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SAS/STAT[®] 12.1 User's Guide The MCMC Procedure (Chapter)



This document is an individual chapter from *SAS/STAT® 12.1 User's Guide*.

The correct bibliographic citation for the complete manual is as follows: SAS Institute Inc. 2012. *SAS/STAT® 12.1 User's Guide*. Cary, NC: SAS Institute Inc.

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Electronic book 1, August 2012

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Chapter 55

The MCMC Procedure

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Overview: MCMC Procedure

The MCMC procedure is a general purpose Markov chain Monte Carlo (MCMC) simulation procedure that is designed to fit Bayesian models. Bayesian statistics is different from traditional statistical methods such as frequentist or classical methods. For a short introduction to Bayesian analysis and related basic concepts, see Chapter 7, “[Introduction to Bayesian Analysis Procedures](#).” Also see the section “[A Bayesian Reading List](#)” on page 156 for a guide to Bayesian textbooks of varying degrees of difficulty.

In essence, Bayesian statistics treats parameters as unknown random variables, and it makes inferences based on the posterior distributions of the parameters. There are several advantages associated with this approach to statistical inference. Some of the advantages include its ability to use prior information and to directly answer specific scientific questions that can be easily understood. For further discussions of the relative advantages and disadvantages of Bayesian analysis, see the section “[Bayesian Analysis: Advantages and Disadvantages](#)” on page 132.

It follows from Bayes’ theorem that a posterior distribution is the product of the likelihood function and the prior distribution of the parameter. In all but the simplest cases, it is very difficult to obtain the posterior distribution directly and analytically. Often, Bayesian methods rely on simulations to generate sample from the desired posterior distribution and use the simulated draws to approximate the distribution and to make all of the inferences.

PROC MCMC is a flexible, simulation-based procedure that is suitable for fitting a wide range of Bayesian models. To use PROC MCMC, you need to specify a likelihood function for the data and a prior distribution for the parameters. If you are fitting hierarchical models, you can specify a hyperprior distribution or distributions for the random-effects parameters. PROC MCMC then obtains samples from the corresponding posterior distributions, produces summary and diagnostic statistics, and saves the posterior samples in an output data set that can be used for further analysis. Although PROC MCMC supports a suite of standard distributions, you can analyze data that have any likelihood, prior, or hyperprior, as long as these functions are programmable using the SAS DATA step functions. There are no constraints on how the parameters can enter the model, in either linear or any nonlinear functional form.

The **MODEL** statement in PROC MCMC can automatically model missing data, response variables, or covariates. In releases before SAS/STAT 12.1, observations with missing values were discarded prior to the analysis. Now, PROC MCMC treats the missing values as unknown parameters and incorporates the sampling of the missing values as part of the simulation.

PROC MCMC selects a sampling method for each parameter or a block of parameters. For example, when conjugacy is available, samples are drawn directly from the full conditional distribution by using standard random number generators. In other cases, PROC MCMC uses an adaptive blocked random walk Metropolis algorithm that uses a normal proposal distribution. You can also choose alternative sampling algorithms, such as the slice sampler.

PROC MCMC Compared with Other SAS Procedures

PROC MCMC is unlike most other SAS/STAT procedures in that the nature of the statistical inference is Bayesian. You specify prior distributions for the parameters with **PRIOR** statements and the likelihood function for the data with **MODEL** statements. PROC MCMC derives inferences from simulation rather than through analytic or numerical methods. You should expect slightly different answers from each run

for the same problem, unless the same random number seed is used. The model specification is similar to PROC NLIN, and PROC MCMC shares some of the syntax of PROC NLMIXED.

You can also carry out a Bayesian analysis with the GENMOD, PHREG, LIFEREG, and FMM procedures for generalized linear models, accelerated life failure models, Cox regression models, piecewise constant baseline hazard models (also known as piecewise exponential models), and finite mixture models. See Chapter 40, “[The GENMOD Procedure](#),” Chapter 67, “[The PHREG Procedure](#),” Chapter 51, “[The LIFEREG Procedure](#),” and Chapter 37, “[The FMM Procedure](#).”

Getting Started: MCMC Procedure

There are three examples in this “Getting Started” section: a simple linear regression, the Behrens-Fisher estimation problem, and a random-effects model. The regression model is chosen for its simplicity; the Behrens-Fisher problem illustrates some advantages of the Bayesian approach; and the random-effects model is one of the most prevalently used models.

Keep in mind that **PARMS** statements declare the parameters in the model, **PRIOR** statements declare the prior distributions, **MODEL** statements declare the likelihood for the data, and **RANDOM** statements declare the random effects. In most cases, you do not need to supply initial values. PROC MCMC advises you if it is unable to generate starting values for the Markov chain.

Simple Linear Regression

This section illustrates some basic features of PROC MCMC by using a linear regression model. The model is as follows:

$$Y_i = \beta_0 + \beta_1 X_i + \epsilon_i$$

for the observations $i = 1, 2, \dots, n$.

The following statements create a SAS data set with measurements of Height and Weight for a group of children:

```

title 'Simple Linear Regression';

data Class;
  input Name $ Height Weight @@;
  datalines;
Alfred 69.0 112.5   Alice 56.5 84.0   Barbara 65.3 98.0
Carol 62.8 102.5   Henry 63.5 102.5   James 57.3 83.0
Jane 59.8 84.5    Janet 62.5 112.5   Jeffrey 62.5 84.0
John 59.0 99.5    Joyce 51.3 50.5    Judy 64.3 90.0
Louise 56.3 77.0   Mary 66.5 112.0   Philip 72.0 150.0
Robert 64.8 128.0  Ronald 67.0 133.0  Thomas 57.5 85.0
William 66.5 112.0
;

```

The equation of interest is as follows:

$$\text{Weight}_i = \beta_0 + \beta_1 \text{Height}_i + \epsilon_i$$

The observation errors, ϵ_i , are assumed to be independent and identically distributed with a normal distribution with mean zero and variance σ^2 .

$$\text{Weight}_i \sim \text{normal}(\beta_0 + \beta_1 \text{Height}_i, \sigma^2)$$

The likelihood function for each of the `Weight`, which is specified in the `MODEL` statement, is as follows:

$$p(\text{Weight}|\beta_0, \beta_1, \sigma^2, \text{Height}_i) = \phi(\beta_0 + \beta_1 \text{Height}_i, \sigma^2)$$

where $p(\cdot|\cdot)$ denotes a conditional probability density and ϕ is the normal density. There are three parameters in the likelihood: β_0 , β_1 , and σ^2 . You use the `PARMS` statement to indicate that these are the parameters in the model.

Suppose you want to use the following three prior distributions on each of the parameters:

$$\begin{aligned}\pi(\beta_0) &= \phi(0, \text{var} = 1e6) \\ \pi(\beta_1) &= \phi(0, \text{var} = 1e6) \\ \pi(\sigma^2) &= f_{i\Gamma}(\text{shape} = 3/10, \text{scale} = 10/3)\end{aligned}$$

where $\pi(\cdot)$ indicates a prior distribution and $f_{i\Gamma}$ is the density function for the inverse-gamma distribution. The normal priors on β_0 and β_1 have large variances, expressing your lack of knowledge about the regression coefficients. The priors correspond to an equal-tail 95% credible intervals of approximately (-2000, 2000) for β_0 and β_1 . Priors of this type are often called *vague* or *diffuse* priors. See the section “[Prior Distributions](#)” on page 127 for more information. Typically diffuse prior distributions have little influence on the posterior distribution and are appropriate when stronger prior information about the parameters is not available.

A frequently used prior for the variance parameter σ^2 is the inverse-gamma distribution. See [Table 55.22](#) in the section “[Standard Distributions](#)” on page 4476 for the density definition. The inverse-gamma distribution is a conjugate prior (see the section “[Conjugate Sampling](#)” on page 4472) for the variance parameter in a normal distribution. Also see the section “[Gamma and Inverse-Gamma Distributions](#)” on page 4512 for typical usages of the gamma and inverse-gamma prior distributions. With a shape parameter of 3/10 and a scale parameter of 10/3, this prior corresponds to an equal-tail 95% credible interval of (1.7, 1E6), with the mode at 2.5641 for σ^2 . Alternatively, you can use any other prior distribution with positive support on this variance component. For example, you can use the gamma prior.

According to Bayes’ theorem, the likelihood function and prior distributions determine the posterior (joint) distribution of β_0 , β_1 , and σ^2 as follows:

$$\pi(\beta_0, \beta_1, \sigma^2 | \text{Weight}, \text{Height}) \propto \pi(\beta_0)\pi(\beta_1)\pi(\sigma^2)p(\text{Weight}|\beta_0, \beta_1, \sigma^2, \text{Height})$$

You do not need to know the form of the posterior distribution when you use PROC MCMC. PROC MCMC automatically obtains samples from the desired posterior distribution, which is determined by the prior and likelihood you supply.

The following statements fit this linear regression model with diffuse prior information:

```
ods graphics on;
proc mcmc data=class outpost=classout nmc=10000 thin=2 seed=246810;
  parms beta0 0 beta1 0;
  parms sigma2 1;
  prior beta0 beta1 ~ normal(mean = 0, var = 1e6);
  prior sigma2 ~ igamma(shape = 3/10, scale = 10/3);
  mu = beta0 + beta1*height;
  model weight ~ n(mu, var = sigma2);
run;
ods graphics off;
```

When ODS Graphics is enabled, diagnostic plots, such as the trace and autocorrelation function plots of the posterior samples, are displayed. For more information about ODS Graphics, see Chapter 21, “[Statistical Graphics Using ODS](#).”

The PROC MCMC statement invokes the procedure and specifies the input data set `Class`. The output data set `Classout` contains the posterior samples for all of the model parameters. The `NMC=` option specifies the number of posterior simulation iterations. The `THIN=` option controls the thinning of the Markov chain and specifies that one of every 2 samples is kept. Thinning is often used to reduce the correlations among posterior sample draws. In this example, 5,000 simulated values are saved in the `Classout` data set. The `SEED=` option specifies a seed for the random number generator, which guarantees the reproducibility of the random stream. For more information about Markov chain sample size, burn-in, and thinning, see the section “[Burn-in, Thinning, and Markov Chain Samples](#)” on page 138.

The `PARMS` statements identify the three parameters in the model: `beta0`, `beta1`, and `sigma2`. Each statement also forms a block of parameters, where the parameters are updated simultaneously in each iteration. In this example, `beta0` and `beta1` are sampled jointly, conditional on `sigma2`; and `sigma2` is sampled conditional on fixed values of `beta0` and `beta1`. In simple regression models such as this, you expect the parameters `beta0` and `beta1` to have high posterior correlations, and placing them both in the same block improves the mixing of the chain—that is, the efficiency that the posterior parameter space is explored by the Markov chain. For more information, see the section “[Blocking of Parameters](#)” on page 4466. The `PARMS` statements also assign initial values to the parameters (see the section “[Initial Values of the Markov Chains](#)” on page 4474). The regression parameters are given 0 as their initial values, and the scale parameter `sigma2` starts at value 1. If you do not provide initial values, PROC MCMC chooses starting values for every parameter.

The `PRIOR` statements specify prior distributions for the parameters. The parameters `beta0` and `beta1` both share the same prior—a normal prior with mean 0 and variance 1e6. The parameter `sigma2` has an inverse-gamma distribution with a shape parameter of 3/10 and a scale parameter of 10/3. For a list of standard distributions that PROC MCMC supports, see the section “[Standard Distributions](#)” on page 4476.

The `MU` assignment statement calculates the expected value of `Weight` as a linear function of `Height`. The `MODEL` statement uses the shorthand notation, `n`, for the normal distribution to indicate that the response variable, `Weight`, is normally distributed with parameters `mu` and `sigma2`. The functional argument `MEAN=` in the normal distribution is optional, but you have to indicate whether `sigma2` is a variance (`VAR=`), a standard deviation (`SD=`), or a precision (`PRECISION=`) parameter. See [Table 55.2](#) in the section “[MODEL Statement](#)” on page 4443 for distribution specifications.

The distribution parameters can contain expressions. For example, you can write the `MODEL` statement as follows:

```
model weight ~ n(beta0 + betal*height, var = sigma2);
```

Before you do any posterior inference, it is essential that you examine the convergence of the Markov chain (see the section “[Assessing Markov Chain Convergence](#)” on page 139). You cannot make valid inferences if the Markov chain has not converged. A very effective convergence diagnostic tool is the trace plot. Although PROC MCMC produces graphs at the end of the procedure output (see [Figure 55.5](#)), you should visually examine the convergence graph first.

The first table that PROC MCMC produces is the “Number of Observations” table, as shown in [Figure 55.1](#). This table lists the number of observations read from the `DATA=` data set and the number of observations used in the analysis.

Figure 55.1 Observation Information

Simple Linear Regression	
The MCMC Procedure	
Number of Observations Read	19
Number of Observations Used	19

The “Parameters” table, shown in [Figure 55.2](#), lists the names of the parameters, the blocking information, the sampling method used, the starting values, and the prior distributions. For more information about blocking information, see the section “[Blocking of Parameters](#)” on page 4466; for more information about starting values, see the section “[Initial Values of the Markov Chains](#)” on page 4474. The first block, which consists of the parameters `beta0` and `beta1`, uses a random walk Metropolis algorithm. The second block, which consists of the parameter `sigma2`, is updated via its full conditional distribution in conjugacy. You should check this table to ensure that you have specified the parameters correctly, especially for complicated models.

Figure 55.2 Parameter Information

Parameters				
Block	Parameter	Sampling Method	Initial Value	Prior Distribution
1	<code>beta0</code>	N-Metropolis	0	<code>normal(mean = 0, var = 1e6)</code>
	<code>beta1</code>		0	<code>normal(mean = 0, var = 1e6)</code>
2	<code>sigma2</code>	Conjugate	1.0000	<code>igamma(shape = 3/10, scale = 10/3)</code>

For each posterior distribution, PROC MCMC also reports summary statistics (posterior means, standard deviations, and quantiles) and interval statistics (95% equal-tail and highest posterior density credible intervals), as shown in [Figure 55.3](#). For more information about posterior statistics, see the section “[Summary Statistics](#)” on page 153.

Figure 55.3 MCMC Summary and Interval Statistics

Simple Linear Regression						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
beta0	5000	-142.8	33.4326	-164.8	-142.3	-120.0
beta1	5000	3.8924	0.5333	3.5361	3.8826	4.2395
sigma2	5000	137.3	51.1030	101.9	127.2	161.2
Posterior Intervals						
Parameter	Alpha	Equal-Tail Interval		HPD Interval		
beta0	0.050	-208.9	-78.7305	-210.8	-81.6714	
beta1	0.050	2.8790	4.9449	2.9056	4.9545	
sigma2	0.050	69.1351	259.8	59.2362	236.3	

By default, PROC MCMC also computes a number of convergence diagnostics to help you determine whether the chain has converged. These are the Monte Carlo standard errors, the autocorrelations at selected lags, the Geweke diagnostics, and the effective sample sizes. These statistics are shown in [Figure 55.4](#). For details and interpretations of these diagnostics, see the section “[Assessing Markov Chain Convergence](#)” on page 139.

The “Monte Carlo Standard Errors” table indicates that the standard errors of the mean estimates for each of the parameters are relatively small, with respect to the posterior standard deviations. The values in the “MCSE/SD” column (ratios of the standard errors and the standard deviations) are small, around 0.03. This means that only a fraction of the posterior variability is due to the simulation. The “Autocorrelations of the Posterior Samples” table shows that the autocorrelations among posterior samples reduce quickly and become almost nonexistent after a few lags. The “Geweke Diagnostics” table indicates that no parameter failed the test, and the “Effective Sample Sizes” table reports the number of effective sample sizes of the Markov chain.

Figure 55.4 MCMC Convergence Diagnostics

Simple Linear Regression			
The MCMC Procedure			
Monte Carlo Standard Errors			
Parameter	MCSE	Standard Deviation	MCSE/SD
beta0	1.0070	33.4326	0.0301
beta1	0.0159	0.5333	0.0299
sigma2	0.9473	51.1030	0.0185

Figure 55.4 *continued*

Posterior Autocorrelations				
Parameter	Lag 1	Lag 5	Lag 10	Lag 50
beta0	0.6177	0.1083	0.0250	-0.0007
beta1	0.6162	0.1052	0.0217	0.0029
sigma2	0.1224	0.0216	0.0098	0.0197

Geweke Diagnostics		
Parameter	z	Pr > z
beta0	1.0267	0.3046
beta1	-0.9305	0.3521
sigma2	-0.3578	0.7205

Effective Sample Sizes			
Parameter	ESS	Autocorrelation	
		Time	Efficiency
beta0	1102.2	4.5366	0.2204
beta1	1119.0	4.4684	0.2238
sigma2	2910.1	1.7182	0.5820

PROC MCMC produces a number of graphs, shown in [Figure 55.5](#), which also aid convergence diagnostic checks. With the trace plots, there are two important aspects to examine. First, you want to check whether the mean of the Markov chain has stabilized and appears constant over the graph. Second, you want to check whether the chain has good mixing and is “dense,” in the sense that it quickly traverses the support of the distribution to explore both the tails and the mode areas efficiently. The plots show that the chains appear to have reached their stationary distributions.

Next, you should examine the autocorrelation plots, which indicate the degree of autocorrelation for each of the posterior samples. High correlations usually imply slow mixing. Finally, the kernel density plots estimate the posterior marginal distributions for each parameter.

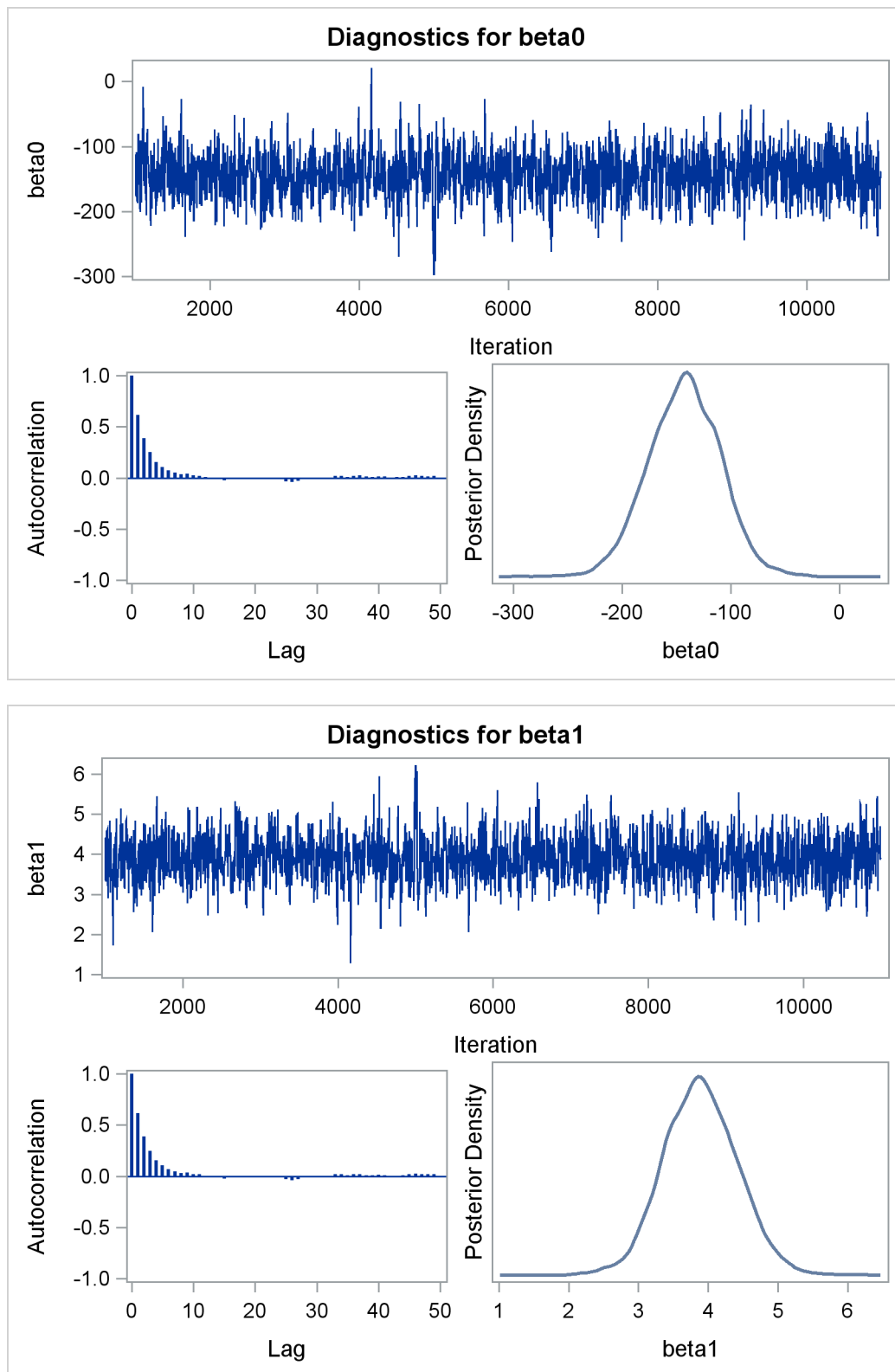
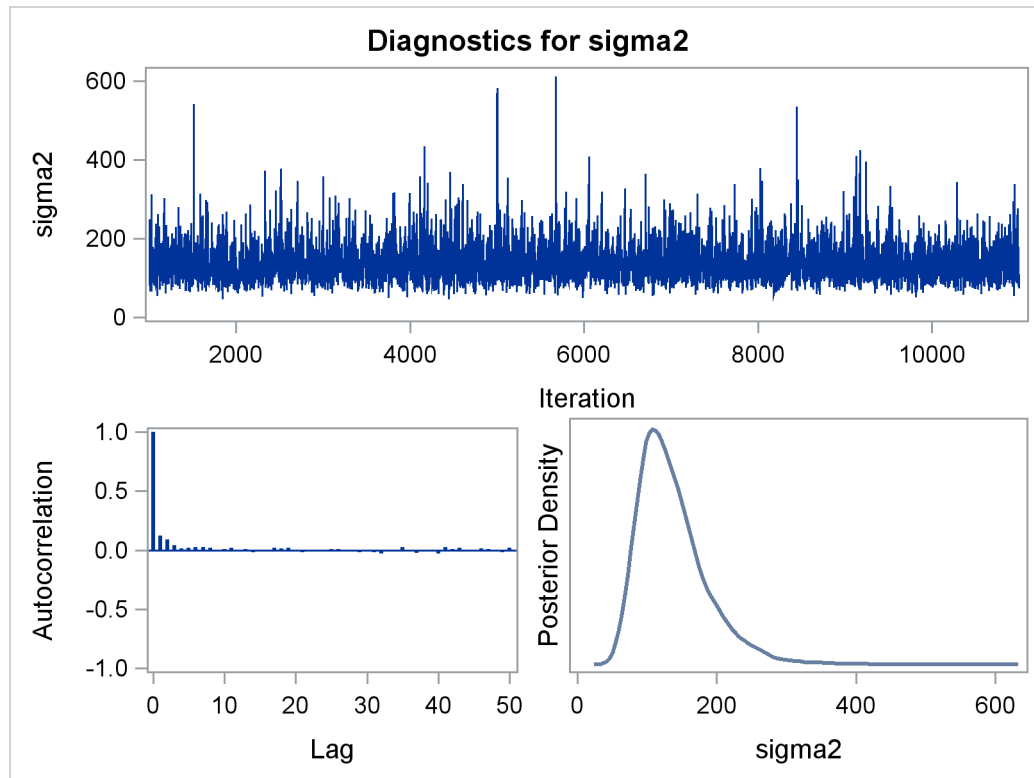
Figure 55.5 Diagnostic Plots for β_0 , β_1 and σ^2 

Figure 55.5 continued



In regression models such as this, you expect the posterior estimates to be very similar to the maximum likelihood estimators with noninformative priors on the parameters. The REG procedure produces the following fitted model (code not shown):

$$\text{Weight} = -143.0 + 3.9 \times \text{Height}$$

These are very similar to the means shown in Figure 55.3. With PROC MCMC, you can carry out informative analysis that uses specifications to indicate prior knowledge on the parameters. Informative analysis is likely to produce different posterior estimates, which are the result of information from both the likelihood and the prior distributions. Incorporating additional information in the analysis is one major difference between the classical and Bayesian approaches to statistical inference.

The Behrens-Fisher Problem

One of the famous examples in the history of statistics is the Behrens-Fisher problem (Fisher 1935). Consider the situation where there are two independent samples from two different normal distributions:

$$\begin{aligned} y_{11}, y_{12}, \dots, y_{1n_1} &\sim \text{normal}(\mu_1, \sigma_1^2) \\ y_{21}, y_{22}, \dots, y_{2n_2} &\sim \text{normal}(\mu_2, \sigma_2^2) \end{aligned}$$

Note that $n_1 \neq n_2$. When you do not want to assume that the variances are equal, testing the hypothesis $H_0 : \mu_1 = \mu_2$ is a difficult problem in the classical statistics framework, because the distribution under H_0

is not known. Within the Bayesian framework, this problem is straightforward because you can estimate the posterior distribution of $\mu_1 - \mu_2$ while taking into account the uncertainties in all of parameters by treating them as random variables.

Suppose you have the following set of data:

```

title 'The Behrens-Fisher Problem';

data behrens;
  input y ind @@;
  datalines;
121 1  94 1 119 1 122 1 142 1 168 1 116 1
172 1 155 1 107 1 180 1 119 1 157 1 101 1
145 1 148 1 120 1 147 1 125 1 126 2 125 2
130 2 130 2 122 2 118 2 118 2 111 2 123 2
126 2 127 2 111 2 112 2 121 2
;

```

The response variable is y , and the ind variable is the group indicator, which takes two values: 1 and 2. There are 19 observations that belong to group 1 and 14 that belong to group 2.

The likelihood functions for the two samples are as follows:

$$\begin{aligned}
 p(y_{1i}|\mu_1, \sigma_1^2) &= \phi(y_{1i}; \mu_1, \sigma_1^2) \text{ for } i = 1, \dots, 19 \\
 p(y_{2j}|\mu_2, \sigma_2^2) &= \phi(y_{2j}; \mu_2, \sigma_2^2) \text{ for } j = 1, \dots, 14
 \end{aligned}$$

Berger (1985) showed that a uniform prior on the support of the location parameter is a noninformative prior. The distribution is invariant under location transformations—that is, $\theta = \mu + c$. You can use this prior for the mean parameters in the model:

$$\begin{aligned}
 \pi(\mu_1) &\propto 1 \\
 \pi(\mu_2) &\propto 1
 \end{aligned}$$

In addition, Berger (1985) showed that a prior of the form $1/\sigma^2$ is noninformative for the scale parameter, and it is invariant under scale transformations (that is $\tau = c\sigma^2$). You can use this prior for the variance parameters in the model:

$$\begin{aligned}
 \pi(\sigma_1^2) &\propto 1/\sigma_1^2 \\
 \pi(\sigma_2^2) &\propto 1/\sigma_2^2
 \end{aligned}$$

The log densities of the prior distributions on σ_1^2 and σ_2^2 are:

$$\begin{aligned}
 \log(\pi(\sigma_1^2)) &= -\log(\sigma_1^2) \\
 \log(\pi(\sigma_2^2)) &= -\log(\sigma_2^2)
 \end{aligned}$$

The following statements generate posterior samples of $\mu_1, \mu_2, \sigma_1^2, \sigma_2^2$, and the difference in the means: $\mu_1 - \mu_2$:

```

proc mcmc data=behrens outpost=postout seed=123
    nmc=40000 thin=10 monitor=(_parms_ mudif)
    statistics(alpha=0.01)=(summary interval);
ods select PostSummaries PostIntervals;
parm mu1 0 mu2 0;
parm sig21 1;
parm sig22 1;
prior mu: ~ general(0);
prior sig21 ~ general(-log(sig21), lower=0);
prior sig22 ~ general(-log(sig22), lower=0);
mudif = mu1 - mu2;
if ind = 1 then do;
    mu = mu1;
    s2 = sig21;
end;
else do;
    mu = mu2;
    s2 = sig22;
end;
model y ~ normal(mu, var=s2);
run;

```

The PROC MCMC statement specifies an input data set (Behrens), an output data set containing the posterior samples (Postout), a random number seed, the simulation size, and the thinning rate. The **MONITOR=** option specifies a list of symbols, which can be either parameters or functions of the parameters in the model, for which inference is to be done. The symbol _parms_ is a shorthand for all model parameters—in this case, μ_1 , μ_2 , sig21 , and sig22 . The symbol `mudif` is defined in the program as the difference between μ_1 and μ_2 .

The **STATISTICS=** option requests the calculation of summary and interval statistics. The global suboption **ALPHA=0.01** specifies 99% equal-tail and highest posterior density (HPD) credible intervals for all parameters.

The ODS SELECT statement displays the summary statistics and interval statistics tables while excluding all other output. For a complete list of ODS tables that PROC MCMC can produce, see the sections “[Displayed Output](#)” on page 4533 and “[ODS Table Names](#)” on page 4537.

The **PARMS** statements assign the parameters μ_1 and μ_2 to the same block, and sig21 and sig22 each to their own separate blocks. There are a total of three blocks. The **PARMS** statements also assign an initial value to each parameter.

The **PRIOR** statements specify prior distributions for the parameters. Because the priors are all nonstandard (uniform on the real axis for μ_1 and μ_2 and $1/\sigma^2$ for σ_1^2 and σ_2^2), you must use the **GENERAL** function here. The argument in the **GENERAL** function is an expression for the log of the distribution, up to an additive constant. This distribution can have any functional form, as long as it is programmable using SAS functions and expressions. The function specifies a distribution on the log scale, not on the original scale. The log of the prior on μ_1 and μ_2 is 0, and the log of the priors on sig21 and sig22 are $-\log(\text{sig21})$ and $-\log(\text{sig22})$ respectively. See the section “[Specifying a New Distribution](#)” on page 4490 for more information about how to specify an arbitrary distribution. The **LOWER=** option indicates that both variance terms must be strictly positive.

The MUDIF assignment statement calculates the difference between μ_1 and μ_2 . The IF-ELSE statements enable different y 's to have different mean and variance, depending on their group indicator ind . The **MODEL** statement specifies the normal likelihood function for each observation in the model.

Figure 55.6 displays the posterior summary and interval statistics.

Figure 55.6 Posterior Summary and Interval Statistics

The Behrens-Fisher Problem						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
mu1	4000	134.8	6.0065	130.9	134.7	138.7
mu2	4000	121.4	1.9150	120.2	121.4	122.7
sig21	4000	683.2	259.9	507.8	630.1	792.3
sig22	4000	51.3975	24.2881	35.0212	45.7449	61.2582
mudif	4000	13.3596	6.3335	9.1732	13.4078	17.6332
Posterior Intervals						
Parameter	Alpha	Equal-Tail Interval		HPD Interval		
mu1	0.010	118.7	150.6	119.3	151.0	
mu2	0.010	115.9	126.6	116.2	126.7	
sig21	0.010	292.0	1821.1	272.8	1643.7	
sig22	0.010	18.5883	158.8	16.3730	140.5	
mudif	0.010	-3.2537	29.9987	-3.1915	30.0558	

The mean difference has a posterior mean value of 13.36, and the lower endpoints of the 99% credible intervals are negative. This suggests that the mean difference is positive with a high probability. However, if you want to estimate the probability that $\mu_1 - \mu_2 > 0$, you can do so as follows.

The following statements produce Figure 55.7:

```
proc format;
  value diffmt low=0 = 'mu1 - mu2 <= 0' 0<-high = 'mu1 - mu2 > 0';
run;

proc freq data = postout;
  tables mudif /nocum;
  format mudif diffmt.;
run;
```

The sample estimate of the posterior probability that $\mu_1 - \mu_2 > 0$ is 0.98. This example illustrates an advantage of Bayesian analysis. You are not limited to making inferences based on model parameters only. You can accurately quantify uncertainties with respect to any function of the parameters, and this allows for flexibility and easy interpretations in answering many scientific questions.

Figure 55.7 Estimated Probability of $\mu_1 - \mu_2 > 0$.

The Behrens-Fisher Problem		
The FREQ Procedure		
mudif	Frequency	Percent

mu1 - mu2 <= 0	77	1.93
mu1 - mu2 > 0	3923	98.08

Random-Effects Model

This example illustrates how you can fit a normal likelihood random-effects model in PROC MCMC. PROC MCMC offers you the ability to model beyond the normal likelihood (see “[Example 55.7: Logistic Regression Random-Effects Model](#)” on page 4579, “[Example 55.8: Nonlinear Poisson Regression Multilevel Random-Effects Model](#)” on page 4581, and “[Example 55.16: Piecewise Exponential Frailty Model](#)” on page 4631).

Consider a scenario in which data are collected in groups and you want to model group-specific effects. You can use a random-effects model (sometimes also known as a variance-components model):

$$y_{ij} = \beta_0 + \beta_1 x_{ij} + \gamma_i + e_{ij}, \quad e_{ij} \sim \text{normal}(0, \sigma^2)$$

where $i = 1, 2, \dots, I$ is the group index and $j = 1, 2, \dots, n_i$ indexes the observations in the i th group. In the regression model, the fixed effects β_0 and β_1 are the intercept and the coefficient for variable x_{ij} , respectively. The random effect γ_i is the mean for the i th group, and e_{ij} are the error term.

Consider the following SAS data set:

```

title 'Random-Effects Model';

data heights;
  input Family G$ Height @@;
  datalines;
1 F 67   1 F 66   1 F 64   1 M 71   1 M 72   2 F 63
2 F 63   2 F 67   2 M 69   2 M 68   2 M 70   3 F 63
3 M 64   4 F 67   4 F 66   4 M 67   4 M 67   4 M 69
;

```

The response variable Height measures the heights (in inches) of 18 individuals. The covariate x is the gender (variable G), and the individuals are grouped according to Family (group index). Since the variable G is a character variable and PROC MCMC does not support a CLASS statement, you need to create the corresponding design matrix. In this example, the design matrix for a factor variable of level 2 (M and F) can be constructed using the following statement:

```

data input;
  set heights;
  if g eq 'F' then gf = 1;
  else gf = 0;
  drop g;
run;

```

The data set variable `gf` is a numeric variable and can be used in the regression model in PROC MCMC.

In data sets with factor variables that have more levels, you can consider using PROC TRANSREG to construct the design matrix. See the section “[Create Design Matrix](#)” on page 4502 for more information.

To model the data, you can assume that `Height` is normally distributed:

$$y_{ij} \sim \text{normal}(\mu_{ij}, \sigma^2), \quad \mu_{ij} = \beta_0 + \beta_1 \text{gf}_{ij} + \gamma_i$$

The priors on the parameters β_0 , β_1 , γ_i are also assumed to be normal:

$$\begin{aligned} \beta_0 &\sim \text{normal}(0, \text{var} = 1e5) \\ \beta_1 &\sim \text{normal}(0, \text{var} = 1e5) \\ \gamma_i &\sim \text{normal}(0, \text{var} = \sigma_\gamma^2) \end{aligned}$$

Priors on the variance terms, σ^2 and σ_γ^2 , are inverse-gamma:

$$\begin{aligned} \sigma^2 &\sim \text{igamma}(\text{shape} = 0.01, \text{scale} = 0.01) \\ \sigma_\gamma^2 &\sim \text{igamma}(\text{shape} = 0.01, \text{scale} = 0.01) \end{aligned}$$

The inverse-gamma distribution is a conjugate prior for the variance in the normal likelihood and the variance in the prior distribution of the random effect.

The following statements fit a linear random-effects model to the data and produce the output shown in [Figure 55.9](#) and [Figure 55.10](#):

```

ods graphics on;
proc mcmc data=input outpost=postout nmc=50000 thin=5 seed=7893 plots=trace;
  ods select Parameters REparameters PostSummaries PostIntervals
    tracepanel;
  parms b0 0 b1 0 s2 1 s2g 1;

  prior b: ~ normal(0, var = 10000);
  prior s: ~ igamma(0.01, scale = 0.01);
  random gamma ~ normal(0, var = s2g) subject=family monitor=(gamma);
  mu = b0 + b1 * gf + gamma;
  model height ~ normal(mu, var = s2);
run;
ods graphics off;

```

Some of the statements are very similar to those shown in the previous two examples. The ODS GRAPHICS ON statement enables ODS Graphics. The PROC MCMC statement specifies the input and output data sets, the simulation size, the thinning rate, and a random number seed. The ODS SELECT statement displays

the model parameter and random-effects parameter information tables, summary statistics table, the interval statistics table, and the trace plots.

The **PARMS** statement lumps all four model parameters in a single block. They are **b0** (overall intercept), **b1** (main effect for **gf**), **s2** (variance of the likelihood function), and **s2g** (variance of the random effect). If a random walk Metropolis sampler is the only applicable sampler for all parameters, then these four parameters are updated in a single block. However, because PROC MCMC updates the parameters **s2** and **s2g** via conjugacy, these parameters are separated into individual blocks. (See the Block column in “Parameters” table in Figure 55.8.)

The **PRIOR** statements specify priors for all the parameters. The notation **b:** is a shorthand for all symbols that start with the letter ‘b’. In this example, **b:** includes **b0** and **b1**. Similarly, **s:** stands for both **s2** and **s2g**. This shorthand notation can save you some typing, and it keeps your statements tidy.

The **RANDOM** statement specifies a single random effect to be **gamma**, and specifies that it has a normal prior centered at 0 with variance **s2g**. The **SUBJECT=** argument in the **RANDOM** statement defines a group index (family) in the model, where all observations from the same family should have the same group indicator value. The **MONITOR=** option outputs analysis for all the random-effects parameters.

Finally, the **MU** assignment statement calculates the expected value of the height of the model. The calculation includes the random-effects term **gamma**. The **MODEL** statement specifies the likelihood function for height.

The “Parameters” and “Random-Effects Parameters” tables, shown in Figure 55.8, contain information about the model parameters and the four random-effects parameters.

Figure 55.8 Model and Random-Effects Parameter Information

Random-Effects Model					
The MCMC Procedure					
Parameters					
Block	Parameter	Sampling Method	Initial Value	Prior Distribution	
1	s2	Conjugate	1.0000	igamma(0.01, scale = 0.01)	
2	s2g	Conjugate	1.0000	igamma(0.01, scale = 0.01)	
3	b0	N-Metropolis	0	normal(0, var = 10000)	
	b1		0	normal(0, var = 10000)	
Random Effect Parameters					
Parameter	Sampling Method	Subject	Number of Subjects	Subject Values	Prior Distribution
gamma	N-Metropolis	Family	4	1 2 3 4	normal(0, var = s2g)

The posterior summary and interval statistics for the model parameters and the random-effects parameters are shown in Figure 55.9.

Figure 55.9 Posterior Summary and Interval Statistics

Random-Effects Model						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
b0	10000	68.4717	1.2735	67.7757	68.4495	69.1213
b1	10000	-3.5533	0.9740	-4.1829	-3.5381	-2.9375
s2	10000	4.1334	1.9372	2.8024	3.7093	4.9790
s2g	10000	5.1508	23.4698	0.2312	1.3104	4.2433
gamma_1	10000	0.9404	1.3219	0.0860	0.6963	1.6322
gamma_2	10000	0.0131	1.1935	-0.4020	0.0214	0.4878
gamma_3	10000	-1.3481	1.6535	-2.1852	-0.9346	-0.1252
gamma_4	10000	0.0945	1.1931	-0.3323	0.0528	0.5643

Posterior Intervals					
Parameter	Alpha	Equal-Tail Interval		HPD Interval	
b0	0.050	65.8646	71.1331	65.9097	71.1712
b1	0.050	-5.5058	-1.6127	-5.4201	-1.5651
s2	0.050	1.7166	9.0766	1.3678	7.8796
s2g	0.050	0.00983	32.7002	0.00105	19.0298
gamma_1	0.050	-1.0884	4.0560	-1.0160	4.0923
gamma_2	0.050	-2.5942	2.5279	-2.5357	2.5636
gamma_3	0.050	-5.4957	0.6638	-4.7168	1.0677
gamma_4	0.050	-2.4901	2.7349	-2.5895	2.5888

Trace plots for all the parameters are shown in [Figure 55.10](#). The mixing looks very reasonable, suggesting convergence.

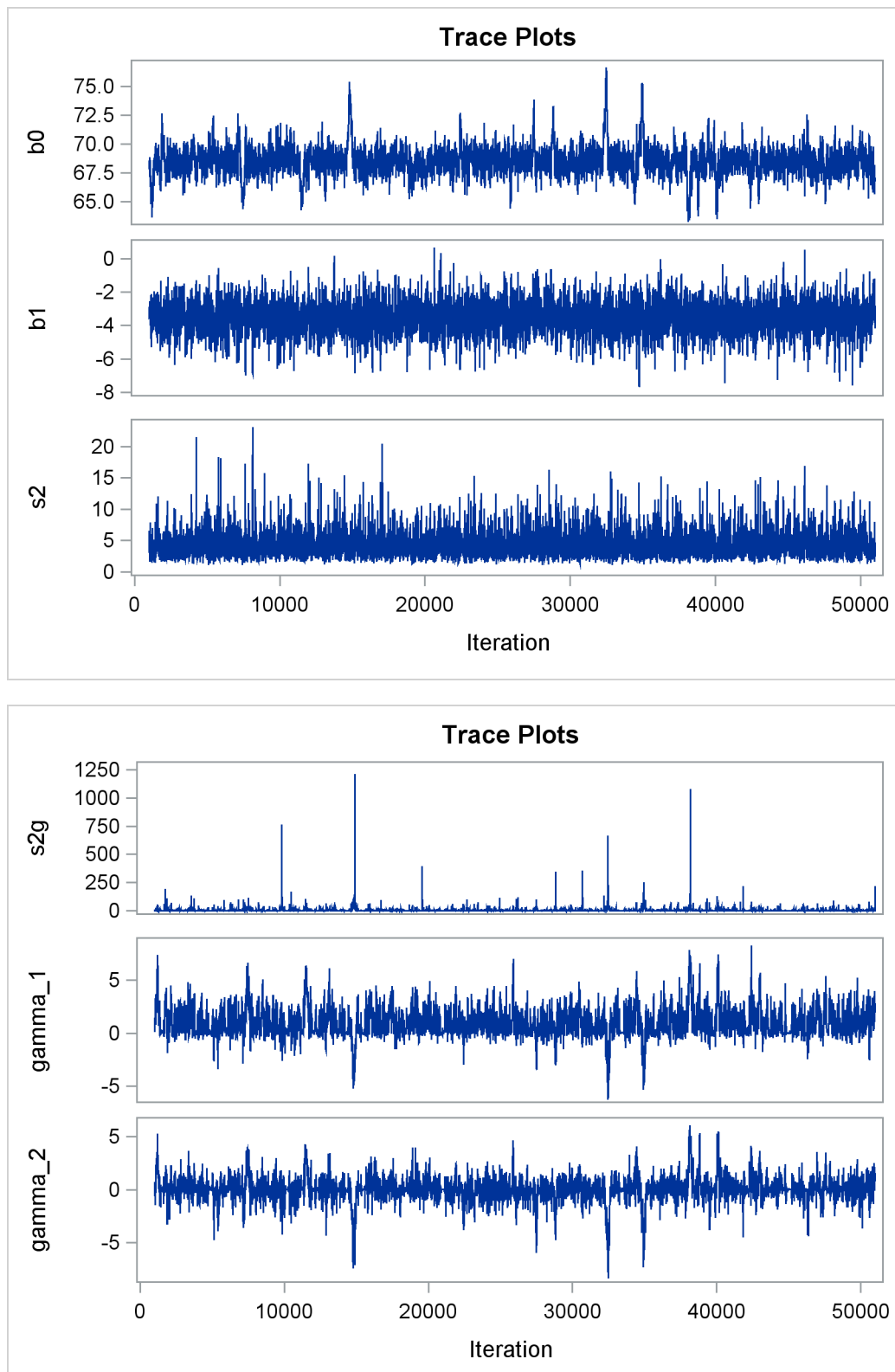
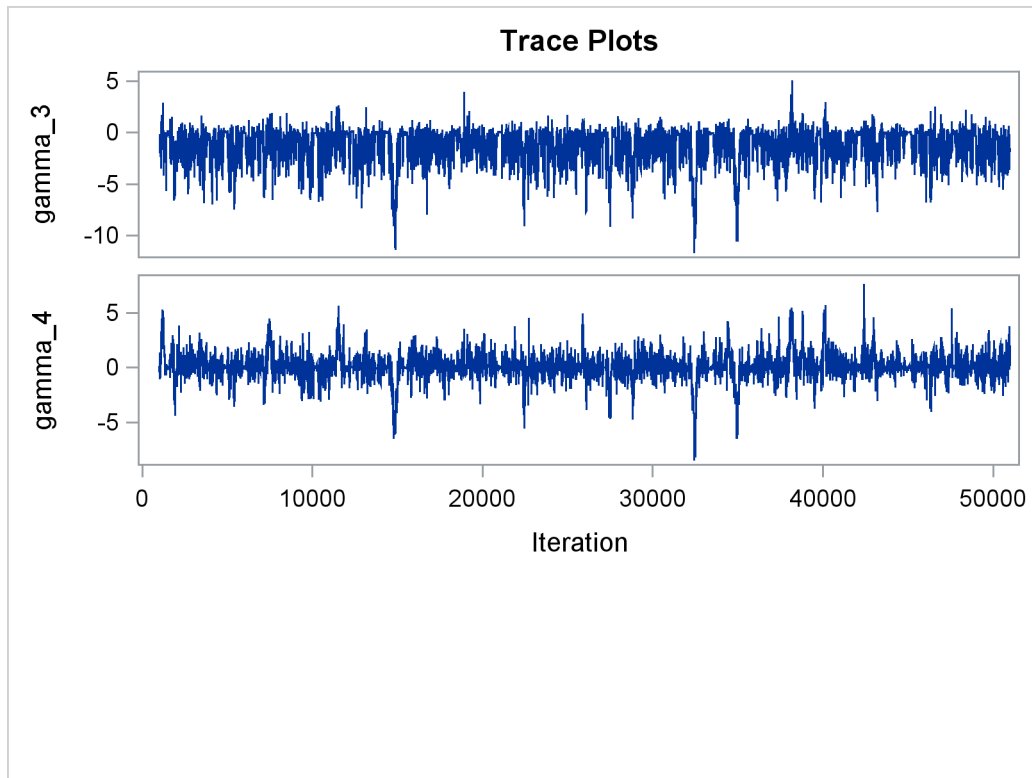
Figure 55.10 Plots for b_1 and Log of the Posterior Density

Figure 55.10 continued



From the interval statistics table, you see that both the equal-tail and HPD intervals for β_0 are positive, strongly indicating the positive effect of the parameter. On the other hand, both intervals for β_1 cover the value zero, indicating that *gf* does not have a strong impact on predicting height in this model.

Syntax: MCMC Procedure

The following statements are available in the MCMC procedure. Items within < > are optional.

```

PROC MCMC < options > ;
  ARRAY arrayname [ dimensions ] < $ > < variables-and-constants > ;
  BEGINCNST/ENDCNST ;
  BEGINNODATA/ENDNODATA ;
  BY variables ;
  MODEL variable ~ distribution < options > ;
  PARMS parameter < = > number < / options > ;
  PREDDIST < 'label' > OUTPRED=SAS-data-set < options > ;
  PRIOR/HYPERPRIOR parameter ~ distribution ;
  Programming statements ;
  RANDOM random-effects-specification < / options > ;
  UDS subroutine-name (subroutine-argument-list) ;

```

The **PARMS** statements declare parameters in the model and assign optional starting values for the Markov chain. The **PRIOR/HYPERPRIOR** statements specify the prior distributions of the parameters. The **MODEL** statements specify the log-likelihood functions for the response variables. These statements form the basis of most Bayesian models.

In addition, you can use the **ARRAY** statement to define constant or parameter arrays, the **BEGINNST/ENDCNST** and **BEGINNODATA/ENDNODATA** statements to omit unnecessary evaluation and reduce simulation time, the **PREDDIST** statement to generate samples from the posterior predictive distribution, the **program statements** to specify more complicated models that you want to fit, the **RANDOM** statement to specify random effects and their prior distributions, and the **UDS** statement to define your own Gibbs samplers to sample parameters in the model.

The following sections provide a description of each of these statements.

PROC MCMC Statement

PROC MCMC *options* ;

The PROC MCMC statement invokes the MCMC procedure. [Table 55.1](#) summarizes the options available in the PROC MCMC statement.

Table 55.1 PROC MCMC Statement Options

Option	Description
Basic options	
DATA=	Names the input data set
OUTPOST=	Names the output data set for posterior samples of parameters
Debugging output	
LIST	Displays model program and variables
LISTCODE	Displays compiled model program
TRACE	Displays detailed model execution messages
Frequently used MCMC options	
MAXTUNE=	Specifies the maximum number of tuning loops
MINTUNE=	Specifies the minimum number of tuning loops
NBI=	Specifies the number of burn-in iterations
NMC=	Specifies the number of MCMC iterations, excluding the burn-in iterations
NTU=	Specifies the number of tuning iterations
PROPCOV=	Controls options for constructing the initial proposal covariance matrix
SEED=	Specifies the random seed for simulation
THIN=	Specifies the thinning rate
Less frequently used MCMC options	
ACCEPTTOL=	Specifies the acceptance rate tolerance
DISCRETE=	Controls sampling discrete parameters
INIT=	Controls generating initial values
MCHISTORY=	Displays Markov chain sampling history
MAXINDEXPRINT=	Specifies the maximum number of observation indices to print in models with missing data

Table 55.1 (continued)

Option	Description
MAXSUBVALUEPRINT=	Specifies the maximum number of subject values to print in the “Random Effects Parameters” table
PROPDIST=	Specifies the proposal distribution
REOBSINFO	Displays more detailed information about each random effect
SCALE=	Specifies the initial scale applied to the proposal distribution
TARGACCEPT=	Specifies the target acceptance rate for random walk sampler
TARGACCEPTI=	Specifies the target acceptance rate for independence sampler
TUNEW=	Specifies the weight used in covariance updating
Summary, diagnostics, and plotting options	
AUTOCORLAG=	Specifies the number of autocorrelation lags used to compute effective sample sizes and Monte Carlo errors
DIAGNOSTICS=	Controls the convergence diagnostics
DIC	Computes deviance information criterion (DIC)
MONITOR=	Outputs analysis for a list of symbols of interest
PLOTS=	Controls plotting
STATISTICS=	Controls posterior statistics
Other Options	
INF=	Specifies the machine numerical limit for infinity
JOINTMODEL	Specifies joint log-likelihood function
MISSING=	Indicates how missing values are handled.
NOLOGDIST	Omits the calculation of the logarithm of the joint distribution of the parameters
SIMREPORT=	Controls the frequency of report for expected run time
SINGDEN=	Specifies the singularity tolerance

These options are described in alphabetical order.

ACCEPTTOL=*n*

specifies a tolerance for acceptance probabilities. By default, ACCEPTTOL=0.075.

AUTOCORLAG=*n***ACLAG=*n***

specifies the maximum number of autocorrelation lags used in computing the effective sample size; see the section “[Effective Sample Size](#)” on page 152 for more details. The value is used in the calculation of the Monte Carlo standard error; see the section “[Standard Error of the Mean Estimate](#)” on page 153. By default, AUTOCORLAG=MIN(500, MCsample/4), where MCsample is the Markov chain sample size kept after thinning—that is, $MCsample = \left\lceil \frac{NMC}{NTHIN} \right\rceil$. If AUTOCORLAG= is set too low, you might observe significant lags, and the effective sample size cannot be calculated accurately. A WARNING message appears, and you can either increase AUTOCORLAG= or [NMC=](#), accordingly.

DISCRETE=*keyword*

specifies the proposal distribution used in sampling discrete parameters. The default is DISCRETE=BINNING.

The *keyword* values are as follows:

BINNING

uses continuous proposal distributions for all discrete parameter blocks. The proposed sample is then discretized (binned) before further calculations. This sampling method approximates the correlation structure among the discrete parameters in the block and could improve mixing in some cases.

GEO

uses independent symmetric geometric proposal distributions for all discrete parameter blocks. This proposal does not take parameter correlations into account. However, it can work better than the BINNING option in cases where the range of the parameters is relatively small and a normal approximation can perform poorly.

DIAGNOSTICS=NONE | (*keyword-list*)**DIAG=NONE** | (*keyword-list*)

specifies options for MCMC convergence diagnostics. By default, PROC MCMC computes the Geweke test, sample autocorrelations, effective sample sizes, and Monte Carlo errors. The Raftery-Lewis and Heidelberger-Welch tests are also available. See the section “[Assessing Markov Chain Convergence](#)” on page 139 for more details on convergence diagnostics. You can request all of the diagnostic tests by specifying DIAGNOSTICS=ALL. You can suppress all the tests by specifying DIAGNOSTICS=NONE.

You can use postprocessing autocall macros to calculate convergence diagnostics of the posterior samples after PROC MCMC has exited. See the section “[Autocall Macros for Postprocessing](#)” on page 4510.

The following *options* are available.

ALL

computes all diagnostic tests and statistics. You can combine the option ALL with any other specific tests to modify test options. For example DIAGNOSTICS=(ALL AUTOCORR(LAGS=(1 5 35))) computes all tests with default settings and autocorrelations at lags 1, 5, and 35.

AUTOCORR < (*autocorr-options*) >

computes default autocorrelations at lags 1, 5, 10, and 50 for each variable. You can choose other lags by using the following *autocorr-options*:

LAGS | **AC=***numeric-list*

specifies autocorrelation lags. The *numeric-list* must take positive integer values.

ESS

computes the effective sample sizes (Kass et al. (1998)) of the posterior samples of each parameter. It also computes the correlation time and the efficiency of the chain for each parameter. Small values of ESS might indicate a lack of convergence. See the section “[Effective Sample Size](#)” on page 152 for more details.

GEWEKE < (*Geweke-options*) >

computes the Geweke spectral density diagnostics; this is a two-sample t -test between the first f_1 portion and the last f_2 portion of the chain. See the section “[Geweke Diagnostics](#)” on page 146 for more details. The default is $\text{FRAC1}=0.1$ and $\text{FRAC2}=0.5$, but you can choose other fractions by using the following *Geweke-options*:

FRAC1 | **F1**=*value*

specifies the beginning FRAC1 proportion of the Markov chain. By default, $\text{FRAC1}=0.1$.

FRAC2 | **F2**=*value*

specifies the end FRAC2 proportion of the Markov chain. By default, $\text{FRAC2}=0.5$.

HEIDELBERGER | **HEIDEL** < (*Heidel-options*) >

computes the Heidelberg and Welch diagnostic (which consists of a stationarity test and a halfwidth test) for each variable. The stationary diagnostic test tests the null hypothesis that the posterior samples are generated from a stationary process. If the stationarity test is passed, a halfwidth test is then carried out. See the section “[Heidelberg and Welch Diagnostics](#)” on page 148 for more details.

These diagnostics are not performed by default. You can specify the `DIAGNOSTICS=HEIDELBERGER` option to request these diagnostics, and you can also specify suboptions, such as `DIAGNOSTICS=HEIDELBERGER(EPS=0.05)`, as follows:

SALPHA=*value*

specifies the α level ($0 < \alpha < 1$) for the stationarity test. By default, $\text{SALPHA}=0.05$.

HALPHA=*value*

specifies the α level ($0 < \alpha < 1$) for the halfwidth test. By default, $\text{HALPHA}=0.05$.

EPS=*value*

specifies a small positive number ϵ such that if the halfwidth is less than ϵ times the sample mean of the retaining iterates, the halfwidth test is passed. By default, $\text{EPS}=0.1$.

MCSE**MCERROR**

computes the Monte Carlo standard error for the posterior samples of each parameter.

NONE

suppresses all of the diagnostic tests and statistics. This is not recommended.

RAFTERY | **RL** < (*Raftery-options*) >

computes the Raftery and Lewis diagnostics, which evaluate the accuracy of the estimated quantile ($\hat{\theta}_Q$ for a given $Q \in (0, 1)$) of a chain. $\hat{\theta}_Q$ can achieve any degree of accuracy when the chain is allowed to run for a long time. The algorithm stops when the estimated probability $\hat{P}_Q = \Pr(\theta \leq \hat{\theta}_Q)$ reaches within $\pm R$ of the value Q with probability S ; that is, $\Pr(Q - R \leq \hat{P}_Q \leq Q + R) = S$. See the section “[Raftery and Lewis Diagnostics](#)” on page 149

for more details. The *Raftery-options* enable you to specify Q, R, S, and a precision level ϵ for a stationary test.

These diagnostics are not performed by default. You can specify the `DIAGNOSTICS=RAFERTY` option to request these diagnostics, and you can also specify suboptions, such as `DIAGNOSTICS=RAFERTY(QUANTILE=0.05)`, as follows:

QUANTILE | Q=value

specifies the order (a value between 0 and 1) of the quantile of interest. By default, `QUANTILE=0.025`.

ACCURACY | R=value

specifies a small positive number as the margin of error for measuring the accuracy of estimation of the quantile. By default, `ACCURACY=0.005`.

PROB | S=value

specifies the probability of attaining the accuracy of the estimation of the quantile. By default, `PROB=0.95`.

EPS=value

specifies the tolerance level (a small positive number) for the stationary test. By default, `EPS=0.001`.

DIC

computes the Deviance Information Criterion (DIC). DIC is calculated using the posterior mean estimates of the parameters. See the section “[Deviance Information Criterion \(DIC\)](#)” on page 155 for more details.

DATA=SAS-data-set

specifies the input data set. Observations in this data set are used to compute the log-likelihood function that you specify with PROC MCMC statements.

INF=value

specifies the numerical definition of infinity in PROC MCMC. The default is `INF=1E15`. For example, PROC MCMC considers `1E16` to be outside of the support of the normal distribution and assigns a missing value to the log density evaluation. You can select a larger value with the `INF=` option. The minimum value allowed is `1E10`.

INIT=(keyword-list)

specifies options for generating the initial values for the parameters. These options apply only to prior distributions that are recognized by PROC MCMC. See the section “[Standard Distributions](#)” on page 4476 for a list of these distributions. If either of the functions `GENERAL` or `DGENERAL` is used, you must supply explicit initial values for the parameters. By default, `INIT=MODE`. The following keywords are used:

MODE

uses the mode of the prior density as the initial value of the parameter, if you did not provide one. If the mode does not exist or if it is on the boundary of the support of the density, the mean value is used. If the mean is outside of the support or on the boundary, which can happen if the prior distribution is truncated, a random number drawn from the prior is used as the initial value.

PINIT

tabulates parameter values after the tuning phase. This option also tabulates the tuned proposal parameters used by the Metropolis algorithm. These proposal parameters include covariance matrices for continuous parameters and probability vectors for discrete parameters for each block. By default, PROC MCMC does not display the initial values or the tuned proposal parameters after the tuning phase.

RANDOM

generates a random number from the prior density and uses it as the initial value of the parameter, if you did not provide one.

REINIT

resets the parameters, after the tuning phase, with the initial values that you provided explicitly or that were assigned by PROC MCMC. By default, PROC MCMC does not reset the parameters because the tuning phase usually moves the Markov chains to a more favorable place in the posterior distribution.

LIST

displays the model program and variable lists. The LIST option is a debugging feature and is not normally needed.

LISTCODE

displays the compiled program code. The LISTCODE option is a debugging feature and is not normally needed.

JOINTMODEL**JOINTLLIKE**

specifies how the likelihood function is calculated. By default, PROC MCMC assumes that the observations in the data set are independent so that the joint log-likelihood function is the sum of the individual log-likelihood functions for the observations, where the individual log-likelihood function is specified in the [MODEL](#) statement. When your data are not independent, you can specify the JOINTMODEL option to modify the way that PROC MCMC computes the joint log-likelihood function. In this situation, PROC MCMC no longer steps through the input data set to sum the individual log likelihood.

To use this option correctly, you need to do the following two things:

- create ARRAY symbols to store all data set variables that are used in the program. This can be accomplished with the [BEGINCNST](#) and [ENDCNST](#) statements.
- program the joint log-likelihood function by using these ARRAY symbols only. The [MODEL](#) statement specifies the joint log-likelihood function for the entire data set. Typically, you use the function [GENERAL](#) in the [MODEL](#) statement.

See the sections “[BEGINCNST/ENDCNST Statement](#)” on page 4441 and “[Modeling Joint Likelihood](#)” on page 4504 for details.

MAXTUNE=*n*

specifies an upper limit for the number of proposal tuning loops. By default, MAXTUNE=24. See the section “[Covariance Tuning](#)” on page 4470 for more details.

MAXINDEXPRINT=*number* | ALL**MAXIPRINT=*number* | ALL**

specifies the maximum number of observation indices to print in the ODS tables “Missing Response Information” table and “Missing Covariates Information” table. This option applies only to programs that model missing data. The default value is 20. MAXINDEXPRINT=ALL prints all observation indices for every missing variable that is modeled in PROC MCMC.

MAXSUBVALUEPRINT=*number* | ALL**MAXSVPRINT=*number* | ALL**

specifies the maximum number of subject values to display in the “Subject Values” column of the ODS table “Random Effects Parameters.” This option applies only to programs that have RANDOM statements. The default value is 20. MAXSUBVALUEPRINT=ALL prints all subject values for every random effect in the program.

MCHISTORY=*keyword***MCHIST=*keyword***

controls the display of the Markov chain sampling history.

BRIEF

produces a summary output for the tuning, burn-in, and sampling history tables. The tables show the following when applicable:

- “RWM Scale” shows the scale, or the range of the scales, used in each random walk Metropolis block that is normal or is based on a *t* distribution.
- “Probability” shows the proposal probability parameter, or the range of the parameters, used in each random walk Metropolis block that is based on a geometric distribution.
- “RWM Acceptance Rate” shows the acceptance rate, or the range of the acceptance rates, for each random walk Metropolis block.
- “IM Acceptance Rate” shows the acceptance rate, or the range of the acceptance rates, for each independent Metropolis block.

DETAILED

produces detailed output of the tuning, burn-in, and sampling history tables, including scale values, acceptance probabilities, blocking information, and so on. Use this option with caution, especially in random-effects models that have a large number of random-effects groups. This option can produce copious output.

NONE

produces none of the tuning history, burn-in history, and sampling history tables.

The default is MCHISTORY=NONE.

MINTUNE=*n*

specifies a lower limit for the number of proposal tuning loops. By default, MINTUNE=2. See the section “[Covariance Tuning](#)” on page 4470 for more details.

MISSING=*keyword*

MISS=*keyword*

specifies how missing values are handled (see the section “[Handling of Missing Data](#)” on page 4518 for more details). The default is MISSING=COMPLETECASE.

ALLCASE | AC

gives you the option to model the missing values in an all-case analysis. You can use any techniques that you see fit, for example, fully Bayesian or multiple imputation.

COMPLETECASE | CC

assumes a complete case analysis, so all observations with missing variable values are discarded prior to the simulation.

MONITOR= (*symbol-list*)

outputs analysis for selected symbols of interest in the program. The symbols can be any of the following: model parameters (symbols in the [PARMS](#) statement), secondary parameters (assigned using the operator “=”), the log of the posterior density (LOGPOST), the log of the prior density (LOGPRIOR), the log of the hyperprior density (LOGHYPER) if the [HYPER](#) statement is used, or the log of the likelihood function (LOGLIKE). You can use the keyword `_PARMS_` as a shorthand for all of the model parameters. PROC MCMC performs only posterior analyses (such as plotting, diagnostics, and summaries) on the symbols selected with the MONITOR= option. You can also choose to monitor an entire array by specifying the name of the array. By default MONITOR=`_PARMS_`.

Posterior samples of any secondary parameters listed in the MONITOR= option are saved in the [OUTPOST=](#) data set. Posterior samples of model parameters are always saved to the [OUTPOST=](#) data set, regardless of whether they appear in the MONITOR= option.

NBI=*n*

specifies the number of burn-in iterations to perform before beginning to save parameter estimate chains. By default, NBI=1000. See the section “[Burn-in, Thinning, and Markov Chain Samples](#)” on page 138 for more details.

NMC=*n*

specifies the number of iterations in the main simulation loop. This is the MCMC sample size if [THIN=1](#). By default, NMC=1000.

NOLOGDIST

omits the calculation of the logarithm of the joint distribution of the model parameters at each iteration. The option applies only if all parameters in the model are updated directly from their target distribution, either from the full conditional posterior via conjugacy or from the marginal distribution. Such algorithms do not require the calculation of the joint posterior distribution; hence PROC MCMC runs faster by avoiding these unnecessary calculations. As a result, the [OUTPOST=](#) data set does not contain the LOGPRIOR, LOGLIKE, and LOGPOST variables.

NTU=*n*

specifies the number of iterations to use in each proposal tuning phase. By default, NTU=500.

OUTPOST=*SAS-data-set*

specifies an output data set that contains the posterior samples of all model parameters, the iteration numbers (variable name ITERATION), the log of the posterior density (LOGPOST), the log of the

prior density (LOGPRIOR), the log of the hyperprior density (LOGHYPER), if the [HYPER](#) statement is used, and the log likelihood (LOGLIKE). Any secondary parameters (assigned using the operator “=”) listed in the [MONITOR=](#) option are saved to this data set. By default, no OUTPOST= data set is created.

PLOTS< (*global-plot-options*)>= (*plot-request* <...*plot-request*>)

PLOT< (*global-plot-options*)>= (*plot-request* <...*plot-request*>)

controls the display of diagnostic plots. Three types of plots can be requested: trace plots, autocorrelation function plots, and kernel density plots. By default, the plots are displayed in panels unless the global plot option UNPACK is specified. Also when more than one type of plot is specified, the plots are grouped by parameter unless the global plot option GROUPBY=TYPE is specified. When you specify only one plot request, you can omit the parentheses around the plot-request, as shown in the following example:

```
plots=none
plots(unpack)=trace
plots=(trace density)
```

ODS Graphics must be enabled before plots can be requested. For example:

```
ods graphics on;
proc mcmc data=exi seed=7 outpost=p1 plots=all;
  parm mu;
  prior mu ~ normal(0, sd=10);
  model y ~ normal(mu, sd=1);
run;
ods graphics off;
```

For more information about enabling and disabling ODS Graphics, see the section “[Enabling and Disabling ODS Graphics](#)” on page 600 in Chapter 21, “[Statistical Graphics Using ODS](#).”

If ODS Graphics is enabled but do not specify the PLOTS= option, then PROC MCMC produces, for each parameter, a panel that contains the trace plot, the autocorrelation function plot, and the density plot. This is equivalent to specifying PLOTS=(TRACE AUTOCORR DENSITY).

The *global-plot-options* include the following:

FRINGE

adds a fringe plot to the horizontal axis of the density plot.

GROUPBY|GROUP=PARAMETER | TYPE

specifies how the plots are grouped when there is more than one type of plot. GROUPBY=PARAMETER is the default. The choices are as follows:

TYPE

specifies that the plots are grouped by type.

PARAMETER

specifies that the plots are grouped by parameter.

LAGS=*n*

specifies the number of autocorrelation lags used in plotting the ACF graph. By default, LAGS=50.

SMOOTH

smooths the trace plot with a fitted penalized B-spline curve (Eilers and Marx 1996).

UNPACKPANEL

UNPACK

specifies that all paneled plots are to be unpacked, so that each plot in a panel is displayed separately.

The *plot-requests* are as follows:

ALL

requests all types of plots. PLOTS=ALL is equivalent to specifying PLOTS=(TRACE AUTOCORR DENSITY).

AUTOCORR | ACF

displays the autocorrelation function plots for the parameters.

DENSITY | D | KERNEL | K

displays the kernel density plots for the parameters.

NONE

suppresses the display of all plots.

TRACE | T

displays the trace plots for the parameters.

Consider a model with four parameters, X1–X4. Displays for various specifications are depicted as follows.

- PLOTS=(TRACE AUTOCORR) displays the trace and autocorrelation plots for each parameter side by side with two parameters per panel:

Display 1	Trace(X1)	Autocorr(X1)
	Trace(X2)	Autocorr(X2)
Display 2	Trace(X3)	Autocorr(X3)
	Trace(X4)	Autocorr(X4)

- PLOTS(GROUPBY=TYPE)=(TRACE AUTOCORR) displays all the paneled trace plots, followed by panels of autocorrelation plots:

Display 1	Trace(X1)	
	Trace(X2)	
Display 2	Trace(X3)	
	Trace(X4)	
Display 3	Autocorr(X1)	Autocorr(X2)
	Autocorr(X3)	Autocorr(X4)

- `PLOTS(UNPACK)=(TRACE AUTOCORR)` displays a separate trace plot and a separate correlation plot, parameter by parameter:

Display 1	Trace(X1)
Display 2	Autocorr(X1)
Display 3	Trace(X2)
Display 4	Autocorr(X2)
Display 5	Trace(X3)
Display 6	Autocorr(X3)
Display 7	Trace(X4)
Display 8	Autocorr(X4)

- `PLOTS(UNPACK GROUPBY=TYPE)=(TRACE AUTOCORR)` displays all the separate trace plots followed by the separate autocorrelation plots:

Display 1	Trace(X1)
Display 2	Trace(X2)
Display 3	Trace(X3)
Display 4	Trace(X4)
Display 5	Autocorr(X1)
Display 6	Autocorr(X2)
Display 7	Autocorr(X3)
Display 8	Autocorr(X4)

PROPCOV=*value*

specifies the method used in constructing the initial covariance matrix for the Metropolis-Hastings algorithm. The QUANEW and NMSIMP methods find numerically approximated covariance matrices at the optimum of the posterior density function with respect to all continuous parameters. The optimization does not apply to discrete parameters. The tuning phase starts at the optimized values; in some problems, this can greatly increase convergence performance. If the approximated covariance matrix is not positive definite, then an identity matrix is used instead. Valid values are as follows:

IND

uses the identity covariance matrix. This is the default. See the section “[Tuning the Proposal Distribution](#)” on page 4469.

CONGRA<(optimize-options)>

performs a conjugate-gradient optimization.

DBLDOG<(optimize-options)>

performs a double-dogleg optimization.

QUANEW<(optimize-options)>

performs a quasi-Newton optimization.

NMSIMP | **SIMPLEX**<(optimize-options)>

performs a Nelder-Mead simplex optimization.

The *optimize-options* are as follows:

ITPRINT

prints optimization iteration steps and results.

PROPDIST=value

specifies a proposal distribution for the Metropolis algorithm. See the section “[Metropolis and Metropolis-Hastings Algorithms](#)” on page 134. You can also use **PARMS** statement option (see the section “[PARMS Statement](#)” on page 4451) to change the proposal distribution for a particular block of parameters. Valid values are as follows:

NORMAL**N**

specifies a normal distribution as the proposal distribution. This is the default.

T<(df)>

specifies a *t* distribution with the degrees of freedom *df*. By default, *df* = 3. If *df* > 100, the normal distribution is used since the two distributions are almost identical.

REOBSINFO <(display-options)>

displays the ODS table “Random Effect Observation Information.” The table lists the name of each random effect, the unique values in the corresponding subject variable, the number of observations in each subject, and the observation indices for each subject value.

To understand how this option works, consider the following statements:

```
data input;
  array names{*} $ n1-n10 ("John" "Mary" "Chris" "Rob" "Greg"
                          "Jen" "Henry" "Alice" "James" "Toby");
  call streaminit(17);
  do i = 1 to 20;
    j = ceil(rand("uniform") * 10 );
    index = names[j];
    output;
  end;
```

```

drop n: j;
run;

proc print data=input;
run;

```

The input data set (Figure 55.11) contains the index variable, which indicates subjects in a hypothetical random-effects model.

Figure 55.11 Subject Variable in an Input Data Set

Obs	i	index
1	1	Mary
2	2	James
3	3	Mary
4	4	Greg
5	5	Chris
6	6	James
7	7	James
8	8	Chris
9	9	James
10	10	James
11	11	Chris
12	12	Rob
13	13	Rob
14	14	Greg
15	15	Greg
16	16	Alice
17	17	Jen
18	18	Alice
19	19	John
20	20	Chris

The following statements illustrate the use of the REOBSINFO option:

```

ods select reobsinfo;
proc mcmc data=input reobsinfo stats=none diag=none;
  random u ~ normal(0, sd=1) subject=index;
  model general(0);
run;

```

Figure 55.12 displays the “Random Effect Observation Information” table. The table contains the name of the random-effect parameter (u), the values of the subject variable index, the total number of observations, and the row index of these observations in each of the subject values.

Figure 55.12 Random Effect Observation Information

The MCMC Procedure			
Random Effect Observation Information			
Parameter	Subject Values	Number of Observations in Subject	Observation Indices
u	Mary	2	1 3
	James	5	2 6 7 9 10
	Greg	3	4 14 15
	Chris	4	5 8 11 20
	Rob	2	12 13
	Alice	2	16 18
	Jen	1	17
	John	1	19

The *display-options* are as follows:

MAXVALUEPRINT=*number* | **ALL**

MAXVPRINT=*number* | **ALL**

prints the number of subject values for each random effect (that is, the number of rows that are displayed in the “Random Effect Observation Information” table for each random effect). The default value is 20. MAXVALUEPRINT=ALL displays all subject values.

MAXOBSPRINT=*number* | **ALL**

MAXOPRINT=*number* | **ALL**

prints the number of observation indices for each subject value of every random effect (that is, the maximum number of indices that are displayed in the “Observation Indices” column in the “Random Effect Observation Information” table). The default value is 20. MAXOBSPRINT=ALL displays indices for every subject value.

SCALE=*value*

controls the initial multiplicative scale to the covariance matrix of the proposal distribution. By default, SCALE=2.38. See the section “[Scale Tuning](#)” on page 4470 for more details.

SEED=*n*

specifies the random number seed. By default, SEED=0, and PROC MCMC gets a random number seed from the clock.

SIMREPORT=*n*

controls the number of times that PROC MCMC reports the expected run time of the simulation. This can be useful for monitoring the progress of CPU-intensive programs. For example, with SIMREPORT=2, PROC MCMC reports the simulation progress twice. By default, SIMREPORT=0, and there is no reporting. The expected run times are displayed in the log file.

SINGDEN=*value*

defines the singularity criterion in PROC MCMC. By default, SINGDEN=1E-11. The *value* indicates the exclusion of an endpoint in an interval. The mathematical notation “(0)” is equivalent to “[*value*” in PROC MCMC—that is, $x < 0$ is treated as $x \leq \text{value}$ in PROC MCMC. The maximum SINGDEN allowed is 1E-6.

STATISTICS< (*global-stats-options*)> = **NONE** | **ALL** | *stats-request***STATS**< (*global-stats-options*)> = **NONE** | **ALL** | *stats-request*

specifies options for posterior statistics. By default, PROC MCMC computes the posterior mean, standard deviation, quantiles, and two 95% credible intervals: equal-tail and highest posterior density (HPD). Other available statistics include the posterior correlation and covariance. See the section “[Summary Statistics](#)” on page 153 for more details. You can request all of the posterior statistics by specifying STATS=ALL. You can suppress all the calculations by specifying STATS=NONE.

You can use postprocessing autocall macros to calculate posterior summary statistics of the posterior samples after PROC MCMC has exited. See the section “[Autocall Macros for Postprocessing](#)” on page 4510.

The *global-stats-options* includes the following:

ALPHA=*numeric-list*

specifies the α level for the equal-tail and HPD intervals. The value α must be between 0 and 0.5. By default, ALPHA=0.05.

PERCENTAGE | **PERCENT**=*numeric-list*

calculates the posterior percentages. The *numeric-list* contains values between 0 and 100. By default, PERCENTAGE=(25 50 75).

The *stats-requests* include the following:

ALL

computes all posterior statistics. You can combine the option ALL with any other options. For example STATS(ALPHA=(0.02 0.05 0.1))=ALL computes all statistics with the default settings and intervals at α levels of 0.02, 0.05, and 0.1.

CORR

computes the posterior correlation matrix.

COV

computes the posterior covariance matrix.

SUMMARY**SUM**

computes the posterior means, standard deviations, and percentile points for each variable. By default, the 25th, 50th, and 75th percentile points are produced, but you can use the global PERCENT= option to request specific percentile points.

INTERVAL**INT**

computes the $100(1 - \alpha)\%$ equal-tail and HPD credible intervals for each variable. See the sections “[Equal-Tail Credible Interval](#)” on page 154 and “[Highest Posterior Density \(HPD\) Interval](#)” on page 154 for details. By default, ALPHA=0.05, but you can use the global ALPHA= option to request other intervals of any probabilities.

NONE

suppresses all of the statistics.

TARGACCEPT=*value*

specifies the target acceptance rate for the random walk based Metropolis algorithm. See the section “[Metropolis and Metropolis-Hastings Algorithms](#)” on page 134. The numeric *value* must be between 0.01 and 0.99. By default, TARGACCEPT=0.45 for models with 1 parameter; TARGACCEPT=0.35 for models with 2, 3, or 4 parameters; and TARGACCEPT=0.234 for models with more than 4 parameters (Roberts, Gelman, and Gilks 1997; Roberts and Rosenthal 2001).

TARGACCEPTI=*value*

specifies the target acceptance rate for the independence sampler algorithm. The independence sampler is used for blocks of binary parameters. See the section “[Independence Sampler](#)” on page 137 for more details. The numeric *value* must be between 0 and 1. By default, TARGACCEPTI=0.6.

THIN=*n***NTHIN=***n*

controls the thinning rate of the simulation. PROC MCMC keeps every *n*th simulation sample and discards the rest. All of the posterior statistics and diagnostics are calculated using the thinned samples. By default, THIN=1. See the section “[Burn-in, Thinning, and Markov Chain Samples](#)” on page 138 for more details.

TRACE

displays the result of each operation in each statement in the model program as it is executed. This debugging option is very rarely needed, and it produces voluminous output. If you use this option, also use small NMC=, NBI=, MAXTUNE=, and NTU= numbers.

TUNEWT=*value*

specifies the multiplicative weight used in updating the covariance matrix of the proposal distribution. The numeric *value* must be between 0 and 1. By default, TUNEWT=0.75. See the section “[Covariance Tuning](#)” on page 4470 for more details.

ARRAY Statement

ARRAY *arrayname* [*dimensions*] < \$ > < *variables-and-constants* > ;

The ARRAY statement associates a name (of no more than eight characters) with a list of variables and constants. The ARRAY statement is similar to, but not the same as, the ARRAY statement in the DATA step, and it is the same as the ARRAY statements in the NLIN, NLP, NLMIXED, and MODEL procedures. The array name is used with subscripts in the program to refer to the array elements, as illustrated in the following statements:

```
array r[8] r1-r8;

do i = 1 to 8;
    r[i] = 0;
end;
```

The ARRAY statement does not support all the features of the ARRAY statement in the DATA step. Implicit indexing of variables cannot be used; all array references must have explicit subscript expressions. Only exact array dimensions are allowed; lower-bound specifications are not supported. A maximum of six dimensions is allowed.

Both variables and constants can be array elements. Constant array elements cannot have values assigned to them while variables can. Both the dimension specification and the list of elements are optional, but at least one must be specified. When the list of elements is not specified or fewer elements than the size of the array are listed, array variables are created by appending element numbers to the array name to complete the element list. You can index array elements by enclosing a subscript in braces ({ }) or brackets ([]), but not in parentheses (()). The parentheses are reserved for function calls only.

For example, the following statement names an array `day`:

```
array day[365];
```

By default, the variables names are `day1` to `day365`. However, since `day` is a SAS function, any subscript that uses parentheses gives you the wrong results. The expression `day(4)` returns the value 5 and does not reference the array element `day4`.

BEGINCNST/ENDCNST Statement

```
BEGINCNST ;
```

```
ENDCNST ;
```

The BEGINCNST and ENDCNST statements define a block within which PROC MCMC processes the programming statements only during the setup stage of the simulation. You can use the BEGINCNST and ENDCNST statements to define constants or import data set variables into arrays. Storing data in arrays enables you to work with data that are not identically distributed (see the section “[Modeling Joint Likelihood](#)” on page 4504) or to implement your own Markov chain sampler (see the section “[UDS Statement](#)” on page 4462). You can also use the BEGINCNST and ENDCNST statements to assign initial values to the parameters (see the section “[Assignments of Parameters](#)” on page 4474).

Assign Constants

Whenever you have programming statements that calculate constants that do not need to be evaluated multiple times throughout the simulation, you should put them within the BEGINCNST and ENDCNST statements. Using these statements can reduce redundant processing. For example, you can assign a constant to a symbol or fill in an array with numbers:

```
array cnst[17];
begincnst;
  offset = 17;
  do i = 1 to 17;
    cnst[i] = i * i;
  end;
endcnst;
```

During the setup process, PROC MCMC evaluates the programming statements within the BEGINCNST/ENDCNST once for each observation in the data set and ignores the statements in the rest of the simulation.

READ_ARRAY Function

Sometimes you might need to store variables, either from the current input data set or from a different data set, in arrays and use these arrays to specify your model. The READ_ARRAY function is convenient for that purpose.

The following two forms of the READ_ARRAY function are available:

```
rc = READ_ARRAY (data-set, array) ;
```

```
rc = READ_ARRAY (data-set, array < , "col-name1"> < , "col-name2"> < , ... > ) ;
```

where

- *rc* returns 0 if the function is able to successfully read the data set.
- *data-set* specifies the name of the data set from which the array data is read. The value specified for *data-set* must be a character literal or a variable that contains the member name (libname.memname) of the data set to be read from.
- *array* specifies the PROC MCMC array variable into which the data is read. The value specified for *array* must be a local temporary array variable because the function might need to grow or shrink its size to accommodate the size of the data set.
- *col-name* specifies optional names for the specific columns of the data set that are read. If specified, *col-name* must be a literal string enclosed in quotation marks. In addition, *col-name* cannot be a PROC MCMC variable. If column names are not specified, PROC MCMC reads all of the columns in the data set.

When SAS translates between an array and a data set, the array is indexed as [row,column].

The READ_ARRAY function attempts to dynamically resize the array to match the dimensions of the input data set. Therefore, the array must be dynamic; that is, the array must be declared with the /NOSYMBOLS option.

For examples that use the READ_ARRAY function, see “Modeling Joint Likelihood” on page 4504, “Example 55.14: Time Independent Cox Model” on page 4617, and “Example 55.19: Implement a New Sampling Algorithm” on page 4645.

BEGINNODATA/ENDNODATA Statements

```
BEGINNODATA ;
```

```
ENDNODATA ;
```

```
BEGINPRIOR ;
```

```
ENDPRIOR ;
```

The BEGINNODATA and ENDNODATA statements define a block within which PROC MCMC processes the programming statements without stepping through the entire data set. The programming statements are executed only twice: at the first and the last observation of the data set. The BEGINNODATA and ENDNODATA statements are best used to reduce unnecessary observation-level computations. Any computations that are identical to every observation, such as transformation of parameters, should be enclosed in these statements.

At the first observation, PROC MCMC executes all programming statements, including those that are enclosed by these two statements. This enables a quick update of all the symbols enclosed by the BEGINNODATA and ENDNODATA statements. The goal is to ensure that subsequent statements (for example, the **MODEL** statement) use symbol values that have been calculated correctly. At the last observation, PROC MCMC executes the enclosed programming statements again and adds the log of the prior density to the log of the posterior density.

The BEGINPRIOR and ENDPRIOR statements are aliases for the BEGINNODATA and ENDNODATA statements, respectively. You can enclose PRIOR statements in the BEGINNODATA and ENDNODATA statements.

BY Statement

BY *variables* ;

You can specify a BY statement with PROC MCMC to obtain separate analyses of observations in groups that are defined by the BY variables. When a BY statement appears, the procedure expects the input data set to be sorted in order of the BY variables. If you specify more than one BY statement, only the last one specified is used.

If your input data set is not sorted in ascending order, use one of the following alternatives:

- Sort the data by using the SORT procedure with a similar BY statement.
- Specify the NOTSORTED or DESCENDING option in the BY statement for the MCMC procedure. The NOTSORTED option does not mean that the data are unsorted but rather that the data are arranged in groups (according to values of the BY variables) and that these groups are not necessarily in alphabetical or increasing numeric order.
- Create an index on the BY variables by using the DATASETS procedure (in Base SAS software).

For more information about BY-group processing, see the discussion in *SAS Language Reference: Concepts*. For more information about the DATASETS procedure, see the discussion in the *Base SAS Procedures Guide*.

MODEL Statement

MODEL *dependent-variable-list* ~ *distribution* < options > ;

The MODEL statement specifies the conditional distribution of the data given the parameters (the likelihood function). You specify a single dependent variable or a list of dependent variables, a tilde ~, and then a

distribution with its arguments. The dependent variables can be variables from the input data set or functions of the symbols in the program. You must specify the dependent variables unless you use the [GENERAL](#) function or the [DGENERAL](#) function (see the section “[Specifying a New Distribution](#)” on page 4490 for more details).

The MODEL statement assumes that the observations are independent of each other, conditional on the model parameters. If you want to model dependent data—that is, $f(y_i|\theta, y_j)$ for $j \neq i$ —you can use the [JOINTMODEL](#) option in the PROC MCMC statement. See the section “[Modeling Joint Likelihood](#)” on page 4504 for more details. By default, the log-likelihood value is the sum of the individual log-likelihood value for each observation.

You can specify multiple MODEL statements. You can define likelihood functions that are independent of each other. For example, in the following statements, the dependent variables y1 and y2 are independent of each other:

```
model y1 ~ normal(alpha, var=s21);
model y2 ~ normal(beta, var=s22);
```

Alternatively, you can use marginal and conditional distributions to define a joint log-likelihood function for multiple dependent variables. For example, the following statements jointly define a distribution over (y1, y2). They specify a marginal distribution for the dependent variable y1 and a conditional distribution for the dependent variable y2:

```
model y1 ~ normal(alpha, var=s21);
model y2 ~ normal(beta * y1, var=s22);
```

Every program must have at least one MODEL statement. If you want to run a Monte Carlo simulation that does not require a response variable, use the [GENERAL](#) function in the MODEL statement:

```
model general(0);
```

PROC MCMC interprets the statement as a flat likelihood function with a constant log-likelihood value of 0.

PROC MCMC is a programming language that is similar to the DATA step, and the order of statement evaluation is important. For example, the MODEL statement must come after any SAS programming statements that define or modify arguments used in the construction of the log likelihood. In PROC MCMC, a symbol can be defined multiple times and used at different places. Using an expression out of order produces erroneous results that can also be hard to detect.

Do not embed the MODEL statement within programming statements. For example, suppose you have three response variables, y1, y2, and y3, and want to model each with a normal distribution. The following statements lead to erroneous output:

```
array Y[3] y1 y2 y3;
do i = 1 to 3;
  model y[i] ~ normal(mu, sd=s);
end;
```

Instead, you should do one of the following.

- Use separate MODEL statements:

```

model y1 ~ normal(mu, sd=s);
model y2 ~ normal(mu, sd=s);
model y3 ~ normal(mu, sd=s);

```

- Use the GENERAL function to construct a joint distribution of the three dependent variables and use a single MODEL statement to specify the log-likelihood function:

```

llike = logpdf("normal", y1, mu, s) +
        logpdf("normal", y2, mu, s) +
        logpdf("normal", y3, mu, s);
model y1 y2 y3 ~ general(llike);

```

See the section “[Specifying a New Distribution](#)” on page 4490 for more information about how to use the GENERAL function to specify an arbitrary distribution.

Missing data are allowed in the response variables; the MODEL statement augments missing data automatically. (In releases before SAS/STAT 12.1, observations with missing values were discarded prior to analysis and PROC MCMC did not attempt to model these values.) In each iteration, PROC MCMC samples missing values from their posterior distributions and incorporates them as part of the simulation. PROC MCMC creates one variable for each missing response value. There are two ways to create the missing value variable names; see the [NAMESUFFIX=](#) option for the naming convention of the variables.

Distributions in MODEL Statement

Standard distributions that the MODEL statement supports are listed in the [Table 55.2](#) (univariate) and [Table 55.3](#) (multivariate). See the section “[Standard Distributions](#)” on page 4476 for density specifications. You can also specify all distributions except the multinomial distribution in the [PRIOR](#) and [HYPERPRIOR](#) statements. The [RANDOM](#) statement supports only a subset of the distributions (see [Table 55.4](#)).

PROC MCMC allows some distributions to be parameterized in multiple ways. For example, you can specify a normal distribution with a variance, standard deviation, or precision parameter. For distributions that have different parameterizations, you must specify an option to clearly name the ambiguous parameter. For example, in the normal distribution, you must indicate whether the second argument represents variance, standard deviation, or precision.

All univariate distributions, with the exception of binary and uniform, can have the optional LOWER= and UPPER= arguments, which specify a truncated density. See the section “[Truncation and Censoring](#)” on page 4494 for more details. Truncation is not supported for multivariate distributions.

Table 55.2 Univariate Distributions

Distribution Name	Definition
beta (< a = α , < b = β)	Beta distribution with shape parameters α and β
binary (< prob p = p)	Binary (Bernoulli) distribution with probability of success p . You can use the alias bern for this distribution.
binomial (< n = n , < prob p = p)	Binomial distribution with count n and probability of success p

Table 55.2 (continued)

Distribution Name	Definition
cauchy (<location loc = > θ , <scale s = > λ)	Cauchy distribution with location θ and scale λ
chisq (<df= > ν)	χ^2 distribution with ν degrees of freedom
dgeneral (//)	General log-likelihood function that you construct using SAS programming statements for single or multiple discrete parameters. Also see the function general . The name dlogden is an alias for this function.
expchisq (<df= > ν)	Log transformation of a χ^2 distribution with ν degrees of freedom: $\theta \sim \mathbf{chisq}(\nu) \Leftrightarrow \log(\theta) \sim \mathbf{expchisq}(\nu)$. You can use the alias echisq for this distribution.
expexpon (scale s= λ) expexpon (iscale is= λ)	Log transformation of an exponential distribution with scale or inverse-scale parameter λ : $\theta \sim \mathbf{expon}(\lambda) \Leftrightarrow \log(\theta) \sim \mathbf{expexpon}(\lambda)$. You can use the alias eexpon for this distribution.
expGamma (<shape sp= > a , scale s= λ) expGamma (<shape sp= > a , iscale is= λ)	Log transformation of a gamma distribution with shape a and scale or inverse-scale λ : $\theta \sim \mathbf{gamma}(a, \lambda) \Leftrightarrow \log(\theta) \sim \mathbf{expgamma}(a, \lambda)$. You can use the alias egamma for this distribution.
expichisq (<df= > ν)	Log transformation of an inverse χ^2 distribution with ν degrees of freedom: $\theta \sim \mathbf{ichisq}(\nu) \Leftrightarrow \log(\theta) \sim \mathbf{expichisq}(\nu)$. You can use the alias eichisq for this distribution.
expiGamma (<shape sp= > a , scale s= λ) expiGamma (<shape sp= > a , iscale is= λ)	Log transformation of an inverse-gamma distribution with shape a and scale or inverse-scale λ : $\theta \sim \mathbf{igamma}(a, \lambda) \Leftrightarrow \log(\theta) \sim \mathbf{expigamma}(a, \lambda)$. You can use the alias eigamma for this distribution.
expsichisq (<df= > ν , <scale s= > s)	Log transformation of a scaled inverse χ^2 distribution with ν degrees of freedom and scale parameter s : $\theta \sim \mathbf{sichisq}(\nu) \Leftrightarrow \log(\theta) \sim \mathbf{expsichisq}(\nu)$. You can use the alias esichisq for this distribution.
expon (scale s= λ) expon (iscale is= λ)	Exponential distribution with scale or inverse-scale parameter λ
gamma (<shape sp= > a , scale s= λ) gamma (<shape sp= > a , iscale is= λ)	Gamma distribution with shape a and scale or inverse-scale λ

Table 55.2 (continued)

Distribution Name	Definition
geo (< prob p= > p)	Geometric distribution with probability p
general (<i>//</i>)	General log-likelihood function that you construct using SAS programming statements for a single or multiple continuous parameters. The argument <i>//</i> is an expression for the log of the distribution. If there are multiple variables specified before the tilde in a MODEL, PRIOR, or HYPERPRIOR statement, <i>//</i> is interpreted as the log of the joint distribution for these variables. Note that in the MODEL statement, the response variable specified before the tilde is just a place holder and is of no consequence; the variable must have appeared in the construction of <i>//</i> in the programming statements. general (<i>constant</i>) is equivalent to a uniform distribution on the real line. You can use the alias logden for this distribution.
ichisq (< df= > ν)	Inverse χ^2 distribution with ν degrees of freedom
igamma (< shape sp= > a, scale s= λ) igamma (< shape sp= > a, iscale is= λ)	Inverse-gamma distribution with shape a and scale or inverse-scale λ
laplace (< location loc = > θ, scale s= λ) laplace (< location loc = > θ, iscale is= λ)	Laplace distribution with location θ and scale or inverse-scale λ . This is also known as the <i>double exponential</i> distribution. You can use the alias dexpon for this distribution.
logistic (< location loc = > a, < scale s= > b)	Logistic distribution with location a and scale b
lognormal (< mean m= > μ, sd= λ) lognormal (< mean m= > μ, var v= λ) lognormal (< mean m= > μ, prec= λ)	Log-normal distribution with mean μ and a value of λ for the standard deviation, variance, or precision. You can use the aliases lognormal or lnorm for this distribution.
negbin (< n= > n, < prob p= > p)	Negative binomial distribution with count n and probability of success p . You can use the alias nb for this distribution.
normal (< mean m= > μ, sd= λ) normal (< mean m= > μ, var v= λ) normal (< mean m= > μ, prec= λ)	Normal (Gaussian) distribution with mean μ and a value of λ for the standard deviation, variance, or precision. You can use the aliases gaussian , norm , or n for this distribution.
pareto (< shape sp= > a, < scale s= > b)	Pareto distribution with shape a and scale b

Table 55.2 (continued)

Distribution Name	Definition
poisson (< mean m= > λ)	Poisson distribution with mean λ
sichisq (< df= > ν , < scale s= > s)	Scaled inverse χ^2 distribution with ν degrees of freedom and scale parameter s
t (< mean m= > μ , sd= λ , < df= > ν) t (< mean m= > μ , var v= λ , < df= > ν) t (< mean m= > μ , prec= λ , < df= > ν)	T distribution with mean μ , standard deviation or variance or precision λ , and ν degrees of freedom
uniform (< left l= > a , < right r= > b)	Uniform distribution with range a and b . You can use the alias unif for this distribution.
wald (< mean m= > μ , < iscale is= > λ)	Wald distribution with mean parameter μ and inverse scale parameter λ . This is also known as the <i>Inverse Gaussian</i> distribution. You can use the alias igaussian for this distribution.
weibull (μ, c, σ)	Weibull distribution with location (threshold) parameter μ , shape parameter c , and scale parameter σ .

Table 55.3 Multivariate Distributions

Distribution Name	Definition
dirichlet (< alpha= > α)	Dirichlet distribution with parameter vector α , where α must be a one-dimensional array of length greater than 1
iwish (< df= > ν , < scale= > S)	Inverse Wishart distribution with ν degrees of freedom and symmetric positive definite scale array S
mvn (< mu= > μ , < cov= > Σ)	Multivariate normal distribution with mean vector μ and covariance matrix Σ
mvnar (< mu= > μ , sd= λ , < rho= > ρ) mvnar (< mu= > μ , var= λ , < rho= > ρ) mvnar (< mu= > μ , prec= λ , < rho= > ρ)	Multivariate normal distribution with mean vector μ and a covariance matrix Σ . The covariance matrix Σ is a multiple of the scale and a matrix with a first-order autoregressive structure. When rho=0 , this distribution becomes a multivariate normal distribution with shared variance.
multinom (< p= > p)	Multinomial distribution with probability vector p

Options for the MODEL Statement

The *options* in the MODEL statement apply only when there are missing values in the response variable. You can specify the following options:

INITIAL=SAS-data-set | constant | numeric-list

specifies the initial values of the missing values. By default, PROC MCMC uses a sample average of the nonmissing values of a response variable as the starting values for all missing values in the simulation for that variable. You can use the INITIAL= option to start the Markov chain at a different place.

If you use a *SAS-data-set* to store initial values, the data set must consist of variable names that agree with the missing variable names that are used by PROC MCMC. The easiest way to find the names of the internally created variables is to run a default analysis with a very small number of simulations and check the variable names in the [OUTPOST=](#) data set. You can provide a subset of the initial values in the *SAS-data-set*, and PROC MCMC uses a default mechanism to fill in the rest of the missing initial values.

For example, the following statement creates a data set with initial values for the first three missing values of a response variable:

```
data RandomInit;
  input y_1 y_2 y_3;
  datalines;
  2.3 3 -3
;
```

The following MODEL statement uses the values in the RandomInit data set as the initial values of the corresponding missing values in the model:

```
model y ~ normal(0,var=s2u) init=randominit;
```

Specifying a *constant* assigns that constant as the initial value to all missing values in that response variable. For example, the following statement assigns the value 5 to be used as an initial value for all missing y_i in the model:

```
model y ~ normal(0,var=s2u) init=5;
```

If you have a multidimensional response variable, you can provide a list of numbers that have the same length as the dimension of your response array. Each number is then given to all corresponding missing variables in order. For example, the following statement assigns the value 2 to be used as an initial value for all missing w_{1i} and the value 3 to be used for all missing w_{2i} in the model:

```
array w[2] w1 w2;
model w ~ mvn(mu, cov) init=(2 3);
```

MONITOR= (symbol-list | number-list | RANDOM(number))

outputs analysis for selected missing data variables. You can choose to monitor the missing values by listing the response variable names, the missing data variable names, or indices, or you can have them randomly selected by PROC MCMC.

For example, suppose that the data set contains 10 observations and the response variable *y* has missing values in observations 2, 3, 7, 9, and 10. To monitor all missing data variables (five in total), you specify the response variable name in the **MONITOR=** option:

```
model y ~ normal(0,var=s2u) monitor=(y);
```

Suppose you want to monitor the missing data variables that correspond to the missing values in observations 2, 3, and 10. You have two options: provide either a list of variable names or a list of indices.

The following statement selects monitored variables by their variable names:

```
model y ~ normal(0,var=s2u) monitor=(y_2 y_3 y_10);
```

The variable names must match the internally created variable names for each missing value. See **NAMESUFFIX=** option for the naming convention of the variables. By default, the names are created by concatenating the response variable with the observation index; hence you use the **name_obs** format to construct the names. The numbers 2, 3, and 10 are the corresponding observation indices to the missing values in the input data set.

The following statement selects monitored variables by indices:

```
model y ~ normal(0,var=s2u) monitor=(1 2 5);
```

The indices are not a list of the observation numbers, but rather the order by which the missing values appear in the data set: PROC MCMC reports back the first, the second, and the fifth missing value variables that it creates. The actual variable names that appear in the output are still *y_2*, *y_3*, and *y_10*, honoring the control of the **NAMESUFFIX=** option.

Lastly, PROC MCMC can randomly choose a subset of the variables to monitor. The following statement randomly selects 3 variables to monitor:

```
model y ~ normal(0,var=s2u) monitor=(random(3));
```

The list of the random indices is controlled by the **SEED=** option in the PROC MCMC statement. Therefore, the selected variables will be the same when the **SEED=** option is the same.

NAMESUFFIX=OBSERVATION | POSITION | ORDER

specifies how the names of the missing data variables are created. By default, the names are created by concatenating the response variable symbol, an underscore (“_”), and the observation number of the missing value.

NAMESUFFIX=OBSERVATION constructs the parameter names by appending the observation number to the response variable symbol. This is the default. **NAMESUFFIX=POSITION** or **NAMESUFFIX=ORDER** construct the parameter names by appending the numbers 1, 2, 3, and so on, where the number indicates the order in which the missing values appear in the data set.

For example, suppose you have a response variable *y* with 10 observations in total, of which five are missing (observations 2, 3, 7, 9, and 10). By default, PROC MCMC creates five variable names *y_2*, *y_3*, *y_7*, *y_9*, and *y_10*. Using **NAMESUFFIX=POSITION** changes the names to *y_1*, *y_2*, *y_3*, *y_4*, and *y_5*.

NOOUTPOST

suppresses the output of the posterior samples of missing data variables to the posterior output data set (which is specified in the [OUTPOST=](#) option in the PROC MCMC statement). In models with a large number of missing values (for example, tens of thousands), PROC MCMC can run faster if it does not save the posterior samples.

When you specify both the NOOUTPOST option and the [MONITOR=](#) option, PROC MCMC outputs the list of variables that are monitored.

The maximum number of variables that can be saved to an [OUTPOST=](#) data set is 32,767. If the total number of parameters in your model, including the number of missing data variables, exceeds the limit, the NOOUTPOST option is evoked automatically and PROC MCMC does not save the missing value draws to the posterior output data set. You can use the [MONITOR=](#) option to select a subset of the parameters to store in the [OUTPOST=](#) data set.

PARMS Statement

```
PARMS  name |(name-list)<=><{> number | number-list <}>
        <name |(name-list)<=><{> number | number-list <}> ... >
        </options> ;
```

The PARMS statement lists the names of the parameters in the model and specifies optional initial values for these parameters. These parameters are referred to as the *model parameters*. You can specify multiple PARMS statements. Each PARMS statement defines a block of parameters, and the blocked Metropolis algorithm updates the parameters in each block simultaneously. See the section “[Blocking of Parameters](#)” on page 4466 for more details. PROC MCMC generates missing initial values from the prior distributions whenever needed, as long as they are the standard distributions and not the [GENERAL](#) or [DGENERAL](#) function.

If your model contains a multidimensional parameter (for example, a parameter with a multivariate normal prior distribution), you must declare the parameter as an array (using the [ARRAY](#) statement). You can use braces { } after the parameter name in the PARM statement to assign initial values. For example:

```
array mu[3];
parms mu {1 2 3};
```

You cannot use the [ARRAY](#) statement to assign initial values. If you use the [ARRAY](#) statement to store values in array elements, the declared array becomes a constant array and cannot be used as parameters in the PARMS statement. For example, the following statement assigns three numbers to mu:

```
array mu[3] (1 2 3);
```

The array mu can no longer be a model parameter.

Every parameter in the PARMS statement must have a corresponding prior distribution in the PRIOR statement. The program exits if this one-to-one requirement is not satisfied.

You can specify the following *options* to control different samplers explicitly for that block of parameters.

NORMAL | N

uses the normal proposal distribution in the random walk Metropolis. This is the default.

T <(df)>

uses the t distribution with df degrees of freedom as an alternative proposal distribution. A t distribution with a small number of degrees of freedom has thicker tails and can sometimes improve the mixing of the Markov chain. When $df > 100$, the normal distribution is used instead.

SLICE

applies the slice sampler to each parameter in the PARMS statement individually. See the section “[Slice Sampler](#)” on page 136 for details. PROC MCMC does not implement a multidimensional version of the slice sampler. Because the slice sampler usually requires multiple evaluations of the objective function (the posterior distribution) in each iteration, the associated computational cost could be potentially high with this sampling algorithm.

UDS

implements a user-defined sampler for any of the parameters in the block. See the section “[UDS Statement](#)” on page 4462 for details and “[Example 55.19: Implement a New Sampling Algorithm](#)” on page 4645 for a realistic example. When you specify the UDS option, PROC MCMC hands off the sampling of these parameters to you at each iteration and relies on your sampler to return a random draw from the conditional posterior distribution. This option is useful if you have a model-specific sampler that you want to implement or a new algorithm that can improve the convergence and mixing of the Markov chain. This functionality is for advanced users, and you should proceed with caution.

PREDDIST Statement

PREDDIST <'label'> **OUTPRED**=SAS-data-set <**NSIM**=n> <**COVARIATES**=SAS-data-set>
<**STATISTICS**=options> ;

The PREDDIST statement creates a new SAS data set that contains random samples from the posterior predictive distribution of the response variable. The posterior predictive distribution is the distribution of unobserved observations (prediction) conditional on the observed data. Let $\mathbf{y}$ be the observed data, $\mathbf{X}$ be the covariates, θ be the parameter, and $\mathbf{y}_{\text{pred}}$ be the unobserved data. The posterior predictive distribution is defined to be the following:

$$\begin{aligned} p(\mathbf{y}_{\text{pred}}|\mathbf{y}, \mathbf{X}) &= \int p(\mathbf{y}_{\text{pred}}, \theta|\mathbf{y}, \mathbf{X}) d\theta \\ &= \int p(\mathbf{y}_{\text{pred}}|\theta, \mathbf{y}, \mathbf{X}) p(\theta|\mathbf{y}, \mathbf{X}) d\theta \end{aligned}$$

Given the assumption that the observed and unobserved data are conditional independent given θ , the posterior predictive distribution can be further simplified as the following:

$$p(\mathbf{y}_{\text{pred}}|\mathbf{y}, \mathbf{X}) = \int p(\mathbf{y}_{\text{pred}}|\theta) p(\theta|\mathbf{y}, \mathbf{X}) d\theta$$

The posterior predictive distribution is an integral of the likelihood function $p(y_{\text{pred}}|\theta)$ with respect to the posterior distribution $p(\theta|y)$. The PREDDIST statement generates samples from a posterior predictive distribution based on draws from the posterior distribution of θ .

The PREDDIST statement works only on response variables that have standard distributions, and it does not support either the GENERAL or DGENERAL functions. Multiple PREDDIST statements can be specified, and an optional label (specified as a quoted string) helps identify the output.

The following list explains specifications in the PREDDIST statement:

COVARIATES=SAS-data-set

names the SAS data set that contains the sets of explanatory variable values for which the predictions are established. This data set must contain data with the same variable names as are used in the likelihood function. If you omit the COVARIATES= option, the DATA= data set specified in the PROC MCMC statement is used instead.

NSIM=*n*

specifies the number of simulated predicted values. By default, NSIM= uses the NMC= option value specified in the PROC MCMC statement.

OUTPRED=SAS-data-set

creates an output data set to contain the samples from the posterior predictive distribution. The output variable names are listed as *resp_1*–*resp_m*, where *resp* is the name of the response variable and *m* is the number of observations in the COVARIATES= data set in the PREDDIST statement. If the COVARIATES= data set is not specified, *m* is the number of observations in the DATA= data set specified in the PROC statement.

STATISTICS<(global-stats-options)> = NONE | ALL |stats-request

STATS<(global-stats-options)> = NONE | ALL |stats-request

specifies options for calculating posterior statistics. This option works identically to the STATISTICS= option in the PROC statement. By default, this option takes the specification of the STATISTICS= option in the PROC MCMC statement.

For an example that uses the PREDDIST statement, see “[Posterior Predictive Distribution](#)” on page 4514.

PRIOR/HYPERPRIOR Statement

PRIOR *parameter-list* ~ *distribution* ;

HYPERPRIOR *parameter-list* ~ *distribution* ;

HYPER *parameter-list* ~ *distribution* ;

The PRIOR statement specifies the prior distribution of the model parameters. You must specify a single parameter or a list of parameters, a tilde ~, and then a distribution with its parameters.

You can specify multiple **PRIOR** statements to define models with multiple prior components. Your model can have as many hierarchical levels as you want. But in many cases, such as random-effects models, it is better to use the **RANDOM** statements to build up the model hierarchy. The log of the prior is the sum of the log prior values from each of the **PRIOR** statements. Similar to the **MODEL** statement, you can use the **PRIOR** statement to specify marginal or conditional prior distributions. See the section “**MODEL Statement**” on page 4443 for the names of the standard distributions and the section “**Standard Distributions**” on page 4476 for density specification.

The **PRIOR** statements are processed twice at every Markov chain simulation—that is, twice per pass through the data set. The statements are called at the first and the last observation of the data set, just as the **BEGINNODATA** and **ENDNODATA** statements are processed. If you run a Monte Carlo simulation that is data-independent, you can specify the **NOLOGDIST** option in the **PROC MCMC** statement to omit the calculation of the prior distribution. Omitting this calculation enables **PROC MCMC** to run faster.

The **HYPERPRIOR** statement is treated internally the same as the **PRIOR** statement. It provides a notational convenience in case you want to fit a multilevel hierarchical model. It specifies the hyperprior distribution of the prior distribution parameters. The log of the hyperprior is the sum of the log hyperprior values from each of the **HYPERPRIOR** statements.

Parameters in the **PRIOR** statements can appear as hyperparameters in the **RANDOM** statement. The reverse is not allowed: random-effects parameters cannot be hyperparameters in a **PRIOR** statement.

You can have a program that contains a **RANDOM** statement but no **PRIOR** statements. (In SAS 9.3 and earlier, each program had to contain a **PRIOR** statement.) A program that contains a **RANDOM** statement but no **PRIOR** statements could be a random-effects model with no fixed-effects parameters or hyperparameters to the random effects. A **MODEL** statement is still required in every program.

Programming Statements

This section lists the programming statements available in **PROC MCMC** to compute the priors and log-likelihood functions. This section also documents the differences between programming statements in **PROC MCMC** and programming statements in the **DATA** step. The syntax of programming statements used in **PROC MCMC** is identical to that used in the **NLMIXED** procedure (see Chapter 64, “**The NLMIXED Procedure**”) and the **MODEL** procedure (see Chapter 19, “**The MODEL Procedure**” (*SAS/ETS User’s Guide*)). Most of the programming statements that can be used in the **DATA** step can also be used in **PROC MCMC**. See *SAS Language Reference: Dictionary* for a description of SAS programming statements.

There are also a number of unique functions in **PROC MCMC** that calculate the log density of various distributions in the procedure. You can find them at the section “**Using Density Functions in the Programming Statements**” on page 4491.

For the list of matrix-based functions that is supported in **PROC MCMC**, see the section “**Matrix Functions in PROC MCMC**” on page 4498.

The following are valid statements:


```

ABORT;
ARRAY arrayname < [ dimensions ] > < $ > < variables-and-constants >;
CALL name < (expression < , expression ... >) >;
DELETE;
DO < variable = expression < TO expression > < BY expression > >
    < , expression < TO expression > < BY expression > > ...
    < WHILE expression > < UNTIL expression >;
END;
GOTO statement-label;
IF expression;
IF expression THEN program-statement;
    ELSE program-statement;
variable = expression;
variable + expression;
LINK statement-label;
PUT < variable > < = > ...;
RETURN;
SELECT < (expression) >;
STOP;
SUBSTR(variable, index, length) = expression;
WHEN (expression) program-statement;
    OTHERWISE program-statement;

```

For the most part, the SAS programming statements work the same as they do in the DATA step, as documented in *SAS Language Reference: Concepts*. However, there are several differences:

- The ABORT statement does not allow any arguments.
- The DO statement does not allow a character index variable. Thus

```
do i = 1, 2, 3;
```

is supported; however, the following statement is not supported:

```
do i = 'A', 'B', 'C';
```

- The PUT statement, used mostly for program debugging in PROC MCMC (see the section “[Handling Error Messages](#)” on page 4530), supports only some of the features of the DATA step PUT statement, and it has some features that are not available with the DATA step PUT statement:
 - The PROC MCMC PUT statement does not support line pointers, factored lists, iteration factors, overprinting, _INFILE_, _OBS_, the colon (:) format modifier, or “\$”.
 - The PROC MCMC PUT statement does support expressions, but the expression must be enclosed in parentheses. For example, the following statement displays the square root of x:

```
put (sqrt(x));
```

- The WHEN and OTHERWISE statements enable you to specify more than one target statement. That is, DO/END groups are not necessary for multiple statement WHENs. For example, the following syntax is valid:

```

select;
  when (exp1) stmt1;
               stmt2;
  when (exp2) stmt3;
               stmt4;
end;

```

You should avoid defining variables that begin with an underscore (_). They might conflict with internal variables created by PROC MCMC. The **MODEL** statement must come after any SAS programming statements that define or modify terms used in the construction of the log likelihood.

RANDOM Statement

RANDOM *random-effect* ~ *distribution* **SUBJECT**=*variable* < *options* > ;

The **RANDOM** statement defines a single random effect and its prior distribution or an array of random effects and their prior distribution. The *random-effect* must be represented by either a symbol or an array. The **RANDOM** statement must consist of the *random-effect*, a tilde (~), the distribution for the random effect, and then a **SUBJECT**= variable.

SUBJECT=*variable* | **_OBS_**

identifies the subjects in the random-effects model. The *variable* must be part of the input data set, and it can be either a numeric variable or character literal. The *variable* does not need to be sorted, and the input data set does not need to be clustered according to it. **SUBJECT**=_OBS_ enables you fit an observation-level random-effects model (each observation has its own random effect) without specifying a subject variable in the input data set.

The random-effects parameters associated with each subject in the same **RANDOM** statement are assumed to be conditionally independent of each other, given other parameters and data set variables in the model. The other parameters include model parameters (declared in the **PARMS** statements), random-effects parameters (from other **RANDOM** statements), and missing data variables.

Table 55.4 shows the distributions that you can specify in the **RANDOM** statement.

Table 55.4 Valid Distributions in the **RANDOM** Statement

Distribution Name	Definition
beta (< a => α , < b => β)	Beta distribution with shape parameters α and β
binary (< prob p => p)	Binary (Bernoulli) distribution with probability of success p . You can use the alias bern for this distribution.
gamma (< shape sp => a , scale s => λ) gamma (< shape sp => a , iscale is => λ)	Gamma distribution with shape a and scale or inverse-scale λ

Table 55.4 (continued)

Distribution Name	Definition
dgeneral (//)	General log-prior function that you construct using SAS programming statements for univariate or multivariate discrete random effects. See the section “ Specifying a New Distribution ” on page 4490 for more details.
general (//)	General log-prior function that you construct using SAS programming statements for univariate or multivariate continuous random effects. See the section “ Specifying a New Distribution ” on page 4490 for more details.
igamma (< shape sp= > a , scale s= λ) igamma (< shape sp= > a , iscale is= λ)	Inverse-gamma distribution with shape a and scale or inverse-scale λ
laplace (< location loc = > θ , scale s= λ) laplace (< location loc = > θ , iscale is= λ)	Laplace distribution with location θ and scale or inverse-scale λ . This is also known as the <i>double exponential</i> distribution. You can use the alias dexpon for this distribution.
normal (< mean m= > μ , sd= λ) normal (< mean m= > μ , var v= λ) normal (< mean m= > μ , prec= λ)	Normal (Gaussian) distribution with mean μ and a value of λ for the standard deviation, variance, or precision. You can use the aliases gaussian , norm , or n for this distribution.
poisson (< mean m= > λ)	Poisson distribution with mean λ
mvn (< mu= > μ , < cov= > Σ)	Multivariate normal distribution with mean vector μ and covariance matrix Σ
mvnar (< mu= > μ , sd= λ , < rho= > ρ) mvnar (< mu= > μ , var= λ , < rho= > ρ) mvnar (< mu= > μ , prec= λ , < rho= > ρ)	Multivariate normal distribution with mean vector μ and a covariance matrix Σ . The covariance matrix Σ is a multiple of the scale and a matrix with a first-order autoregressive structure

The following RANDOM statement specifies a scale effect, where **s2u** can be a constant or a model parameter and **index** is a data set variable that indicates group membership of the random effect **u**:

```
random u ~ normal(0,var=s2u) subject=index;
```

The following statements specify multidimensional effects, where **mu** and **cov** can be either parameters in the model or constant arrays:

```
array w[2];
array mu[2];
array cov[2,2];
random w ~ mvn(mu, cov) subject=index;
```

You can specify multiple RANDOM statements. Hyperparameters in the prior distribution of a random effect can be other random effects in the model. For example, the following statements are allowed because the random effect *g* appears in the distribution for the random effect *u*:

```
random g ~ normal(0,var=s2g) subject=month;
random u ~ normal(g,var=s2u) subject=day;
```

These two RANDOM statements specify a nested hierarchical model in which the random-effects *g* is the hyperparameter of the random-effects *u*. You can build the hierarchical structure as deep as you want. You can also use multiple RANDOM statements to build non-nested random-effects models, where the effects could enter the model on different levels but not in the same hierarchy of each other.

The number of random-effects parameters in each RANDOM statement is determined by the number of unique values in the **SUBJECT=** variable, which can be either unsorted numeric or unsorted character literal. Unlike the model parameters that are explicitly declared in the **PARMS** statement (with therefore a fixed total number), the number of random-effects parameters in a program depends on the values of the **SUBJECT=** data set variable. That number can change from one BY group to another.

The names of the random-effects parameters are created internally. See the **NAMESUFFIX=** option for the naming convention of the random-effects parameters. The random-effects parameters are updated conditionally in the simulation. All posterior draws are saved to the **OUTPOST=** output data set by default, and you can use the **MONITOR=** option to monitor any of the parameters. For more information about available sampling algorithms, see the **ALGORITHM=** option. For more information about how to set a random-effects parameter to a constant (also known as corner-point constraint), see the **CONSTRAINT** option.

You can specify the following *options* in the RANDOM statement:

ALGORITHM=*option*

ALG=*option*

specifies the algorithm to use to sample the posterior distribution. The following *options* are available:

RWM

uses the random-walk Metropolis algorithm with normal proposal.

SLICE

uses the slice sampling algorithm.

GEO

uses the discrete random-walk Metropolis with symmetric geometric proposal.

When possible, PROC MCMC samples directly from the full conditional distribution. Otherwise, the default sampling algorithm is the RWM.

CONSTRAINT(VALUE=*value***) = FIRST | LAST | NONE | 'formatted-value'**

ZERO=**FIRST | LAST | NONE | 'formatted-value'**

sets one of the random-effects parameters to a fixed value. The default is **ZERO=NONE**, which does not fix any of the parameters to be a constant. This option enables you to eliminate one of the parameters.

For example, this option could be useful if you want to fit a regression model with categorical covariates and, instead of creating a design matrix, you treat the parameters as “random effects” and fit an equivalent random-effects model.

Suppose you have a regression that includes a categorical variable X with J levels. You can construct a full-rank design matrix with $J-1$ dummy variables ($X_2 \cdots X_J$ with X_1 being the base group) and fit a regression such as the following:

$$\mu_i = \beta_0 + \beta_2 \cdot X_2 \cdots \beta_J \cdot X_J$$

The following statements in a PROC MCMC step fit such a hypothetical regression model:

```
parms beta0 betax2 ... betaxJ;
prior beta: ~ n(0, sd=100);
mu = beta0 + betax2 * x2 + ... betaxJ * xJ;
...
```

Equivalently, you can also treat this model as a random-effects model such as the following, where β_j are random effects for each category in X :

$$\mu_i = \beta_0 + \beta_j \text{ for } j = 1, \dots, J$$

However, this random-effects model is over-parameterized. The ZERO= option rids the model with one random-effects parameter of choice and fixes it to be zero. The following example statements fit such a hypothetical random-effects model:

```
parms beta0;
prior beta0 ~ n(0, sd=100);
random beta ~ n(0, sd=100) subject=x zero=first;
mu = beta0 + beta;
...
```

The specification ZERO=FIRST sets the first random-effects parameter to 0, implying $\beta_1 = 0$. This random-effects parameter corresponds to the first category in the **SUBJECT=** variable. The category is what the first observation of the **SUBJECT=** variable takes.

The specification ZERO=LAST sets the last random-effects parameter to be 0, implying $\beta_J = 0$. This random-effects parameter corresponds to the last category in the **SUBJECT=** variable. The category is not necessarily the same category that the last observation of the **SUBJECT=** variable takes because the **SUBJECT=** variable does not need to be sorted.

The specification ZERO=*formatted-value* sets the random-effects parameter for the category (in the **SUBJECT=** variable) with a formatted value that matches *formatted-value* to 0. For example, ZERO='3' sets $\beta_3 = 0$.

The CONSTRAINT(VALUE=*value*) option works similarly to the ZERO= option. You can assign an arbitrary *value* to any one of the random-effects parameter. For example, the specification CONSTRAINT(VALUE=0)=FIRST is equivalent to ZERO=FIRST.

INITIAL=SAS-data-set | constant | numeric-list

specifies the initial values of the random-effects parameters. By default, PROC MCMC uses the same option as specified in the **INIT=** option to generate initial values for the random-effects parameter: either it uses the mode of the prior density or it randomly draws a sample from that distribution. You can start the Markov chain at different places by providing a *SAS-data-set*, a constant, or a *numeric-list* for multivariate random-effects parameters.

If you use a *SAS-data-set*, the data set must consist of variable names that agree with the random-effects parameters in the model (see the **NAMESUFFIX=** option for the naming convention of the random-effects parameters). The easiest way to find the names of the internally created parameter names is to run a default analysis with a very small number of simulations and check the variable names in the **OUTPOST=** data set. You can provide a subset of the initial values in the *SAS-data-set* and PROC MCMC will use the default mechanism to fill in the rest of the random-effects parameters.

For example, the following statement creates a data set with initial values for the random-effects parameters `u_1`, `u_2`, and `u_3`:

```
data RandomInit;
  input u_1 u_2 u_3;
  datalines;
  2.3 3 -3
;
```

The following **RANDOM** statement takes the values in the `RandomInit` data set to be the initial values of the corresponding random-effects parameters in the model:

```
random u ~ normal(0,var=s2u) subject=index init=randominit;
```

Specifying a *constant* assigns that constant as the initial value to all random-effects parameters in the statement. For example, the following statement assigns the value 5 to be used as an initial value for all u_i in the model:

```
random u ~ normal(0,var=s2u) subject=index init=5;
```

If you have multiple effects, you can provide a list of numbers, where the length of the list the same as the dimension of your random-effects array. Each number is then given to all corresponding random-effects parameters in order. For example, the following statement assigns the value 2 to be used as an initial value for all w_{1i} and the value 3 to be used for all w_{2i} in the model:

```
array w[2] w1 w2;
random w ~ mvn(mu, cov) subject=index init=(2 3);
```

If you use the **GENERAL** or **DGENERAL** functions in the **RANDOM** statement, you must provide initial values for these parameters.

MONITOR= (symbol-list | number-list | RANDOM(number))

outputs analysis for selected random-effects parameters. You can choose to monitor the random-effects parameters by listing the effect names or effect indices, or you can have them randomly selected by PROC MCMC.

To monitor all random-effects parameters, you specify the effect name in the **MONITOR=** option:

```
random u ~ normal(0,var=s2u) subject=index monitor=(u);
```

You have three options for monitoring a subset of the random-effects parameters. You can provide a list of the parameter names, you can provide a number list of the parameter indices, or you can have PROC MCMC randomly choose a subset of parameters for you.

For example, if you want to monitor analysis for parameters `u_1` through `u_10`, `u_23`, and `u_57`, you can provide the names as follows:

```
random u ~ normal(0,var=s2u) subject=index monitor=(u_1-u_10 u_23 u_57);
```

The naming convention in the *symbol-list* must agree with the `NAMESUFFIX=` option, which controls how the parameter names of the *random-effect* are created. By default, `NAMESUFFIX=SUBJECT`, and the *symbol-list* must use suffixes that correspond to the formatted values¹ in the `SUBJECT=` data set variable. With the `NAMESUFFIX=POSITION` option, the *symbol-list* must use suffixes that agree with the input order of the `SUBJECT=` variable. If the `SUBJECT=` variable has a character value, you cannot use the hyphen (-) in the *symbol-list* to indicate a range of variables.

To monitor the same list of random-effects parameters, you can provide their indices:

```
random u ~ normal(0,var=s2u) subject=index monitor=(1 to 10 by 1 23 57);
```

PROC MCMC can also randomly choose a subset of the parameters to monitor:

```
random u ~ normal(0,var=s2u) subject=index monitor=(random(12));
```

The sequence of the random indices is controlled by the `SEED=` option in the PROC MCMC statement.

By default, PROC MCMC does not monitor any random-effects parameters. When you specify this option, it takes the specification of the `STATISTICS=` and `PLOTS=` options in the PROC MCMC statement. By default, PROC MCMC outputs all the posterior samples of all random-effects parameters to the `OUTPOST=` output data set. You can use the `NOOUTPOST` option to suppress the saving of the random-effects parameters.

NAMESUFFIX=option

specifies how the names of the random-effects parameters are internally created from the `SUBJECT=variable` that is specified in the RANDOM statement. PROC MCMC creates the names by concatenating the *random-effect* symbol with an underscore and a series of numbers or characters. The following *options* control the type of methods that are used in such construction:

SUBJECT

constructs the parameter names by appending the formatted values of the `SUBJECT= variable` in the input data set¹.

¹In SAS/STAT 9.3, the random-effects parameters were created using the unformatted values of the `SUBJECT= variable`.

POSITION

constructs the parameter names by appending the numbers 1, 2, 3, and so on, where the number indicates the order in which the **SUBJECT=** *variable* appears in the data set.

For example, suppose you have an input data set with four observations and the **SUBJECT=** variable *zipcode* has four values (with three of them unique): 27513, 01440, 27513, and 15217. The following SAS statement creates three random-effects parameters named *u_27513*, *u_01440*, and *u_15217*:

```
random u ~ normal(0,var=10) subject=zipcode namesuffix=subject;
```

On the other hand, using **NAMESUFFIX=POSITION** creates three parameters named as *u_1*, *u_2*, and *u_3*:

```
random u ~ normal(0,var=10) subject=zipcode namesuffix=position;
```

By default, **NAMESUFFIX=SUBJECT**.

NOOUTPOST

suppresses the output of the posterior samples of random-effects parameters to the **OUTPOST=** data set. In models with a large number of random-effects parameters (for example, tens of thousands), PROC MCMC can run faster if it does not save the posterior samples of the random-effects parameters.

When you specify both the **NOOUTPOST** option and the **MONITOR=** option, PROC MCMC outputs the list of variables that are monitored.

The maximum number of variables that can be saved to an **OUTPOST=** data set is 32,767. If you run a large-scale random-effects model with the number of parameters exceeding the limit, the **NOOUTPOST** option is evoked automatically and PROC MCMC does not save the random-effects parameter draws to the posterior output data set. You can use the **MONITOR=** option to select a subset of the parameters to store in the **OUTPOST=** data set.

UDS Statement

UDS *subroutine-name* (*subroutine-argument-list*) ;

UDS stands for user defined sampler. The UDS statement enables you to use a separate algorithm, other than the default random walk Metropolis, to update parameters in the model. The purpose of the UDS statement is to give you a greater amount of flexibility and better control over the updating schemes of the Markov chain. Multiple UDS statements are allowed.

For the UDS statement to work properly, you have to do the following:

- write a subroutine by using PROC FCMP (see the FCMP Procedure in the *Base SAS Procedures Guide*) and save it to a SAS catalog (see the example in this section). The subroutine must update some parameters in the model. These are the UDS parameters. The subroutine is called the UDS subroutine.

- declare any UDS parameters in the **PARMS** statement with a sampling option, as in `</ UDS>` (see the section “**PARMS Statement**” on page 4451).
- specify the prior distributions for all UDS parameters, using the **PRIOR** statements.

NOTE: All UDS parameters must appear in three places: the UDS statement, the **PARMS** statement, and the **PRIOR** statement. Otherwise, PROC MCMC exits.

To obtain a valid Markov chain, a UDS subroutine must update a parameter from its full posterior conditional distribution and not the posterior marginal distribution. The posterior conditional is something that you need to provide. This conditional is implicitly based on a prior distribution. PROC MCMC has no means to verify that the implied prior in the UDS subroutine is the same as the prior that you specified in the **PRIOR** statement. You need to make sure that the two distributions agree; otherwise, you will get misleading results.

The priors in the **PRIOR** statements do not directly affect the sampling of the UDS parameters. They could affect the sampling of the other parameters in the model, which, in turn, changes the behavior of the Markov chain. You can see this by noting cases where the hyperparameters of the UDS parameters are model parameters; the priors should be part of the posterior conditional distributions of these hyperparameters, and they cannot be omitted.

Some additional information is listed to help you better understand the UDS statement:

- Most features of the SAS programming language can be used in subroutines processed by PROC FCMP (see the FCMP Procedure in the *Base SAS Procedures Guide*).
- The UDS statement does not support FCMP functions—a FCMP function returns a value, while a subroutine does not. A subroutine updates some of its subroutine arguments. These arguments are called OUTARGS arguments.
- The UDS parameters cannot be in the same block as other parameters. The optional argument `</ UDS>` in the **PARMS** statement prevents parameters that use the default Metropolis from being mixed with those that are updated by the UDS subroutines.
- You can put all the UDS parameters in the same **PARMS** statement or have a separate UDS statement for each of them.
- The same subroutine can be used in multiple UDS statements. This feature comes in handy if you have a generic sampler that can be applied to different parameters.
- PROC MCMC updates the UDS parameters by calling the UDS subroutines directly. At every iteration, PROC MCMC first samples parameters that use the Metropolis algorithm, then the UDS parameters. Sampling of the UDS parameters proceeds in the order in which the UDS statements are listed.
- A UDS subroutine accepts any symbols in the program as well as any input data set variables as its arguments.
- Only the OUTARGS arguments in a UDS subroutine are updated in PROC MCMC. You can modify other arguments in the subroutine, but the changes are not global in PROC MCMC.
- If a UDS subroutine has an argument that is a SAS data set variable, PROC MCMC steps through the data set while updating the UDS parameters. The subroutine is called once per observation in the data set for every iteration.

- If a UDS subroutine does not have any arguments that are data set variables, PROC MCMC does not access the data set while executing the subroutine. The subroutine is called once per iteration.
- To reduce the overhead in calling the UDS subroutine and accessing the data set repeatedly, you might consider reading all the input data set variables into arrays and using the arrays as the subroutine arguments. See the section “[BEGINCNST/ENDCNST Statement](#)” on page 4441 about how to use the [BEGINCNST](#) and [ENDCNST](#) statements to store data set variables.

For an example that uses the UDS statement, see “[Example 55.19: Implement a New Sampling Algorithm](#)” on page 4645.

Details: MCMC Procedure

How PROC MCMC Works

PROC MCMC is a simulation-based procedure that applies a variety of sampling algorithms to the program at hand. The default sampling methods include conjugate sampling (from full conditional), direct sampling from the marginal distribution, inverse cumulative distribution function, random walk Metropolis with normal proposal, and discretized random walk Metropolis with normal proposal. You can request alternate sampling algorithms, such as random walk Metropolis with t distribution proposal, discretized random walk Metropolis with symmetric geometric proposal, and the slice sampling algorithm.

PROC MCMC applies the more efficient sampling algorithms first, whenever possible. When a parameter does not appear in the conditional distributions of other random variables in the program, PROC MCMC generates samples directly from its prior distribution (which is also its marginal distribution). This usually occurs in data-independent Monte Carlo simulation programs (see “[Example 55.1: Simulating Samples From a Known Density](#)” on page 4540 for an example) or missing data problems, where the missing response variables are generated directly from the conditional sampling distribution (or the conditional likelihood). When conjugacy is detected, PROC MCMC uses random number generators to draw values from the full conditional distribution. (For information about detecting conjugacy, see the section “[Conjugate Sampling](#)” on page 4472.) In other situations, PROC MCMC resorts to the random walk Metropolis with normal proposal to generate posterior samples for continuous parameters and a discretized version for discrete parameters. See the section “[Metropolis and Metropolis-Hastings Algorithms](#)” on page 134 for details about the Metropolis algorithm. For the actual implementation details of the Metropolis algorithm in PROC MCMC, such as tuning of the covariance matrices, see the section “[Tuning the Proposal Distribution](#)” on page 4469.

A key component of the Metropolis algorithm is the calculation of the objective function. In most cases, the objective function that PROC MCMC uses in a Metropolis step is the logarithm of the joint posterior distribution, which is calculated with the inclusion of all data and parameters. The rest of this section describes how PROC MCMC calculates the objective function for parameters that use the Metropolis algorithm.

Model Parameters

To calculate the log of the posterior density, PROC MCMC assumes that all observations in the data set are independent,

$$\log(p(\theta|\mathbf{y})) = \log(\pi(\theta)) + \sum_{i=1}^n \log(f(y_i|\theta))$$

where θ is a parameter or a vector of parameters that are defined in the **PARMS** statements (referred to as the *model parameters*). The term $\log(\pi(\theta))$ is the sum of the log of the prior densities specified in the **PRIOR** and **HYPERPRIOR** statements. The term $\log(f(y_i|\theta))$ is the log likelihood specified in the **MODEL** statement. The **MODEL** statement specifies the log likelihood for a single observation in the data set.

If you want to model dependent data—that is, $\log(f(\mathbf{y}|\theta)) \neq \sum_i \log(f(y_i|\theta))$ —you can use the **JOINT-MODEL** option in the PROC MCMC statement. See the section “[Modeling Joint Likelihood](#)” on page 4504 for more details.

The statements in PROC MCMC are similar to DATA step statements; PROC MCMC evaluates every statement in order for each observation. At the beginning of the data set, the log likelihood is set to be 0. As PROC MCMC steps through the data set, it cumulatively adds the log likelihood for each observation. Statements between the **BEGINNODATA** and **ENDNODATA** statements are evaluated only at the first and the last observations. At the last observation, the log of the prior and hyperprior distributions is added to the sum of the log likelihood to obtain the log of the posterior distribution.

Calculation of the $\log(p(\theta|\mathbf{y}))$ objective function involves a complete pass through the data set, making it potentially computationally expensive. If $\theta = \{\theta_1, \theta_2\}$ is multidimensional, you can choose to update a portion of the parameters at each iteration step by declaring them in separate **PARMS** statements (see the section “[Blocking of Parameters](#)” on page 4466 for more information). PROC MCMC updates each block of parameters while holding others constant. The objective functions that are used in each update are the same as the log of the joint posterior density:

$$\log(p(\theta_1|\mathbf{y}, \theta_2)) = \log(p(\theta_2|\mathbf{y}, \theta_1)) = \log(p(\theta|\mathbf{y}))$$

In other words, PROC MCMC does not derive the conditional distribution explicitly for each block of parameters, and it uses the full joint distribution in the Metropolis step for every block update.

Random-Effects Models

For programs that require **RANDOM** statements, PROC MCMC includes the sum of the density evaluation of the random-effects parameters in the calculation of the objective function for θ ,

$$\log(p(\theta|\boldsymbol{\gamma}, \mathbf{y})) = \log(\pi(\theta)) + \sum_{j=1}^J \log(\pi(\gamma_j|\theta)) + \sum_{i=1}^n \log(f(y_i|\theta, \boldsymbol{\gamma}))$$

where $\boldsymbol{\gamma} = \{\gamma_1, \dots, \gamma_J\}$ are random-effects parameters and $\pi(\gamma_j|\theta)$ is the prior distribution of the random-effects parameters. The likelihood function can be conditional on $\boldsymbol{\gamma}$, but the prior distributions of θ , which must be independent of $\boldsymbol{\gamma}$, cannot.

The objective function used in the Metropolis step for the random-effects parameter γ_j contains only the portion of the data that belong to the j th cluster:

$$\log(p(\gamma_j|\theta, \mathbf{y})) = \log(\pi(\gamma_j|\theta)) + \sum_{i \in \{j\text{th cluster}\}} \log(f(y_i|\theta, \gamma_j))$$

The calculation does not include $\log(\theta)$, the prior density piece, because that is a known constant. Evaluation of this objective function involves only a portion of the data set, making it more computationally efficient. In fact, updating every random-effects parameters in a single **RANDOM** statement involves only one pass through the data set.

You can have multiple **RANDOM** statements in a program, which adds more pieces to the posterior calculation, such as

$$\log(p(\theta|\boldsymbol{\gamma}, \boldsymbol{\alpha}, \mathbf{y})) = \log(\pi(\theta)) + \sum_{j=1}^J \log(\pi(\gamma_j|\theta)) + \sum_{k=1}^K \log(\pi(\alpha_k|\theta)) + \sum_{i=1}^n \log(f(y_i|\theta, \boldsymbol{\gamma}, \boldsymbol{\alpha}))$$

where $\boldsymbol{\alpha} = \{\alpha_1, \dots, \alpha_K\}$ is another random effect. The random effects $\boldsymbol{\gamma}$ and $\boldsymbol{\alpha}$ can form their own hierarchy (as in a nested model), or they can enter the program in a non-nested fashion. The objective functions for γ_j and α_k are calculated using only observations that belong to their respective clusters.

Models with Missing Values

Missing values in the response variables of the **MODEL** statement are treated as random variables, and they add another layer in the conditional updates in the simulation. Suppose that

$$\mathbf{y} = \{\mathbf{y}_{\text{obs}}, \mathbf{y}_{\text{mis}}\}$$

The response variable $\mathbf{y}$ consists of n_1 observed values $\mathbf{y}_{\text{obs}}$ and n_2 missing values $\mathbf{y}_{\text{mis}}$. The log of the posterior distribution is thus formed by

$$\log(p(\theta|\boldsymbol{\gamma}, \mathbf{y}_{\text{mis}}, \mathbf{y}_{\text{obs}})) = \log(\pi(\theta)) + \sum_{j=1}^J \log(\pi(\gamma_j|\theta)) + \sum_{i=1}^{n_2} \log(f(y_{\text{mis},i}|\theta, \boldsymbol{\gamma})) + \sum_{i=1}^{n_1} \log(f(y_{\text{obs},i}|\theta, \boldsymbol{\gamma}))$$

where the expression is evaluated at the drawn $\boldsymbol{\gamma}$ and $\mathbf{y}_{\text{obs}}$ values.

The conditional distribution of the random-effects parameter γ_j is

$$\log(p(\gamma_j|\theta, \mathbf{y})) = \log(\pi(\gamma_j|\theta)) + \sum_{i \in \{j\text{th cluster}\}} \log(f(y_i|\theta, \gamma_j))$$

where the y_i are either the observed or the imputed values of the response variable.

The missing values are usually sampled directly from the sampling distribution and do not require the Metropolis sampler. When a response variable takes on a **GENERAL** function, the objective function is simply the likelihood function: $\log(f(y_{\text{mis},i}|\theta, \gamma_j))$.

Blocking of Parameters

In a multivariate parameter model, if all k parameters are proposed with one joint distribution $q(\cdot|\cdot)$, acceptance or rejection would occur for all of them. This can be rather inefficient, especially when parameters have vastly different scales. A way to avoid this difficulty is to allocate the k parameters into d blocks and update them separately. The **PARMS** statement puts model parameters in separate blocks, and each block of parameters is updated sequentially in the procedure.

Suppose you want to sample from a multivariate distribution with probability density function $p(\theta|\mathbf{y})$ where $\theta = \{\theta_1, \theta_2, \dots, \theta_k\}$. Now suppose that these k parameters are separated into d blocks—for example, $p(\theta|\mathbf{x}) = f_d(z)$ where $z = \{z_1, z_2, \dots, z_d\}$, where each z_j contains a nonempty subset of the $\{\theta_i\}$, and where each θ_i is contained in one and only one z_j . In the MCMC context, the z 's are blocks of parameters. In the blocked algorithm, a proposal consists of several parts. Instead of proposing a simultaneous move for all the θ 's, a proposal is made for the θ_i 's in z_1 only, then for the θ_i 's in z_2 , and so on for d subproposals. Any accepted proposal can involve any number of the blocks moving. The parameters do not necessarily all move at once as in the all-at-once Metropolis algorithm.

Formally, the blocked Metropolis algorithm is as follows. Let w_j be the collection of θ_i that are in block z_j , and let $q_j(\cdot|w_j)$ be a symmetric multivariate distribution that is centered at the current values of w_j .

1. Let $t = 0$. Choose points for all w_j^t . A point can be an arbitrary point as long as $p(w_j^t|\mathbf{y}) > 0$.
2. For $j = 1, \dots, d$:
 - a) Generate a new sample, $w_{j,\text{new}}$, using the proposal distribution $q_j(\cdot|w_j^t)$.
 - b) Calculate the following quantity:

$$r = \min \left\{ \frac{p(w_{j,\text{new}}|w_1^t, \dots, w_{j-1}^t, w_{j+1}^{t-1}, \dots, w_d^t, \mathbf{y})}{p(w_j^t|w_1^t, \dots, w_{j-1}^t, w_{j+1}^{t+1}, \dots, w_d^t, \mathbf{y})}, 1 \right\}.$$
 - c) Sample u from the uniform distribution $U(0, 1)$.
 - d) Set $w_j^{t+1} = w_{j,\text{new}}$ if $r < u$; $w_j^{t+1} = w_j^t$ otherwise.
3. Set $t = t + 1$. If $t < T$, the number of desired samples, go back to Step 2; otherwise, stop.

With PROC MCMC, you can sample all parameters simultaneously by putting them all in a single PARMS statement, you can sample parameters individually by putting each parameter in its own PARMS statement, or you can sample certain subsets of parameters together by grouping each subset in its own PARMS statements. For example, if the model you are interested in has five parameters, alpha, beta, gamma, phi, sigma, the all-at-once strategy is as follows:

```
parms alpha beta gamma phi sigma;
```

The one-at-a-time strategy is as follows:

```
parms alpha;
parms beta;
parms gamma;
parms phi;
parms sigma;
```

A two-block strategy could be as follows:

```
parms alpha beta gamma;
parms phi sigma;
```

The exceptions to the previously described blocking strategies are parameters that are sampled directly (either from their full conditional or marginal distributions) and parameters that are array-based (with multivariate prior distributions). In these cases, the parameters are taken out of an existing block and are updated individually. You can use the sampling options in the **PARMS** statement to override the default behavior.

One of the greatest challenges in MCMC sampling is achieving good mixing of the chains—the chains should quickly traverse the support of the stationary distribution. A number of factors determine the behavior of a Metropolis sampler; blocking is one of them, so you want to be extremely careful when you choose a good design. Generally speaking, forming blocks of parameters has its advantages, but it is not true that the larger the block the faster the convergence.

When simultaneously sampling a large number of parameters, the algorithm might find it difficult to achieve good mixing. As the number of parameters gets large, it is much more likely to have (proposal) samples that fall well into the tails of the target distribution, producing too small a test ratio. As a result, few proposed values are accepted and convergence is slow. On the other hand, when the algorithm samples each parameter individually, the computational cost increases linearly. Each block of Metropolis parameters requires one additional pass through the data set, so a five-block updating strategy could take five times longer than a single-block updating strategy. In addition, there is a chance that the chain might mix far too slowly because the conditional distributions (of θ_i given all other θ 's) might be very “narrow,” as a result of posterior correlation among the parameters. When that happens, it takes a long time for the chain to fully explore that dimension alone. There are no theoretical results that can help determine an optimal “blocking” for an arbitrary parametric model. A rule followed in practice is to form small groups of correlated parameters that belong to the same context in the formulation of the model. The best mixing is usually obtained with a blocking strategy somewhere between the all-at-once and one-at-a-time strategies.

Sampling Methods

When suitable, PROC MCMC chooses the optimal sampling method for each parameter. That involves direct sampling either from the conditional posterior via conjugacy (see the section “[Conjugate Sampling](#)” on page 4472) or via the marginal posterior (see the section “[Direct Sampling](#)” on page 4472). Alternatively, PROC MCMC samples according to [Table 55.5](#). Each block of parameters is classified by the nature of the prior distributions. “Continuous” means all priors of the parameters in the same block have a continuous distribution. “Discrete” means all priors are discrete. “Mixed” means that some parameters are continuous and others are discrete. Parameters that have binary priors are treated differently, as indicated in the table.

Table 55.5 Sampling Methods in PROC MCMC

Blocks	Default Method	Alternative Method
Continuous	Multivariate normal (MVN)	Multivariate t (MVT); slice sampler
Discrete (other than binary)	Binned MVN	Binned MVT or symmetric geometric
Mixed	MVN	MVT
Binary (single dimensional)	Inverse CDF	
Binary (multidimensional)	Independence sampler	

For a block of continuous parameters, PROC MCMC uses a multivariate normal distribution as the default proposal distribution. In the tuning phase, PROC MCMC finds an optimal scale c and a tuning covariance matrix Σ .

For a discrete block of parameters, PROC MCMC uses a discretized multivariate normal distribution as the default proposal distribution. The scale c and covariance matrix Σ are tuned. Alternatively, you can use an independent symmetric geometric proposal distribution. The density has form $\frac{p(1-p)^{|\theta|}}{2(1-p)}$ and has variance $\frac{(2-p)(1-p)}{p^2}$. In the tuning phase, the procedure finds an optimal proposal probability p for every parameter in the block.

You can change the proposal distribution, from the normal to a t distribution. You can either use the PROC option **PROPDIST=T(df)** or **PARMS** statement option **</ T(df)>** to make the change. The t distributions have thicker tails, and they can propose to the tail areas more efficiently than the normal distribution. It can help with the mixing of the Markov chain if some of the parameters have a skewed tails. See “[Example 55.6: Nonlinear Poisson Regression Models](#)” on page 4570. The independence sampler (see the section “[Independence Sampler](#)” on page 137) is used for a block of binary parameters. The inverse CDF method is used for a block that consists of a single binary parameter.

For parameters with continuous prior distributions, you can use the slice sampler as an alternative sampling algorithm. To do so, specify the **SLICE** option in the **PARMS**. When you specify the **SLICE** option, all parameters are updated individually. PROC MCMC does not support a multivariate version of the slice sampler. For more in information about the slice sampler, see the section “[Slice Sampler](#)” on page 136.

The sampling algorithms for the random-effects parameters are chosen in a similar fashion. The preferred algorithms are the direct method either from the full conditional or the marginal. When these are not attainable, Metropolis with normal proposal becomes the default for continuous random-effects parameters, and discrete Metropolis with normal proposal becomes the default for discrete random-effects parameters. You can use the **ALGORITHM=** option in the **RANDOM** statement to choose the slice sampler or discrete Metropolis with symmetric geometric as the alternatives.

The sampling preference of the missing data variables is the same as the random-effects parameters. The reserve sampling algorithm is the Metropolis. There is no alternative sampling method available for the missing data variables.

Tuning the Proposal Distribution

One key factor in achieving high efficiency of a Metropolis-based Markov chain is finding a good proposal distribution for each block of parameters. This process is referred to as tuning. The tuning phase consists of a number of loops. The minimum number of loops is controlled by the option **MINTUNE=**, with a default value of 2. The option **MAXTUNE=** controls the maximum number of tuning loops, with a default value of 24. Each loop lasts for **NTU=** iterations, where by default **NTU=** 500. At the end of every loop, PROC MCMC examines the acceptance probability for each block. The acceptance probability is the percentage of **NTU=** proposals that have been accepted. If the probability falls within the acceptance tolerance range (see the section “[Scale Tuning](#)” on page 4470), the current configuration of c/Σ or p is kept. Otherwise, these parameters are modified before the next tuning loop.

Continuous Distribution: Normal or t Distribution

A good proposal distribution should resemble the actual posterior distribution of the parameters. Large sample theory states that the posterior distribution of the parameters approaches a multivariate normal distribution (see Gelman et al. 2004, Appendix B, and Schervish 1995, Section 7.4). That is why a normal proposal distribution often works well in practice. The default proposal distribution in PROC MCMC is

the normal distribution: $q_j(\theta_{\text{new}}|\theta^t) = \text{MVN}(\theta_{\text{new}}|\theta^t, c^2\Sigma)$. As an alternative, you can choose a multivariate t distribution as the proposal distribution. It is a good distribution to use if you think that the posterior distribution has thick tails and a t distribution can improve the mixing of the Markov chain. See “Example 55.6: Nonlinear Poisson Regression Models” on page 4570.

Scale Tuning

The acceptance rate is closely related to the sampling efficiency of a Metropolis chain. For a random walk Metropolis, high acceptance rate means that most new samples occur right around the current data point. Their frequent acceptance means that the Markov chain is moving rather slowly and not exploring the parameter space fully. On the other hand, a low acceptance rate means that the proposed samples are often rejected; hence the chain is not moving much. An efficient Metropolis sampler has an acceptance rate that is neither too high nor too low. The scale c in the proposal distribution $q(\cdot|\cdot)$ effectively controls this acceptance probability. Roberts, Gelman, and Gilks (1997) showed that if both the target and proposal densities are normal, the optimal acceptance probability for the Markov chain should be around 0.45 in a single dimensional problem, and asymptotically approaches 0.234 in higher dimensions. The corresponding optimal scale is 2.38, which is the initial scale set for each block.

Due to the nature of stochastic simulations, it is impossible to fine-tune a set of variables such that the Metropolis chain has the exact desired acceptance rate. In addition, Roberts and Rosenthal (2001) empirically demonstrated that an acceptance rate between 0.15 and 0.5 is at least 80% efficient, so there is really no need to fine-tune the algorithms to reach acceptance probability that is within small tolerance of the optimal values. PROC MCMC works with a probability range, determined by the PROC options `TARGACCEPT ± ACCEPTTOL`. The default value of `TARGACCEPT` is a function of the number of parameters in the model, as outlined in Roberts, Gelman, and Gilks (1997). The default value of `ACCEPTTOL` is 0.075. If the observed acceptance rate in a given tuning loop is less than the lower bound of the range, the scale is reduced; if the observed acceptance rate is greater than the upper bound of the range, the scale is increased. During the tuning phase, a scale parameter in the normal distribution is adjusted as a function of the observed acceptance rate and the target acceptance rate. The following updating scheme is used in PROC MCMC ²:

$$c_{\text{new}} = \frac{c_{\text{cur}} \cdot \Phi^{-1}(p_{\text{opt}}/2)}{\Phi^{-1}(p_{\text{cur}}/2)}$$

where c_{cur} is the current scale, p_{cur} is the current acceptance rate, p_{opt} is the optimal acceptance probability.

Covariance Tuning

To tune a covariance matrix, PROC MCMC takes a weighted average of the old proposal covariance matrix and the recent observed covariance matrix, based on `NTU` samples in the current loop. The `TUNEWT=w` option determines how much weight is put on the recently observed covariance matrix. The formula used to update the covariance matrix is as follows:

$$\text{COV}_{\text{new}} = w \text{COV}_{\text{cur}} + (1 - w)\text{COV}_{\text{old}}$$

There are two ways to initialize the covariance matrix:

² Roberts, Gelman, and Gilks (1997) and Roberts and Rosenthal (2001) demonstrate that the relationship between acceptance probability and scale in a random walk Metropolis is $p = 2\Phi(-\sqrt{I}c/2)$, where c is the scale, p is the acceptance rate, Φ is the CDF of a standard normal, and $I \equiv E_f[(f'(x)/f(x))^2]$, $f(x)$ is the density function of samples. This relationship determines the updating scheme, with I being replaced by the identity matrix to simplify calculation.

- The default is an identity matrix multiplied by the initial scale of 2.38 (controlled by the PROC option `SCALE=`) and divided by the square root of the number of estimated parameters in the model. It can take a number of tuning phases before the proposal distribution is tuned to its optimal stage, since the Markov chain needs to spend time learning about the posterior covariance structure. If the posterior variances of your parameters vary by more than a few orders of magnitude, if the variances of your parameters are much different from 1, or if the posterior correlations are high, then the proposal tuning algorithm might have difficulty with forming an acceptable proposal distribution.
- Alternatively, you can use a numerical optimization routine, such as the quasi-Newton method, to find a starting covariance matrix. The optimization is performed on the joint posterior distribution, and the covariance matrix is a quadratic approximation at the posterior mode. In some cases this is a better and more efficient way of initializing the covariance matrix. However, there are cases, such as when the number of parameters is large, where the optimization could fail to find a matrix that is positive definite. In that case, the tuning covariance matrix is reset to the identity matrix.

A side product of the optimization routine is that it also finds the *maximum a posteriori* (MAP) estimates with respect to the posterior distribution. The MAP estimates are used as the initial values of the Markov chain.

If any of the parameters are discrete, then the optimization is performed conditional on these discrete parameters at their respective fixed initial values. On the other hand, if all parameters are continuous, you can in some cases skip the tuning phase (by setting `MAXTUNE=0`) or the burn-in phase (by setting `NBI=0`).

Discrete Distribution: Symmetric Geometric

By default, PROC MCMC uses the normal density as the proposal distribution in all Metropolis random walks. For parameters that have discrete prior distributions, PROC MCMC discretizes proposed samples. You can choose an alternative symmetric geometric proposal distribution by specifying the option `DIS-CREATE=GEO`.

The density of the symmetric geometric proposal distribution is as follows:

$$\frac{p_g(1 - p_g)^{|\theta|}}{2(1 - p_g)}$$

where the symmetry centers at θ . The distribution has a variance of

$$\sigma^2 = \frac{(2 - p_g)(1 - p_g)}{p_g^2}$$

Tuning for the proposal p_g uses the following formula:

$$\frac{\sigma_{\text{new}}}{\sigma_{\text{cur}}} = \frac{\Phi^{-1}(p_{\text{opt}}/2)}{\Phi^{-1}(p_{\text{cur}}/2)}$$

where σ_{new} is the standard deviation of the new proposal geometric distribution, σ_{cur} is the standard deviation of the current proposal distribution, p_{opt} is the target acceptance probability, and p_{cur} is the current acceptance probability for the discrete parameter block.

The updated p_g is the solution to the following equation that is between 0 and 1 :

$$\sqrt{\frac{(2 - p_g)(1 - p_g)}{p_g^2}} = \frac{\sigma_{\text{cur}} \cdot \Phi^{-1}(p_{\text{opt}}/2)}{\Phi^{-1}(p_{\text{cur}}/2)}$$

Binary Distribution: Independence Sampler

Blocks consisting of a single parameter with a binary prior do not require any tuning; the inverse-CDF method applies. Blocks that consist of multiple parameters with binary prior are sampled by using an independence sampler with binary proposal distributions. See the section “[Independence Sampler](#)” on page 137. During the tuning phase, the success probability p of the proposal distribution is taken to be the probability of acceptance in the current loop. Ideally, an independence sampler works best if the acceptance rate is 100%, but that is rarely achieved. The algorithm stops when the probability of success exceeds the `TARGACCEPTI=`*value*, which has a default value of 0.6.

Direct Sampling

The word “direct” is reserved for sampling that is done directly from the prior distribution of a model or a random-effects parameter or from the sampling distribution of a missing data variable. If the parameter is updated via sampling from its full conditional posterior distribution, the sampling method is referred to as conjugate sampling. (See the section “[Conjugate Sampling](#)” on page 4472.)

Whenever a parameter does not appear in the hierarchy of another parameter in the model, PROC MCMC samples directly from its distribution. For a model parameter or a random-effects parameter, this distribution is its prior distribution. For a missing data variable, this distribution is the sampling distribution of the response variable. Therefore, direct sampling takes place most frequently in data-independent Monte Carlo simulations or the sampling of missing response variables.

Conjugate Sampling

Conjugate prior is a family of prior distributions in which the prior and the posterior distributions are of the same family of distributions. For example, if you model an independently and identically distributed random variable y_i using a normal likelihood with known variance σ^2 ,

$$y_i \sim \text{normal}(\mu, \sigma^2)$$

a normal prior on μ

$$\mu \sim \text{normal}(\mu_0, \sigma_0^2)$$

is a conjugate prior because the posterior distribution of μ is also a normal distribution given $y = \{y_i\}$, σ^2 , μ_0 , and σ_0^2 :

$$\mu|y \sim \text{normal} \left(\left(\frac{1}{\sigma_0^2} + \frac{n}{\sigma^2} \right)^{-1} \cdot \left(\frac{\mu_0}{\sigma_0^2} + \frac{n \cdot \bar{y}}{\sigma^2} \right), \left(\frac{1}{\sigma_0^2} + \frac{n}{\sigma^2} \right)^{-1} \right)$$

Conjugate sampling is efficient because it enables the Markov chain to obtain samples from the target distribution directly. When appropriate, PROC MCMC uses conjugate sampling methods to draw conditional posterior samples. [Table 55.6](#) lists scenarios that lead to conjugate sampling in PROC MCMC.

Table 55.6 Conjugate Sampling in PROC MCMC

Family	Parameter	Prior
Normal with known μ	Variance σ^2	Inverse gamma family
Normal with known μ	Precision τ	Gamma family
Normal with known scale parameter (σ^2 , σ , or τ)	Mean μ	Normal
Multivariate normal with known Σ	Mean $\boldsymbol{\mu}$	Multivariate normal
Multivariate normal with known $\boldsymbol{\mu}$	Covariance Σ	Inverse Wishart
Multinomial	$\mathbf{p}$	Dirichlet
Binomial/binary	p	Beta
Poisson	λ	Gamma family

In most cases, Family in [Output 55.6](#) refers to the likelihood function. However, it does not necessarily have to be the case. The Family is a distribution that is conditional on the parameter of interest, and it can appear in any level of the hierarchical model, including on the random-effects level.

PROC MCMC can detect conjugacy only if the model parameter (not a function or a transformation of the model parameter) is used in the prior and Family distributions. For example, the following statements lead to a conjugate sampler being used on the parameter mu:

```
parm mu;
prior mu ~ n(0, sd=1000);
model y ~ n(mu, var=s2);
```

However, if you modify the program slightly in the following way, although the conjugacy still holds in theory, PROC MCMC cannot detect conjugacy on mu because the parameter enters the normal likelihood function through the symbol w:

```
parm mu;
prior mu ~ n(0, sd=1000);
w = mu;
model y ~ n(w, var=s2);
```

In this case, PROC MCMC resorts to the default sampling algorithm, which is a random walk Metropolis based on a normal kernel.

Similarly, the following statements also prevent PROC MCMC from detecting conjugacy on the parameter mu:

```
parm mu;
prior mu ~ n(0, sd=1000);
model y ~ n(mu + 2, var=s2);
```

In a normal family, an often-used and often-confused conjugate prior on the variance is the inverse gamma distribution, and a conjugate prior on the precision is the gamma distribution. See “[Gamma and Inverse-Gamma Distributions](#)” on page 4512 for typical usages of these prior distributions.

When conjugacy is detected in a model, PROC MCMC performs a numerical optimization on the joint posterior distribution at the start of the MCMC simulation. If the only sampling methods required in the program are conjugate samplers or direct samplers, PROC MCMC omits this optimization step. To turn off this optimization routine, use the [PROPCOV=IND](#) option in the PROC MCMC statement.

Initial Values of the Markov Chains

There are three types of parameters in a PROC MCMC program: the *model parameters* in the **PARMS** statement, the *random-effects parameters* in the **RANDOM** statement, and the *missing data variables* in the **MODEL** statement. The last category is used to model missing values in the input data set.

When the model parameters and random-effects parameters have missing initial values, PROC MCMC generates initial values based on the prior distributions. PROC MCMC either uses the mode value (the default) or draws a random number (if the **INIT=****RANDOM** option is specified). For distributions that do not have modes, such as the uniform distribution, PROC MCMC uses the mean instead. In general, PROC MCMC avoids using starting values that are close to the boundary of support of the prior distribution. For example, the exponential prior has a mode at 0, and PROC MCMC starts an initial value at the mean. This avoids some potential numerical problems. If you use the **GENERAL** or **DGENERAL** function in the **PRIOR** statements, you must provide initial values for those parameters.

With missing data variables, PROC MCMC uses the sample average of the nonmissing values (of the response variable) as the initial value. If all values of a particular variable are missing, PROC MCMC resorts to using the mode value or a random number from the sampling distribution (the likelihood), depending on the specification of the **INIT=** option.

To assign a different set of initial values to the model parameters, you use either the **PARMS** statements or programming statements within the **BEGINCNST** and **ENDCNST** statements. See the section “Assignments of Parameters” on page 4474 for more information about how to assign parameter values within the **BEGINCNST** and **ENDCNST** statements.

To assign initial values to the random-effects parameters, you can use the **INIT=** option in the **RANDOM** statement. Either you can give a constant value to all random-effects parameters that are associated with that statement (for example, use **init=3**), or you can assign values individually by providing a data set that stores different values for different parameters.

A mirroring **INIT=** option in the **MODEL** statement enables you to assign different initial values to the missing data variables.

If you use the **PROPCOV=** optimization option in the PROC MCMC statement, PROC MCMC starts the tuning at the optimized values. PROC MCMC overwrites the initial values that you might have provided at the beginning of the Markov chain unless you use the option **INIT=REINIT**.

Assignments of Parameters

In general, you cannot alter the values of any model parameters in PROC MCMC. For example, the following assignment statement produces an error:

```
parms alpha;  
alpha = 27;
```

This restriction prevents incorrect calculation of the posterior density—assignments of parameters in the program would override the parameter values generated by PROC MCMC and lead to an incorrect value of the density function.

However, you can modify parameter values and assign initial values to parameters within the block defined by the **BEGINCNST** and **ENDCNST** statements. The following syntax is allowed:

```
parms alpha;
begincnst;
    alpha = 27;
endcnst;
```

The initial value of alpha is 27. Assignments within the **BEGINCNST/ENDCNST** block override initial values specified in the **PARMS** statement. For example, with the following statements, the Markov chain starts at alpha = 27, not 23.

```
parms alpha 23;
begincnst;
    alpha = 27;
endcnst;
```

This feature enables you to systematically assign initial values. Suppose that z is an array parameter of the same length as the number of observations in the input data set. You want to start the Markov chain with each z_i having a different value depending on the data set variable y . The following statements set $z_i = |y|$ for the first half of the observations and $z_i = 2.3$ for the rest:

```
/* a rather artificial input data set. */
data inputdata;
    do ind = 1 to 10;
        y = rand('normal');
        output;
    end;
run;

proc mcmc data=inputdata;
    array z[10];
    begincnst;
        if ind <= 5 then z[ind] = abs(y);
        else z[ind] = 2.3;
    endcnst;
    parms z;;
    prior z: ~ normal(0, sd=1);
    model general(0);
run;
```

Elements of z are modified as PROC MCMC executes the programming statements between the **BEGINCNST** and **ENDCNST** statements. This feature could be useful when you use the **GENERAL** function and you find that the **PARMS** statements are too cumbersome for assigning starting values.

Standard Distributions

The section “Univariate Distributions” on page 4476 (Table 55.7 through Table 55.34) lists all univariate distributions that PROC MCMC recognizes. The section “Multivariate Distributions” on page 4486 (Table 55.35 through Table 55.39) lists all multivariate distributions that PROC MCMC recognizes. With the exception of the **multinomial** distribution, all these distributions can be used in the **MODEL**, **PRIOR**, and **HYPERPRIOR** statements. The **multinomial** distribution is supported only in the **MODEL** statement. The **RANDOM** statement supports a limited number of distributions; see Table 55.4 for the complete list.

See the section “Using Density Functions in the Programming Statements” on page 4491 for information about how to use distributions in the programming statements. To specify an arbitrary distribution, you can use the **GENERAL** and **DGENERAL** functions. See the section “Specifying a New Distribution” on page 4490 for more details. See the section “Truncation and Censoring” on page 4494 for tips about how to work with truncated distributions and censoring data.

Univariate Distributions

Table 55.7 Beta Distribution

PROC specification	beta (a, b)
Density	$\frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} \theta^{a-1} (1-\theta)^{b-1}$
Parameter restriction	$a > 0, b > 0$
Range	$\begin{cases} [0, 1] & \text{when } a = 1, b = 1 \\ [0, 1) & \text{when } a = 1, b \neq 1 \\ (0, 1] & \text{when } a \neq 1, b = 1 \\ (0, 1) & \text{otherwise} \end{cases}$
Mean	$\frac{a}{a+b}$
Variance	$\frac{ab}{(a+b)^2(a+b+1)}$
Mode	$\begin{cases} \frac{a-1}{a+b-2} & a > 1, b > 1 \\ 0 \text{ and } 1 & a < 1, b < 1 \\ 0 & \begin{cases} a < 1, b \geq 1 \\ a = 1, b > 1 \end{cases} \\ 1 & \begin{cases} a \geq 1, b < 1 \\ a > 1, b = 1 \end{cases} \\ \text{does not exist uniquely} & a = b = 1 \end{cases}$
Random number	If $\min(a, b) > 1$, see (Cheng 1978); if $\max(a, b) < 1$, see (Atkinson and Whittaker 1976) and (Atkinson 1979); if $\min(a, b) < 1$ and $\max(a, b) > 1$, see (Cheng 1978); if $a = 1$ or $b = 1$, use the inversion method; if $a = b = 1$, use a uniform random number generator.

Table 55.8 Binary Distribution

PROC specification	binary (p)
Density	$p^\theta (1-p)^{1-\theta}$
Parameter restriction	$0 \leq p \leq 1$
Range	$\begin{cases} \{0\} & \text{when } p = 0 \\ \{1\} & \text{when } p = 1 \\ \{0, 1\} & \text{otherwise} \end{cases}$
Mean	$\text{round}(p)$
Variance	$p(1-p)$
Mode	$\begin{cases} \{1\} & \text{when } p = 1 \\ \{0\} & \text{otherwise} \end{cases}$
Random number	Generate $u \sim \text{uniform}(0, 1)$. If $u \leq p$, $\theta = 1$; else, $\theta = 0$.

Table 55.9 Binomial Distribution

PROC specification	binomial (n, p)
Density	$\binom{n}{\theta} p^\theta (1-p)^{n-\theta}$
Parameter restriction	$n = 0, 1, 2, \dots$ $0 \leq p \leq 1$
Range	$\theta \in \{0, \dots, n\}$
Mean	$\lfloor np \rfloor$
Variance	$np(1-p)$
Mode	$\lfloor (n+1)p \rfloor$

Table 55.10 Cauchy Distribution

PROC specification	cauchy (a, b)
Density	$\frac{1}{\pi} \left(\frac{b}{b^2 + (\theta - a)^2} \right)$
Parameter restriction	$b > 0$
Range	$\theta \in (-\infty, \infty)$
Mean	Does not exist.
Variance	Does not exist.
Mode	a
Random number	Generate $u_1, u_2 \sim \text{uniform}(0, 1)$; let $v = 2u_2 - 1$. Repeat the procedure until $u_1^2 + v^2 < 1$. $y = v/u_1$ is a draw from the standard Cauchy, and $\theta = a + by$ (Ripley 1987).

Table 55.11 χ^2 Distribution

PROC specification	chisq (ν)
Density	$\frac{1}{\Gamma(\nu/2)2^{\nu/2}} \theta^{(\nu/2)-1} e^{-\theta/2}$
Parameter restriction	$\nu > 0$
Range	$\theta \in [0, \infty)$ if $\nu = 2$; $(0, \infty)$ otherwise.
Mean	ν
Variance	2ν
Mode	$\nu - 2$ if $\nu \geq 2$; does not exist otherwise.
Random number	χ^2 is a special case of the gamma distribution: $\theta \sim \text{gamma}(\nu/2, \text{scale}=2)$ is a draw from the χ^2 distribution.

Table 55.12 Exponential χ^2 Distribution

PROC specification	expchisq (ν)
Density	$\frac{1}{\Gamma(\nu/2)2^{\nu/2}} \exp(\theta)^{\nu/2} \exp(-\exp(\theta)/2)$
Parameter restriction	$\nu > 0$
Range	$\theta \in (-\infty, \infty)$
Mode	$\log(\nu)$
Random number	Generate $x_1 \sim \chi^2(\nu)$, and $\theta = \log(x_1)$ is a draw from the exponential χ^2 distribution.
Relationship to the χ^2 distribution	$\theta \sim \chi^2(\nu) \Leftrightarrow \log(\theta) \sim \exp \chi^2(\nu)$

Table 55.13 Exponential Exponential Distribution

PROC specification	expexpon (scale = b)	expexpon (iscale = β)
Density	$\frac{1}{b} \exp(\theta) \exp(-\exp(\theta)/b)$	$\beta \exp(\theta) \exp(-\exp(\theta) \cdot \beta)$
Parameter restriction	$b > 0$	$\beta > 0$
Range	$\theta \in (-\infty, \infty)$	Same
Mode	$\log(b)$	$\log(1/\beta)$
Random number	Generate $x_1 \sim \text{expon}(\text{scale}=b)$, and $\theta = \log(x_1)$ is a draw from the exponential exponential distribution. Note that an exponential exponential distribution is not the same as the double exponential distribution.	
Relationship to the exponential distribution	$\theta \sim \text{expon}(b) \Leftrightarrow \log(\theta) \sim \text{expExpon}(b)$	

Table 55.14 Exponential Gamma Distribution

PROC specification	expgamma (a , scale = b)	expgamma (a , iscale = β)
Density	$\frac{1}{b^a \Gamma(a)} e^{a\theta} \exp(-e^\theta/b)$	$\frac{\beta^a}{\Gamma(a)} e^{a\theta} \exp(-e^\theta \cdot \beta)$
Parameter restriction	$a > 0, b > 0$	$a > 0, \beta > 0$
Range	$\theta \in (-\infty, \infty)$	Same
Mode	$\log(ab)$	$\log(a/\beta)$
Random number	Generate $x_1 \sim \text{gamma}(a, \text{scale} = b)$, and $\theta = \log(x_1)$ is a draw from the exponential gamma distribution.	
Relationship to the Γ distribution	$\theta \sim \text{gamma}(a, b) \Leftrightarrow \log(\theta) \sim \text{expGamma}(a, b)$	

Table 55.15 Exponential Inverse χ^2 Distribution

PROC specification	expichisq (ν)
Density	$\frac{1}{\Gamma(\frac{\nu}{2}) 2^{\nu/2}} \exp(-\nu\theta/2) \exp(-1/(2 \exp(\theta)))$
Parameter restriction	$\nu > 0$
Range	$\theta \in (-\infty, \infty)$
Mode	$-\log(\nu)$
Random number	Generate $x_1 \sim i\chi^2(\nu)$, and $\theta = \log(x_1)$ is a draw from the exponential inverse χ^2 distribution.
Relationship to the $i\chi^2$ distribution	$\theta \sim i\chi^2(\nu) \Leftrightarrow \log(\theta) \sim \text{exp} i\chi^2(\nu)$

Table 55.16 Exponential Inverse-Gamma Distribution

PROC specification	expigamma (a , scale = b)	expigamma (a , iscale = β)
Density	$\frac{b^a}{\Gamma(a)} \exp(-\alpha\theta) \exp(-b/\exp(\theta))$	$\frac{1}{\beta^a \Gamma(a)} \exp(-\alpha\theta) \exp(-\frac{1}{\beta \exp(\theta)})$
Parameter restriction	$a > 0, b > 0$	$a > 0, \beta > 0$
Range	$\theta \in (-\infty, \infty)$	Same
Mode	$-\log(a/b)$	$-\log(a\beta)$
Random number	Generate $x_1 \sim \text{igamma}(a, \text{scale} = b)$, and $\theta = \log(x_1)$ is a draw from the exponential inverse-gamma distribution.	
Relationship to the $i\Gamma$ distribution	$\theta \sim \text{igamma}(a, b) \Leftrightarrow \log(\theta) \sim \text{eigamma}(a, b)$	

Table 55.17 Exponential Scaled Inverse χ^2 Distribution

PROC specification	expsichisq (ν, s)
Density	$\frac{(\frac{\nu}{2})^{\nu/2}}{\Gamma(\frac{\nu}{2})} s^\nu \exp(-\nu\theta/2) \exp(-\nu s^2/(2 \exp(\theta)))$
Parameter restriction	$\nu > 0, s > 0$
Range	$\theta \in (-\infty, \infty)$
Mode	$\log(s^2)$
Random number	Generate $x_1 \sim si\chi^2(\nu, s)$, and $\theta = \log(x_1)$ is a draw from the exponential scaled inverse χ^2 distribution.
Relationship to the $si\chi^2$ distribution	$\theta \sim si\chi^2(\nu, s) \Leftrightarrow \log(\theta) \sim \exp si\chi^2(\nu, s)$

Table 55.18 Exponential Distribution

PROC specification	expon (scale = b)	expon (iscale = β)
Density	$\frac{1}{b} e^{-\theta/b}$	$\beta e^{-\beta\theta}$
Parameter restriction	$b > 0$	$\beta > 0$
Range	$\theta \in [0, \infty)$	Same
Mean	b	$1/\beta$
Variance	b^2	$1/\beta^2$
Mode	0	0
Random number	The exponential distribution is a special case of the gamma distribution: $\theta \sim \text{gamma}(1, \text{scale} = b)$ is a draw from the exponential distribution.	

Table 55.19 Gamma Distribution

PROC specification	gamma ($a, \text{scale} = b$)	gamma ($a, \text{iscale} = \beta$)
Density	$\frac{1}{b^a \Gamma(a)} \theta^{a-1} e^{-\theta/b}$	$\frac{\beta^a}{\Gamma(a)} \theta^{a-1} e^{-\beta\theta}$
Parameter restriction	$a > 0, b > 0$	$a > 0, \beta > 0$
Range	$\theta \in [0, \infty)$ if $a = 1$; $(0, \infty)$ otherwise.	Same
Mean	ab	a/β
Variance	ab^2	a/β^2
Mode	$(a-1)b$ if $a \geq 1$	$(a-1)/\beta$ if $a \geq 1$
Random number	See (McGrath and Irving 1973).	

Table 55.20 Geometric Distribution

PROC specification	geo (p)
Density ³	$p(1 - p)^\theta$
Parameter restriction	$0 < p \leq 1$
Range	$\theta \in \begin{cases} \{0, 1, 2, \dots\} & 0 < p < 1 \\ \{0\} & p = 1 \end{cases}$
Mean	$\text{round}(\frac{1-p}{p})$
Variance	$\frac{1-p}{p^2}$
Mode	0
Random number	Based on samples obtained from a Bernoulli distribution with probability p until the first success.

Table 55.21 Inverse χ^2 Distribution

PROC specification	ichisq (ν)
Density	$\frac{1}{\Gamma(\nu/2)2^{\nu/2}} \theta^{-(\nu/2+1)} e^{-1/(2\theta)}$
Parameter restriction	$\nu > 0$
Range	$\theta \in (0, \infty)$
Mean	$\frac{1}{\nu-2}$ if $\nu > 2$
Variance	$\frac{2}{(\nu-2)^2(\nu-4)}$ if $\nu > 4$
Mode	$\frac{1}{\nu+2}$
Random number	Inverse χ^2 is a special case of the inverse-gamma distribution: $\theta \sim \text{igamma}(\nu/2, \text{iscale} = 2)$ is a draw from the inverse χ^2 distribution.

Table 55.22 Inverse-Gamma Distribution

PROC specification	igamma ($a, \text{scale} = b$)	igamma ($a, \text{iscale} = \beta$)
Density	$\frac{b^a}{\Gamma(a)} \theta^{-(a+1)} e^{-b/\theta}$	$\frac{1}{\beta^a \Gamma(a)} \theta^{-(a+1)} e^{-1/\beta\theta}$
Parameter restriction	$a > 0, b > 0$	$a > 0, \beta > 0$
Range	$\theta \in (0, \infty)$	Same
Mean	$\frac{b}{a-1}$ if $a > 1$	$\frac{1}{\beta(a-1)}$ if $a > 1$
Variance	$\frac{b^2}{(a-1)^2(a-2)}$	$\frac{1}{\beta^2(a-1)^2(a-2)}$
Mode	$\frac{b}{a+1}$	$\frac{1}{\beta(a+1)}$
Random number	Generate $x_1 \sim \text{gamma}(a, \text{scale} = b)$, and $\theta = 1/x_1$ is a draw from the $\text{igamma}(a, \text{iscale} = b)$ distribution.	

³The random variable θ is the total number of failures in an experiment *before* the first success. This density function is not to be confused with another popular formulation, $p(1 - p)^{\theta-1}$, which counts the total number of trials *until* the first success.

Relationship to the $\theta \sim \text{gamma}(a, \text{iscale} = b) \Leftrightarrow 1/\theta \sim \text{igamma}(a, \text{scale} = b)$
gamma distribution

Table 55.23 Laplace (Double Exponential) Distribution

PROC specification	laplace ($a, \text{scale} = b$)	laplace ($a, \text{iscale} = \beta$)
Density	$\frac{1}{2b} e^{- \theta-a /b}$	$\frac{\beta}{2} e^{-\beta \theta-a }$
Parameter restriction	$b > 0$	$\beta > 0$
Range	$\theta \in (-\infty, \infty)$	Same
Mean	a	a
Variance	$2b^2$	$2/\beta^2$
Mode	a	a
Random number	Inverse CDF. $F(\theta) = \begin{cases} \frac{1}{2} \exp\left(-\frac{a-\theta}{b}\right) & \theta < a \\ 1 - \frac{1}{2} \exp\left(-\frac{\theta-a}{b}\right) & \theta \geq a \end{cases}$. Generate $u_1, u_2 \sim \text{uniform}(0, 1)$. If $u_1 < 0.5$, $\theta = a + b \log(u_2)$; else $\theta = a - b \log(u_2)$. θ is a draw from the Laplace distribution.	

Table 55.24 Logistic Distribution

PROC specification	logistic (a, b)
Density	$\frac{\exp\left(-\frac{\theta-a}{b}\right)}{b(1+\exp\left(-\frac{\theta-a}{b}\right))^2}$
Parameter restriction	$b > 0$
Range	$\theta \in (-\infty, \infty)$
Mean	a
Variance	$\frac{\pi^2 b^2}{3}$
Mode	a
Random number	Inverse CDF method with $F(\theta) = \left(1 + \exp\left(-\frac{\theta-a}{b}\right)\right)^{-1}$. Generate $u \sim \text{uniform}(0, 1)$, and $\theta = a - b \log(1/u - 1)$ is a draw from the logistic distribution.

Table 55.25 Lognormal Distribution

PROC specification	lognormal ($\mu, \text{sd} = s$)	lognormal ($\mu, \text{var} = v$)	lognormal ($\mu, \text{prec} = \tau$)
Density	$\frac{1}{\theta s \sqrt{2\pi}} \exp\left(-\frac{(\log \theta - \mu)^2}{2s^2}\right)$	$\frac{1}{\theta \sqrt{2\pi v}} \exp\left(-\frac{(\log \theta - \mu)^2}{2v}\right)$	$\frac{1}{\theta} \sqrt{\frac{\tau}{2\pi}} \exp\left(-\frac{\tau(\log \theta - \mu)^2}{2}\right)$
Parameter restriction	$s > 0$	$v > 0$	$\tau > 0$

Range	$\theta \in (0, \infty)$	Same	Same
Mean	$\exp(\mu + s^2/2)$	$\exp(\mu + v/2)$	$\exp(\mu + 1/(2\tau))$
Variance	$\exp(2(\mu + s^2))$ $-\exp(2\mu + s^2)$	$\exp(2(\mu + v))$ $-\exp(2\mu + v)$	$\exp(2(\mu + 1/\tau))$ $-\exp(2\mu + 1/\tau)$
Mode	$\exp(\mu - s^2)$	$\exp(\mu - v)$	$\exp(\mu - 1/\tau)$
Random number	Generate $x_1 \sim \text{normal}(0, 1)$, and $\theta = \exp(\mu + sx_1)$ is a draw from the lognormal distribution.		

Table 55.26 Negative Binomial Distribution

PROC specification	negbin (n, p)
Density	$\binom{\theta + n - 1}{n - 1} p^n (1 - p)^\theta$
Parameter restriction	$n = 1, 2, \dots$, and $0 < p \leq 1$
Range	$\theta \in \begin{cases} \{0, 1, 2, \dots\} & 0 < p < 1 \\ \{0\} & p = 1 \end{cases}$
Mean	$\text{round}\left(\frac{n(1-p)}{p}\right)$
Variance	$\frac{n(1-p)}{p^2}$
Mode	$\begin{cases} 0 & n = 1 \\ \text{round}\left(\frac{(n-1)(1-p)}{p}\right) & n > 1 \end{cases}$
Random number	Generate $x_1 \sim \text{gamma}(n, 1)$, and $\theta \sim \text{Poisson}(x_1 \cdot (1 - p)/p)$ (Fishman 1996).

Table 55.27 Normal Distribution

PROC specification	normal ($\mu, \text{sd} = s$)	normal ($\mu, \text{var} = v$)	normal ($\mu, \text{prec} = \tau$)
Density	$\frac{1}{s\sqrt{2\pi}} \exp\left(-\frac{(\theta-\mu)^2}{2s^2}\right)$	$\frac{1}{\sqrt{2\pi v}} \exp\left(-\frac{(\theta-\mu)^2}{2v}\right)$	$\sqrt{\frac{\tau}{2\pi}} \exp\left(-\frac{\tau(\theta-\mu)^2}{2}\right)$
Parameter restriction	$s > 0$	$v > 0$	$\tau > 0$
Range	$\theta \in (-\infty, \infty)$	Same	Same
Mean	μ	Same	Same
Variance	s^2	v	$1/\tau$
Mode	μ	Same	Same

Table 55.28 Pareto Distribution

PROC specification	pareto (a, b)
Density	$\frac{a}{b} \left(\frac{b}{\theta}\right)^{a+1}$
Parameter restriction	$a > 0, b > 0$
Range	$\theta \in [b, \infty)$
Mean	$\frac{ab}{a-1}$ if $a > 1$
Variance	$\frac{b^2 a}{(a-1)^2(a-2)}$ if $a > 2$
Mode	b
Random number	Inverse CDF method with $F(\theta) = 1 - (b/\theta)^a$. Generate $u \sim \text{uniform}(0, 1)$, and $\theta = \frac{b}{u^{1/a}}$ is a draw from the Pareto distribution.
Useful transformation	$x = 1/\theta$ is $\text{Beta}(a, 1)\mathbf{I}\{x < 1/b\}$.

Table 55.29 Poisson Distribution

PROC specification	poisson (λ)
Density	$\frac{\lambda^\theta}{\theta!} \exp(-\lambda)$
Parameter restriction	$\lambda \geq 0$
Range	$\theta \in \begin{cases} \{0, 1, \dots\} & \text{if } \lambda > 0 \\ \{0\} & \text{if } \lambda = 0 \end{cases}$
Mean	λ
Variance	λ , if $\lambda > 0$
Mode	$\text{round}(\lambda)$

Table 55.30 Scaled Inverse χ^2 Distribution

PROC specification	sichisq (ν, s^2)
Density	$\frac{(s^2 \nu/2)^{\nu/2}}{\Gamma(\nu/2)} \theta^{-(\nu/2+1)} e^{-\nu s^2/(2\theta)}$
Parameter restriction	$\nu > 0, s > 0$
Range	$\theta \in (0, \infty)$
Mean	$\frac{\nu}{\nu-2} s^2$ if $\nu > 2$
Variance	$\frac{2\nu^2}{(\nu-2)^2(\nu-4)} s^4$ if $\nu > 4$
Mode	$\frac{\nu}{\nu+2} s^2$
Random number	Scaled inverse χ^2 is a special case of the inverse-gamma distribution: $\theta \sim \text{igamma}(\nu/2, \text{scale} = (\nu s^2)/2)$ is a draw from the scaled inverse χ^2 distribution.

Table 55.31 *t* Distribution

PROC specification	$\mathbf{t}(\mu, \text{sd} = s, \nu)$	$\mathbf{t}(\mu, \text{var} = v, \nu)$	$\mathbf{t}(\mu, \text{prec} = \tau, \nu)$
Density	$\frac{\Gamma(\frac{\nu+1}{2})}{\Gamma(\frac{\nu}{2})s\sqrt{\nu\pi}}(1 + \frac{(\theta-\mu)^2}{\nu s^2})^{-\frac{\nu+1}{2}}$	$\frac{\Gamma(\frac{\nu+1}{2})}{\Gamma(\frac{\nu}{2})\sqrt{\nu\pi v}}(1 + \frac{(\theta-\mu)^2}{\nu v})^{-\frac{\nu+1}{2}}$	$\frac{\Gamma(\frac{\nu+1}{2})\sqrt{\tau}}{\Gamma(\frac{\nu}{2})\sqrt{\nu\pi}}(1 + \frac{\tau(\theta-\mu)^2}{\nu})^{-\frac{\nu+1}{2}}$
Parm restriction	$s > 0, \nu > 0$	$v > 0, \nu > 0$	$\tau > 0, \nu > 0$
Range	$\theta \in (-\infty, \infty)$	Same	Same
Mean	μ if $\nu > 1$	Same	Same
Variance	$\frac{\nu}{\nu-2}s^2$ if $\nu > 2$	$\frac{\nu}{\nu-2}v$ if $\nu > 2$	$\frac{\nu}{\nu-2}\frac{1}{\tau}$ if $\nu > 2$
Mode	μ	Same	Same
Random number	$x_1 \sim \text{normal}(0, 1), x_2 \sim \chi^2(d)$, and $\theta = m + \sigma x_1 \sqrt{d/x_2}$ is a draw from the t distribution.		

Table 55.32 Uniform Distribution

PROC specification	$\mathbf{uniform}(a, b)$
Density	$\begin{cases} \frac{1}{a-b} & \text{if } a > b \\ \frac{1}{b-a} & \text{if } b > a \\ 1 & \text{if } a = b \end{cases}$
Parameter restriction	none
Range	$\theta \in [a, b]$
Mean	$\frac{a+b}{2}$
Variance	$\frac{ b-a ^2}{12}$
Mode	Does not exist
Random number	Mersenne Twister (Matsumoto and Kurita 1992, 1994; Matsumoto and Nishimura 1998)

Table 55.33 Wald Distribution

PROC specification	$\mathbf{wald}(\mu, \lambda)$
Density	$\sqrt{\frac{\lambda}{2\pi\theta^3}} \exp\left(\frac{-\lambda(\theta-\mu)^2}{2\mu^2\theta}\right)$
Parameter restriction	$\mu > 0, \lambda > 0$
Range	$\theta \in (0, \infty)$
Mean	μ
Variance	μ^3/λ
Mode	$\mu \left[\left(1 + \frac{9\mu^2}{4\lambda^2}\right)^{1/2} - \frac{3\mu}{2\lambda} \right]$

Random number	Generate $v_0 \sim \chi^2_{(1)}$. Let $x_1 = \mu + \frac{\mu^2 v_0}{2\lambda} - \frac{\mu}{2\lambda} \sqrt{4\mu\lambda v_0 + \mu^2 v_0^2}$ and $x_2 = \mu^2/x_1$. Perform a Bernoulli trial, $w \sim \text{Bernoulli}(\frac{\mu}{\mu+x_1})$. If $w = 1$, choose $\theta = x_1$; otherwise, choose $\theta = x_2$ (Michael, Schucany, and Haas 1976).
---------------	---

Table 55.34 Weibull Distribution

PROC specification	weibull (μ, c, σ)
Density	$\exp\left(-\left(\frac{\theta-\mu}{\sigma}\right)^c\right) \frac{c}{\sigma} \left(\frac{\theta-\mu}{\sigma}\right)^{c-1}$
Parameter restriction	$c > 0, \sigma > 0$
Range	$\theta \in [\mu, \infty)$ if $c = 1$; (μ, ∞) otherwise
Mean	$\mu + \sigma \Gamma(1 + 1/c)$
Variance	$\sigma^2[\Gamma(1 + 2/c) - \Gamma^2(1 + 1/c)]$
Mode	$\mu + \sigma(1 - 1/c)^{1/c}$ if $c > 1$
Random number	Inverse CDF method with $F(\theta) = 1 - \exp\left(-\left(\frac{\theta-\mu}{\sigma}\right)^c\right)$. Generate $u \sim \text{uniform}(0, 1)$, and $\theta = \mu + \sigma \cdot (-\ln u)^{1/c}$ is a draw from the Weibull distribution.

Multivariate Distributions

Table 55.35 Dirichlet Distribution

PROC specification	$\boldsymbol{\theta} \sim \text{dirich}(\boldsymbol{\alpha})$, where $\boldsymbol{\theta} = \{\theta_i\}$, $\boldsymbol{\alpha} = \{\alpha_i\}$, for $i = 1 \dots k$
Density	$\frac{\Gamma(\alpha_0)}{\prod_{i=1}^k \Gamma(\alpha_i)} \prod_{i=1}^k \theta_i^{\alpha_i-1}$, where $\alpha_0 = \sum_{i=1}^k \alpha_i$
Parameter restriction	$\alpha_i > 0$
Range	$\theta_i > 0, \sum_{i=1}^k \theta_i = 1$
Mean	α_j / α_0
Mode	$(\alpha_j - 1) / (\alpha_0 - k)$

Table 55.36 Inverse Wishart Distribution

PROC specification	$\boldsymbol{\theta} \sim \text{iwishart}(\nu, \mathbf{S})$, both $\boldsymbol{\theta}$ and $\mathbf{S}$ are $k \times k$ matrices
Density	$\left(2^{\frac{\nu k}{2}} \pi^{\frac{k(k-1)}{4}} \prod_{i=1}^k \Gamma\left(\frac{\nu+1-i}{2}\right)\right)^{-1} \mathbf{S} ^{\frac{\nu}{2}} \boldsymbol{\theta} ^{-\frac{\nu+k+1}{2}} \exp\left(-\frac{1}{2} \text{tr}(\mathbf{S}\boldsymbol{\theta}^{-1})\right)$
Parameter restriction	$\mathbf{S}$ must be symmetric and positive definite; $\nu > k - 1$
Range	$\boldsymbol{\theta}$ is symmetric and positive definite
Mean	$\mathbf{S} / (\nu - k - 1)$
Mode	$\mathbf{S} / (\nu + k + 1)$

Table 55.37 Multivariate Normal Distribution

PROC specification	$\boldsymbol{\theta} \sim \mathbf{mvn}(\boldsymbol{\mu}, \boldsymbol{\Sigma})$, where $\boldsymbol{\theta} = \{\theta_k\}$, $\boldsymbol{\mu} = \{\mu_k\}$, for $i = 1 \cdots k$, and $\boldsymbol{\Sigma}$ is a $k \times k$ variance matrix
Density	$\exp\left(-\frac{1}{2}(\boldsymbol{\theta} - \boldsymbol{\mu})' \boldsymbol{\Sigma}^{-1}(\boldsymbol{\theta} - \boldsymbol{\mu})\right) / \sqrt{(2\pi)^k \boldsymbol{\Sigma} }$
Parameter restriction	$\boldsymbol{\Sigma}$ must be symmetric and positive definite
Range	$-\infty < \theta_i < \infty$
Mean	$\boldsymbol{\mu}$
Mode	$\boldsymbol{\mu}$

Table 55.38 Autoregressive Multivariate Normal Distribution

PROC specification	$\boldsymbol{\theta} \sim \mathbf{mvn}(\boldsymbol{\mu}, \text{sd}=\sigma, \rho)$	$\boldsymbol{\theta} \sim \mathbf{mvn}(\boldsymbol{\mu}, \text{var}=\sigma^2, \rho)$	$\boldsymbol{\theta} \sim \mathbf{mvn}(\boldsymbol{\mu}, \text{prec}=1/\sigma^2, \rho)$
Density	$\exp\left(-\frac{1}{2}(\boldsymbol{\theta} - \boldsymbol{\mu})'(\sigma^2 \boldsymbol{\Sigma})^{-1}(\boldsymbol{\theta} - \boldsymbol{\mu})\right) / \sqrt{(2\pi)^k (\sigma^2 \boldsymbol{\Sigma}) }$ where $\boldsymbol{\Sigma} = \begin{bmatrix} 1 & \rho & \rho^2 & \rho^3 & \cdots & \rho^k \\ \rho & 1 & \rho & \rho^2 & \cdots & \rho^{k-1} \\ \rho^2 & \rho & 1 & \rho & \cdots & \rho^{k-2} \\ \rho^3 & \rho^2 & \rho & 1 & \cdots & \rho^{k-3} \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots \\ \rho^k & \rho^{k-1} & \rho^{k-2} & \rho^{k-3} & \cdots & 1 \end{bmatrix}$		
Parameter restriction	$\sigma > 0$ and $-1 < \rho < 1$		
Range	$-\infty < \theta_i < \infty$		
Mean	$\boldsymbol{\mu}$		
Mode	$\boldsymbol{\mu}$		
Special Case	When $\rho = 0$, the distribution simplifies to $\mathbf{mvn}(\boldsymbol{\mu}, \sigma^2 \cdot \mathbf{I}_k)$, where $\mathbf{I}_k$ denotes the $k \times k$ identity matrix		

Table 55.39 Multinomial Distribution

PROC specification	$\boldsymbol{\theta} \sim \mathbf{multinom}(\mathbf{p})$, where $\boldsymbol{\theta} = \{\theta_i\}$ and $\mathbf{p} = \{p_i\}$, for $i = 1 \cdots k$
Density	$\frac{n!}{\theta_1! \cdots \theta_k!} p_1^{\theta_1} \cdots p_k^{\theta_k}$, where $\sum_i \theta_i = n$
Parameter restriction	$\sum_i p_i = 1$ with all $p_i > 0$
Range	$\theta_i \in \{0, \dots, n\}$, nonnegative integers
Mean	$n \cdot \mathbf{p}$

Usage of Multivariate Distributions

The following simple example illustrates the usage of the multivariate distributions in PROC MCMC. Suppose you are interested in estimating the mean and covariance of multivariate data using this multivariate normal model:

$$\begin{pmatrix} x_1 \\ x_2 \end{pmatrix} \sim \text{MVN} \left(\boldsymbol{\mu} = \begin{pmatrix} \mu_1 \\ \mu_2 \end{pmatrix}, \boldsymbol{\Sigma} = \begin{pmatrix} \sigma_{11} & \sigma_{12} \\ \sigma_{21} & \sigma_{22} \end{pmatrix} \right)$$

where

$$\begin{aligned} \boldsymbol{\mu} &= \begin{pmatrix} 1 \\ 2 \end{pmatrix} \\ \boldsymbol{\Sigma} &= \begin{pmatrix} 2.4 & 3 \\ 3 & 8.1 \end{pmatrix} \end{aligned}$$

You can use the following independent prior on $\boldsymbol{\mu}$ and $\boldsymbol{\Sigma}$:

$$\begin{aligned} \boldsymbol{\mu} &\sim \text{MVN} \left(\boldsymbol{\mu}_0 = \begin{pmatrix} 0 \\ 0 \end{pmatrix}, \boldsymbol{\Sigma}_0 = \begin{pmatrix} 100 & 0 \\ 0 & 100 \end{pmatrix} \right) \\ \boldsymbol{\Sigma} &\sim \text{iWishart} \left(\nu = 2, \mathbf{S} = \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix} \right) \end{aligned}$$

The following IML procedure statements simulate 100 random multivariate normal samples:

```

title 'An Example that Uses Multivariate Distributions';
proc iml;
  N = 100;
  Mean = {1 2};
  Cov = {2.4 3, 3 8.1};
  call randseed(1);
  x = RANDNORMAL( N, Mean, Cov );

  SampleMean = x[, ];
  n = nrow(x);
  y = x - repeat( SampleMean, n );
  SampleCov = y`*y / (n-1);
  print SampleMean Mean, SampleCov Cov;

  cname = {"x1", "x2"};
  create inputdata from x [colname = cname];
  append from x;
  close inputdata;
quit;

```

Figure 55.13 prints the sample mean and covariance of the simulated data, in addition to the true mean and covariance matrix.

Figure 55.13 Simulated Multivariate Normal Data

An Example that Uses Multivariate Distributions			
SampleMean		Mean	
0.9987751	2.115693	1	2
SampleCov		Cov	
2.8252975	3.7190704	2.4	3
3.7190704	9.2916805	3	8.1

The following PROC MCMC statements estimate the posterior mean and covariance of the multivariate normal data:

```
proc mcmc data=inputdata seed=17 nmc=3000 diag=none;
  ods select PostSummaries PostIntervals;
  array data[2] x1 x2;
  array mu[2];
  array Sigma[2,2];
  array mu0[2] (0 0);
  array Sigma0[2,2] (100 0 0 100);
  array S[2,2] (1 0 0 1);
  parm mu Sigma;
  prior mu ~ mvn(mu0, Sigma0);
  prior Sigma ~ iwish(2, S);
  model data ~ mvn(mu, Sigma);
run;
```

To use the multivariate distribution, you must specify parameters (or random variables in the MODEL statement) in an array form. The first **ARRAY** statement creates an one-dimensional array `data`, which contains two numeric variables, `x1` and `x2`, from the input data set. The `data` variable is your response variable. The subsequent statements defines two array-parameters (`mu` and `Sigma`) and three constant array-hyperparameters (`mu0`, `Sigma0`, and `S`). The **PARMS** statement declares `mu` and `Sigma` to be model parameters. The two **PRIOR** statements specify the multivariate normal and inverse Wishart distributions as the prior for `mu` and `Sigma`, respectively. The **MODEL** statement specifies the multivariate normal likelihood with `data` as the random variable, `mu` as the mean, and `Sigma` as the covariance matrix.

Figure 55.14 lists the estimated posterior mean and covariance matrix.

Figure 55.14 Estimated Mean and Covariance

The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
mu1	3000	0.9941	0.1763	0.8761	0.9958	1.1136
mu2	3000	2.1135	0.3112	1.9075	2.1056	2.3254
Sigma1	3000	2.8726	0.4084	2.5799	2.8347	3.1205
Sigma2	3000	3.7573	0.6418	3.3090	3.7057	4.1385
Sigma3	3000	3.7573	0.6418	3.3090	3.7057	4.1385
Sigma4	3000	9.3987	1.3224	8.4705	9.2507	10.1946

Posterior Intervals					
Parameter	Alpha	Equal-Tail Interval		HPD Interval	
mu1	0.050	0.6500	1.3356	0.6338	1.3106
mu2	0.050	1.5081	2.7405	1.4939	2.7165
Sigma1	0.050	2.1725	3.8034	2.1001	3.6723
Sigma2	0.050	2.6659	5.2064	2.5791	5.0223
Sigma3	0.050	2.6659	5.2064	2.5791	5.0223
Sigma4	0.050	7.1260	12.3763	7.0155	12.0969

Specifying a New Distribution

To work with a new density that is not listed in the section “[Standard Distributions](#)” on page 4476, you can use the `GENERAL` and `DGENERAL` functions. The letter “D” stands for discrete. The new distributions have to be specified on the logarithm scale.

Suppose you want to use the inverse-beta distribution:

$$p(\alpha|a, b) = \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} \cdot \alpha^{(a-1)} \cdot (1+\alpha)^{-(a+b)}$$

The following statements in PROC MCMC define the density on its log scale:

```
a = 3; b = 5;
const = lgamma(a + b) - lgamma(a) - lgamma(b);
lp = const + (a - 1) * log(alpha) - (a + b) * log(1 + alpha);
prior alpha ~ general(lp);
```

The symbol `lp` is the expression for the log of an inverse-beta ($a = 3$, $b = 5$). The function `general(lp)` assigns that distribution to `alpha`. The constant term, `const`, can be omitted because the Markov simulation requires only the log of the density kernel.

You can use the `GENERAL` function to specify a distribution for a single variable or for multiple variables. It is important to emphasize that the argument `lp` is an expression for the log of the joint distribution for

these variables. On the contrary, any standard distribution is applied separately to each random variable in the statement.

When you use the **GENERAL** function in the **MODEL** statement, you do not need to specify the dependent variable on the left of the tilde $\sim$. The log-likelihood function takes the dependent variable into account; hence, there is no need to explicitly state the dependent variable in the **MODEL** statement. However, in the **PRIOR** and **RANDOM** statements, you need to explicitly state the parameter names and a tilde with the **GENERAL** function.

You can specify any distribution function by using the **GENERAL** and **DGENERAL** functions as long as the distribution function is programmable with SAS statements. When the function is used in the **PRIOR** statements, you must supply initial values in either the **PARMS** statement or within the **BEGINCNST** and **ENDCNST** statements. See the sections “**PARMS Statement**” on page 4451 and “**BEGINCNST/ENDCNST Statement**” on page 4441. When the function is used in the **RANDOM** statement, you must use the **INITIAL=** option in the **RANDOM** statement to supply initial values

NOTE: PROC MCMC does not verify that the **GENERAL** function you specify is a valid distribution—that is, an integrable density. You must use the function with caution.

Using Density Functions in the Programming Statements

Density Functions in PROC MCMC

PROC MCMC has a number of internally defined log-density functions for univariate and multivariate distributions. These functions have the basic form of $\text{LPDF}_{\text{dist}}(x, \text{parm-list})$, where *dist* is the name of the distribution (see [Table 55.40](#) for univariate distributions and [Table 55.41](#) for multivariate distributions). The argument *x* is the random variable, and *parm-list* is the list of parameters.

In addition, the univariate functions allow for optional boundary arguments, such as $\text{LPDF}_{\text{dist}}(x, \text{parm-list}, <\text{lower}>, <\text{upper}>)$, where *lower* and *upper* are optional but positional boundary arguments. With the exception of the Bernoulli and uniform distribution, you can specify limits on all univariate distributions.

To set a lower bound on the normal density:

```
lpdfnorm(x, 0, 1, -2);
```

To set just an upper bound, specify a missing value for the lower bound argument:

```
lpdfnorm(x, 0, 1, ., 2);
```

Leaving both limits out gives you the unbounded density. You can also specify both bounds:

```
lpdfnorm(x, 0, 1);
lpdfnorm(x, 0, 1, -3, 4);
```

See [Table 55.40](#) for the function names of univariate distributions and [Table 55.41](#) for multivariate distributions.

Table 55.40 Logarithm of Univariate Density Functions in PROC MCMC

Distribution Name	Function Call
Beta	lpdfbeta (<i>x</i> , <i>a</i> , <i>b</i> , < lower >, < upper >);
Binary	lpdfbern (<i>x</i> , <i>p</i>);
Binomial	lpdfbin (<i>x</i> , <i>n</i> , <i>p</i> , < lower >, < upper >);
Cauchy	lpdfcau (<i>x</i> , <i>loc</i> , <i>scale</i> , < lower >, < upper >);
χ^2	lpdfchisq (<i>x</i> , <i>df</i> , < lower >, < upper >);
Exponential χ^2	lpdfechisq (<i>x</i> , <i>df</i> , < lower >, < upper >);
Exponential gamma	lpdfegamma (<i>x</i> , <i>sp</i> , <i>scale</i> , < lower >, < upper >);
Exponential exponential	lpdfeexpon (<i>x</i> , <i>scale</i> , < lower >, < upper >);
Exponential inverse χ^2	lpdfeichisq (<i>x</i> , <i>df</i> , < lower >, < upper >);
Exponential inverse-gamma	lpdfeigamma (<i>x</i> , <i>sp</i> , <i>scale</i> , < lower >, < upper >);
Exponential scaled inverse χ^2	lpdfesichisq (<i>x</i> , <i>df</i> , <i>scale</i> , < lower >, < upper >);
Exponential	lpdfexpon (<i>x</i> , <i>scale</i> , < lower >, < upper >);
Gamma	lpdfgamma (<i>x</i> , <i>sp</i> , <i>scale</i> , < lower >, < upper >);
Geometric	lpdfgeo (<i>x</i> , <i>p</i> , < lower >, < upper >);
Inverse χ^2	lpdfichisq (<i>x</i> , <i>df</i> , < lower >, < upper >);
Inverse-gamma	lpdfigamma (<i>x</i> , <i>sp</i> , <i>scale</i> , < lower >, < upper >);
Laplace	lpdfdexp (<i>x</i> , <i>loc</i> , <i>scale</i> , < lower >, < upper >);
Logistic	lpdflogis (<i>x</i> , <i>loc</i> , <i>scale</i> , < lower >, < upper >);
Lognormal	lpdflnorm (<i>x</i> , <i>loc</i> , <i>sd</i> , < lower >, < upper >);
Negative binomial	lpdfnegbin (<i>x</i> , <i>n</i> , <i>p</i> , < lower >, < upper >);
Normal	lpdfnorm (<i>x</i> , <i>mu</i> , <i>sd</i> , < lower >, < upper >);
Pareto	lpdfpareto (<i>x</i> , <i>sp</i> , <i>scale</i> , < lower >, < upper >);

Table 55.40 (continued)

Distribution Name	Function Call
Poisson	lpdfpoi (<i>x</i> , <i>mean</i> , < <i>lower</i> >, < <i>upper</i> >);
Scaled inverse χ^2	lpdfsichisq (<i>x</i> , <i>df</i> , <i>scale</i> , < <i>lower</i> >, < <i>upper</i> >);
<i>t</i>	lpdfft (<i>x</i> , <i>mu</i> , <i>sd</i> , <i>df</i> , < <i>lower</i> >, < <i>upper</i> >);
Uniform	lpdfunif (<i>x</i> , <i>a</i> , <i>b</i>);
Wald	lpdfwald (<i>x</i> , <i>mean</i> , <i>scale</i> , < <i>lower</i> >, < <i>upper</i> >);
Weibull	lpdfwei (<i>x</i> , <i>loc</i> , <i>sp</i> , <i>scale</i> , < <i>lower</i> >, < <i>upper</i> >);

In the multivariate log-density functions, arrays must be used in place for the random variable and parameters in the model.

Table 55.41 Logarithm of Multivariate Density Functions in PROC MCMC

Distribution Name	Function Call
Dirichlet	lpdfdirch (<i>x_array</i> , <i>alpha_array</i>);
Inverse Wishart	lpdfiwish (<i>x_array</i> , <i>df</i> , <i>S_array</i>);
Multivariate normal	lpdfmvn (<i>x_array</i> , <i>mu_array</i> , <i>cov_array</i>);
Multinomial	lpdfmnom (<i>x_array</i> , <i>p_array</i>);

Standard Distributions, the LOGPDF Functions, and the LPDF*dist* Functions

Standard distributions listed in the section “[Standard Distributions](#)” on page 4476 are *names* only, and they can be used only in the **MODEL**, **PRIOR**, and **HYPERPRIOR** statements to specify either a prior distribution or a conditional distribution of the data given parameters. They do not return any values, and you cannot use them in the programming statements.

The LOGPDF functions are DATA step functions that compute the logarithm of various probability density (mass) functions. For example,

```
logpdf("beta", x, 2, 15);
```

returns the log of a beta density with parameters *a* = 2 and *b* = 15, evaluated at *x*. All the LOGPDF functions are supported in PROC MCMC.

The LPDF*dist* functions are unique to PROC MCMC. They compute the logarithm of various probability density (mass) functions. The functions are the same as the LOGPDF functions when it comes to calculating

the log density. For example,

```
lpdfbeta(x, 2, 15);
```

returns the same value as

```
logpdf("beta", x, 2, 15);
```

The `LPDFdist` functions cover a greater class of probability density functions, and the univariate distribution functions take the optional but positional boundary arguments. There are no corresponding `LCDFdist` or `LSDFdist` functions in PROC MCMC. To work with the cumulative probability function or the survival functions, you need to use the `LOGCDF` and the `LOGSDF DATA` step functions.

Truncation and Censoring

Truncated Distributions

To specify a truncated distribution, you can use the `LOWER=` and/or `UPPER=` options. Almost all of the standard distributions, including the `GENERAL` and `DGENERAL` functions, take these optional truncation arguments. The exceptions are the binary and uniform distributions.

For example, you can specify the following:

```
prior alpha ~ normal(mean = 0, sd = 1, lower = 3, upper = 45);
```

or

```
parms beta;
a = 3; b = 7;
ll = (a + 1) * log(b / beta);
prior beta ~ general(ll, upper = b + 17);
```

The preceding statements state that if `beta` is less than `b+17`, the log of the prior density is `ll`, as calculated by the equation; otherwise, the log of the prior density is missing—the log of zero.

When the same distribution is applied to multiple parameters in a `PRIOR` statement, the `LOWER=` and `UPPER=` truncations apply to all parameters in that statement. For example, the following statements define a Poisson density for `theta` and `gamma`:

```
parms theta gamma;
lambda = 7;
ll = theta * log(lambda) - lgamma(1 + theta);
ll = gamma * log(lambda) - lgamma(1 + gamma);
ll = ll + 12;
prior theta gamma ~ dgeneral(ll, lower = 1);
```

The `LOWER=1` condition is applied to both `theta` and `gamma`, meaning that for the assignment to `ll` to be meaningful, both `theta` and `gamma` have to be greater than 1. If either of the parameters is less than 1, the log of the joint prior density becomes a missing value.

With the exceptions of the normal distribution and the `GENERAL` and `DGENERAL` functions, the `LOWER=` and `UPPER=` options cannot be parameters or functions of parameters. The reason is that most

of the truncated distributions are not normalized. Unnormalized densities do not lead to wrong MCMC answers as long as the bounds are constants. However if the bounds involve model parameters, then the normalizing constant, which is a function of these parameters, must be taken into account in the posterior. Without specifying the normalizing constant, inferences on these boundary parameters are incorrect.

It is not difficult to construct a truncated distribution with a normalizing constant. Any truncated distribution has the probability distribution:

$$p(\theta|a < \theta < b) = \frac{p(\theta)}{F(a) - F(b)}$$

where $p(\cdot)$ is the density function and $F(\cdot)$ is the cumulative distribution function. In SAS functions, $p(\cdot)$ is probability density function and $F(\cdot)$ is cumulative distribution function. The following example shows how to construct a truncated gamma prior on theta, with SHAPE = 3, SCALE = 2, LOWER = a, and UPPER = b:

```
lp = logpdf('gamma', theta, 3, 2)
      - log(cdf('gamma', a, 3, 2) - cdf('gamma', b, 3, 2));
prior theta ~ general(lp);
```

Note the difference from a naive definition of the density, without taking into account of the normalizing constant:

```
lp = logpdf('gamma', theta, 3, 2);
prior theta ~ general(lp, lower=a, upper=b);
```

If a or b are parameters, you get very different results from the two formulations.

Censoring

There is no built-in mechanism in PROC MCMC that models censoring automatically. You need to construct the density function (using a combination of the LOGPDF, LOGCDF, and LOGSDF functions and IF-ELSE statements) for the censored data.

Suppose you partition the data into four categories: uncensored (with observation x), left censored (with observation xl), right censored (with observation xr), and interval censored (with observations xl and xr). The likelihood is the normal with mean mu and standard deviation s. The following statements construct the corresponding log likelihood for the observed data:

```
if uncensored then
  ll = logpdf('normal', x, mu, s);
else if leftcensored then
  ll = logcdf('normal', xl, mu, s);
else if rightcensored then
  ll = logsdf('normal', xr, mu, s);
else /* this is the case of interval censored. */
  ll = log(cdf('normal', xr, mu, s) - cdf('normal', xl, mu, s));
model general(ll);
```

See “[Example 55.17: Normal Regression with Interval Censoring](#)” on page 4638.

Some Useful SAS Functions

Table 55.42 Some Useful SAS Functions

SAS Function	Definition
abs(x);	$ x $
airy(x);	Returns the value of the AIRY function.
beta(x1, x2);	$\int_0^1 z^{x1-1} (1-z)^{x2-1} dz$
call logistic(x);	$\frac{\exp(x)}{1+\exp(x)}$
call softmax(x1,...,xn);	Each element is replaced by $\exp(x_j) / \sum \exp(x_j)$
call stdize(x1,...,xn);	Standardize values
cdf();	Cumulative distribution function
cdf('normal', x, 0, 1);	Standard normal cumulative distribution function
comb(x1, x2);	$\frac{x1!}{x2!(x1-x2)!}$
constant('.');	Calculate commonly used constants
cos(x);	cosine(x)
css(x1, ..., xn);	$\sum_i (x_i - \bar{x})^2$
cv(x1, ..., xn);	$\text{std}(x) / \text{mean}(x) * 100$
dairy(x);	Derivative of the AIRY function
dimN(m);	Returns the numbers of elements in the Nth dim of array <i>m</i>
x1 eq x2	Returns 1 if $x1 = x2$; 0 otherwise
x1**x2	$x1^{x2}$
geomean(x1, ..., xn);	$\exp\left(\frac{\log(x1) + \dots + \log(xn)}{n}\right)$
difN(x);	Returns differences between the argument and its Nth lag
digamma(x1);	$\frac{\Gamma'(x1)}{\Gamma(x1)}$
erf(x);	$\frac{2}{\sqrt{\pi}} \int_0^x \exp(-z^2) dz$
erfc(x);	$1 - \text{erf}(x)$
fact(x);	$x!$
floor(x);	Greatest integer $\leq x$
gamma(x);	$\int_0^\infty z^{x-1} \exp(-1) dz$
harmean(x1, ..., xn);	$\frac{n}{1/x1 + \dots + 1/xn}$
ibessel(nu, x, kode);	Modified Bessel function of order <i>nu</i> evaluated at <i>x</i>
jbessel(nu, x);	Bessel function of order <i>nu</i> evaluated at <i>x</i>
lagN(x);	Returns values from a queue
largest(k, x1, ..., xn);	Returns the k^{th} largest element
lgamma(x);	$\ln(\Gamma(x))$
lgamma(x+1);	$\ln(x!)$
log(x, logN(x));	$\ln(x)$
logbeta(x1, x2);	$\text{lgamma}(x1) + \text{lgamma}(x2) - \text{lgamma}(x1 + x2)$
logcdf();	Log of a left cumulative distribution function
logpdf();	Log of a probability density (mass) function
logsdf();	Log of a survival function
max(x1, x2);	Returns $x1$ if $x1 > x2$; $x2$ otherwise
mean(of x1-xn);	$\sum_i x_i / n$

Table 55.42 (continued)

SAS Function	Definition
median (of $x1-xn$);	Returns the median of nonmissing values
min ($x1, x2$);	Returns x_1 if $x_1 < x_2$; x_2 otherwise
missing (x);	Returns 1 if x is missing; 0 otherwise
mod ($x1, x2$);	Returns the remainder from x_1/x_2
n ($x1, \dots, xn$);	Returns number of nonmissing values
nmiss (of $y1-yn$);	Number of missing values
quantile ();	Computes the quantile from a specific distribution
pdf ();	Probability density (mass) functions
perm (n, r);	$\frac{n!}{(n-r)!}$
put ();	Returns a value that uses a specified format
round (x);	Rounds x
rms (of $x1-xn$);	$\sqrt{\frac{x_1^2 + \dots + x_n^2}{n}}$
sdf ();	Survival function
sign (x);	Returns -1 if $x < 0$; 0 if $x = 0$; 1 if $x > 0$
sin (x);	sine(x)
smallest ($s, x1, \dots, en$);	Returns the s^{th} smallest component of $x_1, \dots, x_n$
sortn (of $x1-xn$);	Sorts the values of the variables
sqrt (x);	$\sqrt{x}$
std ($x1, \dots, xn$);	Standard deviation of $x_1, \dots, x_n$ (n-1 in denominator)
sum (of x);	$\sum_i x_i$
trigamma (x);	Derivative of the DIGAMMA(x) function
uss (of $x1-xn$);	Uncorrected sum of squares

Here are examples of some commonly used transformations:

- logit

```
mu = beta0 + beta1 * z1;
call logistic(mu);
```

- log

```
w = beta0 + beta1 * z1;
mu = exp(w);
```

- probit

```
w = beta0 + beta1 * z1;
mu = cdf('normal', w, 0, 1);
```

- cloglog

```
w = beta0 + beta1 * z1;
mu = 1 - exp(-exp(w));
```

Matrix Functions in PROC MCMC

The MCMC procedure provides you with a number of CALL routines for performing simple matrix operations on declared arrays. With the exception of FILLMATRIX, IDENTITY, and ZEROMATRIX, the CALL routines listed in Table 55.43 do not support matrices or arrays that contain missing values.

Table 55.43 Matrix Functions in PROC MCMC

CALL Routine	Description
ADDMATRIX	Performs an element-wise addition of two matrices or of a matrix and a scalar.
CHOL	Calculates the Cholesky decomposition for a particular symmetric matrix.
DET	Calculates the determinant of a specified matrix, which must be square.
ELEMMULT	Performs an element-wise multiplication of two matrices.
FILLMATRIX	Replaces all of the element values of the input matrix with the specified value. You can use this routine with multidimensional numeric arrays.
IDENTITY	Converts the input matrix to an identity matrix. Diagonal element values of the matrix are set to 1, and the rest of the values are set to 0.
INV	Calculates a matrix that is the inverse of the input matrix. The input matrix must be a square, nonsingular matrix.
MULT	Calculates the matrix product of two input matrices.
SUBTRACTMATRIX	Performs an element-wise subtraction of two matrices or of a matrix and a scalar.
TRANSPOSE	Returns the transpose of a matrix.
ZEROMATRIX	Replaces all of the element values of the numeric input matrix with 0.

ADDMATRIX CALL Routine

The ADDMATRIX CALL routine performs an element-wise addition of two matrices or of a matrix and a scalar.

The syntax of the ADDMATRIX CALL routine is

```
CALL ADDMATRIX (X, Y, Z);
```

where

X specifies a scalar or an input matrix with dimensions $m \times n$ (that is, $X[m, n]$)

Y specifies a scalar or an input matrix with dimensions $m \times n$ (that is, $Y[m, n]$)

Z specifies an output matrix with dimensions $m \times n$ (that is, $Z[m, n]$)

such that

$$Z = X + Y$$

CHOL CALL Routine

The CHOL CALL routine calculates the Cholesky decomposition for a particular symmetric matrix.

The syntax of the CHOL CALL routine is

CALL CHOL (*X*, *Y* <, *validate*>) ;

where

X specifies a symmetric positive-definite input matrix with dimensions $m \times m$ (that is, $X[m, m]$)

Y is a variable that contains the Cholesky decomposition and specifies an output matrix with dimensions $m \times m$ (that is, $Y[m, m]$)

validate specifies an optional argument that can increase the processing speed by avoiding error checking:

If *validate* = 0 or is not specified, then the matrix *X* is checked for symmetry.

If *validate* = 1, then the matrix *X* is assumed to be symmetric.

such that

$$X = YY^*$$

where *Y* is a lower triangular matrix with strictly positive diagonal entries and Y^* denotes the conjugate transpose of *Y*.

Both input and output matrices must be square and have the same dimensions. If *X* is symmetric positive-definite, *Y* is a lower triangle matrix. If *X* is not symmetric positive-definite, *Y* is filled with missing values.

DET CALL Routine

The determinant, the product of the eigenvalues, is a single numeric value. If the determinant of a matrix is zero, then that matrix is singular (that is, it does not have an inverse). The routine performs an LU decomposition and collects the product of the diagonals.

The syntax of the DET CALL routine is

CALL DET (*X*, *a*) ;

where

X specifies an input matrix with dimensions $m \times m$ (that is, $X[m, m]$)

a specifies the returned determinate value

such that

$$a = |X|$$

ELEMMULT CALL Routine

The ELEMMULT CALL routine performs an element-wise multiplication of two matrices.

The syntax of the ELEMMULT CALL routine is

CALL ELEMMULT (X, Y, Z) ;

where

X specifies an input matrix with dimensions $m \times n$ (that is, $X[m, n]$)

Y specifies an input matrix with dimensions $m \times n$ (that is, $Y[m, n]$)

Z specifies an output matrix with dimensions $m \times n$ (that is, $Z[m, n]$)

FILLMATRIX CALL Routine

The FILLMATRIX CALL routine replaces all of the element values of the input matrix with the specified value. You can use the FILLMATRIX CALL routine with multidimensional numeric arrays.

The syntax of the FILLMATRIX CALL routine is

CALL FILLMATRIX (X, Y) ;

where

X specifies an input numeric matrix

Y specifies the numeric value that is used to fill the matrix

IDENTITY CALL Routine

The IDENTITY CALL routine converts the input matrix to an identity matrix. Diagonal element values of the matrix are set to 1, and the rest of the values are set to 0.

The syntax of the IDENTITY CALL routine is

CALL IDENTITY (X) ;

where

X specifies an input matrix with dimensions $m \times m$ (that is, $X[m, m]$)

INV CALL Routine

The INV CALL routine calculates a matrix that is the inverse of the input matrix. The input matrix must be a square, nonsingular matrix.

The syntax of the INV CALL routine is

CALL INV (X, Y) ;

where

X specifies an input matrix with dimensions $m \times m$ (that is, $X[m, m]$)

Y specifies an output matrix with dimensions $m \times m$ (that is, $Y[m, m]$)

MULT CALL Routine

The MULT CALL routine calculates the matrix product of two input matrices.

The syntax of the MULT CALL routine is

CALL MULT (X, Y, Z) ;

where

X specifies an input matrix with dimensions $m \times n$ (that is, $X[m, n]$)

Y specifies an input matrix with dimensions $n \times p$ (that is, $Y[n, p]$)

Z specifies an output matrix with dimensions $m \times p$ (that is, $Z[m, p]$)

The number of columns for the first input matrix must be the same as the number of rows for the second matrix. The calculated matrix is the last argument.

SUBTRACTMATRIX CALL Routine

The SUBTRACTMATRIX CALL routine performs an element-wide subtraction of two matrices or of a matrix and a scalar.

The syntax of the SUBTRACTMATRIX CALL routine is

CALL SUBTRACTMATRIX (X, Y, Z) ;

where

X specifies a scalar or an input matrix with dimensions $m \times n$ (that is, $X[m, n]$)

Y specifies a scalar or an input matrix with dimensions $m \times n$ (that is, $Y[m, n]$)

Z specifies an output matrix with dimensions $m \times n$ (that is, $Z[m, n]$)

such that

$$Z = X - Y$$

TRANSPOSE CALL Routine

The TRANSPOSE CALL routine returns the transpose of a matrix.

The syntax of the TRANSPOSE CALL routine is

CALL TRANSPOSE (X, Y) ;

where

X specifies an input matrix with dimensions $m \times n$ (that is, $X[m, n]$)

Y specifies an output matrix with dimensions $n \times m$ (that is, $Y[n, m]$)

ZEROMATRIX CALL Routine

The ZEROMATRIX CALL routine replaces all of the element values of the numeric input matrix with 0. You can use the ZEROMATRIX CALL routine with multidimensional numeric arrays.

The syntax of the ZEROMATRIX CALL routine is

```
CALL ZEROMATRIX (X) ;
```

where

X specifies a numeric input matrix.

Create Design Matrix

PROC MCMC does not support a CLASS statement; therefore you need to construct the right design matrix (with dummy or indicator variables) prior to calling PROC MCMC. The best tool to use is the TRANSREG procedure (see Chapter 97, “[The TRANSREG Procedure](#)”). This procedure offers both indicator and effects coding methods. You can specify any categorical variables in the CLASS expansion, and use the ZERO= option to select a reference category. You can also specify any other data set variables (predictors, the responses, and so on) to the output data set in the ID statement.

For example, the following statements create a data set that contains two categorical variables (City and G), and two continuous variables (x and resp):

```
title 'Create Design Matrix';
data categorical;
  input City$ G$ x resp @@;
  datalines;
Chicago F 69.0 112.5  Chicago F 56.5  84.0
Chicago M 65.3  98.0  Chicago M 59.8  84.5
NewYork M 62.8 102.5  NewYork M 63.5 102.5
NewYork F 57.3  83.0  NewYork M 57.5  85.0
;
```

Suppose you are interested in creating a design matrix that uses dummy variable coding for the categorical variables City, G and their interaction City * G. You can use the following PROC TRANSREG statements:

```
proc transreg data=categorical design;
  model class(city g city*g / zero=last);
  id x resp;
  output out=input_mcmc(drop=_: Int:);
run;
```

The DESIGN option specifies that the primary goal is to code the design matrix. The MODEL statement indicates the variable of interest. The CLASS option in the MODEL statement expands the variables of interest to a list of “dummy” variables. The ZERO=LAST option sets the reference level. The ID statement includes x and resp in the OUT= data set. And the OUTPUT statement creates a new data set Input_MCMC that stores the design matrix and original variables from the original data set.

A quick call of the PRINT procedure shows the output from the PROC TRANSREG call:

```
proc print data=input_mcmc;
run;
```

Figure 55.15 prints the design matrix that is generated by PROC TRANSREG. The Input_mcmc data set contains all the variables from the original Categorical data set, in addition to corresponding dummy variables (CityChicago, GF, and CityChicagoGF) for the categorical variables.

Figure 55.15 Design Matrix Generated by PROC TRANSREG

Create Design Matrix							
Obs	City Chicago	GF	City Chicago GF	City	G	x	resp
1	1	1	1	Chicago	F	69.0	112.5
2	1	1	1	Chicago	F	56.5	84.0
3	1	0	0	Chicago	M	65.3	98.0
4	1	0	0	Chicago	M	59.8	84.5
5	0	0	0	NewYork	M	62.8	102.5
6	0	0	0	NewYork	M	63.5	102.5
7	0	1	0	NewYork	F	57.3	83.0
8	0	0	0	NewYork	M	57.5	85.0

You can now proceed to call PROC MCMC using this input data set Input_mcmc and the corresponding dummy variables.

PROC TRANSREG automatically creates a macro variable, &_TRGIND, which contains a list of variable names that it creates. The %put &_trgind; statement prints the following:

```
CityChicago GF CityChicagoGF
```

The macro variable &_TRGIND can come handy if you want to build a regression model; you can refer to &_TRGIND in the following way:

```
proc mcmc data=input_mcmc;
  array data[5] 1 &_trgind x;
  array beta[5] beta0-beta4;
  ...;
  call mult(beta, data, mu);
  ...;
```

The first ARRAY statement defines a one-dimensional array of length 5, and it takes on five values: a constant 1 and variables CityChicago, GF, CityChicagoGF, and x. The second ARRAY statement defines an array of beta, which are the model parameters. Later in the program, you can use the CALL MULT function to calculate the regression mean and store the value in the symbol mu.

Modeling Joint Likelihood

PROC MCMC assumes that the input observations are independent and that the joint log likelihood is the sum of individual log-likelihood functions. You specify the log likelihood of one observation in the **MODEL** statement. PROC MCMC evaluates that function for each observation in the data set and cumulatively sums them up. If observations are not independent of each other, this summation produces the incorrect log likelihood.

There are two ways to model dependent data. You can either use the DATA step LAG function or use the PROC option **JOINTMODEL**. The LAG function returns values of a variable from a queue. As PROC MCMC steps through the data set, the LAG function queues each data set variable, and you have access to the current value as well as to all previous values of any variable. If the log likelihood for observation x_i depends only on observations 1 to i in the data set, you can use this SAS function to construct the log-likelihood function for each observation. Note that the LAG function enables you to access observations from different rows, but the log-likelihood function in the **MODEL** statement must be generic enough that it applies to all observations. See “[Example 55.14: Time Independent Cox Model](#)” on page 4617 and “[Example 55.15: Time Dependent Cox Model](#)” on page 4625 for how to use this LAG function.

A second option is to create arrays, store all relevant variables in the arrays, and construct the joint log likelihood for the entire data set instead of for each observation. Following is a simple example that illustrates the usage of this option. For a more realistic example that models dependent data, see “[Example 55.14: Time Independent Cox Model](#)” on page 4617 and “[Example 55.15: Time Dependent Cox Model](#)” on page 4625.

```
/* allocate the sample size. */
data exi;
  call streaminit(17);
  do ind = 1 to 100;
    y = rand("normal", 2.3, 1);
    output;
  end;
run;
```

The log-likelihood function for each observation is as follows:

$$\log(f(y_i|\mu, \sigma)) = \log(\phi(y_i; \mu, \text{var} = \sigma^2))$$

The joint log-likelihood function is as follows:

$$\log(f(\mathbf{y}|\mu, \sigma)) = \sum_i \log(\phi(y_i; \mu, \text{var} = \sigma^2))$$

The following statements fit a simple model with an unknown mean (μ) in PROC MCMC, with the variance in the likelihood assumed known. The **MODEL** statement indicates a normal likelihood for each observation y .

```
proc mcmc data=exi seed=7 outpost=p1;
  parm mu;
  prior mu ~ normal(0, sd=10);
  model y ~ normal(mu, sd=1);
run;
```

The following statements show how you can specify the log-likelihood function for the entire data set:

```
data a;
run;

proc mcmc data=a seed=7 outpost=p2 jointmodel;
  array data[1] / nosymbols;
  begincnst;
    rc = read_array("exi", data, "y");
    n = dim(data, 1);
  endcnst;

  parm mu;
  prior mu ~ normal(0, sd=10);
  ll = 0;
  do i = 1 to n;
    ll = ll + lpdfnorm(data[i], mu, 1);
  end;
  model general(ll);
run;
```

The **JOINTMODEL** option indicates that the function used in the **MODEL** statement calculates the log likelihood for the entire data set, rather than just for one observation. Given this option, PROC MCMC no longer steps through the input data during the simulation. Consequently, you can no longer use any data set variables to construct the log-likelihood function. Instead, you store the data set in arrays and use arrays instead of data set variables to calculate the log likelihood.

The **ARRAY** statement allocates a temporary array (data). The **READ_ARRAY** function selects the y variable from the **exi** data set and stores it in the data array. See the section “**READ_ARRAY Function**” on page 4442. In the programming statements, you use a DO loop to construct the joint log likelihood. The expression **ll** in the **GENERAL** function now takes the value of the joint log likelihood for all data.

You can run the following statements to see that two PROC MCMC runs produce identical results.

```
proc compare data=p1 compare=p2;
  var mu;
run;
```

Regenerating Diagnostics Plots

By default, PROC MCMC generates three plots: the trace plot, the autocorrelation plot, and the kernel density plot. Unless ODS Graphics is enabled before calling the procedure, it is hard to generate the same graph afterwards. Directly using the **Stat.MCMC.Graphics.TraceAutocorrDensity** template is not feasible. The easiest way to regenerate the same graph is with the **%TADPlot** autocall macro. The **%TADPlot** macro requires you to specify an input data set (which usually is the output data set from a previous PROC MCMC call) and a list of variables that you want to plot.

For more information about enabling and disabling ODS Graphics, see the section “[Enabling and Disabling ODS Graphics](#)” on page 600 in Chapter 21, “[Statistical Graphics Using ODS](#).”

A simple regression example, with three parameters, is used here for illustrational purposes. For an explanation of the regression model and the data involved, see the section “[Simple Linear Regression](#)” on page 4408. The following statements generate a SAS data set and fit a regression model:

```

title 'Regenerating Diagnostics Plots';

data Class;
  input Name $ Height Weight @@;
  datalines;
Alfred  69.0 112.5   Alice  56.5  84.0   Barbara 65.3  98.0
Carol   62.8 102.5   Henry  63.5 102.5   James   57.3  83.0
Jane    59.8  84.5   Janet  62.5 112.5   Jeffrey 62.5  84.0
John    59.0  99.5   Joyce  51.3  50.5   Judy    64.3  90.0
Louise  56.3  77.0   Mary   66.5 112.0   Philip  72.0 150.0
Robert  64.8 128.0   Ronald 67.0 133.0   Thomas  57.5  85.0
William 66.5 112.0
;

ods select none;
proc mcmc data=class nmc=50000 thin=5 outpost=classout seed=246810;
  parms beta0 0 beta1 0;
  parms sigma2 1;
  prior beta0 beta1 ~ normal(0, var = 1e6);
  prior sigma2 ~ igamma(3/10, scale = 10/3);
  mu = beta0 + beta1*height;
  model weight ~ normal(mu, var = sigma2);
run;
ods select all;

```

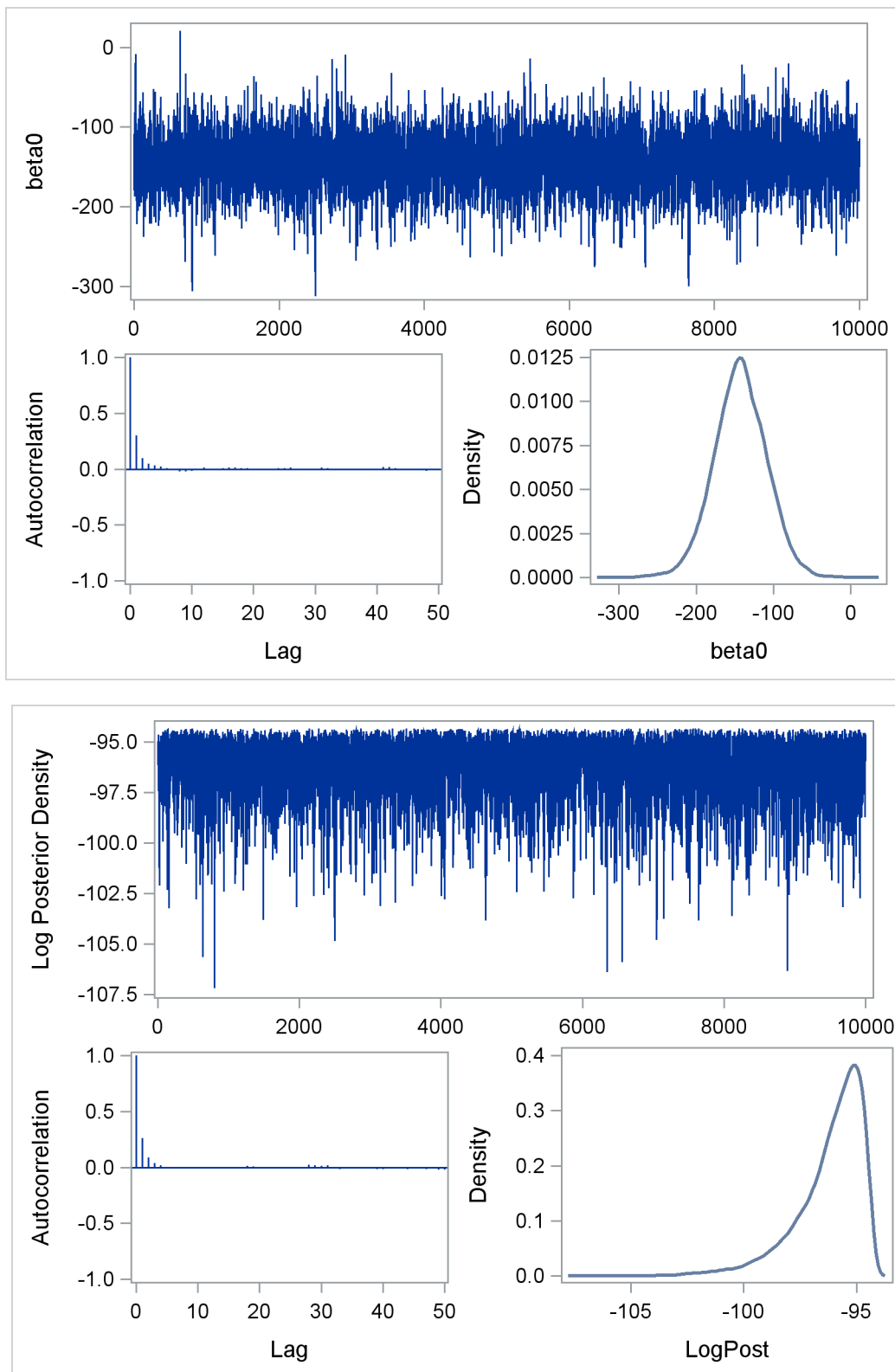
The output data set Classout contains posterior draws for beta0, beta1, and sigma2. It also stores the log of the prior density (LogPrior), log of the likelihood (LogLike), and the log of the posterior density (LogPost). If you want to examine the beta0 and LogPost variable, you can use the following statements to generate the graphs:

```

ods graphics on;
%tadplot(data=classout, var=beta0 logpost);
ods graphics off;

```

[Figure 55.16](#) displays the regenerated diagnostics plots for variables beta0 and Logpost from the data set Classout.

Figure 55.16 Regenerated Diagnostics Plots for beta0 and Logpost

Caterpillar Plot

The caterpillar plot is a side-by-side bar plot of 95% intervals for multiple parameters. Typically, it is used to visualize and compare random-effects parameters, which can come in large numbers in certain models. You can use the %CATER autocall macro to create a caterpillar plot. The %CATER macro requires you specify an input data set and a list of variables that you want to plot.

A random-effects model that has 21 random-effects parameters is used here for illustrational purpose. For an explanation of the random-effects model and the data involved, see “[Example 55.7: Logistic Regression Random-Effects Model](#)” on page 4579. The following statements generate a SAS data set and fit the model:

```

title 'Create a Caterpillar Plot';

data seeds;
  input r n seed extract @@;
  ind = _N_;
  datalines;
10 39 0 0      23 62 0 0      23 81 0 0      26 51 0 0
17 39 0 0      5  6 0 1      53 74 0 1      55 72 0 1
32 51 0 1      46 79 0 1      10 13 0 1      8  16 1 0
10 30 1 0      8  28 1 0      23 45 1 0      0  4  1 0
3  12 1 1      22 41 1 1      15 30 1 1      32 51 1 1
3  7  1 1
;

ods select none;
proc mcmc data=seeds outpost=postout seed=332786 nmc=20000;
  parms beta0 0 beta1 0 beta2 0 beta3 0 s2 1;
  prior s2 ~ igamma(0.01, s=0.01);
  prior beta: ~ general(0);
  w = beta0 + beta1*seed + beta2*extract + beta3*seed*extract;
  random delta ~ normal(w, var=s2) subject=ind;
  pi = logistic(delta);
  model r ~ binomial(n = n, p = pi);
run;
ods select all;

```

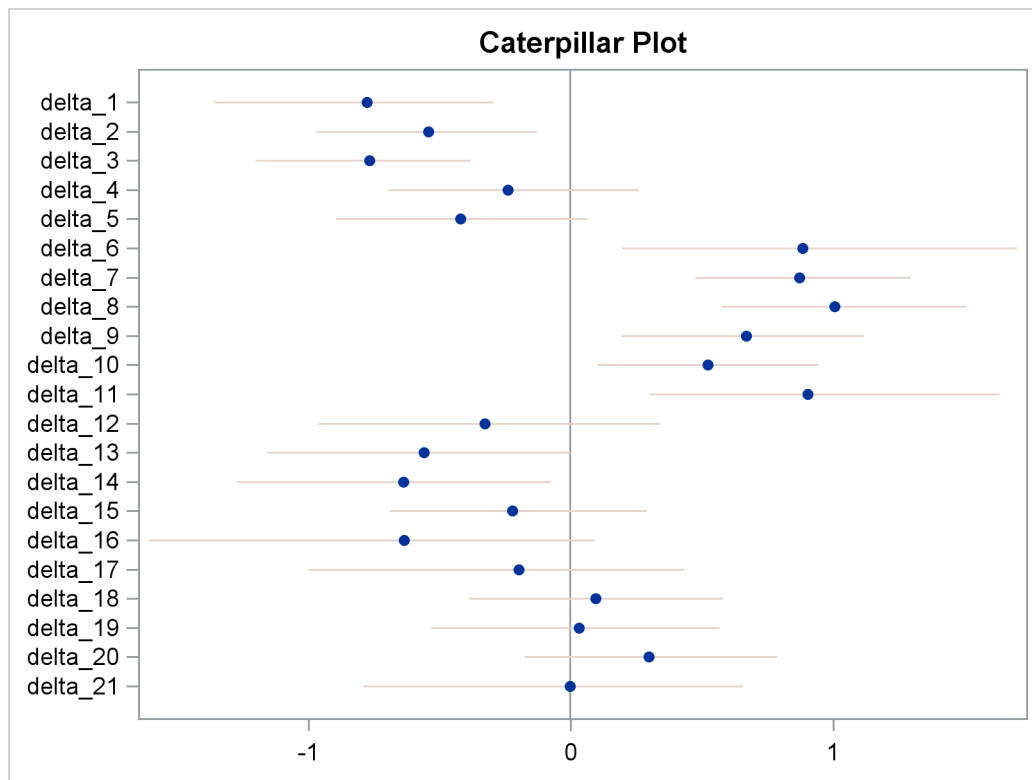
The output data set Postout contains posterior draws for all 21 random-effects parameters, delta_1 ... delta_21. You can use the following statements to generate a caterpillar plot for the 21 parameters:

```

ods graphics on;
%CATER(data=postout, var=delta:);
ods graphics off;

```

Figure 55.17 is a caterpillar plot of the random-effects parameters delta_1–delta_21.

Figure 55.17 Caterpillar Plot of the Random-Effects Parameters

If you want to change the display of the caterpillar plot, such as using a different line pattern, color, or size of the markers, you need to first modify the `Stat.MCMC.Graphics.Caterpillar` template and then call the `%CATER` macro again.

You can use the following statements to view the source of the `Stat.MCMC.Graphics.Caterpillar` template:

```
proc template;
  path sashelp.tmplmst;
  source Stat.MCMC.Graphics.Caterpillar;
run;
```

Figure 55.18 lists the source statements of the template that is used to generate the template for the caterpillar plot.

Figure 55.18 Source Statements for Stat.MCMC.Graphics.Caterpillar Template

```

define statgraph Stat.MCMC.Graphics.Caterpillar;
  dynamic _OverallMean _VarName _VarMean _XLower _XUpper _byline_ _bytitle_
    _byfootnote_;
  begingraph;
    entrytitle "Caterpillar Plot";
    layout overlay / yaxisopts=(offsetmin=0.05 offsetmax=0.05 display=(line
      ticks tickvalues)) xaxisopts=(display=(line ticks tickvalues));
    referenceline x=_OVERALLMEAN / lineattrs=(color=
      GraphReference:ContrastColor);
    HighLowPlot y=_VARNAME high=_XUPPER low=_XLOWER / lineattrs=
      GRAPHCONFIDENCE;
    scatterplot y=_VARNAME x=_VARMEAN / markerattrs=(size=5 symbol=
      circlefilled);
  endlayout;
  if (_BYTITLE_)
    entrytitle _BYLINE_ / textattrs=GRAPHVALUETEXT;
  else
    if (_BYFOOTNOTE_)
      entryfootnote halign=left _BYLINE_;
    endif;
  endif;
endgraph;
end;

```

You can use the `TEMPLATE` procedure (see Chapter 21, “[Statistical Graphics Using ODS](#)”) to run any modified SAS/GRAPH graph template definition and then call the `%CATER` macro again. The `%CATER` macro picks up the change you made to the Caterpillar template and displays the new graph accordingly.

Autocall Macros for Postprocessing

Although PROC MCMC provides a number of convergence diagnostic tests and posterior summary statistics, PROC MCMC performs the calculations only if you specify the options in advance. If you wish to analyze the posterior draws of unmonitored parameters or functions of the parameters that are calculated in later DATA step calls, you can use the autocall macros in [Table 55.44](#).

Table 55.44 Postprocessing Autocall Macros

Macro	Description
<code>%ESS</code>	Effective sample sizes
<code>%GEWEKE</code> ⁴	Geweke diagnostic
<code>%HEIDEL</code> ⁴	Heidelberger-Welch diagnostic
<code>%MCSE</code>	Monte Carlo standard errors
<code>%RAFTERY</code>	Raftery diagnostic
<code>%POSTACF</code>	Autocorrelation
<code>%POSTCOR</code>	Correlation matrix

⁴The `%GEWEKE` and `%HEIDEL` macros use a different optimization routine than that used in PROC MCMC. As a result, there might be numerical differences in some cases, especially when the sample size is small.

Table 55.44 (continued)

Macro	Description
%POSTCOV	Covariance matrix
%POSTINT	Equal-tail and HPD intervals
%POSTSUM	Summary statistics

Table 55.45 lists options that are shared by all postprocessing autocall macros. See Table 55.46 for macro-specific options.

Table 55.45 Shared Options

Option	Description
DATA=SAS-data-set	Input data set that contains posterior samples
VAR=variable-list	Specifies the variables on which you want to carry out the calculation.
PRINT=YES NO	Displays the results. The default is YES.
OUT=SAS-data-set	Specifies a name for the output SAS data set to contain the results.

Suppose that the data set that contains posterior samples is called `post` and that the variables of interest are defined in the macro variable `&PARMS`. The following statements call the `%ESS` macro and calculates the effective sample sizes for each variable:

```
%let parms = alpha beta u_1-u_17;
%ESS(data=post, var=&parms);
```

By default, the ESS estimates are displayed. You can choose not to display the result and save the output to a data set with the following statement:

```
%ESS(data=post, var=&parms, print=NO, out=eout);
```

Some of the macros can take additional options, which are listed in Table 55.46.

Table 55.46 Macro-Specific Options

Macro	Option	Description
%ESS	AUTOCORLAG=numeric	Specifies the maximum number of autocorrelation lags used in computing the ESS estimates. By default, AUTOCORLAG=MIN(500, NOBS/4), where NOBS is the sample size of the input data set.
	HIST=YES NO	Displays a histogram of all ESS estimates. The default is NO.
%HEIDEL	SALPHA=numeric	Specifies the α level for the stationarity test. By default, SALPHA=0.05.
	HALPHA=numeric	Specifies the α level for the halfwidth test. By default, HALPHA=0.05.
	EPS=numeric	Specifies a small positive number ϵ such that if the halfwidth is less than ϵ times the sample mean of the remaining iterations, the halfwidth test is passed. By default, EPS=0.1.

Table 55.46 (continued)

Option	Description	
%GEWEKE	FRAC1= <i>numeric</i>	Specifies the earlier portion of the Markov chain used in the test. By default, FRAC1=0.1.
	FRAC2= <i>numeric</i>	Specifies the latter portion of the Markov chain used in the test. By default, FRAC2=0.5.
%MCSE	AUTOCORLAG= <i>numeric</i>	Specifies the maximum number of autocorrelation lags used in computing the Monte Carlo standard error estimates. By default, AUTOCORLAG=MIN(500, NOBS/4), where NOBS is the sample size of the input data set.
%RAFTERY	Q= <i>numeric</i>	Specifies the order of the quantile of interest. By default, Q=0.025.
	R= <i>numeric</i>	Specifies the margin of error for measuring the accuracy of estimation of the quantile. By default, R=0.005.
	S= <i>numeric</i>	Specifies the probability of attaining the accuracy of the estimation of the quantile. By default, S=0.95.
	EPS= <i>numeric</i>	Specifies the tolerance level for the stationary test. By default, EPS=0.001.
%POSTACF	LAGS=%str(<i>numeric-list</i>)	Specifies autocorrelation lags calculated. The default values are 1, 5, 10, and 50.
%POSTINT	ALPHA= <i>value</i>	Specifies the α level ($0 < \alpha < 1$) for the interval estimates. By default, ALPHA=0.05.

For example, the following statement calculates and displays autocorrelation at lags 1, 6, 11, 50, and 100. Note that the lags in the *numeric-list* need to be separated by commas “,”.

```
%PostACF(data=post, var=&parms, lags=%str(1 to 15 by 5, 50, 100));
```

Gamma and Inverse-Gamma Distributions

The gamma and inverse gamma distributions are widely used in Bayesian analysis. With their respective scale and inverse scale parameterizations, they are a frequent source of confusion in the field. This section aims to clarify their parameterizations and common usages.

The gamma distribution is often used as the conjugate prior for the precision parameter ($\tau = 1/\sigma^2$) in a normal distribution. See Table 55.19 in the section “Standard Distributions” on page 4476 for the density definitions. You can specify the distribution in two ways:

- `gamma(shape=, scale=)` which has mean `shape*scale` and variance `shape * scale2`
- `gamma(shape=, iscale=)` which has mean $\frac{\text{shape}}{\text{iscale}}$ and variance $\frac{\text{shape}}{\text{iscale}^2}$

The parameterization of the gamma distribution that is preferred by most Bayesian analysts is to have the same number in both hyperparameter positions, which results in a prior distribution that has mean 1. To do this, you should use the `iscale=` parameterization. In addition, if you choose a small value (for example,

0.01), the prior distribution takes on a large variance (100 in this example). To specify this prior in PROC MCMC, use `gamma(shape=0.01, iscale=0.01)`⁵, *not* `gamma(shape=0.01, scale=0.01)`.

If you specify the `scale=` parameterization, as in `gamma(shape=0.01, scale=0.01)`, you would get a prior distribution that has mean 0.0001 and variance 0.000001. This would lead to a completely different posterior inference: the prior would push the precision parameter estimate close to 0, or the variance estimate to a large value.

The inverse-gamma distribution is often used as the conjugate prior of the variance parameter (σ^2) in a normal distribution. See Table 55.22 in the section “Standard Distributions” on page 4476 for the density definitions. Similar to the gamma distribution, you can specify the inverse-gamma distribution in two ways:

- `igamma(shape=, scale=)`
- `igamma(shape=, iscale=)`

The inverse gamma distribution does not have a mean when the shape parameter is less than or equal to 1 and does not have a variance when the shape parameter is less than or equal to 2.

A gamma prior distribution on the precision is the equivalent to an inverse gamma prior distribution on the variance. The equivalency is the following:

$$\tau \sim \text{gamma}(\text{shape}=0.01, \text{iscale}=0.01) \Leftrightarrow \sigma^2 \sim \text{igamma}(\text{shape}=0.01, \text{scale}=0.01)$$

NOTE: This mnemonic might help you remember the parameterization scheme of the distributions. If you prefer to have identical hyperparameter values in the distribution, you should specify one and only one “i.” When the “i” appears in the `igamma` distribution name for the variance parameter, choose the `scale=` parameterization; when the “i” appears in the `iscale=` parameterization, choose the `gamma` distribution for the precision parameter.

If you are not sure about the choices of other hyperparameter values and what type of prior distributions they induce, you can write a simple PROC MCMC program and see the distributions as in the following example:

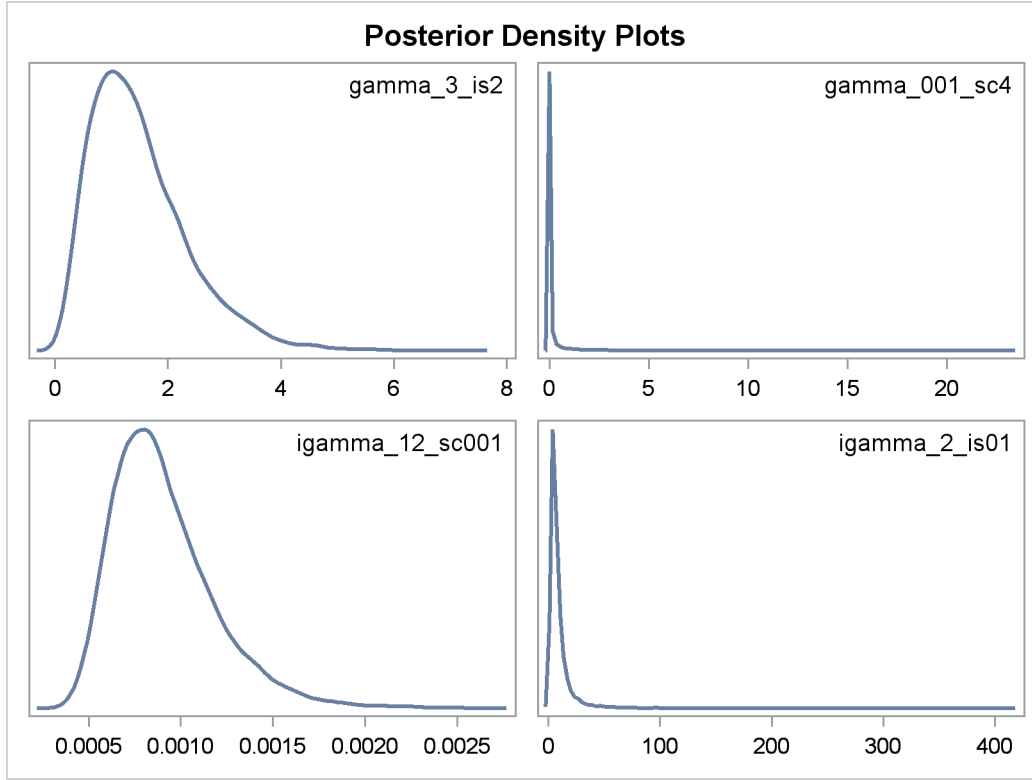
```
data a;
run;

ods graphics on;
ods select DensityPanel;
proc mcmc data=a stats=none diag=none nmc=10000 outpost=gout
  plots=density seed=1;
  parms gamma_3_is2 gamma_001_sc4 igamma_12_sc001 igamma_2_is01;
  prior gamma_3_is2      ~ gamma(shape=3, iscale=2);
  prior gamma_001_sc4    ~ gamma(shape=0.01, scale=4);
  prior igamma_12_sc001 ~ igamma(shape=12, scale=0.01);
  prior igamma_2_is01    ~ igamma(shape=2, iscale=0.1);
  model general(0);
run;
ods graphics off;
```

⁵Specifying the same number at both positions and choosing a small value has been popularized by the WinBUGS software program. The WinBUGS's distribution specification of `dgamma(0.01, 0.01)` is equivalent to specifying `gamma(shape=0.01, iscale=0.01)` in PROC MCMC.

The preceding statements specify four different gamma and inverse gamma distributions with various scale and inverse scale parameter values. The output of kernel density plots of these four prior distributions is shown in Figure 55.19. Note how the X axis scales vary across different distributions.

Figure 55.19 Density Plots of Different Gamma and Inverse Gamma Distributions



Posterior Predictive Distribution

The posterior predictive distribution

$$p(\mathbf{y}_{\text{pred}}|\mathbf{y}) = \int p(\mathbf{y}_{\text{pred}}|\theta) p(\theta|\mathbf{y}) d\theta$$

can often be used to check whether the model is consistent with data. For more information about using predictive distribution as a model checking tool, see Gelman et al. 2004, Chapter 6 and the bibliography in that chapter. The idea is to generate replicate data from $p(\mathbf{y}_{\text{pred}}|\mathbf{y})$ —call them $\mathbf{y}_{\text{pred}}^i$, for $i = 1, \dots, M$, where M is the total number of replicates—and compare them to the observed data to see whether there are any large and systematic differences. Large discrepancies suggest a possible model misfit. One way to compare the replicate data to the observed data is to first summarize the data to some test quantities, such as the mean, standard deviation, order statistics, and so on. Then compute the tail-area probabilities of the test statistics (based on the observed data) with respect to the estimated posterior predictive distribution that uses the M replicate $\mathbf{y}_{\text{pred}}$ samples.

Let $T(\cdot)$ denote the function of the test quantity, $T(\mathbf{y})$ the test quantity that uses the observed data, and $T(\mathbf{y}_{\text{pred}}^i)$ the test quantity that uses the i th replicate data from the posterior predictive distribution. You

calculate the tail-area probability by using the following formula:

$$\Pr(T(\mathbf{y}_{\text{pred}}) > T(\mathbf{y})|\theta)$$

The following example shows how you can use PROC MCMC to estimate this probability.

An Example for the Posterior Predictive Distribution

This example uses a normal mixed model to analyze the effects of coaching programs for the scholastic aptitude test (SAT) in eight high schools. For the original analysis of the data, see Rubin (1981). The presentation here follows the analysis and posterior predictive check presented in Gelman et al. (2004). The data are as follows:

```
title 'An Example for the Posterior Predictive Distribution';

data SAT;
  input effect se @@;
  ind=_n_;
  datalines;
28.39 14.9 7.94 10.2 -2.75 16.3
6.82 11.0 -0.64 9.4 0.63 11.4
18.01 10.4 12.16 17.6
;
```

The variable `effect` is the reported test score difference between coached and uncoached students in eight schools. The variable `se` is the corresponding estimated standard error for each school. In a normal mixed effect model, the variable `effect` is assumed to be normally distributed:

$$\text{effect}_i \sim \text{normal}(\mu_i, \text{se}^2) \quad \text{for } i = 1, \dots, 8$$

The parameter μ_i has a normal prior with hyperparameters (m, v) :

$$\mu_i \sim \text{normal}(m, \text{var} = v)$$

The hyperprior distribution on m is a uniform prior on the real axis, and the hyperprior distribution on v is a uniform prior from 0 to infinity.

The following statements fit a normal mixed model and use the **PREDDIST** statement to generate draws from the posterior predictive distribution.

```
ods listing close;
proc mcmc data=SAT outpost=out nmc=40000 seed=12;
  parms m 0;
  parms v 1 /slice;
  prior m ~ general(0);
  prior v ~ general(1, lower=0);
  random mu ~ normal(m, var=v) subject=ind monitor=(mu);
  model effect ~ normal(mu, sd=se);
  predpdist outpred=pout nsim=5000;
run;
ods listing;
```

The ODS LISTING CLOSE statement disables the listing output because you are primarily interested in the samples of the predictive distribution. The **HYPER**, **PRIOR**, and **MODEL** statements specify the Bayesian model of interest. The **PREDDIST** statement generates samples from the posterior predictive distribution and stores the samples in the Pout data set. The predictive variables are named `effect_1`, ..., `effect_8`. When no **COVARIATES** option is specified, the covariates in the original input data set SAT are used in the prediction. The **NSIM=** option specifies the number of predictive simulation iterations.

The following statements use the Pout data set to calculate the four test quantities of interest: the average (mean), the sample standard deviation (sd), the maximum effect (max), and the minimum effect (min). The output is stored in the Pred data set.

```
data pred;
  set pout;
  mean = mean(of effect:);
  sd = std(of effect:);
  max = max(of effect:);
  min = min(of effect:);
run;
```

The following statements compute the corresponding test statistics, the mean, standard deviation, and the minimum and maximum statistics on the real data and store them in macro variables. You then calculate the tail-area probabilities by counting the number of samples in the data set Pred that are greater than the observed test statistics based on the real data.

```
proc means data=SAT noprint;
  var effect;
  output out=stat mean=mean max=max min=min stddev=sd;
run;

data _null_;
  set stat;
  call symputx('mean',mean);
  call symputx('sd',sd);
  call symputx('min',min);
  call symputx('max',max);
run;

data _null_;
  set pred end=eof nobs=nobs;
  ctmean + (mean>&mean);
  ctmin + (min>&min);
  ctmax + (max>&max);
  ctsd + (sd>&sd);
  if eof then do;
    pmean = ctmean/nobs; call symputx('pmean',pmean);
    pmin = ctmin/nobs; call symputx('pmin',pmin);
    pmax = ctmax/nobs; call symputx('pmax',pmax);
    psd = ctsd/nobs; call symputx('psd',psd);
  end;
run;
```

You can plot histograms of each test quantity to visualize the posterior predictive distributions. In addition, you can see where the estimated *p*-values fall on these densities. [Figure 55.20](#) shows the histograms. To

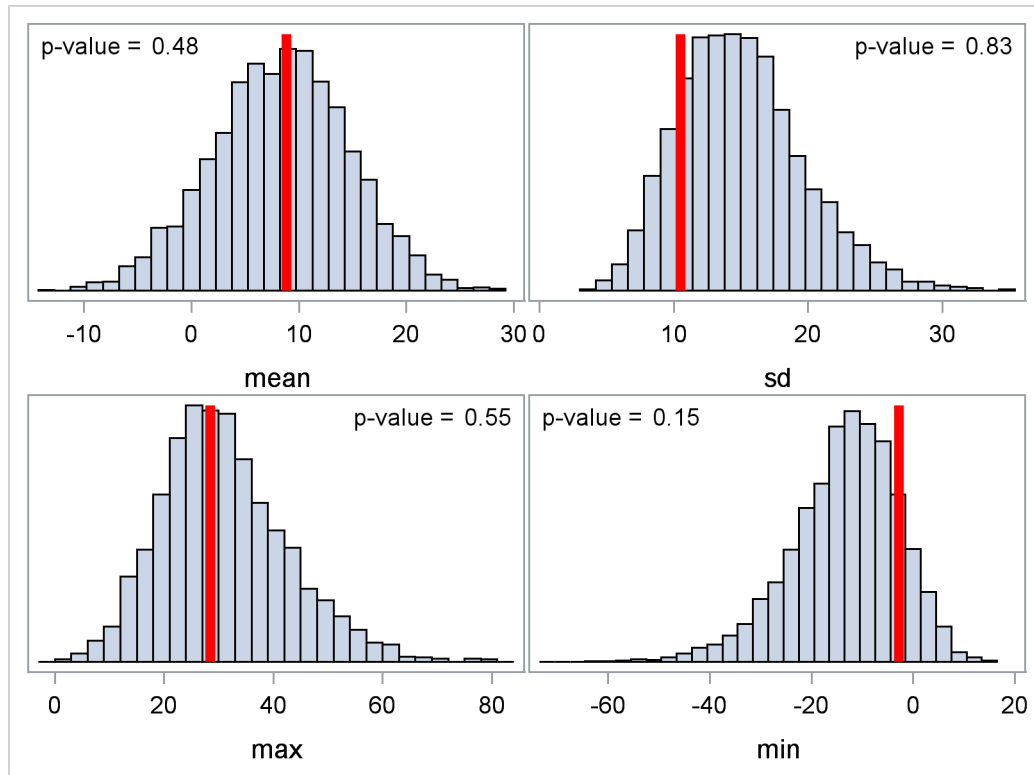
put all four histograms on the same panel, you need to use PROC TEMPLATE to define a new graph template. (See Chapter 21, “[Statistical Graphics Using ODS](#).”) The following statements define the template `twobytwo`:

```
proc template;
  define statgraph twobytwo;
    begingraph;
      layout lattice / rows=2 columns=2;
        layout overlay / yaxisopts=(display=none)
          xaxisopts=(label="mean");
        layout gridded / columns=2 border=false
          autoalign=(topleft topright);
        entry halign=right "p-value =";
        entry halign=left eval(strip(put(&pmean, 12.2)));
      endlayout;
      histogram mean / binaxis=false;
      lineparm x=&mean y=0 slope=. /
        lineattrs=(color=red thickness=5);
    endlayout;
    layout overlay / yaxisopts=(display=none)
      xaxisopts=(label="sd");
    layout gridded / columns=2 border=false
      autoalign=(topleft topright);
    entry halign=right "p-value =";
    entry halign=left eval(strip(put(&psd, 12.2)));
    endlayout;
    histogram sd / binaxis=false;
    lineparm x=&sd y=0 slope=. /
      lineattrs=(color=red thickness=5);
    endlayout;
    layout overlay / yaxisopts=(display=none)
      xaxisopts=(label="max");
    layout gridded / columns=2 border=false
      autoalign=(topleft topright);
    entry halign=right "p-value =";
    entry halign=left eval(strip(put(&pmax, 12.2)));
    endlayout;
    histogram max / binaxis=false;
    lineparm x=&max y=0 slope=. /
      lineattrs=(color=red thickness=5);
    endlayout;
    layout overlay / yaxisopts=(display=none)
      xaxisopts=(label="min");
    layout gridded / columns=2 border=false
      autoalign=(topleft topright);
    entry halign=right "p-value =";
    entry halign=left eval(strip(put(&pmin, 12.2)));
    endlayout;
    histogram min / binaxis=false;
    lineparm x=&min y=0 slope=. /
      lineattrs=(color=red thickness=5);
    endlayout;
  endlayout;
endgraph;
end;
run;
```

You call PROC SGRENDER to create the graph, which is shown in Figure 55.20. (See the SGRENDER procedure in the *SAS/GRAPH: Statistical Graphics Procedures Guide*.) There are no extreme p -values observed; this supports the notion that the predicted results are similar to the actual observations and that the model fits the data.

```
proc sgrender data=pred template=twobytwo;
run;
```

Figure 55.20 Posterior Predictive Distribution Check for the SAT example



Note that the posterior predictive distribution is not the same as the prior predictive distribution. The prior predictive distribution is $p(y)$, which is also known as the marginal distribution of the data. The prior predictive distribution is an integral of the likelihood function with respect to the prior distribution

$$p(y_{\text{pred}}) = \int p(y_{\text{pred}}|\theta)p(\theta)d\theta$$

and the distribution is not conditional on observed data.

Handling of Missing Data

PROC MCMC automatically augments missing values⁶ via the use of the **MODEL** statement. PROC MCMC treats missing values as unknown parameters, assigns distributions to the variables, and incorporates the sampling of the missing data as part of Markov chain.

⁶A missing value is usually, although not necessarily, represented by a single period (.) in the input data set.

(In SAS/STAT 9.3 and earlier releases, by default, PROC MCMC discarded all observations that had missing or partial missing values. PROC MCMC could not model missing values.)

You can use the **MISSING=** option in the PROC MCMC statement to specify how you want PROC MCMC to handle the missing values. If you specify **MISSING=CC** (CC stands for complete cases), PROC MCMC discards all observations that have missing or partial missing values before carrying out the simulation. If you specify **MISSING=AC** (AC stands for all cases), PROC MCMC neither discards any missing values nor augments them.

Generally speaking, there are three types of missing data models, as discussed by Rubin (1976). Also see Little and Rubin (2002) for a comprehensive treatment of missing data analysis. The rest of this section provides an overview of these three types of missing data models and explains how to use PROC MCMC to fit them.

Missing Completely at Random (MCAR)

Data are said to be MCAR if the probability of a missing value (or the failure of observing a value) does not depend on any other observations in the data set, regardless of whether they are observed or missing. That is, the observed and unobserved values are independent of each other: if y_i is missing, it is MCAR if the probability of observing y_i is independent of other y_j (and other covariates x_i) in the data set. Under this assumption, both the observed and unobserved data are random samples of all the data; hence, fitting a model based only on the observed data does not introduce any biases. This type of analysis is called a complete-case analysis. To carry out a complete-case analysis, you must specify **MISSING=CC** in the PROC MCMC statement. (In SAS/STAT 9.3 and earlier, PROC MCMC performed a complete-case analysis when the data contained missing values.)

Missing at Random (MAR)

Data are said to be MAR if the probability of a missing value can depend on some observed quantities but does not depend on any unobserved data. For example, suppose that x_i are completely observed for all observations and some y_i are missing. MAR states that the probability of observing y_i is independent of other missing y_j (values that could have been observed) and that it depends only on x_i (and, potentially, observed y_i).

The MAR assumption states that the missing y_i are no longer random samples and that they need to be modeled (via the likelihood specification of the missing values). At the same time, the independence assumption of the missing values on the unobserved quantities states that the missing mechanism (usually a binary indicator variable such that $r_i = 1$ if y_i is missing and $r_i = 0$ otherwise) can be ignored and does not need to be taken into account. Hence, MAR is sometimes referred to as *ignorably missing*. It is not the missing values that can be ignored, it is the missing mechanism that can be ignored.

By default, PROC MCMC treats the missing data as MAR (this assumes that you do not input a binary indicator variable r_i and model it specifically): each missing value becomes an extra parameter and PROC MCMC updates it in every iteration. PROC MCMC assumes that both the missing values and observed values arise from the same distribution (which is specified in the **MODEL** statement),

$$\mathbf{y} = \{\mathbf{y}_{\text{obs}}, \mathbf{y}_{\text{mis}}\} \sim f(\mathbf{y}|\theta)$$

where $\mathbf{y}$ consists of observed ($\mathbf{y}_{\text{obs}}$) and missing ($\mathbf{y}_{\text{mis}}$) values, and $f(\mathbf{y}|\theta)$ is the likelihood function with parameters θ .

You can use the **MODEL** statement to model missing covariates. Using multiple **MODEL** statements enables you to specify, for example, a marginal distribution for missing values in covariate x and a conditional distribution for the response variable y given x as follows:

```
model x ~ normal(alpha, var=s2_x);
model y ~ normal(beta * x, var=s2_y);
```

In each iteration, PROC MCMC draws samples for every missing value in variable x , then every missing value in variable y , conditional on the drawn values of the x variable.

Missing Not at Random (MNAR)

Data are said to be MNAR if the probability of a missing value depends on unobserved data (or data that could have been observed): the probability that y_i is missing depends on the missing values of other y_i . This is a very general scenario that assumes that the missing mechanism is no longer ignorable (it is sometimes referred to as *nonignorably missing*) and that a model for the missing mechanism is required in order to make correct inferences about the model parameters.

Let $\mathbf{R} = (r_1, \dots, r_n)$ be the missing value indicator for $\mathbf{Y} = (y_1, \dots, y_n)$, where $r_i = 1$ if y_i is missing and $r_i = 0$ otherwise. This $\mathbf{R}$ is usually part of an input data set where you preprocess the response variable and create this missing value indicator variable. Modeling MNAR data implies that you must specify a joint likelihood function over $\mathbf{R}$ and $\mathbf{Y}$: $f(\mathbf{R}, \mathbf{Y} | \mathbf{X}, \boldsymbol{\theta})$, where $\mathbf{X}$ represents the covariates and $\boldsymbol{\theta}$ represents the model parameters. This joint distribution can be factored in two ways: a pattern-mixture model and a selection model.

The *selection model* factors the joint distribution $\mathbf{R}$ and $\mathbf{Y}$ into a marginal distribution for $\mathbf{Y}$ and a conditional distribution for $\mathbf{R}$,

$$f(\mathbf{R}, \mathbf{Y} | \mathbf{X}, \boldsymbol{\theta}) \propto f(\mathbf{Y} | \mathbf{X}, \boldsymbol{\alpha}) \cdot f(\mathbf{R} | \mathbf{Y}, \mathbf{X}, \boldsymbol{\beta})$$

where $\boldsymbol{\theta} = (\boldsymbol{\alpha}, \boldsymbol{\beta})$, $f(\mathbf{R} | \mathbf{Y}, \mathbf{X}, \boldsymbol{\alpha})$ is usually a binary model with a logit or probit link that involves regression parameters $\boldsymbol{\alpha}$, and $f(\mathbf{Y} | \mathbf{X}, \boldsymbol{\beta})$ is the sampling distribution that generates y_i with model parameters $\boldsymbol{\beta}$.

The *pattern-mixture model* factors the opposite way, a marginal distribution for $\mathbf{R}$ and a conditional distribution for $\mathbf{Y}$,

$$f(\mathbf{R}, \mathbf{Y} | \mathbf{X}, \boldsymbol{\theta}) \propto f(\mathbf{R} | \mathbf{X}, \boldsymbol{\gamma}) \cdot f(\mathbf{Y} | \mathbf{R}, \mathbf{X}, \boldsymbol{\delta})$$

where $\boldsymbol{\theta} = (\boldsymbol{\gamma}, \boldsymbol{\delta})$.

You can use PROC MCMC to fit either model by specifying multiple **MODEL** statements: one for the marginal distribution and one for the conditional distribution. Suppose that the variable r is the missing data indicator, which is modeled using a logit model, and that the response variable y is a Poisson regression that includes the missing variable indicator as one of its covariates. The following statements are a PROC MCMC program that fits a pattern-mixture model:

```
pi = logistic(alpha * x1);
model r ~ binary(pi);
mu = beta0 + beta1 * x2 + beta3 * r;
model y ~ poisson(exp(mu));
```

The first **MODEL** statement uses a binary model with logit link to model the missing mechanism, and the second **MODEL** statement models the response variable with a Poisson regression that includes the missing

value indicator as one of its covariates. Each of the two sets of regression has its covariates and regression coefficients. If this hypothetical data set contained missing values in covariates `x1` and `x2`, you could add two more **MODEL** statements to handle each variable as follows:

```
model x1 ~ normal(mu1, var=s2_x1);
pi = logistic(alpha * x1);
model r ~ binary(pi);
model x2 ~ normal(mu2, var=s2_x2);
mu = beta0 + beta1 * x2 + beta3 * r;
model y ~ poisson(exp(mu));
```

Functions of Random-Effects Parameters

When you specify a **RANDOM** statement in a program, PROC MCMC internally creates a random-effects parameter for every unique value in the **SUBJECT=** variable. You can calculate any transformations of these random-effects parameters by applying SAS functions to the effect, and you can use the transformed variable in the subsequent statements. For example, the following statements perform a logit transformation of an effect:

```
random u ~ normal(mu, var=s2) subject=students;
p = logistic(u);
...
```

The value of the variable `p` changes with `u` as the procedure steps through the input data set: for different unique values of the `students` variable, `u` takes on a different parameter value, and `p` changes accordingly.

To save all the transformed values in `p` to the **OUTPOST=** data set, you cannot just specify the **MONITOR=(p)** option in the PROC MCMC statement. With such a specification, PROC MCMC can save only one value of `p` (usually the value associated with the last observation in the data set); it cannot save all values. To output all transformed values, you must create an array to store every transformation and use the **MONITOR=** option to save the entire array to the **OUTPOST=** data set. The difficult part of the programming involves the creation of the correct array index to use in different types of the **SUBJECT=** variables. The rest of this section describes how to monitor functions of random-effects parameters in different situations.

Indexing Subject Variable

This subsection describes how to monitor transformation of an effect `u` when the `students` variable is an indexing subject variable. An indexing subject variable is an integer variable that takes value from one to the total number of unique subjects in a variable. In other words, the variable can be used as an index in a SAS array. The indexing subject variable does not need to be sorted for the example code in this section to work. An example of an indexing variable takes the values of (1 2 3 4 5 1 2 3 4 5), where the total number of observation is $n=10$ and the number of unique values is $m=5$.

The following statements create an indexing variable `students` in the data set `a`:

```
data a;
  input students @@;
  datalines;
  1 1 2 2 3 3 4 4 5 5 6 6 7 7 8 8 9 9 10 10
;
```

The following statements run a random-effects model without any response variables. There are only random-effects parameters in the model; the program calculates the logit transformation of each effect, saves the results to the **OUTPOST=** data set, and produces Figure 55.21:

```
proc mcmc data=a monitor=(p) diag=none stats=none outpost=a1
  plots=none seed=1;
  array p[10];
  random u ~ n(0, sd=1) subject=students;
  p[students] = logistic(u);
  model general(0);
run;

proc print data=a1(obs=3);
run;
```

The **ARRAY** statement creates an array **p** of size 10, which is the number of unique values in **students**. The **p** array stores all the transformed values. The **RANDOM** statement declares **u** to be an effect with the subject variable **students**. The **P[STUDENTS]** assignment statement calculates the logit transformations of **u** and saves them in appropriate array elements—this is why the **students** variable must be an indexing variable. Because the **students** variable used in the **p[]** array is also the subject variable in the **RANDOM** statement, PROC MCMC can match each random-effects parameter with the corresponding element in array **p**. The **MONITOR=** option monitors all elements in **p** and saves the output to the **a1** data set. The **a1** data set contains variables **p1–p10**. Figure 55.21 shows the first three observations of the **OUTPOST=** data set.

Figure 55.21 Monitor Functions of Random Effect **u**

Obs	Iteration	p1	p2	p3	p4	p5	p6	p7
1	1	0.5050	0.7334	0.5375	0.5871	0.6862	0.4944	0.5740
2	2	0.5563	0.4254	0.7260	0.5280	0.4593	0.5797	0.5813
3	3	0.6132	0.8031	0.4735	0.3135	0.7047	0.5273	0.6761
Obs	p8	p9	p10	u_1	u_2	u_3	u_4	u_5
1	0.5991	0.6812	0.8678	0.0198	1.0120	0.1504	0.3521	0.7826
2	0.7360	0.9079	0.3351	0.2261	-0.3006	0.9742	0.1120	-0.1630
3	0.2379	0.2938	0.3986	0.4607	1.4058	-0.1060	-0.7837	0.8698
Obs	u_6	u_7	u_8	u_9	u_10	LogReff	LogLike	LogPost
1	-0.0225	0.2983	0.4019	0.7595	1.8819	-12.2658	0	-12.2658
2	0.3213	0.3281	1.0253	2.2887	-0.6854	-13.2393	0	-13.2393
3	0.1092	0.7361	-1.1641	-0.8772	-0.4112	-12.3984	0	-12.3984

The variable **p1** is the logit transformation of the variable **u_1**, **p2** is the logit transformation of the variable **u_2**, and so on.

The same idea works for a **students** variable that is unsorted. The following statements create an unsorted indexing variable **students** with repeated measures in each subject, fit the same model, and produce Figure 55.22:

```

data a;
  input students @@;
  datalines;
  1 1 1 3 5 3 4 5 3 1 5 5 4 4 2 2 2 2 4 3
;
proc mcmc data=a monitor=(p) diag=none stats=none outpost=a1
  plots=none seed=1;
  array p[5];
  random u ~ n(0, sd=1) subject=students;
  p[students] = logistic(u);
  model general(0);
run;

proc print data=a1(obs=3);
run;

```

Figure 55.22 Monitor Functions of Random Effect u When the students Variable is Unsorted

Obs	Iteration	p1	p2	p3	p4	p5	u_1
1	1	0.5050	0.6862	0.7334	0.5871	0.5375	0.0198
2	2	0.4944	0.8678	0.5740	0.6812	0.5991	-0.0225
3	3	0.5563	0.4593	0.4254	0.5280	0.7260	0.2261
Obs	u_3	u_5	u_4	u_2	LogReff	LogLike	LogPost
1	1.0120	0.1504	0.3521	0.7826	-5.4865	0	-5.4865
2	0.2983	0.4019	0.7595	1.8819	-6.7793	0	-6.7793
3	-0.3006	0.9742	0.1120	-0.1630	-5.1595	0	-5.1595

There are five random-effects parameters in this example, and the array p also has five elements. The values p1–p5 are the transformations of u_1–u_5, respectively. The u variables are not sorted from u_1 to u_5 because PROC MCMC creates the names according to the order by which the subject variable appears in the input data set. Nevertheless, because students is an indexing variable, the first element p[1] stores the transformation that corresponds to **students=1** (which is u_1), the second element p[2] stores the transformation that corresponds to **students=2**, and so on.

Non-Indexing Subject Variable

A non-indexing subject variable can take values of character literals (for example, names) or numerals (for example, ZIP code or a person's weight). This section illustrates how to monitor functions of random-effects parameters in these situations.

Suppose you have unsorted character literals as the subject variable:

```

data a;
  input students$ @@;
  datalines;
  smith john john mary kay smith lizzy ben ben dylan
  ben toby abby mary kay kay lizzy ben dylan mary
;

```

A statement such as following does not work anymore because a character variable cannot be used as an array index:

```
p[students] = logistic(u);
```

In this situation, you usually need to do two things: (1) find out the number of unique values in the subject variable, and (2) create a numeric index variable that replaces the students array index. You can use the following statements to do the first task:

```

proc sql noprint;
  select count(distinct(students)) into :nuniq from a;
quit;
%put &nuniq;

```

The PROC SQL call counts the distinct values in the students variable and saves the count to the macro variable &nuniq. The macro variable is used later to specify the element size of the p array. In this example, the a data set contains 20 observations and 9 unique elements (the value of &nuniq).

The following statements create an Index variable in the a data set that is in the order by which the students names appear in the data set:

```

proc freq data=a order=data noprint;
  tables students / out=_f(keep=students);
run;

proc print data=_f;
run;

data a(drop=n);
  set a;
  do i = 1 to nobs until(students=n);
    set _f(keep=students rename=(students=n)) point=i nobs=nobs;
    Index = i;
  end;
run;

proc print data=a;
run;

```

The PROC FREQ call identifies the unique students names and saves them to the _f data set, which is displayed in [Figure 55.23](#).

Figure 55.23 Unique Names in the Variable Students

Obs	students
1	smith
2	john
3	mary
4	kay
5	lizzy
6	ben
7	dylan
8	toby
9	abby

The DATA step steps through the a data set and creates an Index variable to match the order in which the students names appear in the data set. The new a data set⁷ is displayed in [Figure 55.24](#).

Figure 55.24 New Index Variable in the a Data Set

Obs	students	Index
1	smith	1
2	john	2
3	john	2
4	mary	3
5	kay	4
6	smith	1
7	lizzy	5
8	ben	6
9	ben	6
10	dylan	7
11	ben	6
12	toby	8
13	abby	9
14	mary	3
15	kay	4
16	kay	4
17	lizzy	5
18	ben	6
19	dylan	7
20	mary	3

Student smith is the first subject, and his Index value is one. The same student appears again in the sixth observation, which is given the same Index value. Now, this Index variable can be used to index the p array, in a similar fashion as demonstrated in previous programs:

⁷The programming code that creates and adds the Index variable to the data set a keeps all variables from the original data set and does not discard them.

```

data _f;
  set _f;
  subj = compress('p_'||students);
run;
proc sql noprint;
  select subj into :pnames separated by ' ' from _f;
quit;
%put &pnames;

proc mcmc data=a monitor=(p) diag=none stats=none outpost=a1
  plots=none seed=1;
  array p[&nuniq] &pnames;
  random u ~ n(0, sd=1) subject=students;
  p[index] = logistic(u);
  model general(0);
run;

proc print data=a1(obs=3);
run;

```

The first part of the DATA step and the PROC SQL call create array names for the *p* array that match the subject names in the *students* variable. It is not necessary to include these steps for the PROC MCMC program to work, but it makes the output more readable. The first DATA step steps through the *_f* data set and creates a *subj* variable that concatenates the prefix characters *p_* with the names of the students. The PROC SQL calls put all the *subj* values to a macro called *&pnames*, which looks like the following:

```
p_smith p_john p_mary p_kay p_lizzy p_ben p_dylan p_toby p_abby
```

In the PROC MCMC program, the **ARRAY** statement defines an *p* array with size *&nuniq* (9), and use the macro variable *&pnames* to name the array elements. The *P[INDEX]* assignment statement uses the *Index* variable to find the correct array element to store the transformation. [Figure 55.25](#) displays the first few observations of the **OUTPOST=a1** data set.

Figure 55.25 First Few Observations of the Outpost Data Set

Obs	Iteration	p_smith	p_john	p_mary	p_kay	p_lizzy	p_ben	p_dylan
1	1	0.5050	0.7334	0.5375	0.5871	0.6862	0.4944	0.5740
2	2	0.8678	0.5563	0.4254	0.7260	0.5280	0.4593	0.5797
3	3	0.9079	0.3351	0.6132	0.8031	0.4735	0.3135	0.7047
Obs	p_toby	p_abby	u_smith	u_john	u_mary	u_kay	u_lizzy	u_ben
1	0.5991	0.6812	0.0198	1.0120	0.1504	0.3521	0.7826	-0.0225
2	0.5813	0.7360	1.8819	0.2261	-0.3006	0.9742	0.1120	-0.1630
3	0.5273	0.6761	2.2887	-0.6854	0.4607	1.4058	-0.1060	-0.7837
Obs	u_dylan	u_toby	u_abby	LogReff	LogLike	LogPost		
1	0.2983	0.4019	0.7595	-9.5761	0	-9.5761		
2	0.3213	0.3281	1.0253	-11.2370	0	-11.2370		
3	0.8698	0.1092	0.7361	-13.1867	0	-13.1867		

There are nine random-effects parameters (u_{smith} , u_{john} , and so on). There are nine elements of the p array (p_{smith} , p_{john} , and so on); each is the logit transformation of corresponding u elements.

You can use the same statements for subject variables that are numeric non-indexing variables. The following statements create a `students` variable that take large numbers that cannot be used as indices to an array. The rest of the program monitors functions of the effect u . The output is not displayed here.

```
data a;
  call streaminit(1);
  do i = 1 to 20;
    students = rand("poisson", 20);
    output;
  end;
  drop i;
run;

proc sql noprint;
  select count(distinct(students)) into :nuniq from a;
quit;
%put &nuniq;

proc freq data=a order=data noprint;
  tables students / out=_f(keep=students);
run;

data a(drop=n);
  set a;
  do i = 1 to nobs until(students=n);
    set _f(keep=students rename=(students=n)) point=i nobs=nobs;
    Index = i;
  end;
run;

data _f;
  set _f;
  subj = compress('p_'||students);
proc sql noprint;
  select subj into :pnames separated by ' ' from _f;
quit;
%put &pnames;

proc mcmc data=a monitor=(p) diag=none stats=none outpost=a1
  plots=none seed=1;
  array p[&nuniq] &pnames;
  random u ~ n(0, sd=1) subject=students;
  p[index] = logistic(u);
  model general(0);
run;

proc print data=a1(obs=3);
run;
```

Floating Point Errors and Overflows

When performing a Markov chain Monte Carlo simulation, you must calculate a proposed jump and an objective function (usually a posterior density). These calculations might lead to arithmetic exceptions and overflows. A typical cause of these problems is parameters with widely varying scales. If the posterior variances of your parameters vary by more than a few orders of magnitude, the numerical stability of the optimization problem can be severely reduced and can result in computational difficulties. A simple remedy is to rescale all the parameters so that their posterior variances are all approximately equal. Changing the `SCALE=` option might help if the scale of your parameters is much different than one. Another source of numerical instability is highly correlated parameters. Often a model can be reparameterized to reduce the posterior correlations between parameters.

If parameter rescaling does not help, consider the following actions:

- provide different initial values or try a different seed value
- use boundary constraints to avoid the region where overflows might happen
- change the algorithm (specified in programming statements) that computes the objective function

Problems Evaluating Code for Objective Function

The initial values must define a point for which the programming statements can be evaluated. However, during simulation, the algorithm might iterate to a point where the objective function cannot be evaluated. If you program your own likelihood, priors, and hyperpriors by using SAS statements and the `GENERAL` function in the `MODEL`, `PRIOR`, AND `HYPERPRIOR` statements, you can specify that an expression cannot be evaluated by setting the value you pass back through the `GENERAL` function to missing. This tells the PROC MCMC that the proposed set of parameters is invalid, and the proposal will not be accepted. If you use the shorthand notation that the `MODEL`, `PRIOR`, AND `HYPERPRIOR` statements provide, this error checking is done for you automatically.

Long Run Times

PROC MCMC can take a long time to run for problems with complex models, many parameters, or large input data sets. Although the techniques used by PROC MCMC are some of the best available, they are not guaranteed to converge or proceed quickly for all problems. Ill-posed or misspecified models can cause the algorithms to use more extensive calculations designed to achieve convergence, and this can result in longer run times. You should make sure that your model is specified correctly, that your parameters are scaled to the same order of magnitude, and that your data reasonably match the model that you are specifying.

To speed general computations, you should check over your programming statements to minimize the number of unnecessary operations. For example, you can use the proportional kernel in the priors or the likelihood and not add constants in the densities. You can also use the `BEGINCNST` and `ENDCNST` to reduce unnecessary computations on constants, and the `BEGINNODATA` and `ENDNODATA` statements to reduce observation-level calculations.

Reducing the number of blocks (the number of the `PARMS` statements) can speed up the sampling process. A single-block program is approximately three times faster than a three-block program for the same number

of iterations. On the other hand, you do not want to put too many parameters in a single block, because blocks with large size tend not to produce well-mixed Markov chains.

If some parameters satisfy the conditional independence assumption, such as in the random-effects models or latent variable models, consider using the **RANDOM** statement to model these parameters. This statement takes advantage of the conditional independence assumption and can sample a larger number of parameters at a more efficient pace.

Slow or No Convergence

If the simulator is slow or fails to converge, you can try changing the model as follows:

- Change the number of Monte Carlo iterations (**NMC=**), or the number of burn-in iterations (**NBI=**), or both. Perhaps the chain just needs to run a little longer. Note that after the simulation, you can always use the **DATA** step or the **FIRSTOBS** data set option to throw away initial observations where the algorithm has not yet burned in, so it is not always necessary to set **NBI=** to a large value.
- Increase the number of tuning. The proposal tuning can often work better in large models (models that have more parameters) with larger values of **NTU=**. The idea of tuning is to find a proposal distribution that is a good approximation to the posterior distribution. Sometimes 500 iterations per tuning phase (the default) is not sufficient to find a good approximating covariance.
- Change the initial values to more feasible starting values. Sometimes the proposal tuning starts badly if the initial values are too far away from the main mass of the posterior density, and it might not be able to recover.
- Use the **PROPCOV=** option to start the Markov chain at better starting values. With the **PROPCOV=QUANEW** option, PROC MCMC optimizes the object function and uses the posterior mode as the starting value of the Markov chain. In addition, a quadrature approximation to the posterior mode is used as the proposal covariance matrix. This option works well in many cases and can improve the mixing of the chain and shorten the tuning and burn-in time.
- Parameterize your model to include conjugacy, such as using the gamma prior on the precision parameter in a normal distribution or using an inverse gamma on the variance parameter. For a list of conjugate sampling methods that PROC MCMC supports, see the section “**Conjugate Sampling**” on page 4472.
- Change the blocking by using the **PARMS** statements. Sometimes poor mixing and slow convergence can be attributed to highly correlated parameters being in different parameter blocks.
- Modify the target acceptance rate. A target acceptance rate of about 25% works well for many multi-parameter problems, but if the mixing is slow, a lower target acceptance rate might be better.
- Change the initial scaling or the **TUNEWT=** option to possibly help the proposal tuning.
- Consider using a different proposal distribution. If from a trace plot you see that a chain traverses to the tail area and sometimes takes quite a few simulations before it comes back, you can consider using a *t* proposal distribution. You can do this by either using the PROC option **PROPDIST=T** or using a **PARMS** statement option **T**.

- Transform parameters and sample on a different scale. For example, if a parameter has a gamma distribution, sample on the logarithm scale instead. A parameter a that has a gamma distribution is equivalent to $\log(a)$ that has an egamma distribution, with the same distribution specification. For example, the following two formulations are equivalent:

```
parm a;
prior a ~ gamma(shape = 0.001, scale = 0.001);
```

and

```
parm la;
prior la ~ egamma(shape = 0.001, scale = 0.001);
a = exp(la);
```

See “[Example 55.6: Nonlinear Poisson Regression Models](#)” on page 4570 and “[Example 55.20: Using a Transformation to Improve Mixing](#)” on page 4654. You can also use the logit transformation on parameters that have $\text{uniform}(0, 1)$ priors. This prior is often used on probability parameters. The logit transformation is as follows: $q = \log(\frac{p}{1-p})$. The distribution on q is the Jacobian of the transformation: $\exp(-q)(1 + \exp(-q))^{-2}$. Again, the following two formulations are equivalent:

```
parm p;
prior p ~ uniform(0, 1);
```

and

```
parm q;
lp = -q - 2 * log(1 + exp(-q));
prior q ~ general(lp);
p = 1/(1+exp(-q));
```

Precision of Solution

In some applications, PROC MCMC might produce parameter values that are not precise enough. Usually, this means that there were not enough iterations in the simulation. At best, the precision of MCMC estimates increases with the square of the simulation sample size. Autocorrelation in the parameter values deflate the precision of the estimates. For more information about autocorrelations in Markov chains, see the section “[Autocorrelations](#)” on page 152.

Handling Error Messages

PROC MCMC does not have a debugger. This section covers a few ways to debug and resolve error messages.

Using the PUT Statement

Adding the PUT statement often helps to find errors in a program. The following statements produce an error:

```
data a;
run;

proc mcmc data=a seed=1;
  parms sigma lt w;

  beginnodata;
  prior sigma ~ unif(0.001,100);
  s2 = sigma*sigma;
  prior lt ~ gamma(shape=1, iscale=0.001);
  t = exp(lt);
  c = t/s2;
  d = 1/(s2);
  prior w ~ gamma(shape=c, iscale=d);
  endnodata;

  model general(0);
run;
```

```
ERROR: PROC MCMC is unable to generate an initial value for the
       parameter w. The first parameter in the prior distribution is
       missing.
```

To find out why the shape parameter *c* is missing, you can add the put statement and examine all the calculations that lead up to the assignment of *c*:

```
proc mcmc data=a seed=1;
  parms sigma lt w;

  beginnodata;
  prior sigma ~ unif(0.001,100);
  s2 = sigma*sigma;
  prior lt ~ gamma(shape=1, iscale=0.001);
  t = exp(lt);
  c = t/s2;
  d = 1/(s2);
  put c= t= s2= lt=; /* display the values of these symbols. */
  prior w ~ gamma(shape=c, iscale=d);
  endnodata;

  model general(0);
run;
```

In the log file, you see the following:

```
c=. t=. s2=. lt=.
c=. t=. s2=2500.0500003 lt=1000
c=. t=. s2=2500.0500003 lt=1000
```

```
ERROR: PROC MCMC is unable to generate an initial value for the parameter w.
       The first parameter in the prior distribution is missing.
```

You can ignore the first few lines. They are the results of initial set up by PROC MCMC. The last line is important. The variable `c` is missing because `t` is the exponential of a very large number, 1000, in `lt`. The value 1000 is assigned to `lt` by PROC MCMC because none was given. The gamma prior with shape of 1 and inverse scale of 0.001 has mode 0 (see “[Standard Distributions](#)” on page 4476 for more details). PROC MCMC avoids starting the Markov chain at the boundary of the support of the distribution, and it uses the mean value here instead. The mean of the gamma prior is 1000, hence the problem. You can change how the initial value is generated by using the PROC statement `INIT=RANDOM`. Remember to take out the `put` statement once you identify the problem. Otherwise, you will see a voluminous output in the log file.

Using the HYPER Statement

You can use the `HYPER` statement to narrow down possible errors in the prior distribution specification. With multiple `PRIOR` statements in a program, you might see the following error message if one of the prior distributions is not specified correctly:

```
ERROR: The initial prior parameter specifications must yield log
       of positive prior density values.
```

This message is displayed when PROC MCMC detects an error in the prior distribution calculation but cannot pinpoint the specific parameter at fault. It is frequently, although not necessarily, associated with parameters that have `GENERAL` or `DGENERAL` distributions. If you have a complicated model with many `PRIOR` statements, finding the parameter at fault can be time consuming. One way is to change a subset of the `PRIOR` statements to `HYPER` statements. The two statements are treated the same in PROC MCMC and the simulation is not affected, but you get a different message if the hyperprior distributions are calculated incorrectly:

```
ERROR: The initial hyperprior parameter specifications must yield
       log of positive hyperprior density values.
```

This message can help you identify more easily which distributions are producing the error, and you can then use the `PUT` statement to further investigate.

Computational Resources

It is impossible to estimate how long it will take for a general Markov chain to converge to its stationary distribution. It takes a skilled and thoughtful analysis of the chain to decide whether it has converged to the target distribution and whether the chain is mixing rapidly enough. In some cases, you might be able to estimate how long a particular simulation might take. The running time of a program that does not have `RANDOM` statements is approximately linear to the following factors: the number of samples in the input data set, the number of simulations, the number of blocks in the program, and the speed of your computer. For an analysis that uses a data set of size `nsamples`, a simulation length of `nsim`, and a block design of

nblocks, PROC MCMC evaluates the log-likelihood function the following number of times, excluding the tuning phase:

$$\text{nsamples} \times \text{nsim} \times \text{nblocks}$$

The faster your computer evaluates a single log-likelihood function, the faster this program runs. Suppose you have nsamples equal to 200, nsim equal to 55,000, and nblocks equal to 3. PROC MCMC evaluates the log-likelihood function approximately 3.3×10^7 times. If your computer can evaluate the log likelihood for one observation 10^6 times per second, this program takes approximately a half a minute to run. If you want to increase the number of simulations five-fold, the run time increases approximately five-fold.

Each **RANDOM** statement adds one pass through the input data at each iteration. If the Metropolis algorithm is used to sample the random-effects parameter, the conditional density (objective function) is calculated twice per pass through the data, which requires a computational resource that is approximately equivalent to adding two blocks of parameters.

Of course, larger problems take longer than shorter ones, and if your model is amenable to frequentist treatment, then one of the other SAS procedures might be more suitable. With “regular” likelihoods and a lot of data, the results of standard frequentist analysis are often asymptotically equivalent to a Bayesian approach. If PROC MCMC requires too much CPU time, then perhaps another SAS/STAT tool would be suitable.

Displayed Output

This section describes the output that PROC MCMC displays. For a quick reference of all ODS table names, see the section “[ODS Table Names](#)” on page 4537. ODS tables are arranged under four groups, which are listed in the following sections: “[Model and Data Related ODS Tables](#)” on page 4533, “[Sampling Related ODS Tables](#)” on page 4534, “[Posterior Statistics Related ODS Tables](#)” on page 4535, “[Convergence Diagnostics Related ODS Tables](#)” on page 4535, and “[Optimization Related ODS Tables](#)” on page 4536.

Model and Data Related ODS Tables

Missing Data Information Table

The “Missing Data Information” table (ODS table name MISSDATAINFO) displays the name of the response variable that contains missing values, the number of missing observations, the corresponding observation indices in the input data set, and the sampling method used in the simulation for the missing values.

Number of Observation Table

The “NObs” table (ODS table name NOBS) shows the number of observations that is in the data set and the number of observations that is used in the analysis. By default, observations with missing values are not used (see the section “[Handling of Missing Data](#)” on page 4518 for more details). This table is displayed by default.

Parameters

The “Parameters” table (ODS table name Parameters) shows the name of each parameter, the block number of each parameter, the sampling method used for the block, the initial values, and the prior or hyperprior distributions. This table is displayed by default.

REObsInfo

The “Random Effect Observation Information” table (ODS table name REObsInfo) lists the name of the random effect, each subject value, the number of observations in each subject, and their corresponding observation indices in the input data set. You can request this table by specifying the [REOBSINFO](#) option.

REParameters

The “REParameters” table (ODS table name REParameters) lists the name of the random effect, sampling algorithm, the subject variable, the number of subjects, unique values of the subject variable, and the prior distribution. This table is displayed by default if a [RANDOM](#) statement is used in the program.

Sampling Related ODS Tables**Burn-In History**

The “Burn-In History” table (ODS table name BurnInHistory) shows the scales and acceptance rates for each parameter block in the burn-in phase. The table is not displayed by default and can be requested by specifying the option [MCHISTORY=BRIEF | DETAILED](#).

Parameters Initial Value Table

The “Parameters Initial” table (ODS table name ParametersInit) shows the value of each parameter after the tuning phase. This table is not displayed by default and can be requested by specifying the option [INIT=PINIT](#).

Posterior Samples

The “Posterior Samples” table (ODS table name PosteriorSample) stores posterior draws of all parameters. It is not printed by PROC MCMC. You can create an ODS output data set of the chain by specifying the following:

```
ODS OUTPUT PosteriorSample = SAS-data-set;
```

Sampling History

The “Sampling History” table (ODS table name SamplingHistory) shows the scales and acceptance rates for each parameter block in the main sampling phase. The table is not displayed by default and can be requested by specifying the option [MCHISTORY=BRIEF | DETAILED](#).

Tuning Covariance

The “Tuning Covariance” table (ODS table name TuneCov) shows the proposal covariance matrices for each parameter block after the tuning phase. The table is not displayed by default and can be requested by specifying the option [INIT=PINIT](#). For more details about proposal tuning, see the section “[Tuning the Proposal Distribution](#)” on page 4469.

Tuning History

The “Tuning History” table (ODS table name TuningHistory) shows the number of tuning phases used in establishing the proposal distribution. The table also displays the scales and acceptance rates for each parameter block at each of the tuning phases. For more information about the self-adapting proposal tuning algorithm used by PROC MCMC, see the section “[Tuning the Proposal Distribution](#)” on page 4469. The table is not displayed by default and can be requested by specifying the option [MCHISTORY=BRIEF | DETAILED](#).

Tuning Probability Vector

The “Tuning Probability” table (ODS table name TuneP) shows the proposal probability vector for each discrete parameter block (when the option DISCRETE=GEO is specified and the geometric proposal distribution is used for discrete parameters) after the tuning phase. The table is not displayed by default and can be requested by specifying the option `INIT=PINIT`. For more information about proposal tuning, see the section “[Tuning the Proposal Distribution](#)” on page 4469.

Posterior Statistics Related ODS Tables

PROC MCMC calculates some essential posterior statistics and outputs them to a number of ODS tables that you can request and save individually. For details of the calculations, see the section “[Summary Statistics](#)” on page 153.

Summary Statistics

The “Posterior Summaries” table (ODS table name PostSummaries) contains basic statistics for each parameter. The table lists the number of posterior samples, the posterior mean and standard deviation estimates, and the percentile estimates. This table is displayed by default.

Correlation Matrix

The “Posterior Correlation Matrix” table (ODS table name Corr) contains the posterior correlation of model parameters. The table is not displayed by default and can be requested by specifying the option `STATS=CORR`.

Covariance Matrix

The “Posterior Covariance Matrix” table (ODS table name Cov) contains the posterior covariance of model parameters. The table is not displayed by default and can be requested by specifying the option `STATISTICS=COV`.

Deviance Information Criterion

The “Deviance Information Criterion” table (ODS table name DIC) contains the DIC of the model. The table is not displayed by default and can be requested by specifying the option `DIC`. For details of the calculations, see the section “[Deviance Information Criterion \(DIC\)](#)” on page 155.

Interval Statistics

The “Posterior Intervals” table (ODS table name PostIntervals) contains the equal-tail and highest posterior density (HPD) interval estimates for each parameter. The default α value is 0.05, and you can change it to other levels by using the `STATISTICS=` option. This table is displayed by default.

Convergence Diagnostics Related ODS Tables

PROC MCMC has convergence diagnostic tests that check for Markov chain convergence. PROC MCMC produces a number of ODS tables that you can request and save individually. For details in calculation, see the section “[Statistical Diagnostic Tests](#)” on page 144.

Autocorrelation

The “Autocorrelations” table (ODS table name AUTOCORR) contains the first order autocorrelations of the posterior samples for each parameter. The “Parameter” column states the name of the parameter. By default,

PROC MCMC displays lag 1, 5, 10, and 50 estimates of the autocorrelations. You can request different autocorrelations by using the **DIAGNOSTICS = AUTOCORR(LAGS=)** option. This table is displayed by default.

Effective Sample Size

The “Effective Sample Sizes” table (ODS table name ESS) calculates the effective sample size of each parameter. See the section “Effective Sample Size” on page 152 for more details. The table is displayed by default.

Monte Carlo Standard Errors

The “Monte Carlo Standard Errors” table (ODS table name MCSE) calculates the standard errors of the posterior mean estimate. See the section “Standard Error of the Mean Estimate” on page 153 for more details. The table is displayed by default.

Geweke Diagnostics

The “Geweke Diagnostics” table (ODS table name Geweke) lists the result of the Geweke diagnostic test. See the section “Geweke Diagnostics” on page 146 for more details. The table is displayed by default.

Heidelberger-Welch Diagnostics

The “Heidelberger-Welch Diagnostics” table (ODS table name Heidelberger) lists the result of the Heidelberger-Welch diagnostic test. The test is consisted of two parts: a stationary test and a half-width test. See the section “Heidelberger and Welch Diagnostics” on page 148 for more details. The table is not displayed by default and can be requested by specifying **DIAGNOSTICS = HEIDEL**.

Raftery-Lewis Diagnostics

The “Raftery-Lewis Diagnostics” table (ODS table name Raftery) lists the result of the Raftery-Lewis diagnostic test. See the section “Raftery and Lewis Diagnostics” on page 149 for more details. The table is not displayed by default and can be requested by specifying **DIAGNOSTICS = RAFTERY**.

Summary Statistics for Prediction

The “Posterior Summaries for Prediction” table (ODS table name PredSummaries) contains basic statistics for each prediction. The table lists the number of posterior samples, the posterior mean and standard deviation estimates, and the percentile estimates. This table is displayed by default if any **PREDDIST** statement is used in the program.

Interval Statistics for Prediction

The “Posterior Intervals for Prediction” table (ODS table name PredIntervals) contains the equal-tail and highest posterior density (HPD) interval estimates for each prediction. The default α value is 0.05, and you can change it to other levels by using the **STATISTICS** option in a **PREDDIST** statement, or the **STATISTICS=** option in the PROC MCMC statement if the option is not specified in a statement. This table is displayed by default if any **PREDDIST** statement is used in the program.

Optimization Related ODS Tables

PROC MCMC can perform optimization on the joint posterior distribution. This is requested by the **PROPCOV=** option. The most commonly used optimization method is the quasi-Newton method: **PROPCOV=QUANEW(ITPRINT)**. The **ITPRINT** option displays the ODS tables, listed as follows:

Input Options

The “Input Options” table (ODS table name InputOptions) lists optimization options used in the procedure.

Optimization Start

The “Optimization Start” table (ODS table name ProblemDescription) shows the initial state of the optimization.

Iteration History

The “Iteration History” table (ODS table name IterHist) shows iteration history of the optimization.

Optimization Results

The “Optimization Results” table (ODS table name IterStop) shows the results of the optimization, includes information about the number of function calls, and the optimized objective function, which is the joint log posterior density.

Convergence Status

The “Convergence Status” table (ODS table name ConvergenceStatus) shows whether the convergence criterion is satisfied.

Parameters Value After Optimization Table

The “Parameter Values After Optimization” table (ODS table name OptiEstimates) lists the parameter values that maximize the joint log posterior. These are the maximum a posteriori point estimates, and they are used to start the Markov chain.

Covariance Matrix After Optimization Table

The “Proposal Covariance” table (ODS table name OptiCov) lists covariance matrices for each block parameter by using quadrature approximation at the posterior mode. These covariance matrices are used in the proposal distribution.

ODS Table Names

PROC MCMC assigns a name to each table it creates. You can use these names to refer to the table when you use the Output Delivery System (ODS) to select tables and create output data sets. These names are listed in [Table 55.47](#). For more information about ODS, see Chapter 21, “[Statistical Graphics Using ODS](#).”

Table 55.47 ODS Tables Produced in PROC MCMC

ODS Table Name	Description	Statement or Option
AutoCorr	Autocorrelation statistics for each parameter	Default
BurnInHistory	History of burn-in phase sampling	MCHISTORY=BRIEF DETAILED
ConvergenceStatus	Optimization convergence status	PROPCOV=method(ITPRINT)
Corr	Correlation matrix of the posterior samples	STATS=CORR

Table 55.47 (continued)

ODS Table Name	Description	Statement or Option
Cov	Covariance matrix of the posterior samples	STATS=COV
DIC	Deviance information criterion	DIC
ESS	Effective sample size for each parameter	Default
MCSE	Monte Carlo standard error for each parameter	Default
Geweke	Geweke diagnostics for each parameter	Default
Heidelberger	Heidelberger-Welch diagnostics for each parameter	DIAGNOSTICS=HEIDEL
InputOptions	Optimization input table	PROPCOV=method(ITPRINT)
IterHist	Optimization iteration history	PROPCOV=method(ITPRINT)
IterStop	Optimization results table	PROPCOV=method(ITPRINT)
MissDataInfo	Response variable, number of missing observations, missing observation indices, and sampling algorithm	Default with sampling of missing values
NObs	Number of observations	Default
OptiEstimates	Parameter values after either optimization	PROPCOV=method(ITPRINT)
OptiCov	Covariance used in proposal distribution after optimization	PROPCOV=method(ITPRINT)
Parameters	Summary of the PARMS, BLOCKING, PRIOR, sampling method, and initial value specification	Default
ParametersInit	Parameter values after the tuning phase	INIT=PINIT
PosteriorSample	Posterior samples for each parameter	(For ODS output data set only)
PostIntervals	Equal-tail and HPD intervals for each parameter	Default
PostSummaries	Basic posterior statistics for each parameter, including sample size, mean, standard deviation, and percentiles	Default
PredIntervals	Equal-tail and HPD intervals for each prediction	Default with any PREDDIST statement
PredSummaries	Basic posterior statistics for each prediction	Default with any PREDDIST statement
ProblemDescription	Optimization table	PROPCOV=method(ITPRINT)
REObsInfo	Random effect, subject values, number of observations in each unique subject value, and corresponding observation indices	REOBSINFO

Table 55.47 (continued)

ODS Table Name	Description	Statement or Option
REParameters	Random effect, sampling method, subject variable, number of subjects, unique values of the subject variable, and prior distribution of the random effect	Default with any RANDOM statement
Raftery	Raftery-Lewis diagnostics for each parameter	DIAGNOSTICS=RAFTERY
SamplingHistory TuneCov	History of main phase sampling Proposal covariance matrix (for continuous parameters) after the tuning phase	MCHISTORY=BRIEF DETAILED INIT=PINIT
TuneP	Proposal probability vector (for discrete parameters) after the tuning phase	INIT=PINIT and DISCRETE=GEO
TuningHistory	History of proposal distribution tuning	MCHISTORY=BRIEF DETAILED

ODS Graphics

Statistical procedures use ODS Graphics to create graphs as part of their output. ODS Graphics is described in detail in Chapter 21, “[Statistical Graphics Using ODS.](#)”

Before you create graphs, ODS Graphics must be enabled (for example, by specifying the ODS GRAPHICS ON statement). For more information about enabling and disabling ODS Graphics, see the section “[Enabling and Disabling ODS Graphics](#)” on page 600 in Chapter 21, “[Statistical Graphics Using ODS.](#)”

The overall appearance of graphs is controlled by ODS styles. Styles and other aspects of using ODS Graphics are discussed in the section “[A Primer on ODS Statistical Graphics](#)” on page 599 in Chapter 21, “[Statistical Graphics Using ODS.](#)”

You can reference every graph produced through ODS Graphics with a name. The names of the graphs that PROC MCMC generates are listed in [Table 55.48](#).

Table 55.48 Graphs Produced by PROC MCMC

ODS Graph Name	Plot Description	Statement & Option
ADPanel	Autocorrelation function and density panel	PLOTS=(AUTOCORR DENSITY)
AutocorrPanel	Autocorrelation function panel	PLOTS=AUTOCORR
AutocorrPlot	Autocorrelation function plot	PLOTS(UNPACK)=AUTOCORR
DensityPanel	Density panel	PLOTS=DENSITY
DensityPlot	Density plot	PLOTS(UNPACK)=DENSITY

Table 55.48 *continued*

ODS Graph Name	Plot Description	Statement & Option
TAPanel	Trace and autocorrelation function panel	PLOTS=(TRACE AUTOCORR)
TADPanel	Trace, density, and autocorrelation function panel	PLOTS=(TRACE AUTOCORR DENSITY)
TDPanel	Trace and density panel	PLOTS=(TRACE DENSITY)
TracePanel	Trace panel	PLOTS=TRACE
TracePlot	Trace plot	PLOTS(UNPACK)=TRACE

Examples: MCMC Procedure

Example 55.1: Simulating Samples From a Known Density

This example illustrates how you can obtain random samples from a known function. The target distributions are the normal distribution (a standard distribution) and a mixture of the normal distributions (a nonstandard distribution). For more information, see the sections “[Standard Distributions](#)” on page 4476 and “[Specifying a New Distribution](#)” on page 4490). This example also shows how you can use PROC MCMC to estimate an integral (area under a curve). Monte Carlo simulation is data-independent; hence, you do not need an input data set from which to draw random samples from the desired distribution.

Sampling from a Normal Density

When you run a simulation without an input data set, the posterior distribution is the same as the prior distribution. Hence, if you want to generate samples from a distribution, you declare the distribution in the **PRIOR** statement and set the likelihood function to a constant. Although there is no contribution from any data set variable to the likelihood calculation, you still must specify a data set and the **MODEL** statement needs a distribution. You can input an empty data set and use the **GENERAL** function to provide a flat likelihood. The following statements generate 10,000 samples from a standard normal distribution:

```

title 'Simulating Samples from a Normal Density';
data x;
run;

ods graphics on;
proc mcmc data=x outpost=simout seed=23 nmc=10000
    statistics=(summary interval) diagnostics=none;
    ods exclude nob;
    parm alpha 0;
    prior alpha ~ normal(0, sd=1);
    model general(0);
run;
```

The ODS GRAPHICS ON statement enables ODS Graphics. The PROC MCMC statement specifies the input and output data sets, a random number seed, and the size of the simulation sample. The **STATISTICS=** option displays only the summary and interval statistics. The ODS EXCLUDE statement excludes the display of the **NObs** table. PROC MCMC draws independent samples from the normal distribution directly (see [Output 55.1.1](#)). Therefore, the simulation does not require any tuning, and PROC MCMC omits the default burn-in phrase.

Output 55.1.1 Parameters Information

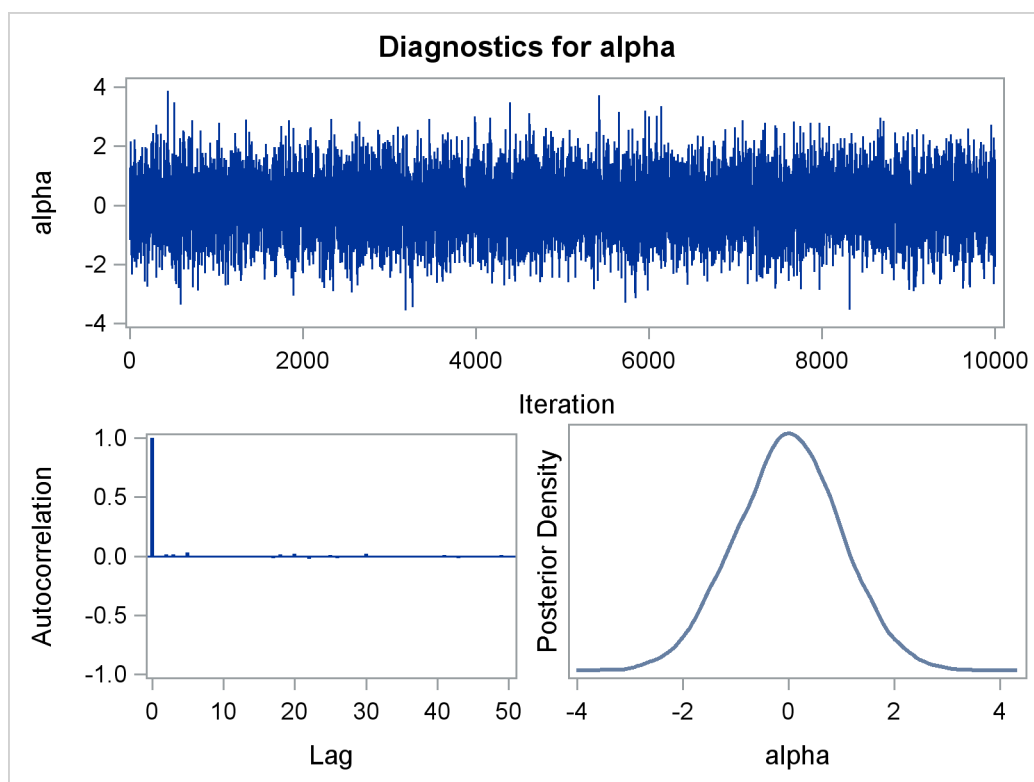
Simulating Samples from a Normal Density				
The MCMC Procedure				
Parameters				
Block	Parameter	Sampling Method	Initial Value	Prior Distribution
1	alpha	Direct	0	normal(0, sd=1)

The summary statistics ([Output 55.1.2](#)) are what you would expect from a standard normal distribution.

Output 55.1.2 MCMC Summary and Interval Statistics from a Normal Target Distribution

Simulating Samples from a Normal Density						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
alpha	10000	0.00195	0.9949	-0.6544	0.00965	0.6709
Posterior Intervals						
Parameter	Alpha	Equal-Tail Interval		HPD Interval		
alpha	0.050	-1.9485	1.9507	-1.9664	1.9302	

The trace plot ([Output 55.1.3](#)) shows perfect mixing with no autocorrelation in the lag plot. This is expected because these are independent draws.

Output 55.1.3 Diagnostics Plots for α 

You can overlay the estimated kernel density with the true density to visually compare the densities, as displayed in [Output 55.1.4](#). To create the kernel comparison plot, you first call PROC KDE (see Chapter 48, “[The KDE Procedure](#)”) to obtain a kernel density estimate of the posterior density on α . Then you evaluate a grid of α values on a normal density. The following statements evaluate kernel density and compute the corresponding normal density:

```
proc kde data=simout;
  ods exclude inputs controls;
  univar alpha /out=sample;
run;

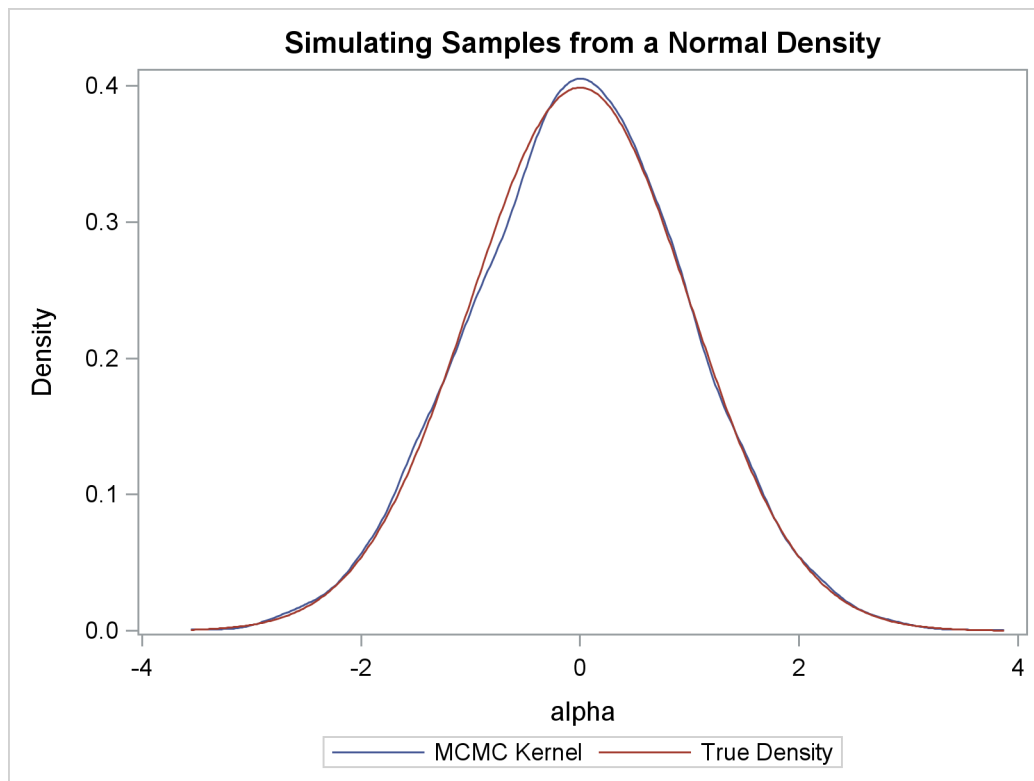
data den;
  set sample;
  alpha = value;
  true = pdf('normal', alpha, 0, 1);
  keep alpha density true;
run;
```


Next you plot the two curves on top of each other by using PROC SGPLOT (see Chapter 21, “[Statistical Graphics Using ODS](#)”) as follows:

```
proc sgplot data=den;
  yaxis label="Density";
  series y=density x=alpha / legendlabel = "MCMC Kernel";
  series y=true x=alpha / legendlabel = "True Density";
  discretelegend;
run;
```

[Output 55.1.4](#) shows the result. You can see that the kernel estimate and the true density are very similar to each other.

Output 55.1.4 Estimated Density versus the True Density



Density Visualization Macro

In programs that do not involve any data set variables, PROC MCMC samples directly from the (joint) prior distributions of the parameters. The modification makes the sampling from a known distribution more efficient and more precise. For example, you can write simple programs, such as the following macro, to understand different aspects of a prior distribution of interest, such as its moments, intervals, shape, spread, and so on:

```

%macro density(dist=, seed=0);
  %let savenote = %sysfunc(getoption(notes));
  options nonotes;
  title "&dist distribution.";
  data _a;
  run;

  ods select densitypanel postsummaries postintervals;
  proc mcmc data=_a nmc=10000 diag=none nologdist
    plots=density seed=&seed;
    parms alpha;
    prior alpha ~ &dist;
    model general(0);
  run;

  proc datasets nolist;
    delete _a;
  run;
  options &savenote;
%mend;

%density(dist=beta(4, 12), seed=1);

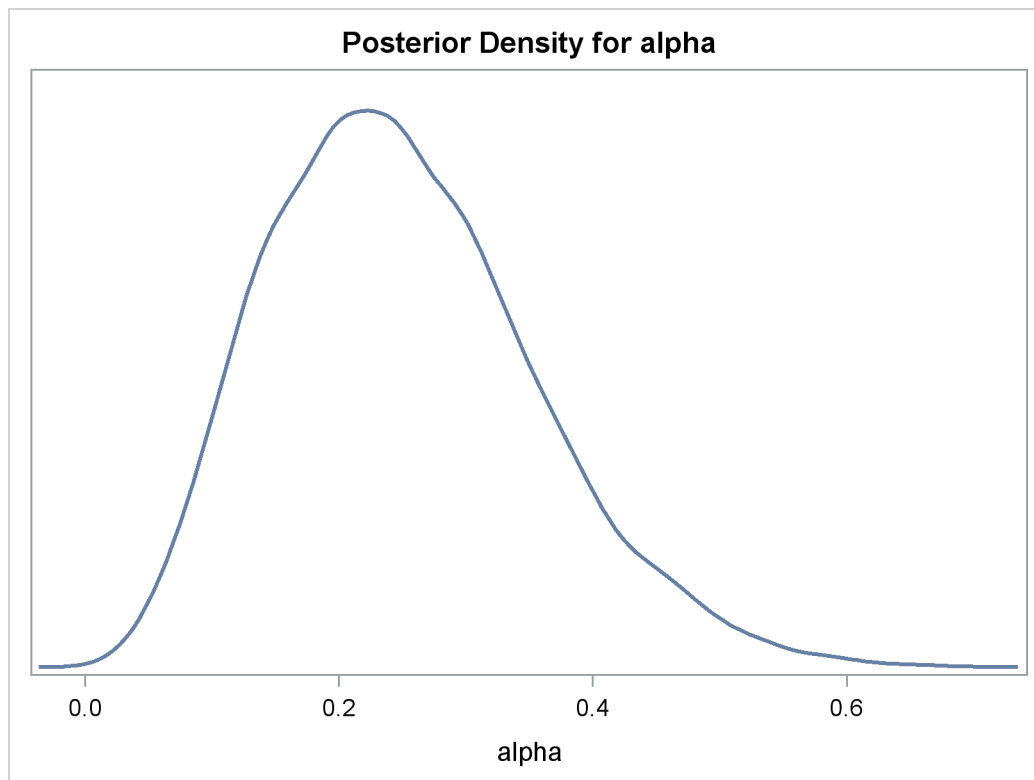
```

The macro %density creates an empty data set, invokes PROC MCMC, draws 10,000 samples from a beta(4, 12) distribution, displays summary and interval statistics, and generates a kernel density plot. Summary and interval statistics from the beta distribution are displayed in [Output 55.1.5](#).

Output 55.1.5 Beta Distribution Statistics

beta(4, 12) distribution.						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
alpha	10000	0.2494	0.1039	0.1731	0.2397	0.3148
Posterior Intervals						
Parameter	Alpha	Equal-Tail Interval		HPD Interval		
alpha	0.050	0.0775	0.4800	0.0657	0.4590	

The distribution is displayed in [Output 55.1.6](#).

Output 55.1.6 Density Plot

Calculation of Integrals

One advantage of MCMC methods is to estimate any integral under the curve of a target distribution. This can be done fairly easily using the MCMC procedure. Suppose you are interested in estimating the following cumulative probability:

$$\int_{\alpha=0}^{1.3} \phi(\alpha|0, 1) d\alpha$$

To estimate this integral, PROC MCMC draws samples from the distribution and counts the portion of the simulated values that fall within the desired range of [0, 1.3]. This becomes a Monte Carlo estimate of the integral. The following statements simulate samples from a standard normal distribution and estimate the integral:

```
proc mcmc data=x outpost=simout seed=23 nmc=10000 nologdist
  monitor=(int) statistics=(summary) diagnostics=none;
  ods select postsummaries;
  parm alpha 0;
  prior alpha ~ normal(0, sd=1);
  int = (0 <= alpha <= 1.3);
  model general(0);
run;
```

The ODS SELECT statement displays the posterior summary statistics table. The **MONITOR=** option outputs analysis on the variable int (the integral estimate). The **STATISTICS=** option computes the summary

statistics. The **NOLOGDIST** option omits the calculation of the log of the prior distribution at each iteration, shortening the simulation time⁸. The **INT** assignment statement sets **int** to be 1 if the simulated **alpha** value falls between 0 and 1.3, and 0 otherwise. PROC MCMC supports the usage of the IF-ELSE logical control if you need to account for more complex conditions. [Output 55.1.7](#) displays the estimated integral value:

Output 55.1.7 Monte Carlo Integral from a Normal Distribution

beta(4, 12) distribution.						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	25%	50%	75%
int	10000	0.4079	0.4915	0	0	1.0000

In this simulation, 4079 samples fall between 0 and 1.3, making the expected probability 0.4079. In this example, you can verify the actual cumulative probability by calling the CDF function in the DATA step:

```
data _null_;
  int = cdf("normal", 1.3, 0, 1) - cdf("normal", 0, 0, 1);
  put int=;
run;
```

The value is 0.4032.

Sampling from a Mixture of Normal Densities

Suppose you are interested in generating samples from a three-component mixture of normal distributions, with the density specified as follows:

$$p(\alpha) = 0.3 \cdot \phi(-3, \sigma = 2) + 0.4 \cdot \phi(2, \sigma = 1) + 0.3 \cdot \phi(10, \sigma = 4)$$

The distribution is not one of the standard distributions that PROC MCMC supports. Hence you need to construct the density function and supply it to the procedure. The following statements generate random samples from this mixture density:

```
title 'Simulating Samples from a Mixture of Normal Densities';
data x;
run;

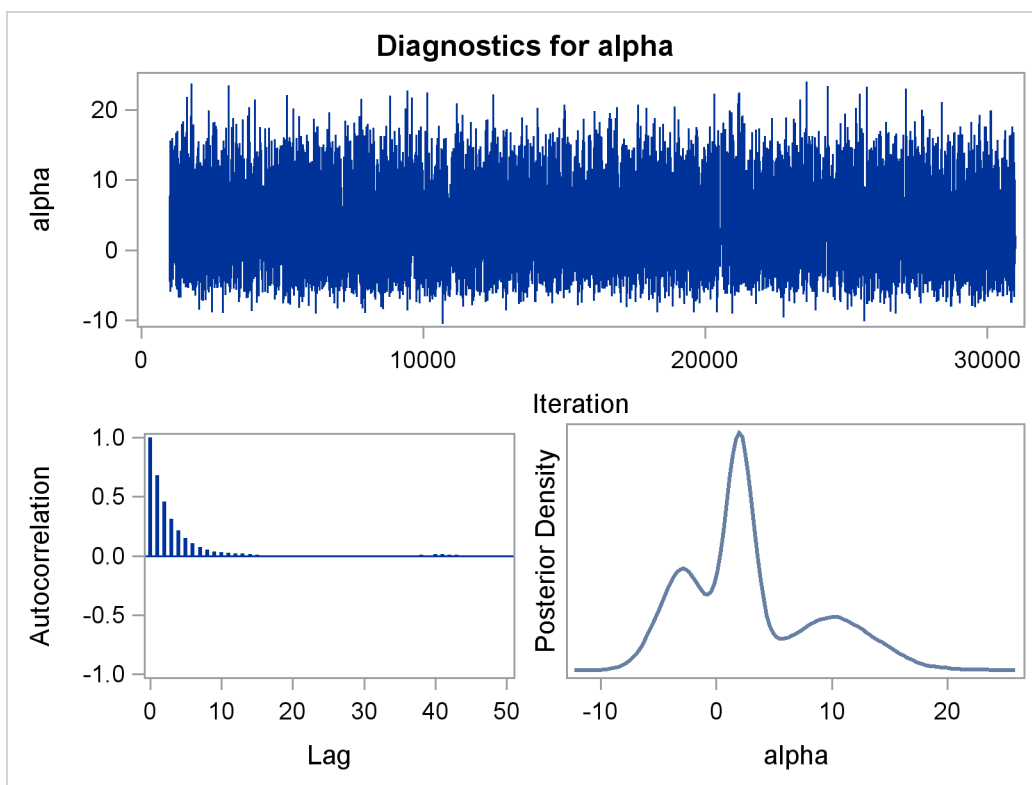
proc mcmc data=x outpost=simout seed=1234 nmc=30000;
  ods select TADpanel;
  parm alpha 0.3;
  lp = logpdf('normalmix', alpha, 3, 0.3, 0.4, 0.3, -3, 2, 10, 2, 1, 4);
  prior alpha ~ general(lp);
  model general(0);
run;
```

⁸In this example, the **NOLOGDIST** option saves only a fraction of the time. But in more complex simulation schemes that involve a larger number of distributions and parameters, the time reduction could be significant.

The ODS SELECT statement displays the diagnostic plots. All other tables, such as the **NObs** tables, are excluded. The PROC MCMC statement uses the input data set X, saves output to the Simout data set, sets a random number seed, and draws 30,000 samples.

The LP assignment statement evaluates the log density of alpha at the mixture density, using the SAS function LOGPDF. The number 3 after alpha in the LOGPDF function indicates that the density is a three-component normal mixture. The following three numbers, 0.3, 0.4, and 0.3, are the weights in the mixture; -3, 2, and 10 are the means; 2, 1, and 4 are the standard deviations. The **PRIOR** statement assigns this log density function to alpha as its prior. Note that the **GENERAL** function interprets the density on the log scale, and not the original scale—you must use the LOGPDF function, not the PDF function. **Output 55.1.8** displays the results. The kernel density clearly shows three modes.

Output 55.1.8 Plots of Posterior Samples from a Mixture Normal Distribution



Using the following set of statements similar to the previous example, you can overlay the estimated kernel density with the true density. The comparison is shown in **Output 55.1.9**.

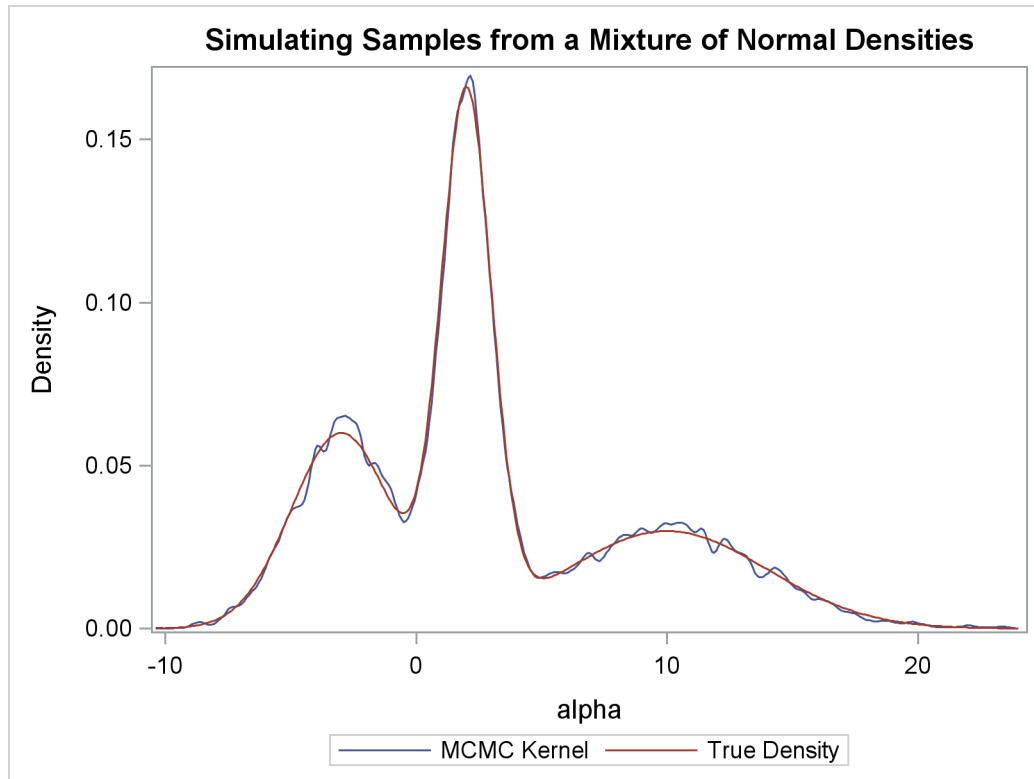
```
proc kde data=simout;
  ods exclude inputs controls;
  univar alpha /out=sample;
run;

data den;
  set sample;
  alpha = value;
  true = pdf('normalmix', alpha, 3, 0.3, 0.4, 0.3, -3, 2, 10, 2, 1, 4);
  keep alpha density true;
run;
```

```

proc sgplot data=den;
  yaxis label="Density";
  series y=density x=alpha / legendlabel = "MCMC Kernel";
  series y=true x=alpha / legendlabel = "True Density";
  discretelegend;
run;

```

Output 55.1.9 Estimated Density versus the True Density

Example 55.2: Box-Cox Transformation

Box-Cox transformations (Box and Cox 1964) are often used to find a power transformation of a dependent variable to ensure the normality assumption in a linear regression model. This example illustrates how you can use PROC MCMC to estimate a Box-Cox transformation for a linear regression model. Two different priors on the transformation parameter λ are considered: a continuous prior and a discrete prior. You can estimate the probability of λ being 0 with a discrete prior but not with a continuous prior. The IF-ELSE statements are demonstrated in the example.

Using a Continuous Prior on λ

The following statements create a SAS data set with measurements of y (the response variable) and x (a single dependent variable):

```

title 'Box-Cox Transformation, with a Continuous Prior on Lambda';
data boxcox;
    input y x @@;
    datalines;
10.0  3.0  72.6  8.3  59.7  8.1  20.1  4.8  90.1  9.8  1.1  0.9
78.2  8.5  87.4  9.0  9.5  3.4  0.1  1.4  0.1  1.1  42.5  5.1
57.0  7.5  9.9  1.9  0.5  1.0 121.1  9.9  37.5  5.9  49.5  6.7

    ... more lines ...

2.6  1.8  58.6  7.9  81.2  8.1  37.2  6.9
;

```

The Box-Cox transformation of y takes on the form of:

$$y(\lambda) = \begin{cases} \frac{y^\lambda - 1}{\lambda} & \text{if } \lambda \neq 0; \\ \log(y) & \text{if } \lambda = 0. \end{cases}$$

The transformed response $y(\lambda)$ is assumed to be normally distributed:

$$y_i(\lambda) \sim \text{normal}(\beta_0 + \beta_1 x_i, \sigma^2)$$

The likelihood with respect to the original response y_i is as follows:

$$p(y_i | \lambda, \beta, \sigma^2, x_i) \propto \phi(y_i | \beta_0 + \beta_1 x_i, \sigma^2) \cdot J(\lambda, y_i)$$

where $J(\lambda, y_i)$ is the Jacobian:

$$J(\lambda, y) = \begin{cases} y_i^{\lambda-1} & \text{if } \lambda \neq 0; \\ 1/y_i & \text{if } \lambda = 0. \end{cases}$$

And on the log-scale, the Jacobian becomes:

$$\log(J(\lambda, y)) = \begin{cases} (\lambda - 1) \cdot \log(y_i) & \text{if } \lambda \neq 0; \\ -\log(y_i) & \text{if } \lambda = 0. \end{cases}$$

There are four model parameters: λ , $\boldsymbol{\beta} = \{\beta_0, \beta_1\}$, and σ^2 . You can consider using a flat prior on $\boldsymbol{\beta}$ and a gamma prior on σ^2 .

To consider only power transformations ($\lambda \neq 0$), you can use a continuous prior (for example, a uniform prior from -2 to 2) on λ . One issue with using a continuous prior is that you cannot estimate the probability of $\lambda = 0$. To do so, you need to consider a discrete prior that places positive probability mass on the point 0 . See “[Modeling \$\lambda = 0\$](#) ” on page 4553.

The following statements fit a Box-Cox transformation model:

```

ods graphics on;
proc mcmc data=boxcox nmc=50000 thin=10 propcov=quanew seed=12567
    monitor=(lda);
    ods select PostSummaries PostIntervals TADpanel;

    parms beta0 0  beta1 0  lda 1 s2 1;

    beginnodata;
    prior beta: ~ general(0);
    prior s2 ~ gamma(shape=3, scale=2);
    prior lda ~ unif(-2,2);
    sd = sqrt(s2);
    endnodata;

    ys = (y**lda-1)/lda;
    mu = beta0+beta1*x;
    ll = (lda-1)*log(y)+lpdfnorm(ys, mu, sd);
    model general(ll);
run;

```

The **PROPCOV=** option initializes the Markov chain at the posterior mode and uses the estimated inverse Hessian matrix as the initial proposal covariance matrix. The **MONITOR=** option selects λ as the variable to report. The ODS SELECT statement displays the summary statistics table, the interval statistics table, and the diagnostic plots.

The **PARMS** statement puts all four parameters, β_0 , β_1 , λ , and σ^2 , in a single block and assigns initial values to each of them. Three **PRIOR** statements specify previously stated prior distributions for these parameters. The assignment to **sd** transforms a variance to a standard deviation. It is better to place the transformation inside the **BEGINNODATA** and **ENDNODATA** statements to save computational time.

The assignment to the symbol **ys** evaluates the Box-Cox transformation of y , where μ is the regression mean and ll is the log likelihood of the transformed variable ys . Note that the log of the Jacobian term is included in the calculation of ll .

Summary statistics and interval statistics for λ are listed in [Output 55.2.1](#).

Output 55.2.1 Box-Cox Transformation

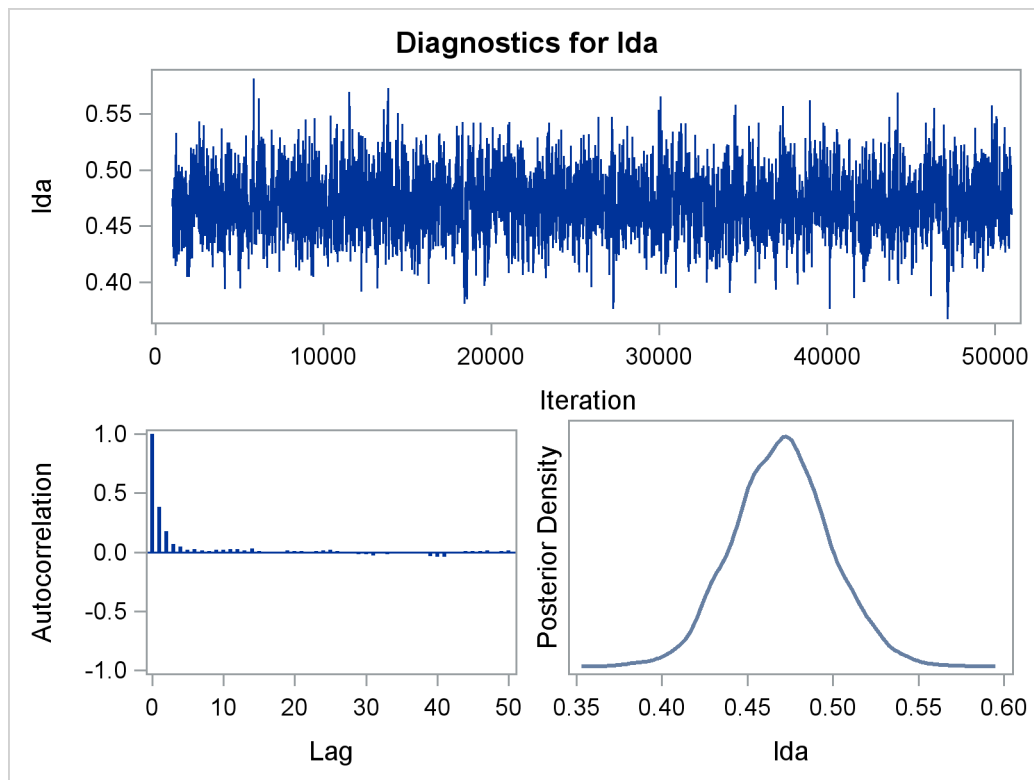
Box-Cox Transformation, with a Continuous Prior on Lambda						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles 25%	50%	75%
lda	5000	0.4702	0.0284	0.4515	0.4703	0.4884

Output 55.2.1 *continued*

Parameter	Alpha	Posterior Intervals			
		Equal-Tail Interval		HPD Interval	
lda	0.050	0.4162	0.5269	0.4197	0.5298

The posterior mean of λ is 0.47, with a 95% equal-tail interval of [0.42, 0.53] and a similar HPD interval. The preferred power transformation would be 0.5 (rounding λ up to the square root transformation).

Output 55.2.2 shows diagnostics plots for lda. The chain appears to converge, and you can proceed to make inferences. The density plot shows that the posterior density is relatively symmetric around its mean estimate.

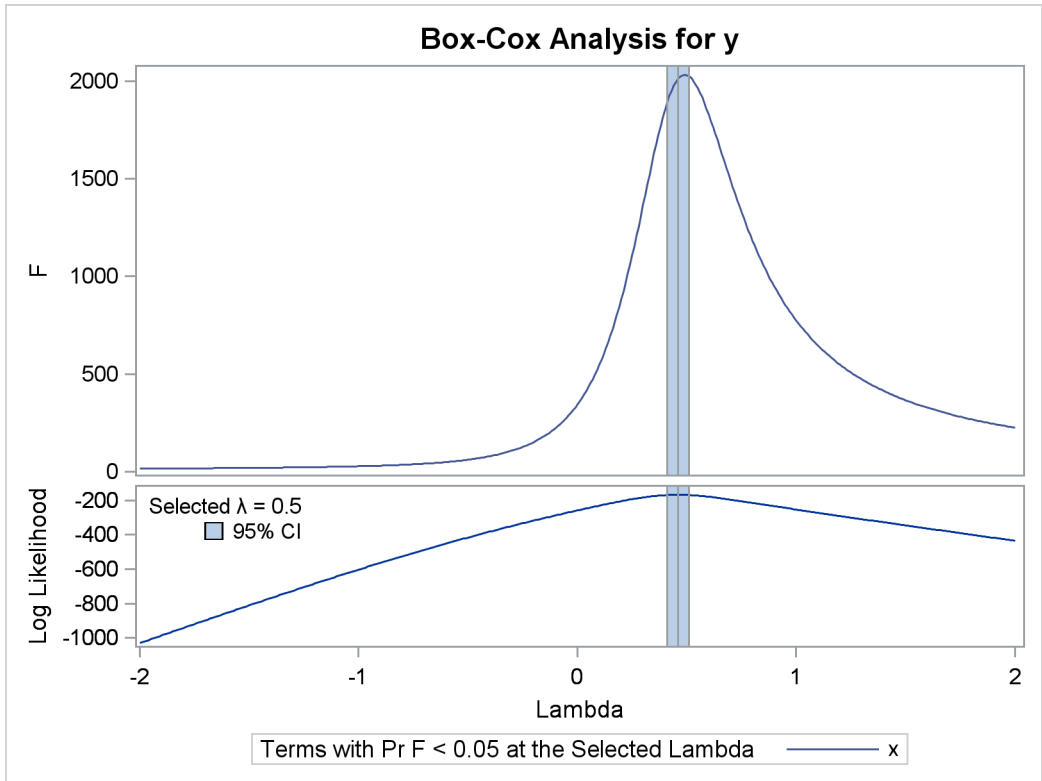
Output 55.2.2 Diagnostic Plots for λ 

To verify the results, you can use PROC TRANSREG (see Chapter 97, “[The TRANSREG Procedure](#)”) to find the estimate of λ .

```
proc transreg data=boxcox details pbo;
  ods output boxcox = bc;
  model boxcox(y / convenient lambda=-2 to 2 by 0.01) = identity(x);
  output out=trans;
run;
```

Output from PROC TRANSREG is shown in [Output 55.2.5](#) and [Output 55.2.4](#). PROC TRANSREG produces a similar point estimate of $\lambda = 0.46$, and the 95% confidence interval is shown in [Output 55.2.5](#).

Output 55.2.3 Box-Cox Transformation Using PROC TRANSREG



Output 55.2.4 Estimates Reported by PROC TRANSREG

Box-Cox Transformation, with a Continuous Prior on Lambda				
The TRANSREG Procedure				
Model Statement Specification Details				
Type	DF	Variable	Description	Value
Dep	1	BoxCox(y)	Lambda Used	0.5
			Lambda	0.46
			Log Likelihood	-167.0
			Conv. Lambda	0.5
			Conv. Lambda LL	-168.3
			CI Limit	-169.0
			Alpha	0.05
			Options	Convenient Lambda Used
Ind	1	Identity(x)	DF	1

The ODS data set Bc contains the 95% confidence interval estimates produced by PROC TRANSREG. This ODS table is rather large, and you want to see only the relevant portion. The following statements generate the part of the table that is important and display [Output 55.2.5](#):

```
proc print noobs label data=bc(drop=rmse);
  title2 'Confidence Interval';
  where ci ne ' ' or abs(lambda - round(lambda, 0.5)) < 1e-6;
  label convenient = '00'x ci = '00'x;
run;
```

The estimated 90% confidence interval is [0.41, 0.51], which is very close to the reported Bayesian credible intervals. The resemblance of the intervals is probably due to the noninformative prior that you used in this analysis.

Output 55.2.5 Estimated Confidence Interval on λ

Box-Cox Transformation, with a Continuous Prior on Lambda				
Confidence Interval				
Dependent	Lambda	R-Square	Log Likelihood	
BoxCox(y)	-2.00	0.14	-1030.56	
BoxCox(y)	-1.50	0.17	-810.50	
BoxCox(y)	-1.00	0.22	-602.53	
BoxCox(y)	-0.50	0.39	-415.56	
BoxCox(y)	0.00	0.78	-257.92	
BoxCox(y)	0.41	0.95	-168.40	*
BoxCox(y)	0.42	0.95	-167.86	*
BoxCox(y)	0.43	0.95	-167.46	*
BoxCox(y)	0.44	0.95	-167.19	*
BoxCox(y)	0.45	0.95	-167.05	*
BoxCox(y)	0.46	0.95	-167.04	<
BoxCox(y)	0.47	0.95	-167.16	*
BoxCox(y)	0.48	0.95	-167.41	*
BoxCox(y)	0.49	0.95	-167.79	*
BoxCox(y)	0.50	+	-168.28	*
BoxCox(y)	0.51	0.95	-168.89	*
BoxCox(y)	1.00	0.89	-253.09	
BoxCox(y)	1.50	0.79	-345.35	
BoxCox(y)	2.00	0.70	-435.01	

Modeling $\lambda = 0$

With a continuous prior on λ , you can get only a continuous posterior distribution, and this makes the probability of $\Pr(\lambda = 0|\text{data})$ equal to 0 by definition. To consider $\lambda = 0$ as a viable solution to the Box-Cox transformation, you need to use a discrete prior that places some probability mass on the point 0 and allows for a meaningful posterior estimate of $\Pr(\lambda = 0|\text{data})$.

This example uses a simulation study where the data are generated from an exponential likelihood. The simulation implies that the correct transformation should be the logarithm and λ should be 0. Consider the

following exponential model:

$$y = \exp(x + \epsilon),$$

where $\epsilon \sim \text{normal}(0, 1)$. The transformed data can be fitted with a linear model:

$$\log(y) = x + \epsilon$$

The following statements generate a SAS data set with a gridded x and corresponding y:

```
title 'Box-Cox Transformation, Modeling Lambda = 0';
data boxcox;
  do x = 1 to 8 by 0.025;
    ly = x + normal(7);
    y = exp(ly);
    output;
  end;
run;
```

The log-likelihood function, after taking the Jacobian into consideration, is as follows:

$$\log p(y_i | \lambda, x_i) = \begin{cases} (\lambda - 1) \log(y_i) - \frac{1}{2} \left(\log \sigma^2 + \frac{((y_i^\lambda - 1)/\lambda - x_i)^2}{\sigma^2} \right) + C_1 & \text{if } \lambda \neq 0; \\ -\log(y_i) - \frac{1}{2} \left(\log \sigma^2 + \frac{(\log(y_i) - x_i)^2}{\sigma^2} \right) + C_2 & \text{if } \lambda = 0. \end{cases}$$

where C_1 and C_2 are two constants.

You can use the function [DGENERAL](#) to place a discrete prior on λ . The function is similar to the function [GENERAL](#), except that it indicates a discrete distribution. For example, you can specify a discrete uniform prior from -2 to 2 using

```
prior lda ~ dgeneral(1, lower=-2, upper=2);
```

This places equal probability mass on five points, -2 , -1 , 0 , 1 , and 2 . This prior might not work well here because the grid is too coarse. To consider smaller values of λ , you can sample a parameter that takes a wider range of integer values and transform it back to the λ space. For example, set α as your model parameter and give it a discrete uniform prior from -200 to 200 . Then define λ as $\alpha/100$ so λ can take values between -2 and 2 but on a finer grid.

The following statements fit a Box-Cox transformation by using a discrete prior on λ :

```
proc mcmc data=boxcox outpost=simout nmc=50000 thin=10 seed=12567
  monitor=(lda);

ods select PostSummaries PostIntervals;
parms s2 1 alpha 10;

beginnodata;
prior s2 ~ gamma(shape=3, scale=2);
if alpha=0 then lp = log(2);
  else lp = log(1);
prior alpha ~ dgeneral(lp, lower=-200, upper=200);
lda = alpha * 0.01;
sd = sqrt(s2);
endnodata;
```

```

if alpha=0 then
  ll = -ly+lpdfnorm(ly, x, sd);
else do;
  ys = (y**lda - 1)/lda;
  ll = (lda-1)*ly+lpdfnorm(ys, x, sd);
end;
model general(ll);
run;

```

There are two parameters, `s2` and `alpha`, in the model. They are placed in a single **PARMS** statement so that they are sampled in the same block.

The parameter `s2` takes a gamma distribution, and `alpha` takes a discrete prior. The IF-ELSE statements state that `alpha` takes twice as much prior density when it is 0 than otherwise. Note that on the original scale, $\Pr(\alpha = 0) = 2 \cdot \Pr(\alpha \neq 0)$. Translating that to the log scale, the densities become $\log(2)$ and $\log(1)$, respectively. The LDA assignment statement transforms `alpha` to the parameter of interest: `lda` takes values between -2 and 2 . You can model `lda` on an even smaller scale by dividing `alpha` by a larger constant. However, an increment of 0.01 in the Box-Cox transformation is usually sufficient. The SD assignment statement calculates the square root of the variance term.

The log-likelihood function uses another set of IF-ELSE statements, separating the case of $\lambda = 0$ from the others. The formulas are stated previously. The output of the program is shown in [Output 55.2.6](#).

Output 55.2.6 Box-Cox Transformation

Box-Cox Transformation, Modeling Lambda = 0						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
lda	5000	-0.00002	0.00201	0	0	0
Posterior Intervals						
Parameter	Alpha	Equal-Tail Interval		HPD Interval		
lda	0.050	0	0	0	0	0

From the summary statistics table, you see that the point estimate for λ is 0 and both of the 95% equal-tail and HPD credible intervals are 0. This strongly suggests that $\lambda = 0$ is the best estimate for this problem. In addition, you can also count the frequency of λ among posterior samples to get a more precise estimate on the posterior probability of λ being 0.

The following statements use PROC FREQ to produce [Output 55.2.7](#) and [Output 55.2.8](#):

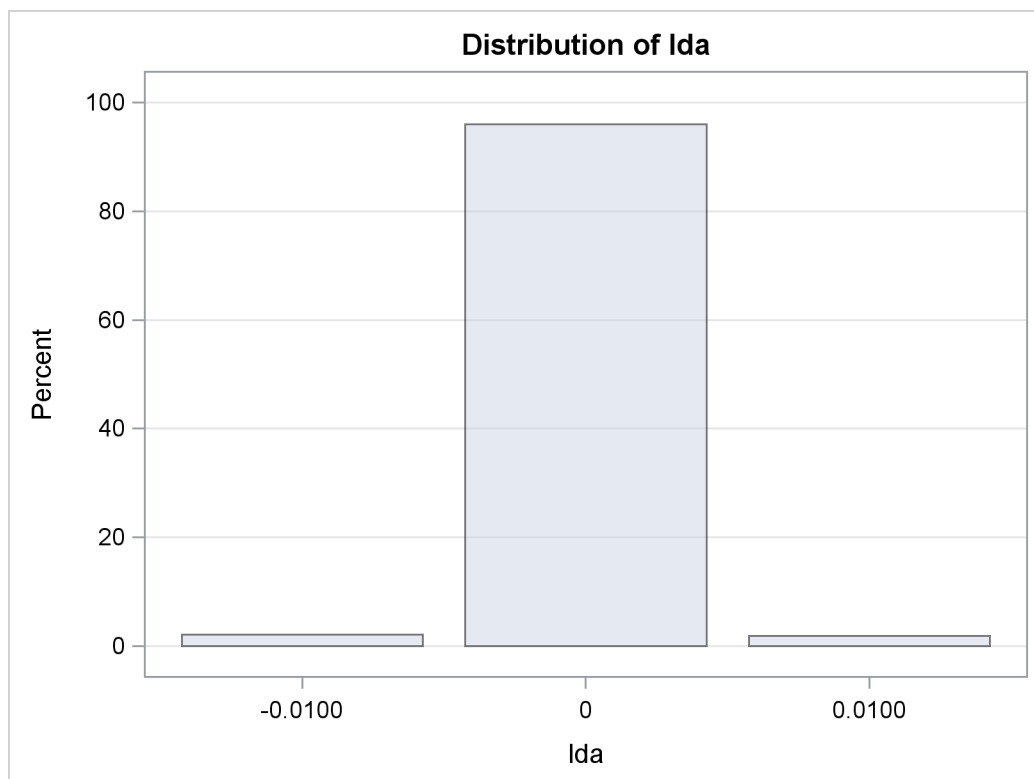
```
proc freq data=simout;
  ods select onewayfreqs freqplot;
  tables lda /nocum plot=freqplot(scale=percent);
run;
ods graphics off;
```

Output 55.2.7 shows the frequency count table. An estimate of $\Pr(\lambda = 0|\text{data})$ is 96%. The conclusion is that the log transformation should be the appropriate transformation used here, which agrees with the simulation setup. Output 55.2.8 shows the histogram of λ .

Output 55.2.7 Frequency Counts of λ

Box-Cox Transformation, Modeling Lambda = 0		
The FREQ Procedure		
lda	Frequency	Percent
-0.0100	106	2.12
0	4798	95.96
0.0100	96	1.92

Output 55.2.8 Histogram of λ



Example 55.3: Logistic Regression Model with a Diffuse Prior

This example illustrates how to fit a logistic regression model with a diffuse prior in PROC MCMC. You can also use the BAYES statement in PROC GENMOD. See Chapter 40, “[The GENMOD Procedure](#).”

The following statements create a SAS data set with measurements of the number of deaths, y , among n beetles that have been exposed to an environmental contaminant x :

```

title 'Logistic Regression Model with a Diffuse Prior';
data beetles;
    input n y x @@;
    datalines;
6 0 25.7 8 2 35.9 5 2 32.9 7 7 50.4 6 0 28.3
7 2 32.3 5 1 33.2 8 3 40.9 6 0 36.5 6 1 36.5
6 6 49.6 6 3 39.8 6 4 43.6 6 1 34.1 7 1 37.4
8 2 35.2 6 6 51.3 5 3 42.5 7 0 31.3 3 2 40.6
;

```

You can model the data points y_i with a binomial distribution,

$$y_i | p_i \sim \text{binomial}(n_i, p_i)$$

where p_i is the success probability and links to the regression covariate x_i through a logit transformation:

$$\text{logit}(p_i) = \log\left(\frac{p_i}{1 - p_i}\right) = \alpha + \beta x_i$$

The priors on α and β are both diffuse normal:

$$\begin{aligned} \alpha &\sim \text{normal}(0, \text{var} = 10000) \\ \beta &\sim \text{normal}(0, \text{var} = 10000) \end{aligned}$$

These statements fit a logistic regression with PROC MCMC:

```

ods graphics on;
proc mcmc data=beetles ntu=1000 nmc=20000 nthin=2 propcov=quanew
    diag=(mcse ess) outpost=beetleout seed=246810;
    ods select PostSummaries PostIntervals mcse ess TADpanel;
    parms (alpha beta) 0;
    prior alpha beta ~ normal(0, var = 10000);
    p = logistic(alpha + beta*x);
    model y ~ binomial(n,p);
run;

```

The key statement in the program is the assignment to p that calculates the probability of death. The SAS function LOGISTIC does the proper transformation. The **MODEL** statement specifies that the response variable, y , is binomially distributed with parameters n (from the input data set) and p . The summary statistics table, interval statistics table, the Monte Carlo standard error table, and the effective sample sizes table are shown in [Output 55.3.1](#).

Output 55.3.1 MCMC Results

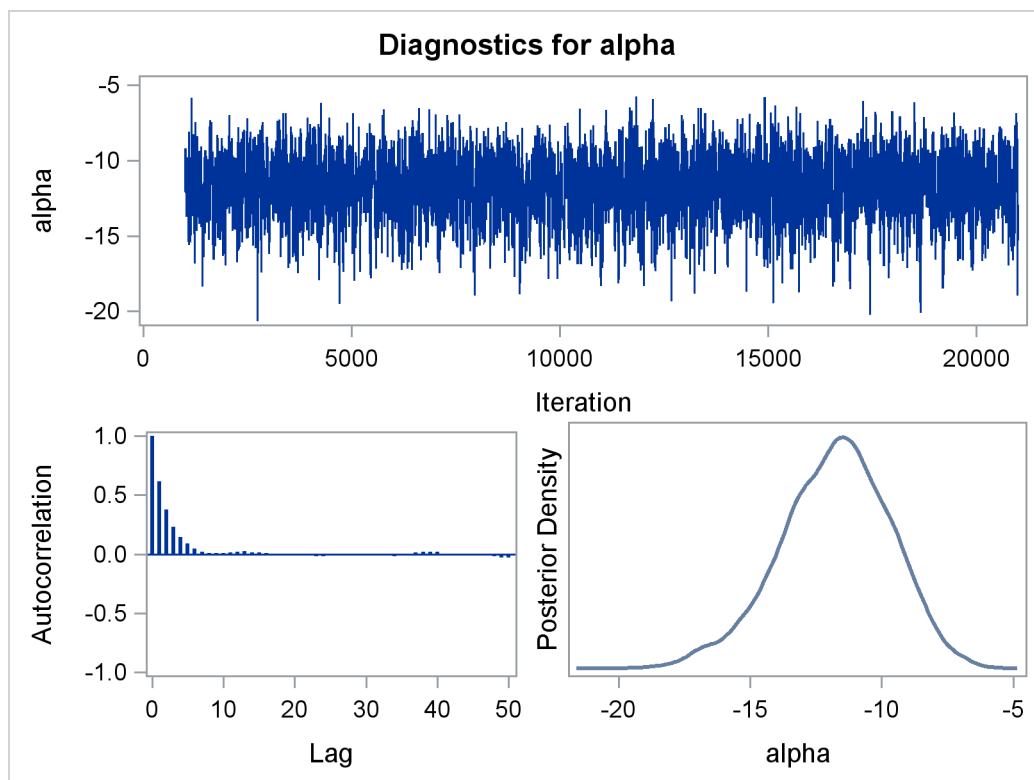
Logistic Regression Model with a Diffuse Prior						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	25%	Percentiles 50%	75%
alpha	10000	-11.7707	2.0997	-13.1243	-11.6683	-10.3003
beta	10000	0.2920	0.0542	0.2537	0.2889	0.3268
Posterior Intervals						
Parameter	Alpha	Equal-Tail Interval		HPD Interval		
alpha	0.050	-16.3332	-7.9675	-15.8822	-7.6673	
beta	0.050	0.1951	0.4087	0.1901	0.4027	
Logistic Regression Model with a Diffuse Prior						
The MCMC Procedure						
Monte Carlo Standard Errors						
Parameter	MCSE	Standard Deviation		MCSE/SD		
alpha	0.0422	2.0997		0.0201		
beta	0.00110	0.0542		0.0203		
Effective Sample Sizes						
Parameter	ESS	Autocorrelation Time		Efficiency		
alpha	2470.1	4.0484		0.2470		
beta	2435.4	4.1060		0.2435		

The summary statistics table shows that the sample mean of the output chain for the parameter alpha is -11.7707. This is an estimate of the mean of the marginal posterior distribution for the intercept parameter alpha. The estimated posterior standard deviation for alpha is 2.0997. The two 95% credible intervals for alpha are both negative, which indicates with very high probability that the intercept term is negative. On the other hand, you observe a positive effect on the regression coefficient beta. Exposure to the environment contaminant increases the probability of death.

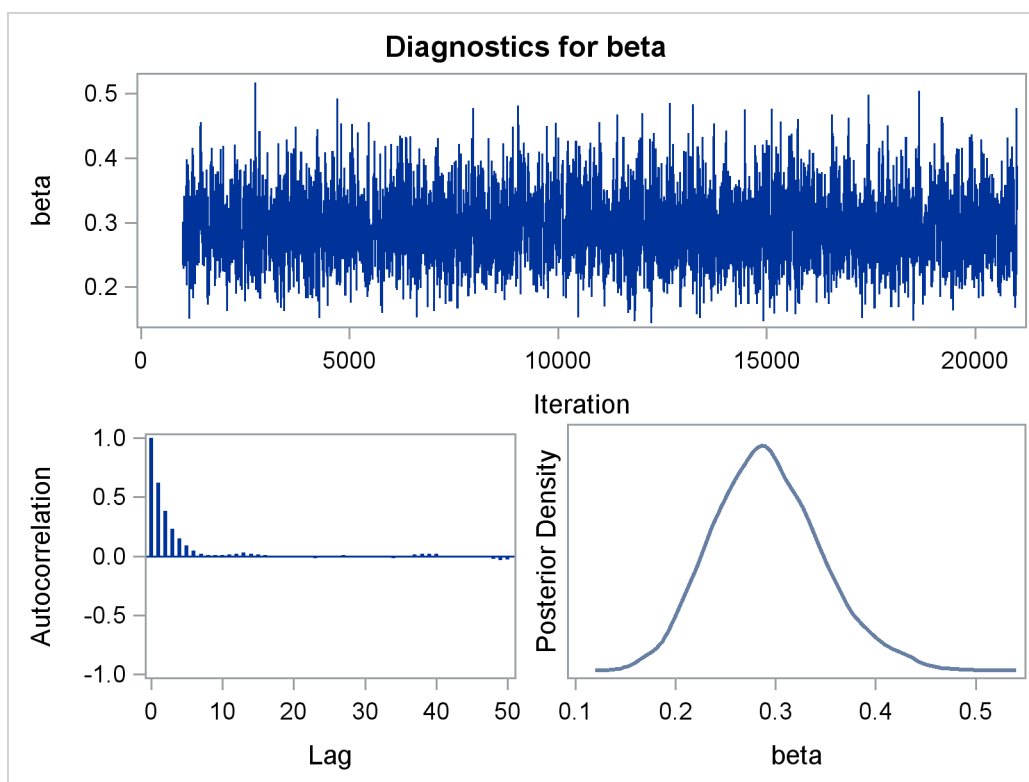
The Monte Carlo standard errors of each parameter are significantly small relative to the posterior standard deviations. A small MCSE/SD ratio indicates that the Markov chain has stabilized and the mean estimates do not vary much over time. Note that the precision in the parameter estimates increases with the square of the MCMC sample size, so if you want to double the precision, you must quadruple the MCMC sample size.

MCMC chains do not produce independent samples. Each sample point depends on the point before it. In this case, the correlation time estimate, read from the effective sample sizes table, is roughly 4. This means that it takes four observations from the MCMC output to make inferences about α with the same precision that you would get from using an independent sample. The effective sample size of 2470 reflects this loss of efficiency. The coefficient β has similar efficiency. You can often observe that some parameters have significantly better mixing (better efficiency) than others, even in a single Markov chain run.

Output 55.3.2 Plots for Parameters in the Logistic Regression Example



Output 55.3.2 continued



Trace plots and autocorrelation plots of the posterior samples are shown in [Output 55.3.2](#). Convergence looks good in both parameters; there is good mixing in the trace plot and quick drop-off in the ACF plot.

One advantage of Bayesian methods is the ability to directly answer scientific questions. In this example, you might want to find out the posterior probability that the environmental contaminant increases the probability of death—that is, $\Pr(\beta > 0|y)$. This can be estimated using the following steps:

```
proc format;
  value betafmt low=0 = 'beta <= 0' 0<-high = 'beta > 0';
run;

proc freq data=beetleout;
  tables beta /nocum;
  format beta betafmt.;
run;
```

Output 55.3.3 Frequency Counts

Logistic Regression Model with a Diffuse Prior		
The FREQ Procedure		
beta	Frequency	Percent

beta > 0	10000	100.00

All of the simulated values for β are greater than zero, so the sample estimate of the posterior probability that $\beta > 0$ is 100%. The evidence overwhelmingly supports the hypothesis that increased levels of the environmental contaminant increase the probability of death.

If you are interested in making inference based on any quantities that are transformations of the random variables, you can either do it directly in PROC MCMC or by using the DATA step after you run the simulation. Transformations sometimes can make parameter inference quite formidable using direct analytical methods, but with simulated chains, it is easy to compute chains for any set of parameters. Suppose you are interested in the lethal dose and want to estimate the level of the covariate x that corresponds to a probability of death, p . Abbreviate this quantity as ldp . In other words, you want to solve the logit transformation with a fixed value p . The lethal dose is as follows:

$$ldp = \frac{\log\left(\frac{p}{1-p}\right) - \alpha}{\beta}$$

You can obtain an estimate of any ldp by using the posterior mean estimates for α and β . For example, $lp95$, which corresponds to $p = 0.95$, is calculated as follows:

$$lp95 = \frac{\log\left(\frac{0.95}{1-0.95}\right) + 11.77}{0.29} = 50.79$$

where -11.77 and 0.29 are the posterior mean estimates of α and β , respectively, and 50.79 is the estimated lethal dose that leads to a 95% death rate.

While it is easy to obtain the point estimates, it is harder to estimate other posterior quantities, such as the standard deviation directly. However, with PROC MCMC, you can trivially get estimates of any posterior quantities of $lp95$. Consider the following program in PROC MCMC:

```
proc mcmc data=beetles ntu=1000 nmc=20000 nthin=2 propcov=quanew
    outpost=beetleout seed=246810 plot=density
    monitor=(pi30 ld05 ld50 ld95);
    ods select PostSummaries PostIntervals densitypanel;
    parms (alpha beta) 0;
    begincnst;
        c1 = log(0.05 / 0.95);
        c2 = -c1;
    endcnst;

    beginnodata;
    prior alpha beta ~ normal(0, var = 10000);
    pi30 = logistic(alpha + beta*30);
    ld05 = (c1 - alpha) / beta;
    ld50 = - alpha / beta;
    ld95 = (c2 - alpha) / beta;
    endnodata;
    pi = logistic(alpha + beta*x);
    model y ~ binomial(n,pi);
run;
ods graphics off;
```

The program estimates four additional posterior quantities. The three lpd quantities, ld05, ld50, and ld95, are the three levels of the covariate that kills 5%, 50%, and 95% of the population, respectively. The predicted probability when the covariate x takes the value of 30 is π_{30} . The **MONITOR=** option selects the quantities of interest. The **PLOTS=** option selects kernel density plots as the only ODS graphical output, excluding the trace plot and autocorrelation plot.

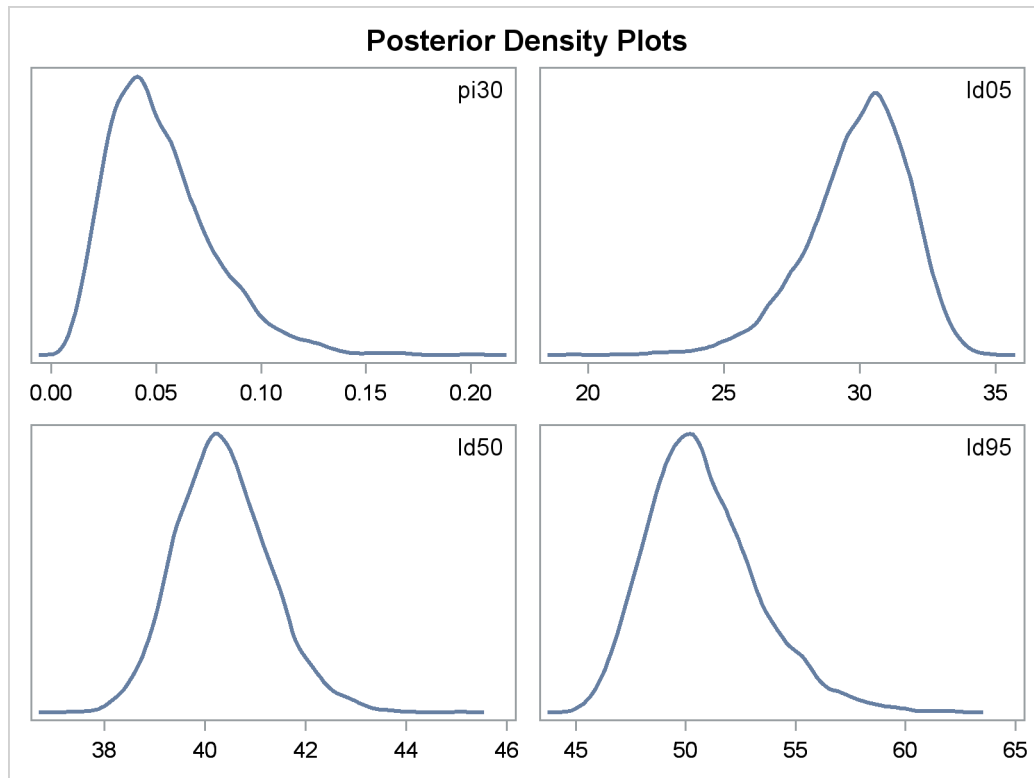
Programming statements between the **BEGINCNST** and **ENDCNST** statements define two constants. These statements are executed once at the beginning of the simulation. The programming statements between the **BEGINNODATA** and **ENDNODATA** statements evaluate the quantities of interest. The symbols, π_{30} , ld05, ld50, and ld95, are functions of the parameters alpha and beta only. Hence, they should not be processed at the observation level and should be included in the **BEGINNODATA** and **ENDNODATA** statements. [Output 55.3.4](#) lists the posterior summary and [Output 55.3.5](#) shows the density plots of these posterior quantities.

Output 55.3.4 PROC MCMC Results

Logistic Regression Model with a Diffuse Prior						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
π_{30}	10000	0.0524	0.0253	0.0340	0.0477	0.0662
ld05	10000	29.9281	1.8814	28.8430	30.1727	31.2563
ld50	10000	40.3745	0.9377	39.7271	40.3165	40.9612
ld95	10000	50.8210	2.5353	49.0372	50.5157	52.3100
Posterior Intervals						
Parameter	Alpha	Equal-Tail Interval		HPD Interval		
π_{30}	0.050	0.0161	0.1133	0.0109	0.1008	
ld05	0.050	25.6409	32.9660	26.2193	33.2774	
ld50	0.050	38.6706	42.3718	38.6194	42.2811	
ld95	0.050	46.7180	56.7667	46.3221	55.8774	

The posterior mean estimate of π_{95} is 50.82, which is close to the estimate of 50.79 by using the posterior mean estimates of the parameters. With PROC MCMC, in addition to the mean estimate, you can get the standard deviation, quantiles, and interval estimates at any level of significance.

From the density plots, you can see, for example, that the sample distribution for π_{30} is skewed to the right, and almost all of your posterior belief concerning π_{30} is concentrated in the region between zero and 0.15.

Output 55.3.5 Density Plots of Quantities of Interest in the Logistic Regression Example

It is easy to use the DATA step to calculate these quantities of interest. The following DATA step uses the simulated values of α and β to create simulated values from the posterior distributions of ld_{05} , ld_{50} , ld_{95} , and π_{30} :

```
data transout;
  set beetleout;
  pi30 = logistic(alpha + beta*30);
  ld05 = (log(0.05 / 0.95) - alpha) / beta;
  ld50 = (log(0.50 / 0.50) - alpha) / beta;
  ld95 = (log(0.95 / 0.05) - alpha) / beta;
run;
```

Subsequently, you can use SAS/INSIGHT, or the UNIVARIATE, CAPABILITY, or KDE procedures to analyze the posterior sample. If you want to regenerate the default ODS graphs from PROC MCMC, see “Regenerating Diagnostics Plots” on page 4505.

Example 55.4: Logistic Regression Model with Jeffreys' Prior

A controlled experiment was run to study the effect of the rate and volume of air inspired on a transient reflex vasoconstriction in the skin of the fingers. Thirty-nine tests under various combinations of rate and volume of air inspired were obtained (Finney 1947). The result of each test is whether or not vasoconstriction occurred. Pregibon (1981) uses this set of data to illustrate the diagnostic measures he proposes for detecting influential observations and to quantify their effects on various aspects of the maximum likelihood fit. The following statements create the data set Vaso:

```

title 'Logistic Regression Model with Jeffreys Prior';
data vaso;
  input vol rate resp @@;
  lvol = log(vol);
  lrate = log(rate);
  ind = _n_;
  cnst = 1;
  datalines;
3.7 0.825 1 3.5 1.09 1 1.25 2.5 1 0.75 1.5 1
0.8 3.2 1 0.7 3.5 1 0.6 0.75 0 1.1 1.7 0
0.9 0.75 0 0.9 0.45 0 0.8 0.57 0 0.55 2.75 0
0.6 3.0 0 1.4 2.33 1 0.75 3.75 1 2.3 1.64 1
3.2 1.6 1 0.85 1.415 1 1.7 1.06 0 1.8 1.8 1
0.4 2.0 0 0.95 1.36 0 1.35 1.35 0 1.5 1.36 0
1.6 1.78 1 0.6 1.5 0 1.8 1.5 1 0.95 1.9 0
1.9 0.95 1 1.6 0.4 0 2.7 0.75 1 2.35 0.03 0
1.1 1.83 0 1.1 2.2 1 1.2 2.0 1 0.8 3.33 1
0.95 1.9 0 0.75 1.9 0 1.3 1.625 1
;

```

The variable `resp` represents the outcome of a test. The variable `lvol` represents the log of the volume of air intake, and the variable `lrate` represents the log of the rate of air intake. You can model the data by using logistic regression. You can model the response with a binary likelihood:

$$\text{resp}_i \sim \text{binary}(p_i)$$

with

$$p_i = \frac{1}{1 + \exp(-(\beta_0 + \beta_1 \text{lvol}_i + \beta_2 \text{lrate}_i))}$$

Let $\mathbf{X}$ be the design matrix in the regression. Jeffreys' prior for this model is

$$p(\boldsymbol{\beta}) \propto |\mathbf{X}'\mathbf{M}\mathbf{X}|^{1/2}$$

where $\mathbf{M}$ is a 39 by 39 matrix with off-diagonal elements being 0 and diagonal elements being $p_i(1 - p_i)$. For details on Jeffreys' prior, see “[Jeffreys' Prior](#)” on page 129. You can use a number of matrix functions, such as the determinant function, in PROC MCMC to construct Jeffreys' prior. The following statements illustrate how to fit a logistic regression with Jeffreys' prior:

```

%let n = 39;
proc mcmc data=vaso nmc=10000 outpost=mcmcout seed=17;
  ods select PostSummaries PostIntervals;

  array beta[3] beta0 beta1 beta2;
  array m[&n, &n];
  array x[1] / nosymbols;
  array xt[3, &n];
  array xtm[3, &n];
  array xmx[3, 3];
  array p[&n];

  parms beta0 1 beta1 1 beta2 1;

```

```

begincnst;
  if (ind eq 1) then do;
    rc = read_array("vaso", x, "cnst", "lvol", "lrate");
    call transpose(x, xt);
    call zeromatrix(m);
  end;
endcnst;

beginnodata;
call mult(x, beta, p);           /* p = x * beta */
do i = 1 to &n;
  p[i] = 1 / (1 + exp(-p[i]));  /* p[i] = 1/(1+exp(-x*beta)) */
  m[i,i] = p[i] * (1-p[i]);
end;
call mult (xt, m, xtm);          /* xtm = xt * m */
call mult (xtm, x, xmx);         /* xmx = xtm * x */
call det (xmx, lp);              /* lp = det(xmx) */
lp = 0.5 * log(lp);              /* lp = -0.5 * log(lp) */
prior beta: ~ general(lp);
endnodata;

model resp ~ bern(p[ind]);
run;

```

The first **ARRAY** statement defines an array `beta` with three elements: `beta0`, `beta1`, and `beta2`. The subsequent statements define arrays that are used in the construction of Jeffreys' prior. These include `m` (the **M** matrix), `x` (the design matrix), `xt` (the transpose of `x`), and some additional work spaces.

The explanatory variables `lvol` and `lrate` are saved in the array `x` in the **BEGINCNST** and **ENDCNST** statements. See “**BEGINCNST/ENDCNST Statement**” on page 4441 for details. After all the variables are read into `x`, you transpose the `x` matrix and store it to `xt`. The **ZEROMATRIX** function call assigns all elements in matrix `m` the value zero. To avoid redundant calculation, it is best to perform these calculations as the last observation of the data set is processed—that is, when `ind` is 39.

You calculate Jeffreys' prior in the **BEGINNODATA** and **ENDNODATA** statements. The probability vector `p` is the product of the design matrix `x` and parameter vector `beta`. The diagonal elements in the matrix `m` are $p_i(1 - p_i)$. The expression `lp` is the logarithm of Jeffreys' prior. The **PRIOR** statement assigns `lp` as the prior for the β regression coefficients. The **MODEL** statement assigns a binary likelihood to `resp`, with probability `p[ind]`. The `p` array is calculated earlier using the matrix function **MULT**. You use the `ind` variable to pick out the right probability value for each `resp`.

Posterior summary statistics are displayed in [Output 55.4.1](#).

Output 55.4.1 PROC MCMC Results, Jeffreys' prior

Logistic Regression Model with Jeffreys Prior						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	25%	50%	75%
beta0	10000	-2.9587	1.3258	-3.8117	-2.7938	-2.0007
beta1	10000	5.2905	1.8193	3.9861	5.1155	6.4145
beta2	10000	4.6889	1.8189	3.3570	4.4914	5.8547
Posterior Intervals						
Parameter	Alpha	Equal-Tail Interval		HPD Interval		
beta0	0.050	-5.8247	-0.7435	-5.5936	-0.6027	
beta1	0.050	2.3001	9.3789	1.8590	8.7222	
beta2	0.050	1.6788	8.6643	1.3611	8.2490	

You can also use PROC GENMOD to fit the same model by using the following statements:

```
proc genmod data=vaso descending;
  ods select PostSummaries PostIntervals;
  model resp = lvol lrate / d=bin link=logit;
  bayes seed=17 coeffprior=jeffreys nmc=20000 thin=2;
run;
```

The MODEL statement indicates that resp is the response variable and lvol and lrate are the covariates. The options in the MODEL statement specify a binary likelihood and a logit link function. The BAYES statement requests Bayesian capability. The SEED=, NMC=, and THIN= arguments work in the same way as in PROC MCMC. The COEFFPRIOR=JEFFREYS option requests Jeffreys' prior in this analysis.

The PROC GENMOD statements produce [Output 55.4.2](#), with estimates very similar to those reported in [Output 55.4.1](#). Note that you should not expect to see identical output from PROC GENMOD and PROC MCMC, even with the simulation setup and identical random number seed. The two procedures use different sampling algorithms. PROC GENMOD uses the adaptive rejection metropolis algorithm (ARMS) (Gilks and Wild 1992; Gilks 2003) while PROC MCMC uses a random walk Metropolis algorithm. The asymptotic answers, which means that you let both procedures run an very long time, would be the same as they both generate samples from the same posterior distribution.

Output 55.4.2 PROC GENMOD Results

Logistic Regression Model with Jeffreys Prior						
The GENMOD Procedure						
Bayesian Analysis						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	25%	50%	75%
Intercept	10000	-2.8773	1.3213	-3.6821	-2.7326	-1.9097
lvol	10000	5.2059	1.8707	3.8535	4.9574	6.3337
lrate	10000	4.5525	1.8140	3.2281	4.3722	5.6643
Posterior Intervals						
Parameter	Alpha	Equal-Tail Interval		HPD Interval		
Intercept	0.050	-5.7447	-0.6877	-5.4593	-0.5488	
lvol	0.050	2.2066	9.4415	2.0729	9.2343	
lrate	0.050	1.5906	8.5272	1.3351	8.1152	

Example 55.5: Poisson Regression

You can use the Poisson distribution to model the distribution of cell counts in a multiway contingency table. Aitkin et al. (1989) have used this method to model insurance claims data. Suppose the following hypothetical insurance claims data are classified by two factors: age group (with two levels) and car type (with three levels). The following statements create the data set:

```

title 'Poisson Regression';
data insure;
  input n c car $ age;
  ln = log(n);
  datalines;
500  42  small  0
1200 37  medium 0
100   1  large  0
400 101  small  1
500  73  medium 1
300  14  large  1
;

proc transreg data=insure design;
  model class(car / zero=last);
  id n c age ln;
  output out=input_insure(drop=_: Int:);
run;

```

The variable *n* represents the number of insurance policy holders and the variable *c* represents the number of insurance claims. The variable *car* is the type of car involved (classified into three groups), and it is coded into two levels. The variable *age* is the age group of a policy holder (classified into two groups).

Assume that the number of claims *c* has a Poisson probability distribution and that its mean, μ_i , is related to the factors *car* and *age* for observation *i* by

$$\begin{aligned}\log(\mu_i) &= \log(n_i) + \mathbf{x}'\boldsymbol{\beta} \\ &= \log(n_i) + \beta_0 + \\ &\quad \text{car}_i(1)\beta_1 + \text{car}_i(2)\beta_2 + \text{car}_i(3)\beta_3 + \\ &\quad \text{age}_i(1)\beta_4 + \text{age}_i(2)\beta_5\end{aligned}$$

The indicator variables $\text{car}_i(j)$ is associated with the *j*th level of the variable *car* for observation *i* in the following way:

$$\text{car}_i(j) = \begin{cases} 1 & \text{if } \text{car} = j \\ 0 & \text{if } \text{car} \neq j \end{cases}$$

A similar coding applies to *age*. The $\boldsymbol{\beta}$'s are parameters. The logarithm of the variable *n* is used as an offset—that is, a regression variable with a constant coefficient of 1 for each observation. Having the offset constant in the model is equivalent to fitting an expanded data set with 3000 observations, each with response variable *y* observed on an individual level. The log link relates the mean and the factors *car* and *age*.

The following statements run PROC MCMC:

```
proc mcmc data=input_insure outpost=insureout nmc=5000 propcov=quanew
    maxtune=0 seed=7;
    ods select PostSummaries PostIntervals;
    array data[4] 1 &_trgind age;
    array beta[4] alpha beta_car1 beta_car2 beta_age;
    parms alpha beta;
    prior alpha beta: ~ normal(0, prec = 1e-6);
    call mult(data, beta, mu);
    model c ~ poisson(exp(mu+ln));
run;
```

The analysis uses a relatively flat prior on all the regression coefficients, with mean at 0 and precision at 10^{-6} . The option **MAXTUNE=0** skips the tuning phase because the optimization routine (**PROPCOV=QUANEW**) provides good initial values and proposal covariance matrix.

There are four parameters in the model: *alpha* is the intercept; *beta_car1* and *beta_car2* are coefficients for the class variable *car*, which has three levels; and *beta_age* is the coefficient for *age*. The symbol *mu* connects the regression model and the Poisson mean by using the log link. The **MODEL** statement specifies a Poisson likelihood for the response variable *c*.

Posterior summary and interval statistics are shown in [Output 55.5.1](#).

Output 55.5.1 MCMC Results

Poisson Regression						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	25%	50%	75%
alpha	5000	-2.6403	0.1344	-2.7261	-2.6387	-2.5531
beta_car1	5000	-1.8335	0.2917	-2.0243	-1.8179	-1.6302
beta_car2	5000	-0.6931	0.1255	-0.7775	-0.6867	-0.6118
beta_age	5000	1.3151	0.1386	1.2153	1.3146	1.4094
Posterior Intervals						
Parameter	Alpha	Equal-Tail Interval		HPD Interval		
alpha	0.050	-2.9201	-2.3837	-2.9133	-2.3831	
beta_car1	0.050	-2.4579	-1.3036	-2.4692	-1.3336	
beta_car2	0.050	-0.9462	-0.4497	-0.9485	-0.4589	
beta_age	0.050	1.0442	1.5898	1.0387	1.5812	

To fit the same model by using PROC GENMOD, you can do the following. Note that the default normal prior on the coefficients β is $N(0, \text{prec} = 1e - 6)$, the same as used in the PROC MCMC. The following statements run PROC GENMOD and create [Output 55.5.2](#):

```
proc genmod data=insure;
  ods select PostSummaries PostIntervals;
  class car age(descending);
  model c = car age / dist=poisson link=log offset=ln;
  bayes seed=17 nmc=5000 coeffprior=normal;
run;
```

To compare, posterior summary and interval statistics from PROC GENMOD are reported in [Output 55.5.2](#), and they are very similar to PROC MCMC results in [Output 55.5.1](#).

Output 55.5.2 PROC GENMOD Results

Poisson Regression						
The GENMOD Procedure						
Bayesian Analysis						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles 25%	50%	75%
Intercept	5000	-2.6424	0.1336	-2.7334	-2.6391	-2.5547
carlarge	5000	-1.8040	0.2764	-1.9859	-1.7929	-1.6101
carmedium	5000	-0.6908	0.1311	-0.7797	-0.6898	-0.6044
age1	5000	1.3207	0.1384	1.2264	1.3209	1.4140

Posterior Intervals					
Parameter	Alpha	Equal-Tail Interval		HPD Interval	
Intercept	0.050	-2.9154	-2.3893	-2.8997	-2.3850
carlarge	0.050	-2.3668	-1.2891	-2.2992	-1.2378
carmedium	0.050	-0.9437	-0.4231	-0.9434	-0.4230
age1	0.050	1.0455	1.5871	1.0266	1.5629

Note that the descending option in the CLASS statement reverses the sort order of the class variable `age` so that the results agree with PROC MCMC. If this option is not used, the estimate for `age` has a reversed sign as compared to [Output 55.5.2](#).

Example 55.6: Nonlinear Poisson Regression Models

This example illustrates how to fit a nonlinear Poisson regression with PROC MCMC. In addition, it shows how you can improve the mixing of the Markov chain by selecting a different proposal distribution or by sampling on the transformed scale of a parameter. This example shows how to analyze count data for calls to a technical support help line in the weeks immediately following a product release. This information could be used to decide upon the allocation of technical support resources for new products. You can model the number of daily calls as a Poisson random variable, with the average number of calls modeled as a nonlinear function of the number of weeks that have elapsed since the product's release. The data are input into a SAS data set as follows:

```

title 'Nonlinear Poisson Regression';
data calls;
  input weeks calls @@;
  datalines;
1   0   1   2   2   2   1   3   1   3   3
4   5   4   8   5   5   5   9   6  17   6   9
7  24   7  16   8  23   8  27
;

```

During the first several weeks after a new product is released, the number of questions that technical support receives concerning the product increases in a sigmoidal fashion. The expression for the mean value in the classic Poisson regression involves the log link. There is some theoretical justification for this link, but with MCMC methodologies, you are not constrained to exploring only models that are computationally convenient. The number of calls to technical support tapers off after the initial release, so in this example you can use a logistic-type function to model the mean number of calls received weekly for the time period immediately following the initial release. The mean function $\lambda(t)$ is modeled as follows:

$$\lambda_i = \frac{\gamma}{1 + \exp[-(\alpha + \beta t_i)]}$$

The likelihood for every observation calls_i is

$$\text{calls}_i \sim \text{Poisson}(\lambda_i)$$

Past experience with technical support data for similar products suggests the following prior distributions:

$$\begin{aligned}\gamma &\sim \text{gamma}(\text{shape} = 3.5, \text{scale} = 12) \\ \alpha &\sim \text{normal}(-5, \text{sd} = 0.5) \\ \beta &\sim \text{normal}(0.75, \text{sd} = 0.5)\end{aligned}$$

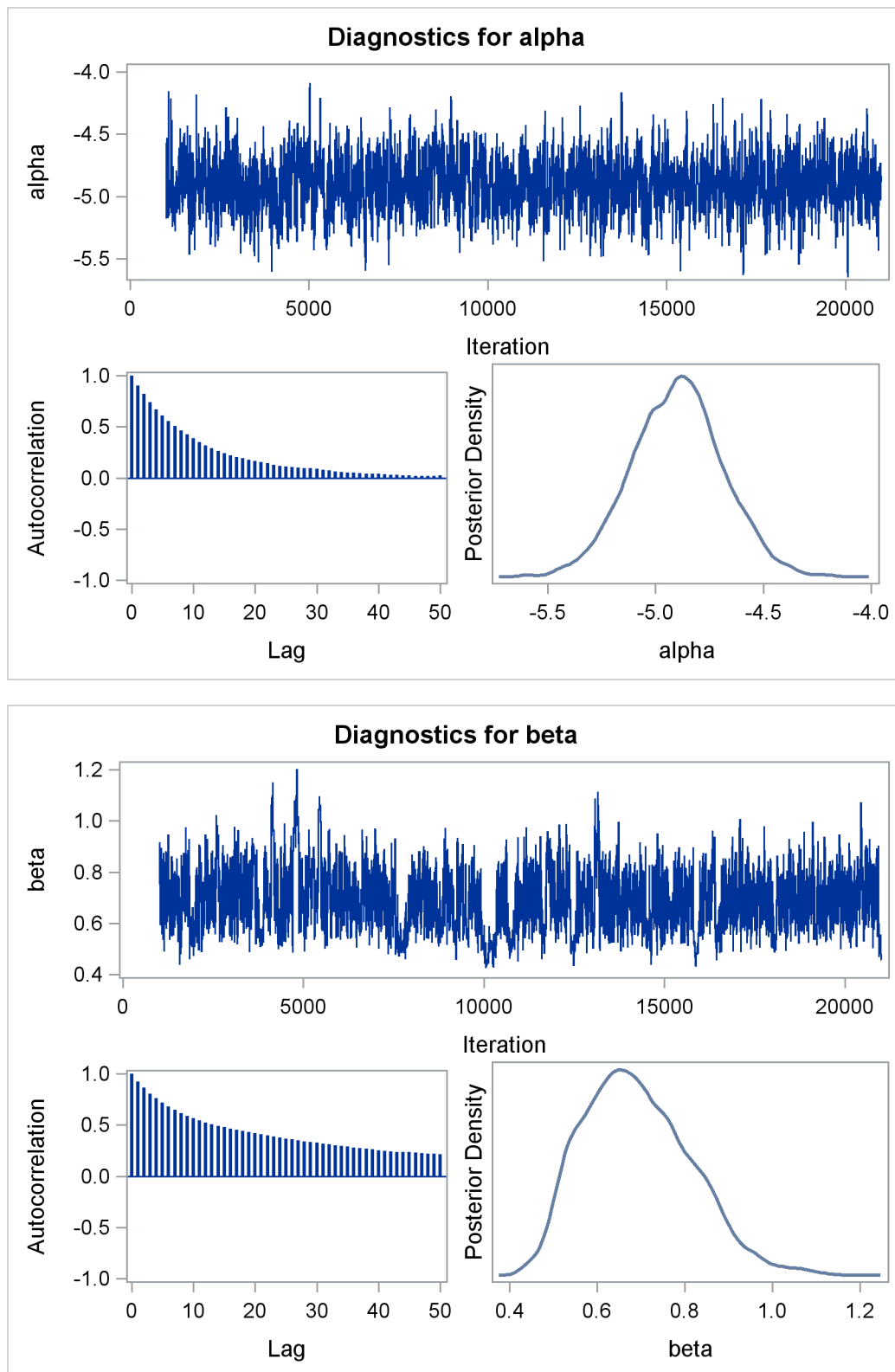
The following PROC MCMC statements fit this model:

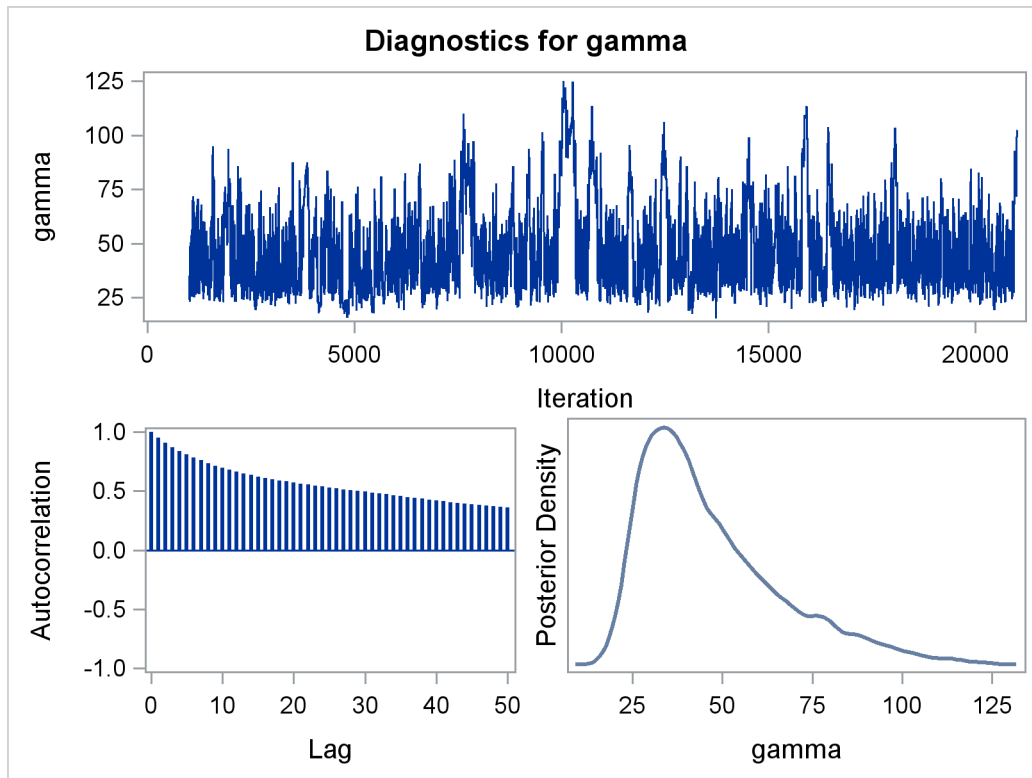
```
ods graphics on;
proc mcmc data=calls outpost=callout seed=53197 ntu=1000 nmc=20000
    propcov=quanew stats=none diag=ess;
    ods select TADpanel ess;
    parms alpha -4 beta 1 gamma 2;
    prior gamma ~ gamma(3.5, scale=12);
    prior alpha ~ normal(-5, sd=0.25);
    prior beta ~ normal(0.75, sd=0.5);
    lambda = gamma*logistic(alpha+beta*weeks);
    model calls ~ poisson(lambda);
run;
```

The one **PARMS** statement defines a block of all parameters and sets their initial values individually. The **PRIOR** statements specify the informative prior distributions for the three parameters. The assignment statement defines λ , the mean number of calls. Instead of using the SAS function LOGISTIC, you can use the following statement to calculate λ and get the same result:

```
lambda = gamma / (1 + exp(-(alpha+beta*weeks)));
```

Mixing is not particularly good with this run of PROC MCMC. The ODS SELECT statement displays the diagnostic graphs and effective sample sizes (ESS) calculation while excluding all other output. The graphical output is shown in [Output 55.6.1](#), and the ESS of each parameters are all relatively low ([Output 55.6.2](#)).

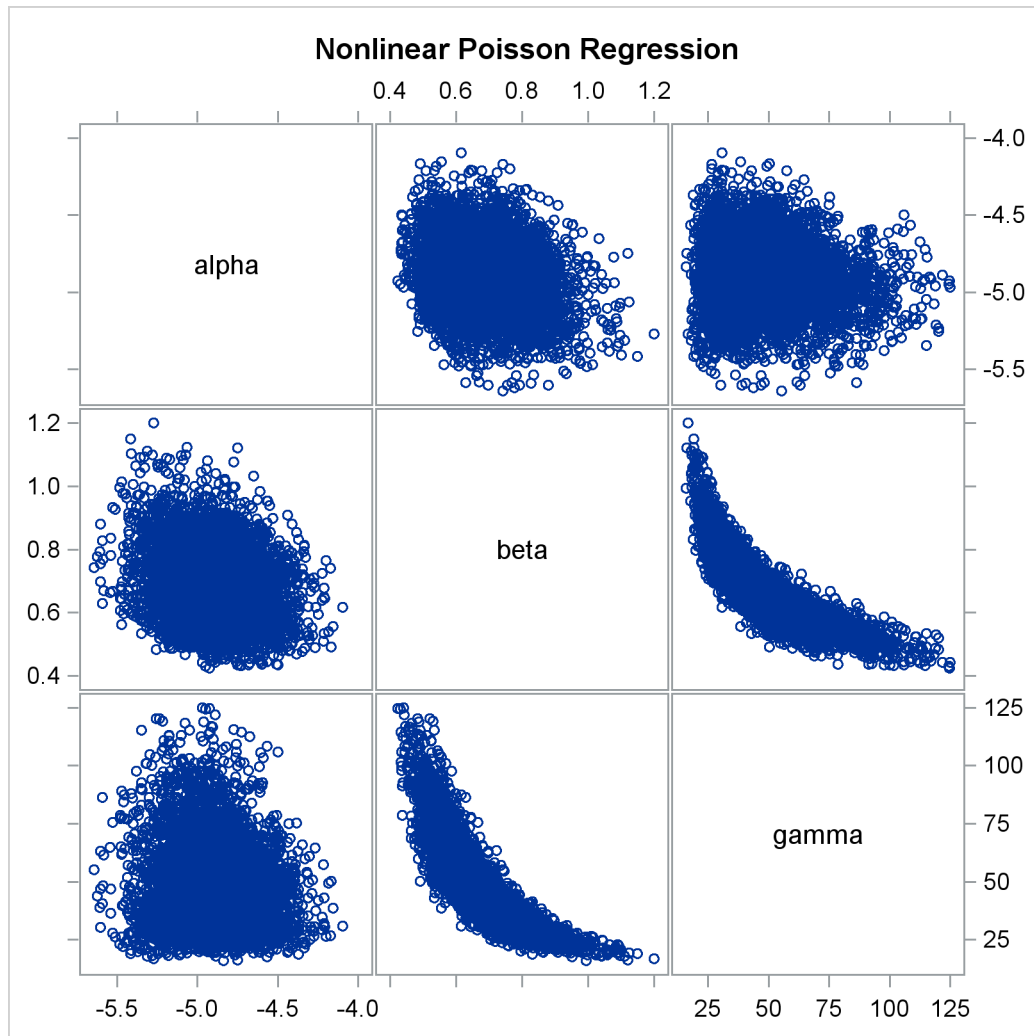
Output 55.6.1 Plots for Parameters

Output 55.6.1 continued**Output 55.6.2** Effective Sample Sizes

Nonlinear Poisson Regression			
The MCMC Procedure			
Effective Sample Sizes			
Parameter	ESS	Autocorrelation Time	Efficiency
alpha	897.4	22.2870	0.0449
beta	231.6	86.3540	0.0116
gamma	162.9	122.8	0.0081

Often a simple scatter plot of the posterior samples can reveal a potential cause of the bad mixing. You can use PROC SGSCATTER to generate pairwise scatter plots of the three model parameters. The following statements generate [Output 55.6.3](#):

```
proc sgscatter data=callout;
  matrix alpha beta gamma;
run;
```

Output 55.6.3 Pairwise Scatter Plots of the Parameters

The nonlinearity in parameters β and γ stands out immediately. This explains why a random walk Metropolis with normal proposal has a difficult time exploring the joint distribution efficiently—the algorithm works best when the target distribution is unimodal and symmetric (normal-like). When there is nonlinearity in the parameters, it is impossible to find a single proposal scale parameter that optimally adapts to different regions of the joint parameter space. As a result, the Markov chain can be inefficient in traversing some parts of the distribution. This is evident in examining the trace plot of the γ parameter. You see that the Markov chain sometimes gets stuck in the far-right tail and does not travel back to the high-density area quickly. This effect can be seen around the simulations 8,000 and 18,000 in [Output 55.6.1](#).

Reparameterization can often improve the mixing of the Markov chain. Note that the parameter γ has a positive support and that the posterior distribution is right-skewed. This suggests that the chain might mix more rapidly if you sample on the logarithm of the parameter γ .

Let $\delta = \log(\gamma)$, and reparameterize the mean function as follows:

$$\lambda_i = \frac{\exp(\delta)}{1 + \exp[-(\alpha + \beta t_i)]}$$

To obtain the same inference, you use an induced prior on δ based on the gamma prior on the gamma parameter. This involves a transformation of variables, and you can obtain the following equivalency, where $|\exp(\delta)|$ is the Jacobian:

$$\pi(\gamma) = \text{gamma}(\gamma; a, \text{scale} = b) = \frac{1}{b^a \Gamma(a)} \gamma^{a-1} \exp(-\gamma/b)$$

$$\Leftrightarrow \pi(\delta) = \text{gamma}(\gamma = \exp(\delta); a, \text{scale} = b) \cdot |\exp(\delta)|$$

The distribution on δ simplifies to the following:

$$\pi(\delta) = \frac{1}{b^a \Gamma(a)} \exp(a\delta) \exp(-\exp(\delta)/b)$$

PROC MCMC supports such a distribution on the logarithm transformation of a gamma random variable. It is called the [ExpGamma](#) distribution.

In the original model, you specify a prior on gamma:

```
prior gamma ~ gamma(3.5, scale=12);
```

You can obtain the same inference by specifying an [ExpGamma](#) prior on δ and take an exponential transformation to get back to gamma:

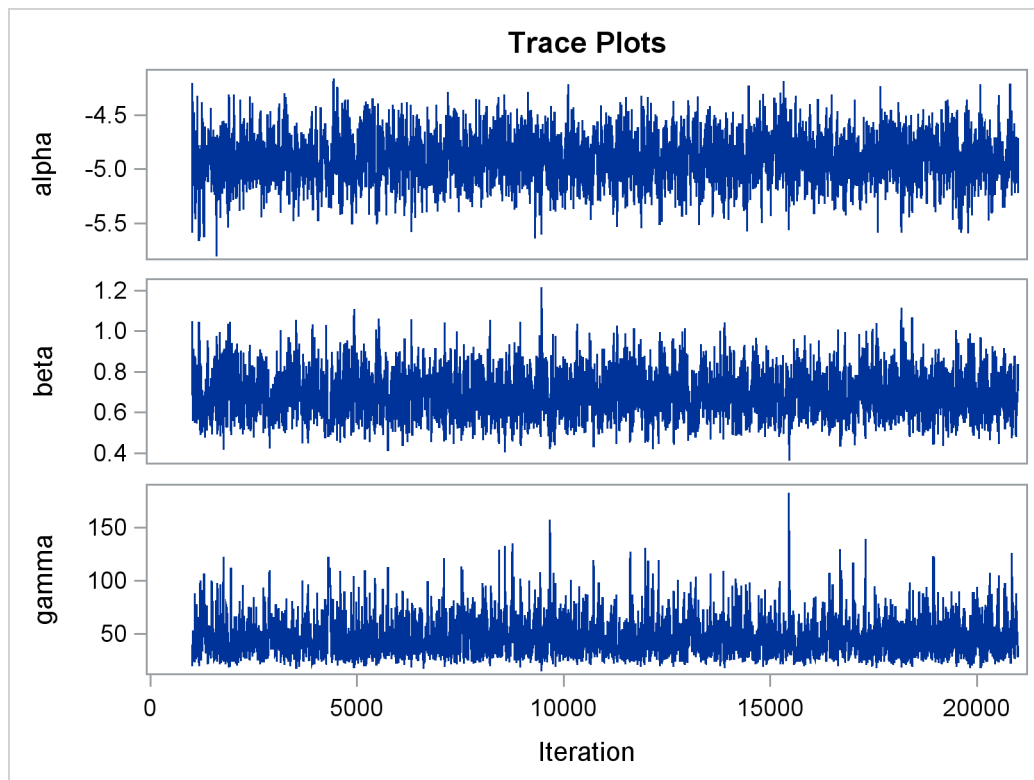
```
prior delta ~ egamma(3.5, scale=12);
gamma = exp(delta);
```

The following statements produce [Output 55.6.6](#) and [Output 55.6.4](#):

```
proc mcmc data=calls outpost=tcallout seed=53197 ntu=1000 nmc=20000
  propcov=quanew diag=ess plots=(trace) monitor=(alpha beta gamma);
  ods select PostSummaries PostIntervals ESS TRACEpanel;
  parms alpha -4 beta 1 delta 2;
  prior alpha ~ normal(-5, sd=0.25);
  prior beta ~ normal(0.75, sd=0.5);
  prior delta ~ egamma(3.5, scale=12);
  gamma = exp(delta);
  lambda = gamma*logistic(alpha+beta*weeks);
  model calls ~ poisson(lambda);
run;
```

The [PARMS](#) statement declares δ , instead of gamma, as a model parameter. The prior distribution of δ is [egamma](#), as opposed to the [gamma](#) distribution. The [GAMMA](#) assignment statement transforms δ to gamma. The [LAMBDA](#) assignment statement calculates the mean for the Poisson by using the gamma parameter. The [MODEL](#) statement specifies a Poisson likelihood for the calls response.

The trace plots in [Output 55.6.4](#) show better mixing of the parameters, and the effective sample sizes in [Output 55.6.5](#) show substantial improvements over the original formulation of the model. The improvements are especially obvious in beta and gamma, where the increase is fivefold to tenfold.

Output 55.6.4 Plots for Parameters, Sampling on the Log Scale of Gamma**Output 55.6.5** Effective Sample Sizes, Sampling on the Log Scale of Gamma

Nonlinear Poisson Regression			
The MCMC Procedure			
Effective Sample Sizes			
Parameter	ESS	Autocorrelation Time	Efficiency
alpha	1338.4	14.9430	0.0669
beta	1254.9	15.9379	0.0627
gamma	1073.4	18.6320	0.0537

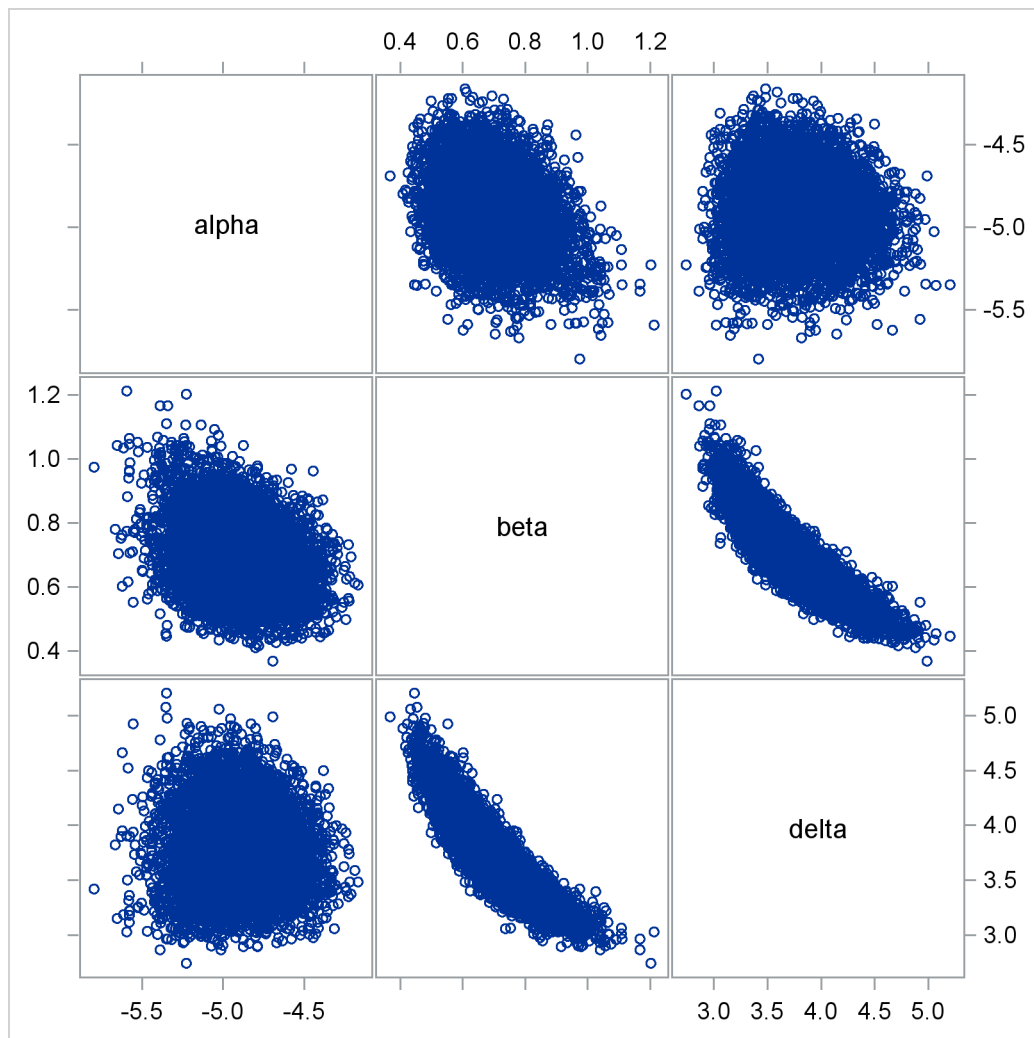
Output 55.6.6 shows the posterior summary and interval statistics of the nonlinear Poisson regression.

Output 55.6.6 MCMC Results, Sampling on the Log Scale of Gamma

Nonlinear Poisson Regression						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles 25%	50%	75%
alpha	20000	-4.9040	0.2234	-5.0555	-4.9055	-4.7530
beta	20000	0.6899	0.1154	0.6055	0.6787	0.7662
gamma	20000	46.7199	19.4977	32.3528	41.9888	55.4315
Posterior Intervals						
Parameter	Alpha	Equal-Tail Interval		HPD Interval		
alpha	0.050	-5.3392	-4.4659	-5.3217	-4.4544	
beta	0.050	0.4919	0.9327	0.4841	0.9169	
gamma	0.050	23.2996	96.7209	19.6588	86.2425	

Note that the delta parameter has a more symmetric density than the skewed gamma parameter. A pairwise scatter plot (Output 55.6.7) shows a more linear relationship between beta and delta. The Metropolis algorithm always works better if the target distribution is approximately normal.

```
proc sgscatter data=tcallout;
  matrix alpha beta delta;
run;
```

Output 55.6.7 Pairwise Scatter Plots of the Transformed Parameters

If you are still unsatisfied with the slight nonlinearity in the parameters β and δ , you can try another transformation on β . Normally you would not want to do a logarithm transformation on a parameter that has support on the real axis, because you would risk taking the logarithm of negative values. However, because all the β samples are positive and the marginal posterior distribution is away from 0, you can try a such a transformation.

Let $\kappa = \log(\beta)$. The prior distribution on κ is the following:

$$\pi(\kappa) = \text{normal}(\beta = \exp(\kappa); \mu, \sigma^2) \cdot |\exp(\kappa)|$$

You can specify the prior distribution in PROC MCMC by using a **GENERAL** function:

```
parms kappa;
lprior = logpdf("normal", exp(kappa), 0.75, 0.5) + kappa;
prior kappa ~ general(lp);
beta = exp(kappa);
```

The **PARMS** statement declares the transformed parameter kappa, which will be sampled. The **LPRIOR** assignment statement defines the logarithm of the prior distribution on kappa. The **LOGPDF** function is used here to simplify the specification of the distribution. The **PRIOR** statement specifies the nonstandard distribution as the prior on kappa. Finally, the **BETA** assignment statement transforms kappa back to the beta parameter.

Applying logarithm transformations on both beta and gamma yields the best mixing. (The results are not shown here, but you can find the code in the file *mcmcex6.sas* in the SAS Sample Library.) The transformed parameters kappa and delta have much clearer linear correlation. However, the improvement over the case where gamma alone is transformed is only marginally significant (50% increase in ESS).

This example illustrates that PROC MCMC can fit Bayesian nonlinear models just as easily as Bayesian linear models. More importantly, transformations can sometimes improve the efficiency of the Markov chain, and that is something to always keep in mind. Also see “[Example 55.20: Using a Transformation to Improve Mixing](#)” on page 4654 for another example of how transformations can improve mixing of the Markov chains.

Example 55.7: Logistic Regression Random-Effects Model

This example illustrates how you can use PROC MCMC to fit random-effects models. In the example “[Random-Effects Model](#)” on page 4419 in “[Getting Started: MCMC Procedure](#)” on page 4408, you already saw PROC MCMC fit a linear random-effects model. This example shows how to fit a logistic random-effects model in PROC MCMC. Although you can use PROC MCMC to analyze random-effects models, you might want to first consider some other SAS procedures. For example, you can use PROC MIXED (see Chapter 59, “[The MIXED Procedure](#)”) to analyze linear mixed effects models, PROC NL MIXED (see Chapter 64, “[The NL MIXED Procedure](#)”) for nonlinear mixed effects models, and PROC GLIMMIX (see Chapter 41, “[The GLIMMIX Procedure](#)”) for generalized linear mixed effects models. In addition, a sampling-based Bayesian analysis is available in the MIXED procedure through the **PRIOR** statement (see “[PRIOR Statement](#)” on page 4935).

The data are taken from Crowder (1978). The *Seeds* data set is a 2×2 factorial layout, with two types of seeds, *O. aegyptiaca* 75 and *O. aegyptiaca* 73, and two root extracts, *bean* and *cucumber*. You observe *r*, which is the number of germinated seeds, and *n*, which is the total number of seeds. The independent variables are seed and extract.

The following statements create the data set:

```

title 'Logistic Regression Random-Effects Model';
data seeds;
    input r n seed extract @@;
    ind = _N_;
    datalines;
10 39 0 0    23 62 0 0    23 81 0 0    26 51 0 0
17 39 0 0    5  6 0 1    53 74 0 1    55 72 0 1
32 51 0 1    46 79 0 1    10 13 0 1    8  16 1 0
10 30 1 0    8  28 1 0    23 45 1 0    0  4  1 0
3  12 1 1    22 41 1 1    15 30 1 1    32 51 1 1
3  7  1 1
;

```

You can model each observation r_i as having its own probability of success p_i , and the likelihood is as follows:

$$r_i \sim \text{binomial}(n_i, p_i)$$

You can use the logit link function to link the covariates of each observation, `seed` and `extract`, to the probability of success,

$$\begin{aligned}\mu_i &= \beta_0 + \beta_1 \cdot \text{seed}_i + \beta_2 \cdot \text{extract}_i + \beta_3 \cdot \text{seed}_i \cdot \text{extract}_i \\ p_i &= \text{logistic}(\mu_i + \delta_i)\end{aligned}$$

where δ_i is assumed to be an iid random effect with a normal prior:

$$\delta_i \sim \text{normal}(0, \text{var} = \sigma^2)$$

The four β regression coefficients and the standard deviation σ^2 in the random effects are model parameters; they are given noninformative priors as follows:

$$\begin{aligned}\pi(\beta_0, \beta_1, \beta_2, \beta_3) &\propto 1 \\ \sigma^2 &\sim \text{igamma}(\text{shape} = 0.01, \text{scale} = 0.01)\end{aligned}$$

Another way of expressing the same model is as

$$p_i = \text{logistic}(\delta_i)$$

where

$$\delta_i \sim \text{normal}(\beta_0 + \beta_1 \cdot \text{seed}_i + \beta_2 \cdot \text{extract}_i + \beta_3 \cdot \text{seed}_i \cdot \text{extract}_i, \sigma^2)$$

The two models are equivalent. In the first model, the random effects δ_i centers at 0 in the normal distribution, and in the second model, δ_i centers at the regression mean. This hierarchical centering can sometimes improve mixing.

The following statements fit the second model and generate [Output 55.7.1](#):

```
proc mcmc data=seeds outpost=postout seed=332786 nmc=20000;
  ods select PostSummaries PostIntervals;
  parms beta0 0 beta1 0 beta2 0 beta3 0 s2 1;
  prior s2 ~ igamma(0.01, s=0.01);
  prior beta: ~ general(0);
  w = beta0 + beta1*seed + beta2*extract + beta3*seed*extract;
  random delta ~ normal(w, var=s2) subject=ind;
  pi = logistic(delta);
  model r ~ binomial(n = n, p = pi);
run;
```

The PROC MCMC statement specifies the input and output data sets, sets a seed for the random number generator, and requests a large simulation size. The ODS SELECT statement displays the summary statistics and interval statistics tables. The [PARMS](#) statement declares the model parameters, and the [PRIOR](#) statements specify the prior distributions for β and σ^2 .

The symbol w calculates the regression mean, and the **RANDOM** statement specifies the random effect, with a normal prior distribution, centered at w with variance σ^2 . Note that the variable w is a function of the input data set variables. You can use data set variable in constructing the hyperparameters of the random-effects parameters, as long as the hyperparameters remain constant within each subject group. The **SUBJECT=** option indicates the group index for the random-effects parameters.

The symbol π is the logit transformation. The **MODEL** specifies the response variable r as a binomial distribution with parameters n and π .

Output 55.7.1 lists the posterior mean and interval estimates of the regression parameters.

Output 55.7.1 Logistic Regression Random-Effects Model

Logistic Regression Random-Effects Model						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
beta0	20000	-0.5570	0.1929	-0.6842	-0.5535	-0.4368
beta1	20000	0.0776	0.3276	-0.1185	0.0745	0.2765
beta2	20000	1.3667	0.2923	1.1759	1.3453	1.5577
beta3	20000	-0.8469	0.4718	-1.1487	-0.8280	-0.5364
s2	20000	0.1171	0.0993	0.0497	0.0921	0.1546
Posterior Intervals						
Parameter	Alpha	Equal-Tail Interval		HPD Interval		
beta0	0.050	-0.9379	-0.1753	-0.9422	-0.1816	
beta1	0.050	-0.6183	0.7186	-0.5690	0.7499	
beta2	0.050	0.8326	1.9642	0.8463	1.9724	
beta3	0.050	-1.8074	0.0604	-1.7741	0.0742	
s2	0.050	0.0103	0.3749	0.00163	0.3045	

Example 55.8: Nonlinear Poisson Regression Multilevel Random-Effects Model

This example uses the pump failure data of Gaver and O'Muircheartaigh (1987) to illustrate how to fit a multilevel random-effects model with PROC MCMC. The number of failures and the time of operation are recorded for 10 pumps. Each of the pumps is classified into one of two groups that correspond to either continuous or intermittent operation. The following statements generate the data set:

```

title 'Nonlinear Poisson Regression Random-Effects Model';
data pump;
  input y t group @@;
  pump = _n_;
  logtstd = log(t) - 2.4564900;
  datalines;
5   94.320 1    1   15.720 2    5   62.880 1
14  125.760 1    3    5.240 2   19   31.440 1
1    1.048 2    1    1.048 2    4    2.096 2
22   10.480 2
;

```

Each row denotes data for a single pump, and the variable `logtstd` contains the centered operation times. Letting y_{ij} denote the number of failures for the j th pump in the i th group, Draper (1996) considers the following hierarchical model for these data, where the data set variable `logtstd` is $\log t_{ij} - \overline{\log t}$:

$$\begin{aligned}
 y_{ij} | \lambda_{ij} &\sim \text{Poisson}(\lambda_{ij}) \\
 \log \lambda_{ij} &= \alpha_i + \beta_i (\log t_{ij} - \overline{\log t}) + e_{ij}
 \end{aligned}$$

This model specifies different intercepts and slopes for each group ($i = 1, 2$), and the random effect e_{ij} is a mechanism for accounting for overdispersion. You can use noninformative priors on the parameters α_i , β_i , and σ^2 , and a normal prior on e_{ij} ,

$$\begin{aligned}
 u_i &= \begin{pmatrix} \alpha_i \\ \beta_i \end{pmatrix} \sim \text{mvn} \left(\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} 1e6 & 0 \\ 0 & 1e6 \end{pmatrix} \right) \text{ for } i = 1, 2 \\
 \sigma^2 &\sim \text{igamma}(\text{shape} = 0.01, \text{scale} = 0.01) \\
 e_{ij} | \sigma^2 &\sim \text{normal}(0, \sigma^2)
 \end{aligned}$$

where u_i is a multidimensional random effect. The following statements fit such a random-effects model:

```

ods graphics on;
proc mcmc data=pump outpost=postout seed=248601 nmc=10000
  plots=trace stats=none diag=none;
  ods select tracepanel;
  array u[2] alpha beta;
  array mu[2] (0 0);
  parms s2;
  prior s2 ~ igamma(0.01, scale=0.01);
  random u ~ mvn(mu, sd=1e6, rho=0) subject=group monitor=(u);
  random e ~ normal(0, var=s2) subject=pump monitor=(random(1));
  w = alpha + beta * logtstd;
  lambda = exp(w+e);
  model y ~ poisson(lambda);
run;

```

The PROC MCMC statement specifies the input data set (Pump), the output data set (Postout), a seed for the random number generator, and a simulation sample size of 10,000. The program requests that only trace plots be produced, disabling all posterior calculations and convergence diagnostics tests. The ODS SELECT statement displays the trace plots, which are the primary focus.

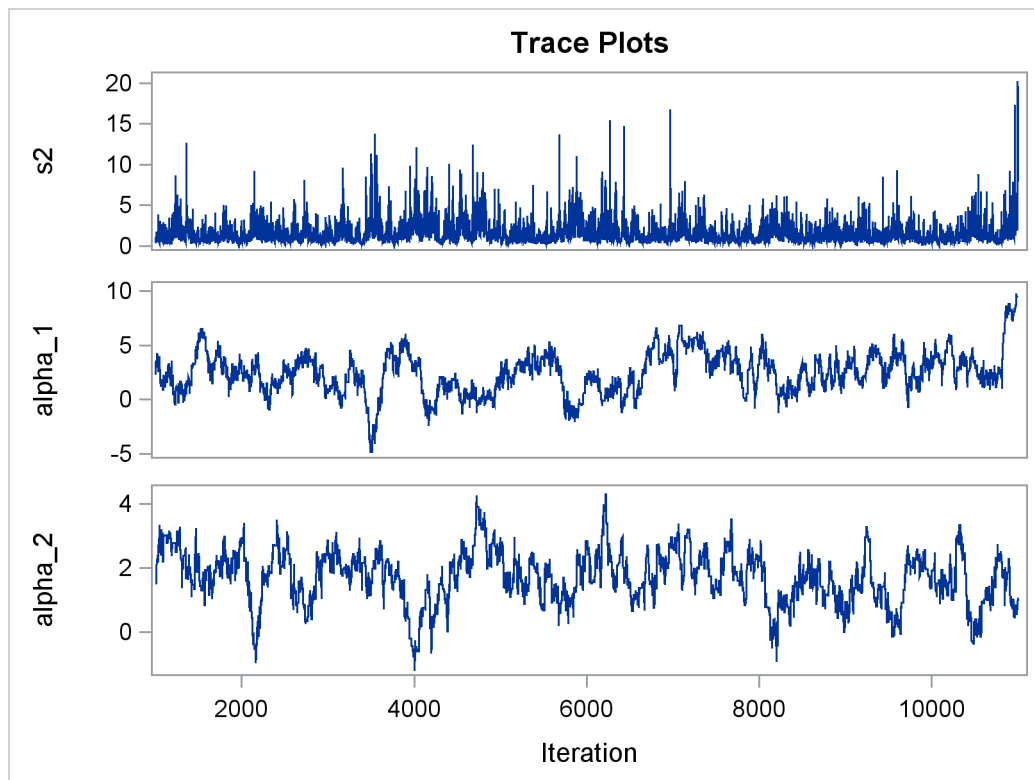
The first **ARRAY** statement declares an array `u` of size 2 and names the elements `alpha` and `beta`. The array `u` stores the random-effects parameters `alpha` and `beta`. The next **ARRAY** statement defines the mean of the multivariate normal prior on `u`.

The **PARMS** statement declares the only model parameter here, the variance `s2` in the prior distribution for the random effect e_{ij} . The **PRIOR** statement specifies an inverse-gamma prior on the variance. The first **RANDOM** statement specifies a multivariate normal prior on `u`. The `mvn` distribution is a multivariate normal distribution with a first-order autoregressive covariance. When the argument `rho` is set to 0, this distribution simplifies to a multivariate normal distribution with a shared variance. The **RANDOM** statement also indicates the group variable as its subject index and monitors all elements `u`. The second **RANDOM** statement specifies a normal prior on the effect `e`, where the subject index variable is `pump`. The **MONITOR=** option requests that PROC MCMC randomly choose one of the 10 `e` random-effects parameters to monitor.

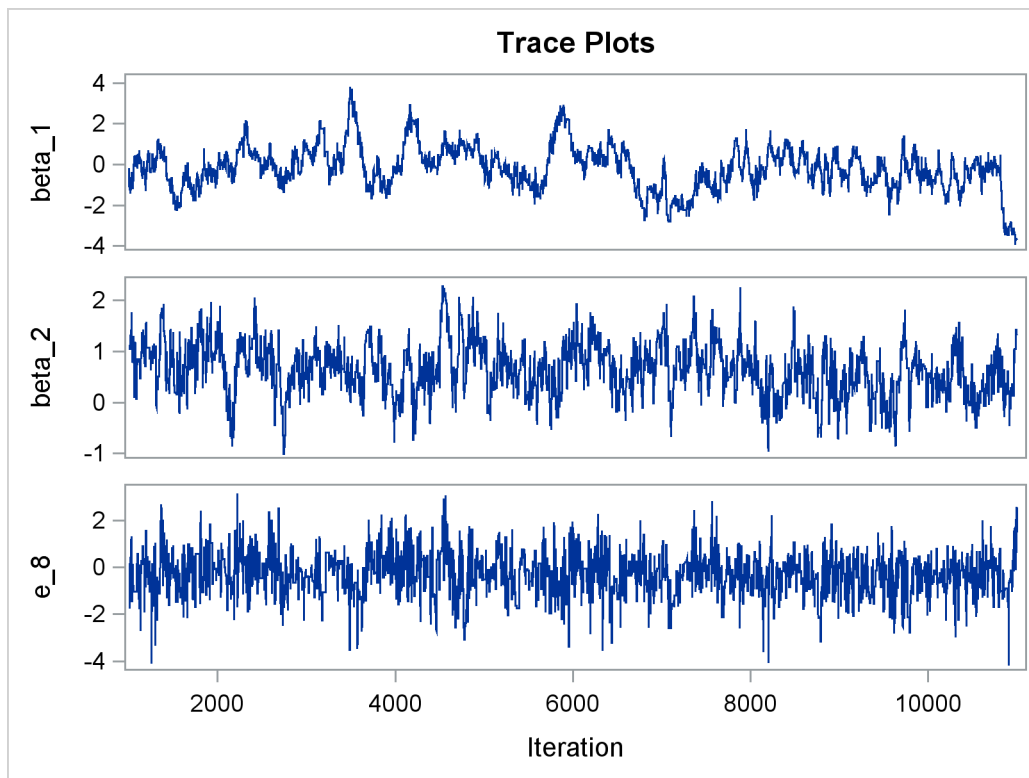
Next, programming statements construct the mean of the Poisson likelihood, and the **MODEL** statement specifies the likelihood function for each observation.

Output 55.8.1 shows trace plots for σ^2 , α_1 , α_2 , β_1 , β_2 , and e_8 . You can see that the chains are mixing poorly.

Output 55.8.1 Trace Plots of σ^2 , α , β , and e_8 without Hierarchical Centering



Output 55.8.1 continued



To improve mixing, you can repeat the same analysis by using a hierarchical centering technique, where instead of using a normal prior centered at 0 on e_{ij} , you center the random effects on the group means:

$$y_{ij} | \lambda_{ij} \sim \text{Poisson}(\lambda_{ij})$$

$$\log \lambda_{ij} \sim \text{normal}(\alpha_i + \beta_i (\log t_{ij} - \overline{\log t}), \text{var} = \sigma^2)$$

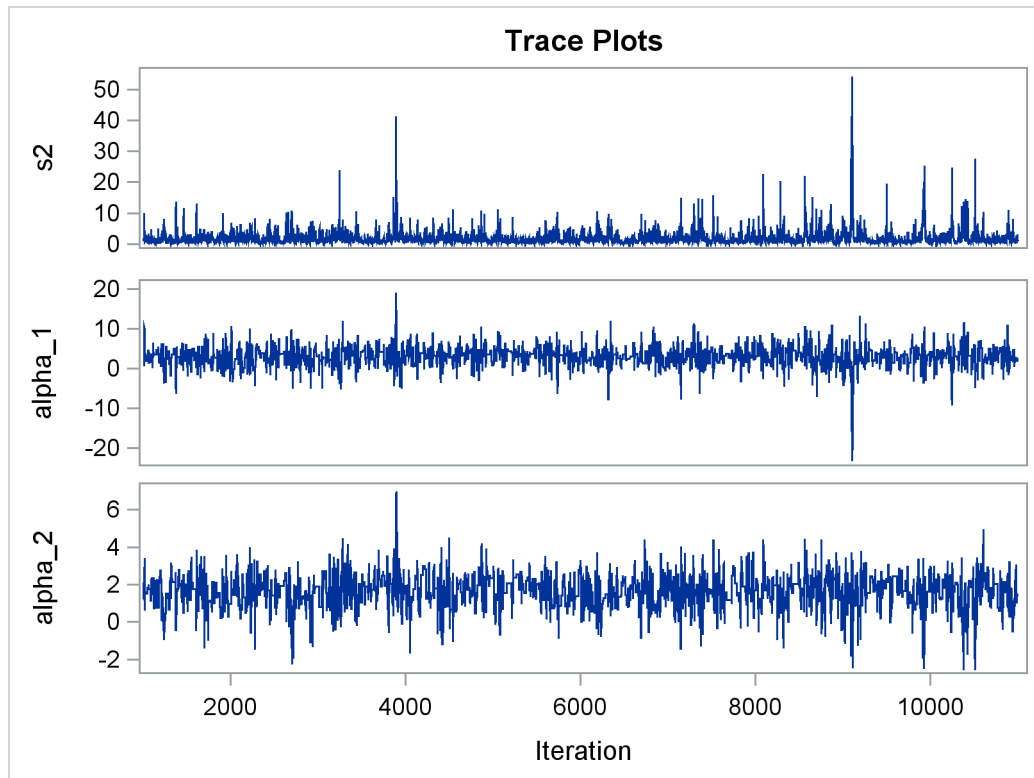
The following statements illustrate how to fit a multilevel hierarchical centering random-effects model:

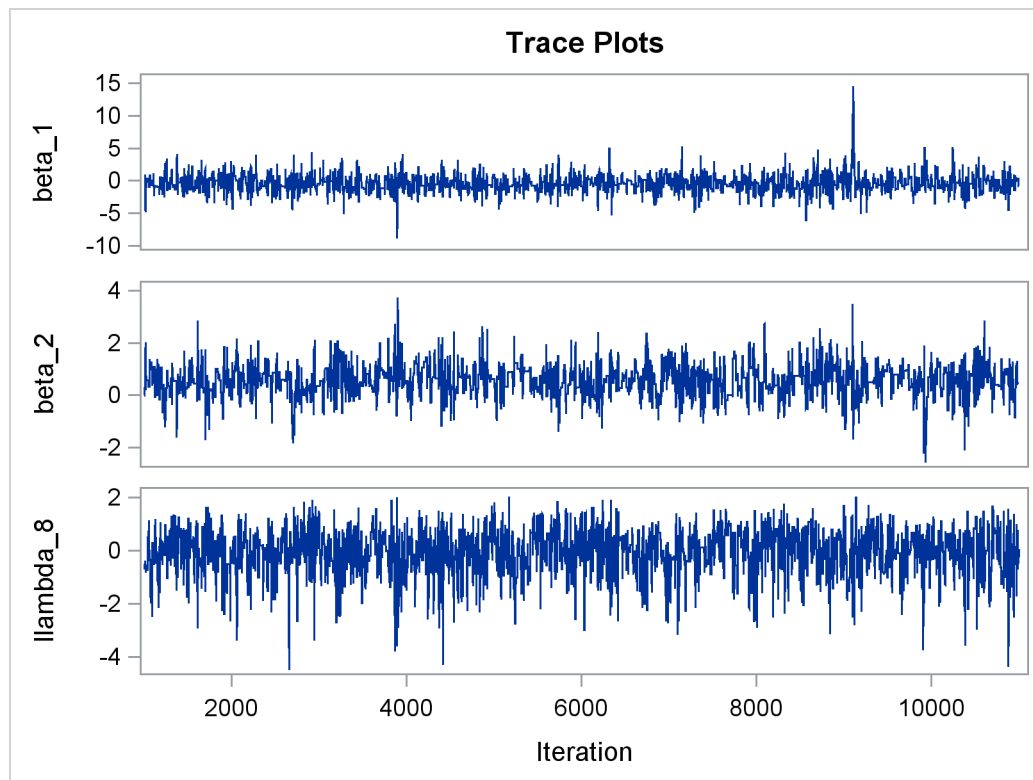
```
proc mcmc data=pump outpost=postout_c seed=248601 nmc=10000
  plots=trace diag=none;
  ods select tracepanel postsummaries postintervals;
  array u[2] alpha beta;
  array mu[2] (0 0);
  parms s2 1;
  prior s2 ~ igamma(0.01, scale=0.01);
  random u ~ mvn(mu, sd=1e6, rho=0) subject=group monitor=(u);
  w = alpha + beta * logtstd;
  random llambda ~ normal(w, var = s2) subject=pump monitor=(random(1));
  lambda = exp(llambda);
  model y ~ poisson(lambda);
run;
```

The difference between these statements and the previous statements on page 4582 is that these statements have the variable w as the prior mean of the random effect llambda . The symbol llambda is the exponential of the corresponding $\log \lambda_{ij}$ (llambda), and the **MODEL** statement assigns the response variable y a Poisson likelihood with a mean parameter llambda , the same way it did in the previous statements.

The trace plots of the monitored parameters are shown in [Output 55.8.2](#). The mixing is significantly improved over the previous model. The posterior summary and interval statistics tables are shown in [Output 55.8.3](#).

Output 55.8.2 Trace Plots of σ^2 , α , and β with Hierarchical Centering



Output 55.8.2 *continued***Output 55.8.3** Posterior Summary Statistics

Nonlinear Poisson Regression Random-Effects Model						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	25%	Percentiles 50%	75%
s2	10000	1.7606	2.2022	0.7338	1.1862	2.0067
alpha_1	10000	2.9286	2.4247	1.6030	3.0767	4.2536
alpha_2	10000	1.6105	0.8801	1.0728	1.6514	2.1775
beta_1	10000	-0.4018	1.3110	-1.1276	-0.4925	0.3198
beta_2	10000	0.5652	0.5804	0.2198	0.5701	0.9124
llambda_8	10000	-0.0560	0.8395	-0.5437	0.0244	0.5479

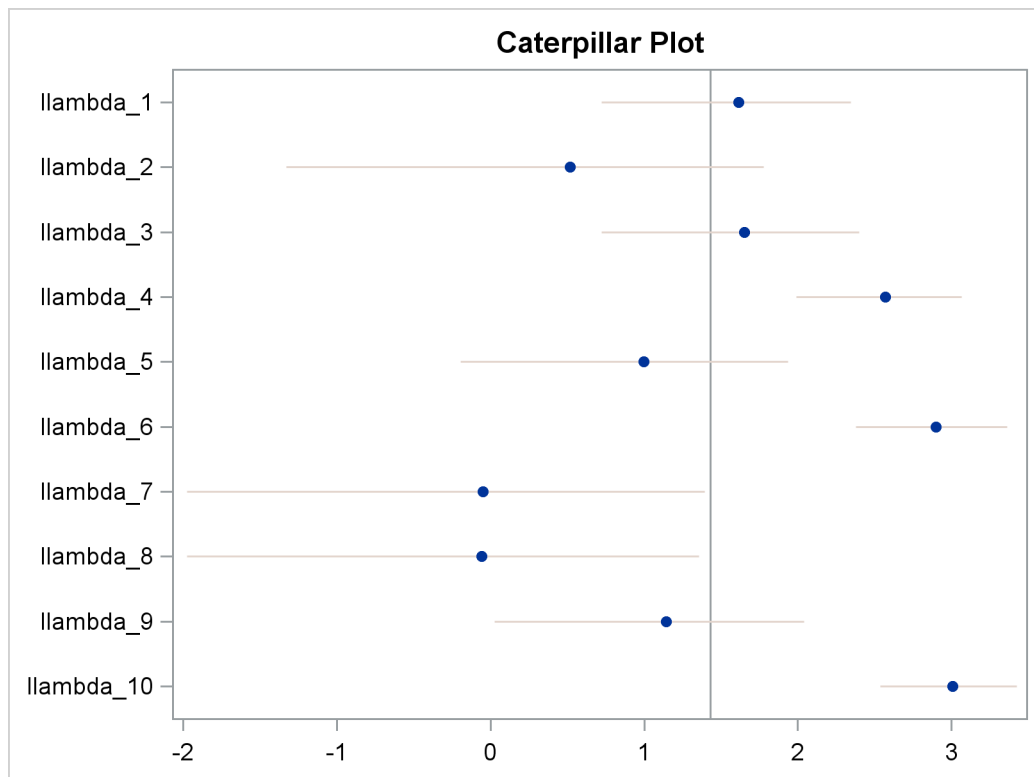
Output 55.8.3 *continued*

Parameter	Alpha	Posterior Intervals			
		Equal-Tail Interval		HPD Interval	
s2	0.050	0.2957	6.5641	0.1039	4.7631
alpha_1	0.050	-1.8812	7.5363	-1.9416	7.4115
alpha_2	0.050	-0.2736	3.1647	-0.0436	3.2985
beta_1	0.050	-2.8784	2.2091	-2.9323	2.0623
beta_2	0.050	-0.5864	1.7179	-0.5469	1.7381
llambda_8	0.050	-1.9763	1.3552	-1.6933	1.4612

You can generate a caterpillar plot (Output 55.8.4) of the random-effects parameters by calling the %CATER macro:

```
%CATER(data=postout_c, var=llambda_:);
ods graphics off;
```

Varying llambda indicates nonconstant dispersion in the Poisson model.

Output 55.8.4 Caterpillar Plots of the Random-Effects Parameters

Example 55.9: Multivariate Normal Random-Effects Model

Gelfand et al. (1990) use a multivariate normal hierarchical model to estimate growth regression coefficients for the growth of 30 young rats in a control group over a period of 5 weeks. The following statements create a SAS data set with measurements of Weight, Age (in days), and Subject.

```

title 'Multivariate Normal Random-Effects Model';
data rats;
  array days[5] (8 15 22 29 36);
  input weight @@;
  subject = ceil(_n_/5);
  index = mod(_n_-1, 5) + 1;
  age = days[index];
  drop index days;;
  datalines;
151 199 246 283 320 145 199 249 293 354
147 214 263 312 328 155 200 237 272 297
135 188 230 280 323 159 210 252 298 331
141 189 231 275 305 159 201 248 297 338
177 236 285 350 376 134 182 220 260 296
160 208 261 313 352 143 188 220 273 314
154 200 244 289 325 171 221 270 326 358
163 216 242 281 312 160 207 248 288 324
142 187 234 280 316 156 203 243 283 317
157 212 259 307 336 152 203 246 286 321
154 205 253 298 334 139 190 225 267 302
146 191 229 272 302 157 211 250 285 323
132 185 237 286 331 160 207 257 303 345
169 216 261 295 333 157 205 248 289 316
137 180 219 258 291 153 200 244 286 324
;

```

The model assumes normal measurement errors,

$$\text{Weight}_{ij} \sim \text{normal}(\alpha_i + \beta_i \text{Age}_{ij}, \sigma^2), \quad i = 1 \cdots 30; j = 1 \cdots 5$$

where i indexes rat (Subject variable), j indexes the time period, Weight_{ij} and Age_{ij} denote the weight and age of the i th rat in week j , and σ^2 is the variance in the normal likelihood. The individual intercept and slope coefficients are modeled as the following:

$$\theta_i = \begin{pmatrix} \alpha_i \\ \beta_i \end{pmatrix} \sim \text{MVN} \left(\theta_c = \begin{pmatrix} \alpha_c \\ \beta_c \end{pmatrix}, \Sigma_c \right), \quad i = 1, \dots, 30$$

You can use the following independent prior distributions on θ_c , Σ_c , and σ^2 :

$$\begin{aligned} \theta_c &\sim \text{MVN} \left(\mu_0 = \begin{pmatrix} 0 \\ 0 \end{pmatrix}, \Sigma_0 = \begin{pmatrix} 1000 & 0 \\ 0 & 1000 \end{pmatrix} \right) \\ \Sigma_c &\sim \text{iwishart} \left(\rho = 2, S = \rho \cdot \begin{pmatrix} 0.01 & 0 \\ 0 & 10 \end{pmatrix} \right) \\ \sigma^2 &\sim \text{igamma}(\text{shape} = 0.01, \text{scale} = 0.01) \end{aligned}$$

The following statements fit this multivariate normal random-effects model:

```
proc mcmc data=rats nmc=10000 outpost=postout
  seed=17 init=random;
  ods select Parameters REParameters PostSummaries;
  array theta[2] alpha beta;
  array theta_c[2];
  array Sig_c[2,2];
  array mu0[2] (0 0);
  array Sig0[2,2] (1000 0 0 1000);
  array S[2,2] (0.02 0 0 20);

  parms theta_c Sig_c {121 0 0 0.26} var_y;
  prior theta_c ~ mvn(mu0, Sig0);
  prior Sig_c ~ iwish(2, S);
  prior var_y ~ igamma(0.01, scale=0.01);

  random theta ~ mvn(theta_c, Sig_c) subject=subject
    monitor=(alpha_9 beta_9 alpha_25 beta_25);
  mu = alpha + beta * age;
  model weight ~ normal(mu, var=var_y);
run;
```

The ODS SELECT statement displays information about model parameters, random-effects parameters, and the posterior summary statistics. The ARRAY statements allocate memory space for the multivariate parameters and hyperparameters in the model. The parameters are θ (theta where the variable name of each element is alpha or beta), θ_c (theta_c), and Σ_c (Sig_c). The hyperparameters are μ_0 (mu0), Σ_0 (Sig0), and S (S). The multivariate hyperparameters are assigned with constant values using parentheses ().

The PARMS statement declares model parameters and assigns initial values to Sig_c using braces { }. The PRIOR statements specify the prior distributions. The RANDOM statement defines an array random effect theta and specifies a multivariate normal prior distribution. The SUBJECT= option indicates cluster membership for each of the random-effects parameter. The MONITOR= option monitors the individual intercept and slope coefficients of subjects 9 and 25.

You can use the following syntax in the RANDOM statement to monitor all parameters in an array random effect:

```
monitor=(theta)
```

This would produce posterior summary statistics on $\alpha_1 \cdots \alpha_{30}$ and $\beta_1 \cdots \beta_{30}$.

The following syntax monitors all α_i parameters:

```
monitor=(alpha)
```

If you did not name elements of theta to be alpha and beta, the SAS System creates variable names automatically in a consecutive fashion, as in theta1 and theta2.

Output 55.9.1 Parameter and Random-Effects Parameter Information Table

Multivariate Normal Random-Effects Model					
The MCMC Procedure					
Parameters					
Block	Parameter	Array Index	Sampling Method	Initial Value	Prior Distribution
1	theta_c1		Conjugate	-4.5834	MVNormal(mu0, Sig0)
	theta_c2			5.7930	
2	Sig_c1	[1,1]	Conjugate	121.0	iWishart(2, S)
	Sig_c2	[1,2]		0	
	Sig_c3	[2,1]		0	
	Sig_c4	[2,2]		0.2600	
3	var_y		Conjugate	2806714	igamma(0.01, scale=0.01)
Random Effect Parameters					
Parameter	Sampling Method	Subject	Number of Subjects	Subject Values	Prior Distribution
theta	N-Metropolis	subject	30	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 ...	MVNormal(theta_c, Sig_c)

Output 55.9.1 displays the parameter and random-effects parameter information tables. The Array Index column in “Parameters” table shows the index reference of the elements in the array parameter Sig_c. The total number of subjects in the study is 30.

Output 55.9.2 Multivariate Normal Random-Effects Model

Multivariate Normal Random-Effects Model						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	25%	50%	75%
theta_c1	10000	106.1	2.2486	104.6	106.1	107.5
theta_c2	10000	6.1975	0.1988	6.0639	6.1966	6.3286
Sig_c1	10000	110.8	45.9169	78.2354	103.6	135.9
Sig_c2	10000	-1.4267	2.3320	-2.7324	-1.2288	0.0789
Sig_c3	10000	-1.4267	2.3320	-2.7324	-1.2288	0.0789
Sig_c4	10000	1.0591	0.2979	0.8472	1.0104	1.2145
var_y	10000	37.6855	5.9591	33.4151	36.9994	41.2448
alpha_9	10000	119.4	5.6756	115.6	119.2	123.2
alpha_25	10000	86.5673	6.3694	82.4621	86.7183	90.7307
beta_9	10000	7.4670	0.2382	7.3109	7.4730	7.6260
beta_25	10000	6.7804	0.2612	6.6144	6.7756	6.9526

Output 55.9.2 displays posterior summary statistics for model parameters and the random-effects parameters for subjects 9 and 25. You can see that there is a substantial difference in the intercepts and growth rates between the two rats.

A seemingly confusing message might occur if a symbol name matches an internally generated variable name for elements of an array. For example, if, instead of using the symbol `var_y` in the SAS program for the model variance σ^2 , you used `s2`, the SAS System produces the following error message:

```
ERROR: The initial value 0 for the parameter S2 is outside of the prior
distribution support set.
```

This is confusing because the program does not assign an initial value for the parameter `s2` in the **PARMS** statement, and you might expect that PROC MCMC would not generate an invalid initial value. The confusion is caused by the **ARRAY** statement that defines the array variable `S`:

```
array S[2,2] (0.02 0 0 20);
```

Elements of `S` are automatically given names `s1`–`s4`. PROC MCMC interprets `s2` as an element in `S` that was given a value of 0, hence producing this error message.

Example 55.10: Missing at Random Analysis

This example illustrates how PROC MCMC treats missing at random (MAR) data. For a short overview of missing data problems, see the section “[Handling of Missing Data](#)” on page 4518.

Researchers studied the effects of air pollution on respiratory disease in children. The response variable (`y`) represented whether a child exhibited wheezing symptoms; it was recorded as 1 for symptoms exhibited and

0 for no symptoms exhibited. City of residency (x1) and maternal smoking status (x2) were the explanatory variables. The variable x1 was coded as 1 if the child lived in the more polluted city, Steel City, and 0 if the child lived in Green Hills. The variable x2 was the number of cigarettes the mother reported that she smoked per day. Both the covariates contain missing values: 17 for x1 and 30 for x2, respectively. The total number of observations in the data set is 390. The following statements generate the data set air:

```

title 'Missing at Random Analysis';
data air;
  input y x1 x2 @@;
  datalines;
0 0 0 0 0 0 0 1 0 0 0 0 0 0 11 0 1 7
0 0 8 0 1 10 0 1 9 0 0 0 1 1 6 0 1 10
0 1 12 0 0 . 0 0 0 0 1 0 0 1 7 1 1 15
0 0 8 0 0 0 1 1 0 1 0 6 0 0 0 1 1 11
0 0 0 1 0 0 1 0 5 0 0 8 0 0 0 0 1 9

... more lines ...

0 0 11 0 0 0 0 0 6 0 0 12 0 0 10 0 1 10
0 1 11 0 0 9 1 0 11 0 1 7 0 0 7 0 0 0
0 . 11 1 1 6 0 0 8 0 0 0 0 1 12 0 0 0
0 1 0 1 1 8 0 0 0 0 1 11 0 1 0 0 1 8
0 . 0 1 0 0 1 1 10 0 . 4 1 1 16 0 . 13
;

```

Suppose you want to fit a logistic regression model for whether the subject develops wheezing symptoms with density for the $i = 1, \dots, 390$ subjects as follows:

$$\begin{aligned}
 y_i &\sim \text{binary}(p_i) \\
 \text{logit}(p_i) &= \beta_0 + \beta_1 \cdot x1_i + \beta_2 \cdot x2_i \\
 \pi(\beta_0), \pi(\beta_1), \pi(\beta_2) &= \text{normal}(0, \sigma^2 = 10)
 \end{aligned}$$

Suppose you specify a joint distribution of x1 and x2 in terms of the product of a conditional and marginal distribution; that is,

$$p(x1, x2 | \alpha) = p(x1 | x2, \alpha_{10}, \alpha_{11}) p(x2 | \alpha_{20})$$

where $p(x1_i | x2_i, \alpha_{10}, \alpha_{11})$ could be a logistic model and $p(x2_i | \alpha_{20})$ could be a Poisson distribution that models the following counts:

$$\begin{aligned}
 p(x1_i | x2_i, \alpha_{10}, \alpha_{11}) &= \text{binary}(p_{c,i}) \\
 \text{logit}(p_{c,i}) &= \alpha_{10} + \alpha_{11} \cdot x2_i \\
 \pi(\alpha_{10}), \pi(\alpha_{11}) &= \text{normal}(0, \sigma^2 = 10) \\
 p(x2_i | \alpha_{20}) &= \text{Poisson}(e^{\alpha_{20}}) \\
 \pi(\alpha_{20}) &= \text{normal}(0, \sigma^2 = 2)
 \end{aligned}$$

The researchers are interested in interpreting how the odds of developing a wheeze changes for a child living in the more polluted city. The odds ratio can be written as the follows:

$$OR_{x1} = \exp(\beta_1)$$

Similarly, the odds ratio for the maternal smoking effect can be written as follows:

$$OR_{x2} = \exp(\beta_2)$$

The following statements fit a Bayesian logistic regression with missing covariates:

```
proc mcmc data=air seed=1181 nmc=10000 monitor=(_parms_ orx1 orx2)
  stats=(summary interval) diag=none plots=none;
  parms beta0 -1 beta1 0.1 beta2 .01;
  parms alpha10 0 alpha11 0 alpha20 0;

  prior beta: alpha1: ~ normal(0,var=10);
  prior alpha20 ~ normal(0,var=2);

  beginnodata;
  pm = exp(alpha20);
  orx1 = exp(beta1);
  orx2 = exp(beta2);
  endnodata;
  model x2 ~ poisson(pm) monitor=(1 3 10);
  p1 = logistic(alpha10 + alpha11 * x2);
  model x1 ~ binary(p1) monitor=(random(3));
  p = logistic(beta0 + beta1*x1 + beta2*x2);
  model y ~ binary(p);
run;
```

The **PARMS** statements specify the parameters in the model and assign initial values to each of them. The **PRIOR** statements specify priors for all the model parameters. The notations **beta:** and **alpha:** in the **PRIOR** statements are shorthand for all variables that start with “beta,” and “alpha,” respectively. The shorthand notation is not necessary, but it keeps your code succinct.

The **BEGINNODATA** and **ENDNODATA** statements enclose three programming statements that calculate the Poisson mean (pm) and the two odds ratios (ORX1 and ORX2). These enclosed statements are independent of any data set variables, and they are run only once per iteration to reduce unnecessary observation-level computations.

The first **MODEL** statement assigns a Poisson likelihood with mean pm to x2. The statement models missing values in x2 automatically, creating one variable for each of the missing values, and augments them accordingly. By default, PROC MCMC does not output analyses of the posterior samples of the missing values. You can use the **MONITOR=** option to choose the missing values that you want to monitor. In the example, the first, third, and tenth missing values are monitored.

The P1 assignment statement calculates $p_{c,i}$. The second **MODEL** statement assigns a binary likelihood with probability p1 and requests a random choice of three missing data variables of x1 to monitor.

The P assignment statement calculates p_i in the logistic model. The third **MODEL** statement specifies the complete data likelihood function for Y.

Output 55.10.1 displays the number of observations read from the DATA= data set, the number of observations used in the analysis, and the “Missing Data Information” table. No observations were omitted from the data set in the analysis.

The “Missing Data Information” table lists the variables that contain missing values, which are x1 and x2, the number of missing observations in each variable, the observation indices of these missing values, and the sampling algorithms used. By default, the first 20 observation indices of each variable are printed in the table.

Output 55.10.1 Observation Information and Missing Data Information

Missing at Random Analysis											
The MCMC Procedure											
Number of Observations Read										390	
Number of Observations Used										390	
Missing Data Information Table											
Variable	Number of Missing Obs	Observation Indices									Sampling Method
x2	30	14	41	50	55	59	66	71	83	N-Metropolis	
		88	90	118	158	174	175				
		178	183	196	203	210	212				
		...									
x1	17	50	92	93	167	194	231	273	Inverse CDF		
		296	303	304	308	330	349				
		373	385	388	390						

There are 30 missing values in the variable x2, and 17 in x1. Internally, PROC MCMC creates 30 and 17 variables for the missing values in x2 and x1, respectively. The default naming convention for these missing values is to concatenate the response variable and the observation number. For example, the first missing value in x2 is the fourteenth observation, and the corresponding variable is x2_14.

Output 55.10.2 displays the summary and interval statistics for each parameter, the odds ratios, and the monitored missing values.

Output 55.10.2 Posterior Summary and Interval Statistics

Missing at Random Analysis						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles 25%	50%	75%
beta0	10000	-1.3585	0.1986	-1.4891	-1.3515	-1.2192
beta1	10000	0.4763	0.2355	0.3195	0.4675	0.6334
beta2	10000	0.0146	0.0227	0.000049	0.0124	0.0299
alpha10	10000	-0.2244	0.1446	-0.3190	-0.2187	-0.1273
alpha11	10000	0.0140	0.0214	-0.00113	0.0136	0.0289
alpha20	10000	1.5635	0.0247	1.5466	1.5644	1.5803
orx1	10000	1.6557	0.4002	1.3765	1.5960	1.8841
orx2	10000	1.0149	0.0231	1.0000	1.0125	1.0303
x2_14	10000	4.9229	2.1745	3.0000	5.0000	6.0000
x2_50	10000	4.9569	2.1758	3.0000	5.0000	6.0000
x2_90	10000	4.9214	2.2152	3.0000	5.0000	6.0000
x1_296	10000	0.4183	0.4933	0	0	1.0000
x1_304	10000	0.4569	0.4982	0	0	1.0000
x1_373	10000	0.4461	0.4971	0	0	1.0000

Posterior Intervals					
Parameter	Alpha	Equal-Tail Interval		HPD Interval	
beta0	0.050	-1.7749	-0.9914	-1.7669	-0.9899
beta1	0.050	0.0125	0.9526	0.0481	0.9806
beta2	0.050	-0.0295	0.0599	-0.0305	0.0580
alpha10	0.050	-0.5175	0.0506	-0.5142	0.0508
alpha11	0.050	-0.0271	0.0547	-0.0267	0.0549
alpha20	0.050	1.5137	1.6095	1.5127	1.6078
orx1	0.050	1.0126	2.5924	0.9007	2.4030
orx2	0.050	0.9709	1.0617	0.9699	1.0597
x2_14	0.050	1.0000	10.0000	1.0000	9.0000
x2_50	0.050	1.0000	10.0000	1.0000	9.0000
x2_90	0.050	1.0000	10.0000	1.0000	9.0000
x1_296	0.050	0	1.0000	0	1.0000
x1_304	0.050	0	1.0000	0	1.0000
x1_373	0.050	0	1.0000	0	1.0000

The odds ratio for x1 is the multiplicative change in the odds of a child wheezing in Steel City compared to the odds of the child wheezing in Green Hills. The estimated odds ratio (ORX1) value is 1.6736 with a corresponding 95% equal-tail credible interval of (1.0248, 2.5939). City of residency is a significant factor in a child's wheezing status. The estimated odds ratio for x2 is the multiplicative change in the odds of developing a wheeze for each additional reported cigarette smoked per day. The odds ratio of ORX2 indicates that the odds of a child developing a wheeze is 1.0150 times higher for each reported cigarette a mother smokes. The corresponding 95% equal-tail credible interval is (0.9695, 1.0619). Since this interval contains the value 1, maternal smoking is not considered to be an influential effect.

Example 55.11: Nonignorably Missing Data (MNAR) Analysis

This example illustrates how to fit a nonignorably missing data model (MNAR) with PROC MCMC. For a short overview of missing data problems, see the section “[Handling of Missing Data](#)” on page 4518.

This data set comes from an environmental study that involve workers in a cotton factory. A similar data set was analyzed from Ibrahim, Chen, and Lipsitz (2001). There are 912 workers in the data set, and the response variable of interest is whether they develop dyspnea (difficult or labored respiration). The data are collected over three time points, and there are six covariates. The following statements create the data set:

```

title 'Nonignorably Missing Data Analysis';
data dyspnea;
  input smoke1 smoke2 smoke3 y1 y2 y3 yrswrk1 yrswrk2 yrswrk3
        age expd sex hgt;
  datalines;
0 0 0 0 0 0 28.1 33.1 39.1 48 1 1 165.0
0 0 0 0 . 0 5.1 10.1 16.1 45 1 0 147.0
0 0 0 0 . 0 26.0 31.0 37.0 46 1 0 156.0

... more lines ...

1 1 1 0 . . 6.0 11.0 17.0 25 0 1 180.0
0 0 0 0 . . 20.0 25.0 31.0 42 0 0 159.0
;

```

The following variables are included in the data set:

- y1, y2, and y3: dichotomous outcome at the three time periods, which takes the value 1 if the worker has dyspnea, 0 if not (there are missing values in y2 and y3)
- smoke1, smoke2, smoke3: smoking status (0=no, and 1=yes)
- yrswrk1, yrswrk2, yrswrk3: years worked at the cotton factory
- age: age of the worker
- expd: cotton dust exposure (0=no, 1=yes)
- sex: gender (0=female, 1=male)
- hgt: height of the worker

Prior to the analysis, three missing data indicator variables (r1, r2, and r3, one for each of the response variables) are created, and they are set to 1 if the response variable is missing, and 0 otherwise. The covariates age, hgt, yrswrk1, yrswrk2, and yrswrk3 are standardized:

```

data dyspnea;
  array y[3] y1-y3;
  array r[3];
  set dyspnea;
  do i = 1 to 3;
    if y[i] = . then r[i] = 1;
    else r[i] = 0;
  end;
  output;
run;

proc standard data=dyspnea out=dyspnea mean=0 std=1;
  var age hgt yrswrk;;
run;

```

There are no missing values in response variable y_1 , 128 missing values in y_2 , and 131 in y_3 . Ibrahim, Chen, and Lipsitz (2001) used a logistic regression for each of the response variables, where δ_i is a scalar random effect on the observational level:

$$\begin{aligned}
 y_{ki} &\sim \text{binary}(p_{ki}) \quad k = 1, 2, 3; \quad i = 1, \dots, 912 \\
 p_{ki} &= \text{logistic}(\mu_{ki} + \delta_i) \\
 \mu_{ki} &= \beta_1 + \beta_2 \cdot \text{expd}_i + \beta_3 \cdot \text{sex}_i + \beta_4 \cdot \text{hgt}_i + \beta_5 \cdot \text{age}_i + \beta_6 \cdot \text{yrswrk}_{ki} + \beta_7 \cdot \text{smoke}_{ki} \\
 \delta_i &\sim n(0, \sigma^2)
 \end{aligned}$$

Ibrahim, Chen, and Lipsitz (2001) noted that taking δ_i to be higher dimensional (3) would make the model either not identifiable or nearly not identifiable because of the multiple missing values for some subjects.

The first response variable y_1 does not contain any missing values, making it meaningless to model the corresponding r_1 because every value is 1. Hence, only r_2 and r_3 are considered in the missing mechanism part of the model. Ibrahim, Chen, and Lipsitz (2001) suggest the following logistic regression for r_2 and r_3 , where the regression mean for each r depends not only on the current response variable y but also the response from previous time period:

$$\begin{aligned}
 r_{ki} &\sim \text{binary}(q_{ki}) \quad k = 2, 3; \quad i = 1, \dots, 912 \\
 q_{ki} &= \text{logistic}(v_{ki}) \\
 \mu_c &= \phi_1 + \phi_2 \cdot \text{expd}_i + \phi_3 \cdot \text{sex}_i + \phi_4 \cdot \text{hgt}_i + \phi_5 \cdot \text{age}_i + \phi_6 \cdot \text{yrswrk}_{ki} + \phi_7 \cdot \text{smoke}_{ki} \\
 v_{2i} &= \mu_c + \phi_8 \cdot y_{1i} + \phi_9 \cdot y_{2i} \\
 v_{3i} &= \mu_c + \phi_9 \cdot y_{2i} + \phi_{10} \cdot y_{3i}
 \end{aligned}$$

The missing mechanism model introduces an additional 10 parameters to the model. Normal priors with large standard deviations are used here.

The following statements fit a nonignorably missing model to the dyspnea data set:

```

ods select MissDataInfo REParameters PostSummaries PostIntervals;
proc mcmc data=dyspnea seed=17 outpost=dysp2 nmc=20000
    propcov=simplex diag=none monitor=(beta1-beta7);
    array p[3];
    array yrswrk[3];
    array smoke[3];

    parms beta1-beta7 s2;
    parms phi1-phi10;
    prior beta: phi: ~ n(0, var=1e6);
    prior s2 ~ igamma(2, scale=2);
    random d ~ n(0, var=s2) subject=_obs_;
    mu = beta1 + beta2*expd + beta3*sex + beta4*hgt + beta5*age + d;
    do i = 1 to 3;
        p[i] = logistic(mu + beta6*yrswrk[i] + beta7*smoke[i]);
    end;
    model y1 ~ binary(p1);
    model y2 ~ binary(p2);
    model y3 ~ binary(p3);

    nu = phi1 + phi2*expd + phi3*sex + phi4*hgt + phi5*age;
    q2 = logistic(nu + phi6*yrswrk[2] + phi7*smoke[2] +
        phi8*y1 + phi9*y2);
    model r2 ~ binary(q2);
    q3 = logistic(nu + phi6*yrswrk[3] + phi7*smoke[3] +
        phi9*y2 + phi10*y3);
    model r3 ~ binary(q3);
run;

```

The first **ARRAY** statement declares an array `p` of size 3. This array stores three binary probabilities of the response variables. The next two **ARRAY** statements create storage arrays for some of `yrswrk` and `smoke` variables for later programming convenience. The first **PARMS** statement declares eight parameters, $\beta_1 - \beta_7$ and σ^2 . The second **PARMS** statement declares the 10 ϕ parameters for the missing mechanism model. The **PRIOR** statements assign prior distributions to these parameters.

The **RANDOM** statement defines an observational-level random effect `d` that has a normal prior with variance `s2`. The **SUBJECT=_OBS_** option enables the specification of individual random effects without an explicit input data set variable.

The **MU** assignment statement and the following **DO** loop statements calculate the binary probabilities for the three response variables. Note that different `yrswrk` and `smoke` variables are used in the **DO** loop for different years. The three **MODEL** statements assign three binary distributions to the response variables.

The **NU** assignment statement starts the calculation for the regression mean in the logistic model for `r2` and `r3`. The variables `q2` and `q3` are the binary probabilities for the missing mechanisms. Note that their calculations are conditional on the response variables `y` (pattern mixture model). The last two **MODEL** statements for `r2` and `r3` complete the specification of the models.

Missing data information and random-effects parameters information are displayed in [Output 55.11.1](#). You can read the total number of missing observations from each variable and its indices from the table. The missing values are sampled using the inverse CDF method. There are 912 random-effects parameters in the model.

Output 55.11.1 Missing Data and Random-Effects Information

Nonignorably Missing Data Analysis												
The MCMC Procedure												
Missing Data Information Table												
Variable	Number of Missing Obs	Observation Indices									Sampling Method	
y2	128	2 3 9 11 13 19 20 21 30							Inverse CDF			
		31 32 35 39 40 43 56 58										
		71 75 95 ...										
y3	131	9 14 16 20 21 29 31 32							Inverse CDF			
		43 45 56 72 86 115 117										
		121 124 142 149 160 ...										
Random Effect Parameters												
Parameter	Sampling Method	Subject	Number of Subjects	Subject Values								Prior Distribution
d	N-Metropolis	_OBS_	912	1 2 3 4 5 6 7 8						normal(0, var=s2)		
				9 10 11 12 13 14								
				15 16 17 18 19								
				20 ...								

The posterior summary and interval statistics of all the β parameters are shown in [Output 55.11.2](#). There are a number of significant regression coefficients in modeling the probability of a worker developing dyspnea, including those for expd (β_2), sex (β_3), age (β_5), and smoke (β_7).

Output 55.11.2 Posterior Summary Statistics for β

Nonignorably Missing Data Analysis						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	25%	Percentiles 50% 75%	
beta1	20000	-2.3256	0.1771	-2.4443	-2.3266	-2.2069
beta2	20000	0.5327	0.1530	0.4270	0.5316	0.6352
beta3	20000	-0.5966	0.2593	-0.7709	-0.5990	-0.4244
beta4	20000	-0.0682	0.1061	-0.1389	-0.0679	0.00196
beta5	20000	0.6252	0.1640	0.5133	0.6245	0.7324
beta6	20000	-0.1776	0.1574	-0.2784	-0.1742	-0.0693
beta7	20000	0.5862	0.2214	0.4357	0.5854	0.7285

Output 55.11.2 *continued*

Parameter	Alpha	Posterior Intervals			
		Equal-Tail Interval		HPD Interval	
beta1	0.050	-2.6692	-1.9826	-2.6670	-1.9826
beta2	0.050	0.2383	0.8308	0.2306	0.8193
beta3	0.050	-1.1085	-0.0785	-1.0906	-0.0691
beta4	0.050	-0.2815	0.1400	-0.2734	0.1462
beta5	0.050	0.3074	0.9613	0.2992	0.9490
beta6	0.050	-0.5047	0.1191	-0.4971	0.1218
beta7	0.050	0.1599	1.0301	0.1433	1.0051

Example 55.12: Change Point Models

Consider the data set from Bacon and Watts (1971), where y_i is the logarithm of the height of the stagnant surface layer and the covariate x_i is the logarithm of the flow rate of water. The following statements create the data set:

```

title 'Change Point Model';
data stagnant;
  input y x @@;
  ind = _n_;
  datalines;
1.12 -1.39 1.12 -1.39 0.99 -1.08 1.03 -1.08
0.92 -0.94 0.90 -0.80 0.81 -0.63 0.83 -0.63
0.65 -0.25 0.67 -0.25 0.60 -0.12 0.59 -0.12
0.51 0.01 0.44 0.11 0.43 0.11 0.43 0.11
0.33 0.25 0.30 0.25 0.25 0.34 0.24 0.34
0.13 0.44 -0.01 0.59 -0.13 0.70 -0.14 0.70
-0.30 0.85 -0.33 0.85 -0.46 0.99 -0.43 0.99
-0.65 1.19
;

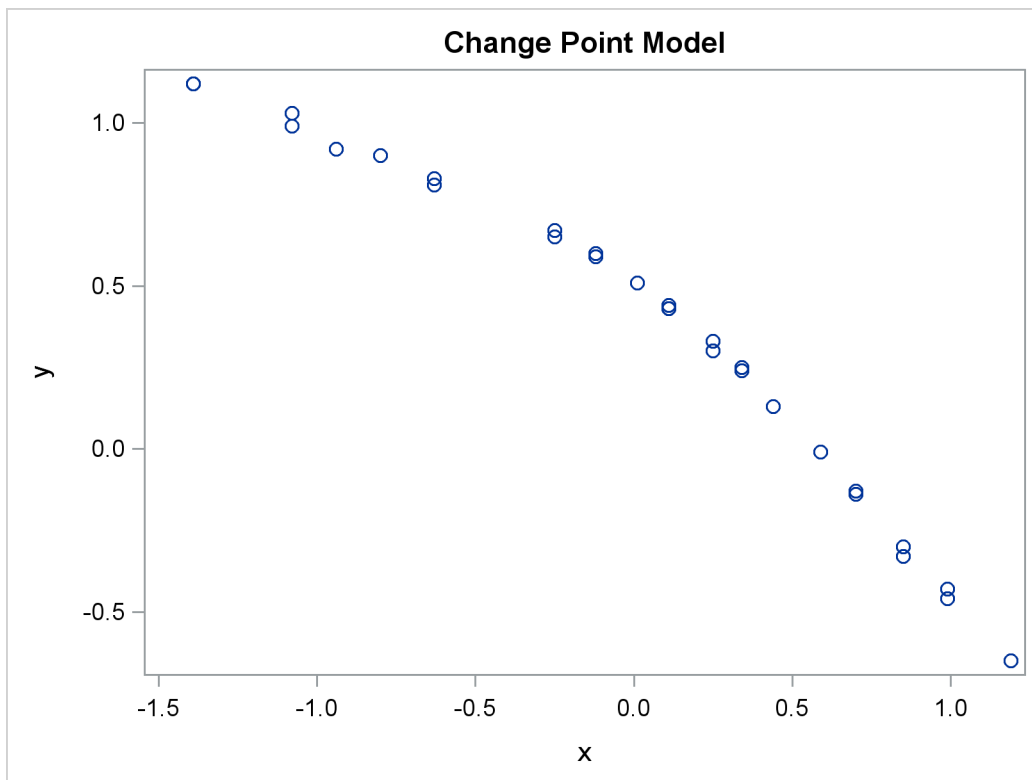
```

A scatter plot (Output 55.12.1) shows the presence of a nonconstant slope in the data. This suggests a change point regression model (Carlin, Gelfand, and Smith 1992). The following statements generate the scatter plot in Output 55.12.1:

```

ods graphics on;
proc sgplot data=stagnant;
  scatter x=x y=y;
run;

```

Output 55.12.1 Scatter Plot of the Stagnant Data Set

Let the change point be cp . Following formulation by Spiegelhalter et al. (1996b), the regression model is as follows:

$$y_i \sim \begin{cases} \text{normal}(\alpha + \beta_1(x_i - cp), \sigma^2) & \text{if } x_i < cp \\ \text{normal}(\alpha + \beta_2(x_i - cp), \sigma^2) & \text{if } x_i \geq cp \end{cases}$$

You might consider the following diffuse prior distributions:

$$\begin{aligned} cp &\sim \text{uniform}(-1.3, 1.1) \\ \alpha, \beta_1, \beta_2 &\sim \text{normal}(0, \text{var} = 1e6) \\ \sigma^2 &\sim \text{uniform}(0, 5) \end{aligned}$$

The following statements generate [Output 55.12.2](#):

```
proc mcmc data=stagnant outpost=postout seed=24860 ntu=1000
      nmc=20000;
      ods select PostSummaries;
      ods output PostSummaries=ds;

      array beta[2];
      parms alpha cp beta1 beta2;
      parms s2;

      prior cp ~ unif(-1.3, 1.1);
      prior s2 ~ uniform(0, 5);
```

```

prior alpha beta: ~ normal(0, v = 1e6);

j = 1 + (x >= cp);
mu = alpha + beta[j] * (x - cp);
model y ~ normal(mu, var=s2);
run;

```

The PROC MCMC statement specifies the input data set (Stagnant), the output data set (Postout), a random number seed, a tuning sample of 1000, and an MCMC sample of 20000. The ODS SELECT statement displays only the summary statistics table. The ODS OUTPUT statement saves the summary statistics table to the data set Ds.

The **ARRAY** statement allocates an array of size 2 for the beta parameters. You can use beta1 and beta2 as parameter names without allocating an array, but having the array makes it easier to construct the likelihood function. The two **PARMS** statements put the five model parameters in two blocks. The three **PRIOR** statements specify the prior distributions for these parameters.

The symbol j indicates the segment component of the regression. When x is less than the change point, (x < cp) returns 0 and j is assigned the value 1; if x is greater than or equal to the change point, (x >= cp) returns 1 and j is 2. The symbol mu is the mean for the jth segment, and beta[j] changes between the two regression coefficients depending on the segment component. The **MODEL** statement assigns the normal model to the response variable y.

Posterior summary statistics are shown in [Output 55.12.2](#).

Output 55.12.2 MCMC Estimates of the Change Point Regression Model

Change Point Model						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
alpha	20000	0.5349	0.0249	0.5188	0.5341	0.5509
cp	20000	0.0283	0.0314	0.00728	0.0303	0.0493
beta1	20000	-0.4200	0.0146	-0.4293	-0.4198	-0.4111
beta2	20000	-1.0136	0.0167	-1.0248	-1.0136	-1.0023
s2	20000	0.000451	0.000145	0.000348	0.000425	0.000522

You can use PROC SGPLOT to visualize the model fit. [Output 55.12.3](#) shows the fitted regression lines over the original data. In addition, on the bottom of the plot is the kernel density of the posterior marginal distribution of cp, the change point. The kernel density plot shows the relative variability of the posterior distribution on the data plot. You can use the following statements to create the plot:

```

data _null_;
  set ds;
  call symputx(parameter, mean);
run;

data b;
  missing A;
  input x1 @@;
  if x1 eq .A then x1 = &cp;
  if _n_ <= 2 then y1 = &alpha + &beta1 * (x1 - &cp);
  else y1 = &alpha + &beta2 * (x1 - &cp);
  datalines;
-1.5 A 1.2
;

proc kde data=postout;
  univar cp / out=m1 (drop=count);
run;

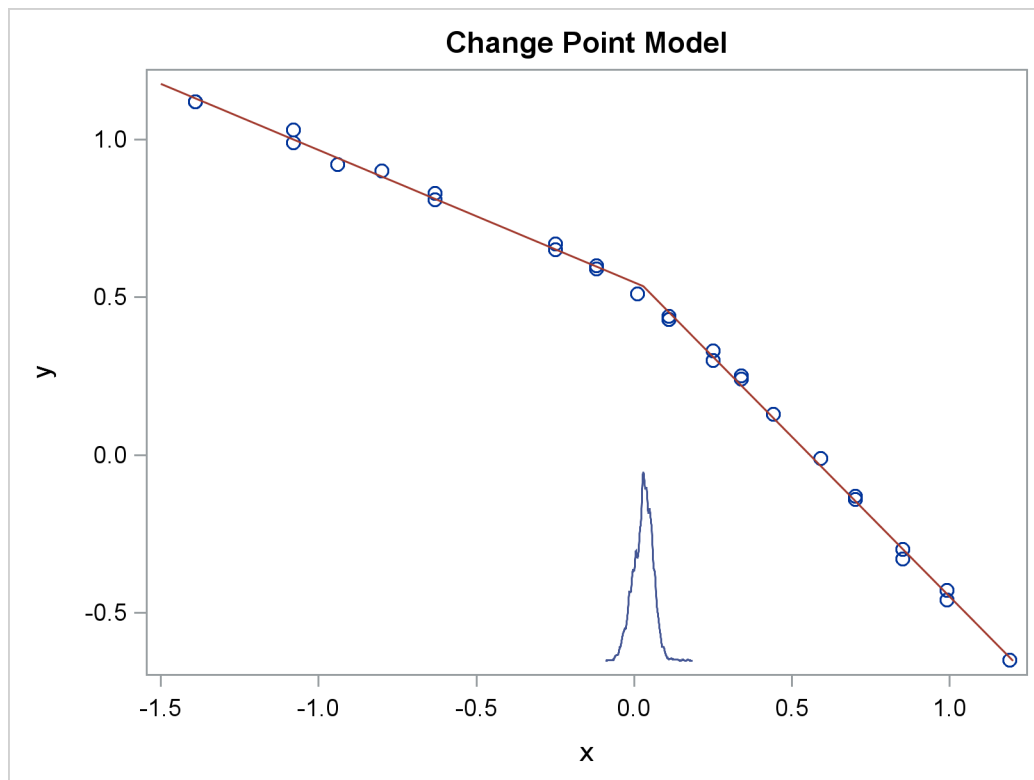
data m1;
  set m1;
  density = (density / 25) - 0.653;
run;

data all;
  set stagnant b m1;
run;

proc sgplot data=all noautolegend;
  scatter x=x y=y;
  series x=x1 y=y1 / lineattrs = graphdata2;
  series x=value y=density / lineattrs = graphdata1;
run;
ods graphics off;

```

The macro variables &alpha, &beta1, &beta2, and &cp store the posterior mean estimates from the data set Ds. The data set b contains three predicted values, at the minimum and maximum values of x and the estimated change point &cp. These input values give you fitted values from the regression model. Data set M1 contains the kernel density estimates of the parameter cp. The density is scaled down so the curve would fit in the plot. Finally, you use PROC SGPLOT to overlay the scatter plot, regression line and kernel density plots in the same graph.

Output 55.12.3 Estimated Fit to the Stagnant Data Set

Example 55.13: Exponential and Weibull Survival Analysis

This example covers two commonly used survival analysis models: the exponential model and the Weibull model. The deviance information criterion (DIC) is used to do model selections, and you can also find programs that visualize posterior quantities. Exponential and Weibull models are widely used for survival analysis. This example shows you how to use PROC MCMC to analyze the treatment effect for the E1684 melanoma clinical trial data. These data were collected to assess the effectiveness of using interferon alpha-2b in chemotherapeutic treatment of melanoma. The following statements create the data set:

```

data e1684;
  input t t_cen treatment @@;
  if t = . then do;
    t = t_cen;
    v = 0;
  end;
  else
    v = 1;
  ifn = treatment - 1;
  et = exp(t);
  lt = log(t);
  drop t_cen;
  datalines;
1.57808 0.00000 2 1.48219 0.00000 2 . 7.33425 1
2.23288 0.00000 1 . 9.38356 2 3.27671 0.00000 1
. 9.64384 1 1.66575 0.00000 2 0.94247 0.00000 1
1.68767 0.00000 2 2.34247 0.00000 2 0.89863 0.00000 1

... more lines ...

3.39178 0.00000 1 . 4.36164 2 . 4.81918 2
;

```

The data set E1684 contains the following variables: t is the failure time that equals the censoring time whether the observation was censored, v indicates whether the observation is an actual failure time or a censoring time, $treatment$ indicates two levels of treatments, and ifn indicates the use of interferon as a treatment. The variables et and lt are the exponential and logarithm transformation of the time t . The published data contains other potential covariates that are not listed here. This example concentrates on the effectiveness of the interferon treatment.

Exponential Survival Model

The density function for exponentially distributed survival times is as follows:

$$p(t_i | \lambda_i) = \lambda_i \exp(-\lambda_i t_i)$$

Note that this formulation of the exponential distribution is different from what is used in the SAS probability function PDF. The definition used in PDF for the exponential distributions is as follows:

$$p(t_i | v_i) = \frac{1}{v_i} \exp\left(-\frac{t_i}{v_i}\right)$$

The relationship between λ and v is as follows:

$$\lambda_i = \frac{1}{v_i}$$

The corresponding survival function, using the λ_i formulation, is as follows:

$$S(t_i | \lambda_i) = \exp(-\lambda_i t_i)$$

If you have a sample $\{t_i\}$ of n independent exponential survival times, each with mean λ_i , then the likelihood function in terms of λ is as follows:

$$\begin{aligned} L(\lambda|t) &= \prod_{i=1}^n p(t_i|\lambda_i)^{v_i} S(t_i|\lambda_i)^{1-v_i} \\ &= \prod_{i=1}^n (\lambda_i \exp(-\lambda_i t_i))^{v_i} (\exp(-\lambda_i t_i))^{1-v_i} \\ &= \prod_{i=1}^n \lambda_i^{v_i} \exp(-\lambda_i t_i) \end{aligned}$$

If you link the covariates to λ with $\lambda_i = \exp \mathbf{x}_i' \boldsymbol{\beta}$, where $\mathbf{x}_i$ is the vector of covariates corresponding to the i th observation and $\boldsymbol{\beta}$ is a vector of regression coefficients, then the log-likelihood function is as follows:

$$l(\boldsymbol{\beta}|t, \mathbf{x}) = \sum_{i=1}^n v_i \mathbf{x}_i' \boldsymbol{\beta} - t_i \exp(\mathbf{x}_i' \boldsymbol{\beta})$$

In the absence of prior information about the parameters in this model, you can choose diffuse normal priors for the $\boldsymbol{\beta}$:

$$\boldsymbol{\beta} \sim \text{normal}(0, \text{sd}=10000)$$

There are two ways to program the log-likelihood function in PROC MCMC. You can use the SAS functions LOGPDF and LOGSDF. Alternatively, you can use the simplified log-likelihood function, which is more computationally efficient. You get identical results by using either approaches.

The following PROC MCMC statements fit an exponential model with simplified log-likelihood function:

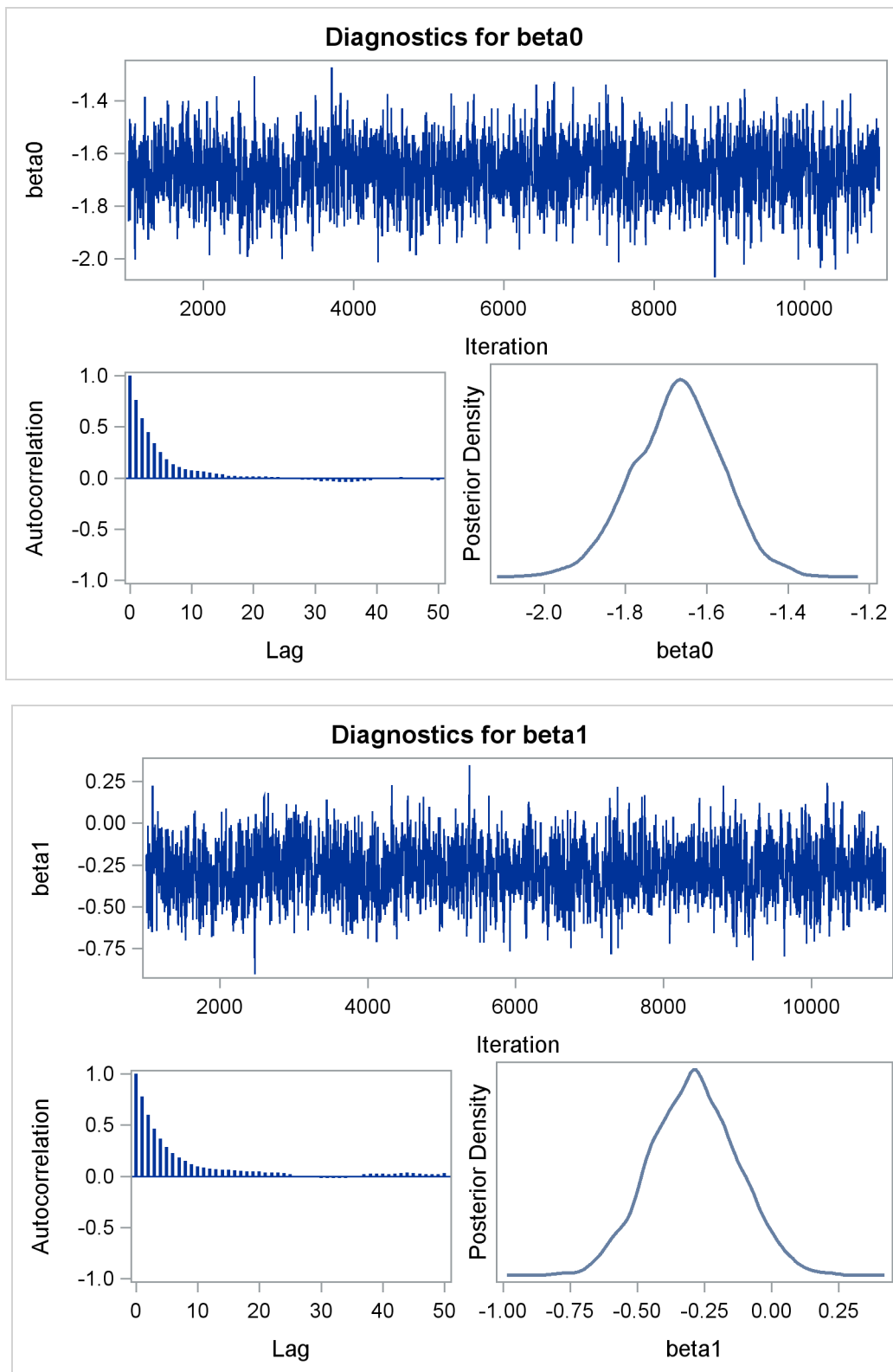
```

title 'Exponential Survival Model';
ods graphics on;
proc mcmc data=e1684 outpost=expsurvout nmc=10000 seed=4861;
  ods select PostSummaries PostIntervals TADpanel
            ess mcse;
  parms (beta0 beta1) 0;
  prior beta: ~ normal(0, sd = 10000);
  /* *****
  /* (1) the logpdf and logsdf functions are not used */
  /* *****
  /*      nu = 1/exp(beta0 + beta1*ifn);
  /*      llike = v*logpdf("exponential", t, nu) +
  /*              (1-v)*logsdf("exponential", t, nu);
  /*
  /* *****
  /* (2) the simplified likelihood formula is used */
  /* *****
  l_h = beta0 + beta1*ifn;
  llike = v*(l_h) - t*exp(l_h);
  model general(llike);
run;

```

The two assignment statements that are commented out calculate the log-likelihood function by using the SAS functions LOGPDF and LOGSDF for the exponential distribution. The next two assignment statements calculate the log likelihood by using the simplified formula. The first approach is slower because of the redundant calculation involved in calling both LOGPDF and LOGSDF.

An examination of the trace plots for β_0 and β_1 (see [Output 55.13.1](#)) reveals that the sampling has gone well with no particular concerns about the convergence or mixing of the chains.

Output 55.13.1 Posterior Plots for β_0 and β_1 in the Exponential Survival Analysis

The MCMC results are shown in [Output 55.13.2](#).

Output 55.13.2 Posterior Summary and Interval Statistics

Exponential Survival Model						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
beta0	10000	-1.6715	0.1091	-1.7426	-1.6684	-1.5964
beta1	10000	-0.2879	0.1615	-0.4001	-0.2892	-0.1803
Posterior Intervals						
Parameter	Alpha	Equal-Tail Interval		HPD Interval		
beta0	0.050	-1.8907	-1.4639	-1.8930	-1.4673	
beta1	0.050	-0.5985	0.0300	-0.6104	0.0169	

The Monte Carlo standard errors and effective sample sizes are shown in [Output 55.13.3](#). The posterior means for β_0 and β_1 are estimated with high precision, with small standard errors with respect to the standard deviation. This indicates that the mean estimates have stabilized and do not vary greatly in the course of the simulation. The effective sample sizes are roughly the same for both parameters.

Output 55.13.3 MCSE and ESS

Exponential Survival Model			
The MCMC Procedure			
Monte Carlo Standard Errors			
Parameter	MCSE	Standard Deviation	MCSE/SD
beta0	0.00302	0.1091	0.0277
beta1	0.00485	0.1615	0.0301
Effective Sample Sizes			
Parameter	ESS	Autocorrelation Time	Efficiency
beta0	1304.1	7.6682	0.1304
beta1	1107.2	9.0319	0.1107

The next part of this example shows fitting a Weibull regression to the data and then comparing the two models with DIC to see which one provides a better fit to the data.

Weibull Survival Model

The density function for Weibull distributed survival times is as follows:

$$p(t_i | \alpha, \lambda_i) = \alpha t_i^{\alpha-1} \exp(\lambda_i - \exp(\lambda_i) t_i^\alpha)$$

Note that this formulation of the Weibull distribution is different from what is used in the SAS probability function PDF. The definition used in PDF is as follows:

$$p(t_i | \alpha, \gamma_i) = \exp\left(-\left(\frac{t_i}{\gamma_i}\right)^\alpha\right) \frac{\alpha}{\gamma_i} \left(\frac{t_i}{\gamma_i}\right)^{\alpha-1}$$

The relationship between λ and γ in these two parameterizations is as follows:

$$\lambda_i = -\alpha \log \gamma_i$$

The corresponding survival function, using the λ_i formulation, is as follows:

$$S(t_i | \alpha, \lambda_i) = \exp(-\exp(\lambda_i) t_i^\alpha)$$

If you have a sample $\{t_i\}$ of n independent Weibull survival times, with parameters α , and λ_i , then the likelihood function in terms of α and λ is as follows:

$$\begin{aligned} L(\alpha, \lambda | t) &= \prod_{i=1}^n p(t_i | \alpha, \lambda_i)^{v_i} S(t_i | \alpha, \lambda_i)^{1-v_i} \\ &= \prod_{i=1}^n (\alpha t_i^{\alpha-1} \exp(\lambda_i - \exp(\lambda_i) t_i^\alpha))^{v_i} (\exp(-\exp(\lambda_i) t_i^\alpha))^{1-v_i} \\ &= \prod_{i=1}^n (\alpha t_i^{\alpha-1} \exp(\lambda_i))^{v_i} (\exp(-\exp(\lambda_i) t_i^\alpha)) \end{aligned}$$

If you link the covariates to λ with $\lambda_i = \mathbf{x}_i' \boldsymbol{\beta}$, where $\mathbf{x}_i$ is the vector of covariates corresponding to the i th observation and $\boldsymbol{\beta}$ is a vector of regression coefficients, the log-likelihood function becomes this:

$$l(\alpha, \boldsymbol{\beta} | t, \mathbf{x}) = \sum_{i=1}^n v_i (\log(\alpha) + (\alpha - 1) \log(t_i) + \mathbf{x}_i' \boldsymbol{\beta}) - \exp(\mathbf{x}_i' \boldsymbol{\beta}) t_i^\alpha$$

As with the exponential model, in the absence of prior information about the parameters in this model, you can use diffuse normal priors on $\boldsymbol{\beta}$. You might want to choose a diffuse gamma distribution for α . Note that when $\alpha = 1$, the Weibull survival likelihood reduces to the exponential survival likelihood. Equivalently, by looking at the posterior distribution of α , you can conclude whether fitting an exponential survival model would be more appropriate than the Weibull model.

PROC MCMC also enables you to make inference on any functions of the parameters. Quantities of interest in survival analysis include the value of the survival function at specific times for specific treatments and the relationship between the survival curves for different treatments. With PROC MCMC, you can compute a sample from the posterior distribution of the interested survival functions at any number of points. The data in this example range from about 0 to 10 years, and the treatment of interest is the use of interferon.

Like in the previous exponential model example, there are two ways to fit this model: using the SAS functions LOGPDF and LOGSDF, or using the simplified log likelihood functions. The example uses the latter method. The following statements run PROC MCMC and produce [Output 55.13.4](#):

```

title 'Weibull Survival Model';
proc mcmc data=e1684 outpost=weisurvout nmc=10000 seed=1234
    monitor=(_parms_ surv_ifn surv_noifn);
    ods select PostSummaries;
    ods output PostSummaries=ds PostIntervals=is;
    array surv_ifn[10];
    array surv_noifn[10];
    parms alpha 1 (beta0 beta1) 0;
    prior beta: ~ normal(0, var=10000);
    prior alpha ~ gamma(0.001,is=0.001);

    beginnodata;
        do t1 = 1 to 10;
            surv_ifn[t1] = exp(-exp(beta0+beta1)*t1**alpha);
            surv_noifn[t1] = exp(-exp(beta0)*t1**alpha);
        end;
    endnodata;

    lambda = beta0 + beta1*ifn;
    /******
    /* (1) the logpdf and logsdf functions are not used */
    /******
    /*      gamma = exp(-lambda /alpha);
    /*      llike = v*logpdf('weibull', t, alpha, gamma) +
    /*              (1-v)*logsdf('weibull', t, alpha, gamma);
    /*
    /******
    /* (2) the simplified likelihood formula is used */
    /******
    llike = v*(log(alpha) + (alpha-1)*log(t) + lambda) -
            exp(lambda)*(t**alpha);
    model general(llike);
run;

```

The **MONITOR=** option indicates the parameters and quantities of interest that PROC MCMC tracks. The symbol **_PARMS_** specifies all model parameters. The array **surv_ifn** stores the expected survival probabilities for patients who received interferon over a period of 10 years. Similarly, **surv_noifn** stores the expected survival probabilities for patients who did not received interferon.

The **BEGINNODATA** and **ENDNODATA** statements enclose the calculations for the survival probabilities. The assignment statements proceeding the **MODEL** statement calculate the log likelihood for the Weibull survival model. The **MODEL** statement specifies the log likelihood that you programmed.

An examination of the trace plots for α , β_0 , and β_1 (not displayed here) reveals that the sampling has gone well, with no particular concerns about the convergence or mixing of the chains.

Output 55.13.4 displays the posterior summary statistics.

Output 55.13.4 Posterior Summary Statistics

Weibull Survival Model						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	25%	50%	75%
alpha	10000	0.7891	0.0539	0.7514	0.7880	0.8260
beta0	10000	-1.3581	0.1369	-1.4519	-1.3597	-1.2624
beta1	10000	-0.2512	0.1541	-0.3541	-0.2606	-0.1521
surv_ifn1	10000	0.8175	0.0227	0.8027	0.8187	0.8331
surv_ifn2	10000	0.7066	0.0291	0.6874	0.7072	0.7265
surv_ifn3	10000	0.6203	0.0331	0.5983	0.6205	0.6436
surv_ifn4	10000	0.5495	0.0360	0.5253	0.5497	0.5747
surv_ifn5	10000	0.4899	0.0381	0.4635	0.4895	0.5170
surv_ifn6	10000	0.4390	0.0396	0.4118	0.4382	0.4666
surv_ifn7	10000	0.3949	0.0406	0.3669	0.3934	0.4223
surv_ifn8	10000	0.3564	0.0413	0.3281	0.3551	0.3840
surv_ifn9	10000	0.3225	0.0416	0.2940	0.3212	0.3505
surv_ifn10	10000	0.2926	0.0416	0.2638	0.2911	0.3208
surv_noifn1	10000	0.7719	0.0274	0.7535	0.7736	0.7913
surv_noifn2	10000	0.6401	0.0339	0.6171	0.6415	0.6635
surv_noifn3	10000	0.5415	0.0374	0.5161	0.5428	0.5662
surv_noifn4	10000	0.4635	0.0395	0.4365	0.4636	0.4890
surv_noifn5	10000	0.4001	0.0406	0.3725	0.3995	0.4261
surv_noifn6	10000	0.3475	0.0411	0.3195	0.3459	0.3745
surv_noifn7	10000	0.3034	0.0411	0.2758	0.3012	0.3299
surv_noifn8	10000	0.2661	0.0406	0.2384	0.2630	0.2921
surv_noifn9	10000	0.2342	0.0399	0.2069	0.2311	0.2592
surv_noifn10	10000	0.2069	0.0389	0.1803	0.2035	0.2312

An examination of the α parameter reveals that the exponential model might not be inappropriate here. The estimated posterior mean of α is 0.7856 with a posterior standard deviation of 0.0533. As noted previously, if $\alpha = 1$, then the Weibull survival distribution is the exponential survival distribution. With these data, you can see that the evidence is in favor of $\alpha < 1$. The value 1 is almost 4 posterior standard deviations away from the posterior mean. The following statements compute the posterior probability of the hypothesis that $\alpha < 1$:

```
proc format;
  value alphafmt low-<1 = 'alpha < 1' 1-high = 'alpha >= 1';
run;

proc freq data=weisurvout;
  tables alpha /nocum;
  format alpha alphafmt.;
run;
```

The PROC FREQ results are shown in [Output 55.13.5](#).

Output 55.13.5 Frequency Analysis of α

Weibull Survival Model		
The FREQ Procedure		
alpha	Frequency	Percent

alpha < 1	9998	99.98
alpha >= 1	2	0.02

The output from PROC FREQ shows that 100% of the 10000 simulated values for α are less than 1. This is a very strong indication that the exponential model is too restrictive to model these data well.

You can examine the estimated survival probabilities over time individually, either through the posterior summary statistics or by looking at the kernel density plots. Alternatively, you might find it more informative to examine these quantities in relation with each other. For example, you can use a side-by-side box plot to display these posterior distributions by using PROC SGPLOT (“[Statistical Graphics Using ODS](#)” on page 579). First you need to take the posterior output data set `Weisurvout` and stack variables that you want to plot. For example, to plot all the survival times for patients who received interferon, you want to stack `surv_inf1–surv_inf10`. The macro `%Stackdata` takes an input data set `dataset`, stacks the wanted variables `vars`, and outputs them into the output data set.

The following statements define the macro `stackdata`:

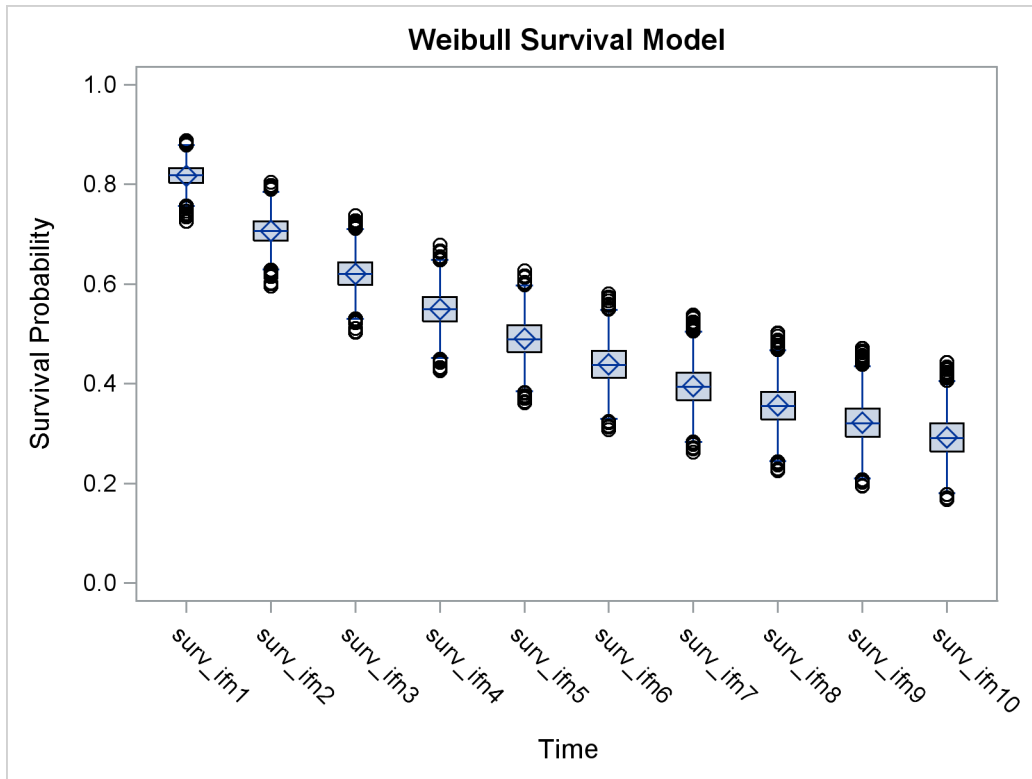
```
/* define macro stackdata */
%macro StackData(dataset,output,vars);
  data &output;
    length var $ 32;
    if 0 then set &dataset nobs=nnn;
    array l11[*] &vars;
    do jjj=1 to dim(l11);
      do iii=1 to nnn;
        set &dataset point=iii;
        value = l11[jjj];
        call vname(l11[jjj],var);
        output;
      end;
    end;
  stop;
  keep var value;
run;
%mend;

/* stack the surv_ifn variables and saved them to survifn. */
%StackData(weisurvout, survifn, surv_ifn1–surv_ifn10);
```

Once you stack the data, use PROC SGPLOT to create the side-by-side box plots. The following statements generate [Output 55.13.6](#):

```
proc sgplot data=survifn;
  yaxis label='Survival Probability' values=(0 to 1 by 0.2);
  xaxis label='Time' discreteorder=data;
  vbox value / category=var;
run;
```

Output 55.13.6 Side-by-Side Box Plots of Estimated Survival Probabilities



There is a clear decreasing trend over time of the survival probabilities for patients who receive the treatment. You might ask how does this group compare to those who did not receive the treatment? In this case, you want to overlay the two predicted curves for the two groups of patients and add the corresponding credible interval. See [Output 55.13.7](#). To generate the graph, you first take the posterior mean estimates from the ODS output table ds and the lower and upper HPD interval estimates is, store them in the data set Surv, and draw the figure by using PROC SGPLOT.

The following statements generate data set Surv:

```
data surv;
  set ds;
  if _n_ >= 4 then do;
    set is point=_n_;
    group = 'with interferon';
    time = _n_ - 3;
    if time > 10 then do;
      time = time - 10;
      group = 'without interferon';
    end;
  end;
```

```

output;
end;
keep time group mean hpdlower hpdupper;
run;

```

The following SGLOT statements generate [Output 55.13.7](#):

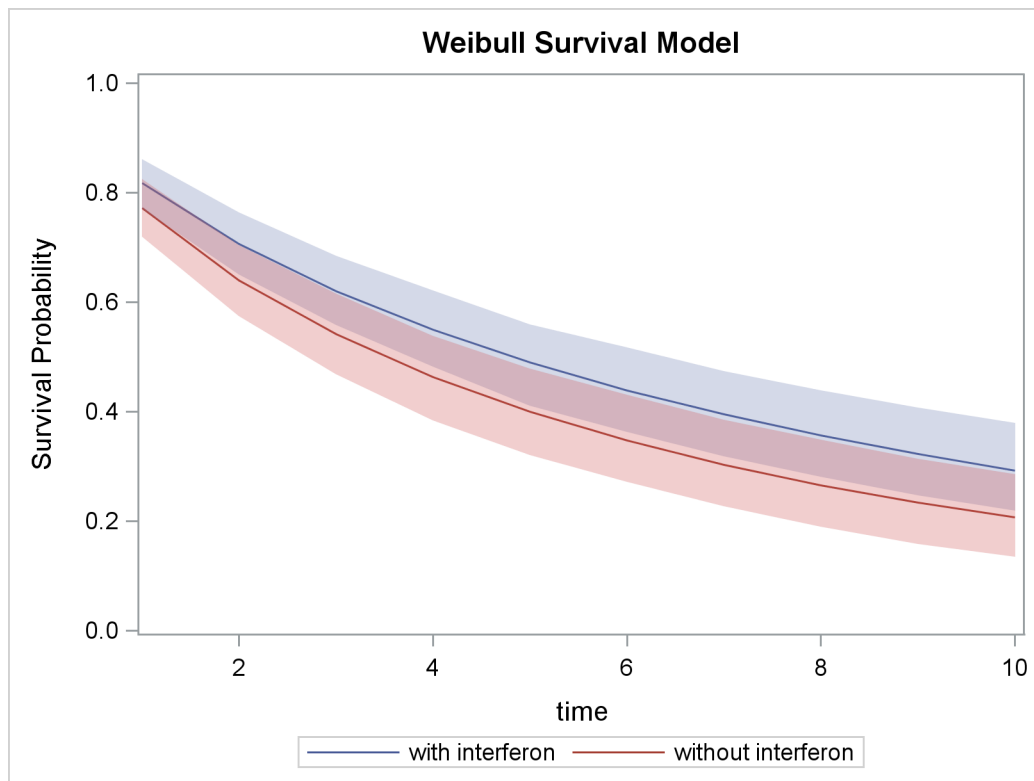
```

proc sgplot data=surv;
  yaxis label="Survival Probability" values=(0 to 1 by 0.2);
  series x=time y=mean / group = group name='i';
  band x=time lower=hpdlower upper=hpdupper / group = group transparency=0.7;
  keylegend 'i';
run;
ods graphics off;

```

In [Output 55.13.7](#), the solid line is the survival curve for patients who received interferon; the shaded region centers at the solid line is the 95% HPD intervals; the medium-dashed line is the survival curve for patients who did not receive interferon; and the shaded region around the dashed line is the corresponding 95% HPD intervals.

Output 55.13.7 Predicted Survival Probability Curves with 95% HPD Intervals



The plot suggests that there is an effect of using interferon because patients who received interferon have sustained better survival probabilities than those who did not. However, the effect might not be very significant, as the 95% credible intervals of the two groups do overlap. For more on these interferon studies, see Ibrahim, Chen, and Lipsitz (2001).

Weibull or Exponential?

Although the evidence from the Weibull model fit shows that the posterior distribution of α has a significant amount of density mass less than 1, suggesting that the Weibull model is a better fit to the data than the exponential model, you might still be interested in comparing the two models more formally. You can use the Bayesian model selection criterion (see the section “[Deviance Information Criterion \(DIC\)](#)” on page 155) to determine which model fits the data better.

The PROC MCMC [DIC](#) option requests the calculation of DIC, and the procedure displays the ODS output table [DIC](#). The table includes the posterior mean of the deviation, $\overline{D(\theta)}$, deviation at the estimate, $D(\hat{\theta})$, effective number of parameters, p_D , and DIC. It is important to remember that the standardizing term, $p(y)$, which is a function of the data alone, is not taken into account in calculating the DIC. This term is irrelevant only if you compare two models that have the *same* likelihood function. If you do not have identical likelihood functions, using DIC for model selection purposes without taking this standardizing term into account can produce incorrect results. In addition, you want to be careful in interpreting the DIC whenever you use the [GENERAL](#) function to construct the log-likelihood, as the case in this example. Using the [GENERAL](#) function, you can obtain identical posterior samples with two log-likelihood functions that differ only by a constant. This difference translates to a difference in the DIC calculation, which could be very misleading.

If $\alpha = 1$, the Weibull likelihood is identical to the exponential likelihood. It is safe in this case to directly compare DICs from these two models. However, if you do not want to work out the mathematical detail or you are uncertain of the equivalence, a better way of comparing the DICs is to run the Weibull model twice: once with α being a parameter and once with $\alpha = 1$. This ensures that the likelihood functions are the same, and the DIC comparison is meaningful.

The following statements fit a Weibull model:

```
title 'Model Comparison between Weibull and Exponential';
proc mcmc data=e1684 outpost=weisurvout nmc=10000 seed=4861 dic;
  ods select dic;
  parms alpha 1 (beta0 betal) 0;
  prior beta: ~ normal(0, var=10000);
  prior alpha ~ gamma(0.001,is=0.001);

  lambda = beta0 + betal*ifn;
  llike = v*(log(alpha) + (alpha-1)*log(t) + lambda) -
          exp(lambda)*(t**alpha);
  model general(llike);
run;
```

The **DIC** option requests the calculation of DIC, and the table is displayed in [Output 55.13.8](#).

Output 55.13.8 DIC Table from the Weibull Model

Model Comparison between Weibull and Exponential	
The MCMC Procedure	
Deviance Information Criterion	
Dbar (posterior mean of deviance)	858.623
Dmean (deviance evaluated at posterior mean)	855.633
pD (effective number of parameters)	2.990
DIC (smaller is better)	861.614
The GENERAL or DGENERAL function is used in this program. To make meaningful comparisons, you must ensure that all GENERAL or DGENERAL functions include appropriate normalizing constants. Otherwise, DIC comparisons can be misleading.	

The note in [Output 55.13.8](#) reminds you of the importance of ensuring identical likelihood functions when you use the **GENERAL** function. The DIC value is 861.6.

Based on the same set of code, the following statements fit an exponential model by setting $\alpha = 1$:

```
proc mcmc data=e1684 outpost=expsurvout nmc=10000 seed=4861 dic;
  ods select dic;
  parms beta0 beta1 0;
  prior beta: ~ normal(0, var=10000);
  begincnst;
    alpha = 1;
  endcnst;

  lambda = beta0 + beta1*ifn;
  llike = v*(log(alpha) + (alpha-1)*log(t) + lambda) -
    exp(lambda)*(t**alpha);
  model general(llike);
run;
```

[Output 55.13.9](#) displays the DIC table.

Output 55.13.9 DIC Table from the Exponential Model

Model Comparison between Weibull and Exponential	
The MCMC Procedure	
Deviance Information Criterion	
Dbar (posterior mean of deviance)	870.133
Dmean (deviance evaluated at posterior mean)	868.190
pD (effective number of parameters)	1.943
DIC (smaller is better)	872.075
The GENERAL or DGENERAL function is used in this program. To make meaningful comparisons, you must ensure that all GENERAL or DGENERAL functions include appropriate normalizing constants. Otherwise, DIC comparisons can be misleading.	

The DIC value of 872.075 is greater than 861. A smaller DIC indicates a better fit to the data; hence, you can conclude that the Weibull model is more appropriate for this data set. You can see the equivalencing of the exponential model you fitted in “[Exponential Survival Model](#)” on page 4605 by running the following comparison.

The following statements are taken from the section “[Exponential Survival Model](#)” on page 4605, and they fit the same exponential model:

```
proc mcmc data=e1684 outpost=expsurvout1 nmc=10000 seed=4861 dic;
  ods select none;
  parms (beta0 beta1) 0;
  prior beta: ~ normal(0, sd = 10000);
  l_h = beta0 + beta1*ifn;
  llike = v*(l_h) - t*exp(l_h);
  model general(llike);
run;

proc compare data=expsurvout compare=expsurvout1;
  var beta0 beta1;
run;
```

The posterior samples of beta0 and beta1 in the data set Expsurvout1 are identical to those in the data set Expsurvout. The comparison results are not shown here.

Example 55.14: Time Independent Cox Model

This example has two purposes. One is to illustrate how to use PROC MCMC to fit a Cox proportional hazard model. Specifically, the time independent model. See “[Example 55.15: Time Dependent Cox Model](#)” on page 4625 for an example on fitting time dependent Cox model. Note that it is much easier to fit a Bayesian Cox model by specifying the BAYES statement in PROC PHREG (see Chapter 67, “[The PHREG Procedure](#)”). If you are interested only in fitting a Cox regression survival model, you should use PROC PHREG.

The second objective of this example is to demonstrate how to model data that are not independent. That is the case where the likelihood for observation i depends on other observations in the data set. In other words, if you work with a likelihood function that cannot be broken down simply as $L(\mathbf{y}) = \prod_i^n L(y_i)$, you can use this example for illustrative purposes. By default, PROC MCMC assumes that the programming statements and model specification is intended for a single row of observations in the data set. The Cox model is chosen because the complexity in the data structure requires more elaborate coding.

The Cox proportional hazard model is widely used in the analysis of survival time, failure time, or other duration data to explain the effect of exogenous explanatory variables. The data set used in this example is taken from Krall, Uthoff, and Harley (1975), who analyzed data from a study on myeloma in which researchers treated 65 patients with alkylating agents. Of those patients, 48 died during the study and 17 survived. The following statements generate the data set that is used in this example:

```
data Myeloma;
  input Time Vstatus LogBUN HGB Platelet Age LogWBC Frac
        LogPBM Protein SCalc;
  label Time='survival time'
        VStatus='0=alive 1=dead';
  datalines;
1.25 1 2.2175 9.4 1 67 3.6628 1 1.9542 12 10
1.25 1 1.9395 12.0 1 38 3.9868 1 1.9542 20 18
2.00 1 1.5185 9.8 1 81 3.8751 1 2.0000 2 15
2.00 1 1.7482 11.3 0 75 3.8062 1 1.2553 0 12

... more lines ...

77.00 0 1.0792 14.0 1 60 3.6812 0 0.9542 0 12
;

proc sort data = Myeloma;
  by descending time;
run;

data _null_;
  set Myeloma nobs=_n;
  call symputx('N', _n);
  stop;
run;
```

The variable Time represents the survival time in months from diagnosis. The variable VStatus consists of two values, 0 and 1, indicating whether the patient was alive or dead, respectively, at the end of the study. If the value of VStatus is 0, the corresponding value of Time is censored. The variables thought to be related to survival are LogBUN (log(BUN) at diagnosis), HGB (hemoglobin at diagnosis), Platelet (platelets at diagnosis: 0=abnormal, 1=normal), Age (age at diagnosis in years), LogWBC (log(WBC) at diagnosis), Frac (fractures at diagnosis: 0=none, 1=present), LogPBM (log percentage of plasma cells in bone marrow), Protein (proteinuria at diagnosis), and SCalc (serum calcium at diagnosis). Interest lies in identifying important prognostic factors from these explanatory variables. In addition, there are 65 (&n) observations in the data set Myeloma. The likelihood used in these examples is the Breslow likelihood:

$$L(\boldsymbol{\beta}) = \prod_{i=1}^n \left[\prod_{j=1}^{d_i} \frac{\exp(\boldsymbol{\beta}' \mathbf{Z}_j(t_i))}{\sum_{l \in \mathcal{R}_i} \exp(\boldsymbol{\beta}' \mathbf{Z}_l(t_i))} \right]^{v_i}$$

where

- β is the vector parameters
- n is the total number of observations in the data set
- t_i is the i th time, which can be either event time or censored time
- $\mathbf{Z}_l(t)$ is the vector explanatory variables for the l th individual at time t
- d_i is the multiplicity of failures at t_i . If there are no ties in time, d_i is 1 for all i .
- $\mathcal{R}_i$ is the risk set for the i th time t_i , which includes all observations that have survival time greater than or equal to t_i
- v_i indicates whether the patient is censored. The value 0 corresponds to censoring. Note that the censored time t_i enters the likelihood function only through the formation of the risk set $\mathcal{R}_i$.

Priors on the coefficients are independent normal priors with very large variance (1e6). Throughout this example, the symbol $\mathbf{bZ}$ represents the regression term $\beta' \mathbf{Z}_j(t_i)$ in the likelihood, and the symbol $\mathbf{S}$ represents the term $\sum_{l \in \mathcal{R}_i} \exp(\beta' \mathbf{Z}_l(t_i))$.

The regression model considered in this example uses the following formula:

$$\begin{aligned} \beta' \mathbf{Z}_j = & \beta_1 \text{logbun} + \beta_2 \text{hgb} + \beta_3 \text{platelet} + \beta_4 \text{age} + \\ & \beta_5 \text{logwbc} + \beta_6 \text{frac} + \beta_7 \text{logpbm} + \beta_8 \text{protein} + \beta_9 \text{scal} \end{aligned}$$

The hard part of coding this in PROC MCMC is the construction of the risk set $\mathcal{R}_i$. $\mathcal{R}_i$ contains all observations that have survival time greater than or equal to t_i . First suppose that there are no ties in time. Sorting the data set by the variable time into descending order gives you $\mathcal{R}_i$ that is in the right order. Observation i 's risk set consists of all data points j such that $j \leq i$ in the data set. You can cumulatively increment $\mathbf{S}$ in the SAS statements.

With potential ties in time, at observation i , you need to know whether any subsequent observations, $i + 1$ and so on, have the same survival time as t_i . Suppose that the i th, the $i + 1$, and the $i + 2$ observations all have the same survival time; all three of them need to be included in the risk set calculation. This means that to calculate the likelihood for some observations, you need to access both the previous and subsequent observations in the data set. There are two ways to do this. One is to use the LAG function; the other is to use the option [JOINTMODEL](#).

The LAG function returns values from a queue (see *SAS Language Reference: Dictionary*). So for the i th observation, you can use LAG1 to access variables from the previous row in the data set. You want to compare the lag1 value of time with the current time value. Depending on whether the two time values are equal, you can add correction terms in the calculation for the risk set $\mathbf{S}$.

The following statements sort the data set by time into descending order, with the largest survival time on top:

```

title 'Cox Model with Time Independent Covariates';
proc freq data=myeloma;
    ods select none;
    tables time / out=freqs;
run;

proc sort data = freqs;
    by descending time;
run;

data myelomaM;
    set myeloma;
    ind = _N_;
run;
ods select all;

```

The following statements run PROC MCMC and produce [Output 55.14.1](#):

```

proc mcmc data=myelomaM outpost=outi nmc=50000 ntu=3000 seed=1;
    ods select PostSummaries PostIntervals;
    array beta[9];
    parms beta: 0;
    prior beta: ~ normal(0, var=1e6);

    bZ = beta1 * LogBUN + beta2 * HGB + beta3 * Platelet
        + beta4 * Age + beta5 * LogWBC + beta6 * Frac +
        beta7 * LogPBM + beta8 * Protein + beta9 * SCalc;

    if ind = 1 then do;                /* first observation          */
        S = exp(bZ);
        l = vstatus * bZ;
        v = vstatus;
    end;
    else if (1 < ind < &N) then do;
        if (lag1(time) ne time) then do;
            l = vstatus * bZ;
            l = l - v * log(S); /* correct the loglike value */
            v = vstatus;        /* reset v count value   */
            S = S + exp(bZ);
        end;
        else do;                /* still a tie           */
            l = vstatus * bZ;
            S = S + exp(bZ);
            v = v + vstatus;    /* add # of nonsensored values */
        end;
    end;
    else do;                    /* last observation      */
        if (lag1(time) ne time) then do;
            l = - v * log(S); /* correct the loglike value */
            S = S + exp(bZ);
            l = l + vstatus * (bZ - log(S));
        end;
        else do;

```

```

      S = S + exp(bZ) ;
      l = vstatus * bZ - (v + vstatus) * log(S) ;
    end;
  end;
  model general(l) ;
run;

```

The symbol bZ is the regression term, which is independent of the time variable. The symbol ind indexes observation numbers in the data set. The symbol S keeps track of the risk set term for every observation. The symbol l calculates the log likelihood for each observation. Note that the value of l for observation ind is not necessarily the correct log likelihood value for that observation, especially in cases where the observation ind is in the tied times. Correction terms are added to subsequent values of l when the time variable becomes different in order to make up the difference. The total sum of l calculated over the entire data set is correct. The symbol v keeps track of the sum of $vstatus$, as censored data do not enter the likelihood and need to be taken out.

You use the function `LAG1` to detect if two adjacent time values are different. If they are, you know that the current observation is in a different risk set than the last one. You then need to add a correction term to the log likelihood value of l . The IF-ELSE statements break the observations into three parts: the first observation, the last observation and everything in the middle.

Output 55.14.1 Summary Statistics on Cox Model with Time Independent Explanatory Variables and Ties in the Survival Time, Using PROC MCMC

Cox Model with Time Independent Covariates						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	25%	Percentiles 50%	75%
beta1	50000	1.7600	0.6441	1.3275	1.7651	2.1947
beta2	50000	-0.1308	0.0720	-0.1799	-0.1304	-0.0817
beta3	50000	-0.2017	0.5148	-0.5505	-0.1965	0.1351
beta4	50000	-0.0126	0.0194	-0.0257	-0.0128	0.000641
beta5	50000	0.3373	0.7256	-0.1318	0.3505	0.8236
beta6	50000	0.3992	0.4337	0.0973	0.3864	0.6804
beta7	50000	0.3749	0.4861	0.0464	0.3636	0.6989
beta8	50000	0.0106	0.0271	-0.00723	0.0118	0.0293
beta9	50000	0.1272	0.1064	0.0579	0.1300	0.1997

Output 55.14.1 *continued*

Parameter	Alpha	Posterior Intervals			
		Equal-Tail Interval		HPD Interval	
beta1	0.050	0.4649	3.0214	0.5117	3.0465
beta2	0.050	-0.2704	0.0114	-0.2746	0.00524
beta3	0.050	-1.2180	0.8449	-1.2394	0.7984
beta4	0.050	-0.0501	0.0257	-0.0512	0.0245
beta5	0.050	-1.1233	1.7232	-1.1124	1.7291
beta6	0.050	-0.4136	1.2970	-0.4385	1.2575
beta7	0.050	-0.5551	1.3593	-0.5423	1.3689
beta8	0.050	-0.0451	0.0618	-0.0451	0.0616
beta9	0.050	-0.0933	0.3272	-0.0763	0.3406

An alternative to using the LAG function is to use the PROC option [JOINTMODEL](#). With this option, the log-likelihood function you specify applies not to a single observation but to the entire data set. See “[Modeling Joint Likelihood](#)” on page 4504 for details on how to properly use this option. The basic idea is that you store all necessary data set variables in arrays and use only the arrays to construct the log likelihood of the entire data set. This approach works here because for every observation i , you can use index to access different values of arrays to construct the risk set S . To use the [JOINTMODEL](#) option, you need to do some additional data manipulation. You want to create a stop variable for each observation, which indicates the observation number that should be included in S for that observation. For example, if observations 4, 5, 6 all have the same survival time, the stop value for all of them is 6.

The following statements generate a new data set MyelomaM that contains the stop variable:

```
data myelomaM;
  merge myelomaM freqs(drop=percent);
  by descending time;
  retain stop;
  if first.time then do;
    stop = _n_ + count - 1;
  end;
run;
```

The following SAS program fits the same Cox model by using the [JOINTMODEL](#) option:

```
data a;
run;

proc mcmc data=a outpost=outa nmc=50000 ntu=3000 seed=1 jointmodel;
  ods select none;
  array beta[9];
  array data[1] / nosymbols;
  array timeA[1] / nosymbols;
  array vstatusA[1] / nosymbols;
  array stopA[1] / nosymbols;
  array bZ[&n];
  array S[&n];

  beginncnst;
```



```

rc = read_array("myelomam", data, "logbun", "hgb", "platelet",
               "age", "logwbc", "frac", "logpbm", "protein", "scalp");
rc = read_array("myelomam", timeA, "time");
rc = read_array("myelomam", vstatusA, "vstatus");
rc = read_array("myelomam", stopA, "stop");
endcnst;

parms (beta:) 0;
prior beta: ~ normal(0, var=1e6);

jl = 0;
/* calculate each bZ and cumulatively adding S as if there are no ties.*/
call mult(data, beta, bZ);
S[1] = exp(bZ[1]);
do i = 2 to &n;
    S[i] = S[i-1] + exp(bZ[i]);
end;

do i = 1 to &n;
    /* correct the S[i] term, when needed. */
    if(stopA[i] > i) then do;
        do j = (i+1) to stopA[i];
            S[i] = S[i] + exp(bZ[j]);
        end;
    end;
    jl = jl + vstatusA[i] * (bZ[i] - log(S[i]));
end;
model general(jl);
run;
ods select all;

```

No output tables were produced because this PROC MCMC run produces identical posterior samples as does the previous example.

Because the [JOINTMODEL](#) option is specified here, you do not need to specify myelomaM as the input data set. An empty data set a is used to speed up the procedure run.

Multiple [ARRAY](#) statements allocate array symbols that are used to store the parameters (beta), the response and the covariates (data, timeA, vstatusA, and stopA), and the work space (bZ and S). The data, timeA, vstatusA, and stopA arrays are declared with the [/NOSYMBOLS](#) option. This option enables PROC MCMC to dynamically resize these arrays to match the dimensions of the input data set. See the section “[READ_ARRAY Function](#)” on page 4442. The bZ and S arrays store the regression term and the risk set term for every observation.

The [BEGINCNST](#) and [ENDCNST](#) statements enclose programming statements that read the data set variables into these arrays. The rest of the programming statements construct the log likelihood for the entire data set.

The CALL MULT function calculates the regression term in the model and stores the result in the array bZ. In the first DO loop, you sum the risk set term S as if there are no ties in time. This underevaluates some of the S elements. For observations that have a tied time, you make the necessary correction to the corresponding S values. The correction takes place in the second DO loop. Any observation that has a tied time also has a stopA[i] that is different from i. You add the right terms to S and sum up the joint log likelihood jl. The [MODEL](#) statement specifies that the log likelihood takes on the value of jl.

To see that you get identical results from these two approaches, use PROC COMPARE to compare the posterior samples from two runs:

```
proc compare data=outi compare=outa;
  ods select comparesummary;
  var beta1-beta9;
run;
```

The output is not shown here.

Generally, the **JOINTMODEL** option can be slightly faster than using the default setup. The savings come from avoiding the overhead cost of accessing the data set repeatedly at every iteration. However, the speed gain is not guaranteed because it largely depends on the efficiency of your programs.

PROC PHREG fits the same model, and you get very similar results to PROC MCMC. The following statements fit the model using PROC PHREG and produce [Output 55.14.2](#):

```
proc phreg data=Myeloma;
  ods select PostSummaries PostIntervals;
  model Time*VStatus(0)=LogBUN HGB Platelet Age LogWBC
    Frac LogPBM Protein ScalC;
  bayes seed=1 nmc=10000 outpost=phout;
run;
```

Output 55.14.2 Summary Statistics for Cox Model with Time Independent Explanatory Variables and Ties in the Survival Time, Using PROC PHREG

Cox Model with Time Independent Covariates						
The PHREG Procedure						
Bayesian Analysis						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
LogBUN	10000	1.7610	0.6593	1.3173	1.7686	2.2109
HGB	10000	-0.1279	0.0727	-0.1767	-0.1287	-0.0789
Platelet	10000	-0.2179	0.5169	-0.5659	-0.2360	0.1272
Age	10000	-0.0130	0.0199	-0.0264	-0.0131	0.000492
LogWBC	10000	0.3150	0.7451	-0.1718	0.3321	0.8253
Frac	10000	0.3766	0.4152	0.0881	0.3615	0.6471
LogPBM	10000	0.3792	0.4909	0.0405	0.3766	0.7023
Protein	10000	0.0102	0.0267	-0.00745	0.0106	0.0283
SCalc	10000	0.1248	0.1062	0.0545	0.1273	0.1985

Output 55.14.2 continued

Parameter	Posterior Intervals				
	Alpha	Equal-Tail Interval		HPD Interval	
LogBUN	0.050	0.4418	3.0477	0.4107	2.9958
HGB	0.050	-0.2718	0.0150	-0.2801	0.00599
Platelet	0.050	-1.1952	0.8296	-1.1871	0.8341
Age	0.050	-0.0514	0.0259	-0.0519	0.0251
LogWBC	0.050	-1.2058	1.7228	-1.1783	1.7483
Frac	0.050	-0.3995	1.2316	-0.4273	1.2021
LogPBM	0.050	-0.5652	1.3671	-0.5939	1.3241
Protein	0.050	-0.0437	0.0611	-0.0405	0.0637
SCalc	0.050	-0.0935	0.3264	-0.0846	0.3322

Example 55.15: Time Dependent Cox Model

This example uses the same Myeloma data set as in “[Example 55.14: Time Independent Cox Model](#)” on page 4617, and illustrates the fitting of a time dependent Cox model. The following statements generate the data set once again:

```
data Myeloma;
  input Time Vstatus LogBUN HGB Platelet Age LogWBC Frac
        LogPBM Protein SCalc;
  label Time='survival time'
        VStatus='0=alive 1=dead';
  datalines;
1.25 1 2.2175 9.4 1 67 3.6628 1 1.9542 12 10
1.25 1 1.9395 12.0 1 38 3.9868 1 1.9542 20 18
2.00 1 1.5185 9.8 1 81 3.8751 1 2.0000 2 15
2.00 1 1.7482 11.3 0 75 3.8062 1 1.2553 0 12

... more lines ...

77.00 0 1.0792 14.0 1 60 3.6812 0 0.9542 0 12
;
```

To model $\mathbf{Z}_i(t_i)$ as a function of the survival time, you can relate time t_i to covariates by using this formula:

$$\boldsymbol{\beta}'\mathbf{Z}_j(t_i) = (\beta_1 + \beta_2 t_i)\text{logbun} + (\beta_3 + \beta_4 t_i)\text{hgb} + (\beta_5 + \beta_6 t_i)\text{platelet}$$

For illustrational purposes, only three explanatory variables, LOGBUN, HGB, and PLATELET, are used in this example.

Since $\mathbf{Z}_j(t_i)$ depends on t_i , every term in the summation of $\sum_{l \in \mathcal{R}_i} \exp(\boldsymbol{\beta}'\mathbf{Z}_l(t_i))$ is a product of the current time t_i and all observations that are in the risk set. You can use the **JOINTMODEL** option, as in the last example, or you can modify the input data set such that every row contains not only the current observation but also all observations that are in the corresponding risk set. When you construct the log likelihood for each observation, you have all the relevant data at your disposal.

The following statements illustrate how you can create a new data set with different risk sets at different rows:

```

title 'Cox Model with Time Dependent Covariates';
proc sort data = Myeloma;
    by descending time;
run;

data _null_;
    set Myeloma nobs=_n;
    call symputx('N', _n);
    stop;
run;

ods select none;
proc freq data=myeloma;
    tables time / out=freqs;
run;
ods select all;

proc sort data = freqs;
    by descending time;
run;

data myelomaM;
    set myeloma;
    ind = _N_;
run;

data myelomaM;
    merge myelomaM freqs(drop=percent); by descending time;
    retain stop;
    if first.time then do;
        stop = _n_ + count - 1;
    end;
run;

%macro array(list);
    %global mcmccarray;
    %let mcmccarray = ;
    %do i = 1 %to 32000;
        %let v = %scan(&list, &i, %str( ));
        %if %nrbquote(&v) ne %then %do;
            array _&v[&n];
            %let mcmccarray = &mcmccarray array _&v[&n] _&v.1 - _&v.&n%str(;;);
            do i = 1 to stop;
                set myelomaM(keep=&v) point=i;
                _&v[i] = &v;
            end;
        %end;
    %else %let i = 32001;
    %end;
%mend;

```

```

data z;
    set myelomaM;
    %array(logbun hgb platelet);
    drop vstatus logbun hgb platelet count stop;
run;

data myelomaM;
    merge myelomaM z; by descending time;
run;

```

The data set MyelomaM contains 65 observations and 209 variables. For each observation, you see added variables stop, _logbun1 through _logbun65, _hgb1 through _hgb65, and _platelet1 through _platelet65. The variable stop indicates the number of observations that are in the risk set of the current observation. The rest are transposed values of model covariates of the entire data set. The data set contains a number of missing values. This is due to the fact that only the relevant observations are kept, such as _logbun1 to _logbunstop. The rest of the cells are filled in with missing values. For example, the first observation has a unique survival time of 92 and stop is 1, making it a risk set of itself. You see nonmissing values only in _logbun1, _hgb1, and _platelet1.

The following statements fit the Cox model by using PROC MCMC:

```

proc mcmc data=myelomaM outpost=outi nmc=50000 ntu=3000 seed=17
    missing=ac;
    ods select PostSummaries PostIntervals;
    array beta[6];
    &mcmcarray
    parms (beta:) 0;
    prior beta: ~ normal(0, prec=1e-6);

    b = (beta1 + beta2 * time) * logbun +
        (beta3 + beta4 * time) * hgb +
        (beta5 + beta6 * time) * platelet;
    S = 0;
    do i = 1 to stop;
        S = S + exp( (beta1 + beta2 * time) * _logbun[i] +
                    (beta3 + beta4 * time) * _hgb[i] +
                    (beta5 + beta6 * time) * _platelet[i]);
    end;
    loglike = vstatus * (b - log(S));

    model general(loglike);
run;

```

Note that the option **MISSING=** is set to AC. This is due to missing cells in the input data set. You must use this option so that PROC MCMC retains observations that contain missing values.

The macro variable &mcmcarray is defined in the earlier part in this example. You can use a **%put** statement to print its value:

```
%put &mcmcarray;
```

This statement prints the following:

```
array _logbun[65] _logbun1 - _logbun65; array _hgb[65] _hgb1 - _hgb65; array
```

```
_platelet[65] _platelet1 - _platelet65;
```

The macro uses the [ARRAY](#) statement to allocate three arrays, each of which links their corresponding data set variables. This makes it easier to reference these data set variables in the program. The [PARMS](#) statement puts all the parameters in the same block. The [PRIOR](#) statement gives them normal priors with large variance. The symbol *b* is the regression term, and *S* is cumulatively added from 1 to stop for each observation in the DO loop. The symbol *loglike* completes the construction of log likelihood for each observation and the [MODEL](#) statement completes the model specification.

Posterior summary and interval statistics are shown in [Output 55.15.1](#).

Output 55.15.1 Summary Statistics on Cox Model with Time Dependent Explanatory Variables and Ties in the Survival Time, Using PROC MCMC

Cox Model with Time Dependent Covariates						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
beta1	50000	3.2397	0.8226	2.6835	3.2413	3.7830
beta2	50000	-0.1411	0.0471	-0.1722	-0.1406	-0.1092
beta3	50000	-0.0369	0.1017	-0.1064	-0.0373	0.0315
beta4	50000	-0.00409	0.00360	-0.00656	-0.00408	-0.00167
beta5	50000	0.3548	0.7359	-0.1634	0.3530	0.8445
beta6	50000	-0.0417	0.0359	-0.0661	-0.0423	-0.0181
Posterior Intervals						
Parameter	Alpha	Equal-Tail Interval		HPD Interval		
beta1	0.050	1.6399	4.8667	1.6664	4.8752	
beta2	0.050	-0.2351	-0.0509	-0.2294	-0.0458	
beta3	0.050	-0.2337	0.1642	-0.2272	0.1685	
beta4	0.050	-0.0111	0.00282	-0.0112	0.00264	
beta5	0.050	-1.0317	1.8202	-1.0394	1.8100	
beta6	0.050	-0.1107	0.0295	-0.1122	0.0269	

You can also use the option [JOINTMODEL](#) to get the same inference and avoid transposing the data for every observation:

```
proc mcmc data=myelomaM outpost=outa nmc=50000 ntu=3000 seed=17 jointmodel;
ods select none;
array beta[6];          array timeA[&n];          array vstatusA[&n];
array logbunA[&n];      array hgbA[&n];          array plateletA[&n];
array stopA[&n];        array bZ[&n];            array S[&n];

begincnst;
timeA[ind]=time;          vstatusA[ind]=vstatus;
```

```

        logbunA[ind]=logbun;      hgbA[ind]=hgb;
        plateletA[ind]=platelet;  stopA[ind]=stop;
    endcnst;

    parms (beta:) 0;
    prior beta: ~ normal(0, prec=1e-6);

    j1 = 0;
    do i = 1 to &n;
        v1 = beta1 + beta2 * timeA[i];
        v2 = beta3 + beta4 * timeA[i];
        v3 = beta5 + beta6 * timeA[i];
        bZ[i] = v1 * logbunA[i] + v2 * hgbA[i] + v3 * plateletA[i];

        /* sum over risk set without considering ties in time. */
        S[i] = exp(bZ[i]);
        if (i > 1) then do;
            do j = 1 to (i-1);
                b1 = v1 * logbunA[j] + v2 * hgbA[j] + v3 * plateletA[j];
                S[i] = S[i] + exp(b1);
            end;
        end;
    end;

    /* make correction to the risk set due to ties in time. */
    do i = 1 to &n;
        if(stopA[i] > i) then do;
            v1 = beta1 + beta2 * timeA[i];
            v2 = beta3 + beta4 * timeA[i];
            v3 = beta5 + beta6 * timeA[i];
            do j = (i+1) to stopA[i];
                b1 = v1 * logbunA[j] + v2 * hgbA[j] + v3 * plateletA[j];
                S[i] = S[i] + exp(b1);
            end;
        end;
        j1 = j1 + vstatusA[i] * (bZ[i] - log(S[i]));
    end;
    model general(j1);
run;

```

The multiple **ARRAY** statements allocate array symbols that are used to store the parameters (beta), the response (timeA), the covariates (vstatusA, logbunA, hgbA, plateletA, and stopA), and work space (bZ and S). The bZ and S arrays store the regression term and the risk set term for every observation. Programming statements in the **BEGINCNST** and **ENDCNST** statements input the response and covariates from the data set to the arrays.

Using the same technique shown in the example “[Example 55.14: Time Independent Cox Model](#)” on page 4617, the next DO loop calculates the regression term and corresponding S for every observation, pretending that there are no ties in time. This means that the risk set for observation *i* involves only observation 1 to *i*. The correction terms are added to the corresponding S[i] in the second DO loop, conditional on whether the stop variable is greater than the observation count itself. The symbol j1 cumulatively adds the log likelihood for the entire data set, and the **MODEL** statement specifies the joint log-likelihood function.

The following statements run PROC COMPARE and show that the output data set outa contains identical posterior samples as outi:

```
proc compare data=outi compare=outa;
  ods select comparesummary;
  var betal-beta6;
run;
```

The results are not shown here.

The following statements use PROC PHREG to fit the same time dependent Cox model:

```
proc phreg data=Myeloma;
  ods select PostSummaries PostIntervals;
  model Time*VStatus(0)=LogBUN z2 hgb z3 platelet z4;
  z2 = Time*logbun;
  z3 = Time*hgb;
  z4 = Time*platelet;
  bayes seed=1 nmc=10000 outpost=phout;
run;
```

Coding is simpler than PROC MCMC. See [Output 55.15.2](#) for posterior summary and interval statistics:

Output 55.15.2 Summary Statistics on Cox Model with Time Dependent Explanatory Variables and Ties in the Survival Time, Using PROC PHREG

Cox Model with Time Dependent Covariates						
The PHREG Procedure						
Bayesian Analysis						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles 25%	50%	75%
LogBUN	10000	3.2423	0.8311	2.6838	3.2445	3.7929
z2	10000	-0.1401	0.0482	-0.1723	-0.1391	-0.1069
HGB	10000	-0.0382	0.1009	-0.1067	-0.0385	0.0297
z3	10000	-0.00407	0.00363	-0.00652	-0.00404	-0.00162
Platelet	10000	0.3778	0.7524	-0.1500	0.3389	0.8701
z4	10000	-0.0419	0.0364	-0.0660	-0.0425	-0.0178
Posterior Intervals						
Parameter	Alpha	Equal-Tail Interval		HPD Interval		
LogBUN	0.050	1.6059	4.8785	1.5925	4.8582	
z2	0.050	-0.2361	-0.0494	-0.2354	-0.0492	
HGB	0.050	-0.2343	0.1598	-0.2331	0.1603	
z3	0.050	-0.0113	0.00297	-0.0109	0.00322	
Platelet	0.050	-0.9966	1.9464	-1.1342	1.7968	
z4	0.050	-0.1124	0.0296	-0.1142	0.0274	

Example 55.16: Piecewise Exponential Frailty Model

This example illustrates how to fit a piecewise exponential frailty model using PROC MCMC. Part of the notation and presentation in this example follows Clayton (1991) and the Luek example in Spiegelhalter et al. (1996a).

Generally speaking, the proportional hazards model assumes the hazard function,

$$\lambda_i(t|\mathbf{z}_i) = \lambda_0(t) \exp\{\boldsymbol{\beta}'\mathbf{z}_i\}$$

where $i = 1 \cdots n$ indexes subject, $\lambda_0(t)$ is the baseline hazard function, and $\mathbf{z}_i$ are the covariates for subject i . If you define $N_i(t)$ to be the number of observed failures of the i th subject up to time t , then the hazard function for the i th subject can be seen as a special case of a *multiplicative intensity model* (Clayton 1991). The intensity process for $N_i(t)$ becomes

$$I_i(t) = Y_i(t)\lambda_0(t) \exp(\boldsymbol{\beta}'\mathbf{z}_i)$$

where $Y_i(t)$ indicates observation of the subject at time t (taking the value of 1 if the subject is observed and 0 otherwise). Under *noninformative censoring*, the corresponding likelihood is proportional to

$$\prod_{i=1}^n \left[\prod_{t \geq 0} I_i(t) \right]^{dN_i(t)} \exp \left[- \int_{t \geq 0} I_i(t) dt \right]$$

where $dN_i(t)$ is the increment of $N_i(t)$ over the small time interval $[t, t + dt)$: it takes a value of 1 if the subject i fails in the time interval, 0 otherwise. This is a Poisson kernel with the random variable being the increments of dN_i and the means $I_i(t)dt$

$$dN_i(t) \sim \text{Poisson}(I_i(t)dt)$$

where

$$I_i(t)dt = Y_i(t) \exp(\boldsymbol{\beta}'\mathbf{z}_i) d\Lambda_0(t)$$

and

$$\Lambda_0(t) = \int_0^t \lambda_0(u) du.$$

The integral is the increment in the integrated baseline hazard function that occurs during the time interval $[t, t + dt)$.

This formulation provides an alternative way to fit a piecewise exponential model. You partition the time axis to a few intervals, where each interval has its own hazard rate, $\Lambda_0(t)$. You count the $Y_i(t)$ and $dN_i(t)$ in each interval, and fit a Poisson model to each count.

The following DATA step creates the data set Blind (Lin 1994) that represents 197 diabetic patients who have a high risk of experiencing blindness in both eyes as defined by DRS criteria:

```

title 'Piecewise Exponential Model';
data Blind;
    input ID Time Status DiabeticType Treatment @@;
    datalines;
        5 46.23 0 1 1      5 46.23 0 1 0      14 42.50 0 0 1      14 31.30 1 0 0
        16 42.27 0 0 1      16 42.27 0 0 0      25 20.60 0 0 1      25 20.60 0 0 0
        29 38.77 0 0 1      29  0.30 1 0 0      46 65.23 0 0 1      46 54.27 1 0 0
        49 63.50 0 0 1      49 10.80 1 0 0      56 23.17 0 0 1      56 23.17 0 0 0

        ... more lines ...

        1705  8.00 0 0 1 1705  8.00 0 0 0 1717 51.60 0 1 1 1717 42.33 1 1 0
        1727 49.97 0 1 1 1727  2.90 1 1 0 1746 45.90 0 0 1 1746  1.43 1 0 0
        1749 41.93 0 1 1 1749 41.93 0 1 0
    ;

```

One eye of each patient is treated with laser photocoagulation. The hypothesis of interest is whether the laser treatment delays the occurrence of blindness. The following variables are included in `Blind`:

- ID, patient's identification
- Time, failure time
- Status, event indicator (0=censored and 1=uncensored)
- Treatment, treatment received (1=laser photocoagulation and 0=otherwise)
- DiabeticType, type of diabetes (0=juvenile onset with age of onset at 20 or under, and 1= adult onset with age of onset over 20)

For illustrational purposes, a piecewise exponential model that ignores the patient-level frailties is first fit to the entire data set. The formulation of the Poisson counting process makes it straightforward to add the frailty terms, as it is demonstrated later.

The following statements create a partition (of length 8) along the time axis, with $s_0 < s_1 < s_2 < \dots < s_J$, with $s_0 = 0.1 < y_i$ and $s_J = 80 > y_i$ for all i . The time intervals are stored in the `Partition` data set:

```

data partition;
    input int_1-int_9;
    datalines;
        0.1  6.545  13.95  26.47  38.8  45.88  54.35  62 80
    ;

```

To obtain reasonable estimates, placing an equal number of observations in each interval is recommended. You can find the partition points by calculating the percentile statistics of the time variable (for example, by using the `UNIVARIATE` procedure).

The following regression model and prior distributions are used in the analysis:

$$\begin{aligned}\beta'z_i &= \beta_1\text{treatment} + \beta_2\text{diabetictype} + \beta_3\text{treatment} * \text{diabetictype} \\ \beta_1, \beta_2, \beta_3 &\sim \text{normal}(0, \text{var} = 1e6) \\ \lambda_j &\sim \text{gamma}(\text{shape} = 0.01, \text{iscale} = 0.01) \quad \text{for } j = 1 \dots 8\end{aligned}$$

The following statements calculate $Y_i(t)$ for each observation i , at every time point t in the Partition data set. The statements also find the observed failure time interval, $dN_i(t)$, for each observation:

```
%let n = 8;
data _a;
  set blind;
  if _n_ eq 1 then set partition;
  array int[*] int_;;
  array Y[&n];
  array dN[&n];
  do k = 1 to (dim(int)-1);
    Y[k] = (time - int[k] + 0.001 >= 0);
    dN[k] = Y[k] * (int[k+1] - time - 0.001 >= 0) * status;
  end;
  output;
  drop int_: k;
run;
```

The DATA step reads in the Blind data set. At the first observation, it also reads in the Partition data set. The first **ARRAY** statement creates the int array and name the elements int_:. Because the names match the variable names in the Partition data set, all values of the int_ variables (there is only one observation) in the Partition data set are therefore stored in the int array. The next two **ARRAY** statements create arrays Y and dN, each with length 8. They store values of $Y_i(t)$ and $dN_i(t)$, resulting from each failure time in the Blind data set.

The following statements print the first 10 observations of the constructed data set _a and display them in [Output 55.16.1](#):

```
proc print data=_a(obs=10);
run;
```

Output 55.16.1 First 10 Observations of the Data Set _a

Piecewise Exponential Model																							
				D																			
				i																			
				a																			
				b	T																		
				e	r																		
				t	e																		
				S	i	a																	
				t	c	t																	
				a	T	m																	
O		T																					
b	I	m	u	p	n	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	N	N	N	N	N	N	N	N
s	D	e	s	e	t	1	2	3	4	5	6	7	8	1	2	3	4	5	6	7	8		
1	5	46.23	0	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0
2	5	46.23	0	1	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0
3	14	42.50	0	0	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0
4	14	31.30	1	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0
5	16	42.27	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
6	16	42.27	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
7	25	20.60	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	25	20.60	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
9	29	38.77	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10	29	0.30	1	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0

The first subject in _a experienced blindness in the left eye at time 46.23, and the time falls in the sixth interval as defined in the Partition data set. Therefore, Y1 through Y6 all take a value of 1, and Y7 and Y8 are 0. The variable dN# takes on a value of 1 if the subject is observed to go blind in that interval. Since the first observation is censored (status == 1), the actual failure time is unknown. Hence all dN# are 0. The first observed failure time occurs in observation number 4 (the right eye of the second subject), where the time variable takes a value of 31.30, Y1 through Y4 are 1, and dN4 is 1.

Note that each observation in the _a data set has 8 Y and 8 dN, meaning that you would need eight **MODEL** statements in a PROC MCMC call, each for a Poisson likelihood. Alternatively, you can expand _a, put one Y and one dN in every observation, and fit the data using a single **MODEL** statement in PROC MCMC. The following statements expand the data set _a and save the results in the data set _b:

```
data _b;
  set _a;
  array y[*] y;;
  array dn[*] dn;;
  do i = 1 to (dim(y));
    y_val      = y[i];
    dn_val     = dn[i];
    int_index  = i;
    output;
  end;
  keep y_ dn_ diabetictype treatment int_index id;
run;
```

```
data _b;
  set _b;
  rename y_val=Y dn_val=dN;
run;
```

You can use the following PROC PRINT statements to see the first few observations in `_b`:

```
proc print data=_b(obs=10);
run;
```

Output 55.16.2 First 20 Observations of the Data Set `_b`

Obs	ID	Diabetic Type	Treatment	Y	dN	int_ index
1	5	1	1	1	0	1
2	5	1	1	1	0	2
3	5	1	1	1	0	3
4	5	1	1	1	0	4
5	5	1	1	1	0	5
6	5	1	1	1	0	6
7	5	1	1	0	0	7
8	5	1	1	0	0	8
9	5	1	0	1	0	1
10	5	1	0	1	0	2

The data set `_b` now contains 3,152 observations (see [Output 55.16.2](#) for the first few observations). The Time and Status variables are no longer needed; hence they are discarded from the data set. The `int_index` variable is an index variable that indicates interval membership of each observation.

Because the variable `Y` does not contribute to the likelihood calculation when it takes a value of 0 (it amounts to a Poisson likelihood that has a mean and response variable that are both 0), you can remove these observations. This speeds up the calculation in PROC MCMC:

```
data inputdata;
  set _b;
  if Y > 0;
run;
```

The data set `Inputdata` has 1,775 observations, as opposed to 3,152 observations in `_b`. The following statements fit a piecewise exponential model in PROC MCMC:

```
proc mcmc data=inputdata nmc=10000 outpost=postout seed=12351
  maxtune=5 stats=summary diag=none;
ods select PostSummaries;
parms beta1-beta3 0;
prior beta: ~ normal(0, var = 1e6);
random lambda ~ gamma(0.01, iscale = 0.01) subject=int_index;
bZ = beta1*treatment + beta2*diabetictype + beta3*treatment*diabetictype;
idt = exp(bZ) * lambda;
model dN ~ poisson(idt);
run;
```

The **PARMS** statement declares three regression parameters, beta1–beta3. The **PRIOR** statement specifies a noninformative normal prior on the regression coefficients. The **RANDOM** statement specifies the random effect, lambda, its prior distribution, and interval membership which is indexed by the data set variable int_index.

The symbol bZ calculates the regression mean, and the symbol idt is the mean of the Poisson likelihood. It corresponds to the equation

$$I_i(t)dt = Y_i(t) \exp(\beta'z) d\Lambda_0(t)$$

Note that the $Y_i(t)$ term is omitted in the assignment statement because Y takes only the value of 1 in the input data set.

Output 55.16.3 displays posterior estimates of the three regression parameters.

Output 55.16.3 Posterior Summary Statistics

The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
beta1	10000	−0.4174	0.2129	−0.5612	−0.4282	−0.2770
beta2	10000	0.3138	0.1956	0.1881	0.3121	0.4387
beta3	10000	−0.7899	0.3308	−0.9999	−0.7935	−0.5741

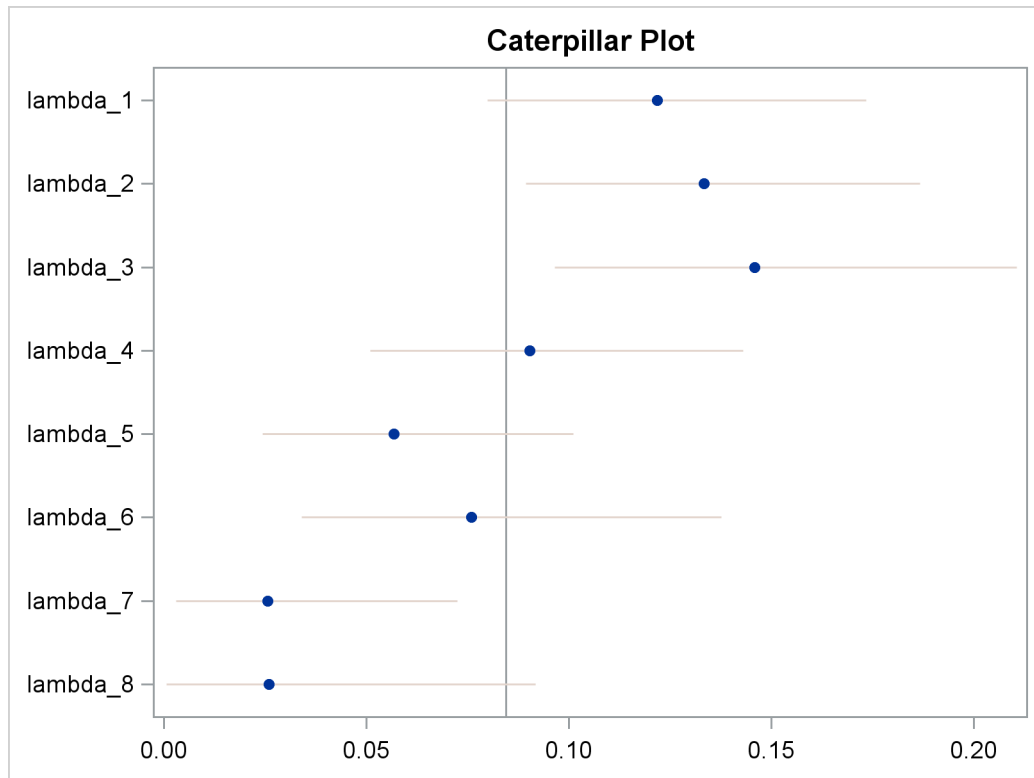
To understand the results, you can create a 2×2 table (Table 55.49) and plug in the posterior mean estimates to the regression model. A −0.41 estimate for subjects who received laser treatment and had juvenile diabetes suggests that the laser treatment is effective in delaying blindness. And the effect is much more pronounced (−0.80) for adult subjects who have diabetes and received treatment.

Table 55.49 Estimates of Regression Effects in the Survival Model

$\hat{\beta}'z$		Diabetic Type	
		0	1
Treatment	0	0	0.32
	1	−0.41	−0.80

You can also use the macro %CATER (“Caterpillar Plot” on page 4508) to draw a caterpillar plot to visualize the eight hazards in the model:

```
ods graphics on;
%cater(data=postout, var=lambda_);
ods graphics off;
```

Output 55.16.4 Caterpillar Plot of the Hazards in the Piecewise Exponential Model

The fitted hazards show a nonconstant underlying hazard function (read along the y-axis as $\lambda_{\#}$ are hazards along the time-axis) in the model.

Now suppose you want to include patient-level information and fit a frailty model to the blind data set, where the random effect enters the model through the regression term, where the subject is indexed by the variable ID in the data.

$$\begin{aligned}\beta'z_i &= \beta_1 \text{treatment} + \beta_2 \text{diabetictype} + \beta_3 \text{treatment} * \text{diabetictype} + u_{id} \\ u_{id} &\sim \text{normal}(0, \text{var} = \sigma^2) \\ \sigma^2 &\sim \text{igamma}(\text{shape} = 0.01, \text{scale} = 0.01)\end{aligned}$$

where id indexes patient.

The actual coding in PROC MCMC of a piecewise exponential frailty model is rather straightforward:

```
ods select none;
proc mcmc data=inputdata nmc=10000 outpost=postout seed=12351
  stats=summary diag=none;
  parms beta1-beta3 0 s2;
  prior beta: ~ normal(0, var = 1e6);
  prior s2 ~ igamma(0.01, scale=0.01);
  random lambda ~ gamma(0.01, iscale = 0.01) subject=int_index;
  random u ~ normal(0, var=s2) subject=id;
  bZ = beta1*treatment + beta2*diabetictype + beta3*treatment*diabetictype + u;
  idt = exp(bZ) * lambda;
  model dN ~ poisson(idt);
run;
```

A second **RANDOM** statement defines a subject-level random effect u , and the random-effects parameters enter the model in the term for the regression mean, bZ . An additional model parameter, $s2$, the variance of the random-effects parameters, is needed for the model. The results are not shown here.

Example 55.17: Normal Regression with Interval Censoring

You can use PROC MCMC to fit failure time data that can be right, left, or interval censored. To illustrate, a normal regression model is used in this example.

Assume that you have the following simple regression model with no covariates:

$$y = \mu + \sigma\epsilon$$

where y is a vector of response values (the failure times), μ is the grand mean, σ is an unknown scale parameter, and ϵ are errors from the standard normal distribution. Instead of observing y_i directly, you only observe a truncated value t_i . If the true y_i occurs after the censored time t_i , it is called *right censoring*. If y_i occurs before the censored time, it is called *left censoring*. A failure time y_i can be censored at both ends, and this is called *interval censoring*. The likelihood for y_i is as follows:

$$p(y_i|\mu) = \begin{cases} \phi(y_i|\mu, \sigma) & \text{if } y_i \text{ is uncensored} \\ S(t_{l,i}|\mu) & \text{if } y_i \text{ is right censored by } t_{l,i} \\ 1 - S(t_{r,i}|\mu) & \text{if } y_i \text{ is left censored by } t_{r,i} \\ S(t_{l,i}|\mu) - S(t_{r,i}|\mu) & \text{if } y_i \text{ is interval censored by } t_{l,i} \text{ and } t_{r,i} \end{cases}$$

where $S(\cdot)$ is the survival function, $S(t) = \Pr(T > t)$.

Gentleman and Geyer (1994) uses the following data on cosmetic deterioration for early breast cancer patients treated with radiotherapy:

```

title 'Normal Regression with Interval Censoring';
data cosmetic;
  label tl = 'Time to Event (Months)';
  input tl tr @@;
  datalines;
45 . 6 10 . 7 46 . 46 . 7 16 17 . 7 14
37 44 . 8 4 11 15 . 11 15 22 . 46 . 46 .
25 37 46 . 26 40 46 . 27 34 36 44 46 . 36 48
37 . 40 . 17 25 46 . 11 18 38 . 5 12 37 .
. 5 18 . 24 . 36 . 5 11 19 35 17 25 24 .
32 . 33 . 19 26 37 . 34 . 36 .
;

```

The data consist of time interval endpoints (in months). Nonmissing equal endpoints ($tl = tr$) indicates noncensoring; a nonmissing lower endpoint ($tl \neq .$) and a missing upper endpoint ($tr = .$) indicates right censoring; a missing lower endpoint ($tl = .$) and a nonmissing upper endpoint ($tr \neq .$) indicates left censoring; and nonmissing unequal endpoints ($tl \neq tr$) indicates interval censoring.

With this data set, you can consider using proper but diffuse priors on both μ and σ , for example:

$$\begin{aligned} \mu &\sim \text{normal}(0, \text{sd} = 1000) \\ \sigma &\sim \text{gamma}(0.001, \text{iscale} = 0.001) \end{aligned}$$

The following SAS statements fit an interval censoring model and generate [Output 55.17.1](#):

```
proc mcmc data=cosmetic outpost=postout seed=1 nmc=20000 missing=AC;
  ods select PostSummaries PostIntervals;
  parms mu 60 sigma 50;

  prior mu ~ normal(0, sd=1000);
  prior sigma ~ gamma(shape=0.001, iscale=0.001);

  if (tl^=. and tr^=. and tl=tr) then
    llike = logpdf('normal', tr, mu, sigma);
  else if (tl^=. and tr=.) then
    llike = logsdf('normal', tl, mu, sigma);
  else if (tl=. and tr^=.) then
    llike = logcdf('normal', tr, mu, sigma);
  else
    llike = log(sdf('normal', tl, mu, sigma) -
      sdf('normal', tr, mu, sigma));

  model general(llike);
run;
```

Because there are missing cells in the input data, you want to use the **MISSING=AC** option so that PROC MCMC does not delete any observations that contain missing values. The IF-ELSE statements distinguish different censoring cases for y_i , according to the likelihood. The SAS functions LOGCDF, LOGSDF, LOGPDF, and SDF are useful here. The **MODEL** statement assigns `llike` as the log likelihood to the response. The Markov chain appears to have converged in this example (evidence not shown here), and the posterior estimates are shown in [Output 55.17.1](#).

Output 55.17.1 Interval Censoring

Normal Regression with Interval Censoring						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
mu	20000	41.7807	5.7882	37.7220	41.3468	45.2249
sigma	20000	29.1122	6.0503	24.8774	28.2210	32.4250
Posterior Intervals						
Parameter	Alpha	Equal-Tail Interval		HPD Interval		
mu	0.050	32.0499	54.6104	31.3604	53.6115	
sigma	0.050	20.0889	43.1335	19.4041	41.6742	

Example 55.18: Constrained Analysis

Conjoint analysis uses regression techniques to model consumer preferences and to estimate consumer utility functions. A problem with conventional conjoint analysis is that sometimes your estimated utilities do not make sense. Your results might suggest, for example, that the consumers would prefer to spend more on a product than to spend less. With PROC MCMC, you can specify constraints on the part-worth utilities (parameter estimates). Suppose that the consumer product being analyzed is an off-road motorcycle. The relevant attributes are how large each motorcycle is (less than 300cc, 301–550cc, and more than 551cc), how much it costs (less than \$5000, \$5001–\$6000, \$6001–\$7000, and more than \$7000), whether or not it has an electric starter, whether or not the engine is counter-balanced, and whether the bike is from Japan or Europe. The preference variable is a ranking of the bikes. You could perform an ordinary conjoint analysis with PROC TRANSREG (see Chapter 97, “[The TRANSREG Procedure](#)”) as follows:

```
options validvarname=any;
proc format;
  value sizef 1 = '< 300cc' 2 = '300-550cc' 3 = '> 551cc';
  value pricef 1 = '< $5000' 2 = '$5000 - $6000'
               3 = '$6001 - $7000' 4 = '> $7000';
  value startf 1 = 'Electric Start' 2 = 'Kick Start';
  value balf 1 = 'Counter Balanced' 2 = 'Unbalanced';
  value orif 1 = 'Japanese' 2 = 'European';
run;

data bikes;
  input Size Price Start Balance Origin Rank @@;
  format size sizef. price pricef. start startf.
         balance balf. origin orif.;
  datalines;
2 1 2 1 2 3 1 4 2 2 2 7 1 2 1 1 2 6
3 3 1 1 2 1 1 3 2 1 1 5 3 4 2 2 2 12
2 3 2 2 1 9 1 1 1 2 1 8 2 2 1 2 2 10
2 4 1 1 1 4 3 1 1 2 1 11 3 2 2 1 1 2
;

title 'Ordinary Conjoint Analysis by PROC TRANSREG';
proc transreg data=bikes utilities cprefix=0 lprefix=0;
  ods select Utilities;
  model identity(rank / reflect) =
    class(size price start balance origin / zero=sum);
  output out=coded(drop=intercept) replace;
run;
```

The DATA step reads the experimental design and dependent variable Rank and assigns formats to label the factor levels. PROC TRANSREG is run specifying UTILITIES, which requests a conjoint analysis. The rank variable is reflected around its mean ($1 \rightarrow 12$, $2 \rightarrow 11$, ..., $12 \rightarrow 1$) so that in the analysis, larger part-worth utilities correspond to higher preference. The OUT=CODED data set contains the reflected ranks and a binary coding of the factors that can be used in other analyses. See Kuhfeld (2004) for more information about conjoint analysis and coding with PROC TRANSREG.

The Utilities table from the conjoint analysis is shown in [Output 55.18.1](#). Notice the part-worth utilities for price. The part-worth utility for < \$5000 is 0.25. As price increases to the \$5000–\$6000 range, utility

decreases to -0.5 . Then as price increases to the \$6001–\$7000 range, part-worth utility *increases* to 0.5. Finally, for the most expensive bikes, utility decreases again to -0.25 . In cases like this, you might want to impose constraints on the solution so that the part-worth utility for price never increases as prices go up.

Output 55.18.1 Ordinary Conjoint Analysis by PROC TRANSREG

Ordinary Conjoint Analysis by PROC TRANSREG				
The TRANSREG Procedure				
Utilities Table Based on the Usual Degrees of Freedom				
Label	Utility	Standard Error	Importance (% Utility Range)	Variable
Intercept	6.5000	0.95743		Intercept
< 300cc	-0.0000	1.35401	0.000	Class.< 300cc
300–550cc	-0.0000	1.35401		Class.300–550cc
> 551cc	0.0000	1.35401		Class.> 551cc
< \$5000	0.2500	1.75891	13.333	Class.< \$5000
\$5000 – \$6000	-0.5000	1.75891		Class.\$5000 – \$6000
\$6001 – \$7000	0.5000	1.75891		Class.\$6001 – \$7000
> \$7000	-0.2500	1.75891		Class.> \$7000
Electric Start	-0.1250	1.01550	3.333	Class.Electric Start
Kick Start	0.1250	1.01550		Class.Kick Start
Counter Balanced	3.0000	1.01550	80.000	Class.Counter Balanced
Unbalanced	-3.0000	1.01550		Class.Unbalanced
Japanese	-0.1250	1.01550	3.333	Class.Japanese
European	0.1250	1.01550		Class.European

You could run PROC TRANSREG again, specifying monotonicity constraints on the part-worth utilities for price:

```

title 'Constrained Conjoint Analysis by PROC TRANSREG';
proc transreg data=bikes utilities cprefix=0 lprefix=0;
  ods select ConservUtilities;
  model identity(rank / reflect) =
    monotone(price / tstandard=center)
    class(size start balance origin / zero=sum);
run;

```

The output from this PROC TRANSREG step is shown in [Output 55.18.2](#).

Output 55.18.2 Constrained Conjoint Analysis by PROC TRANSREG

Constrained Conjoint Analysis by PROC TRANSREG				
The TRANSREG Procedure				
Utilities Table Based on Conservative Degrees of Freedom				
Label	Utility	Standard Error	Importance (% Utility Range)	Variable
Intercept	6.5000	0.97658		Intercept
Price	-0.1581	.	7.143	Monotone(Price)
< \$5000	0.2500	.		
\$5000 - \$6000	0.0000	.		
\$6001 - \$7000	0.0000	.		
> \$7000	-0.2500	.		
< 300cc	-0.0000	1.38109	0.000	Class.< 300cc
300-550cc	0.0000	1.38109		Class.300-550cc
> 551cc	0.0000	1.38109		Class.> 551cc
Electric Start	-0.2083	1.00663	5.952	Class.Electric Start
Kick Start	0.2083	1.00663		Class.Kick Start
Counter Balanced	3.0000	0.97658	85.714	Class.Counter Balanced
Unbalanced	-3.0000	0.97658		Class.Unbalanced
Japanese	-0.0417	1.00663	1.190	Class.Japanese
European	0.0417	1.00663		Class.European

This monotonicity constraint is one of the few constraints on the part-worth utilities that you can specify in PROC TRANSREG. In contrast, PROC MCMC enables you to specify any constraint that can be written in the DATA step language. You can perform the restricted conjoint analysis with PROC MCMC by using the coded factors that were output from PROC TRANSREG. The data set is Coded.

The likelihood is a simple regression model:

$$\text{rank}_i \sim \text{normal}(\mathbf{x}_i' \boldsymbol{\beta}, \sigma)$$

where rank is the response, the covariates are '< 300cc'n, '300-500cc'n, '< \$5000'n, '\$5000 - \$6000'n, '\$6001 - \$7000'n, 'Electric Start'n, 'Counter Balanced'n, and Japanese. Note that OPTIONS VALIDVAR-NAME=ANY enables PROC TRANSREG to create names for the coded variables with blanks and special characters. That is why the name-literal notation ('variable-name'n) is used for the input data set variables.

Suppose that there are two constraints you want to put on some of the parameters: one is that the parameters for '< \$5000'n, '\$5000 - \$6000'n, and '\$6001 - \$7000'n decrease in order, and the other is that the parameter for 'Counter Balanced'n is strictly positive. You can consider a truncated multivariate normal prior as follows:

$$(\beta_{< \$5000'n}, \beta_{\$5000 - \$6000'n}, \beta_{\$6001 - \$7000'n}, \beta_{\text{Counter Balanced'n}}) \sim \text{MVN}(0, \sigma \mathbf{I})$$

with the following set of constraints:

$$\begin{aligned}\beta_{< \$5000'n} &> \beta_{\$5000 - \$6000'n} > \beta_{\$6001 - \$7000'n} > 0 \\ \beta_{\text{Counter Balanced}'n} &> 0\end{aligned}$$

The condition that $\beta_{\$6001 - \$7000'n} > 0$ reflects an implied constraint that, by definition, 0 is the utility for the highest price range, $> \$7000$, which is the reference level for the binary coded price variable. The following statements fit the desired model:

```

title 'Bayesian Constrained Conjoint Analysis by PROC MCMC';
proc mcmc data=coded outpost=bikesout ntu=3000 nmc=50000
  propcov=quanew seed=448 diag=none;
  ods select PostSummaries;
  array pw[4] pw5000 pw5000_6000 pw6001_7000 pwCounterBalanced;
  array sigma[4,4];
  array mu[4];

  begincnst;
    call identity(sigma);
    call mult(sigma, 100, sigma);
    call zeromatrix(mu);
  endcnst;

  parms intercept pw300cc pw300_550cc pwElectricStart pwJapanese tau 1;
  parms pw5000 0.3 pw5000_6000 0.2 pw6001_7000 0.1 pwCounterBalanced 1;

  beginnodata;
  prior intercept pw300: pwE: pwJ: ~ normal(0, var=100);
  if (pw5000 >= pw5000_6000 & pw5000_6000 >= pw6001_7000 &
    pw6001_7000 >= 0 & pwCounterBalanced > 0) then
    lp = lpdfmvn(pw, mu, sigma);
  else
    lp = .;
  prior pw5000 pw5000_6000 pw6001_7000 pwC: ~ general(lp);
  prior tau ~ gamma(0.01, iscale=0.01);
  endnodata;

  mean = intercept +
    pw300cc          * '< 300cc'n          +
    pw300_550cc      * '300-550cc'n        +
    pw5000           * '< $5000'n          +
    pw5000_6000      * '$5000 - $6000'n    +
    pw6001_7000      * '$6001 - $7000'n    +
    pwElectricStart  * 'Electric Start'n    +
    pwCounterBalanced * 'Counter Balanced'n +
    pwJapanese       * Japanese;
  model rank ~ normal(mean, prec=tau);
run;

```

The two [ARRAY](#) statements allocate a 4×4 dimensional array for the prior covariance and an array of size 4 for the prior means. In the [BEGINCNST](#) and [ENDCNST](#) statements, the [CALL IDENTITY](#) function sets sigma to be an identity matrix; the [CALL MULT](#) function sets sigma's diagonal elements to be 100 (the diagonal variance terms); and the [CALL ZEROMATRIX](#) function sets mu to be a vector of zeros (the prior

means). For matrix functions in PROC MCMC, see the section “[Matrix Functions in PROC MCMC](#)” on page 4498.

There are two [PARMS](#) statements, with each of them naming a block of parameters. The first [PARMS](#) statement blocks the following: the intercept, the two size parameters, the one start-type parameter, the one origin parameter, and the precision. The second [PARMS](#) statement blocks the three price parameters and the one balance parameter, parameters that have the constraint multivariate normal prior. The second [PARMS](#) statement also specifies initial values for the parameter estimates. The initial values reflect the constraints on these parameters. The initial part-worth utilities all decrease from 0.3 to 0.2 to 0.1 to 0.0 (for the implicit reference level) as the prices increase. Also, the initial part-worth utility for the counter-balanced engine is set to a positive value, 1.

In the [PRIOR](#) statements, regression coefficients without constraints are given an independent normal prior with mean at 0 and variance of 100. The next IF-ELSE construction imposes the constraints. When these constraints are met, pw5000, pw5000_6000, pw6001_7000, pwCounterBalanced are jointly distributed as a multivariate normal prior with mean mu and covariance sigma. Otherwise, the prior is not defined and lp is assigned a missing value. The parameter tau is given a gamma prior, which is a conjugate prior for that parameter.

The model specification is linear. The mean is comprised of an intercept and the sum of terms like pw300cc * '< 300cc'n, which is a parameter times an input data set variable. The [MODEL](#) statement specifies that the linear model for rank is normally distributed with mean mean and precision tau.

The MCMC results are shown in [Output 55.18.3](#).

Output 55.18.3 MCMC Results

Bayesian Constrained Conjoint Analysis by PROC MCMC						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
intercept	50000	2.2570	2.5131	0.8315	2.3661	3.8234
pw300cc	50000	0.00983	2.4903	-1.4461	-0.00002	1.4821
pw300_550cc	50000	0.0549	2.5097	-1.4175	0.0106	1.4695
pwElectricStart	50000	-1.1319	2.1195	-2.3710	-1.0665	0.1562
pwJapanese	50000	-0.4567	2.1232	-1.6836	-0.4134	0.7903
tau	50000	0.1135	0.0765	0.0578	0.0952	0.1499
pw5000	50000	4.1614	2.1803	2.6082	3.7947	5.2823
pw5000_6000	50000	2.6147	1.6188	1.4316	2.3400	3.4779
pw6001_7000	50000	1.5040	1.2530	0.5432	1.1838	2.1456
pwCounterBalanced	50000	5.8880	2.0638	4.6274	5.8946	7.1094

The estimates of the part-worth utility for the price categories are ordered as expected. This agrees with the intuition that there is a higher preference for a less expensive motor bike when all other things are equal, and that is what you see when you look at the estimated posterior means for the price part-worths. The estimated standard deviations of the price part-worths in this model are of approximately the same order of magnitude as the posterior means. This indicates that the part-worth utilities for this subject are

not significantly far from each other, and that this subject's ranking of the options was not significantly influenced by the difference in price.

One advantage of Bayesian analysis is that you can incorporate prior information in the data analysis. Constraints on the parameter space are one possible source of information that you might have before you examine the data. This example shows that it can be accomplished in PROC MCMC.

Example 55.19: Implement a New Sampling Algorithm

This example illustrates using the `UDS` statement to implement a new Markov chain sampler. The algorithm demonstrated here is proposed by Holmes and Held (2006), hereafter referred to as HH. They presented a Gibbs sampling algorithm for generating draws from the posterior distribution of the parameters in a probit regression model. The notation follows closely to HH.

The data used here is the remission data set from a PROC LOGISTIC example:

```
title 'Implement a New Sampling Algorithm';
data inputdata;
  input remiss cell smear infil li blast temp;
  ind = _n_;
  cnst = 1;
  label remiss='Complete Remission';
  datalines;
1  0.8  0.83  0.66  1.9  1.1    0.996

... more lines ...

0  1    0.73  0.73  0.7  0.398  0.986
;
```

The variable `remiss` is the cancer remission indicator variable with a value of 1 for remission and a value of 0 for nonremission. There are six explanatory variables: `cell`, `smear`, `infil`, `li`, `blast`, and `temp`. These variables are the risk factors thought to be related to cancer remission. The binary regression model is as follows:

$$\text{remiss}_i \sim \text{binary}(p_i)$$

where the covariates are linked to p_i through a probit transformation:

$$\text{probit}(p_i) = \mathbf{x}'\boldsymbol{\beta}$$

$\boldsymbol{\beta}$ are the regression coefficients and $\mathbf{x}'$ the explanatory variables. Suppose you want to use independent normal priors on the regression coefficients:

$$\beta_i \sim \text{normal}(0, \text{var} = 25)$$

Fitting a probit model with PROC MCMC is straightforward. You can use the following statements:

```
proc mcmc data=inputdata nmc=100000 propcov=quanew seed=17
  outpost=mcmcout;
  ods select PostSummaries ess;
  parms beta0-beta6;
```

```

prior beta: ~ normal(0,var=25);
mu = beta0 + beta1*cell + beta2*smear +
      beta3*infil + beta4*li + beta5*blast + beta6*temp;
p = cdf('normal', mu, 0, 1);
model remiss ~ bern(p);
run;

```

The expression `mu` is the regression mean, and the CDF function links `mu` to the probability of remission `p` in the binary likelihood.

The summary statistics and effective sample sizes tables are shown in [Output 55.19.1](#). There are high autocorrelations among the posterior samples, and efficiency is relatively low. The correlation time is reduced only after a large amount of thinning.

Output 55.19.1 Random Walk Metropolis

Implement a New Sampling Algorithm						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
beta0	100000	-2.0531	3.8299	-4.6418	-2.0354	0.5638
beta1	100000	2.6300	2.8270	0.6563	2.5272	4.4846
beta2	100000	-0.8426	3.2108	-3.0270	-0.8263	1.3429
beta3	100000	1.5933	3.5491	-0.7993	1.6190	3.9695
beta4	100000	2.0390	0.8796	1.4312	2.0028	2.6194
beta5	100000	-0.3184	0.9543	-0.9613	-0.3123	0.3418
beta6	100000	-3.2611	3.7806	-5.8050	-3.2736	-0.7243

Implement a New Sampling Algorithm			
The MCMC Procedure			
Effective Sample Sizes			
Parameter	ESS	Autocorrelation Time	Efficiency
beta0	4280.8	23.3602	0.0428
beta1	4496.5	22.2398	0.0450
beta2	3434.1	29.1199	0.0343
beta3	3856.6	25.9294	0.0386
beta4	3659.7	27.3245	0.0366
beta5	3229.9	30.9610	0.0323
beta6	4430.7	22.5696	0.0443

As an alternative to the random walk Metropolis, you can use the Gibbs algorithm to sample from the posterior distribution. The Gibbs algorithm is described in the section “[Gibbs Sampler](#)” on page 135. While the Gibbs algorithm generally applies to a wide range of statistical models, the actual implementation can be problem-specific. In this example, performing a Gibbs sampler involves introducing a class of auxil-

iary variables (also known as latent variables). You first reformulate the model by adding a z_i for each observation in the data set:

$$\begin{aligned} y_i &= \begin{cases} 1 & \text{if } z_i > 0 \\ 0 & \text{otherwise} \end{cases} \\ z_i &= \mathbf{x}_i' \boldsymbol{\beta} + \epsilon_i \\ \epsilon &\sim \text{normal}(0, 1) \\ \boldsymbol{\beta} &\sim \pi(\boldsymbol{\beta}) \end{aligned}$$

If $\boldsymbol{\beta}$ has a normal prior, such as $\pi(\boldsymbol{\beta}) = N(\mathbf{b}, \mathbf{v})$, you can work out a closed form solution to the full conditional distribution of $\boldsymbol{\beta}$ given the data and the latent variables z_i . The full conditional distribution is also a multivariate normal, due to the conjugacy of the problem. See the section “Conjugate Priors” on page 129. The formula is shown here:

$$\begin{aligned} \boldsymbol{\beta} | \mathbf{z}, \mathbf{x} &\sim \text{normal}(\mathbf{B}, \mathbf{V}) \\ \mathbf{B} &= \mathbf{V}((\mathbf{v})^{-1} \mathbf{b} + \mathbf{x}' \mathbf{z}) \\ \mathbf{V} &= (\mathbf{v}^{-1} + \mathbf{x}' \mathbf{x})^{-1} \end{aligned}$$

The advantage of creating the latent variables is that the full conditional distribution of $\mathbf{z}$ is also easy to work with. The distribution is a truncated normal distribution:

$$z_i | \boldsymbol{\beta}, \mathbf{x}_i, y_i \sim \begin{cases} \text{normal}(\mathbf{x}_i \boldsymbol{\beta}, 1) I(z_i > 0) & \text{if } y_i = 1 \\ \text{normal}(\mathbf{x}_i \boldsymbol{\beta}, 1) I(z_i \leq 0) & \text{otherwise} \end{cases}$$

You can sample $\boldsymbol{\beta}$ and $\mathbf{z}$ iteratively, by drawing $\boldsymbol{\beta}$ given $\mathbf{z}$ and vice versa. HH point out that a high degree of correlation could exist between $\boldsymbol{\beta}$ and $\mathbf{z}$, and it makes this iterative way of sampling inefficient. As an improvement, HH proposed an algorithm that samples $\boldsymbol{\beta}$ and $\mathbf{z}$ jointly. At each iteration, you sample z_i from the posterior marginal distribution (this is the distribution that is conditional only on the data and not on any parameters) and then sample $\boldsymbol{\beta}$ from the same posterior full conditional distribution as described previously:

1. Sample z_i from its posterior marginal distribution:

$$\begin{aligned} z_i | \mathbf{z}_{-i}, y_i &\sim \begin{cases} \text{normal}(m_i, v_i) I(z_i > 0) & \text{if } y_i = 1 \\ \text{normal}(m_i, v_i) I(z_i \leq 0) & \text{otherwise} \end{cases} \\ m_i &= \mathbf{x}_i \mathbf{B} - w_i (z_i - \mathbf{x}_i \mathbf{B}) \\ v_i &= 1 + w_i \\ w_i &= h_i / (1 - h_i) \\ h_i &= (\mathbf{H})_{ii}, \mathbf{H} = \mathbf{x} \mathbf{V} \mathbf{x}' \end{aligned}$$

2. Sample $\boldsymbol{\beta}$ from the same posterior full conditional distribution described previously.

For a detailed description of each of the conditional terms, refer to the original paper.

PROC MCMC cannot sample from the probit model by using this sampling scheme but you can implement the algorithm by using the `UDS` statement. To sample z_i from its marginal, you need a function that draws random variables from a truncated normal distribution. The functions, `RLTNORM` and `RRTNORM`, generate left- and right-truncated normal variates, respectively. The algorithm is taken from Robert (1995).

The functions are written in PROC FCMP (see the FCMP Procedure in the *Base SAS Procedures Guide*):

```
proc fcmp outlib=sasuser.funcs.uds;
  /*****
  /* Generate left-truncated normal variate */
  *****/
  function rltnorm(mu,sig,lwr);
  if lwr<mu then do;
    ans = lwr-1;
    do while(ans<lwr);
      ans = rand('normal',mu,sig);
    end;
  end;
  else do;
    mul = (lwr-mu)/sig;
    alpha = (mul + sqrt(mul**2 + 4))/2;
    accept=0;
    do while(accept=0);
      z = mul + rand('exponential')/alpha;
      lrho = -(z-alpha)**2/2;
      u = rand('uniform');
      lu = log(u);
      if lu <= lrho then accept=1;
    end;
    ans = sig*z + mu;
  end;
  return(ans);
endsub;

  /*****
  /* Generate right-truncated normal variate */
  *****/
  function rrtnorm(mu,sig,uppr);
  ans = 2*mu - rltnorm(mu,sig, 2*mu-uppr);
  return(ans);
endsub;
run;
```

The function call to RLTNORM(mu,sig,lwr) generates a random number from the left-truncated normal distribution:

$$\theta \sim \text{normal}(\mu, \text{sd} = \text{sig}) I(\theta > \text{lwr})$$

Similarly, the function call to RRTNORM(mu,sig,uppr) generates a random number from the right-truncated normal distribution:

$$\theta \sim \text{normal}(\mu, \text{sd} = \text{sig}) I(\theta < \text{uppr})$$

These functions are used to generate the latent variables z_i .

Using the algorithm A1 from the HH paper as an example, [Output 55.50](#) lists a line-by-line implementation with the PROC MCMC coding style. The table is broken into three portions: set up the constants, initialize the parameters, and sample one draw from the posterior distribution. The left column of the table is identical to the A1 algorithm stated in the appendix of HH. The right column of the table lists SAS statements.

Table 55.50 Holmes and Held (2006), algorithm A1. Side-by-Side Comparison to SAS

Define Constants	In the BEGINCNST/ENDCNST Statements
$V \leftarrow (X'X + v^{-1})^{-1}$	<pre>call transpose(x,xt); /* xt = transpose(x) */ call mult(xt,x,xtx); call inv(v,v); /* v = inverse(v) */ call addmatrix(xtx,v,xtx); /* xtx = xtx+v */ call inv(xtx,v); /* v = inverse(xtx) */</pre>
$L \leftarrow \text{Chol}(V)$	<pre>call chol(v,L);</pre>
$S \leftarrow VX'$	<pre>call mult(v,xt,S);</pre>
FOR $j = 1$ to n $H[j] \leftarrow X[j,]S[,j]$ $W[j] \leftarrow H[j]/(1 - H[j])$ $Q[j] \leftarrow W[j] + 1$ END	<pre>call mult(x,S,HatMat); do j=1 to &n; H = HatMat[j,j]; W[j] = H/(1-H); sQ[j] = sqrt(W[j] + 1); /* use s.d. in SAS */ end;</pre>
Initial Values	In the BEGINCNST/ENDCNST Statements
$Z \sim \text{normal}(0, I_n) \text{Ind}(Y, Z)$	<pre>do j=1 to &n; if(y[j]=1) then Z[j] = rltnorm(0,1,0); else Z[j] = rrltnorm(0,1,0); end;</pre>
$B \leftarrow SZ$	<pre>call mult(S,Z,B);</pre>

Draw One Sample	Subroutine HH
<pre> FOR j = 1 to n $z_{old} \leftarrow Z[j]$ $m \leftarrow X[j,]B$ $m \leftarrow m - W[j](Z[j] - m)$ $Z[j] \sim \text{normal}(m, Q[j])\text{Ind}(Y[j], Z[j])$ $B \leftarrow B + (Z[j] - z_{old})S[,j]$ END $T \sim \text{normal}(0, I_p)$ $\beta[,i] \leftarrow B + LT$ </pre>	<pre> do j=1 to &n; zold = Z[j]; m = 0; do k= 1 to &p; m = m + X[j,k] * B[k]; end; m = m - W[j]*(Z[j]-m); if (y[j]=1) then Z[j] = rltnorm(m,sQ[j],0); else Z[j] = rrtnorm(m,sQ[j],0); diff = Z[j] - zold; do k= 1 to &p; B[k] = B[k] + diff * S[k,j]; end; end; do j = 1 to &p; T[j] = rand('normal'); end; call mult(L,T,T); call addmatrix(B,T,beta); </pre>

The following statements define the subroutine HH (algorithm A1) in PROC FCMP and store it in library `sasuser.funcs.uds`:

```

/* define the HH algorithm in PROC FCMP. */
%let n = 27;
%let p = 7;
options cmplib=sasuser.funcs;
proc fcmp outlib=sasuser.funcs.uds;
  subroutine HH(beta[*],Z[*],B[*],x[*,*],y[*],W[*],sQ[*],S[*,*],L[*,*]);
    outargs beta, Z, B;
    array T[&p] / nosym;
    do j=1 to &n;
      zold = Z[j];
      m = 0;
      do k = 1 to &p;
        m = m + X[j,k] * B[k];
      end;
      m = m - W[j]*(Z[j]-m);
      if (y[j]=1) then
        Z[j] = rltnorm(m,sQ[j],0);
      else
        Z[j] = rrtnorm(m,sQ[j],0);
      diff = Z[j] - zold;
      do k = 1 to &p;
        B[k] = B[k] + diff * S[k,j];
      end;
    end;
  endsubr;
endproc;

```

```

end;
do j=1 to &p;
    T[j] = rand('normal');
end;
call mult(L,T,T);
call addmatrix(B,T,beta);
endsub;
run;

```

Note that one-dimensional array arguments take the form of *name*[*] and two-dimensional array arguments take the form of *name*[*,*]. Three variables, *beta*, *Z*, and *B*, are OUTARGS variables, making them the only arguments that can be modified in the subroutine. For the **UDS** statement to work, all OUTARGS variables have to be model parameters. Technically, only *beta* and *Z* are model parameters, and *B* is not. The reason that *B* is declared as an OUTARGS is because the array must be updated throughout the simulation, and this is the only way to modify its values. The input array *x* contains all of the explanatory variables, and the array *y* stores the response. The rest of the input arrays, *W*, *sQ*, *S*, and *L*, store constants as detailed in the algorithm. The following statements illustrate how to fit a Bayesian probit model by using the HH algorithm:

```

options cmplib=sasuser.funcs;

proc mcmc data=inputdata nmc=5000 monitor=(beta) outpost=hhout;
    ods select PostSummaries ess;
    array xtx[&p,&p];          /* work space */
    array xt[&p,&n];           /* work space */
    array v[&p,&p];            /* work space */
    array HatMat[&n,&n];       /* work space */
    array S[&p,&n];            /* V * Xt */
    array W[&n];
    array y[1]/ nosymbols; /* y stores the response variable */
    array x[1]/ nosymbols; /* x stores the explanatory variables */
    array sQ[&n];             /* sqrt of the diagonal elements of Q */
    array B[&p];              /* conditional mean of beta */
    array L[&p,&p];            /* Cholesky decomp of conditional cov */
    array Z[&n];              /* latent variables Z */
    array beta[&p] beta0-beta6; /* regression coefficients */

    beginncnst;
        call streaminit(83101);
        if ind=1 then do;
            rc = read_array("inputdata", x, "cnst", "cell", "smear", "infil",
                           "li", "blast", "temp");
            rc = read_array("inputdata", y, "remiss");
            call identity(v);
            call mult(v, 25, v);
            call transpose(x,xt);
            call mult(xt,x,xtx);
            call inv(v,v);
            call addmatrix(xtx,v,xtx);
            call inv(xtx,v);
            call chol(v,L);
            call mult(v,xt,S);
            call mult(x,S,HatMat);

```

```

do j=1 to &n;
    H = HatMat[j,j];
    W[j] = H/(1-H);
    sQ[j] = sqrt(W[j] + 1);
end;

do j=1 to &n;
    if(y[j]=1) then
        Z[j] = rltnorm(0,1,0);
    else
        Z[j] = rrtnorm(0,1,0);
    end;
    call mult(S,Z,B);
end;
endcnst;

uds HH(beta,Z,B,x,y,W,sQ,S,L);
parms z: beta: 0 B1-B7 / uds;
prior z: beta: B1-B7 ~ general(0);

model general(0);
run;

```

The **OPTIONS** statement names the catalog of FCMP subroutines to use. The **cmplib** library stores the subroutine **HH**. You do not need to set a random number seed in the **PROC MCMC** statement because all random numbers are generated from the **HH** subroutine. The initialization of the **rand** function is controlled by the **streaminit** function, which is called in the program with a seed value of 83101.

A number of arrays are allocated. Some of them, such as **xtx**, **xt**, **v**, and **HatMat**, allocate work space for constant arrays. Other arrays are used in the subroutine sampling. Explanations of the arrays are shown in comments in the statements.

In the **BEGINCNST** and **ENDCNST** statement block, you read data set variables in the arrays **x** and **y**, calculate all the constant terms, and assign initial values to **Z** and **B**. For the **READ_ARRAY** function, see the section “**READ_ARRAY Function**” on page 4442. For listings of all array functions and their definitions, see the section “**Matrix Functions in PROC MCMC**” on page 4498.

The **UDS** statement declares that the subroutine **HH** is used to sample the parameters **beta**, **Z**, and **B**. You also specify the **UDS** option in the **PARMS** statement. Because all parameters are updated through the **UDS** interface, it is not necessary to declare the actual form of the prior for any of the parameters. Each parameter is declared to have a prior of **general(0)**. Similarly, it is not necessary to declare the actual form of the likelihood. The **MODEL** statement also takes a flat likelihood of the form **general(0)**.

Summary statistics and effective sample sizes are shown in [Output 55.19.2](#). The posterior estimates are very close to what was shown in [Output 55.19.1](#). The **HH** algorithm produces samples that are much less correlated.

Output 55.19.2 Holms and Held

Implement a New Sampling Algorithm						
The MCMC Procedure						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
beta0	5000	-2.0567	3.8260	-4.6537	-2.0777	0.5495
beta1	5000	2.7254	2.8079	0.7812	2.6678	4.5370
beta2	5000	-0.8318	3.2017	-2.9987	-0.8626	1.2918
beta3	5000	1.6319	3.5108	-0.7481	1.6636	4.0302
beta4	5000	2.0567	0.8800	1.4400	2.0266	2.6229
beta5	5000	-0.3473	0.9490	-0.9737	-0.3267	0.2752
beta6	5000	-3.3787	3.7991	-5.9089	-3.3504	-0.7928

Implement a New Sampling Algorithm			
The MCMC Procedure			
Effective Sample Sizes			
Parameter	ESS	Autocorrelation Time	Efficiency
beta0	3651.3	1.3694	0.7303
beta1	1563.8	3.1973	0.3128
beta2	5005.9	0.9988	1.0012
beta3	4853.2	1.0302	0.9706
beta4	2611.2	1.9148	0.5222
beta5	3049.2	1.6398	0.6098
beta6	3503.2	1.4273	0.7006

It is interesting to compare the two approaches of fitting a generalized linear model. The random walk Metropolis on a seven-dimensional parameter space produces autocorrelations that are substantially higher than the HH algorithm. A much longer chain is needed to produce roughly equivalent effective sample sizes. On the other hand, the Metropolis algorithm is faster to run. The running time of these two examples is roughly the same, with the random walk Metropolis with 100000 samples, a 20-fold increase over that in the HH algorithm example. The speed difference can be attributed to a number of factors, ranging from the implementation of the software and the overhead cost of calling PROC FCMP subroutine and functions. In addition, the HH algorithm requires more parameters by creating an equal number of latent variables as the sample size. Sampling more parameters takes time. A larger number of parameters also increases the challenge in convergence diagnostics, because it is imperative to have convergence in all parameters before you make valid posterior inferences. Finally, you might feel that coding in PROC MCMC is easier. However, this really is not a fair comparison to make here. Writing a Metropolis algorithm from scratch would have probably taken just as much, if not more, effort than the HH algorithm.

Example 55.20: Using a Transformation to Improve Mixing

Proper transformations of parameters can often improve the mixing in PROC MCMC. You already saw this in “[Example 55.6: Nonlinear Poisson Regression Models](#)” on page 4570, which sampled using the log scale of parameters that are strictly positive, such as the gamma priors. This example shows another useful transformation: the logit transformation on parameters that take a uniform prior on $[0, 1]$.

The data set is taken from Sharples (1990). It is used in Chaloner and Brant (1988) and Chaloner (1994) to identify outliers in the data set in a two-level hierarchical model. Congdon (2003) also uses this data set to demonstrate the same technique. This example uses the data set to illustrate how mixing can be improved using transformation and does not address the question of outlier detection as in those papers. The following statements create the data set:

```
data inputdata;
  input nobs grp y @@;
  ind = _n_;
  datalines;
1 1 24.80 2 1 26.90 3 1 26.65
4 1 30.93 5 1 33.77 6 1 63.31
1 2 23.96 2 2 28.92 3 2 28.19
4 2 26.16 5 2 21.34 6 2 29.46
1 3 18.30 2 3 23.67 3 3 14.47
4 3 24.45 5 3 24.89 6 3 28.95
1 4 51.42 2 4 27.97 3 4 24.76
4 4 26.67 5 4 17.58 6 4 24.29
1 5 34.12 2 5 46.87 3 5 58.59
4 5 38.11 5 5 47.59 6 5 44.67
;
```

There are five groups (grp , $j = 1, \dots, 5$) with six observations (nobs , $i = 1, \dots, 6$) in each. The two-level hierarchical model is specified as follows:

$$\begin{aligned} y_{ij} &\sim \text{normal}(\theta_j, \text{prec} = \tau_w) \\ \theta_j &\sim \text{normal}(\mu, \text{prec} = \tau_b) \\ \mu &\sim \text{normal}(0, \text{prec} = 1e-6) \\ \tau &\sim \text{gamma}(0.001, \text{iscale} = 0.001) \\ p &\sim \text{uniform}(0, 1) \end{aligned}$$

with the precision parameters related to each other in the following way:

$$\begin{aligned} \tau_b &= \tau/p \\ \tau_w &= \tau_b - \tau \end{aligned}$$

The total number of parameters in this model is eight: $\theta_1, \dots, \theta_5, \mu, \tau$, and p .

The following statements fit the model:

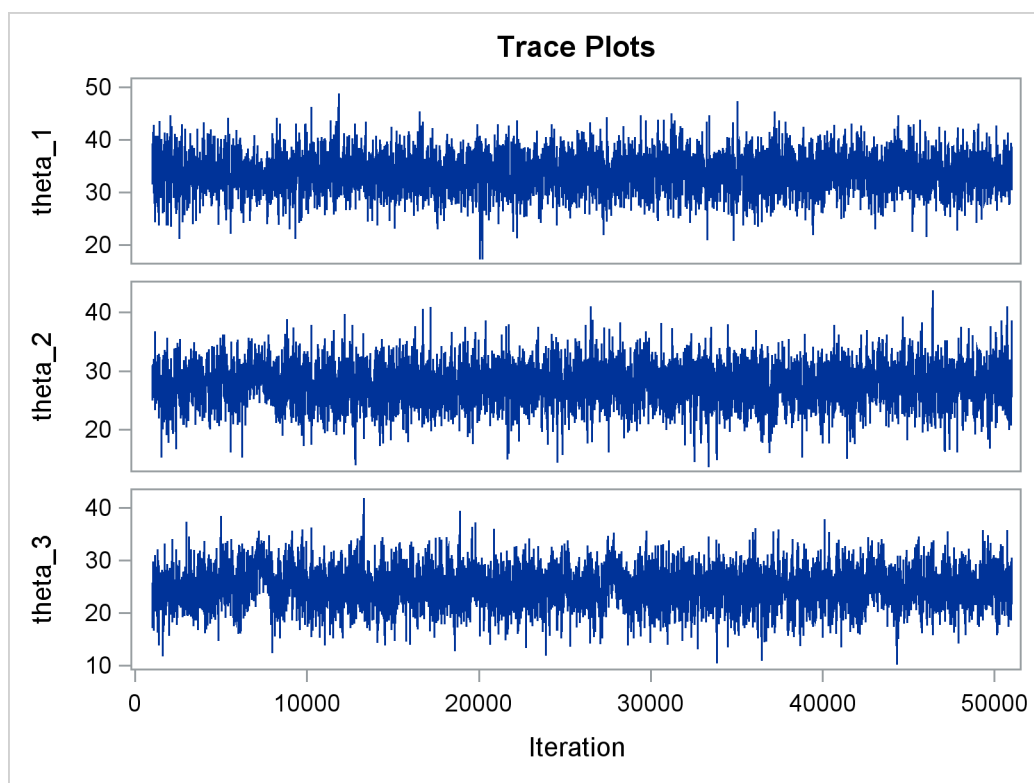
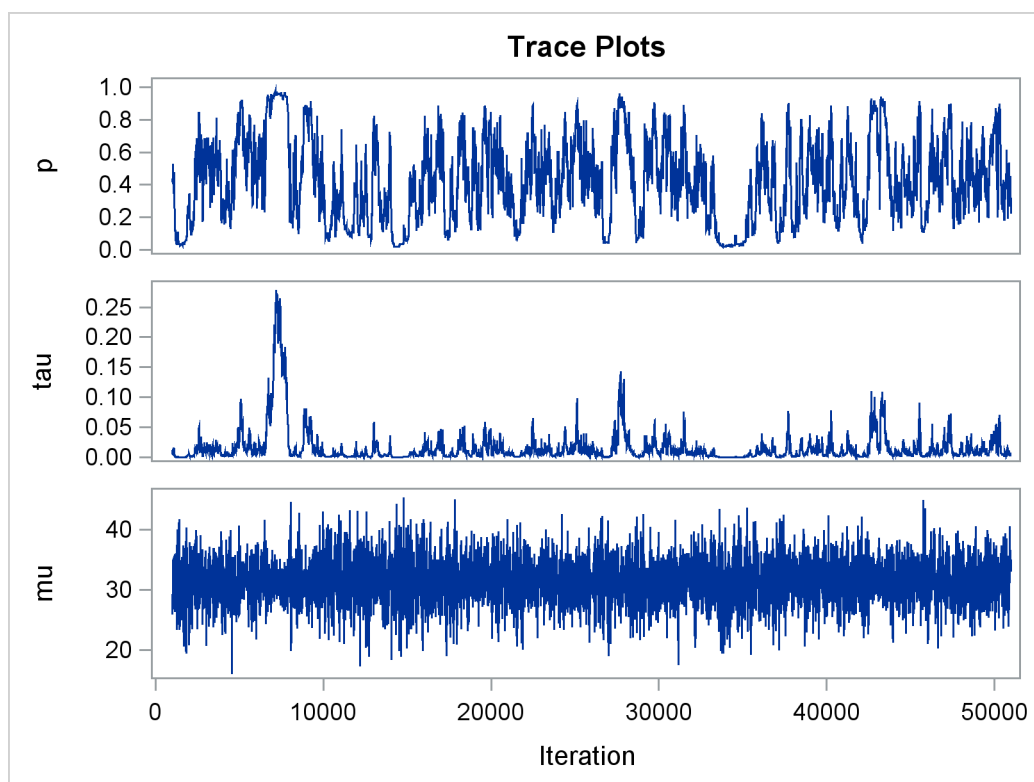
```
ods graphics on;
proc mcmc data=inputdata nmc=50000 thin=10 outpost=m1 seed=17
    plot=trace;
    ods select ess tracepanel;
    parms p;
    parms tau;
    parms mu;

    prior p ~ uniform(0,1);
    prior tau ~ gamma(shape=0.001, iscale=0.001);
    prior mu ~ normal(0, prec=0.00000001);
    beginnodata;
    taub = tau/p;
    tauw = taub-tau;
    endnodata;

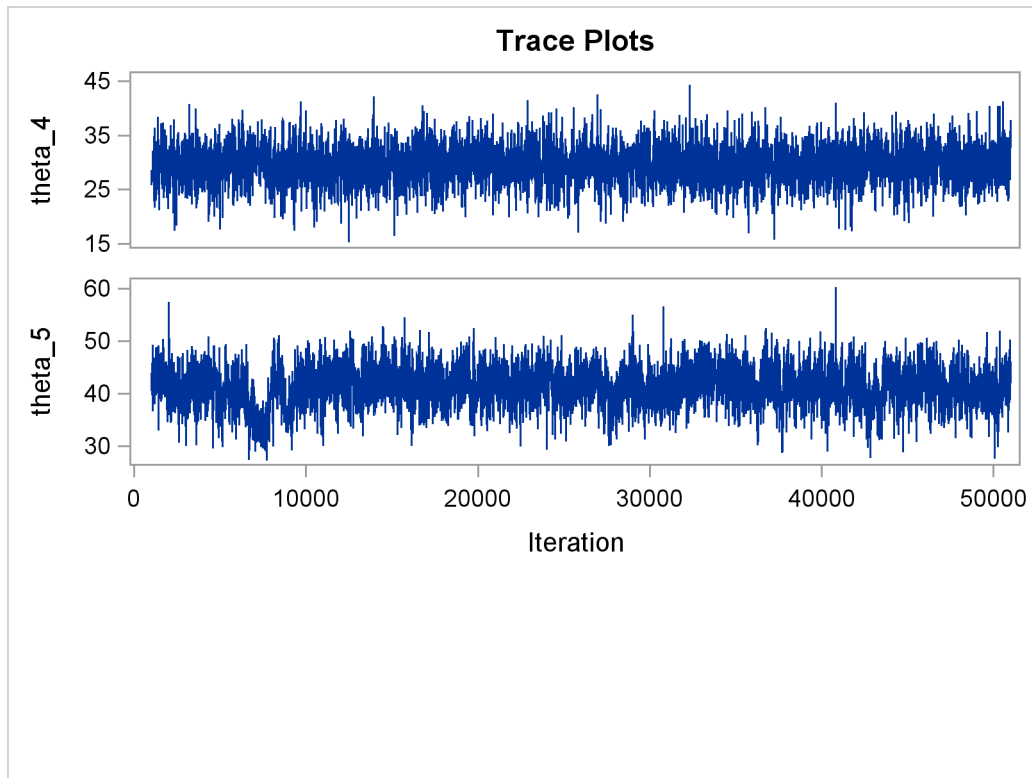
    random theta ~ normal(mu, prec=taub) subject=grp monitor=(theta);
    model y ~ normal(theta, prec=tauw);
run;
```

The ODS SELECT statement displays the effective sample size table and the trace plots. The ODS GRAPHICS ON statement enables ODS Graphics. The PROC MCMC statement specifies the usual options for the procedure run and produces trace plots (**PLOTS=TRACE**). The three **PARMS** statements put three model parameters, p , τ , and μ , in three different blocks. The **PRIOR** statements specify the prior distributions, and the programming statements enclosed with the **BEGINNODATA** and **ENDNODATA** statements calculate the transformation to τ_{aub} and τ_{uw} . The **RANDOM** statement specifies the random effect, its prior distribution, and the subject variable. The resulting trace plots are shown in [Output 55.20.1](#), and the effective sample size table is shown in [Output 55.20.2](#).

Output 55.20.1 Trace Plots



Output 55.20.1 *continued*



Output 55.20.2 Bad Effective Sample Sizes

Implement a New Sampling Algorithm			
The MCMC Procedure			
Effective Sample Sizes			
Parameter	ESS	Autocorrelation Time	Efficiency
p	81.3	61.5342	0.0163
tau	61.2	81.7440	0.0122
mu	5000.0	1.0000	1.0000
theta_1	4839.9	1.0331	0.9680
theta_2	2739.7	1.8250	0.5479
theta_3	1346.6	3.7130	0.2693
theta_4	4897.5	1.0209	0.9795
theta_5	338.1	14.7866	0.0676

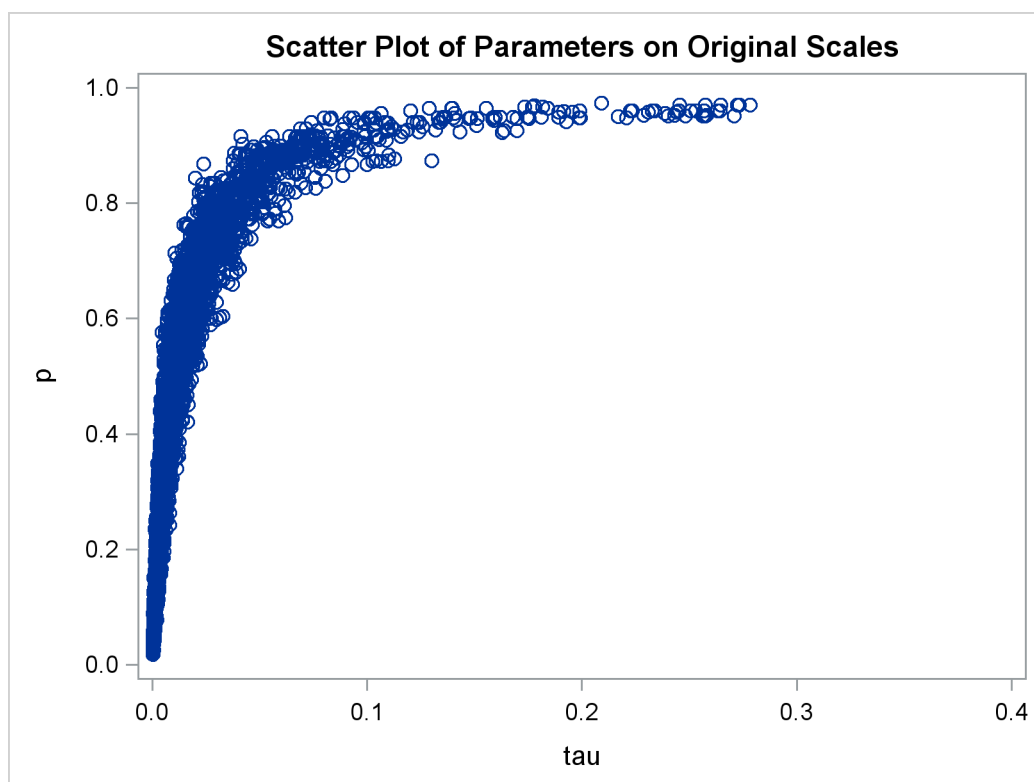
The trace plots show that most parameters have relatively good mixing. Two exceptions appear to be p and τ . The trace plot of p shows a slow periodic movement. The τ parameter does not have good mixing either. When the values are close to zero, the chain stays there for periods of time. An inspection of the effective sample sizes table reveals the same conclusion: p and τ have much smaller ESSs than the rest of the parameters.

A scatter plot of the posterior samples of p and τ reveals why mixing is bad in these two dimensions. The following statements generate the scatter plot in [Output 55.20.3](#):

```
title 'Scatter Plot of Parameters on Original Scales';

proc sgplot data=m1;
  yaxis label = 'p';
  xaxis label = 'tau' values=(0 to 0.4 by 0.1);
  scatter x = tau y = p;
run;
```

Output 55.20.3 Scatter Plot of τ versus p



The two parameters clearly have a nonlinear relationship. It is not surprising that the Metropolis algorithm does not work well here. The algorithm is designed for cases where the parameters are linearly related with each other.

To improve on mixing, you can sample on the log of τ , instead of sampling on τ . The formulation is:

$$\begin{aligned}\tau &\sim \text{gamma}(\text{shape} = 0.001, \text{iscale} = 0.001) \\ \log(\tau) &\sim \text{egamma}(\text{shape} = 0.001, \text{iscale} = 0.001)\end{aligned}$$

See the section “[Standard Distributions](#)” on page 4476 for the definitions of the [gamma](#) and [egamma](#) distributions. In addition, you can sample on the logit of p . Note that

$$p \sim \text{uniform}(0, 1)$$

is equivalent to

$$\text{lgp} = \text{logit}(p) \sim \text{logistic}(0, 1)$$

The following statements fit the same model by using transformed parameters:

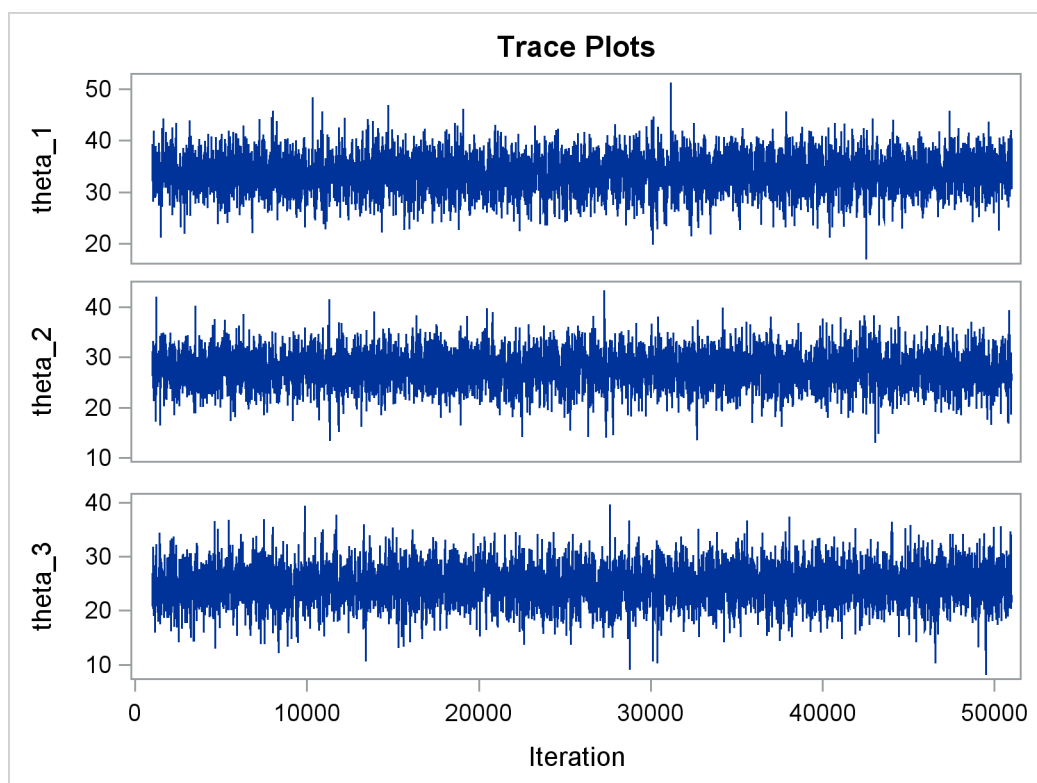
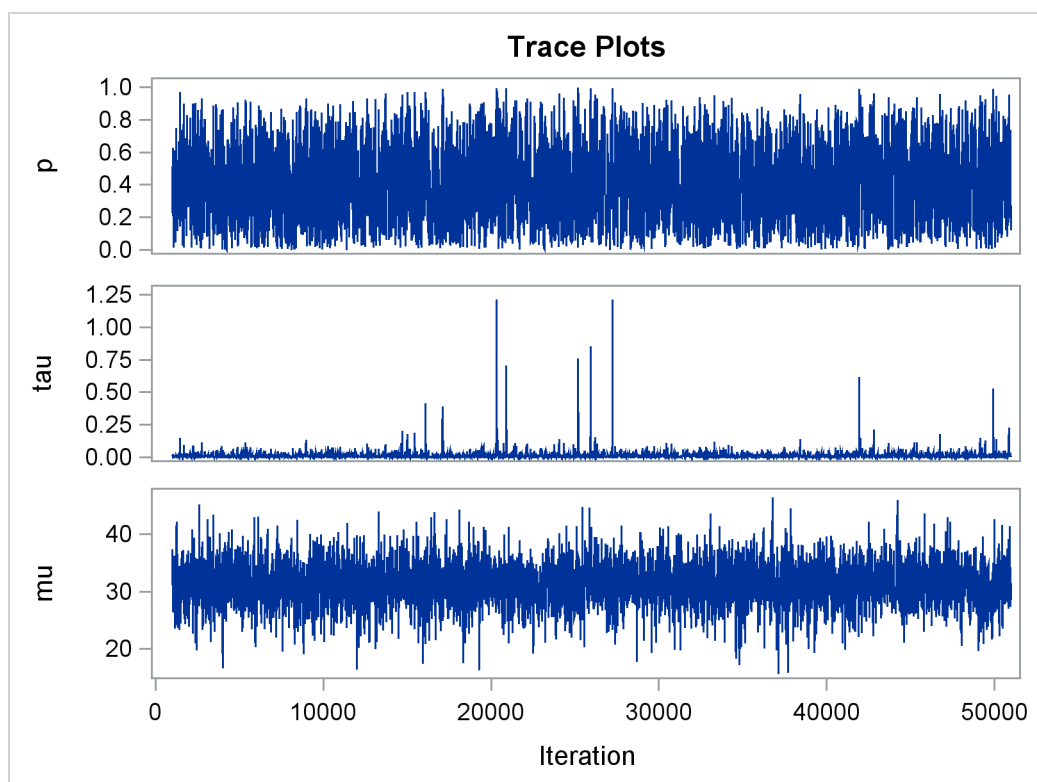
```
proc mcmc data=inputdata nmc=50000 thin=10 outpost=m2 seed=17
    monitor=(p tau mu) plot=trace;
    ods select ess tracepanel;
    parms ltau lgp mu ;

    prior ltau ~ egamma(shape=0.001,iscale=0.001);
    prior lgp ~ logistic(0,1);
    prior mu ~ normal(0,prec=0.00000001);

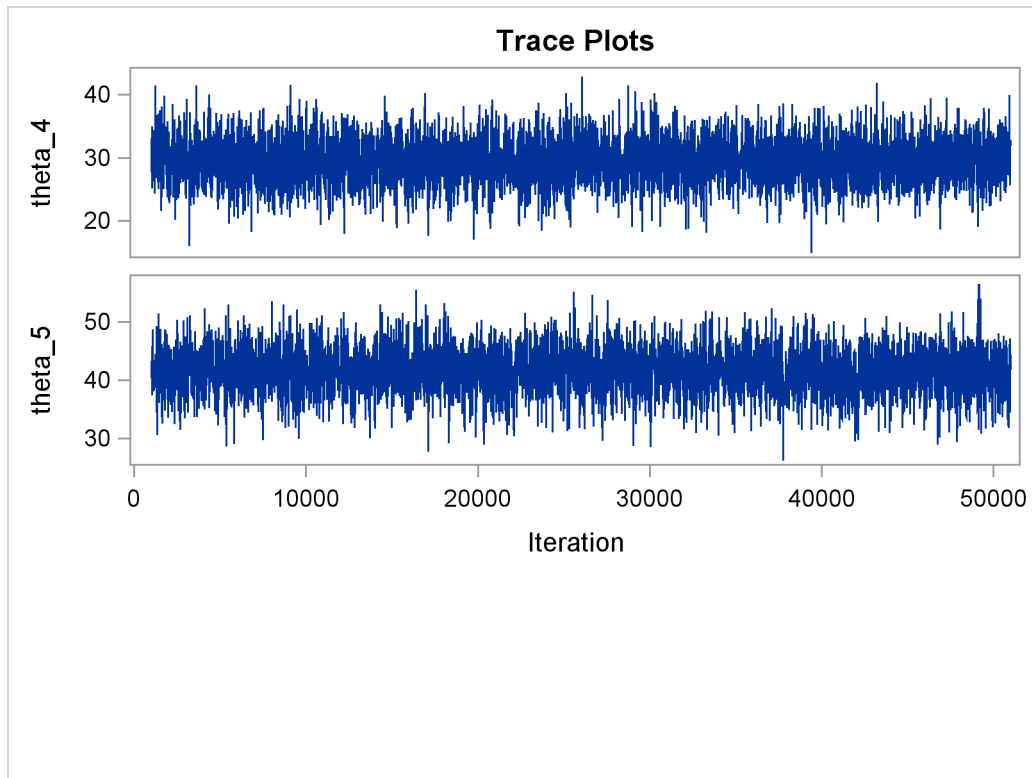
    beginnodata;
    tau = exp(ltau);
    p = logistic(lgp);
    taub = tau/p;
    tauw = taub-tau;
    endnodata;

    random theta ~ normal(mu, prec=taub) subject=grp monitor=(theta);
    model y ~ normal(theta,prec=tauw);
run;
```

The variable `lgp` is the logit transformation of p , and `ltau` is the log transformation of τ . The prior for `ltau` is [egamma](#), and the prior for `lgp` is [logistic](#). The TAU and P assignment statements transform the parameters back to their original scales. The rest of the programs remain unchanged. Trace plots ([Output 55.20.4](#)) and effective sample size ([Output 55.20.5](#)) both show significant improvements in the mixing for both p and τ .

Output 55.20.4 Trace Plots after Transformation

Output 55.20.4 *continued*



Output 55.20.5 Effective Sample Sizes after Transformation

The MCMC Procedure			
Effective Sample Sizes			
Parameter	ESS	Autocorrelation Time	Efficiency
p	3119.4	1.6029	0.6239
tau	2588.0	1.9320	0.5176
mu	5000.0	1.0000	1.0000
theta_1	4866.0	1.0275	0.9732
theta_2	5244.5	0.9534	1.0489
theta_3	5000.0	1.0000	1.0000
theta_4	5000.0	1.0000	1.0000
theta_5	4054.8	1.2331	0.8110

The following statements generate [Output 55.20.6](#) and [Output 55.20.7](#):

```

title 'Scatter Plot of Parameters on Transformed Scales';

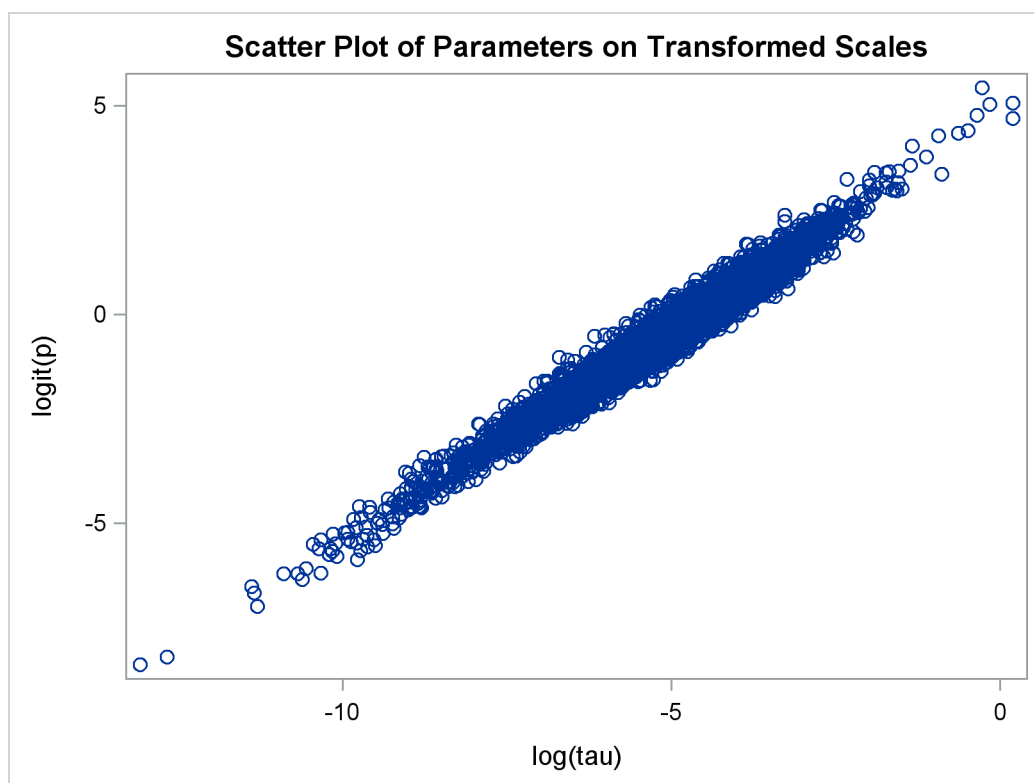
proc sgplot data=m2;
  yaxis label = 'logit(p)';
  xaxis label = 'log(tau)';
  scatter x = ltau y = lgp;
run;

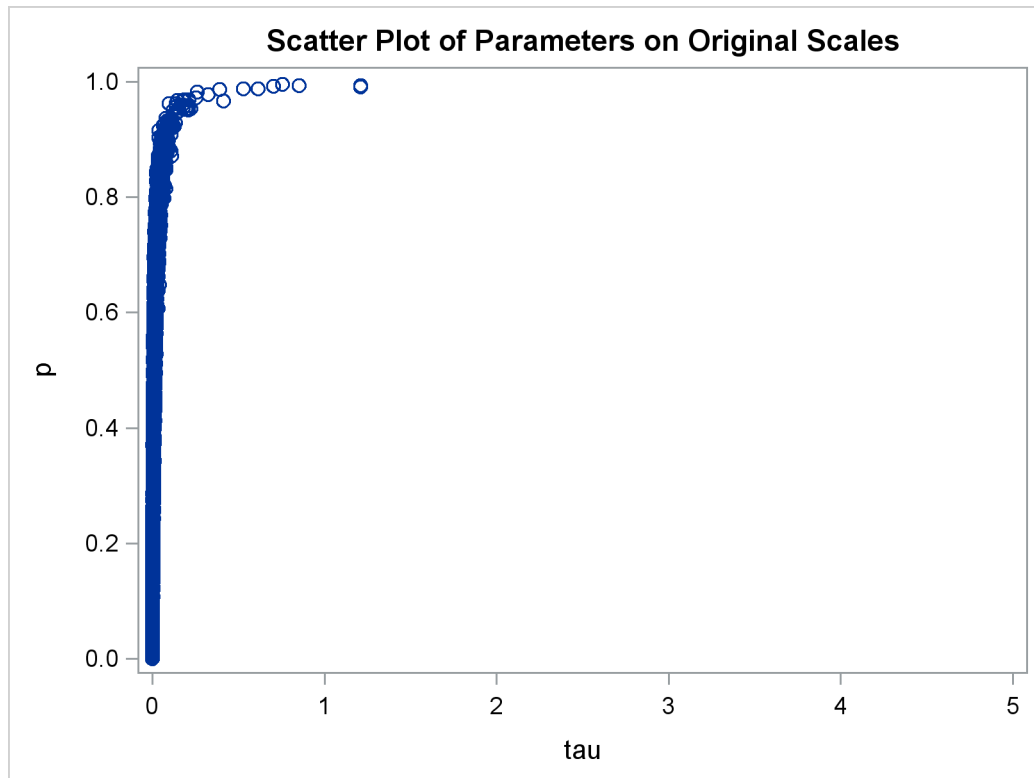
title 'Scatter Plot of Parameters on Original Scales';

proc sgplot data=m2;
  yaxis label = 'p';
  xaxis label = 'tau' values=(0 to 5.0 by 1);
  scatter x = tau y = p;
run;
ods graphics off;

```

Output 55.20.6 Scatter Plot of $\log(\tau)$ versus $\logit(p)$, After Transformation



Output 55.20.7 Scatter Plot of τ versus p , After Transformation

The scatter plot of $\log(\tau)$ versus $\text{logit}(p)$ shows a linear relationship between the two transformed parameters, and this explains the improvement in mixing. In addition, the transformations also help the Markov chain better explore in the original parameter space. [Output 55.20.7](#) shows a scatter plot of τ versus p . The plot is similar to [Output 55.20.3](#). However, note that τ has a far longer tail in [Output 55.20.7](#), extending all the way to 5 as opposed to 0.15 in [Output 55.20.3](#). This means that the second Markov chain can explore this dimension of the parameter more efficiently, and as a result, you are able to draw more precise inference with an equal number of simulations.

Example 55.21: Gelman-Rubin Diagnostics

PROC MCMC does not have the Gelman-Rubin test (see the section “[Gelman and Rubin Diagnostics](#)” on page 145) as a part of its diagnostics. The Gelman-Rubin diagnostics rely on parallel chains to test whether they all converge to the same posterior distribution. This example demonstrates how you can carry out this convergence test. The regression model from the section “[Simple Linear Regression](#)” on page 4408 is used. The model has three parameters: β_0 and β_1 are the regression coefficients, and σ^2 is the variance of the error distribution.

The following statements generate the data set:

```

title 'Simple Linear Regression, Gelman-Rubin Diagnostics';

data Class;
  input Name $ Height Weight @@;
  datalines;
Alfred 69.0 112.5   Alice 56.5 84.0   Barbara 65.3 98.0
Carol 62.8 102.5   Henry 63.5 102.5   James 57.3 83.0
Jane 59.8 84.5    Janet 62.5 112.5   Jeffrey 62.5 84.0
John 59.0 99.5    Joyce 51.3 50.5    Judy 64.3 90.0
Louise 56.3 77.0   Mary 66.5 112.0    Philip 72.0 150.0
Robert 64.8 128.0  Ronald 67.0 133.0  Thomas 57.5 85.0
William 66.5 112.0
  ;

```

To run a Gelman-Rubin diagnostic test, you want to start Markov chains at different places in the parameter space. Suppose you want to start β_0 at 10, -15, and 0; β_1 at -5, 10, and 0; and σ^2 at 1, 20, and 50. You can put these starting values in the following Init SAS data set:

```

data init;
  input Chain beta0 beta1 sigma2;
  datalines;
1 10 -5 1
2 -15 10 20
3 0 0 50
  ;

```

The following statements run PROC MCMC three times, each with starting values specified in the data set Init:

```

/* define constants */
%let nchain = 3;
%let nparm = 3;
%let nsim = 50000;
%let var = beta0 beta1 sigma2;

%macro gmcmmc;
  %do i=1 %to &nchain;
    data _null_;
      set init;
      if Chain=&i;
        %do j = 1 %to &nparm;
          call symputx("init&j", %scan(&var, &j));
        %end;
      stop;
    run;

    proc mcmc data=class outpost=out&i init=reinit nbi=0 nmc=&nsim
      stats=none seed=7;
      parms beta0 &init1 beta1 &init2;
      parms sigma2 &init3 / n;
      prior beta0 beta1 ~ normal(0, var = 1e6);
      prior sigma2 ~ igrmm(3/10, scale = 10/3);

```

```

        mu = beta0 + beta1*height;
        model weight ~ normal(mu, var = sigma2);
    run;
%end;
%mend;

ods listing close;
%gmcmc;
ods listing;

```

The macro variables `nchain`, `nparm`, `nsim`, and `var` define the number of chains, the number of parameters, the number of Markov chain simulations, and the parameter names, respectively. The macro `GMCMC` gets initial values from the data set `Init`, assigns them to the macro variables `init1`, `init2` and `init3`, starts the Markov chain at these initial values, and stores the posterior draws to three output data sets: `Out1`, `Out2`, and `Out3`.

In the `PROC MCMC` statement, the `INIT=REINIT` option restarts the Markov chain after tuning at the assigned initial values. No burn-in is requested.

You can use the autocall macro `GELMAN` to calculate the Gelman-Rubin statistics by using the three chains. The `GELMAN` macro has the following arguments:

```
%macro gelman(dset, nparm, var, nsim, nc=3, alpha=0.05);
```

The argument `dset` is the name of the data set that stores the posterior samples from all the runs, `nparm` is the number of parameters, `var` is the name of the parameters, `nsim` is the number of simulations, `nc` is the number of chains with a default value of 3, and `alpha` is the α significant level in the test with a default value of 0.05. This macro creates two data sets: `_Gelman_Ests` stores the diagnostic estimates and `_Gelman_Parms` stores the names of the parameters.

The following statements calculate the Gelman-Rubin diagnostics:

```

data all;
    set out1(in=in1) out2(in=in2) out3(in=in3);
    if in1 then Chain=1;
    if in2 then Chain=2;
    if in3 then Chain=3;
run;

%gelman(all, &nparm, &var, &nsim);

data GelmanRubin(label='Gelman-Rubin Diagnostics');
    merge _Gelman_Parms _Gelman_Ests;
run;

proc print data=GelmanRubin;
run;

```

The Gelman-Rubin statistics are shown in [Output 55.21.1](#).

Output 55.21.1 Gelman-Rubin Diagnostics of the Regression Example

Simple Linear Regression, Gelman-Rubin Diagnostics					
Obs	Parameter	Between- chain	Within- chain	Estimate	Upper Bound
1	beta0	5384.76	1168.64	1.0002	1.0001
2	beta1	1.20	0.30	1.0002	1.0002
3	sigma2	8034.41	2890.00	1.0010	1.0011

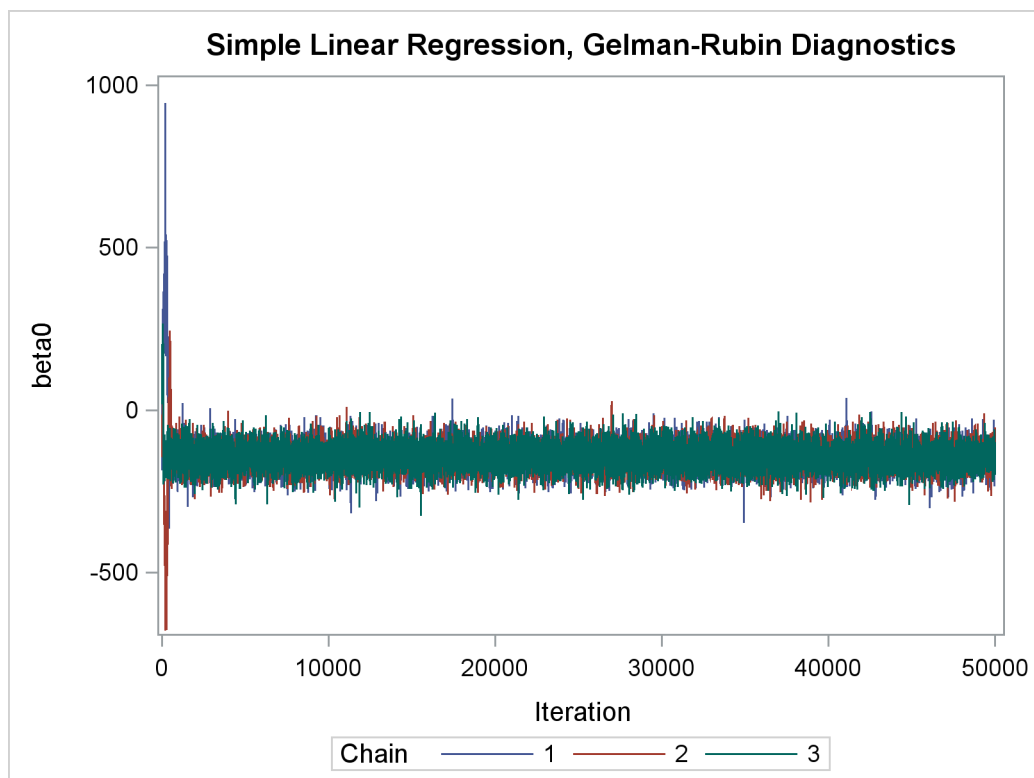
The Gelman-Rubin statistics do not reveal any concerns about the convergence or the mixing of the multiple chains. To get a better visual picture of the multiple chains, you can draw overlapping trace plots of these parameters from the three Markov chains runs.

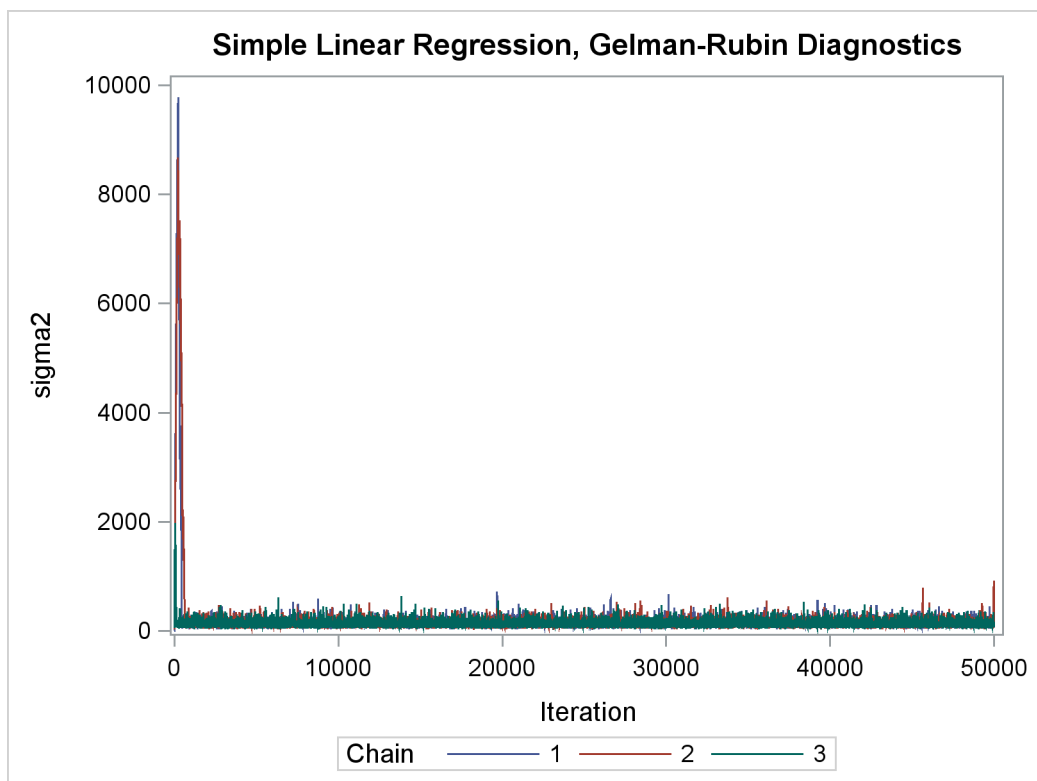
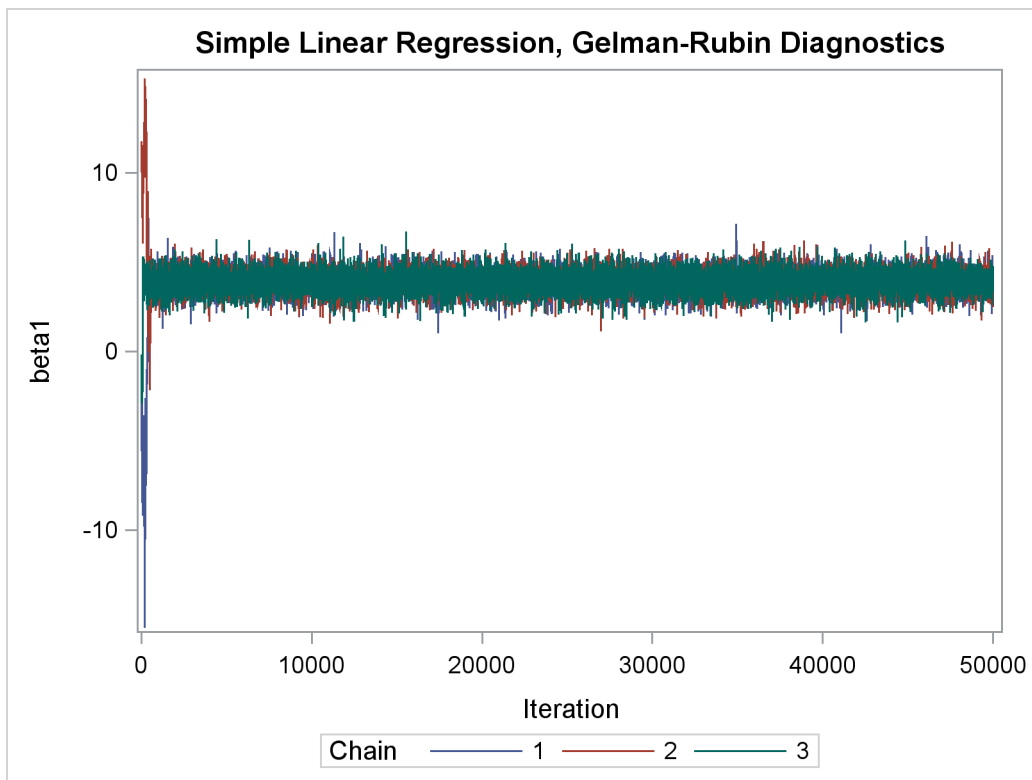
The following statements create [Output 55.21.2](#):

```

/* plot the trace plots of three Markov chains. */
%macro trace;
  %do i = 1 %to &nparm;
    proc sgplot data=all cycleattr;
      series x=Iteration y=%scan(&var, &i) / group=Chain;
    run;
  %end;
%mend;
%trace;

```

Output 55.21.2 Trace Plots of Three Chains for Each of the Parameters

Output 55.21.2 *continued*

The trace plots show that three chains all eventually converge to the same regions even though they started at very different locations. In addition to the trace plots, you can also plot the potential scale reduction factor (PSRF). See the section “[Gelman and Rubin Diagnostics](#)” on page 145 for definition and details.

The following statements calculate PSRF for each parameter. They use the GELMAN macro repeatedly and can take a while to run:

```

/* define sliding window size */
%let nwin = 200;
data PSRF;
run;

%macro PSRF(nsim);
  %do k = 1 %to %sysevalf(&nsim/&nwin, floor);
    %gelman(all, &nparm, &var, nsim=%sysevalf(&k*&nwin));
    data GelmanRubin;
      merge _Gelman_Parms _Gelman_Ests;
    run;

    data PSRF;
      set PSRF GelmanRubin;
    run;
  %end;
%mend PSRF;

options nonotes;
%PSRF(&nsim);
options notes;

data PSRF;
  set PSRF;
  if _n_ = 1 then delete;
run;

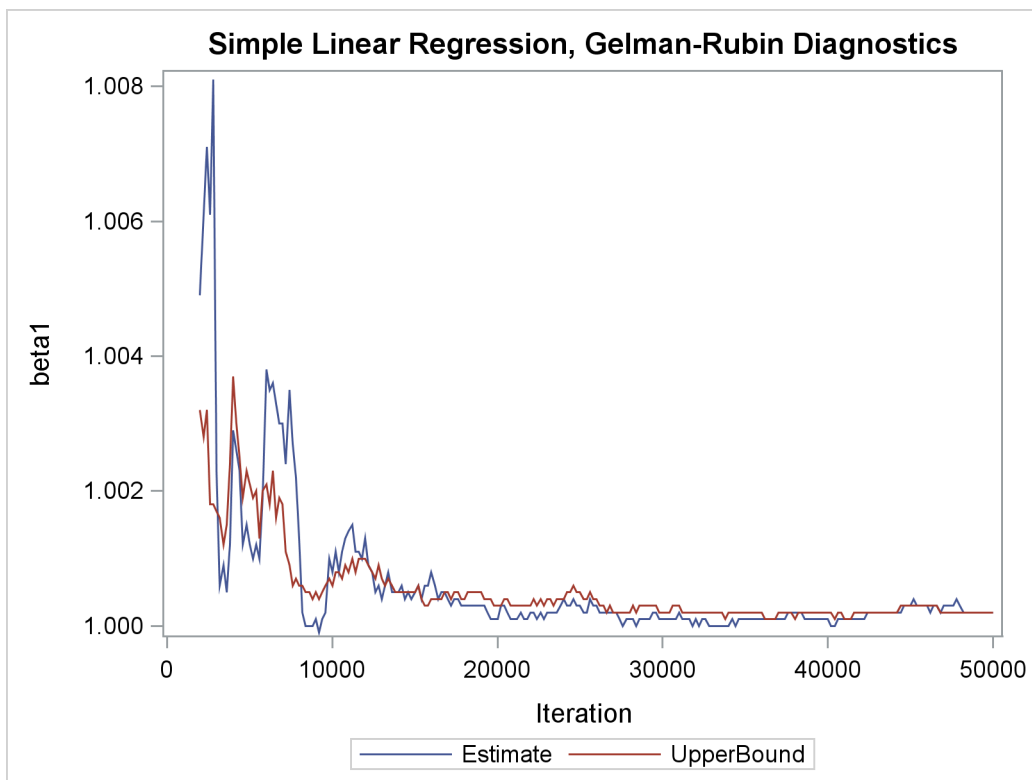
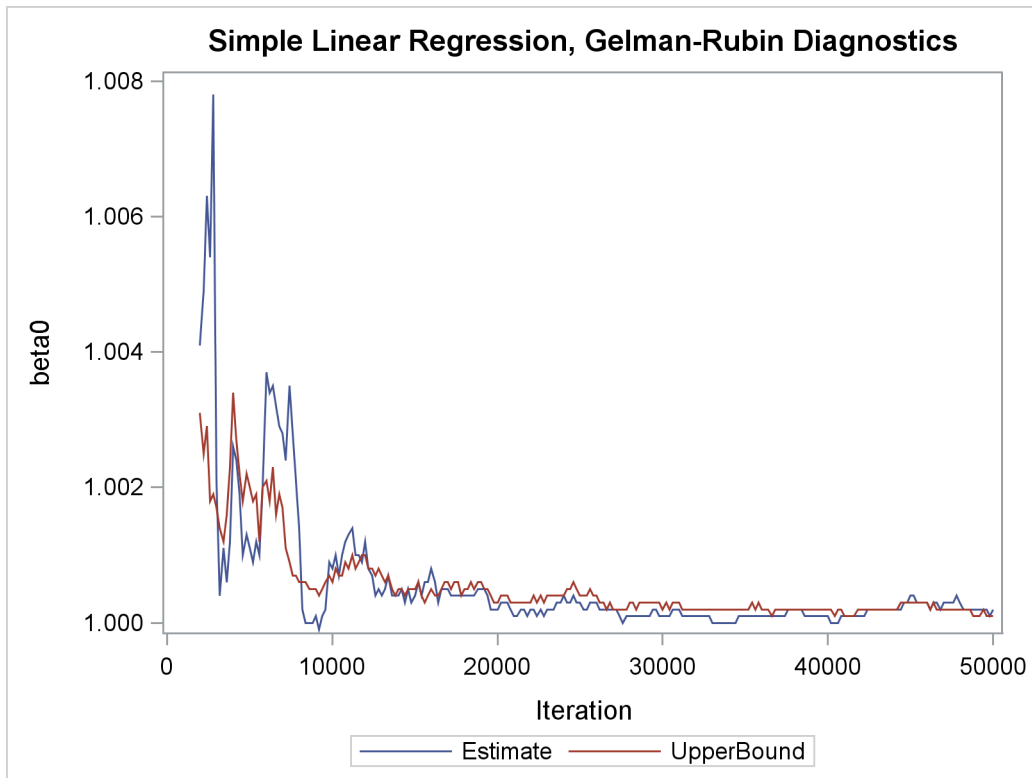
proc sort data=PSRF;
  by Parameter;
run;

%macro sepPSRF(nparm=, var=, nsim=);
  %do k = 1 %to &nparm;
    data save&k; set PSRF;
      if _n_ > %sysevalf(&k*&nsim/&nwin, floor) then delete;
      if _n_ < %sysevalf((&k-1)*&nsim/&nwin + 1, floor) then delete;
      Iteration + &nwin;
    run;

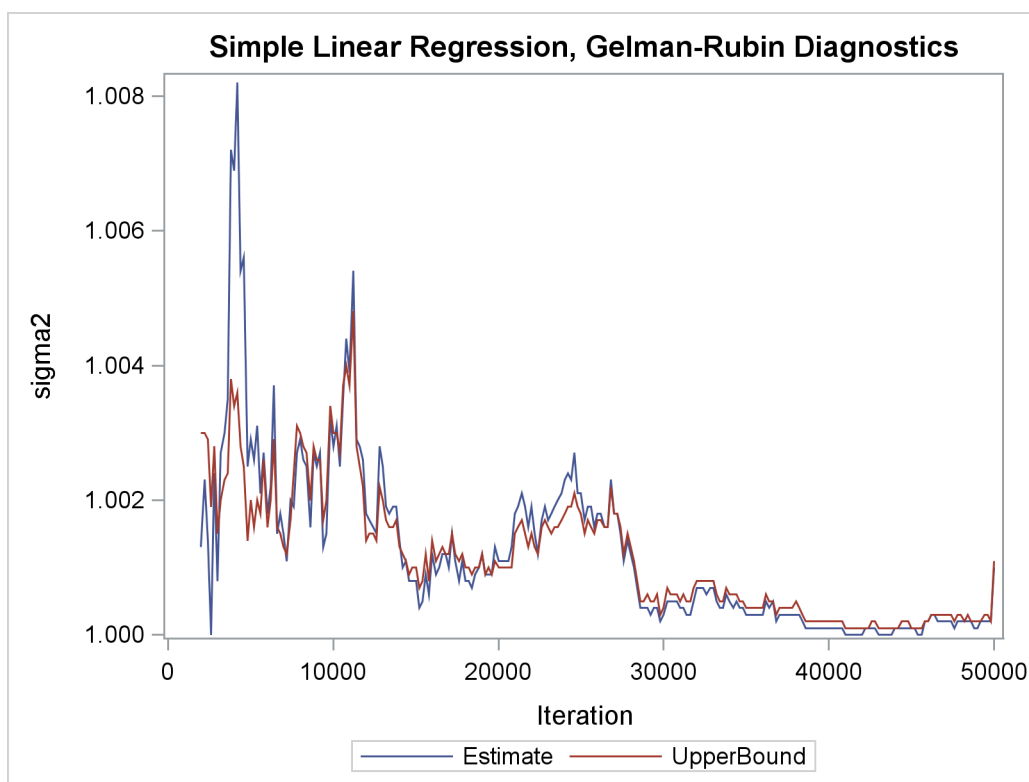
    proc sgplot data=save&k(firstobs=10) cycleattrs;
      series x=Iteration y=Estimate;
      series x=Iteration y=upperbound;
      yaxis label="%scan(&var, &k)";
    run;
  %end;
%mend sepPSRF;

%sepPSRF(nparm=&nparm, var=&var, nsim=&nsim);

```

Output 55.21.3 PSRF Plot for Each Parameter

Output 55.21.3 continued



PSRF is the square root of the ratio of the between-chain variance and the within-chain variance. A large PSRF indicates that the between-chain variance is substantially greater than the within-chain variance, so that longer simulation is needed. You want the PSRF to converge to 1 eventually, as it appears to be the case in this simulation study.

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