specifies a method for approximating the marginal likelihood. *method* is either `lmetropolis`, the default, for Laplace–Metropolis approximation or `hmean` for harmonic-mean approximation. This option is rarely used.

Remarks and examples

Remarks are presented under the following headings:

Bayesian information criteria
Bayes factors
Using bayesstats ic

Bayesian information criteria

Bayesian information criteria are used for selecting a model among a set of candidate models that best fits the data. Likelihood-based inference is known to be prone to overfitting the data. Indeed, it is often possible to increase the likelihood by simply including more parameters in a model. Bayesian information criteria address this problem by applying a penalty proportional to the complexity of the models to the likelihood.

Consider a finite set of Bayesian models M_1, ..., M_r, which we want to compare with a base model M_b. All models M_js are fit to the same dataset but may differ in their likelihood or prior specification.

Three commonly used information criteria are Akaike information criterion (AIC), Bayesian information criterion (BIC), and DIC. All three criteria are likelihood based and include a goodness-of-fit term proportional to the negative likelihood of the model and a penalty term proportional to the number of parameters in the model. Models with smaller values of these criteria are preferable.

The BIC, originally derived for the exponential family of distributions, is based on the assumption that the model has a flat, noninformative prior. In frequentist statistics, BIC is widely used as a variable-selection criterion, particularly in linear regression. In BIC, the penalty term is a product of the number of parameters in the model and the log of the sample size. The penalty of BIC thus increases not only with the number of parameters but also with the sample size. In the AIC, the penalty term is two times the number of parameters and does not depend on the sample size. As a result, BIC is more conservative than AIC and prefers simpler models. DIC is similar to AIC, but its penalty term is based on a complexity term that measures the difference between the expected log likelihood and the log likelihood at the posterior mean point. DIC is designed specifically for Bayesian estimation that involves MCMC simulations.

The limitation of all three criteria is that they either ignore prior distributions or assume that prior distributions are noninformative. They are thus not well suited for Bayesian sensitivity analysis, when models with the same parameters but different priors are being compared.

The `bayesstats ic` command reports DIC. See [R] **estat ic** after the corresponding maximum likelihood estimation command for values of AIC and BIC.

Bayes factors

In Bayesian inference, BFs are preferred to model-selection criteria because, unlike BIC, AIC, and DIC, they incorporate the information about model priors. Taking into account prior information is essential for Bayesian sensitivity analysis, when models with the same parameters but different priors are being compared.

The BF of two models is just the ratio of their marginal likelihoods calculated using the same dataset. Unlike BIC, AIC, and DIC, BFs include all information about the specified Bayesian model. Thus BFs are not applicable to models with improper priors, whereas BIC, AIC, and DIC are still applicable because they ignore prior information. BFs, however, are often difficult to compute reliably because of the difficulty in computing marginal likelihoods.

BFs also require that posterior distributions be completely specified, including the normalizing constants. The latter is especially important in Bayesian estimation using MCMC simulations, when the normalizing constants are often omitted from the specification of a posterior distribution. The Bayesian estimation commands always simulate from a complete posterior distribution when you select one of the supported Bayesian models, but you need to make sure to include all normalizing constants with your posterior distribution when you are programming your own Bayesian model (see [BAYES] **bayesmh evaluators**) and would like to use BFs during postestimation.

Let BF_{jb}, $j = 1, \dots, r$, be the BF of model M_j with respect to the base model M_b. All models M_j are fit to the same dataset; otherwise, BFs are meaningless. The `bayesstats ic` command calculates BF_{jb}'s and reports them in log metric or in absolute metric when the `bayesfactor` option is specified.

Jeffreys (1961) proposes the following interpretation of the values of BF_{jb} based on half-units of the log metric:

$\log_{10}(\text{BF}_{jb})$	BF_{jb}	Evidence against M_b
0 to 1/2	1 to 3.2	Bare mention
1/2 to 1	3.2 to 10	Substantial
1 to 2	10 to 100	Strong
>2	>100	Decisive

Kass and Raftery (1995) suggest using twice the natural logarithm of the BF to make it have the same scale as the DIC and likelihood-ratio test statistic. They suggest the following interpretation table:

$2\log_e(\text{BF}_{jb})$	BF_{jb}	Evidence against M_b
0 to 2	1 to 3	Bare mention
2 to 6	3 to 20	Positive
6 to 10	20 to 150	Strong
>10	>150	Very strong

Typically, the worst-fitting model is chosen as a base model. If the base model happens to be better than the comparison model, the corresponding BF will be negative. In this case, you can apply results above to the absolute value of the BF.

BFs compute relative probabilities of how well each model fits the data compared with the base model. Being relative quantities, BFs cannot be used to measure goodness of fit of a particular model unless one assumes that the base model fits the data well. Some researchers view this as a limitation of BFs (Gelman et al. 2014). Kass and Raftery (1995), on the other hand, show that BFs can be viewed as differences between predictive scores and thus can be used to measure success of different models at predicting the data.

BFs have several advantages over the more traditional, frequentist testing methods. For example, they do not have the limitation of the p-value approach to systematically reject the null hypothesis in large samples. BFs are also suitable for comparing both nonnested and nested models. Also see *Comparing Bayesian models* in [BAYES] **intro** for more information about Bayesian model comparison.

A key element in computing BFs is calculating the marginal likelihood. Except for some rare cases, marginal likelihood does not have a closed form and needs to be approximated. A detailed review of different approximation methods is given by Kass and Raftery (1995). The default method implemented in `bayesstats ic` (and `bayesmh`) is the Laplace–Metropolis approximation (Lewis and Raftery 1997). The harmonic-mean approximation of the marginal likelihood is also available via the `marglmethod(hmean)` option, but we recommend that you use the default method. See *Methods and formulas* in [BAYES] **bayesmh** for technical details.

Using bayesstats ic

▷ Example 1

The bayesstats ic command provides several model-selection statistics that can be used to compare models. To illustrate the use of bayesstats ic, we consider auto.dta. We model the fuel-efficiency variable mpg using a normal distribution with fixed variance but unknown, random mean. There is only one random parameter in this model—{mpg:_cons}. We compare the models with three different prior distributions to find the best one among them. We fit the three models using bayesmh and save the corresponding estimation results as uniform1, uniform2, and normal.

First, for comparison purposes, let's obtain the maximum likelihood estimate (MLE) of the mean of mpg, which is simply the sample mean in our example:

```
. use http://www.stata-press.com/data/r15/auto
(1978 Automobile Data)
. summarize mpg
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
         mpg |         74     21.2973    5.785503         12         41
```

The sample mean of mpg is roughly 21.3.

Next, we use bayesmh to fit our first model of interest. We fix the variance of the normal distribution to 30, which is close to the estimated variance of mpg of $5.79^2 = 33.52$.

```
. set seed 14
. bayesmh mpg, likelihood(normal(30))
> prior({mpg:_cons}, uniform(-10, 10))
> initial({mpg:_cons} 2) saving(uniform1_simdata)
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},30)
Prior:
  {mpg:_cons} ~ uniform(-10,10)
------------------------------------------------------------------------------

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  =      .4102
Log marginal likelihood = -397.42978             Efficiency       =     .08018

------------------------------------------------------------------------------
             |                                                Equal-tailed
         mpg |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
       _cons |  9.965511   .0342812   .001211   9.975729   9.871825   9.998796
------------------------------------------------------------------------------
file uniform1_simdata.dta saved
. estimates store uniform1
```

In the first model, we deliberately chose a prior for {mpg:_cons}, uniform(-10,10), that does not include the value of the sample mean. We thus expect this model to fit poorly. Because of the restricted domain of the specified uniform prior, we also needed to specify an initial value for {mpg:_cons} for MCMC to start from a point of positive posterior probability.

We also specified the `saving()` option to save the MCMC simulation dataset so that we could use **`estimates store`** to store our estimation results for future use. See *Storing estimation results after Bayesian estimation* in [BAYES] **bayesian postestimation** for details.

```
. set seed 14

. bayesmh mpg, likelihood(normal(30))
> prior({mpg:_cons}, uniform(10, 30))
> initial({mpg:_cons} 20) saving(uniform2_simdata)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},30)

Prior:
  {mpg:_cons} ~ uniform(10,30)
------------------------------------------------------------------------------

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  =      .4272
Log marginal likelihood = -237.08583             Efficiency       =      .2414

------------------------------------------------------------------------------
             |                                                Equal-tailed
         mpg |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
       _cons |  21.31085   .6447073   .013123   21.31485   20.06381   22.57936
------------------------------------------------------------------------------

file uniform2_simdata.dta saved

. estimates store uniform2
```

In the second model, we used a uniform prior that included the value of the sample mean in its domain.

```
. set seed 14
. bayesmh mpg, likelihood(normal(30))
> prior({mpg:_cons}, normal(30)) saving(normal_simdata)
Burn-in ...
Simulation ...
Model summary
──────────────────────────────────────────────────────────────────────────────
Likelihood:
  mpg ~ normal({mpg:_cons},30)
Prior:
  {mpg:_cons} ~ normal(30)
──────────────────────────────────────────────────────────────────────────────

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  =      .4295
Log marginal likelihood = -244.16624             Efficiency       =      .2319

──────────────────────────────────────────────────────────────────────────────
             │                                                Equal-tailed
         mpg │      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
─────────────┼────────────────────────────────────────────────────────────────
       _cons │  21.01901   .6461194   .013417   21.01596   19.76637    22.3019
──────────────────────────────────────────────────────────────────────────────
file normal_simdata.dta saved
. estimates store normal
```

In the third model, we used a normal prior with a variance fixed at 30. Note that we did not need to specify an initial value for `{mpg:_cons}` in this model, because the domain of the normal distribution is the whole real line.

Both the `uniform2` and `normal` models yield estimates close to the MLE of 21.3. According to their credible intervals, the domain of the posterior distribution of `{mpg:_cons}` is concentrated around MLE. For example, the 95% credible interval for the `uniform2` model is [20.06, 22.60].

Now, let's use `bayesstats ic` to compare the three models. We list all the models following the command name and use the `normal` model as a reference model.

```
. bayesstats ic uniform1 uniform2 normal, basemodel(normal)
Bayesian information criteria

─────────────┬─────────────────────────────────
             │       DIC    log(ML)    log(BF)
─────────────┼─────────────────────────────────
    uniform1 │  785.8891  -397.4298  -153.2635
    uniform2 │  471.1909  -237.0858   7.080404
      normal │  471.3905  -244.1662          .
─────────────┴─────────────────────────────────
Note: Marginal likelihood (ML) is computed
      using Laplace-Metropolis approximation.
```

The `uniform1` model performs worse than the other two models according to the log marginal-likelihood, `log(ML)`, and DIC—the `DIC` value is much larger, and the `log(ML)` value is much smaller for the `uniform1` model. The other two models have only slightly different values for `DIC` and `log(ML)`, according to which the `uniform2` model is preferable.

Although the `uniform2` and `normal` models have different prior distributions, they have almost identical posterior domain, that is, the range of values of `{mpg:_cons}` where the posterior is strictly positive. As such, they will have the same values for AIC and BIC, and we will not be able to discriminate between the two models based on these information criteria.

The most decisive factor between the `uniform2` and `normal` models is the BF. The value of log BF, `log(BF)`, is 7.08, which provides very strong evidence in favor of the `uniform2` model.

We thus conclude that `uniform2` is the best model among the three considered models. This may be explained by the fact that the specified `uniform(10,30)` prior is in more agreement with the likelihood of the data than the specified `normal(0,30)` prior.

After your analysis, remember to erase the saved simulation datasets you no longer need. For example, we erase all of them by typing

```
. erase uniform1_simdata.dta
. erase uniform2_simdata.dta
. erase normal_simdata.dta
```

◁

Stored results

`bayesstats ic` stores the following in `r()`:

Scalars	
`r(bayesfactor)`	1 if `bayesfactor` is specified, 0 otherwise
Macros	
`r(names)`	names of estimation results used
`r(basemodel)`	name of the base or reference model
`r(marglmethod)`	method for approximating marginal likelihood: `lmetropolis` or `hmean`
Matrices	
`r(ic)`	matrix reporting `DIC`, `log(ML)`, and `log(BF)` or `BF` if `bayesfactor` is used

Methods and formulas

DIC was introduced by Spiegelhalter et al. (2002) for Bayesian model selection using MCMC simulations. DIC is based on the deviance statistics

$$D(\boldsymbol{\theta}) = -2\left\{\log f(\mathbf{y};\boldsymbol{\theta}) - \log f^*(\mathbf{y};\boldsymbol{\theta}^*)\right\}$$

where $f(\cdot;\cdot)$ is the likelihood function of the model and $f^*(\mathbf{y};\boldsymbol{\theta}^*)$ is the likelihood of the full model that fits data perfectly. Because $f^*(\mathbf{y};\boldsymbol{\theta}^*)$ is constant across models fit to the same data, it is ignored in the actual calculation of DIC. Given an MCMC sample $\{\boldsymbol{\theta}_t\}_{t=1}^T$, the expected deviance can be estimated by the sample average $\overline{D}(\boldsymbol{\theta}) = 1/T\sum_{t=1}^T D(\boldsymbol{\theta}_t)$. Similarly to AIC and BIC, DIC is a sum of two components: the goodness-of-fit term $\overline{D}(\boldsymbol{\theta})$ and the model complexity term p_D: DIC $= \overline{D}(\boldsymbol{\theta}) + p_D$. The complexity is defined as the difference between the expected deviance and the deviance at the sample posterior mean: $p_D = \overline{D}(\boldsymbol{\theta}) - D(\overline{\boldsymbol{\theta}})$. We thus have

$$\text{DIC} = D(\overline{\boldsymbol{\theta}}) + 2p_D$$

Models with smaller values of DIC are preferred to models with larger values of DIC.

BFs were introduced by Jeffreys (1961). The BF of two models, M_1 and M_2, is given by

$$\text{BF}_{12} = \frac{P(\mathbf{y}|M_1)}{P(\mathbf{y}|M_2)} = \frac{m_1(\mathbf{y})}{m_2(\mathbf{y})}$$

where $m_1(\cdot)$ and $m_2(\cdot)$ are the corresponding marginal likelihoods associated with models M_1 and M_2. (See *Methods and formulas* in [BAYES] **bayesmh** for details about computing marginal likelihood.) BFs are defined only for proper marginal densities. Comparing models with improper priors is allowed as long as the resulting marginal densities are proper. The methodological importance of BFs comes from the fact that the so-called posterior odds is a product of prior odds and BF:

$$\frac{P(M_1|\mathbf{y})}{P(M_2|\mathbf{y})} = \frac{P(M_1)}{P(M_2)} \times \mathrm{BF}_{12}$$

Therefore, if we assume that M_1 and M_2 are equally probable a priori, the posterior odds will be equal to the BF. We thus prefer model M_1 if $\mathrm{BF}_{12} > 1$ and model M_2 otherwise. In practice, because of the higher numerical stability, we often calculate BFs in the (natural) log metric and compare its value against 0.

$$\log\mathrm{BF}_{12} = \log m_1(\mathbf{y}) - \log m_2(\mathbf{y})$$

References

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 & Hall/CRC.

Jeffreys, H. 1961. *Theory of Probability*. 3rd ed. Oxford: Oxford University Press.

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Lewis, S. M., and A. E. Raftery. 1997. Estimating Bayes factors via posterior simulation with the Laplace–Metropolis estimator. *Journal of the American Statistical Association* 92: 648–655.

Spiegelhalter, D. J., N. G. Best, B. P. Carlin, and A. Van Der Linde. 2002. Bayesian measures of model complexity and fit. *Journal of the Royal Statistical Society, Series B* 64: 583–639.

Also see

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

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

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

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

[BAYES] **bayestest model** — Hypothesis testing using model posterior probabilities

[R] **estimates** — Save and manipulate estimation results

Title

bayesstats summary — Bayesian summary statistics

Description Quick start Menu Syntax
Options Remarks and examples Stored results Methods and formulas
References Also see

Description

bayesstats summary calculates and reports posterior summary statistics for model parameters and functions of model parameters using current Bayesian estimation results. Posterior summary statistics include posterior means, posterior standard deviations, MCMC standard errors (MCSE), posterior medians, and equal-tailed credible intervals or highest posterior density (HPD) credible intervals.

Quick start

Posterior summaries for all model parameters after a Bayesian regression model

```
bayesstats summary
```

As above, but only for parameters {y:x1} and {y:x2}

```
bayesstats summary {y:x1} {y:x2}
```

Same as above

```
bayesstats summary {y:x1 x2}
```

Posterior summaries for elements 1,1 and 2,1 of matrix parameter {S}

```
bayesstats summary {S_1_1 S_2_1}
```

Posterior summaries for all elements of matrix parameter {S}

```
bayesstats summary {S}
```

Posterior summaries with HPD instead of equal-tailed credible intervals and with credible level of 90%

```
bayesstats summary, hpd clevel(90)
```

Posterior summaries with MCSE calculated using batch means

```
bayesstats summary, batch(100)
```

Posterior summaries for functions of scalar model parameters

```
bayesstats summary ({y:x1}-{y:_cons}) (sd:sqrt({var}))
```

Posterior summaries for the log-likelihood and log-posterior functions

```
bayesstats summary _loglikelihood _logposterior
```

Posterior summaries for selected model parameters and functions of model parameters and for log-likelihood and log-posterior functions using abbreviated syntax

```
bayesstats summary {var} ({y:x1}-{y:_cons}) _ll _lp
```

Menu

Statistics > Bayesian analysis > Summary statistics

Syntax

Summary statistics for all model parameters

```
bayesstats summary [, options showreffects[(reref)]]

bayesstats summary _all [, options showreffects[(reref)]]
```

Summary statistics for selected model parameters

```
bayesstats summary paramspec [, options]
```

Summary statistics for functions of model parameters

```
bayesstats summary exprspec [, options]
```

Summary statistics of log-likelihood or log-posterior functions

```
bayesstats summary _loglikelihood | _logposterior [, options]
```

Full syntax

```
bayesstats summary spec [spec ...] [, options]
```

paramspec can be one of the following:

{*eqname*:*param*} refers to a parameter *param* with equation name *eqname*;

{*eqname*:} refers to all model parameters with equation name *eqname*;

{*eqname*:*paramlist*} refers to parameters with names in *paramlist* and with equation name *eqname*; or

{*param*} refers to all parameters named *param* from all equations.

In the above, *param* can refer to a matrix name, in which case it will imply all elements of this matrix. See *Different ways of specifying model parameters* in [BAYES] **bayesian postestimation** for examples.

exprspec is an optionally labeled expression of model parameters specified in parentheses:

([*exprlabel*:]*expr*)

exprlabel is a valid Stata name, and *expr* is a scalar expression that may not contain matrix model parameters. See *Specifying functions of model parameters* in [BAYES] **bayesian postestimation** for examples.

`_loglikelihood` and `_logposterior` also have respective synonyms `_ll` and `_lp`.

spec is one of *paramspec*, *exprspec*, `_loglikelihood` (or `_ll`), or `_logposterior` (or `_lp`).

options	Description
Main	
`clevel(#)`	set credible interval level; default is `clevel(95)`
`hpd`	display HPD credible intervals instead of the default equal-tailed credible intervals
`batch(#)`	specify length of block for batch-means calculations; default is `batch(0)`
`skip(#)`	skip every # observations from the MCMC sample; default is `skip(0)`
`nolegend`	suppress table legend
display_options	control spacing, line width, and base and empty cells
Advanced	
`corrlag(#)`	specify maximum autocorrelation lag; default varies
`corrtol(#)`	specify autocorrelation tolerance; default is `corrtol(0.01)`

Options

Main

`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` specifies the display of HPD credible intervals instead of the default equal-tailed credible intervals.

`batch(#)` specifies the length of the block for calculating batch means, batch standard deviation, and MCSE using batch means. The default is `batch(0)`, which means no batch calculations. When `batch()` is not specified, MCSE is computed using effective sample sizes instead of batch means. Option `batch()` may not be combined with `corrlag()` or `corrtol()`.

`skip(#)` specifies that every # observations from the MCMC sample not be used for computation. The default is `skip(0)` or to use all observations in the MCMC sample. Option `skip()` can be used to subsample or thin the chain. `skip(#)` is equivalent to a thinning interval of #+1. For example, if you specify `skip(1)`, corresponding to the thinning interval of 2, the command will skip every other observation in the sample and will use only observations 1, 3, 5, and so on in the computation. If you specify `skip(2)`, corresponding to the thinning interval of 3, the command will skip every 2 observations in the sample and will use only observations 1, 4, 7, and so on in the computation. `skip()` does not thin the chain in the sense of physically removing observations from the sample, as is done by, for example, `bayesmh`'s `thinning()` option. It only discards selected observations from the computation and leaves the original sample unmodified.

`nolegend` suppresses the display of the table legend. The table legend identifies the rows of the table with the expressions they represent.

`showreffects` and `showreffects(`*reref*`)` are for use after multilevel models, and they specify that the results for all or a list *reref* of random-effects parameters be provided in addition to other model parameters. By default, all random-effects parameters are excluded from the results to conserve computation time.

display_options: `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `nofvlabel`, `fvwrap(#)`, `fvwrapon(`*style*`)`, and `nolstretch`; see [R] **estimation options**.

Advanced

`corrlag(#)` specifies the maximum autocorrelation lag used for calculating effective sample sizes. The default is min{500, `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

Remarks are presented under the following headings:

Introduction
Bayesian summaries for an auto data example

Introduction

`bayesstats summary` reports posterior summary statistics for model parameters and their functions using the current Bayesian estimation results. When typed without arguments, the command displays results for all model parameters. Alternatively, you can specify a subset of model parameters following the command name; see *Different ways of specifying model parameters* in [BAYES] **bayesian postestimation**. You can also obtain results for scalar functions of model parameters; see *Specifying functions of model parameters* in [BAYES] **bayesian postestimation**.

Sometimes, it may be useful to obtain posterior summaries of log-likelihood and log-posterior functions. This can be done by specifying `_loglikelihood` and `_logposterior` (or the respective synonyms `_ll` and `_lp`) following the command name.

`bayesstats summary` reports the following posterior summary statistics: posterior mean, posterior standard deviation, MCMC standard error, posterior median, and equal-tailed credible intervals or, if the `hpd` option is specified, HPD credible intervals. The default credible level is set to 95%, but you can change this by specifying the `clevel()` option. Equal-tailed and HPD intervals may produce very different results for asymmetric or highly skewed marginal posterior distributions. The HPD intervals are preferable in this situation.

You should not confuse the term "HPD interval" with the term "HPD region". A $\{100\times(1-\alpha)\}\%$ HPD interval is defined such that it contains $\{100\times(1-\alpha)\}\%$ of the posterior density. A $\{100\times(1-\alpha)\}\%$ HPD region also satisfies the condition that the density inside the region is never lower than that outside the region. For multimodal univariate marginal posterior distributions, the HPD regions may include unions of nonintersecting HPD intervals. For unimodal univariate marginal posterior distributions, HPD regions are indeed simply HPD intervals. The `bayesstats summary` command thus calculates HPD intervals assuming unimodal marginal posterior distributions (Chen and Shao 1999).

Some authors use the term "posterior intervals" instead of "credible intervals" and the term "central posterior intervals" instead of "equal-tailed credible intervals" (for example, Gelman et al. [2014]).

Bayesian summaries for an auto data example

Recall our analysis of `auto.dta` from example 4 in [BAYES] **bayesmh** using the mean-only normal model for `mpg` with a noninformative prior.

```
. use http://www.stata-press.com/data/r15/auto
(1978 Automobile Data)

. 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
------------------------------------------------------------------------------
```

▷ Example 1: Summaries for all parameters

If we type bayesstats summary without arguments after the bayesmh command, we will obtain the same summary table as reported by bayesmh.

```
. bayesstats summary

Posterior summary statistics                      MCMC sample size =    10,000

------------------------------------------------------------------------------
             |                                                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
------------------------------------------------------------------------------
```

The posterior mean of {mpg:_cons} is 21.29 and of {var} is 34.8. They are close to their respective frequentist analogs (the sample mean of mpg is 21.297, and the sample variance is 33.47), because we used a noninformative prior. Posterior standard deviations are 0.68 for {mpg:_cons} and 5.92 for {var}, and they are comparable to frequentist standard errors under this noninformative prior. The standard error estimates of the posterior means, MCSEs, are low. For example, MCSE is 0.022 for {mpg:_cons}. This means that the precision of our estimate is, up to one decimal point, 21.3 provided that MCMC converged. The posterior means and medians of {mpg:_cons} are close, which suggests that the posterior distribution for {mpg:_cons} may be symmetric. According to the credible intervals, we are 95% certain that the posterior mean of {mpg:_cons} is roughly between 20 and 23 and that the posterior mean of {var} is roughly between 25 and 48. We can infer from this that {mpg:_cons} is greater than, say, 15, and that {var} is greater than, say, 20, with a very high probability. (We can use [BAYES] **bayestest interval** to compute the actual probabilities.)

The above is also equivalent to typing

```
. bayesstats summary {mpg:_cons} {var}
  (output omitted)
```

◁

▷ Example 2: Credible intervals

By default, `bayesstats summary` reports 95% equal-tailed credible intervals. We can change the default credible level by specifying the `clevel()` option.

```
. bayesstats summary, clevel(90)
Posterior summary statistics                      MCMC sample size =    10,000
------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [90% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |  21.29222   .6828864   .021906   21.27898   20.18807   22.44172
-------------+----------------------------------------------------------------
         var |  34.76572    5.91534   .180754   34.18391   26.28517   44.81732
------------------------------------------------------------------------------
```

As expected, 90% credible intervals are more narrow.

To calculate and report HPD intervals, we specify the `hpd` option.

```
. bayesstats summary, hpd
Posterior summary statistics                      MCMC sample size =    10,000
------------------------------------------------------------------------------
             |                                                     HPD
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |  21.29222   .6828864   .021906   21.27898   19.94985   22.54917
-------------+----------------------------------------------------------------
         var |  34.76572    5.91534   .180754   34.18391   24.34876   46.12339
------------------------------------------------------------------------------
```

The posterior distribution of {mpg:_cons} is symmetric about the posterior mean; thus there is little difference between the 95% equal-tailed credible interval from example 1 and this 95% HPD credible interval for {mpg:_cons}. The 95% HPD interval for {var} has a smaller width than the corresponding equal-tailed interval in example 1.

◁

▷ Example 3: Batch-means estimator

`bayesstats summary` provides two estimators for MCSE: effective-sample-size and batch-means. Estimation using effective sample sizes is the default. You can use the `batch(#)` option to request the batch-means estimator, where # is the batch size. The optimal batch size depends on the autocorrelation in the MCMC sample. For example, if we observe that the autocorrelation for the parameters of interest is negligible after lag 100, we can specify `batch(100)` to estimate MCSE.

In our example, autocorrelation dies out after about lag 10 (see, for example, *Autocorrelation plots* in [BAYES] **bayesgraph** and example 1 in [BAYES] **bayesstats ess**), so we use 10 as our batch size:

```
. bayesstats summary, batch(10)

Posterior summary statistics                      MCMC sample size =     10,000
                                                  Batch size       =         10

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |  21.29222   .4842889   .015315   21.27898   19.99152   22.61904
-------------+----------------------------------------------------------------
         var |  34.76572   4.278417   .135295   34.18391    24.9129   47.61286
------------------------------------------------------------------------------
Note: Mean, Std. Dev., and MCSE are estimated using batch means.
```

The batch-means MCSE estimates are somewhat smaller than those obtained by default using effective sample sizes.

Use caution when choosing the batch size for the batch-means method. For example, if you use the batch size of 1, you will obtain MCSE estimates under the assumption that the draws in the MCMC sample are independent, which is not true.

◁

▷ Example 4: Subsampling or thinning the chain

You can reduce correlation between MCMC draws by thinning or subsampling the MCMC chain. You can use the `skip(`*#*`)` option to skip every *#* observations from the MCMC sample, which is equivalent to a thinning interval of $\# + 1$. For example, if you specify `skip(1)`, corresponding to the thinning interval of 2, `bayesstats summary` will skip every other observation in the sample and will use only observations 1, 3, 5, and so on in the computation. If you specify `skip(2)`, corresponding to the thinning interval of 3, `bayesstats summary` will skip every two observations in the sample and will use only observations 1, 4, 7, and so on in the computation. By default, no observations are skipped—`skip(0)`. Note that `skip()` does not thin the chain in the sense of physically removing observations from the sample, as is done by `bayesmh`'s `thinning()` option. It discards only selected observations from the computation and leaves the original sample unmodified.

```
. bayesstats summary, skip(9)
note: skipping every 9 sample observations; using observations 1,11,21,...

Posterior summary statistics                      MCMC sample size =      1,000

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |  21.29554   .6813796   .029517   21.27907   19.98813   22.58582
-------------+----------------------------------------------------------------
         var |   34.7396   5.897313   .206269   33.91782    24.9554   48.11452
------------------------------------------------------------------------------
```

We selected to skip every 9 observations, which led to a significant reduction of the MCMC sample size and thus increased our standard deviations. In some cases, with larger MCMC sample sizes, subsampling may decrease standard deviations because of the decreased autocorrelation in the reduced MCMC sample.

◁

▷ Example 5: Summaries for functions of model parameters

bayesstats summary accepts expressions to provide summaries of functions of model parameters. For example, we can use expression (sd:sqrt({var})) with a label, sd, to summarize the standard deviation of mpg in addition to the variance.

```
. bayesstats summary (sd:sqrt({var})) {var}

Posterior summary statistics                      MCMC sample size =    10,000

          sd : sqrt({var})

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
          sd |   5.87542   .4951654   .014972   5.846701   4.991282   6.900207
         var |  34.76572    5.91534   .180754   34.18391    24.9129   47.61286
------------------------------------------------------------------------------
```

Expressions can also be used for calculating posterior probabilities, although this can be more easily done using bayestest interval (see [BAYES] **bayestest interval**). For illustration, let's verify the probability that {var} is within the endpoints of the reported credible interval, indeed 0.95.

```
. bayesstats summary (prob:{var}>24.913 & {var}<47.613)

Posterior summary statistics                      MCMC sample size =    10,000

        prob : {var}>24.913 & {var}<47.613

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
        prob |     .9502   .2175424   .005301          1          0          1
------------------------------------------------------------------------------
```

◁

▷ Example 6: Summaries for log likelihood and log posterior

We can use reserved names _loglikelihood (or the synonym _ll) and _logposterior (or the synonym _lp) to obtain summaries of the log likelihood and log posterior for the simulated MCMC sample.

```
. bayesstats summary _ll _lp

Posterior summary statistics                      MCMC sample size =    10,000

         _ll : _loglikelihood
         _lp : _logposterior

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
         _ll | -235.4162    .990654   .032232  -235.1379  -238.1236  -234.4345
         _lp | -238.9507   1.037785   .034535  -238.6508  -241.7889  -237.9187
------------------------------------------------------------------------------
```

◁

Stored results

`bayesstats summary` stores the following in `r()`:

Scalars	
`r(clevel)`	credible interval level
`r(hpd)`	`1` if `hpd` is specified, `0` otherwise
`r(batch)`	batch length for batch-means calculations
`r(skip)`	number of MCMC observations to skip in the computation; every `r(skip)` observations are skipped
`r(corrlag)`	maximum autocorrelation lag
`r(corrtol)`	autocorrelation tolerance
Macros	
`r(expr_#)`	#th expression
`r(names)`	names of model parameters and expressions
`r(exprnames)`	expression labels
Matrices	
`r(summary)`	matrix with posterior summaries statistics for parameters in `r(names)`

Methods and formulas

Methods and formulas are presented under the following headings:

Point estimates
Credible intervals

Most of the summary statistics employed in Bayesian analysis are based on the marginal posterior distributions of individual model parameters or functions of model parameters.

Let θ be a scalar model parameter and $\{\theta_t\}_{t=1}^T$ be an MCMC chain of size T drawn from the marginal posterior distribution of θ. For a function $g(\theta)$, substitute $\{\theta_t\}_{t=1}^T$ with $\{g(\theta_t)\}_{t=1}^T$ in the formulas below. If θ is a covariance matrix model parameter, the formulas below are applied to each element of the lower-diagonal portion of θ.

Point estimates

Marginal posterior moments are approximated using the Monte Carlo integration applied to the simulated samples $\{\theta_t\}_{t=1}^T$.

Sample posterior mean and sample standard deviation are defined as follows,

$$\widehat{\theta} = \frac{1}{T}\sum_{t=1}^{T}\theta_t, \ \ \widehat{s}^2 = \frac{1}{T-1}\sum_{t=1}^{T}(\theta_t - \widehat{\theta})^2$$

where $\widehat{\theta}$ and $\widehat{s}^2$ are sample estimators of the population posterior mean $E(\theta_t)$ and posterior variance $\mathrm{Var}(\theta_t)$.

The precision of the sample posterior mean is evaluated by its standard error, also known as the Monte Carlo standard error (MCSE). Note that MCSE cannot be estimated using the classical formula for the standard error, $\widehat{s}/\sqrt{T}$, because of the dependence between θ_t's.

Let

$$\sigma^2 = \mathrm{Var}(\theta_t) + 2\sum_{k=1}^{\infty}\mathrm{Cov}(\theta_t, \theta_{t+k})$$

Then, $\sqrt{T}\times$MCSE approaches σ^2 asymptotically in T.

`bayesstats summary` provides two different approaches for estimating MCSE. Both approaches try to adjust for the existing autocorrelation in the MCMC sample. The first one uses the so-called effective sample size (ESS), and the second one uses batch means (Roberts 1996; Jones et al. 2006).

The ESS-based estimator for MCSE, the default in `bayesstats summary`, is given by

$$\text{MCSE}(\widehat{\theta}) = \widehat{s}/\sqrt{\text{ESS}}$$

ESS is defined as

$$\text{ESS} = T/(1 + 2\sum_{k=1}^{\text{max\_lags}} \rho_k)$$

where ρ_k is the lag-k autocorrelation, and max_lags is the maximum number less than or equal to ρ_{lag} such that for all $k = 1, \ldots, \text{max\_lags}$, $|\rho_k| > \rho_{\text{tol}}$, where ρ_{lag} and ρ_{tol} are specified in options `corrlag()` and `corrtol()` with the respective default values of 500 and 0.01. ρ_k is estimated as γ_k/γ_0, where

$$\gamma_k = \frac{1}{T}\sum_{t=1}^{T-k}(\theta_t - \widehat{\theta})(\theta_{t+k} - \widehat{\theta})$$

is the lag-k empirical autocovariance.

The batch-means estimator of MCSE is obtained as follows. For a given batch of length b, the initial MCMC chain is split into m batches of size b,

$$\{\theta_{j'+1}, \ldots, \theta_{j'+b}\}\ \{\theta_{j'+b+1}, \ldots, \theta_{j'+2b}\}\ \ldots\ \{\theta_{T-b+1}, \ldots, \theta_T\}$$

where $j' = T - m \times b$ and m batch means $\widehat{\mu}_1, \ldots, \widehat{\mu}_m$ are calculated as sample means of each batch. m is chosen as the maximum number such that $m \times b \leq T$. If m is not a divisor of T, the first $T - m \times b$ observations of the sample are not used in the batch-means computation. The batch-means estimator of the posterior variance, $\widehat{s}^2_{\text{batch}}$, is based on the assumption that $\widehat{\mu}_j$s are much less correlated than the original sample draws.

The batch-means estimators of the posterior mean and posterior variance are

$$\widehat{\theta}_{\text{batch}} = \frac{1}{m}\sum_{j=1}^{m}\widehat{\mu}_j,\ \ \widehat{s}^2_{\text{batch}} = \frac{1}{m-1}\sum_{j=1}^{m}(\widehat{\mu}_j - \widehat{\theta}_{\text{batch}})^2$$

We have $\widehat{\theta}_{\text{batch}} = \widehat{\theta}$, whenever $m \times b = T$. Under the assumption that the batch means are uncorrelated, $\widehat{s}^2_{\text{batch}}$ can be used as an estimator of σ^2/b. This fact justifies the batch-means estimator of MCSE given by

$$\text{MCSE}_{\text{batch}}(\widehat{\theta}) = \frac{\widehat{s}_{\text{batch}}}{\sqrt{m}}$$

The accuracy of the batch-means estimator depends on the choice of the batch length b. The higher the autocorrelation in the original MCMC sample, the larger the batch length b should be, provided that the number of batches m does not become too small; $\sqrt{T}$ is typically used as the maximum value for b. The batch length is commonly determined by inspecting the autocorrelation plot for θ. Under certain assumptions, Flegal and Jones (2010) establish that an asymptotically optimal batch size is of order $T^{1/3}$.

Credible intervals

Let $\theta_{(1)}, \ldots, \theta_{(T)}$ be an MCMC sample ordered from smallest to largest. Let $(1-\alpha)$ be a credible level. Then, a $\{100 \times (1-\alpha)\}\%$ equal-tailed credible interval is

$$(\theta_{([T\alpha/2])}, \theta_{([T(1-\alpha/2)])})$$

where [ ] in the above imply an integer number.

A $\{100 \times (1-\alpha)\}\%$ HPD interval is defined as the shortest interval among the $\{100 \times (1-\alpha)\}\%$ credible intervals $(\theta_{(j)}, \theta_{(j+[T(1-\alpha)])})$, $j = 1, \ldots, T - [T(1-\alpha)]$.

References

Chen, M.-H., and Q.-M. Shao. 1999. Monte Carlo estimation of Bayesian credible and HPD intervals. *Journal of Computational and Graphical Statistics* 8: 69–92.

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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 & Hall/CRC.

Jones, G. L., M. Haran, B. S. Caffo, and R. Neath. 2006. Fixed-width output analysis for Markov chain Monte Carlo. *Journal of the American Statistical Association* 101: 1537–1547.

Roberts, G. O. 1996. Markov chain concepts related to sampling algorithms. In *Markov Chain Monte Carlo in Practice*, ed. W. R. Gilks, S. Richardson, and D. J. Spiegelhalter, 45–57. Boca Raton, FL: Chapman and Hall.

Also see

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

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

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

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

[BAYES] **bayesgraph** — Graphical summaries and convergence diagnostics

[BAYES] **bayesstats ess** — Effective sample sizes and related statistics

[BAYES] **bayestest interval** — Interval hypothesis testing

Title

bayestest — Bayesian hypothesis testing

Description   Remarks and examples   Also see

Description

`bayestest` provides two types of Bayesian hypothesis testing, interval hypothesis testing and model hypothesis testing, using current Bayesian estimation results.

`bayestest interval` performs interval hypothesis tests for model parameters and functions of model parameters; see [BAYES] **bayestest interval**.

`bayestest model` tests hypotheses about models by computing posterior probabilities of the models; see [BAYES] **bayestest model**.

Remarks and examples

Bayesian hypothesis testing is fundamentally different from the conventional frequentist hypothesis testing using p-values. Frequentist hypothesis testing is based on the deterministic decision of whether to reject a null hypothesis against an alternative hypothesis based on the obtained p-value. Bayesian hypothesis testing is built upon a probabilistic formulation for a parameter of interest. For example, it can provide a probabilistic summary of how likely that parameter of interest belongs to some prespecified set of values. Also, Bayesian testing can assign a probability to a hypothesis of interest or model of interest given the observed data. This cannot be done in the frequentist testing. The ability to assign a probability to a hypothesis often provides a more natural interpretation of the results. For example, Bayesian hypothesis testing provides a direct answer to the following questions. How likely is it that the mean height of males is larger than six feet? What is the probability that a person is guilty versus being innocent? How likely is one model over the other model? Frequentist hypothesis testing cannot be used to answer these questions.

We consider two forms of Bayesian hypothesis testing: interval hypothesis testing and what we call model hypothesis testing.

The goal of interval hypothesis testing is to estimate the probability that a model parameter lies in a certain interval; see [BAYES] **bayestest interval** for details.

The goal of model hypothesis testing is to test hypotheses about models by computing probabilities of the specified models given the observed data; see [BAYES] **bayestest model** for details.

Also see

[BAYES] **bayestest interval** — Interval hypothesis testing

[BAYES] **bayestest model** — Hypothesis testing using model posterior probabilities

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

Title

bayestest interval — Interval hypothesis testing

Description

`bayestest interval` performs interval hypothesis tests for model parameters and functions of model parameters using current Bayesian estimation results. `bayestest interval` reports mean estimates, standard deviations, and MCMC standard errors of posterior probabilities associated with an interval hypothesis.

Quick start

Posterior probability of the hypothesis that 45 < `{y:_cons}` < 50

```
bayestest interval {y:_cons}, lower(45) upper(50)
```

As above, but skip every 5 observations from the full MCMC sample

```
bayestest interval {y:_cons}, lower(45) upper(50) skip(5)
```

Posterior probability of a hypothesis about a function of model parameter `{y:x1}`

```
bayestest interval (OR:exp({y:x1})), lower(1.1) upper(1.5)
```

Posterior probability of hypotheses 45 < `{y:_cons}` < 50 and 0 < `{var}` < 10 tested independently

```
bayestest interval ({y:_cons}, lower(45) upper(50))  ///
     ({var}, lower(0) upper(10))
```

As above, but tested jointly

```
bayestest interval (({y:_cons}, lower(45) upper(50))  ///
     ({var}, lower(0) upper(10)), joint)
```

Posterior probability of the hypothesis `{mean}` = 2 for discrete parameter `{mean}`

```
bayestest interval ({mean}==2)
```

Posterior probability of the interval hypothesis 0 ≤ `{mean}` ≤ 4

```
bayestest interval {mean}, lower(0, inclusive) upper(4, inclusive)
```

Menu

Statistics > Bayesian analysis > Interval hypothesis testing

Syntax

Test one interval hypothesis about continuous or discrete parameter

`bayestest interval` *exspec* [, *luspec* *options*]

Test one point hypothesis about discrete parameter

`bayestest interval` *exspec*`==`*#* [, *options*]

Test multiple hypotheses separately

`bayestest interval (`*testspec*`)` [`(`*testspec*`)` ...] [, *options*]

Test multiple hypotheses jointly

`bayestest interval (`*jointspec*`)` [, *options*]

Full syntax

`bayestest interval (`*spec*`)` [`(`*spec*`)` ...] [, *options*]

exspec is optionally labeled expression of model parameters, [*prlabel*`:`]*expr*, where *prlabel* is a valid Stata name (or `prob`*#* by default), and *expr* is a scalar model parameter or scalar expression (parentheses are optional) containing scalar model parameters. The expression *expr* may not contain variable names.

testspec is *exspec*[, *luspec*] or *exspec*`==`*#* for discrete parameters only.

jointspec is [*prlabel:*]`(`*testspec*`) (`*testspec*`)` ... `, joint`. The labels (if any) of *testspec* are ignored.

spec is one of *testspec* or *jointspec*.

luspec	Null hypothesis
`lower(`*#*`)` [`upper(.)`]	$\theta > \#$
`lower(`*#*`, inclusive)` [`upper(.)`]	$\theta \geq \#$
[`lower(.)`] `upper(`*#*`)`	$\theta < \#$
[`lower(.)`] `upper(`*#*`, inclusive)`	$\theta \leq \#$
`lower(`$\#_l$`) upper(`$\#_u$`)`	$\#_l < \theta < \#_u$
`lower(`$\#_l$`) upper(`$\#_u$`, inclusive)`	$\#_l < \theta \leq \#_u$
`lower(`$\#_l$`, inclusive) upper(`$\#_u$`)`	$\#_l \leq \theta < \#_u$
`lower(`$\#_l$`, inclusive) upper(`$\#_u$`, inclusive)`	$\#_l \leq \theta \leq \#_u$

`lower(`*intspec*`)` and `upper(`*intspec*`)` specify the lower- and upper-interval values, respectively.

intspec is *#* [, `inclusive`]

where *#* is the interval value, and suboption `inclusive` specifies that this value should be included in the interval, meaning a closed interval. Closed intervals make sense only for discrete parameters.

intspec may also contain a dot (`.`), meaning negative infinity for `lower()` and positive infinity for `upper()`. Either option `lower(.)` or option `upper(.)` must be specified.

options	Description
Main	
skip(#)	skip every # observations from the MCMC sample; default is skip(0)
nolegend	suppress table legend
Advanced	
corrlag(#)	specify maximum autocorrelation lag; default varies
corrtol(#)	specify autocorrelation tolerance; default is corrtol(0.01)

Options

Main

skip(#) specifies that every # observations from the MCMC sample not be used for computation. The default is skip(0) or to use all observations in the MCMC sample. Option skip() can be used to subsample or thin the chain. skip(#) is equivalent to a thinning interval of #+1. For example, if you specify skip(1), corresponding to the thinning interval of 2, the command will skip every other observation in the sample and will use only observations 1, 3, 5, and so on in the computation. If you specify skip(2), corresponding to the thinning interval of 3, the command will skip every 2 observations in the sample and will use only observations 1, 4, 7, and so on in the computation. skip() does not thin the chain in the sense of physically removing observations from the sample, as is done by, for example, bayesmh's thinning() option. It only discards selected observations from the computation and leaves the original sample unmodified.

nolegend suppresses the display of the table legend. The table legend identifies the rows of the table with the expressions they represent.

Advanced

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().

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.

Remarks and examples

Remarks are presented under the following headings:

Introduction

In this entry, we describe interval hypothesis testing, the goal of which is to estimate the probability that a model parameter lies in a certain interval. Interval hypothesis testing is inversely related to credible intervals. For example, if we have a 95% credible interval for θ with endpoints U and L, then the probability of a hypothesis H_0: $\theta \in [U, L]$ is 0.95. For hypothesis testing using model posterior probabilities, see [BAYES] **bayestest model**.

In frequentist hypothesis testing, we often consider a point hypothesis such as H_0: $\theta = \theta_0$ versus H_a: $\theta \neq \theta_0$. In Bayesian hypothesis testing, the probability $P(\theta = \theta_0)$ is 0 whenever θ has a continuous posterior distribution. A point hypothesis is relevant only to parameters with discrete posterior distributions. For continuous parameters, all hypotheses should be formulated as intervals. One possibility is to consider an interval hypothesis H_0: $\theta \in (\theta_0 - \epsilon, \theta_0 + \epsilon)$, where ϵ is some small value.

Note that Bayesian hypothesis testing does not really need a distinction between the null and alternative hypotheses, in the sense that they are defined in a frequentist statistic. There is no need to “protect” the null hypothesis: if $P\{H_0\text{: } \theta \in (a, b)\} = p$, then $P\{H_a\text{: } \theta \notin (a, b)\} = 1 - p$. In what follows, when we refer to H_0, we imply a hypothesis of interest H_0: $\theta \in \Theta$, and when we refer to H_a, we imply the complement hypothesis H_a: $\theta \in \Theta^c$, where Θ is a set of points from the domain of θ and Θ^c is its complement.

The `bayestest interval` command estimates the posterior probability of a null interval hypothesis H_0 using the simulated posterior distributions of model parameters produced by Bayesian estimation. Essentially, `bayestest interval` reports posterior summaries for a dichotomous expression that represents H_0.

For example, suppose we would like to test the following hypothesis: H_0: $\theta \in (a, b)$. Then,

```
bayestest interval ({theta}, lower(a) upper(b))
```

is equivalent to

```
bayesstats summary ({theta} > a & {theta} < b)
```

`bayestest interval` reports the estimated posterior mean probability for H_0, which is not a p-value—as reported by classical frequentist tests—used to decide whether to reject H_0 in favor of the alternative H_a. The p-value interpretation is based on the dichotomous problem formulation of H_0 versus H_a, assuming that one of these two alternatives is actually true. The answer in the Bayesian context is a probability statement about θ that is free of any deterministic presumptions. For example, if you estimate $P(H_0)$ to be 0.15, you cannot ask whether this value is significant or whether you can reject the null hypothesis. Bayesian interpretation of this probability is that if you draw θ from the specified prior distribution and update your knowledge about θ based on the observed data, then there is a 15% chance that θ will belong to the interval (a, b). So the conclusion of Bayesian hypothesis testing is not an acceptance or rejection of the null hypothesis but an explicit probability statement about the tested hypothesis.

Interval tests for continuous parameters

Let's continue our analysis of `auto.dta` from example 4 in [BAYES] **bayesmh** using the mean-only normal model for `mpg` with a noninformative prior.

```
. use http://www.stata-press.com/data/r15/auto
(1978 Automobile Data)

. 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
------------------------------------------------------------------------------
```

▷ Example 1: Interval hypothesis and credible intervals

In the introduction, we commented on the inverse relationship that exists between interval hypothesis tests and credible intervals. Let's verify this using `bayestest interval`. We are interested in a hypothesis H_0: `{mpg:_cons}` $\in (19.992, 22.619)$, where the specified numbers are the endpoints of the credible interval for `{mpg:_cons}` from the `bayesmh` output. To compute the posterior probability for this hypothesis, we specify the parameter following the command line and specify interval endpoints in `lower()` and `upper()`.

```
. bayestest interval {mpg:_cons}, lower(19.992) upper(22.619)

Interval tests     MCMC sample size =    10,000

       prob1 : 19.992 < {mpg:_cons} < 22.619

-----------------------------------------------
             |      Mean    Std. Dev.      MCSE
-------------+---------------------------------
       prob1 |     .9496     0.21878   .0053652
-----------------------------------------------
```

The estimated posterior probability is close to 0.95, as we expected, because we used the endpoints of the 95% credible intervals for `{mpg:_cons}`.

By default, bayestest interval labels probabilities as prob# (prob1 in our example). You can specify your own label as long as you enclose the parameter in parentheses:

```
. bayestest interval (mean:{mpg:_cons}), lower(19.992) upper(22.619)
Interval tests     MCMC sample size =     10,000
        mean : 19.992 < {mpg:_cons} < 22.619
──────────────────────────────────────────────────
             │       Mean    Std. Dev.       MCSE
─────────────┼────────────────────────────────────
        mean │      .9496      0.21878   .0053652
──────────────────────────────────────────────────
```

◁

▷ Example 2: Testing multiple hypotheses separately

Continuing example 1, we can verify that the probability associated with the credible interval for {var} is also close to 0.95.

We can specify multiple hypotheses with bayestest interval, but we must enclose them in parentheses.

```
. bayestest interval ({mpg:_cons}, lower(19.992) upper(22.619))
>                     ({var}, lower(24.913) upper(47.613))
Interval tests     MCMC sample size =     10,000
       prob1 : 19.992 < {mpg:_cons} < 22.619
       prob2 : 24.913 < {var} < 47.613
──────────────────────────────────────────────────
             │       Mean    Std. Dev.       MCSE
─────────────┼────────────────────────────────────
       prob1 │      .9496      0.21878   .0053652
       prob2 │      .9502      0.21754   .0053011
──────────────────────────────────────────────────
```

The estimated posterior probability prob2 is also close to 0.95.

◁

▷ Example 3: Testing multiple hypotheses jointly

We can perform joint tests of multiple hypotheses by enclosing hypothesis to be tested jointly in parentheses and by specifying suboption joint. Notice that each individual hypothesis must also be enclosed in parentheses.

```
. bayestest interval (({mpg:_cons}, lower(19.992) upper(22.619))
>                      ({var}, lower(24.913) upper(47.613)), joint)
Interval tests     MCMC sample size =     10,000
       prob1 : 19.992 < {mpg:_cons} < 22.619,
               24.913 < {var} < 47.613
──────────────────────────────────────────────────
             │       Mean    Std. Dev.       MCSE
─────────────┼────────────────────────────────────
       prob1 │      .9034      0.29543   .0076789
──────────────────────────────────────────────────
```

The joint posterior probability of both {mpg:_cons} and {var} belonging to their respective intervals is 0.9 with a posterior variance of 0.3 and MCSE of 0.008.

◁

▷ Example 4: Full syntax

We can specify multiple separate hypotheses and hypotheses tested jointly in one call to `bayestest interval`.

```
. bayestest interval (({mpg:_cons}, lower(19.992) upper(22.619))
>                       ({var}, lower(24.913) upper(47.613)), joint)
>                      ({mpg:_cons}, lower(21))
>                      ({var}, upper(40))

Interval tests     MCMC sample size =     10,000

       prob1 : 19.992 < {mpg:_cons} < 22.619,
               24.913 < {var} < 47.613
       prob2 : {mpg:_cons} > 21
       prob3 : {var} < 40

-----------------------------------------------
             |      Mean    Std. Dev.      MCSE
-------------+---------------------------------
       prob1 |     .9034     0.29543   .0076789
       prob2 |     .6505     0.47684    .015786
       prob3 |     .8136     0.38945   .0110613
-----------------------------------------------
```

In addition to the joint hypothesis from the previous example, we specified two new separate interval hypotheses for testing `{mpg:_cons}` $>$ 21 and for testing `{var}` $<$ 40. The estimated posterior probabilities for these hypotheses are 0.65 and 0.81, respectively.

◁

▷ Example 5: Point hypothesis for continuous parameters

As we discussed in *Introduction* above, point hypothesis for continuous parameters do not make sense, because the corresponding probability is 0:

```
. bayestest interval ({mpg:_cons}==21)

Interval tests     MCMC sample size =     10,000

       prob1 : {mpg:_cons}==21

-----------------------------------------------
             |      Mean    Std. Dev.      MCSE
-------------+---------------------------------
       prob1 |         0     0.00000          0
-----------------------------------------------
```

We can consider a small window around the value of interest and test an interval hypothesis instead:

```
. bayestest interval ({mpg:_cons}, lower(20.5) upper(21.5))

Interval tests     MCMC sample size =     10,000

       prob1 : 20.5 < {mpg:_cons} < 21.5

-----------------------------------------------
             |      Mean    Std. Dev.      MCSE
-------------+---------------------------------
       prob1 |     .4932     0.49998   .0138391
-----------------------------------------------
```

The probability that `{mpg:_cons}` is between 20.5 and 21.5 is about 50%.

Note that the probability of a continuous parameter belonging to a closed interval or semiclosed interval is the same as that for the open interval. Below we use suboption `inclusive` within `lower()` and `upper()` to request the closed interval.

```
. bayestest interval ({mpg:_cons}, lower(20.5,inclusive) upper(21.5,inclusive))

Interval tests      MCMC sample size =     10,000

       prob1 : 20.5 <= {mpg:_cons} <= 21.5

--------------------------------------------------
             |      Mean    Std. Dev.       MCSE
-------------+------------------------------------
       prob1 |     .4932     0.49998   .0138391
--------------------------------------------------
```

We obtain the same results as above for the corresponding open interval.

◁

▷ Example 6: Functions of parameters

We can test functions of model parameters. For example, let's compute the probability that the posterior standard deviation is greater than 6.

```
. bayestest interval (sd: sqrt({var}), lower(6))

Interval tests      MCMC sample size =     10,000

          sd : sqrt({var}) > 6

--------------------------------------------------
             |      Mean    Std. Dev.       MCSE
-------------+------------------------------------
          sd |     .3793     0.48524   .0143883
--------------------------------------------------
```

The estimated probability is 0.38.

◁

Interval tests for discrete parameters

In this section, we demonstrate how to perform hypothesis testing for a discrete parameter.

First, we simulate data from the Poisson distribution with a mean of 2.

```
. clear

. set seed 12345

. set obs 20
number of observations (_N) was 0, now 20

. generate double y = rpoisson(2)
```

We fit a Bayesian Poisson model to the data and specify a discrete prior for the mean $P(\mu = k) = 0.25$ for $k = 1, 2, 3, 4$.

```
. set seed 14

. bayesmh y, likelihood(dpoisson({mu}))
> prior({mu}, index(0.25,0.25,0.25,0.25)) initial({mu} 2)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------

Likelihood:
  y ~ poisson({mu})

Prior:
  {mu} ~ index(0.25,0.25,0.25,0.25)
------------------------------------------------------------------------------

Bayesian Poisson model                           MCMC iterations  =     12,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      2,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         20
                                                 Acceptance rate  =      .2552
Log marginal likelihood =  -31.58903             Efficiency       =      .4428

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
          mu |    2.0014   .1039188   .001562          2          2          2
------------------------------------------------------------------------------
```

▷ Example 7: Point hypotheses for discrete parameters

We can compute probabilities for each of the four discrete values of {mu}.

```
. bayestest interval ({mu}==1) ({mu}==2) ({mu}==3) ({mu}==4)

Interval tests     MCMC sample size =    10,000

       prob1 : {mu}==1
       prob2 : {mu}==2
       prob3 : {mu}==3
       prob4 : {mu}==4

-----------------------------------------------
             |      Mean    Std. Dev.      MCSE
-------------+---------------------------------
       prob1 |     .0047     0.06840   .0013918
       prob2 |     .9892     0.10337   .0027909
       prob3 |     .0061     0.07787   .0017691
       prob4 |         0     0.00000          0
-----------------------------------------------
```

The posterior probability that {mu} equals 2 is 0.99.

◁

▷ Example 8: Interval hypotheses for discrete parameters

As we can with continuous parameters, we can test interval hypotheses for discrete parameters. For example, we can compute the probability of whether `{mu}` is between 2 and 4.

```
. bayestest interval {mu}, lower(2) upper(4)
Interval tests      MCMC sample size =    10,000
       prob1 : 2 < {mu} < 4
─────────────────────────────────────────────────
             │      Mean     Std. Dev.       MCSE
─────────────┼───────────────────────────────────
       prob1 │     .0061       0.07787   .0017691
─────────────────────────────────────────────────
```

The estimated probability is very small.

Note that unlike hypotheses for continuous parameters, hypotheses including open intervals and closed or semiclosed intervals for discrete parameters may have different probabilities.

```
. bayestest interval {mu}, lower(2, inclusive) upper(4, inclusive)
Interval tests      MCMC sample size =    10,000
       prob1 : 2 <= {mu} <= 4
─────────────────────────────────────────────────
             │      Mean     Std. Dev.       MCSE
─────────────┼───────────────────────────────────
       prob1 │     .9953       0.06840   .0013918
─────────────────────────────────────────────────
```

The estimated posterior probability that `{mu}` is between 2 and 4, inclusively, is drastically different compared with the results for the corresponding open interval.

◁

Stored results

`bayestest interval` stores the following in `r()`:

Scalars

`r(skip)`	number of MCMC observations to skip in the computation; every `r(skip)` observations are skipped
`r(corrlag)`	maximum autocorrelation lag
`r(corrtol)`	autocorrelation tolerance

Macros

`r(expr_#)`	#th probability expression
`r(names)`	names of probability expressions

Matrices

`r(summary)`	test results for parameters in `r(names)`

Methods and formulas

Let θ be a model parameter and $\{\theta_t\}_{t=1}^{T}$ be an MCMC sample of size T drawn from the marginal posterior distribution of θ. It is often of interest to test how likely it is that θ belongs to a particular range of values. Note that testing a point null hypothesis such as H_0: $\theta = \theta_0$ is usually of no interest for parameters with continuous posterior distributions, because the posterior probability $P(H_0)$ is 0.

To perform an open-interval test of the form

$$H_0\text{:}\ \ \theta \in (a, b) \text{ versus } H_a\text{:}\ \ \theta \notin (a, b)$$

we estimate the posterior probability of H_0 from the given MCMC sample. The `bayestest interval` command calculates the probability $P(H_0)$ based on the simulated marginal posterior distribution of θ. The estimate is given by the frequency of inclusion of θ_ts in the test interval

$$\widehat{P}(H_0) = \frac{1}{T}\sum_{t=1}^{T} 1_{\{\theta_t \in (a,b)\}} \qquad (1)$$

where $1_{\{A\}}$ is an indicator function and equals 1 if A is true and 0 otherwise.

When a model parameter θ is discrete, the following closed- and semiclosed-interval tests may be of interest in addition to open-interval tests:

$$H_0\colon\ \theta = a \text{ versus } H_a\colon\ \theta \neq a$$

$$H_0\colon\ \theta \in [a,b] \text{ versus } H_a\colon\ \theta \notin [a,b]$$

$$H_0\colon\ \theta \in [a,b) \text{ versus } H_a\colon\ \theta \notin [a,b)$$

$$H_0\colon\ \theta \in (a,b] \text{ versus } H_a\colon\ \theta \notin (a,b]$$

The corresponding probabilities are calculated as follows:

$$\widehat{P}(H_0) = \frac{1}{T}\sum_{t=1}^{T} 1_{\{\theta_t = a\}}$$

$$\widehat{P}(H_0) = \frac{1}{T}\sum_{t=1}^{T} 1_{\{\theta_t \in [a,b]\}}$$

$$\widehat{P}(H_0) = \frac{1}{T}\sum_{t=1}^{T} 1_{\{\theta_t \in [a,b)\}}$$

$$\widehat{P}(H_0) = \frac{1}{T}\sum_{t=1}^{T} 1_{\{\theta_t \in (a,b]\}}$$

The probability of an alternative hypothesis is always given by $P(H_a) = 1 - P(H_0)$.

The formulas above can be modified to accommodate joint hypotheses tests by multiplying the indicator functions of the individual hypothesis statements. For example, for a joint hypothesis $H_0\colon \theta_1 > a, \theta_2 < b$, we would replace the indicator function with $1_{\{\theta_{1t} > a\}} \times 1_{\{\theta_{2t} < b\}}$ in (1), where $\{\theta_{1t}\}_{t=1}^{T}$ and $\{\theta_{2t}\}_{t=1}^{T}$ are the corresponding MCMC samples for θ_1 and θ_2.

Reference

Huber, C. 2016. 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/.

Also see

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

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

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

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

[BAYES] **bayesstats summary** — Bayesian summary statistics

[BAYES] **bayestest model** — Hypothesis testing using model posterior probabilities

Title

bayestest model — Hypothesis testing using model posterior probabilities

Description Quick start Menu Syntax
Options Remarks and examples Stored results Methods and formulas
Also see

Description

`bayestest model` computes posterior probabilities of Bayesian models fit using the `bayesmh` command or the `bayes` prefix. These posterior probabilities can be used to test hypotheses about model parameters. The command reports marginal likelihoods, prior probabilities, and posterior probabilities for all tested models.

Quick start

Compute posterior probabilities of models corresponding to previously saved estimation results `M1` and `M2`

```
bayestest model M1 M2
```

As above, but specify prior probabilities for models

```
bayestest model M1 M2, prior(0.3 0.7)
```

Menu

Statistics > Bayesian analysis > Hypothesis testing using model posterior probabilities

Syntax

`bayestest model` [*namelist*] [, *options*]

where *namelist* is a name, a list of names, `_all`, or `*`. A name may be `.`, meaning the current (active) estimates. `_all` and `*` mean the same thing.

options	Description
Main	
`prior(`*numlist*`)`	specify prior probabilities for tested models; default is all models are equally likely
Advanced	
`marglmethod(`*method*`)`	specify marginal-likelihood approximation method; default is to use Laplace–Metropolis approximation, `lmetropolis`; rarely used

method	Description
`lmetropolis`	Laplace–Metropolis approximation; default
`hmean`	harmonic-mean approximation

Options

Main

`prior(`*numlist*`)` specifies prior probabilities for models. By default, all models are assumed to be equally likely. You may specify probabilities for all tested models, in which case the probabilities must sum to one. Alternatively, you may specify probabilities for all but the last model, in which case the sum of the specified probabilities must be less than one, and the probability for the last model is computed as one minus this sum.

Advanced

`marglmethod(`*method*`)` specifies a method for approximating the marginal likelihood. *method* is either `lmetropolis`, the default, for Laplace–Metropolis approximation or `hmean` for harmonic-mean approximation. This option is rarely used.

Remarks and examples

Remarks are presented under the following headings:

Introduction

In this entry, we describe hypothesis testing by computing model posterior probabilities, probabilities of Bayesian models given observed data. For interval hypothesis testing, see [BAYES] **bayestest interval**.

The `bayestest model` command computes posterior probabilities for specified models. The computed probabilities can be used to compare which model is more likely among considered models given observed data. You can compare models that differ only in several covariates or models with completely different regression functions, such as linear and nonlinear models. You can compare models with different outcome distributions or with different prior distributions or both. The only requirements are that the considered models have proper posterior distributions and that the same data are used to fit the models. If MCMC is used to approximate posterior distributions, convergence of MCMC should also be verified before model comparison.

The results reported by `bayestest model` are related to Bayes factors; see [BAYES] **bayesstats ic** to compute Bayes factors.

To use `bayestest model`, you must store estimation results after each Bayesian model of interest. You can use `estimates store` (see [R] **estimates store**) to store estimation results after `bayesmh` or the `bayes` prefix, as you can with other estimation commands, provided you also saved simulation results from `bayesmh` or the `bayes` prefix using the `saving()` option. See *Storing estimation results after Bayesian estimation* in [BAYES] **bayesian postestimation** for details.

Testing nested hypotheses

Consider the following Bayesian regression model for `auto.dta`,

$$\texttt{mpg} = \beta_0 + \beta_1\texttt{weight1} + \beta_2\texttt{length1} + \epsilon$$

where `weight1` and `length1` are the original `weight` and `length` variables rescaled to have similar scale as `mpg`.

We assume that errors are normally distributed: $\epsilon \sim \text{normal}(0, \sigma^2)$. We also assume a noninformative Jeffreys prior for the parameters: $(\boldsymbol{\beta}, \sigma^2) \sim 1/\sigma^2$. Suppose that we are interested in testing whether there is a relationship between mileage and weight and length of cars. We will consider four models: the mean-only model, the model with weight only, the model with length only, and the full model with both covariates.

In a frequentist setting, the four models correspond to the following hypotheses: H_0: $\beta_1 = 0$, $\beta_2 = 0$, H_0: $\beta_1 = 0$, and H_0: $\beta_2 = 0$. In a Bayesian setting, we cannot formulate point hypotheses for parameters with continuous distributions; see [BAYES] **bayestest interval** for examples. However, we can compute probabilities of how likely each of the four models is given the observed data.

Let's load auto.dta and generate rescaled versions of weight and length.

```
. use http://www.stata-press.com/data/r15/auto
(1978 Automobile Data)
. generate weight1 = weight/100
. generate length1 = length/10
```

Next, we fit the four models using bayesmh. We use the saving() option to save the simulation datasets so that we can store estimation results of each model for later use with bayestest model.

The first model we fit is the mean-only model. We store its estimation results as meanonly.

```
. set seed 14
. bayesmh mpg, likelihood(normal({var}))
> prior({mpg:}, flat) prior({var}, jeffreys)
> saving(meanonly_simdata) burnin(3500)
note: adaptation option maxiter() changed to 35
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},{var})
Priors:
  {mpg:_cons} ~ 1 (flat)
        {var} ~ jeffreys
------------------------------------------------------------------------------

Bayesian normal regression                       MCMC iterations  =     13,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      3,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         74
                                                 Acceptance rate  =      .2627
                                                 Efficiency:  min =       .105
                                                              avg =      .1064
Log marginal likelihood = -234.64617                          max =      .1078

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |  21.29355   .6768607   .020887   21.28059   20.00132   22.61904
-------------+----------------------------------------------------------------
         var |  34.80707   5.963995   .181615   34.23247    24.9129    47.6883
------------------------------------------------------------------------------

file meanonly_simdata.dta saved
. estimates store meanonly
```

To accommodate the Jeffreys prior for the parameters, we specify suboption flat within the prior() option for coefficients to request the flat prior with the density of 1 and suboption jeffreys within prior() for the variance parameter to request a Jeffreys prior. We also specify a longer burn-in period to improve convergence of MCMC samples for all examples. (Remember to use bayesgraph to check convergence of MCMC.)

We fit the second model containing only covariate `length1` and store its results as `length`:

```
. set seed 14

. bayesmh mpg length1, likelihood(normal({var}))
> prior({mpg:}, flat) prior({var}, jeffreys)
> saving(length_simdata) burnin(3500)
note: adaptation option maxiter() changed to 35
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal(xb_mpg,{var})

Priors:
  {mpg:length1 _cons} ~ 1 (flat)                                           (1)
                {var} ~ jeffreys
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.

Bayesian normal regression                       MCMC iterations  =     13,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      3,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         74
                                                 Acceptance rate  =      .2865
                                                 Efficiency:  min =      .0771
                                                              avg =     .07938
Log marginal likelihood =  -198.7678                          max =     .08286

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
     length1 | -2.069861   .1882345   .006539  -2.068094   -2.44718  -1.706264
       _cons |  60.20346   3.562119   .127411   60.20927   53.34306   67.22423
-------------+----------------------------------------------------------------
         var |  12.88852   2.273808   .081887   12.62042   9.169482   18.16685
------------------------------------------------------------------------------

file length_simdata.dta saved

. estimates store length
```

We fit the third model containing only covariate `weight1` and store its results as `weight`:

```
. set seed 14

. bayesmh mpg weight1, likelihood(normal({var}))
> prior({mpg:}, flat) prior({var}, jeffreys)
> saving(weight_simdata) burnin(3500)
note: adaptation option maxiter() changed to 35
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal(xb_mpg,{var})

Priors:
  {mpg:weight1 _cons} ~ 1 (flat)                                           (1)
                {var} ~ jeffreys
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.

Bayesian normal regression                       MCMC iterations  =     13,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      3,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         74
                                                 Acceptance rate  =      .1735
                                                 Efficiency:  min =      .0463
                                                              avg =     .06694
Log marginal likelihood = -198.20751                          max =     .07989

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
     weight1 | -.6014409   .0506121   .001791  -.6013071  -.6996976    -.50121
       _cons |  39.45934   1.574673   .057646   39.49735   36.31386   42.33547
-------------+----------------------------------------------------------------
         var |  12.13997   2.141741   .099534   11.87332   8.883221   17.14041
------------------------------------------------------------------------------

file weight_simdata.dta saved

. estimates store weight
```

Finally, we fit the last model containing both covariates and store its results as `full`:

```
. set seed 14
. bayesmh mpg weight1 length1, likelihood(normal({var}))
> prior({mpg:}, flat) prior({var}, jeffreys)
> saving(full_simdata) burnin(3500)
note: adaptation option maxiter() changed to 35
Burn-in ...
Simulation ...
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal(xb_mpg,{var})
Priors:
  {mpg:weight1 length1 _cons} ~ 1 (flat)                                  (1)
                        {var} ~ jeffreys
------------------------------------------------------------------------------
(1) Parameters are elements of the linear form xb_mpg.
Bayesian normal regression                       MCMC iterations  =     13,500
Random-walk Metropolis-Hastings sampling         Burn-in          =      3,500
                                                 MCMC sample size =     10,000
                                                 Number of obs    =         74
                                                 Acceptance rate  =      .2323
                                                 Efficiency:  min =     .05455
                                                              avg =     .06647
Log marginal likelihood = -196.86195                          max =     .08085
------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
     weight1 | -.3977027   .1580411   .005558  -.401646  -.6965175  -.0721332
     length1 | -.7599159   .5546754   .021944 -.7502182  -1.907818   .3106868
       _cons |   47.5913   6.132597   .262563   47.5656   35.89593   60.18002
-------------+----------------------------------------------------------------
         var |  11.81753    1.96315    .07608  11.59273   8.729182   16.14065
------------------------------------------------------------------------------
file full_simdata.dta saved
. estimates store full
```

▷ Example 1: Computing posterior probabilities of models

We now use `bayestest model` to compute posterior probabilities of the four models.

```
. bayestest model meanonly length weight full
Bayesian model tests
------------------------------------------
             |    log(ML)      P(M)   P(M|y)
-------------+----------------------------
    meanonly |  -234.6462    0.2500   0.0000
      length |  -198.7678    0.2500   0.1055
      weight |  -198.2075    0.2500   0.1848
        full |  -196.8619    0.2500   0.7097
------------------------------------------
Note: Marginal likelihood (ML) is computed using
      Laplace-Metropolis approximation.
```

The mean-only model is very unlikely compared with other models. The length and weight models are somewhat likely with the respective posterior probabilities of 0.11 and 0.18, and the full model has the highest posterior probability of 0.71.

◁

▷ Example 2: Specifying prior probabilities of models

If we have some prior knowledge about each of the models, we can use the `prior()` option to specify prior probabilities for each model. For example, suppose that we have prior knowledge that the weight model is much more likely than the full model so that the prior probabilities are 0.1 for the mean-only model and the length model, 0.6 for the weight model, and only 0.2 for the full model.

```
. bayestest model meanonly length weight full, prior(0.1 0.1 0.6 0.2)
Bayesian model tests

─────────────────────────────────────────────
             │   log(ML)        P(M)    P(M|y)
─────────────┼───────────────────────────────
    meanonly │ -234.6462      0.1000    0.0000
      length │ -198.7678      0.1000    0.0401
      weight │ -198.2075      0.6000    0.4210
        full │ -196.8619      0.2000    0.5389
─────────────────────────────────────────────
Note: Marginal likelihood (ML) is computed using
      Laplace-Metropolis approximation.
```

Under the specified prior, posterior probabilities of the weight and full models are now more similar: 0.42 and 0.54, respectively, but the full model is still preferable.

The above is equivalent to the following prior specification:

```
. bayestest model meanonly length weight full, prior(0.1 0.1 0.6)
  (output omitted)
```

◁

Using our results, we conclude that `mpg` is related to both `weight` and `length` and would proceed with the full model.

After your analysis, remember to erase the saved simulation datasets you no longer need. For example, we erase all of them by typing

```
. erase meanonly_simdata.dta
. erase weight_simdata.dta
. erase length_simdata.dta
. erase full_simdata.dta
```

Comparing models with different priors

In the previous section, we used `bayestest model` to compare nested hypotheses about which covariates to include in the regression function. We can use `bayestest model` to compare models with not only different covariates but also different outcome distributions and priors for parameters.

We continue our analysis of `auto.dta`, but for simplicity, we now consider the mean-only model for `mpg`. Let's compare models with two slightly different informative priors. We use an informative normal–inverse-gamma prior for both models,

$$
\begin{aligned}
(\beta_0|\sigma^2) &\sim N(\mu_0, \sigma^2/n_0) \\
\sigma^2 &\sim \text{InvGamma}(\nu_0/2, \nu_0\sigma_0^2/2)
\end{aligned}
$$

with $\mu_0 = 25$, $n_0 = 10$, and $\sigma_0^2 = 30$, but we consider two different values for the degrees of freedom: $\nu_0 = 5$ and $\nu_0 = 1$.

We use `bayesmh` to fit our models. Following the formulas, we specify a `normal()` prior for the constant `{mpg:_cons}` (mean parameter) and an inverse-gamma prior `igamma()` for the variance parameter `{var}`. We specify an expression for the variance of the normal prior distribution in parentheses.

We fit the first model with $\nu_0 = 5$ and store its estimation results as `informative1`.

```
. set seed 14

. bayesmh mpg, likelihood(normal({var}))
> prior({mpg:}, normal(25,{var}/10))
> prior({var}, igamma(2.5,75)) saving(inf1_simdata)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},{var})

Priors:
  {mpg:_cons} ~ normal(25,{var}/10)
        {var} ~ igamma(2.5,75)
------------------------------------------------------------------------------

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  =      .2548
                                                 Efficiency:  min =     .09065
                                                              avg =      .1049
Log marginal likelihood = -238.55856                          max =      .1192

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |  21.71853   .6592655   .019091   21.69554   20.44644   23.04896
-------------+----------------------------------------------------------------
         var |  35.47405   5.823372   .193417   34.72454   25.84419     48.228
------------------------------------------------------------------------------

file inf1_simdata.dta saved

. estimates store informative1
```

We fit the second model with $\nu_0 = 1$ and store its estimation results as `informative2`.

```
. set seed 14

. bayesmh mpg, likelihood(normal({var}))
> prior({mpg:}, normal(25,{var}/10))
> prior({var}, igamma(0.5,15)) saving(inf2_simdata)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},{var})

Priors:
  {mpg:_cons} ~ normal(25,{var}/10)
        {var} ~ igamma(0.5,15)
------------------------------------------------------------------------------

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  =      .2261
                                                 Efficiency:  min =      .0941
                                                              avg =       .109
Log marginal likelihood =  -239.4049                          max =      .1239

------------------------------------------------------------------------------
             |                                                Equal-tailed
             |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
mpg          |
       _cons |   21.7175   .6539814   .021319    21.7295   20.47311   23.02638
-------------+----------------------------------------------------------------
         var |  35.89504   6.288571   .178665   35.17056   25.86084   50.21624
------------------------------------------------------------------------------

file inf2_simdata.dta saved

. estimates store informative2
```

▷ Example 3: Comparing models with informative priors

We now use `bayestest model` to compare our models with two different informative priors.

```
. bayestest model informative1 informative2

Bayesian model tests

----------------------------------------------
             |   log(ML)       P(M)     P(M|y)
-------------+--------------------------------
informative1 | -238.5586     0.5000     0.6998
informative2 | -239.4049     0.5000     0.3002
----------------------------------------------
Note: Marginal likelihood (ML) is computed using
      Laplace-Metropolis approximation.
```

Assuming that both models are equally likely a priori, the posterior probability of the `informative1` stored results, 0.70, is much higher than the probability of the `informative2` stored results, 0.3.

◁

▷ Example 4: Comparing a model with noninformative prior

A note of caution regarding comparing models with informative and noninformative priors—models with noninformative priors will often win because they are typically in most agreement with the observed data. For models with noninformative priors, most of the information about parameters is contained in a likelihood. As such, any model with an informative prior that is not in perfect agreement with the data will not fit data as well as a model with a noninformative prior.

For example, let's fit our constant-only model using a noninformative Jeffreys prior for the parameters.

```
. set seed 14

. bayesmh mpg, likelihood(normal({var}))
> prior({mpg:}, flat) prior({var}, jeffreys)
> saving(jeffreys_simdata)
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
------------------------------------------------------------------------------

file jeffreys_simdata.dta saved

. estimates store jeffreys
```

Let's now compare this model with our two informative models.

```
. bayestest model informative1 informative2 jeffreys

Bayesian model tests

---------------------------------------------
             |    log(ML)       P(M)   P(M|y)
-------------+-------------------------------
informative1 |  -238.5586     0.3333   0.0194
informative2 |  -239.4049     0.3333   0.0083
    jeffreys |  -234.6450     0.3333   0.9723
---------------------------------------------
Note: Marginal likelihood (ML) is computed using
      Laplace-Metropolis approximation.
```

The posterior probability of the Jeffreys model is 0.97.

◁

Finally, at the end of our analysis, we erase all the simulation datasets we no longer need. We erase all of them by typing

```
. erase inf1_simdata.dta
. erase inf2_simdata.dta
. erase jeffreys_simdata.dta
```

Stored results

`bayestest model` stores the following in `r()`:

Macros

`r(names)`	names of estimation results used
`r(marglmethod)`	method for approximating marginal likelihood: `lmetropolis` or `hmean`

Matrices

`r(test)`	test results for parameters in `r(names)`

Methods and formulas

Suppose we have r models M_j for $j = 1, \ldots, r$ with prior probabilities $P(M_j)$ such that $\sum_{j=1}^{r} p(M_j) = 1$. Then, posterior probability for model J is

$$P(M_j|\mathbf{y}) = \frac{P(\mathbf{y}|M_j)P(M_j)}{P(\mathbf{y})}$$

where $P(\mathbf{y}|M_j) = m_j(y)$ is the marginal likelihood of M_j with respect to $\mathbf{y}$, and $P(\mathbf{y}) = \sum_{j=1}^{r} P(\mathbf{y}|M_j)P(M_j)$. See *Methods and formulas* in [BAYES] **bayesmh** for details about computing marginal likelihood.

Also see

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

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

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

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

[BAYES] **bayesstats ic** — Bayesian information criteria and Bayes factors

[BAYES] **bayesstats summary** — Bayesian summary statistics

[BAYES] **bayestest interval** — Interval hypothesis testing

Title

set clevel — Set default credible level

Description Syntax Option Remarks and examples Also see

Description

`set clevel` specifies the default credible level for credible intervals for all Bayesian commands (see [BAYES] **bayesian commands**) that report credible intervals. The initial value is 95, meaning 95% credible intervals.

Syntax

```
set clevel # [, permanently]
```

# is any number between 10.00 and 99.99 and may be specified with at most two digits after the decimal point.

Option

`permanently` specifies that in addition to making the change right now, the `clevel` setting be remembered and become the default setting when you invoke Stata.

Remarks and examples

To change the level of credible intervals reported by a particular command, you need not reset the default credible level. All commands that report credible intervals have a `clevel(#)` option. When you do not specify the option, the credible intervals are calculated for the default level set by `set clevel` or for 95% if you have not reset `set clevel`.

▷ Example 1

We use the bayesmh command to obtain the credible interval for the mean of mpg:

```
. use http://www.stata-press.com/data/r15/auto
(1978 Automobile Data)

. set seed 14

. bayesmh mpg, likelihood(normal(30)) prior({mpg:_cons}, flat)
Burn-in ...
Simulation ...

Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},30)

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  =      .4195
Log marginal likelihood = -234.09275             Efficiency       =      .2378

------------------------------------------------------------------------------
             |                                                Equal-tailed
         mpg |      Mean   Std. Dev.     MCSE     Median  [95% Cred. Interval]
-------------+----------------------------------------------------------------
       _cons |  21.30364   .6429995   .013186   21.30381   20.03481    22.5555
------------------------------------------------------------------------------
```

To obtain 90% credible intervals, we would type

```
. bayesmh, clevel(90)

Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},30)

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  =      .4195
Log marginal likelihood = -234.09275             Efficiency       =      .2378

------------------------------------------------------------------------------
             |                                                Equal-tailed
         mpg |      Mean   Std. Dev.     MCSE     Median  [90% Cred. Interval]
-------------+----------------------------------------------------------------
       _cons |  21.30364   .6429995   .013186   21.30381   20.24172   22.35158
------------------------------------------------------------------------------
```

or we could type

```
. set clevel 90
. bayesmh
Model summary
------------------------------------------------------------------------------
Likelihood:
  mpg ~ normal({mpg:_cons},30)
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  =      .4195
Log marginal likelihood = -234.09275             Efficiency       =      .2378

------------------------------------------------------------------------------
             |                                                Equal-tailed
         mpg |      Mean   Std. Dev.     MCSE     Median  [90% Cred. Interval]
-------------+----------------------------------------------------------------
       _cons |  21.30364   .6429995   .013186   21.30381   20.24172   22.35158
------------------------------------------------------------------------------
```

If we opt for the second alternative, the next time that we fit a model, 90% credible intervals will be reported. If we wanted 95% credible intervals, we could specify `clevel(95)` on the estimation command, or we could reset the default by typing `set clevel 95`.

The current setting of `clevel()` is stored as the c-class value `c(clevel)`; see [P] **creturn**.

◁

Also see

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

[BAYES] **bayesmh** — Bayesian models using Metropolis–Hastings algorithm

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

[R] **query** — Display system parameters

[P] **creturn** — Return c-class values

Title

bayes: betareg — Bayesian beta regression

Description | Quick start | Menu | Syntax
Remarks and examples | Stored results | Methods and formulas | Also see

Description

`bayes: betareg` fits a Bayesian beta regression to a fractional outcome whose values are greater than 0 and less than 1; see [BAYES] **bayes** and [R] **betareg** for details.

Quick start

Bayesian beta regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: betareg y x1 x2
```

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

```
bayes, normalprior(10): betareg y x1 x2
```

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)): betareg y x1 x2
```

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

```
bayes, saving(simdata) rseed(123): betareg y x1 x2
```

Specify 20,000 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): betareg y x1 x2
```

In the above, request that the 90% 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] **betareg**.

Menu

Statistics > Fractional outcomes > Bayesian beta regression

Syntax

`bayes` [, *bayesopts*] `:` `betareg` *depvar* *indepvars* [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
`noconstant`	suppress constant term
`scale(`*varlist* [, `noconstant`]`)`	specify independent variables for scale
`link(`*linkname*`)`	specify link function for the conditional mean; default is `link(logit)`
`slink(`*slinkname*`)`	specify link function for the conditional scale; default is `slink(log)`
Reporting	
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

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

`fweight`s are allowed; see **[U] 11.1.6 weight**.

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

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

bayesopts	Description
Priors	
*`normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`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	
*`blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [, *blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
*`noblocking`	do not block parameters by default
Initialization	
`initial(`*initspec*`)`	initial values for model parameters
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
*`noisily`	display output from the estimation command during initialization

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*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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 {scale:*varlist*} for the scale 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] **betareg**.

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

Stored results

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

Methods and formulas

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

Also see

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

[R] **betareg** — Beta 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**

Title

bayes: binreg — Bayesian generalized linear models: Extensions to the binomial family

Description | Quick start | Menu | Syntax
Remarks and examples | Stored results | Methods and formulas | Also see

Description

`bayes: binreg` fits a Bayesian binomial regression to a binary outcome, assuming different link functions; see [BAYES] **bayes** and [R] **binreg** for details.

Quick start

Bayesian binomial regression of `y` on `x1` and `x2`, using the default logit link and using default normal priors for regression coefficients

```
bayes: binreg y x1 x2
```

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

```
bayes, normalprior(10): binreg y x1 x2
```

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)): binreg y x1 x2
```

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

```
bayes, saving(simdata) rseed(123): binreg y x1 x2
```

Specify 20,000 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): binreg y x1 x2
```

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

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

Display odds ratios instead of coefficients

```
bayes: binreg y x1 x2, or
```

Use the log link and report risk ratios

```
bayes: binreg y x1 x2, rr
```

Display coefficients instead of risk ratios

```
bayes, coefficients
```

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

Menu

Statistics > Generalized linear models > Bayesian GLM for the binomial family

Syntax

bayes [, *bayesopts*] : binreg *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
noconstant	suppress constant term
or	use logit link and report odds ratios
rr	use log link and report risk ratios
hr	use log-complement link and report health ratios
rd	use identity link and report risk differences
n(# | *varname*)	use # or *varname* for number of trials
exposure(*varname*)	include ln(*varname*) in model with coefficient constrained to 1
offset(*varname*)	include *varname* in model with coefficient constrained to 1
collinear	keep collinear variables
mu(*varname*)	use *varname* as the initial estimate for the mean of *depvar*
init(*varname*)	synonym for mu(*varname*)
Reporting	
coefficients	report nonexponentiated coefficients
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

depvar 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: binreg, level() is equivalent to bayes, clevel(): binreg.

For a detailed description of *options*, see *Options* in [R] **binreg**. binreg's option ml is implied with bayes: binreg.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref*[, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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
coefficients	report nonexponentiated coefficients
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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] **binreg**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Logistic regression with perfect predictors* in [BAYES] **bayes**.

Stored results

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

Methods and formulas

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

Also see

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

[R] **binreg** — Generalized linear models: Extensions to the binomial family

[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**

Title

bayes: biprobit — Bayesian bivariate probit regression

Description

`bayes: biprobit` fits a Bayesian bivariate probit regression to two binary outcomes; see [BAYES] **bayes** and [R] **biprobit** for details.

Quick start

Bayesian bivariate probit regression of `y1` and `y2` on `x1` and `x2`, using default normal priors for regression coefficients and atanh-transformed correlation

```
bayes: biprobit y1 y2 x1 x2
```

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

```
bayes, normalprior(10): biprobit y1 y2 x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept of the dependent variable `y2`

```
bayes, prior({y2: x1 x2}, uniform(-10,10)) ///
prior({y2:_cons}, normal(0,10)): biprobit y1 y2 x1 x2
```

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

```
bayes, saving(simdata) rseed(123): biprobit y1 y2 x1 x2
```

Specify 20,000 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): biprobit y1 y2 x1 x2
```

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

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

Bayesian seemingly unrelated bivariate probit regression using default priors

```
bayes: biprobit (y1 = x1 x2 x3) (y2 = x1 x2)
```

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

Menu

Statistics > Binary outcomes > Bayesian regression > Bivariate probit regression

Statistics > Binary outcomes > Bayesian regression > Seemingly unrelated bivariate probit

Syntax

Bayesian bivariate probit regression

`bayes` [, *bayesopts*] `:` `biprobit` *depvar*$_1$ *depvar*$_2$ [*indepvars*] [*if*] [*in*] [*weight*]
[, *options*]

Bayesian seemingly unrelated bivariate probit regression

`bayes` [, *bayesopts*] `:` `biprobit` *equation*$_1$ *equation*$_2$ [*if*] [*in*] [*weight*] [, *options*]

where *equation*$_1$ and *equation*$_2$ are specified as

`(` [*eqname*`:`] *depvar* [`=`] [*indepvars*] [, `noconstant` `offset(`*varname*`)`] `)`

options	Description
Model	
`noconstant`	suppress constant term
`offset1(`*varname*`)`	offset variable for first equation
`offset2(`*varname*`)`	offset variable for second equation
`collinear`	keep collinear variables
Reporting	
display_options	control spacing, line width, and base and empty cells
`level(`*#*`)`	set credible level; default is `level(95)`

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

depvar$_1$, *depvar*$_2$, *depvar*, and *indepvars* may contain time-series operators; see **[U] 11.4.4 Time-series varlists**.

`fweight`s are allowed; see **[U] 11.1.6 weight**.

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

For a detailed description of *options*, see *Options* in **[R] biprobit**. Options `noconstant`, `offset1()`, and `offset2()` are not allowed with seemingly unrelated bivariate probit regression.

bayesopts	Description
Priors	
*`normalprior(`*#*`)`	specify standard deviation of default normal priors for regression coefficients and atanh-transformed correlation; default is `normalprior(100)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref*[, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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

Model parameters are regression coefficients {*depvar*$_1$:*indepvars*} and {*depvar*$_2$:*indepvars*} and atanh-transformed correlation {athrho}. 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] **biprobit**.

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

Stored results

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

Methods and formulas

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

Also see

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

[R] **biprobit** — Bivariate probit 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**

Title

bayes: clogit — Bayesian conditional logistic regression

Description	Quick start	Menu	Syntax
Remarks and examples	Stored results	Methods and formulas	Also see

Description

`bayes: clogit` fits a Bayesian conditional logistic regression to matched case–control data; see [BAYES] **bayes** and [R] **clogit** for details.

Quick start

Bayesian conditional logistic regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: clogit y x1 x2, group(id)
```

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

```
bayes, normalprior(10): clogit y x1 x2, group(id)
```

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)): clogit y x1 x2, group(id)
```

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

```
bayes, saving(simdata) rseed(123): clogit y x1 x2, group(id)
```

Specify 20,000 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): clogit y x1 x2, group(id)
```

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

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

Display odds ratios instead of coefficients

```
bayes: clogit y x1 x2, group(id) or
```

Display odds ratios on replay

```
bayes, or
```

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

Menu

Statistics > Categorical outcomes > Bayesian conditional logistic regression

Syntax

bayes [, *bayesopts*] : clogit *depvar* [*indepvars*] [*if*] [*in*] [*weight*] ,

group(*varname*) [*options*]

options	Description
Model	
*group(*varname*)	matched group variable
offset(*varname*)	include *varname* in model with coefficient constrained to 1
collinear	keep collinear variables
Reporting	
or	report odds ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

*group(*varname*) is required.

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

fweights are allowed; see [U] **11.1.6 weight**. fweights are interpreted to apply to groups as a whole, not to individual observations. See *Use of weights* in [R] **clogit**.

bayes: clogit, level() is equivalent to bayes, clevel(): clogit.

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

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref*[, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization	
`initial(`*initspec*`)`	initial values for model parameters
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
*`noisily`	display output from the estimation command during initialization
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
*`or`	report odds ratios
`eform`[`(`*string*`)`]	report exponentiated coefficients and, optionally, label as *string*
`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
[`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
`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)`

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

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

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

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

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] **clogit**.

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

Stored results

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

Methods and formulas

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

Also see

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

[R] **clogit** — Conditional (fixed-effects) logistic 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**

Title

bayes: cloglog — Bayesian complementary log-log regression

Description	Quick start	Menu	Syntax
Remarks and examples	Stored results	Methods and formulas	Also see

Description

`bayes: cloglog` fits a Bayesian complementary log-log regression to a binary outcome; see [BAYES] **bayes** and [R] **cloglog** for details.

Quick start

Bayesian complementary log-log regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: cloglog y x1 x2
```

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

```
bayes, normalprior(10): cloglog y x1 x2
```

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)): cloglog y x1 x2
```

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

```
bayes, saving(simdata) rseed(123): cloglog y x1 x2
```

Specify 20,000 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): cloglog y x1 x2
```

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

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

Display results as exponentiated coefficients

```
bayes: cloglog y x1 x2, eform
```

Display exponentiated coefficients on replay

```
bayes, eform
```

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

Menu

Statistics > Binary outcomes > Bayesian regression > Complementary log-log regression

Syntax

```
bayes [, bayesopts] : cloglog depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
asis	retain perfect predictor variables
collinear	keep collinear variables
Reporting	
eform	report exponentiated coefficients
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

depvar 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: cloglog, level() is equivalent to bayes, clevel(): cloglog.

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

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

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*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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] **cloglog**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Logistic regression with perfect predictors* in [BAYES] **bayes**.

Stored results

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

Methods and formulas

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

Also see

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

[R] **cloglog** — Complementary log-log 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**

Title

bayes: fracreg — Bayesian fractional response regression

Description Quick start Menu Syntax
Remarks and examples Stored results Methods and formulas Also see

Description

`bayes: fracreg` fits a Bayesian fractional response regression to a fractional outcome whose values are greater than or equal to 0 and less than or equal to 1; see [BAYES] **bayes** and [R] **fracreg** for details.

Quick start

Bayesian fractional probit regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: fracreg probit y x1 x2
```

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

```
bayes, normalprior(10): fracreg probit y x1 x2
```

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)): fracreg probit y x1 x2
```

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

```
bayes, saving(simdata) rseed(123): fracreg probit y x1 x2
```

Specify 20,000 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): fracreg probit y x1 x2
```

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

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

Fit a fractional logistic regression and display results as odds ratios

```
bayes: fracreg logit y x1 x2, or
```

Display odds ratios on replay

```
bayes, or
```

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

Menu

Statistics > Fractional outcomes > Bayesian fractional regression

Syntax

Syntax for fractional probit regression

bayes [, *bayesopts*] : fracreg probit *depvar* [*indepvars*] [*if*] [*in*] [*weight*]
[, *options*]

Syntax for fractional logistic regression

bayes [, *bayesopts*] : fracreg logit *depvar* [*indepvars*] [*if*] [*in*] [*weight*]
[, *options*]

Syntax for fractional heteroskedastic probit regression

bayes [, *bayesopts*] : fracreg probit *depvar* [*indepvars*] [*if*] [*in*] [*weight*],
het(*varlist*[, offset(*varname*$_o$)]) [*options*]

options	Description
Model	
noconstant	suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
collinear	keep collinear variables
* het(*varlist*[, offset(*varname*$_o$)])	independent variables to model the variance and possible offset variable with fracreg probit
Reporting	
or	report odds ratios; only valid with fracreg logit
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

* het() may be used only with fracreg probit to compute fractional heteroskedastic probit regression.
indepvars may contain factor variables; see **[U] 11.4.3 Factor variables**.
depvar 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: fracreg, level() is equivalent to bayes, clevel(): fracreg.
For a detailed description of *options*, see *Options* in [R] **fracreg**.

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation

Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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
*or	report odds ratio; only valid with fracreg logit
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
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
[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
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)

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

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

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

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

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

Model parameters are regression coefficients {*depvar*:*indepvars*} and, if option `het()` is specified, regression coefficients {`lnsigma`:*varlist*} for the log-standard deviation 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] **fracreg**.

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

Stored results

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

Methods and formulas

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

Also see

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

[R] **fracreg** — Fractional response 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**

Title

bayes: glm — Bayesian generalized linear models

Description | Quick start | Menu | Syntax
Remarks and examples | Stored results | Methods and formulas | Also see

Description

`bayes: glm` fits a Bayesian generalized linear model to outcomes of different types such as continuous, binary, count, and so on; see [BAYES] **bayes** and [R] **glm** for details.

Quick start

Bayesian generalized linear model of `y` on `x1` and `x2`, using the Gaussian family and log link and using default normal priors for regression coefficients

```
bayes: glm y x1 x2, family(gaussian) link(log)
```

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

```
bayes, normalprior(10): glm y x1 x2, family(gaussian) link(log)
```

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)):  ///
glm y x1 x2, family(gaussian) link(log)
```

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

```
bayes, saving(simdata) rseed(123):  ///
glm y x1 x2, family(gaussian) link(log)
```

Specify 20,000 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):  ///
glm y x1 x2, family(gaussian) link(log)
```

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

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

Fit a logit model and display results as odds ratios

```
bayes: glm z x1 x2, family(binomial) eform
```

Display odds ratios on replay

```
bayes, eform
```

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

Menu

Statistics > Generalized linear models > Bayesian generalized linear models (GLM)

Syntax

bayes [, *bayesopts*] : glm *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
family(*familyname*)	distribution of *depvar*; default is family(gaussian)
link(*linkname*)	link function; default is canonical link for family() specified
Model 2	
noconstant	suppress constant term
exposure(*varname*)	include ln(*varname*) in model with coefficient constrained to 1
offset(*varname*)	include *varname* in model with coefficient constrained to 1
collinear	keep collinear variables
asis	retain perfect predictor variables
mu(*varname*)	use *varname* as the initial estimate for the mean of *depvar*
init(*varname*)	synonym for mu(*varname*)
Reporting	
eform	report exponentiated coefficients
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

depvar 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: glm, level() is equivalent to bayes, clevel(): glm.

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

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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] **glm**.

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

bayes: glm does not estimate the scale parameter but uses a fixed value as provided by the glm command. If you want to fit a GLM and estimate the scale parameter, use bayes: meglm without specifying random effects.

Stored results

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

Methods and formulas

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

Also see

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

[R] **glm** — Generalized linear models

[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**

Title

bayes: gnbreg — Bayesian generalized negative binomial regression

Description Quick start Menu Syntax
Remarks and examples Stored results Methods and formulas Also see

Description

bayes: gnbreg fits a Bayesian generalized negative binomial regression to a nonnegative count outcome; see [BAYES] **bayes** and [R] **nbreg** for details.

Quick start

Bayesian generalized negative binomial regression of y on x1 and x2, using z to model the log-overdispersion and using default normal priors for regression coefficients and log-overdispersion parameter

```
bayes: gnbreg y x1 x2, lnalpha(z)
```

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

```
bayes, normalprior(10): gnbreg y x1 x2, lnalpha(z)
```

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)): gnbreg y x1 x2, lnalpha(z)
```

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

```
bayes, saving(simdata) rseed(123): gnbreg y x1 x2, lnalpha(z)
```

Specify 20,000 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): gnbreg y x1 x2, lnalpha(z)
```

In the above, request that the 90% 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: gnbreg y x1 x2, lnalpha(z) irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

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

Menu

Statistics > Count outcomes > Bayesian regression > Generalized negative binomial regression

Syntax

`bayes` [, *bayesopts*] : `gnbreg` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
`noconstant`	suppress constant term
`lnalpha(`*varlist*`)`	dispersion model variables
`exposure(`*varname*$_e$`)`	include ln(*varname*$_e$) in model with coefficient constrained to 1
`offset(`*varname*$_o$`)`	include *varname*$_o$ in model with coefficient constrained to 1
`collinear`	keep collinear variables
Reporting	
`irr`	report incidence-rate ratios
display_options	control spacing, line width, and base and empty cells
`level(`*#*`)`	set credible level; default is `level(95)`

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

`fweight`s are allowed; see **[U] 11.1.6 weight**.

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

For a detailed description of *options*, see *Options for gnbreg* in **[R] nbreg**.

bayesopts	Description
Priors	
* `normalprior(`*#*`)`	specify standard deviation of default normal priors for regression coefficients and log-overdispersion parameter; default is `normalprior(100)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`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	
* `blocksize(`*#*`)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [, *blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
* `noblocking`	do not block parameters by default
Initialization	
`initial(`*initspec*`)`	initial values for model parameters
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
* `noisily`	display output from the estimation command during initialization

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
* irr	report incidence-rate ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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 {lnalpha:*varlist*} for the log-dispersion 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] **nbreg**.

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

Stored results

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

Methods and formulas

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

Also see

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

[R] **nbreg** — Negative binomial 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**

Title

bayes: heckman — Bayesian Heckman selection model

Description

`bayes: heckman` fits a Bayesian sample-selection linear regression to a partially observed continuous outcome; see [BAYES] **bayes** and [R] **heckman** for details.

Quick start

Bayesian Heckman model of `y` on `x1` and `x2`, using `z1` and `z2` to model selection and using default normal priors for regression coefficients, log-standard-deviation, and atanh-correlation

```
bayes: heckman y x1 x2, select(z1 z2)
```

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

```
bayes, normalprior(10): heckman y x1 x2, select(z1 z2)
```

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)): heckman y x1 x2, select(z1 z2)
```

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

```
bayes, saving(simdata) rseed(123):, ///
heckman y x1 x2, select(z1 z2)
```

Specify 20,000 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):, ///
heckman y x1 x2, select(z1 z2)
```

In the above, request that the 90% 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] **heckman**.

Menu

Statistics > Linear models and related > Bayesian regression > Heckman selection model

Syntax

bayes [, *bayesopts*] : heckman *depvar* [*indepvars*] [*if*] [*in*] [*weight*] ,

select([*depvar*$_s$ =] *varlist*$_s$ [, noconstant offset(*varname*$_o$)]) [*options*]

options	Description
Model	
*select()	specify selection equation: dependent and independent variables; whether to have constant term and offset variable
noconstant	suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
collinear	keep collinear variables
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

*select( ) is required.

The full specification is select([*depvar*$_s$ =] *varlist*$_s$ [, noconstant offset(*varname*$_o$)]).

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

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

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

bayes: heckman, level() is equivalent to bayes, clevel(): heckman.

For a detailed description of *options*, see *Options for Heckman selection model (ML)* and *Options for Heckman selection model (two-step)* in [R] **heckman**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients, log-standard-deviation, and atanh-correlation; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization	
`initial(`*initspec*`)`	initial values for model parameters
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
* `noisily`	display output from the estimation command during initialization
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*
`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
[`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
`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)`

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

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

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

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

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 `{select:`*varlist_s*`}` for the selection equation, atanh-transformed correlation `{athrho}`, and log-standard deviation `{lnsigma}`. 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] **heckman**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Heckman selection model* in [BAYES] **bayes**.

Stored results

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

Methods and formulas

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

Also see

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

[R] **heckman** — Heckman selection 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**

Title

bayes: heckoprobit — Bayesian ordered probit model with sample selection

Description	Quick start	Menu	Syntax
Remarks and examples	Stored results	Methods and formulas	Also see

Description

bayes: heckoprobit fits a Bayesian sample-selection ordered probit regression to a partially observed ordinal outcome; see [BAYES] **bayes** and [R] **heckoprobit** for details.

Quick start

Bayesian sample-selection ordered probit regression of y on x1 and x2, using z1 and z2 to model selection and using default normal priors for regression coefficients and atanh-correlation and flat priors for cutpoints

```
bayes: heckoprobit y x1 x2, select(z)
```

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

```
bayes, normalprior(10): heckoprobit y x1 x2, select(z)
```

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)): heckoprobit y x1 x2, select(z)
```

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

```
bayes, saving(simdata) rseed(123):, ///
heckoprobit y x1 x2, select(z)
```

Specify 20,000 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):, ///
heckoprobit y x1 x2, select(z)
```

In the above, request that the 90% 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] **heckoprobit**.

Menu

Statistics > Ordinal outcomes > Bayesian regression > Ordered probit regression with sample selection

Syntax

> bayes [, *bayesopts*] : heckoprobit *depvar* *indepvars* [*if*] [*in*] [*weight*] ,
>
> select([$depvar_s$ =] $varlist_s$ [, noconstant offset($varname_o$)]) [*options*]

options	Description
Model	
*select()	specify selection equation: dependent and independent variables; whether to have constant term and offset variable
offset(*varname*)	include *varname* in model with coefficient constrained to 1
collinear	keep collinear variables
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

*select() is required.

The full specification is select([$depvar_s$ =] $varlist_s$ [, noconstant offset($varname_o$)]).

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

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

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

bayes: heckoprobit, level() is equivalent to bayes, clevel(): heckoprobit.

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

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients and atanh-correlation; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization	
`initial(`*initspec*`)`	initial values for model parameters
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
* `noisily`	display output from the estimation command during initialization
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*
`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
[`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
`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)`

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

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

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

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

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 `{select:`*varlist_s*`}` for the selection equation, atanh-transformed correlation `{athrho}`, and cutpoints `{cut1}`, `{cut2}`, and so on. Use the `dryrun` option to see the definitions of model parameters prior to estimation.

Flat priors, `flat`, are used by default for cutpoints.

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] **heckoprobit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Heckman selection model* in [BAYES] **bayes**.

Stored results

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

Methods and formulas

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

Also see

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

[R] **heckoprobit** — Ordered probit model with sample selection

[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**

Title

bayes: heckprobit — Bayesian probit model with sample selection

Description

`bayes: heckprobit` fits a Bayesian sample-selection probit regression to a partially observed binary outcome; see [BAYES] **bayes** and [R] **heckprobit** for details.

Quick start

Bayesian sample-selection probit regression of `y` on `x1` and `x2`, using `z1` and `z2` to model selection and using default normal priors for regression coefficients and atanh-correlation

```
bayes: heckprobit y x1 x2, select(z1 z2)
```

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

```
bayes, normalprior(10): heckprobit y x1 x2, select(z1 z2)
```

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)): heckprobit y x1 x2, select(z1 z2)
```

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

```
bayes, saving(simdata) rseed(123):, ///
heckprobit y x1 x2, select(z1 z2)
```

Specify 20,000 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):, ///
heckprobit y x1 x2, select(z1 z2)
```

In the above, request that the 90% 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] **heckprobit**.

Menu

Statistics > Binary outcomes > Bayesian regression > Probit model with sample selection

Syntax

bayes [, *bayesopts*] : heckprobit *depvar* *indepvars* [*if*] [*in*] [*weight*] ,

select([*depvar*$_s$ =] *varlist*$_s$ [, noconstant offset(*varname*$_o$)]) [*options*]

options	Description
Model	
*select()	specify selection equation: dependent and independent variables; whether to have constant term and offset variable
noconstant	suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
collinear	keep collinear variables
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

*select( ) is required.

The full specification is select([*depvar*$_s$ =] *varlist*$_s$ [, noconstant offset(*varname*$_o$)]).

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

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

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

bayes: heckprobit, level() is equivalent to bayes, clevel(): heckprobit.

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

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients and atanh-correlation; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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 {select:*varlist_s*} for the selection equation, and atanh-transformed correlation {athrho}. 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] **heckprobit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Heckman selection model* in [BAYES] **bayes**.

Stored results

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

Methods and formulas

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

Also see

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

[R] **heckprobit** — Probit model with sample selection

[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**

Title

bayes: hetprobit — Bayesian heteroskedastic probit regression

Description Quick start Menu Syntax
Remarks and examples Stored results Methods and formulas Also see

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 `x1` and `x2`, using `z1` to model the variance and using default normal priors for regression coefficients and log-variance coefficients

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

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

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

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(z)
```

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

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

Specify 20,000 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(z)
```

In the above, request that the 90% 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**.

Menu

Statistics > Binary outcomes > Bayesian regression > Heteroskedastic probit regression

Syntax

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

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

*het() is required. The full specification is het(*varlist* [, offset(*varname*$_o$)]).

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

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

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

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients and log-variance coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
* blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref*[, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
* noblocking	do not block parameters by default

Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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 {lnsigma2:*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] **bayesmh**.

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**

Title

bayes: hetregress — Bayesian heteroskedastic linear regression

Description Quick start Menu Syntax
Remarks and examples Stored results Methods and formulas Also see

Description

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

Quick start

Bayesian heteroskedastic linear regression of y on x1 and x2, using z1 to model the variance and using default normal priors for regression coefficients and log-variance coefficients

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

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

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

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

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

Specify 20,000 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):  ///
hetregress y x1 x2, het(z1)
```

In the above, request that the 90% 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] **hetregress**.

Menu

Statistics > Linear models and related > Bayesian regression > Heteroskedastic linear regression

Syntax

bayes [, *bayesopts*] : hetregress *depvar* [*indepvars*] [*if*] [*in*] [*weight*]
[, *options*]

options	Description
Model	
het(*varlist*)	independent variables to model the variance
noconstant	suppress constant term
collinear	keep collinear variables
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

depvar 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: hetregress, level() is equivalent to bayes, clevel(): hetregress.

For a detailed description of *options*, see *Options for maximum likelihood estimation* and *Options for two-step GLS estimation* in [R] **hetregress**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients and log-variance coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

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*
`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
[`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
`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)`

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

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

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

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

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 `{lnsigma2:`*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] **hetregress**.

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

Stored results

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

Methods and formulas

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

Also see

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

[R] **hetregress** — Heteroskedastic linear 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**

Title

bayes: intreg — Bayesian interval regression

Description Quick start Menu Syntax
Remarks and examples Stored results Methods and formulas Also see

Description

`bayes: intreg` fits a Bayesian interval regression to a continuous, interval-measured outcome; see [BAYES] **bayes** and [R] **intreg** for details.

Quick start

Bayesian interval regression of `y_lower` and `y_upper` on `x1` and `x2`, using default normal priors for regression coefficients and log-variance

```
bayes: intreg y_lower y_upper x1 x2
```

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

```
bayes, normalprior(10): intreg y_lower y_upper x1 x2
```

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

```
bayes, prior({y_lower: x1 x2}, uniform(-10,10)) ///
prior({y_lower:_cons}, normal(0,10)): intreg y_lower y_upper x1 x2
```

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

```
bayes, saving(simdata) rseed(123):  ///
intreg y_lower y_upper x1 x2
```

Specify 20,000 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):  ///
intreg y_lower y_upper x1 x2
```

In the above, request that the 90% 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] **intreg**.

Menu

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

Syntax

bayes [, *bayesopts*] : intreg *depvar*$_1$ *depvar*$_2$ [*indepvars*] [*if*] [*in*] [*weight*]
[, *options*]

options	Description
Model	
noconstant	suppress constant term
het(*varlist*[, noconstant])	independent variables to model the variance; use noconstant to suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
collinear	keep collinear variables
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

depvar$_1$, *depvar*$_2$, *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: intreg, level() is equivalent to bayes, clevel(): intreg.

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

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients and log-variance; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref*[, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

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*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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

Model parameters are regression coefficients {*depvar*$_1$:*indepvars*} and log-standard deviation {lnsigma} or, if option het(*varlist*) is specified, coefficients {lnsigma:*varlist*} of the log-standard-deviation 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] **intreg**.

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

Stored results

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

Methods and formulas

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

Also see

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

[R] **intreg** — Interval 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**

Title

bayes: logistic — Bayesian logistic regression, reporting odds ratios

Description	Quick start	Menu	Syntax
Remarks and examples	Stored results	Methods and formulas	Also see

Description

`bayes: logistic` fits a Bayesian logistic regression to a binary outcome; see [BAYES] **bayes** and [R] **logistic** for details.

Quick start

Bayesian logistic regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: logistic y x1 x2
```

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

```
bayes, normalprior(10): logistic y x1 x2
```

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)): logistic y x1 x2
```

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

```
bayes, saving(simdata) rseed(123): logistic y x1 x2
```

Specify 20,000 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): logistic y x1 x2
```

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

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

Display coefficients instead of odds ratios

```
bayes: logistic y x1 x2, coef
```

Display coefficients on replay

```
bayes, coef
```

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

Menu

Statistics > Binary outcomes > Bayesian regression > Logistic regression

Syntax

bayes [, *bayesopts*] : logistic *depvar* *indepvars* [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
noconstant	suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
asis	retain perfect predictor variables
collinear	keep collinear variables
Reporting	
coef	report estimated coefficients
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

depvar 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: logistic, level() is equivalent to bayes, clevel(): logistic.

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

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

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
* coef	report estimated coefficients
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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] **logistic**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Logistic regression with perfect predictors* in [BAYES] **bayes**.

Stored results

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

Methods and formulas

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

Also see

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

[R] **logistic** — Logistic regression, reporting odds ratios

[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**

Title

bayes: logit — Bayesian logistic regression, reporting coefficients

Description | Quick start | Menu | Syntax
Remarks and examples | Stored results | Methods and formulas | Also see

Description

`bayes: logit` fits a Bayesian logistic regression to a binary outcome; see [BAYES] **bayes** and [R] **logit** for details.

Quick start

Bayesian logistic regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: logit y x1 x2
```

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

```
bayes, normalprior(10): logit y x1 x2
```

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)): logit y x1 x2
```

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

```
bayes, saving(simdata) rseed(123): logit y x1 x2
```

Specify 20,000 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): logit y x1 x2
```

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

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

Display odds ratios instead of coefficients

```
bayes: logit y x1 x2, or
```

Display odds ratios on replay

```
bayes, or
```

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

Menu

Statistics > Binary outcomes > Bayesian regression > Logistic regression

Syntax

bayes [, *bayesopts*] : logit *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
noconstant	suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
asis	retain perfect predictor variables
collinear	keep collinear variables
Reporting	
or	report odds ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

depvar 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: logit, level() is equivalent to bayes, clevel(): logit.

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

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

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
* `or`	report odds ratios
`eform[(`*string*`)]`	report exponentiated coefficients and, optionally, label as *string*
`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
`[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
`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)`

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

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

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

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

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] **logit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Logistic regression with perfect predictors* in [BAYES] **bayes**.

Stored results

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

Methods and formulas

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

Also see

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

[R] **logit** — Logistic regression, reporting coefficients

[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**

Title

bayes: mecloglog — Bayesian multilevel complementary log-log regression

Description | Quick start | Menu | Syntax
Remarks and examples | Stored results | Methods and formulas | Also see

Description

bayes: mecloglog fits a Bayesian multilevel complementary log-log regression to a binary outcome; see [BAYES] **bayes** and [ME] **mecloglog** for details.

Quick start

Bayesian two-level complementary log-log regression of y on x1 and x2 with random intercepts by id, using default normal priors for regression coefficients and default inverse-gamma prior for the variance of random intercepts

```
bayes: mecloglog y x1 x2 || id:
```

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

```
bayes, normalprior(10): mecloglog y x1 x2 || id:
```

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)): mecloglog y x1 x2 || id:
```

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

```
bayes, saving(simdata) rseed(123): mecloglog y x1 x2 || id:
```

Specify 20,000 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): mecloglog y x1 x2 || id:
```

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

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

Display results as exponentiated coefficients

```
bayes: mecloglog y x1 x2 || id: , eform
```

Display exponentiated coefficients on replay

```
bayes, eform
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **mecloglog**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Complementary log-log regression

Syntax

```
bayes [, bayesopts] : mecloglog depvar fe_equation
    [|| re_equation] [|| re_equation ...] [, options]
```

where the syntax of *fe_equation* is

```
[indepvars] [if] [in] [weight] [, fe_options]
```

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

```
levelvar: [varlist] [, re_options]
```

for random effects among the values of a factor variable

```
levelvar: R.varname
```

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`noconstant`	suppress constant term from the fixed-effects equation
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`asis`	retain perfect predictor variables

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `identity`, and `unstructured` supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Model	
`binomial(`*varname* | *#*`)`	set binomial trials if data are in binomial form
`collinear`	keep collinear variables
Reporting	
`eform`	report exponentiated coefficients
`notable`	suppress coefficient table
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(`*#*`)`	set credible level; default is `level(95)`

indepvars 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: mecloglog, level() is equivalent to bayes, clevel(): mecloglog.

For a detailed description of *options*, see *Options* in **[ME] mecloglog**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
*igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance components; default is igammaprior(0.01 0.01)
*iwishartprior(# [...])	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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
restubs(*restub1 restub2* ...)	specify stubs for random-effects parameters for all levels
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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
`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
`nomesummary`	suppress multilevel-structure summary
[`no`]`dots`	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is `dots`
`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
`melabel`	display estimation table using the same row labels as `mecloglog`
`nogroup`	suppress table summarizing groups
`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)`

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

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

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

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

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

Model parameters are regression coefficients `{`*depvar*`:`*indepvars*`}`, random effects `{`*rename*`}`, and either variance components `{`*rename*`:sigma2}` or, if option `covariance(unstructured)` is specified, matrix parameter `{`*restub*`:Sigma,matrix}`; see *Likelihood model* in [BAYES] **bayes** for how *rename*s and *restub* are defined. 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 [ME] **mecloglog**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. For multilevel examples, see *Multilevel models* in [BAYES] **bayes**. Also see *Crossed-effects model* in [BAYES] **bayes**.

Stored results

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

Methods and formulas

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

Also see

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

[ME] **mecloglog** — Multilevel mixed-effects complementary log-log 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**

Title

bayes: meglm — Bayesian multilevel generalized linear model

Description | Quick start | Menu | Syntax
Remarks and examples | Stored results | Methods and formulas | Also see

Description

`bayes: meglm` fits a Bayesian multilevel generalized linear model to outcomes of different types such as continuous, binary, count, and so on; see [BAYES] **bayes** and [ME] **meglm** for details.

Quick start

Bayesian two-level generalized linear model of `y` on `x1` and `x2` with random intercepts by `id`, using the Gaussian family and log link and using default normal priors for regression coefficients and default inverse-gamma prior for the variance of random intercepts

```
bayes: meglm y x1 x2 || id:, family(gaussian) link(log)
```

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

```
bayes, normalprior(10): meglm y x1 x2 || id:, family(gaussian) link(log)
```

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)): meglm y x1 x2 || id:, family(gaussian) link(
```

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

```
bayes, saving(simdata) rseed(123):  ///
meglm y x1 x2 || id:, family(gaussian) link(log)
```

Specify 20,000 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):  ///
meglm y x1 x2 || id:, family(gaussian) link(log)
```

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

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

Fit a logit model and display results as odds ratios

```
bayes: meglm z x1 x2 || id:, family(binomial) eform
```

Display odds ratios on replay

```
bayes, eform
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **meglm**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Generalized linear models (GLM)

Syntax

bayes [, *bayesopts*] : `meglm` *depvar* *fe_equation*
  [|| *re_equation*] [|| *re_equation* . . .] [, *options*]

where the syntax of *fe_equation* is

  [*indepvars*] [*if*] [*in*] [*weight*] [, *fe_options*]

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

  levelvar: [*varlist*] [, *re_options*]

for random effects among the values of a factor variable

  levelvar: `R.`*varname*

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`noconstant`	suppress constant term from the fixed-effects equation
`exposure(`*varname*$_e$`)`	include ln(*varname*$_e$) in model with coefficient constrained to 1
`offset(`*varname*$_o$`)`	include *varname*$_o$ in model with coefficient constrained to 1
`asis`	retain perfect predictor variables

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `identity`, and `unstructured` supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Model	
family(*family*)	distribution of *depvar*; default is family(gaussian)
link(*link*)	link function; default varies per family
collinear	keep collinear variables
Reporting	
eform	report exponentiated coefficients
irr	report incidence-rate ratios
or	report odds ratios
notable	suppress coefficient table
noheader	suppress output header
nogroup	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

indepvars 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: meglm, level() is equivalent to bayes, clevel(): meglm.

For a detailed description of *options*, see *Options* in [ME] **meglm**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
*igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance components; default is igammaprior(0.01 0.01)
*iwishartprior(# [...])	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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
restubs(*restub1 restub2* ...)	specify stubs for random-effects parameters for all levels
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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
*irr	report incidence-rate ratios
*or	report odds ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal likelihood
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
nomesummary	suppress multilevel-structure summary
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
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
melabel	display estimation table using the same row labels as meglm
nogroup	suppress table summarizing groups
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)

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

Options prior() and block() can be repeated.

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

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

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

Model parameters are regression coefficients {*depvar*:*indepvars*}, parameters as described in *Additional model parameters*, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *renames* and *restub* are defined. 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 [ME] **meglm**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**. For multilevel examples, see *Multilevel models* in [BAYES] **bayes**. Also see *Crossed-effects model* in [BAYES] **bayes**.

Additional model parameters

In addition to regression coefficients {*depvar*:*indepvars*}, bayes: meglm defines extra parameters that depend on the chosen family; see table 1 below.

Table 1. Additional model parameters defined by bayes: meglm

Family	Parameter	Model parameter	Default prior
Gaussian	Error variance	{e.*depvar*:sigma2}	InvGamma$(0.01, 0.01)$
Bernoulli/Binomial	None	None	None
Ordinal	Cutpoints	{cut1}, {cut2}, ...	Flat
Poisson	None	None	None
Negative binomial	Log-overdispersion	{lnalpha} (mean disp.)	$N(0, 10000)$
		{lndelta} (constant disp.)	$N(0, 10000)$
Gamma	Log-scale	{lnscale}	$N(0, 10000)$

Use the dryrun option with the bayes prefix to see the definitions of model parameters prior to estimation.

Stored results

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

Methods and formulas

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

Also see

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

[ME] **meglm** — Multilevel mixed-effects generalized linear 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**

Title

bayes: meintreg — Bayesian multilevel interval regression

Description	Quick start	Menu	Syntax
Remarks and examples	Stored results	Methods and formulas	Also see

Description

`bayes: meintreg` fits a Bayesian multilevel interval regression to a continuous, interval-measured outcome; see [BAYES] **bayes** and [ME] **meintreg** for details.

Quick start

Bayesian two-level interval regression of `y_lower` and `y_upper` on `x1` and `x2` with random intercepts by `id`, using default normal priors for regression coefficients and default inverse-gamma priors for the error variance and for the variance of random intercepts

```
bayes: meintreg y_lower y_upper x1 x2 || id:
```

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

```
bayes, normalprior(10): meintreg y_lower y_upper x1 x2 || id:
```

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

```
bayes, prior({y_lower: x1 x2}, uniform(-10,10)) ///
prior({y_lower:_cons}, normal(0,10)):  ///
meintreg y_lower y_upper x1 x2 || id:
```

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

```
bayes, saving(simdata) rseed(123):  ///
meintreg y_lower y_upper x1 x2 || id:
```

Specify 20,000 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):  ///
meintreg y_lower y_upper x1 x2 || id:
```

In the above, request that the 90% 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 [ME] **meintreg**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Interval regression

Syntax

bayes [, *bayesopts*] : meintreg *depvar*$_{\text{lower}}$ *depvar*$_{\text{upper}}$ *fe_equation*
  [|| *re_equation*] [|| *re_equation* . . .] [, *options*]

where the syntax of *fe_equation* is

[*indepvars*] [*if*] [*in*] [*weight*] [, *fe_options*]

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

levelvar: [*varlist*] [, *re_options*]

for random effects among the values of a factor variable

levelvar: R.*varname*

levelvar either is a variable identifying the group structure for the random effects at that level or is _all, representing one group comprising all observations.

fe_options	Description
Model	
noconstant	suppress constant term from the fixed-effects equation
offset(*varname*)	include *varname* in model with coefficient constrained to 1

re_options	Description
Model	
covariance(*vartype*)	variance–covariance structure of the random effects; only structures independent, identity, and unstructured supported
noconstant	suppress constant term from the random-effects equation

options	Description
Model	
collinear	keep collinear variables
Reporting	
notable	suppress coefficient table
noheader	suppress output header
nogroup	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
level(*#*)	set credible level; default is level(95)

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

depvar$_{\text{lower}}$, *depvar*$_{\text{upper}}$, *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: meintreg, level() is equivalent to bayes, clevel(): meintreg.

For a detailed description of *options*, see *Options* in [ME] **meintreg**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
*igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance components; default is igammaprior(0.01 0.01)
*iwishartprior(# [...])	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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
restubs(*restub1 restub2* ...)	specify stubs for random-effects parameters for all levels
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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
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
nomesummary	suppress multilevel-structure summary
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
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
melabel	display estimation table using the same row labels as meintreg
nogroup	suppress table summarizing groups
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)

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

Options prior() and block() can be repeated.

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

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

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

Model parameters are regression coefficients {*depvar*$_{\text{lower}}$:*indepvars*}, error variance {e.*depvar*$_{\text{lower}}$:sigma2}, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *rename*s and *restub* are defined. 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 [ME] **meintreg**.

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

Stored results

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

Methods and formulas

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

Also see

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

[ME] **meintreg** — Multilevel mixed-effects interval 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**

Title

bayes: melogit — Bayesian multilevel logistic regression

Description | Quick start | Menu | Syntax
Remarks and examples | Stored results | Methods and formulas | Also see

Description

bayes: melogit fits a Bayesian multilevel logistic regression to a binary outcome; see [BAYES] **bayes** and [ME] **melogit** for details.

Quick start

Bayesian two-level logistic regression of y on x1 and x2 with random intercepts by id, using default normal priors for regression coefficients and default inverse-gamma prior for the variance of random intercepts

```
bayes: melogit y x1 x2 || id:
```

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

```
bayes, normalprior(10): melogit y x1 x2 || id:
```

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)): melogit y x1 x2 || id:
```

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

```
bayes, saving(simdata) rseed(123): melogit y x1 x2 || id:
```

Specify 20,000 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): melogit y x1 x2 || id:
```

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

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

Display odds ratios instead of coefficients

```
bayes: melogit y x1 x2 || id: , or
```

Display odds ratios on replay

```
bayes, or
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **melogit**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Logistic regression

Syntax

`bayes` [`,` *bayesopts*] `: melogit` *depvar* *fe_equation*
    [`||` *re_equation*] [`||` *re_equation* ...] [`,` *options*]

where the syntax of *fe_equation* is

[*indepvars*] [*if*] [*in*] [*weight*] [`,` *fe_options*]

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

levelvar`:` [*varlist*] [`,` *re_options*]

for random effects among the values of a factor variable

levelvar`: R.`*varname*

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`noconstant`	suppress constant term from the fixed-effects equation
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`asis`	retain perfect predictor variables

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `identity`, and `unstructured` supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Model	
`binomial(`*varname* | *#*`)`	set binomial trials if data are in binomial form
`collinear`	keep collinear variables
Reporting	
`or`	report odds ratios
`notable`	suppress coefficient table
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(`*#*`)`	set credible level; default is `level(95)`

indepvars 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**.

`fweight`s are allowed; see [U] **11.1.6 weight**.

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

For a detailed description of *options*, see *Options* in [ME] **melogit**.

bayesopts	Description
Priors	
*`normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
*`igammaprior(# #)`	specify shape and scale of default inverse-gamma prior for variance components; default is `igammaprior(0.01 0.01)`
*`iwishartprior(#` [...]`)`	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`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
`restubs(`*restub1 restub2* ...`)`	specify stubs for random-effects parameters for all levels
Blocking	
*`blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [, *blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
*`noblocking`	do not block parameters by default
Initialization	
`initial(`*initspec*`)`	initial values for model parameters
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
*`noisily`	display output from the estimation command during initialization
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
* or	report odds ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal likelihood
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
nomesummary	suppress multilevel-structure summary
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
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
melabel	display estimation table using the same row labels as melogit
nogroup	suppress table summarizing groups
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)

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

Options prior() and block() can be repeated.

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

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

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

Model parameters are regression coefficients {*depvar*:*indepvars*}, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *renames* and *restub* are defined. 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 [ME] **melogit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. For multilevel examples, see *Multilevel models* in [BAYES] **bayes**.

Stored results

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

Methods and formulas

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

Also see

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

[ME] **melogit** — Multilevel mixed-effects logistic 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**

Title

bayes: menbreg — Bayesian multilevel negative binomial regression

Description | Quick start | Menu | Syntax
Remarks and examples | Stored results | Methods and formulas | Also see

Description

`bayes: menbreg` fits a Bayesian multilevel negative binomial regression to a nonnegative count outcome; see [BAYES] **bayes** and [ME] **menbreg** for details.

Quick start

Bayesian two-level negative binomial regression of `y` on `x1` and `x2` with random intercepts by `id`, using default normal priors for regression coefficients and log-overdispersion parameter and default inverse-gamma prior for the variance of random intercepts

```
bayes: menbreg y x1 x2 || id:
```

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

```
bayes, normalprior(10): menbreg y x1 x2 || id:
```

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)): menbreg y x1 x2 || id:
```

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

```
bayes, saving(simdata) rseed(123): menbreg y x1 x2 || id:
```

Specify 20,000 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): menbreg y x1 x2 || id:
```

In the above, request that the 90% 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: menbreg y x1 x2 || id: , irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **menbreg**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Negative binomial regression

Syntax

```
bayes [, bayesopts] : menbreg depvar fe_equation
    [|| re_equation] [|| re_equation ...] [, options]
```

where the syntax of *fe_equation* is

```
        [indepvars] [if] [in] [weight] [, fe_options]
```

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

```
        levelvar: [varlist] [, re_options]
```

for random effects among the values of a factor variable

```
        levelvar: R.varname
```

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`noconstant`	suppress constant term from the fixed-effects equation
`exposure(`*varname*$_e$`)`	include ln(*varname*$_e$) in model with coefficient constrained to 1
`offset(`*varname*$_o$`)`	include *varname*$_o$ in model with coefficient constrained to 1

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `identity`, and `unstructured` supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Model	
`dispersion(`*dispersion*`)`	parameterization of the conditional overdispersion; *dispersion* may be `mean` (default) or `constant`
`collinear`	keep collinear variables
Reporting	
`irr`	report incidence-rate ratios
`notable`	suppress coefficient table
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

indepvars 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.

`fweight`s are allowed; see [U] 11.1.6 weight.

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

For a detailed description of *options*, see *Options* in [ME] menbreg.

bayesopts	Description
Priors	
*`normalprior(#)`	specify standard deviation of default normal priors for regression coefficients and log-overdispersion parameter; default is `normalprior(100)`
*`igammaprior(# #)`	specify shape and scale of default inverse-gamma prior for variance components; default is `igammaprior(0.01 0.01)`
*`iwishartprior(#` [...]`)`	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`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
`restubs(`*restub1 restub2* ...`)`	specify stubs for random-effects parameters for all levels
Blocking	
*`blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [, *blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
*`noblocking`	do not block parameters by default
Initialization	
`initial(`*initspec*`)`	initial values for model parameters
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
*`noisily`	display output from the estimation command during initialization
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
*irr	report incidence-rate ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal likelihood
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
nomesummary	suppress multilevel-structure summary
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
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
melabel	display estimation table using the same row labels as menbreg
nogroup	suppress table summarizing groups
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)

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

Options prior() and block() can be repeated.

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

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

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

Model parameters are regression coefficients {*depvar*:*indepvars*}, log-overdispersion parameter {lnalpha} with mean dispersion or {lndelta} with constant dispersion, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *renames* and *restub* are defined. 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 [ME] **menbreg**.

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

Stored results

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

Methods and formulas

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

Also see

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

[ME] **menbreg** — Multilevel mixed-effects negative binomial 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**

Title

bayes: meologit — Bayesian multilevel ordered logistic regression

Description | Quick start | Menu | Syntax
Remarks and examples | Stored results | Methods and formulas | Also see

Description

`bayes: meologit` fits a Bayesian multilevel ordered logistic regression to an ordinal outcome; see [BAYES] **bayes** and [ME] **meologit** for details.

Quick start

Bayesian two-level ordered logistic regression of `y` on `x1` and `x2` with random intercepts by `id`, using default normal priors for regression coefficients, flat priors for cutpoints, and default inverse-gamma prior for the variance of random intercepts

```
bayes: meologit y x1 x2 || id:
```

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

```
bayes, normalprior(10): meologit y x1 x2 || id:
```

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)): meologit y x1 x2 || id:
```

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

```
bayes, saving(simdata) rseed(123): meologit y x1 x2 || id:
```

Specify 20,000 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): meologit y x1 x2 || id:
```

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

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

Display odds ratios instead of coefficients

```
bayes: meologit y x1 x2 || id: , or
```

Display odds ratios on replay

```
bayes, or
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **meologit**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Ordered logistic regression

Syntax

`bayes` [, *bayesopts*] `:` `meologit` *depvar* *fe_equation*
  [`||` *re_equation*] [`||` *re_equation* . . .] [, *options*]

where the syntax of *fe_equation* is

  [*indepvars*] [*if*] [*in*] [*weight*] [, *fe_options*]

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

  levelvar: [*varlist*] [, *re_options*]

for random effects among the values of a factor variable

  levelvar: `R.`*varname*

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `identity`, and `unstructured` supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Model	
`collinear`	keep collinear variables
Reporting	
`or`	report odds ratios
`notable`	suppress coefficient table
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(`*#*`)`	set credible level; default is `level(95)`

indepvars 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**.

`fweight`s are allowed; see **[U] 11.1.6 weight**.

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

For a detailed description of *options*, see *Options* in **[ME] meologit**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
*igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance components; default is igammaprior(0.01 0.01)
*iwishartprior(# [...])	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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
restubs(*restub1 restub2* ...)	specify stubs for random-effects parameters for all levels
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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
* or	report coefficients as odds ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal likelihood
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
nomesummary	suppress multilevel-structure summary
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
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
melabel	display estimation table using the same row labels as meologit
nogroup	suppress table summarizing groups
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)

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

Options prior() and block() can be repeated.

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

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

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

Model parameters are regression coefficients {*depvar*:*indepvars*}, cutpoints {cut1}, {cut2}, and so on, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *renames* and *restub* are defined. Use the dryrun option to see the definitions of model parameters prior to estimation.

Flat priors, flat, are used by default for cutpoints.

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 [ME] **meologit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. For multilevel examples, see *Multilevel models* in [BAYES] **bayes**.

Stored results

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

Methods and formulas

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

Also see

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

[ME] **meologit** — Multilevel mixed-effects ordered logistic 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**

Title

bayes: meoprobit — Bayesian multilevel ordered probit regression

Description　　Quick start　　Menu　　Syntax
Remarks and examples　　Stored results　　Methods and formulas　　Also see

Description

`bayes: meoprobit` fits a Bayesian multilevel ordered probit regression to an ordinal outcome; see [BAYES] **bayes** and [ME] **meoprobit** for details.

Quick start

Bayesian two-level ordered probit regression of `y` on `x1` and `x2` with random intercepts by `id`, using default normal priors for regression coefficients, flat priors for cutpoints, and default inverse-gamma prior for the variance of random intercepts

```
bayes: meoprobit y x1 x2 || id:
```

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

```
bayes, normalprior(10): meoprobit y x1 x2 || id:
```

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)): meoprobit y x1 x2 || id:
```

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

```
bayes, saving(simdata) rseed(123): meoprobit y x1 x2 || id:
```

Specify 20,000 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): meoprobit y x1 x2 || id:
```

In the above, request that the 90% 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 [ME] **meoprobit**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Ordered probit regression

Syntax

bayes [, *bayesopts*] : meoprobit *depvar* *fe_equation*
  [|| *re_equation*] [|| *re_equation* ...] [, *options*]

where the syntax of *fe_equation* is

[*indepvars*] [*if*] [*in*] [*weight*] [, *fe_options*]

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

levelvar: [*varlist*] [, *re_options*]

for random effects among the values of a factor variable

levelvar: R.*varname*

levelvar either is a variable identifying the group structure for the random effects at that level or is _all, representing one group comprising all observations.

fe_options	Description
Model	
offset(*varname*)	include *varname* in model with coefficient constrained to 1

re_options	Description
Model	
covariance(*vartype*)	variance–covariance structure of the random effects; only structures independent, identity, and unstructured supported
noconstant	suppress constant term from the random-effects equation

options	Description
Model	
collinear	keep collinear variables
Reporting	
notable	suppress coefficient table
noheader	suppress output header
nogroup	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
level(*#*)	set credible level; default is level(95)

indepvars 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: meoprobit, level() is equivalent to bayes, clevel(): meoprobit.

For a detailed description of *options*, see *Options* in **[ME] meoprobit**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
*igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance components; default is igammaprior(0.01 0.01)
*iwishartprior(# [...])	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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
restubs(*restub1 restub2* ...)	specify stubs for random-effects parameters for all levels
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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
`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
`nomesummary`	suppress multilevel-structure summary
[`no`]`dots`	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is `dots`
`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
`melabel`	display estimation table using the same row labels as `meoprobit`
`nogroup`	suppress table summarizing groups
`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)`

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

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

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

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

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

Model parameters are regression coefficients {*depvar*:*indepvars*}, cutpoints `{cut1}`, `{cut2}`, and so on, random effects {*rename*}, and either variance components {*rename*`:sigma2`} or, if option `covariance(unstructured)` is specified, matrix parameter {*restub*`:Sigma,matrix`}; see *Likelihood model* in [BAYES] **bayes** for how *renames* and *restub* are defined. Use the `dryrun` option to see the definitions of model parameters prior to estimation.

Flat priors, `flat`, are used by default for cutpoints.

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 [ME] **meoprobit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. For multilevel examples, see *Multilevel models* in [BAYES] **bayes**.

Stored results

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

Methods and formulas

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

Also see

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

[ME] **meoprobit** — Multilevel mixed-effects ordered probit 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**

Title

bayes: mepoisson — Bayesian multilevel Poisson regression

Description Quick start Menu Syntax
Remarks and examples Stored results Methods and formulas Also see

Description

`bayes: mepoisson` fits a Bayesian multilevel Poisson regression to a nonnegative count outcome; see [BAYES] **bayes** and [ME] **mepoisson** for details.

Quick start

Bayesian two-level Poisson regression of `y` on `x1` and `x2` with random intercepts by `id`, using default normal priors for regression coefficients and default inverse-gamma prior for the variance of random intercepts

```
bayes: mepoisson y x1 x2 || id:
```

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

```
bayes, normalprior(10): mepoisson y x1 x2 || id:
```

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)): mepoisson y x1 x2 || id:
```

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

```
bayes, saving(simdata) rseed(123): mepoisson y x1 x2 || id:
```

Specify 20,000 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): mepoisson y x1 x2 || id:
```

In the above, request that the 90% 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: mepoisson y x1 x2 || id: , irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **mepoisson**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Poisson regression

Syntax

`bayes` [, *bayesopts*] : `mepoisson` *depvar* *fe_equation*
  [|| *re_equation*] [|| *re_equation* ...] [, *options*]

where the syntax of *fe_equation* is

  [*indepvars*] [*if*] [*in*] [*weight*] [, *fe_options*]

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

  levelvar: [*varlist*] [, *re_options*]

for random effects among the values of a factor variable

  levelvar: `R.`*varname*

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`noconstant`	suppress constant term from the fixed-effects equation
`exposure(`*varname*$_e$`)`	include ln(*varname*$_e$) in model with coefficient constrained to 1
`offset(`*varname*$_o$`)`	include *varname*$_o$ in model with coefficient constrained to 1

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `identity`, and `unstructured` supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Model	
`collinear`	keep collinear variables
Reporting	
`irr`	report incidence-rate ratios
`notable`	suppress coefficient table
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(`*#*`)`	set credible level; default is `level(95)`

indepvars 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**.

`fweight`s are allowed; see **[U] 11.1.6 weight**.

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

For a detailed description of *options*, see *Options* in **[ME] mepoisson**.

bayesopts	Description
Priors	
*`normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
*`igammaprior(# #)`	specify shape and scale of default inverse-gamma prior for variance components; default is `igammaprior(0.01 0.01)`
*`iwishartprior(#` [...]`)`	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`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
`restubs(`*restub1 restub2* ...`)`	specify stubs for random-effects parameters for all levels
Blocking	
*`blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [`,` *blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
*`noblocking`	do not block parameters by default
Initialization	
`initial(`*initspec*`)`	initial values for model parameters
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
*`noisily`	display output from the estimation command during initialization
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
*irr	report incidence-rate ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
remargl	compute log marginal likelihood
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
nomesummary	suppress multilevel-structure summary
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
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
melabel	display estimation table using the same row labels as mepoisson
nogroup	suppress table summarizing groups
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)

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

Options prior() and block() can be repeated.

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

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

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

Model parameters are regression coefficients {*depvar*:*indepvars*}, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *rename*s and *restub* are defined. 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 [ME] **mepoisson**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. For multilevel examples, see *Multilevel models* in [BAYES] **bayes**.

Stored results

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

Methods and formulas

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

Also see

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

[ME] **mepoisson** — Multilevel mixed-effects 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**

Title

bayes: meprobit — Bayesian multilevel probit regression

Description Quick start Menu Syntax
Remarks and examples Stored results Methods and formulas Also see

Description

`bayes: meprobit` fits a Bayesian multilevel probit regression to a binary outcome; see [BAYES] **bayes** and [ME] **meprobit** for details.

Quick start

Bayesian two-level probit regression of `y` on `x1` and `x2` with random intercepts by `id`, using default normal priors for regression coefficients and default inverse-gamma prior for the variance of random intercepts

```
bayes: meprobit y x1 x2 || id:
```

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

```
bayes, normalprior(10): meprobit y x1 x2 || id:
```

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)): meprobit y x1 x2 || id:
```

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

```
bayes, saving(simdata) rseed(123): meprobit y x1 x2 || id:
```

Specify 20,000 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): meprobit y x1 x2 || id:
```

In the above, request that the 90% 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 [ME] **meprobit**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Probit regression

Syntax

bayes [, *bayesopts*] : meprobit *depvar* *fe_equation*
  [|| *re_equation*] [|| *re_equation* ...] [, *options*]

where the syntax of *fe_equation* is

[*indepvars*] [*if*] [*in*] [*weight*] [, *fe_options*]

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

levelvar: [*varlist*] [, *re_options*]

for random effects among the values of a factor variable

levelvar: R.*varname*

levelvar either is a variable identifying the group structure for the random effects at that level or is _all, representing one group comprising all observations.

fe_options	Description
Model	
noconstant	suppress constant term from the fixed-effects equation
offset(*varname*)	include *varname* in model with coefficient constrained to 1
asis	retain perfect predictor variables

re_options	Description
Model	
covariance(*vartype*)	variance–covariance structure of the random effects; only structures independent, identity, and unstructured supported
noconstant	suppress constant term from the random-effects equation

options	Description
Model	
binomial(*varname* | *#*)	set binomial trials if data are in binomial form
collinear	keep collinear variables
Reporting	
notable	suppress coefficient table
noheader	suppress output header
nogroup	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
level(*#*)	set credible level; default is level(95)

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

For a detailed description of *options*, see *Options* in [ME] **meprobit**.

bayesopts	Description
Priors	
*`normalprior(`#`)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
*`igammaprior(`# #`)`	specify shape and scale of default inverse-gamma prior for variance components; default is `igammaprior(0.01 0.01)`
*`iwishartprior(`# [...]`)`	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`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
`restubs(`*restub1 restub2* ...`)`	specify stubs for random-effects parameters for all levels
Blocking	
*`blocksize(`#`)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [, *blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
*`noblocking`	do not block parameters by default
Initialization	
`initial(`*initspec*`)`	initial values for model parameters
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
*`noisily`	display output from the estimation command during initialization
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
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
nomesummary	suppress multilevel-structure summary
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
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
melabel	display estimation table using the same row labels as meprobit
nogroup	suppress table summarizing groups
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)

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

Options prior() and block() can be repeated.

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

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

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

Model parameters are regression coefficients {*depvar*:*indepvars*}, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *renames* and *restub* are defined. 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 [ME] **meprobit**.

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

Stored results

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

Methods and formulas

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

Also see

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

[ME] **meprobit** — Multilevel mixed-effects probit 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**

Title

bayes: mestreg — Bayesian multilevel parametric survival model

Description   Quick start   Menu   Syntax
Remarks and examples   Stored results   Methods and formulas   Also see

Description

`bayes: mestreg` fits a Bayesian multilevel parametric survival model to a survival-time outcome; see [BAYES] **bayes** and [ME] **mestreg** for details.

Quick start

Bayesian two-level Weibull survival model of `stset` survival-time outcome on `x1` and `x2` with random intercepts by `id`, using default normal priors for regression coefficients and log-ancillary parameters and default inverse-gamma prior for the variance of random intercepts

```
bayes: mestreg x1 x2 || id:, distribution(weibull)
```

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

```
bayes, normalprior(10): mestreg x1 x2 || id:, distribution(weibull)
```

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

```
bayes, prior({_t: x1 x2}, uniform(-10,10)) ///
prior({_t:_cons}, normal(0,10)):  ///
mestreg x1 x2 || id:, distribution(weibull)
```

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

```
bayes, saving(simdata) rseed(123):  ///
mestreg x1 x2 || id:, distribution(weibull)
```

Specify 20,000 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):  ///
mestreg x1 x2 || id:, distribution(weibull)
```

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

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

Use accelerated failure-time metric instead of proportional-hazards parameterization, and display time ratios instead of coefficients

```
bayes, tratio: mestreg x1 x2 || id:, distribution(weibull) time
```

Display time ratios on replay

```
bayes, tratio
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ME] **mestreg**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Parametric survival regression

Syntax

bayes [, *bayesopts*] : mestreg *fe_equation*
  [|| *re_equation*] [|| *re_equation* ...] , distribution(*distname*) [*options*]

where the syntax of *fe_equation* is

[*indepvars*] [*if*] [*in*] [*weight*] [, *fe_options*]

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

levelvar: [*varlist*] [, *re_options*]

for random effects among the values of a factor variable

levelvar: R.*varname*

levelvar either is a variable identifying the group structure for the random effects at that level or is _all, representing one group comprising all observations.

fe_options	Description
Model	
noconstant	suppress constant term from the fixed-effects equation
offset(*varname*)	include *varname* in model with coefficient constrained to 1

re_options	Description
Model	
covariance(*vartype*)	variance–covariance structure of the random effects; only structures independent, identity, and unstructured supported
noconstant	suppress constant term from the random-effects equation

options	Description
Model	
* distribution(*distname*)	specify survival distribution
time	use accelerated failure-time metric
collinear	keep collinear variables
Reporting	
nohr	do not report hazard ratios
tratio	report time ratios
noshow	do not show st setting information
notable	suppress coefficient table
noheader	suppress output header
nogroup	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

*distribution(*distname*) is required.

You must stset your data before using bayes: mestreg; see [ST] **stset**.

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

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

bayes: mestreg, level() is equivalent to bayes, clevel(): mestreg.

For a detailed description of *options*, see *Options* in [ME] **mestreg**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients and log-ancillary parameters; default is normalprior(100)
*igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance components; default is igammaprior(0.01 0.01)
*iwishartprior(# [...])	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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
restubs(*restub1 restub2 ...*)	specify stubs for random-effects parameters for all levels
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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
* `nohr`	do not report hazard ratios
* `tratio`	report time ratios; requires option `time` with `mestreg`
`eform`[`(`*string*`)`]	report exponentiated coefficients and, optionally, label as *string*
`remargl`	compute log marginal likelihood
`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
`nomesummary`	suppress multilevel-structure summary
[`no`]`dots`	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is `dots`
`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
`melabel`	display estimation table using the same row labels as `mestreg`
`nogroup`	suppress table summarizing groups
`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)`

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

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

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

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

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

Model parameters are regression coefficients `{`*depvar*`:`*indepvars*`}`, ancillary parameters as described in *Ancillary model parameters*, random effects `{`*rename*`}`, and either variance components `{`*rename*`:sigma2}` or, if option `covariance(unstructured)` is specified, matrix parameter `{`*restub*`:Sigma,matrix}`; see *Likelihood model* in [BAYES] **bayes** for how *renames* and *restub* are defined. 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 [ME] **mestreg**.

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

Ancillary model parameters

In addition to regression coefficients {_t:*varlist*}, bayes: mestreg defines ancillary parameters that depend on the chosen survival model; see table 1 below. Positive ancillary parameters are transformed to be defined on the whole real line. All ancillary parameters are assigned default normal priors with zero mean and variance of 10,000.

Table 1. Ancillary model parameters defined by bayes: mestreg

	Ancillary	Transformed
Distribution	parameters	model parameters
Exponential	None	None
Weibull	p	{ln_p}
Lognormal	σ	{lnsigma}
Loglogistic	γ	{lngamma}
Gamma	s	{lnscale}

Use the dryrun option with the bayes prefix to see the definitions of model parameters prior to estimation.

Stored results

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

Methods and formulas

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

Also see

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

[ME] **mestreg** — Multilevel mixed-effects parametric survival models

[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**

Title

bayes: metobit — Bayesian multilevel tobit regression

Description	Quick start	Menu	Syntax
Remarks and examples	Stored results	Methods and formulas	Also see

Description

`bayes: metobit` fits a Bayesian multilevel tobit regression to a censored continuous outcome; see [BAYES] **bayes** and [ME] **metobit** for details.

Quick start

Bayesian two-level tobit regression of `y` on `x1` and `x2` with random intercepts by `id`, using a lower censoring limit of 17 and using default normal priors for regression coefficients and default inverse-gamma priors for the error variance and for the variance of random intercepts

```
bayes: metobit y x1 x2 || id:, ll(17)
```

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

```
bayes, normalprior(10): metobit y x1 x2 || id:, 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)): metobit y x1 x2 || id:, ll(17)
```

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

```
bayes, saving(simdata) rseed(123):  ///
metobit y x1 x2 || id:, ll(17)
```

Specify 20,000 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):  ///
metobit y x1 x2 || id:, ll(17)
```

In the above, request that the 90% 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 [ME] **metobit**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Tobit regression

Syntax

`bayes` [, *bayesopts*] `:` `metobit` *depvar* *fe_equation*
[`||` *re_equation*] [`||` *re_equation* ...] [, *options*]

where the syntax of *fe_equation* is

[*indepvars*] [*if*] [*in*] [*weight*] [, *fe_options*]

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

levelvar`:` [*varlist*] [, *re_options*]

for random effects among the values of a factor variable

levelvar`:` `R.`*varname*

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`noconstant`	suppress constant term from the fixed-effects equation
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `identity`, and `unstructured` supported
`noconstant`	suppress constant term from the random-effects equation

options	Description
Model	
`ll(`*varname* | *#*`)`	left-censoring variable or limit
`ul(`*varname* | *#*`)`	right-censoring variable or limit
`collinear`	keep collinear variables
Reporting	
`notable`	suppress coefficient table
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(`*#*`)`	set credible level; default is `level(95)`

indepvars 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**.

`fweight`s are allowed; see **[U] 11.1.6 weight**.

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

For a detailed description of *options*, see *Options* in **[ME] metobit**.

bayesopts	Description
Priors	
`normalprior(`#*`)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
`igammaprior(`# #*`)`	specify shape and scale of default inverse-gamma prior for variance components; default is `igammaprior(0.01 0.01)`
`iwishartprior(`#* [*...*]`)`	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`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
`restubs(`*restub1 restub2 ...*`)`	specify stubs for random-effects parameters for all levels
Blocking	
`blocksize(`#*`)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [`,` *blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
*`noblocking`	do not block parameters by default
Initialization	
`initial(`*initspec*`)`	initial values for model parameters
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
*`noisily`	display output from the estimation command during initialization
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
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
nomesummary	suppress multilevel-structure summary
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
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
melabel	display estimation table using the same row labels as metobit
nogroup	suppress table summarizing groups
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)

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

Options prior() and block() can be repeated.

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

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

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

Model parameters are regression coefficients {*depvar*:*indepvars*}, error variance {e.*depvar*:sigma2}, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *rename*s and *restub* are defined. 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 [ME] **metobit**.

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

Stored results

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

Methods and formulas

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

Also see

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

[ME] **metobit** — Multilevel mixed-effects tobit 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**

Title

bayes: mixed — Bayesian multilevel linear regression

Description

`bayes: mixed` fits a Bayesian multilevel linear regression to a continuous outcome; see [BAYES] **bayes** and [ME] **mixed** for details.

Quick start

Bayesian two-level linear regression of `y` on `x1` and `x2` with random intercepts by `id`, using default normal priors for regression coefficients and default inverse-gamma priors for the error variance and for the variance of random intercepts

```
bayes: mixed y x1 x2 || id:
```

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

```
bayes, normalprior(10): mixed y x1 x2 || id:
```

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)): mixed y x1 x2 || id:
```

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

```
bayes, saving(simdata) rseed(123): mixed y x1 x2 || id:
```

Specify 20,000 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): mixed y x1 x2 || id:
```

In the above, request that the 90% 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 [ME] **mixed**.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Linear regression

Syntax

`bayes` [, *bayesopts*] `:` `mixed` *depvar* *fe_equation*
[`||` *re_equation*] [`||` *re_equation* ...] [, *options*]

where the syntax of *fe_equation* is

[*indepvars*] [*if*] [*in*] [*weight*] [, *fe_options*]

and the syntax of *re_equation* is one of the following:

for random coefficients and intercepts

levelvar`:` [*varlist*] [, *re_options*]

for random effects among the values of a factor variable

levelvar`:` `R.`*varname*

levelvar either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

fe_options	Description
Model	
`noconstant`	suppress constant term from the fixed-effects equation

re_options	Description
Model	
`covariance(`*vartype*`)`	variance–covariance structure of the random effects; only structures `independent`, `identity`, and `unstructured` supported
`noconstant`	suppress constant term from the random-effects equation
`collinear`	keep collinear variables

options	Description
Reporting	
`noheader`	suppress output header
`nogroup`	suppress table summarizing groups
display_options	control spacing, line width, and base and empty cells
`level(`*#*`)`	set credible level; default is `level(95)`

indepvars 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**.

`fweight`s are allowed; see **[U] 11.1.6 weight**.

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

For a detailed description of *options*, see *Options* in **[ME] mixed**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
*igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance components; default is igammaprior(0.01 0.01)
*iwishartprior(# [...])	specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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
restubs(*restub1 restub2* ...)	specify stubs for random-effects parameters for all levels
Blocking	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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
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
nomesummary	suppress multilevel-structure summary
[no]dots	suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots
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
melabel	display estimation table using the same row labels as mixed
nogroup	suppress table summarizing groups
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)

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

Options prior() and block() can be repeated.

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

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

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

Model parameters are regression coefficients {*depvar*:*indepvars*}, error variance {e.*depvar*:sigma2}, random effects {*rename*}, and either variance components {*rename*:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {*restub*:Sigma,matrix}; see *Likelihood model* in [BAYES] **bayes** for how *renames* and *restub* are defined. 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 adaptive Metropolis–Hastings and Gibbs algorithms, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [ME] **mixed**.

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

By default, `bayes: mixed` uses Gibbs sampling for all model parameters except the random-effects parameters. If you specify a `prior()` distribution for which Gibbs sampling is not available, `bayes: mixed` will switch to adaptive Metropolis–Hastings sampling. In general, `bayes: mixed` will try to use a more efficient Gibbs sampling for the model parameters whenever available.

Stored results

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

Methods and formulas

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

Also see

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

[ME] **mixed** — Multilevel mixed-effects linear 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**

Title

bayes: mlogit — Bayesian multinomial logistic regression

Description Quick start Menu Syntax
Remarks and examples Stored results Methods and formulas Also see

Description

`bayes: mlogit` fits a Bayesian multinomial logistic regression to a categorical outcome; see [BAYES] **bayes** and [R] **mlogit** for details.

Quick start

Bayesian multinomial logistic regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: mlogit y x1 x2
```

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

```
bayes, normalprior(10): mlogit y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept for the category 2

```
bayes, prior({2: x1 x2}, uniform(-10,10)) ///
prior({2:_cons}, normal(0,10)): mlogit y x1 x2
```

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

```
bayes, saving(simdata) rseed(123): mlogit y x1 x2
```

Specify 20,000 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): mlogit y x1 x2
```

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

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

Display relative-risk ratios instead of coefficients

```
bayes: mlogit y x1 x2, rrr
```

Display relative-risk ratios on replay

```
bayes, rrr
```

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

Menu

Statistics > Categorical outcomes > Bayesian multinomial logistic regression

Syntax

bayes [, *bayesopts*] : mlogit *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
noconstant	suppress constant term
baseoutcome(#)	value of *depvar* that will be the base outcome
collinear	keep collinear variables
Reporting	
rrr	report relative-risk ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

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

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

bayes: mlogit, level() is equivalent to bayes, clevel(): mlogit.

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

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref*[, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

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
*rrr	report relative-risk ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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

Model parameters are regression coefficients {*outcome*$_1$:*indepvars*}, {*outcome*$_2$:*indepvars*}, and so on, where *outcome*$_\#$'s are the values of the dependent variable or the value labels of the dependent variable if they exist. 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] **mlogit**.

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

Stored results

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

Methods and formulas

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

Also see

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

[R] **mlogit** — Multinomial (polytomous) logistic 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**

Title

bayes: mprobit — Bayesian multinomial probit regression

Description Quick start Menu Syntax
Remarks and examples Stored results Methods and formulas Also see

Description

`bayes: mprobit` fits a Bayesian multinomial probit regression to a categorical outcome; see [BAYES] **bayes** and [R] **mprobit** for details.

Quick start

Bayesian multinomial probit regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: mprobit y x1 x2
```

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

```
bayes, normalprior(10): mprobit y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept for the category `2`

```
bayes, prior({2: x1 x2}, uniform(-10,10)) ///
prior({2:_cons}, normal(0,10)): mprobit y x1 x2
```

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

```
bayes, saving(simdata) rseed(123): mprobit y x1 x2
```

Specify 20,000 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): mprobit y x1 x2
```

In the above, request that the 90% 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] **mprobit**.

Menu

Statistics > Categorical outcomes > Bayesian multinomial probit regression

Syntax

```
bayes [, bayesopts] : mprobit depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
`noconstant`	suppress constant term
`baseoutcome(#)`	value of *depvar* that will be the base outcome
`probitparam`	use the probit variance parameterization
`collinear`	keep collinear variables
Reporting	
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

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

`fweight`s are allowed; see **[U] 11.1.6 weight**.

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

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

bayesopts	Description
Priors	
*`normalprior(#)`	specify standard deviation of default normal priors for regression coefficients; default is `normalprior(100)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`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	
*`blocksize(#)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [, *blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
*`noblocking`	do not block parameters by default
Initialization	
`initial(`*initspec*`)`	initial values for model parameters
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
*`noisily`	display output from the estimation command during initialization

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*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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

Model parameters are regression coefficients {$outcome_1$:*indepvars*}, {$outcome_2$:*indepvars*}, and so on, where $outcome_{\#}$'s are the values of the dependent variable or the value labels of the dependent variable if they exist. 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] **mprobit**.

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

Stored results

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

Methods and formulas

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

Also see

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

[R] **mprobit** — Multinomial probit 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**

Title

bayes: mvreg — Bayesian multivariate regression

Description	Quick start	Menu	Syntax
Remarks and examples	Stored results	Methods and formulas	Also see

Description

`bayes: mvreg` fits a Bayesian multivariate regression to multiple continuous outcomes; see [BAYES] **bayes** and [MV] **mvreg** for details.

Quick start

Bayesian multivariate regression of `y1` and `y2` on `x1` and `x2`, using default normal priors for regression coefficients and Jeffreys prior for the covariance matrix

```
bayes: mvreg y1 y2 = x1 x2
```

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

```
bayes, normalprior(10): mvreg y1 y2 = x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept of the dependent variable `y2`

```
bayes, prior({y2: x1 x2}, uniform(-10,10)) ///
prior({y2:_cons}, normal(0,10)): mvreg y1 y2 = x1 x2
```

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

```
bayes, saving(simdata) rseed(123): mvreg y1 y2 = x1 x2
```

Specify 20,000 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): mvreg y1 y2 = x1 x2
```

In the above, request that the 90% 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 [MV] **mvreg**.

Menu

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

Syntax

bayes [, *bayesopts*] : mvreg *depvars* = *indepvars* [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
noconstant	suppress constant term
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

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

bayes: mvreg, level() is equivalent to bayes, clevel(): mvreg.

For a detailed description of *options*, see *Options* in [MV] **mvreg**.

bayesopts	Description
Priors	
*gibbs	specify Gibbs sampling; available only with normal priors for regression coefficients and multivariate Jeffreys prior for covariance
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

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*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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

Model parameters are regression coefficients {*depvar*$_1$:*indepvars*}, {*depvar*$_2$:*indepvars*}, and so on, and covariance matrix {Sigma,matrix}. Use the dryrun option to see the definitions of model parameters prior to estimation.

Multivariate Jeffreys prior, jeffreys(*d*), is used by default for the covariance matrix of dimension *d*.

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 adaptive Metropolis–Hastings and Gibbs algorithms, see [BAYES] **bayesmh**. For remarks and examples specific to the bayes prefix, see [BAYES] **bayes**. For details about the estimation command, see [MV] **mvreg**.

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

Stored results

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

Methods and formulas

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

Also see

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

[MV] **mvreg** — Multivariate 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**

Title

bayes: nbreg — Bayesian negative binomial regression

Description Quick start Menu Syntax
Remarks and examples Stored results Methods and formulas Also see

Description

`bayes: nbreg` fits a Bayesian negative binomial regression to a nonnegative count outcome; see [BAYES] **bayes** and [R] **nbreg** for details.

Quick start

Bayesian negative binomial regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients and log-overdispersion parameter

```
bayes: nbreg y x1 x2
```

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

```
bayes, normalprior(10): nbreg y x1 x2
```

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)): nbreg y x1 x2
```

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

```
bayes, saving(simdata) rseed(123): nbreg y x1 x2
```

Specify 20,000 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): nbreg y x1 x2
```

In the above, request that the 90% 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: nbreg y x1 x2, irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

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

Menu

Statistics > Count outcomes > Bayesian regression > Negative binomial regression

Syntax

```
bayes [, bayesopts] : nbreg depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
dispersion(mean)	parameterization of dispersion; the default
dispersion(constant)	constant dispersion for all observations
exposure(*varname*$_e$)	include ln(*varname*$_e$) in model with coefficient constrained to 1
offset(*varname*$_o$)	include *varname*$_o$ in model with coefficient constrained to 1
collinear	keep collinear variables
Reporting	
irr	report incidence-rate ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

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

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

bayes: nbreg, level() is equivalent to bayes, clevel(): nbreg.

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

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients and log-overdispersion parameter; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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
*irr	report incidence-rate ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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

Model parameters are regression coefficients {*depvar*:*indepvars*} and log-overdispersion parameter {lnalpha} with mean dispersion or {lndelta} with constant dispersion. 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] **nbreg**.

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

Stored results

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

Methods and formulas

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

Also see

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

[R] **nbreg** — Negative binomial 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**

Title

bayes: ologit — Bayesian ordered logistic regression

Description | Quick start | Menu | Syntax
Remarks and examples | Stored results | Methods and formulas | Also see

Description

`bayes: ologit` fits a Bayesian ordered logistic regression to an ordinal outcome; see [BAYES] **bayes** and [R] **ologit** for details.

Quick start

Bayesian ordered logistic regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients and flat priors for cutpoints

```
bayes: ologit y x1 x2
```

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

```
bayes, normalprior(10): ologit y x1 x2
```

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)): ologit y x1 x2
```

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

```
bayes, saving(simdata) rseed(123): ologit y x1 x2
```

Specify 20,000 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): ologit y x1 x2
```

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

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

Display odds ratios instead of coefficients

```
bayes: ologit y x1 x2, or
```

Display odds ratios on replay

```
bayes, or
```

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

Menu

Statistics > Ordinal outcomes > Bayesian regression > Ordered logistic regression

Syntax

```
bayes [, bayesopts] : ologit depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
offset(*varname*)	include *varname* in model with coefficient constrained to 1
collinear	keep collinear variables
Reporting	
or	report odds ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

depvar 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: ologit, level() is equivalent to bayes, clevel(): ologit.

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

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref*[, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

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
* or	report odds ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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

Model parameters are regression coefficients {*depvar*:*indepvars*} and cutpoints {cut1}, {cut2}, and so on. Use the dryrun option to see the definitions of model parameters prior to estimation.

Flat priors, flat, are used by default for cutpoints.

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] **ologit**.

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

Stored results

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

Methods and formulas

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

Also see

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

[R] **ologit** — Ordered logistic 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**

Title

bayes: oprobit — Bayesian ordered probit regression

Description | Quick start | Menu | Syntax
Remarks and examples | Stored results | Methods and formulas | Also see

Description

`bayes: oprobit` fits a Bayesian ordered probit regression to an ordinal outcome; see [BAYES] **bayes** and [R] **oprobit** for details.

Quick start

Bayesian ordered probit regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients and flat priors for cutpoints

```
bayes: oprobit y x1 x2
```

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

```
bayes, normalprior(10): oprobit y x1 x2
```

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)): oprobit y x1 x2
```

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

```
bayes, saving(simdata) rseed(123): oprobit y x1 x2
```

Specify 20,000 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): oprobit y x1 x2
```

In the above, request that the 90% 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] **oprobit**.

Menu

Statistics > Ordinal outcomes > Bayesian regression > Ordered probit regression

Syntax

bayes [, *bayesopts*] : oprobit *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
offset(*varname*)	include *varname* in model with coefficient constrained to 1
collinear	keep collinear variables
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

depvar 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: oprobit, level() is equivalent to bayes, clevel(): oprobit.

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

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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*
`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
`[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
`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)`

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

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

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

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

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

Model parameters are regression coefficients `{`*depvar*`:`*indepvars*`}` and cutpoints `{cut1}`, `{cut2}`, and so on. Use the `dryrun` option to see the definitions of model parameters prior to estimation.

Flat priors, `flat`, are used by default for cutpoints.

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] **oprobit**.

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

Stored results

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

Methods and formulas

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

Also see

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

[R] **oprobit** — Ordered probit 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**

Title

bayes: poisson — Bayesian Poisson regression

Description

`bayes: poisson` fits a Bayesian Poisson regression to a nonnegative count outcome; see [BAYES] **bayes** and [R] **poisson** for details.

Quick start

Bayesian Poisson regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: poisson y x1 x2
```

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

```
bayes, normalprior(10): poisson y x1 x2
```

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)): poisson y x1 x2
```

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

```
bayes, saving(simdata) rseed(123): poisson y x1 x2
```

Specify 20,000 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): poisson y x1 x2
```

In the above, request that the 90% 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: poisson y x1 x2, irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

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

Menu

Statistics > Count outcomes > Bayesian regression > Poisson regression

Syntax

bayes [, *bayesopts*] : poisson *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
noconstant	suppress constant term
exposure($varname_e$)	include ln($varname_e$) in model with coefficient constrained to 1
offset($varname_o$)	include $varname_o$ in model with coefficient constrained to 1
collinear	keep collinear variables
Reporting	
irr	report incidence-rate ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

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

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

bayes: poisson, level() is equivalent to bayes, clevel(): poisson.

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

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

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
*irr	report incidence-rate ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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] **poisson**.

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

Stored results

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

Methods and formulas

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

Also see

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

[R] **poisson** — 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**

Title

bayes: probit — Bayesian probit regression

Description | Quick start | Menu | Syntax
Remarks and examples | Stored results | Methods and formulas | Also see

Description

`bayes: probit` fits a Bayesian probit regression to a binary outcome; see [BAYES] **bayes** and [R] **probit** for details.

Quick start

Bayesian probit regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: probit y x1 x2
```

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

```
bayes, normalprior(10): probit y x1 x2
```

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)): probit y x1 x2
```

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

```
bayes, saving(simdata) rseed(123): probit y x1 x2
```

Specify 20,000 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): probit y x1 x2
```

In the above, request that the 90% 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] **probit**.

Menu

Statistics > Binary outcomes > Bayesian regression > Probit regression

Syntax

```
bayes [, bayesopts] : probit depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
asis	retain perfect predictor variables
collinear	keep collinear variables
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

depvar 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: probit, level() is equivalent to bayes, clevel(): probit.

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

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
* blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
* noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
* noisily	display output from the estimation command during initialization

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*
`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
[`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
`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)`

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

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

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

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

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] **probit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Logistic regression with perfect predictors* in [BAYES] **bayes**.

Stored results

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

Methods and formulas

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

Also see

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

[R] **probit** — Probit 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**

Title

bayes: regress — Bayesian linear regression

Description Quick start Menu Syntax
Remarks and examples Stored results Methods and formulas Also see

Description

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

Quick start

Bayesian linear regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients and default inverse-gamma prior for the variance

```
bayes: regress y x1 x2
```

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

```
bayes, normalprior(10): regress y x1 x2
```

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): regress y x1 x2
```

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)): regress y x1 x2
```

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

```
bayes, saving(simdata) rseed(123): regress y x1 x2
```

Specify 20,000 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): regress y x1 x2
```

In the above, request that the 90% 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] **regress**.

Menu

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

Syntax

bayes [, *bayesopts*] : regress *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
noconstant	suppress constant term
Reporting	
eform(*string*)	report exponentiated coefficients and label as *string*
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

depvar 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: regress, level() is equivalent to bayes, clevel(): regress.

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

bayesopts	Description
Priors	
*gibbs	specify Gibbs sampling; available only with normal priors for regression coefficients and an inverse-gamma prior for variance
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
*igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance; default is igammaprior(0.01 0.01)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

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*
`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
[`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
`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)`

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

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

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

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

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

For a general introduction to Bayesian analysis, see [BAYES] **intro**. For a general introduction to Bayesian estimation using adaptive Metropolis–Hastings and Gibbs algorithms, see [BAYES] **bayesmh**. For remarks and examples specific to the `bayes` prefix, see [BAYES] **bayes**. For details about the estimation command, see [R] **regress**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Linear regression: A case of informative default priors* in [BAYES] **bayes**.

Video examples

Bayesian linear regression using the bayes prefix: How to specify custom priors

Stored results

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

Methods and formulas

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

Also see

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

[R] **regress** — Linear 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**

Title

bayes: streg — Bayesian parametric survival models

Description · Quick start · Menu · Syntax
Remarks and examples · Stored results · Methods and formulas · Also see

Description

`bayes: streg` fits a Bayesian parametric survival model to a survival-time outcome; see [BAYES] **bayes** and [ST] **streg** for details.

Quick start

Bayesian Weibull survival model of `stset` survival-time outcome on `x1` and `x2`, using default normal priors for regression coefficients and log-ancillary parameters

```
bayes: streg x1 x2, distribution(weibull)
```

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

```
bayes, normalprior(10): streg x1 x2, distribution(weibull)
```

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

```
bayes, prior({_t: x1 x2}, uniform(-10,10)) ///
prior({_t:_cons}, normal(0,10)): streg x1 x2, distribution(weibull)
```

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

```
bayes, saving(simdata) rseed(123):  ///
streg x1 x2, distribution(weibull)
```

Specify 20,000 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):  ///
streg x1 x2, distribution(weibull)
```

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

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

Use accelerated failure-time metric instead of proportional-hazards parameterization, and display time ratios instead of coefficients

```
bayes, tratio: streg x1 x2, distribution(weibull) time
```

Display time ratios on replay

```
bayes, tratio
```

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [ST] **streg**.

Menu

Statistics > Survival analysis > Regression models > Bayesian parametric survival models

Syntax

```
bayes [, bayesopts] : streg [varlist] [if] [in] [, options]
```

options	Description
Model	
`noconstant`	suppress constant term
`distribution(exponential)`	exponential survival distribution
`distribution(gompertz)`	Gompertz survival distribution
`distribution(loglogistic)`	loglogistic survival distribution
`distribution(llogistic)`	synonym for `distribution(loglogistic)`
`distribution(weibull)`	Weibull survival distribution
`distribution(lognormal)`	lognormal survival distribution
`distribution(lnormal)`	synonym for `distribution(lognormal)`
`distribution(ggamma)`	generalized gamma survival distribution
`frailty(gamma)`	gamma frailty distribution
`frailty(invgaussian)`	inverse-Gaussian distribution
`time`	use accelerated failure-time metric
Model 2	
`strata(`*varname*`)`	strata ID variable
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`shared(`*varname*`)`	shared frailty ID variable
`ancillary(`*varlist*`)`	use *varlist* to model the first ancillary parameter
`anc2(`*varlist*`)`	use *varlist* to model the second ancillary parameter
`collinear`	keep collinear variables
Reporting	
`nohr`	do not report hazard ratios
`tratio`	report time ratios
`noshow`	do not show st setting information
display_options	control spacing, line width, and base and empty cells
`level(#)`	set credible level; default is `level(95)`

You must `stset` your data before using `bayes: streg`; see [ST] **stset**.

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

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

For a detailed description of *options*, see *Options* in [ST] **streg**.

bayesopts	Description
Priors	
*`normalprior(#)`	specify standard deviation of default normal priors for regression coefficients and log-ancillary parameters; default is `normalprior(100)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation

Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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
*nohr	do not report hazard ratios
*tratio	report time ratios; requires option time with streg
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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

Model parameters are regression coefficients {*depvar*:*indepvars*} and ancillary parameters as described in *Ancillary model parameters*. 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 [ST] **streg**.

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

Ancillary model parameters

In addition to regression coefficients {_t:*varlist*}, bayes: streg defines ancillary parameters that depend on the chosen survival model; see table 1 below. Positive ancillary parameters are transformed to be defined on the whole real line. All ancillary parameters are assigned default normal priors with zero mean and variance of 10,000.

Table 1. Ancillary model parameters defined by bayes: streg

Distribution	Ancillary parameters	Transformed model parameters
Exponential	None	None
Weibull	p	{ln_p}
Gompertz	γ	{gamma}
Lognormal	σ	{lnsigma}
Loglogistic	γ	{lngamma}
Generalized gamma	σ, κ	{lnsigma}, {kappa}

For frailty models, when option frailty() or option shared() is specified with streg, bayes: streg also defines the log-frailty parameter {lntheta}.

If option ancillary(*varlist*) is specified, regression coefficients {ln_p:*varlist*}, {gamma:*varlist*}, and so on are defined for all ancillary parameters except κ. If option anc2(*varlist*) is specified, then regression coefficients {kappa:*varlist*} are defined for κ.

If option strata(*varname*) is specified, additional stratum-specific coefficients of the form {*eqname*:*#*.*varname*} are defined for the main regression and ancillary parameters. For example, if drug contains three strata, then specifying option strata(drug) will result in additional main regression coefficients {_t:2.drug} and {_t:3.drug} and—say, for Weibull regression—in additional parameters {ln_p:2.drug} and {ln_p:3.drug}. In the model summary with default priors, you may see these parameters labeled as {_t:i.drug} and {ln_p:i.drug}, for short.

Use the dryrun option with the bayes prefix to see the definitions of model parameters prior to estimation.

Stored results

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

Methods and formulas

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

Also see

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

[ST] **streg** — Parametric survival models

[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**

Title

bayes: tnbreg — Bayesian truncated negative binomial regression

Description
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Description

`bayes: tnbreg` fits a Bayesian truncated negative binomial regression to a positive count outcome whose values are all above the truncation point; see [BAYES] **bayes** and [R] **tnbreg** for details.

Quick start

Bayesian truncated negative binomial regression of `y` on `x1` and `x2`, using a lower truncation limit of 5 and using default normal priors for regression coefficients and log-overdispersion parameter

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

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

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

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

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

Specify 20,000 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): tnbreg y x1 x2, ll(5)
```

In the above, request that the 90% 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: tnbreg 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] **tnbreg**.

Menu

Statistics > Count outcomes > Bayesian regression > Truncated negative binomial regression

Syntax

`bayes` [, *bayesopts*] : `tnbreg` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
`noconstant`	suppress constant term
`ll(`# | *varname*`)`	truncation point; default value is `ll(0)`, zero truncation
`dispersion(mean)`	parameterization of dispersion; the default
`dispersion(constant)`	constant dispersion for all observations
`exposure(`$varname_e$`)`	include ln($varname_e$) in model with coefficient constrained to 1
`offset(`$varname_o$`)`	include $varname_o$ in model with coefficient constrained to 1
`collinear`	keep collinear variables
Reporting	
`irr`	report incidence-rate ratios
display_options	control spacing, line width, and base and empty cells
`level(`#`)`	set credible level; default is `level(95)`

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

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

`fweight`s are allowed; see **[U] 11.1.6 weight**.

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

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

bayesopts	Description
Priors	
*`normalprior(`#`)`	specify standard deviation of default normal priors for regression coefficients and log-overdispersion parameter; default is `normalprior(100)`
`prior(`*priorspec*`)`	prior for model parameters; this option may be repeated
`dryrun`	show model summary without estimation
Simulation	
`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	
*`blocksize(`#`)`	maximum block size; default is `blocksize(50)`
`block(`*paramref* [, *blockopts*]`)`	specify a block of model parameters; this option may be repeated
`blocksummary`	display block summary
*`noblocking`	do not block parameters by default

Initialization	
`initial(`*initspec*`)`	initial values for model parameters
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
* `noisily`	display output from the estimation command during initialization
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
* `irr`	report incidence-rate ratios
`eform`[`(`*string*`)`]	report exponentiated coefficients and, optionally, label as *string*
`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
[`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
`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)`

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

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

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

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

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

Model parameters are regression coefficients `{`*depvar*`:`*indepvars*`}` and log-overdispersion parameter `{lnalpha}` with mean dispersion or `{lndelta}` with constant dispersion. 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] **tnbreg**.

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] **bayesmh**.

Methods and formulas

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

Also see

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

[R] **tnbreg** — Truncated negative binomial 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**

Title

bayes: tobit — Bayesian tobit regression

Description | Quick start | Menu | Syntax
Remarks and examples | Stored results | Methods and formulas | Also see

Description

`bayes: tobit` fits a Bayesian tobit regression to a censored continuous outcome; see [BAYES] **bayes** and [R] **tobit** for details.

Quick start

Bayesian tobit regression of `y` on `x1` and `x2`, using a lower censoring limit of 17 and using default normal priors for regression coefficients and default inverse-gamma prior for the variance

```
bayes: tobit y x1 x2, ll(17)
```

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

```
bayes, normalprior(10): tobit 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): tobit 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)): tobit y x1 x2, ll(17)
```

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

```
bayes, saving(simdata) rseed(123): tobit y x1 x2, ll(17)
```

Specify 20,000 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): tobit y x1 x2, ll(17)
```

In the above, request that the 90% 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] **tobit**.

Menu

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

Syntax

bayes [, *bayesopts*] : tobit *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
noconstant	suppress constant term
ll[(*varname* | #)]	left-censoring variable or limit
ul[(*varname* | #)]	right-censoring variable or limit
offset(*varname*)	include *varname* in model with coefficient constrained to 1
collinear	keep collinear variables
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

depvar 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: tobit, level() is equivalent to bayes, clevel(): tobit.

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

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
*igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance; default is igammaprior(0.01 0.01)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref*[, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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

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] **tobit**.

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

Stored results

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

Methods and formulas

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

Also see

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

[R] **tobit** — Tobit 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**

Title

bayes: tpoisson — Bayesian truncated Poisson regression

Description | Quick start | Menu | Syntax
Remarks and examples | Stored results | Methods and formulas | 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 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% 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 *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
noconstant	suppress constant term
ll(# | *varname*)	lower limit for truncation; default is ll(0)
ul(# | *varname*)	upper limit for truncation
exposure(*varname$_e$*)	include ln(*varname$_e$*) in model with coefficient constrained to 1
offset(*varname$_o$*)	include *varname$_o$* in model with coefficient constrained to 1
collinear	keep collinear variables
Reporting	
irr	report incidence-rate ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

depvar 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**.

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization	
`initial(`*initspec*`)`	initial values for model parameters
`nomleinitial`	suppress the use of maximum likelihood estimates as starting values
`initrandom`	specify random initial values
`initsummary`	display initial values used for simulation
* `noisily`	display output from the estimation command during initialization
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
* `irr`	report incidence-rate ratios
`eform`[`(`*string*`)`]	report exponentiated coefficients and, optionally, label as *string*
`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
[`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
`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)`

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

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

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

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

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] **bayesmh**.

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**

Title

bayes: truncreg — Bayesian truncated regression

Description Quick start Menu Syntax
Remarks and examples Stored results Methods and formulas 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 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% 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

bayes [, *bayesopts*] : truncreg *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
noconstant	suppress constant term
ll(*varname* | #)	left-truncation variable or limit
ul(*varname* | #)	right-truncation variable or limit
offset(*varname*)	include *varname* in model with coefficient constrained to 1
collinear	keep collinear variables
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

depvar 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: truncreg, level() is equivalent to bayes, clevel(): truncreg.

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

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
*igammaprior(# #)	specify shape and scale of default inverse-gamma prior for variance; default is igammaprior(0.01 0.01)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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

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] **bayesmh**.

Methods and formulas

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

Also see

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

[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**

Title

bayes: zinb — Bayesian zero-inflated negative binomial regression

Description	Quick start	Menu	Syntax
Remarks and examples	Stored results	Methods and formulas	Also see

Description

`bayes: zinb` fits a Bayesian zero-inflated negative binomial regression to a nonnegative count outcome with a high fraction of zeros; see [BAYES] **bayes** and [R] **zinb** for details.

Quick start

Bayesian zero-inflated negative binomial regression of `y` on `x1` and `x2`, using `z` to model excess zeros and using default normal priors for regression coefficients and log-overdispersion parameter

```
bayes: zinb y x1 x2, inflate(z)
```

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

```
bayes, normalprior(10): zinb y x1 x2, inflate(z)
```

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)): zinb y x1 x2, inflate(z)
```

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

```
bayes, saving(simdata) rseed(123): zinb y x1 x2, inflate(z)
```

Specify 20,000 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): zinb y x1 x2, inflate(z)
```

In the above, request that the 90% 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: zinb y x1 x2, inflate(z) irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

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

Menu

Statistics > Count outcomes > Bayesian regression > Zero-inflated negative binomial regression

Syntax

bayes [, *bayesopts*] : zinb *depvar* [*indepvars*] [*if*] [*in*] [*weight*] ,

inflate(*varlist*[, offset(*varname*)] | _cons) [*options*]

options	Description
Model	
*inflate( )	equation that determines whether the count is zero
noconstant	suppress constant term
exposure(*varname$_e$*)	include ln(*varname$_e$*) in model with coefficient constrained to 1
offset(*varname$_o$*)	include *varname$_o$* in model with coefficient constrained to 1
collinear	keep collinear variables
probit	use probit model to characterize excess zeros; default is logit
Reporting	
irr	report incidence-rate ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

*inflate(*varlist*[, offset(*varname*)] | _cons) is required.

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

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

bayes: zinb, level() is equivalent to bayes, clevel(): zinb.

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

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients and log-overdispersion parameter; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref*[, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default

Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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
*irr	report incidence-rate ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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 {inflate:*varlist*} for the inflation equation and log-overdispersion parameter {lnalpha}. 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] **zinb**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Zero-inflated negative binomial model* in [BAYES] **bayes**.

Stored results

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

Methods and formulas

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

Also see

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

[R] **zinb** — Zero-inflated negative binomial 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**

Title

bayes: zioprobit — Bayesian zero-inflated ordered probit regression

Description

`bayes: zioprobit` fits a Bayesian zero-inflated ordered probit regression to an ordinal outcome with a high fraction of zeros; see [BAYES] **bayes** and [R] **zioprobit** for details.

Quick start

Bayesian zero-inflated ordered probit regression of `y` on `x1` and `x2`, using `z` to model excess zeros and using default normal priors for regression coefficients and flat priors for cutpoints

```
bayes: zioprobit y x1 x2, inflate(z)
```

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

```
bayes, normalprior(10): zioprobit y x1 x2, inflate(z)
```

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)): zioprobit y x1 x2, inflate(z)
```

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

```
bayes, saving(simdata) rseed(123):  ///
zioprobit y x1 x2, inflate(z)
```

Specify 20,000 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):  ///
zioprobit y x1 x2, inflate(z)
```

In the above, request that the 90% 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] **zioprobit**.

Menu

Statistics > Ordinal outcomes > Bayesian regression > Zero-inflated ordered probit regression

Syntax

bayes [, *bayesopts*] : zioprobit *depvar* [*indepvars*] [*if*] [*in*] [*weight*] ,

inflate(*varlist* [, noconstant offset(*varname*)] | _cons) [*options*]

options	Description
Model	
*inflate()	equation that determines excess zero values
offset(*varname*)	include *varname* in model with coefficient constrained to 1
collinear	keep collinear variables
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

*inflate(*varlist* [, noconstant offset(*varname*)] | _cons) is required.

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

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

bayes: zioprobit, level() is equivalent to bayes, clevel(): zioprobit.

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

bayesopts	Description
Priors	
*normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
*blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
*noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization

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*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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 {inflate:*varlist*} for the inflation equation and cutpoints {cut1}, {cut2}, and so on. Use the dryrun option to see the definitions of model parameters prior to estimation.

Flat priors, flat, are used by default for cutpoints.

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] **zioprobit**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Zero-inflated negative binomial models* in [BAYES] **bayes**.

Stored results

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

Methods and formulas

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

Also see

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

[R] **zioprobit** — Zero-inflated ordered probit 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**

Title

bayes: zip — Bayesian zero-inflated Poisson regression

Description

`bayes: zip` fits a Bayesian zero-inflated Poisson regression to a nonnegative count outcome with a high fraction of zeros; see [BAYES] **bayes** and [R] **zip** for details.

Quick start

Bayesian zero-inflated Poisson regression of `y` on `x1` and `x2`, using `z` to model excess zeros and using default normal priors for regression coefficients

```
bayes: zip y x1 x2, inflate(z)
```

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

```
bayes, normalprior(10): zip y x1 x2, inflate(z)
```

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)): zip y x1 x2, inflate(z)
```

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

```
bayes, saving(simdata) rseed(123): zip y x1 x2, inflate(z)
```

Specify 20,000 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): zip y x1 x2, inflate(z)
```

In the above, request that the 90% 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: zip y x1 x2, inflate(z) irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

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

Menu

Statistics > Count outcomes > Bayesian regression > Zero-inflated Poisson regression

Syntax

bayes [, *bayesopts*] : zip *depvar* [*indepvars*] [*if*] [*in*] [*weight*] ,

inflate(*varlist*[, offset(*varname*)] | _cons) [*options*]

options	Description
Model	
* inflate( )	equation that determines whether the count is zero
noconstant	suppress constant term
exposure(*varname$_e$*)	include ln(*varname$_e$*) in model with coefficient constrained to 1
offset(*varname$_o$*)	include *varname$_o$* in model with coefficient constrained to 1
collinear	keep collinear variables
probit	use probit model to characterize excess zeros; default is logit
Reporting	
irr	report incidence-rate ratios
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

* inflate(*varlist*[, offset(*varname*)] | _cons) is required.

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

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

bayes: zip, level() is equivalent to bayes, clevel(): zip.

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

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
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	
* blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref*[, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
* noblocking	do not block parameters by default

Initialization	
initial(*initspec*)	initial values for model parameters
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
*noisily	display output from the estimation command during initialization
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
*irr	report incidence-rate ratios
eform[(*string*)]	report exponentiated coefficients and, optionally, label as *string*
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
[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
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)

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

Options prior() and block() can be repeated.

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

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

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 {inflate:*varlist*} for the inflation 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] **zip**.

For a simple example of the bayes prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Zero-inflated negative binomial model* in [BAYES] **bayes**.

Stored results

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

Methods and formulas

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

Also see

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

[R] **zip** — Zero-inflated 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**

Glossary

a posteriori. In the context of Bayesian analysis, we use a posteriori to mean "after the sample is observed". For example, a posteriori information is any information obtained after the data sample is observed. See *posterior distribution, posterior*.

a priori. In the context of Bayesian analysis, we use a priori to mean "before the sample is observed". For example, a priori information is any information obtained before the data sample is observed. In a Bayesian model, a priori information about model parameters is specified by prior distributions.

acceptance rate. In the context of the MH algorithm, acceptance rate is the fraction of the proposed samples that is accepted. The optimal acceptance rate depends on the properties of the target distribution and is not known in general. If the target distribution is normal, however, the optimal acceptance rate is known to be 0.44 for univariate distributions and 0.234 for multivariate distributions.

adaptation. In the context of the MH algorithm, adaptation refers to the process of tuning or adapting the proposal distribution to optimize the MCMC sampling. Typically, adaptation is performed periodically during the MCMC sampling. The `bayesmh` command performs adaptation every # of iterations as specified in option `adaptation(every(#))` for a maximum of `adaptation(maxiter())` iterations. In a continuous-adaptation regimes, the adaptation lasts during the entire process of the MCMC sampling. See [BAYES] **bayesmh**.

adaptation period. Adaptation period includes all MH adaptive iterations. It equals the length of the adaptation interval, as specified by `adaptation(every())`, times the maximum number of adaptations, `adaptation(maxiter())`.

adaptive iteration. In the adaptive MH algorithm, adaptive iterations are iterations during which adaptation is performed.

Akaike information criterion, AIC. Akaike information criterion (AIC) is an information-based model-selection criterion. It is given by the formula $-2 \times \log \text{likelihood} + 2k$, where k is the number of parameters. AIC favors simpler models by penalizing for the number of model parameters. It does not, however, account for the sample size. As a result, the AIC penalization diminishes as the sample size increases, as does its ability to guard against overparameterization.

batch means. Batch means are means obtained from batches of sample values of equal size. Batch means provide an alternative method for estimating MCMC standard errors (MCSE). The batch size is usually chosen to minimize the correlation between different batches of means.

Bayes factor. Bayes factor is given by the ratio of the marginal likelihoods of two models, M_1 and M_2. It is a widely used criterion for Bayesian model comparison. Bayes factor is used in calculating the posterior odds ratio of model M_1 versus M_2,

$$\frac{P(M_1|\mathbf{y})}{P(M_2|\mathbf{y})} = \frac{P(\mathbf{y}|M_1)}{P(\mathbf{y}|M_2)} \frac{P(M_1)}{P(M_2)}$$

where $P(M_i|\mathbf{y})$ is a posterior probability of model M_i, and $P(M_i)$ is a prior probability of model M_i. When the two models are equally likely, that is, when $P(M_1) = P(M_2)$, the Bayes factor equals the posterior odds ratio of the two models.

Bayes's rule. The Bayes's rule is a formal method for relating conditional probability statements. For two (random) events X and Y, the Bayes's rule states that

$$P(X|Y) \propto P(Y|X)P(X)$$

that is, the probability of X conditional on Y is proportional to the probability of X and the probability of Y conditional on X. In Bayesian analysis, the Bayes's rule is used for combining prior information about model parameters and evidence from the observed data to form the posterior distribution.

Bayesian analysis. Bayesian analysis is a statistical methodology that considers model parameters to be random quantities and estimates their posterior distribution by combining prior knowledge about parameters with the evidence from the observed data sample. Prior knowledge about parameters is described by prior distributions and evidence from the observed data is incorporated through a likelihood model. Using the Bayes's rule, the prior distribution and the likelihood model are combined to form the posterior distribution of model parameters. The posterior distribution is then used for parameter inference, hypothesis testing, and prediction.

Bayesian estimation. Bayesian estimation consists of fitting Bayesian models and estimating their parameters based on the resulting posterior distribution. Bayesian estimation in Stata can be done using the convenient `bayes` prefix or the more general `bayesmh` command. See [BAYES] **bayesian estimation** for details.

Bayesian estimation results. Estimation results obtained after the `bayes` prefix or the `bayesmh` command.

Bayesian hypothesis testing. Bayesian hypothesis testing computes probabilities of hypotheses conditional on the observed data. In contrast to the frequentist hypothesis testing, the Bayesian hypothesis testing computes the actual probability of a hypothesis H by using the Bayes's rule,

$$P(H|\mathbf{y}) \propto P(\mathbf{y}|H)P(H)$$

where $\mathbf{y}$ is the observed data, $P(\mathbf{y}|H)$ is the marginal likelihood of $\mathbf{y}$ given H, and $P(H)$ is the prior probability of H. Two different hypotheses, H_1 and H_2, can be compared by simply comparing $P(H_1|\mathbf{y})$ to $P(H_2|\mathbf{y})$.

Bayesian information criterion, BIC. The Bayesian information criterion (BIC), also known as Schwarz criterion, is an information based criterion used for model selection in classical statistics. It is given by the formula $-0.5 \times \log \text{likelihood} + k \times \ln n$, where k is the number of parameters and n is the sample size. BIC favors simpler, in terms of complexity, models and it is more conservative than AIC.

blocking. In the context of the MH algorithm, blocking refers to the process of separating model parameters into different subsets or blocks to be sampled independently of each other. MH algorithm generates proposals and applies the acceptance–rejection rule sequentially for each block. It is recommended that correlated parameters are kept in one block. Separating less-correlated or independent model parameters in different blocks may improve the mixing of the MH algorithm.

burn-in period. The burn-in period is the number of iterations it takes for an MCMC sequence to reach stationarity.

central posterior interval. See *equal-tailed credible interval*.

conditional conjugacy. See *semiconjugate prior*.

conjugate prior. A prior distribution is conjugate for a family of likelihood distributions if the prior and posterior distributions belong to the same family of distributions. For example, the gamma distribution is a conjugate prior for the Poisson likelihood. Conjugacy may provide an efficient way of sampling from posterior distributions and is used in Gibbs sampling.

continuous parameters. Continuous parameters are parameters with continuous prior distributions.

credible interval. In Bayesian analysis, the credible interval of a scalar model parameter is an interval from the domain of the marginal posterior distribution of that parameter. Two types of credible intervals are typically used in practice: equal-tailed credible intervals and HPD credible intervals.

credible level. The credible level is a probability level between 0% and 100% used for calculating credible intervals in Bayesian analysis. For example, a 95% credible interval for a scalar parameter is an interval the parameter belongs to with the probability of 95%.

cusum plot, CUSUM plot. The cusum (CUSUM) plot of an MCMC sample is a plot of cumulative sums of the differences between sample values and their overall mean against the iteration number. Cusum plots are useful graphical summaries for detecting early drifts in MCMC samples.

deviance information criterion, DIC. The deviance information criterion (DIC) is an information based criterion used for Bayesian model selection. It is an analog of AIC and is given by the formula $D(\overline{\theta}) + 2 \times p_D$, where $D(\overline{\theta})$ is the deviance at the sample mean and p_D is the effective complexity, a quantity equivalent to the number of parameters in the model. Models with smaller DIC are preferred.

diminishing adaptation. Diminishing adaptation of the adaptive algorithm is the type of adaptation in which the amount of adaptation decreases with the size of the MCMC chain.

discrete parameters. Discrete parameters are parameters with discrete prior distributions.

effective sample size, ESS. Effective sample size (ESS) is the MCMC sample size T adjusted for the autocorrelation in the sample. It represents the number of independent observations in an MCMC sample. ESS is used instead of T in calculating MCSE. Small ESS relative to T indicates high autocorrelation and consequently poor mixing of the chain.

efficiency. In the context of MCMC, efficiency is a term used for assessing the mixing quality of an MCMC procedure. Efficient MCMC algorithms are able to explore posterior domains in less time (using fewer iterations). Efficiency is typically quantified by the sample autocorrelation and effective sample size. An MCMC procedure that generates samples with low autocorrelation and consequently high ESS is more efficient.

equal-tailed credible interval. An equal-tailed credible interval is a credible interval defined in such a way that both tails of the marginal posterior distribution have the same probability. A $\{100 \times (1-\alpha)\}\%$ equal-tailed credible interval is defined by the $\alpha/2$th and $\{(1-\alpha)/2\}$th quantiles of the marginal posterior distribution.

feasible initial value. An initial-value vector is feasible if it corresponds to a state with a positive posterior probability.

fixed effects. See *fixed-effects parameters*.

fixed-effects parameters. In the Bayesian context, the term “fixed effects” or “fixed-effects parameters” is a misnomer, because all model parameters are inherently random. We use this term in the context of Bayesian multilevel models to refer to regression model parameters and to distinguish them from the random-effects parameters. You can think of fixed-effects parameters as parameters modeling population averaged or marginal relationship of the response and the variables of interest.

frequentist analysis. Frequentist analysis is a form of statistical analysis where model parameters are considered to be unknown but fixed constants and the observed data are viewed as a repeatable random sample. Inference is based on the sampling distribution of the data.

full conditionals. A full conditional is the probability distribution of a random variate conditioned on all other random variates in a joint probability model. Full conditional distributions are used in Gibbs sampling.

full Gibbs sampling. See *Gibbs sampling, Gibbs sampler*.

Gibbs sampling, Gibbs sampler. Gibbs sampling is an MCMC method, according to which each random variable from a joint probability model is sampled according to its full conditional distribution.

highest posterior density credible interval, HPD credible interval. The highest posterior density (HPD) credible interval is a type of a credible interval with the highest marginal posterior density. An HPD interval has the shortest width among all other credible intervals. For some multimodal marginal distributions, HPD may not exists. See *highest posterior density region, HPD region*.

highest posterior density region, HPD region. The highest posterior density (HPD) region for model parameters has the highest marginal posterior probability among all domain regions. Unlike an HPD credible interval, an HPD region always exist.

hybrid MH sampling, hybrid MH sampler. A hybrid MH sampler is an MCMC method in which some blocks of parameters are updated using the MH algorithms and other blocks are updated using Gibbs sampling.

hyperparameter. In Bayesian analysis, hyperparameter is a parameter of a prior distribution, in contrast to a model parameter.

hyperprior. In Bayesian analysis, hyperprior is a prior distribution of hyperparameters. See *hyperparameter*.

improper prior. A prior is said to be improper if it does not integrate to a finite number. Uniform distributions over unbounded intervals are improper. Improper priors may still yield proper posterior distributions. When using improper priors, however, one has to make sure that the resulting posterior distribution is proper for Bayesian inference to be invalid.

independent a posteriori. Parameters are considered independent a posteriori if their marginal posterior distributions are independent; that is, their joint posterior distribution is the product of their individual marginal posterior distributions.

independent a priori. Parameters are considered independent a priori if their prior distributions are independent; that is, their joint prior distribution is the product of their individual marginal prior distributions.

informative prior. An informative prior is a prior distribution that has substantial influence on the posterior distribution.

interval hypothesis testing. Interval hypothesis testing performs interval hypothesis tests for model parameters and functions of model parameters.

interval test. In Bayesian analysis, an interval test applied to a scalar model parameter calculates the marginal posterior probability for the parameter to belong to the specified interval.

Jeffreys prior. The Jeffreys prior of a vector of model parameters $\boldsymbol{\theta}$ is proportional to the square root of the determinant of its Fisher information matrix $I(\boldsymbol{\theta})$. Jeffreys priors are locally uniform and, by definition, agree with the likelihood function. Jeffreys priors are considered noninformative priors that have minimal impact on the posterior distribution.

marginal distribution. In Bayesian context, a distribution of the data after integrating out parameters from the joint distribution of the parameters and the data.

marginal likelihood. In the context of Bayesian model comparison, a marginalized over model parameters $\boldsymbol{\theta}$ likelihood of data $\mathbf{y}$ for a given model M, $P(\mathbf{y}|M) = m(\mathbf{y}) = \int P(\mathbf{y}|\boldsymbol{\theta}, M)P(\boldsymbol{\theta}|M)d\boldsymbol{\theta}$. Also see *Bayes factor*.

marginal posterior distribution. In Bayesian context, a marginal posterior distribution is a distribution resulting from integrating out all but one parameter from the joint posterior distribution.

Markov chain. Markov chain is a random process that generates sequences of random vectors (or states) and satisfies the Markov property: the next state depends only on the current state and not on any of the previous states. MCMC is the most common methodology for simulating Markov chains.

matrix model parameter. A matrix model parameter is any model parameter that is a matrix. Matrix elements, however, are viewed as scalar model parameters.

Matrix model parameters are defined and referred to within the bayesmh command as {*param*,matrix} or {*eqname*:*param*,matrix} with the equation name *eqname*. For example, {Sigma, matrix} and {Scale:Omega, matrix} are matrix model parameters. Individual matrix elements cannot be referred to within the bayesmh command, but they can be referred within postestimation commands accepting parameters. For example, to refer to the individual elements of the defined above, say, 2×2 matrices, use {Sigma_1_1}, {Sigma_2_1}, {Sigma_1_2}, {Sigma_2_2} and {Scale:Omega_1_1}, {Scale:Omega_2_1}, {Scale:Omega_1_2}, {Scale:Omega_2_2}, respectively. See [BAYES] **bayesmh**.

matrix parameter. See *matrix model parameter*.

MCMC, Markov chain Monte Carlo. MCMC is a class of simulation-based methods for generating samples from probability distributions. Any MCMC algorithm simulates a Markov chain with a target distribution as its stationary or equilibrium distribution. The precision of MCMC algorithms increases with the number of iterations. The lack of a stopping rule and convergence rule, however, makes it difficult to determine for how long to run MCMC. The time needed to converge to the target distribution within a prespecified error is referred to as mixing time. Better MCMC algorithms have faster mixing times. Some of the popular MCMC algorithms are random-walk Metropolis, Metropolis–Hastings, and Gibbs sampling.

MCMC sample. An MCMC sample is obtained from MCMC sampling. An MCMC sample approximates a target distribution and is used for summarizing this distribution.

MCMC sample size. MCMC sample size is the size of the MCMC sample. It is specified in bayesmh's option mcmcsize(); see [BAYES] **bayesmh**.

MCMC sampling, MCMC sampler. MCMC sampling is an MCMC algorithm that generates samples from a target probability distribution.

MCMC standard error, MCSE MCSE is the standard error of the posterior mean estimate. It is defined as the standard deviation divided by the square root of ESS. MCSEs are analogs of standard errors in frequentist statistics and measure the accuracy of the simulated MCMC sample.

Metropolis–Hastings (MH) sampling, MH sampler. A Metropolis–Hastings (MH) sampler is an MCMC method for simulating probability distributions. According to this method, at each step of the Markov chain, a new proposal state is generated from the current state according to a prespecified proposal distribution. Based on the current and new state, an acceptance probability is calculated and then used to accept or reject the proposed state. Important characteristics of MH sampling is the acceptance rate and mixing time. The MH algorithm is very general and can be applied to an arbitrary target distribution. However, its efficiency is limited, in terms of mixing time, and decreases as the dimension of the target distribution increases. Gibbs sampling, when available, can provide much more efficient sampling than MH sampling.

mixing of Markov chain. Mixing refers to the rate at which a Markov chain traverses the parameter space. It is a property of the Markov chain that is different from convergence. Poor mixing indicates a slow rate at which the chain explores the stationary distribution and will require more iterations to provide inference at a given precision. Poor (slow) mixing is typically a result of high correlation between model parameters or of weakly-defined model specifications.

model hypothesis testing. Model hypothesis testing tests hypotheses about models by computing model posterior probabilities.

model parameter. A model parameter refers to any (random) parameter in a Bayesian model. Model parameters can be scalars or matrices. Examples of model parameters as defined in bayesmh are {mu}, {scale:s}, {Sigma,matrix}, and {Scale:Omega,matrix}. See [BAYES] **bayesmh** and, specifically, *Declaring model parameters* and *Referring to model parameters* in that entry. Also see *Different ways of specifying model parameters* in [BAYES] **bayesian postestimation**.

model posterior probability. Model posterior probability is probability of a model M computed conditional on the observed data $\mathbf{y}$,

$$P(M|\mathbf{y}) = P(M)P(\mathbf{y}|M) = P(M)m(\mathbf{y})$$

where $P(M)$ is the prior probability of a model M and $m(\mathbf{y})$ is the marginal likelihood under model M.

noninformative prior. A noninformative prior is a prior with negligible influence on the posterior distribution. See, for example, *Jeffreys prior*.

objective prior. See *noninformative prior*.

one-at-a-time MCMC sampling. A one-at-a-time MCMC sample is an MCMC sampling procedure in which random variables are sampled individually, one at a time. For example, in Gibbs sampling, individual variates are sampled one at a time, conditionally on the most recent values of the rest of the variates.

posterior distribution, posterior. A posterior distribution is a probability distribution of model parameters conditional on observed data. The posterior distribution is determined by the likelihood of the parameters and their prior distribution. For a parameter vector $\boldsymbol{\theta}$ and data $\mathbf{y}$, the posterior distribution is given by

$$P(\boldsymbol{\theta}|\mathbf{y}) = \frac{P(\boldsymbol{\theta})P(\mathbf{y}|\boldsymbol{\theta})}{P(\mathbf{y})}$$

where $P(\boldsymbol{\theta})$ is the prior distribution, $P(\mathbf{y}|\boldsymbol{\theta})$ is the model likelihood, and $P(\mathbf{y})$ is the marginal distribution for $\mathbf{y}$. Bayesian inference is based on a posterior distribution.

posterior independence. See *independent a posteriori*.

posterior interval. See *credible interval*.

posterior odds. Posterior odds for $\boldsymbol{\theta}_1$ compared with $\boldsymbol{\theta}_2$ is the ratio of posterior density evaluated at $\boldsymbol{\theta}_1$ and $\boldsymbol{\theta}_2$ under a given model,

$$\frac{p(\boldsymbol{\theta}_1|\mathbf{y})}{p(\boldsymbol{\theta}_2|\mathbf{y})} = \frac{p(\boldsymbol{\theta}_1)}{p(\boldsymbol{\theta}_2)}\frac{p(\mathbf{y}|\boldsymbol{\theta}_1)}{p(\mathbf{y}|\boldsymbol{\theta}_2)}$$

In other words, posterior odds are prior odds times the likelihood ratio.

posterior predictive distribution. A posterior predictive distribution is a distribution of unobserved (future) data conditional on the currently observed data. Posterior predictive distribution is derived by marginalizing the likelihood function with respect to the posterior distribution of model parameters.

prior distribution, prior. In Bayesian statistics, prior distributions are probability distributions of model parameters formed based on some a priori knowledge about parameters. Prior distributions are independent of the observed data.

prior independence. See *independent a priori*.

prior odds. Prior odds for $\boldsymbol{\theta}_1$ compared with $\boldsymbol{\theta}_2$ is the ratio of prior density evaluated at $\boldsymbol{\theta}_1$ and $\boldsymbol{\theta}_2$ under a given model, $p(\boldsymbol{\theta}_1)/p(\boldsymbol{\theta}_2)$. Also see *posterior odds*.

proposal distribution. In the context of the MH algorithm, a proposal distribution is used for defining the transition steps of the Markov chain. In the standard random-walk Metropolis algorithm, the proposal distribution is a multivariate normal distribution with zero mean and adaptable covariance matrix.

pseudoconvergence. A Markov chain may appear to converge when in fact it did not. We refer to this phenomenon as pseudoconvergence. Pseudoconvergence is typically caused by multimodality of the stationary distribution, in which case the chain may fail to traverse the weakly connected regions of the distribution space. A common way to detect pseudoconvergence is to run multiple chains using different starting values and to verify that all of the chain converge to the same target distribution.

random effects. See *random-effects parameters*.

random-effects linear form. A linear form representing a random-effects variable that can be used in substitutable expressions.

random-effects parameters. In the context of Bayesian multilevel models, random-effects parameters are parameters associated with a random-effects variable. Random-effects parameters are assumed to be conditionally independent across levels of the random-effects variable given all other model parameters. Often, random-effects parameters are assumed to be normally distributed with a zero mean and an unknown variance–covariance matrix.

random-effects variable. A variable identifying the group structure for the random effects at a specific level of hierarchy.

reference prior. See *noninformative prior*.

scalar model parameter. A scalar model parameter is any model parameter that is a scalar. For example, `{mean}` and `{hape:alpha}` are scalar parameters, as declared by the `bayesmh` command. Elements of matrix model parameters are viewed as scalar model parameters. For example, for a 2 × 2 matrix parameter `{Sigma,matrix}`, individual elements `{Sigma_1_1}`, `{Sigma_2_1}`, `{Sigma_1_2}`, and `{Sigma_2_2}` are scalar parameters. If a matrix parameter contains a label, the label should be included in the specification of individual elements as well. See [BAYES] **bayesmh**.

scalar parameter. See *scalar model parameter*.

semiconjugate prior. A prior distribution is semiconjugate for a family of likelihood distributions if the prior and (full) conditional posterior distributions belong to the same family of distributions. For semiconjugacy to hold, parameters must typically be independent a priori; that is, their joint prior distribution must be the product of the individual marginal prior distributions. For example, the normal prior distribution for a mean parameter of a normal data distribution with an unknown variance (which is assumed to be independent of the mean a priori) is a semiconjugate prior. Semiconjugacy may provide an efficient way of sampling from posterior distributions and is used in Gibbs sampling.

stationary distribution. Stationary distribution of a stochastic process is a joint distribution that does not change over time. In the context of MCMC, stationary distribution is the target probability distribution to which the Markov chain converges. When MCMC is used for simulating a Bayesian model, the stationary distribution is the target joint posterior distribution of model parameters.

subjective prior. See *informative prior*.

subsampling the chain. See *thinning*.

thinning. Thinning is a way of reducing autocorrelation in the MCMC sample by subsampling the MCMC chain every prespecified number of iterations determined by the thinning interval. For example, the thinning interval of 1 corresponds to using the entire MCMC sample; the thinning interval of 2 corresponds to using every other sample value; and the thinning interval of 3 corresponds to using values from iterations 1, 4, 7, 10, and so on. Thinning should be applied with caution when used to reduce autocorrelation because it may not always be the most appropriate way of improving the precision of estimates.

vague prior. See *noninformative prior*.

valid initial state. See *feasible initial value*.

vanishing adaptation. See *diminishing adaptation*.

Zellner's g-prior. Zellner's g-prior is a form of a weakly informative prior for the regression coefficients in a linear model. It accounts for the correlation between the predictor variables and controls the impact of the prior of the regression coefficients on the posterior with parameter g. For example, $g = 1$ means that prior weight is 50% and $g \to \infty$ means diffuse prior.

Subject and author index

See the combined subject index and the combined author index in the *Glossary and Index*.