# Chapter 37

## The FMM Procedure (Experimental)

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Overview: FMM Procedure

The FMM procedure fits statistical models to data for which the distribution of the response is a finite mixture of univariate distributions—that is, each response comes from one of several random univariate distributions with unknown probabilities. You can use PROC FMM to model the component distributions in addition to the mixing probabilities; see “A Gentle Introduction to Finite Mixture Models” on page 2490 for more precise definitions and discussion of similar but distinct modeling methodologies.

Classical statistical models are a special case of the finite mixture models in which the distribution of the data has only a single component.

Finite mixture models are useful for the following applications:

- estimating multimodal or heavy-tailed densities
- fitting zero-inflated or hurdle models to count data with excess zeros
- modeling overdispersed data
- fitting regression models with complex error distributions
Basic Features

The FMM procedure is designed to fit finite mixtures of regression models or finite mixtures of generalized linear models in which the covariates and regression structure can be the same across components or might be different. You can fit finite mixture models by maximum likelihood or Bayesian methods.

For more information about the differences between the FMM procedure and other statistical modeling procedures in SAS/STAT software, see the section “PROC FMM Contrasted with Other SAS Procedures” on page 2425.

Basic Features

The FMM procedure estimates the parameters in univariate finite mixture models and produces various statistics to evaluate parameters and model fit. The following list summarizes some basic features of the FMM procedure:

- maximum likelihood estimation for all models
- Markov chain Monte Carlo estimation for many models, including zero-inflated Poisson models
- many built-in link and distribution functions for modeling, including the beta, shifted $t$, Weibull, beta-binomial, and generalized Poisson distributions, in addition to many standard members of the exponential family of distributions
- specialized built-in mixture models such as the binomial cluster model (Morel and Nagaraj 1993, Morel and Neerchal 1997, Neerchal and Morel 1998)
- acceptance of multiple MODEL statements to build mixture models in which the model effects, distributions, or link functions vary across mixture components
- model-building syntax using CLASS and effect-based MODEL statements familiar from many other SAS/STAT procedures (for example, the GLM, GLIMMIX, and MIXED procedures)
- evaluation of sequences of mixture models when you specify ranges for the number of components
- simple syntax to impose linear equality and inequality constraints among parameters
- ability to model regression and classification effects in the mixing probabilities through the PROBMODEL statement
- ability to incorporate full or partially known component membership into the analysis through the PARTIAL= option in the PROC FMM statement
- OUTPUT statement that produces a SAS data set with important statistics for interpreting mixture models, such as component log likelihoods and prior and posterior probabilities
The FMM procedure uses ODS Graphics to create graphs as part of its output. For general information about ODS Graphics, see Chapter 21, “Statistical Graphics Using ODS.” For specific information about the statistical graphics available with the FMM procedure, see the PLOTS options in the PROC FMM statement.

Assumptions

The FMM procedure makes the following assumptions in fitting statistical models:

- The number of components $k$ in the finite mixture is known a priori and is not a parameter to be estimated.
- The parameters of the components are distinct a priori.
- The observations are uncorrelated.

Notation for the Finite Mixture Model

The general expression for the finite mixture model fitted with the FMM procedure is as follows:

$$f(y) = \sum_{j=1}^{k} \pi_j(z, \alpha_j) p_j(y; x_j' \beta_j, \phi_j)$$

The number of components in the mixture is denoted as $k$. The mixture probabilities $\pi_j$ can depend on regressor variables $z$ and parameters $\alpha_j$. By default, the FMM procedure models these probabilities using a logit transform if $k = 2$ and as a generalized logit model if $k > 2$. The component distributions $p_j$ can also depend on regressor variables in $x_j$, regression parameters $\beta_j$, and possibly scale parameters $\phi_j$. Notice that the component distributions $p_j$ are indexed by $j$ since the distributions might belong to different families. For example, in a two-component model, you might model one component as a normal (Gaussian) variable and the second component as a variable with a $t$ distribution with low degrees of freedom to manage overdispersion.

The mixture probabilities $\pi_j$ satisfy $\pi_j \geq 0$, for all $j$, and

$$\sum_{j=1}^{k} \pi_j(z, \alpha_j) = 1$$
Homogeneous Mixtures

If the component distributions are of the same distributional form, the mixture is called homogeneous. In most applications of homogeneous mixtures, the mixing probabilities do not depend on regression parameters. The general model then simplifies to

\[ f(y) = \sum_{j=1}^{k} \pi_j p(y; \mathbf{x}' \beta_j, \phi_j) \]

Since the component distributions depend on regression parameters \( \beta_j \), this model is known as a homogeneous regression mixture. A homogeneous regression mixture assumes that the regression effects are the same across the components, although the FMM procedure does not impose such a restriction. If the component distributions do not contain regression effects, the model

\[ f(y) = \sum_{j=1}^{k} \pi_j p(y; \mu_j, \phi_j) \]

is the homogeneous mixture model. A classical case is the estimation of a continuous density as a \( k \)-component mixture of normal distributions.

Special Mixtures

The FMM procedure enables you to fit several special mixture models. The Morel-Neerchal binomial cluster model (Morel and Nagaraj 1993, Morel and Neerchal 1997, and Neerchal and Morel 1998) is a mixture of binomial distributions in which the success probabilities depend on the mixing probabilities.

Zero-inflated count models are obtained as two-component mixtures where one component is a classical count model—such as the Poisson or negative binomial model—and the other component is a distribution that is concentrated at zero. If the nondegenerate part of this special mixture is a zero-truncated model, the resulting two-component mixture is known as a hurdle model (Cameron and Trivedi 1998).

PROC FMM Contrasted with Other SAS Procedures

Since the FMM procedure fits finite mixtures of generalized linear models, it can also fit standard forms of these models in which the distribution of the data does not follow a mixture. This enables you to use the FMM procedure to estimate parameters in models that can be fit with the CATMOD, LOGISTIC, GENMOD, or GLIMMIX procedures. However, the FMM procedure does not fit models for multinomial data or models with random effects.

The FMM procedure has limited postprocessing capabilities compared to some other statistical procedures that are based on linear models. Concepts that are well understood and commonplace in linear models, such as (linear) estimable functions, estimability, and least squares means, do not apply to mixture models in the same way. For example, even the computation of a predicted value is not without ambiguity. You can estimate the means in the component distributions in addition to the overall mean of the mixture.
The FMM procedure provides a limited number of built-in distributions and link functions. User-defined distributions or link functions are not supported. Mixture models with component distributions that are not supported by the FMM procedure can be fit with the NLMIXED procedure.

For Bayesian estimation, the FMM procedure implements a small number of highly specialized sampling algorithms. These algorithms are very efficient and specifically designed for generalized linear models and their mixtures. This limits, for example, the allowable specifications for prior distributions of the model parameters. Models that do not fit the targeted algorithms of the FMM procedure can be fit with the MCMC procedure.

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**Getting Started: FMM Procedure**

**Mixture Modeling for Binomial Overdispersion: “Student,” Pearson, Beer, and Yeast**

The following example demonstrates how you can model a complicated, two-component binomial mixture distribution, either with maximum likelihood or with Bayesian methods, with a few simple PROC FMM statements.

William Sealy Gosset, a chemist at the Arthur Guinness Son and Company brewery in Dublin, joined the statistical laboratory of Karl Pearson in 1906–1907 to study statistics. At first Gosset—who published all but one paper under the pseudonym “Student” because his employer forbade publications by employees after a co-worker had disclosed trade secrets—worked on the Poisson limit to the binomial distribution, using haemacytometer yeast cell counts. Gosset’s interest in studying small-sample (and limit) problems was motivated by the small sample sizes he typically saw in his work at the brewery.

Subsequently, Gosset’s yeast count data have been examined and revisited by many authors. In 1915, Karl Pearson undertook his own examination and realized that the variability in “Student’s” data exceeded that consistent with a Poisson distribution. Pearson (1915) bemoans the fact that if this were so, “it is certainly most unfortunate that such material should have been selected to illustrate Poisson’s limit to the binomial.”

Using a count of Gosset’s yeast cell counts on the 400 squares of a haemacytometer (Table 37.1), Pearson argues that a mixture process would explain the heterogeneity (beyond the Poisson).

<table>
<thead>
<tr>
<th>Table 37.1</th>
<th>“Student’s” Yeast Cell Counts</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Cells</td>
<td>0 1 2 3 4 5</td>
</tr>
<tr>
<td>Frequency</td>
<td>213 128 37 18 3 1</td>
</tr>
</tbody>
</table>

Pearson fits various models to these data, chief among them a mixture of two binomial series

\[ v_1(p_1 + q_1)^\theta + v_2(p_2 + q_2)^\theta \]
where $\theta$ is real-valued and thus the binomial series expands to

$$(p + q)^\theta = \sum_{k=0}^{\infty} \frac{\Gamma(\theta + 1)}{\Gamma(k + 1) \Gamma(\theta - k + 1)} p^k q^{\theta-k}$$

Pearson’s fitted model has $\theta = 4.89997, \nu_1 = 356.986, \nu_2 = 43.014$ (corresponding to a mixing proportion of $356.986/(43.014 + 356.986) = 0.892$), and estimated success probabilities in the binomial components of 0.1017 and 0.4514, respectively. The success probabilities indicate that although the data have about a 90% chance of coming from a distribution with small success probability of about 0.1, there is a 10% chance of coming from a distribution with a much larger success probability of about 0.45.

If $\theta$ is an integer, the binomial series is the cumulative mass function of a binomial random variable. The value of $\theta$ suggests that a suitable model for these data could also be constructed as a two-component mixture of binomial random variables as follows:

$$f(y) = \pi \text{binomial}(5, \mu_1) + (1 - \pi) \text{binomial}(5, \mu_2)$$

The binomial sample size $n = 5$ is suggested by Pearson’s estimate of $\theta = 4.89997$ and the fact that the largest cell count in Table 37.1 is 5.

The following DATA step creates a SAS data set from the data in Table 37.1.

```sas
data yeast;
  input count f;
  n = 5;
  datalines;
  0 213
  1 128
  2 37
  3 18
  4 3
  5 1
;
```

The two-component binomial model is fit with the FMM procedure with the following statements:

```sas
proc fmm data=yeast;
  model count/n = / k=2;
  freq f;
run;
```

Because the events/trials syntax is used in the MODEL statement, PROC FMM defaults to the binomial distribution. The K=2 option specifies that the number of components is fixed and known to be two. The FREQ statement indicates that the data are grouped; for example, the first observation represents 213 squares on the haemacytometer where no yeast cells were found.

The “Model Information” and “Number of Observations” tables in Figure 37.1 convey that the fitted model is a two-component homogeneous binomial mixture with a logit link function. The mixture is homogeneous because there are no model effects in the MODEL statement and because both component distributions belong to the same distributional family. By default, PROC FMM estimates the model parameters by maximum likelihood.
Although only six observations are read from the data set, the data represent 400 observations (squares on the haemacytometer). Since a constant binomial sample size of 5 is assumed, the data represent 273 successes (finding a yeast cell) out of 2,000 Bernoulli trials.

**Figure 37.1** Model Information for Yeast Cell Model

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<tr>
<td>Model Information</td>
</tr>
<tr>
<td>Data Set</td>
</tr>
<tr>
<td>Response Variable (Events)</td>
</tr>
<tr>
<td>Response Variable (Trials)</td>
</tr>
<tr>
<td>Frequency Variable</td>
</tr>
<tr>
<td>Type of Model</td>
</tr>
<tr>
<td>Distribution</td>
</tr>
<tr>
<td>Components</td>
</tr>
<tr>
<td>Link Function</td>
</tr>
<tr>
<td>Estimation Method</td>
</tr>
</tbody>
</table>

| Number of Observations Read | 6       |
| Number of Observations Used | 6       |
| Sum of Frequencies Read    | 400     |
| Sum of Frequencies Used    | 400     |
| Number of Events           | 273     |
| Number of Trials           | 2000    |

The estimated intercepts (on the logit scale) for the two binomial means are \(-2.2316\) and \(-0.2974\), respectively. These values correspond to binomial success probabilities of \(0.09695\) and \(0.4262\), respectively (Figure 37.2). The two components mix with probabilities \(0.8799\) and \(0.1201\). These values are generally close to the values found by Pearson (1915) using infinite binomial series instead of binomial mass functions.

**Figure 37.2** Maximum Likelihood Estimates

<table>
<thead>
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<th>Parameter Estimates for 'Binomial' Model</th>
</tr>
</thead>
<tbody>
<tr>
<td>Component Parameter</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>2</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Parameter Estimates for Mixing Probabilities</th>
</tr>
</thead>
<tbody>
<tr>
<td>Probability Parameter</td>
</tr>
<tr>
<td>Probability</td>
</tr>
</tbody>
</table>
To obtain fitted values and other observationwise statistics under the stipulated two-component model, you can add the OUTPUT statement to the previous PROC FMM run. The following statements request componentwise predicted values and the posterior probabilities:

```plaintext
proc fmm data=yeast;
   model count/n = / k=2;
   freq f;
   output out=fmmout pred(components) posterior;
run;
data fmmout; set fmmout;
   PredCount_1 = post_1 * f;
   PredCount_2 = post_2 * f;
proc print data=fmmout;
run;
```

The DATA step following the PROC FMM step computes the predicted cell counts in each component (Figure 37.3). The predicted means in the components, 0.48476 and 2.13099, are close to the values determined by Pearson (0.4983 and 2.2118), as are the predicted cell counts.

<table>
<thead>
<tr>
<th>Obs</th>
<th>count</th>
<th>f</th>
<th>n</th>
<th>Pred_1</th>
<th>Pred_2</th>
<th>Post_1</th>
<th>Post_2</th>
<th>Pred Count_1</th>
<th>Pred Count_2</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0</td>
<td>213</td>
<td>5</td>
<td>0.48476</td>
<td>2.13099</td>
<td>0.98606</td>
<td>0.01394</td>
<td>210.030</td>
<td>2.9698</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>128</td>
<td>5</td>
<td>0.48476</td>
<td>2.13099</td>
<td>0.91089</td>
<td>0.08911</td>
<td>116.594</td>
<td>11.4058</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>37</td>
<td>5</td>
<td>0.48476</td>
<td>2.13099</td>
<td>0.59638</td>
<td>0.40362</td>
<td>22.066</td>
<td>14.9341</td>
</tr>
<tr>
<td>4</td>
<td>3</td>
<td>18</td>
<td>5</td>
<td>0.48476</td>
<td>2.13099</td>
<td>0.17598</td>
<td>0.82402</td>
<td>3.168</td>
<td>14.8323</td>
</tr>
<tr>
<td>5</td>
<td>4</td>
<td>3</td>
<td>5</td>
<td>0.48476</td>
<td>2.13099</td>
<td>0.02994</td>
<td>0.97006</td>
<td>0.090</td>
<td>2.9102</td>
</tr>
<tr>
<td>6</td>
<td>5</td>
<td>1</td>
<td>5</td>
<td>0.48476</td>
<td>2.13099</td>
<td>0.00444</td>
<td>0.99556</td>
<td>0.004</td>
<td>0.9956</td>
</tr>
</tbody>
</table>

Gosset, who was interested in small-sample statistical problems, investigated the use of prior knowledge in mathematical-statistical analysis—for example, deriving the sampling distribution of the correlation coefficient after having assumed a uniform prior distribution for the coefficient in the population (Aldrich 1997). Pearson also was not opposed to using prior information, especially uniform priors that reflect “equal distribution of ignorance.” Fisher, on the other hand, would not have any of it: the best estimator in his opinion is obtained by a criterion that is absolutely independent of prior assumptions about probabilities of particular values. He objected to the insinuation that his derivations in the work on the correlation were deduced from Bayes theorem (Fisher 1921).

The preceding analysis of the yeast cell count data uses maximum likelihood methods that are free of prior assumptions. The following analysis takes instead a Bayesian approach, assuming a beta prior distribution for the binomial success probabilities and a uniform prior distribution for the mixing probabilities. The changes from the previous FMM run are the addition of the ODS GRAPHICS, PERFORMANCE, and BAYES statements and the SEED=12345 option.
ods graphics on;
proc fmm data=yeast seed=12345;
  model count/n = / k=2;
  freq f;
  performance cpucount=2;
  bayes;
run;
ods graphics off;

With ODS Graphics enabled, PROC FMM produces diagnostic trace plots for the posterior samples. Bayesian analyses are sensitive to the random number seed and thread count; the SEED= and CPUCOUNT= options ensure consistent results for the purposes of this example. The SEED=12345 option in the PROC FMM statement determines the random number seed for the random number generator used in the analysis. The CPUCOUNT=2 option in the PERFORMANCE statement sets the number of available processors to two. The BAYES statement requests a Bayesian analysis.

The “Bayes Information” table in Figure 37.4 provides basic information about the Markov chain Monte Carlo sampler. Because the model is a homogeneous mixture, the FMM procedure applies an efficient conjugate sampling algorithm with a posterior sample size of 10,000 samples after a burn-in size of 2,000 samples. The “Prior Distributions” table displays the prior distribution for each parameter along with its mean and variance and the initial value in the chain. Notice that in this situation all three prior distributions reduce to a uniform distribution on (0, 1).

![Figure 37.4 Basic Information about MCMC Sampler](image)

The FMM procedure produces a log note for this model, indicating that the sampled quantities are not the linear predictors on the logit scale, but are the actual population parameters (on the data scale):
NOTE: Bayesian results for this model (no regressor variables, non-identity link) are displayed on the data scale, not the linked scale. You can obtain results on the linked (=linear) scale by requesting a Metropolis-Hastings sampling algorithm.

The trace panel for the success probability in the first binomial component is shown in Figure 37.5. Note that the first component in this Bayesian analysis corresponds to the second component in the MLE analysis. The graphics in this panel can be used to diagnose the convergence of the Markov chain. If the chain has not converged, inferences cannot be made based on quantities derived from the chain. You generally look for the following:

- a smooth unimodal distribution of the posterior estimates in the density plot displayed on the lower right
- good mixing of the posterior samples in the trace plot at the top of the panel (good mixing is indicated when the trace traverses the support of the distribution and appears to have reached a stationary distribution)

Figure 37.5 Trace Panel for Success Probability in First Component
The autocorrelation plot in Figure 37.5 shows fairly high and sustained autocorrelation among the posterior estimates. While this is generally not a problem, you can affect the degree of autocorrelation among the posterior estimates by running a longer chain and thinning the posterior estimates; see the NMC= and THIN= options in the BAYES statement.

Both the trace plot and the density plot in Figure 37.5 are indications of successful convergence.

Figure 37.6 reports selected results that summarize the 10,000 posterior samples. The arithmetic means of the success probabilities in the two components are 0.3884 and 0.0905, respectively. The posterior mean of the mixing probability is 0.1771. These values are similar to the maximum likelihood parameter estimates in Figure 37.2 (after swapping components).

**Figure 37.6** Summaries for Posterior Estimates

<table>
<thead>
<tr>
<th>Component</th>
<th>Parameter</th>
<th>N</th>
<th>Mean</th>
<th>Std Dev</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Success Probability</td>
<td>10000</td>
<td>0.3884</td>
<td>0.0861</td>
</tr>
<tr>
<td>2</td>
<td>Success Probability</td>
<td>10000</td>
<td>0.0905</td>
<td>0.0162</td>
</tr>
<tr>
<td>1</td>
<td>Probability</td>
<td>10000</td>
<td>0.1771</td>
<td>0.0978</td>
</tr>
</tbody>
</table>

**Posterior Summaries**

<table>
<thead>
<tr>
<th>Component</th>
<th>Parameter</th>
<th>25%</th>
<th>50%</th>
<th>75%</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Success Probability</td>
<td>0.3254</td>
<td>0.3835</td>
<td>0.4457</td>
</tr>
<tr>
<td>2</td>
<td>Success Probability</td>
<td>0.0811</td>
<td>0.0923</td>
<td>0.1017</td>
</tr>
<tr>
<td>1</td>
<td>Probability</td>
<td>0.1073</td>
<td>0.1534</td>
<td>0.2227</td>
</tr>
</tbody>
</table>

**Posterior Intervals**

<table>
<thead>
<tr>
<th>Component</th>
<th>Parameter</th>
<th>Alpha</th>
<th>Lower</th>
<th>Upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Success Probability</td>
<td>0.050</td>
<td>0.2355</td>
<td>0.5663</td>
</tr>
<tr>
<td>2</td>
<td>Success Probability</td>
<td>0.050</td>
<td>0.0538</td>
<td>0.1171</td>
</tr>
<tr>
<td>1</td>
<td>Probability</td>
<td>0.050</td>
<td>0.0564</td>
<td>0.4311</td>
</tr>
</tbody>
</table>

Note that the standard errors in Figure 37.2 are not comparable to those in Figure 37.6, since the standard errors for the MLEs are expressed on the logit scale and the Bayes estimates are expressed on the data scale. You can add the METROPOLIS option in the BAYES statement to sample the quantities on the logit scale.

The “Posterior Intervals” table in Figure 37.6 displays 95% credible intervals (equal-tail intervals and intervals of highest posterior density). It can be concluded that the component with the higher success probability contributes less than 40% to the process.
Modeling Zero-Inflation: Is it Better to Fish Poorly or Not to Have Fished At All?

The following example shows how you can use PROC FMM to model data with more zero values than expected.

Many count data show an excess of zeros relative to the frequency of zeros expected under a reference model. An excess of zeros leads to overdispersion since the process is more variable than a standard count data model. Different mechanisms can lead to excess zeros. For example, suppose that the data are generated from two processes with different distribution functions—one process generates the zero counts, and the other process generates nonzero counts. In the vernacular of Cameron and Trivedi (1998), such a model is called a hurdle model. With a certain probability—the probability of a nonzero count—a hurdle is crossed, and events are being generated. Hurdle models are useful, for example, to model the number of doctor visits per year. Once the decision to see a doctor has been made—the hurdle has been overcome—a certain number of visits follow.

Hurdle models are closely related to zero-inflated models. Both can be expressed as two-component mixtures in which one component has a degenerate distribution at zero and the other component is a count model. In a hurdle model, the count model follows a zero-truncated distribution. In a zero-inflated model, the count model has a nonzero probability of generating zeros. Formally, a zero-inflated model can be written as

\[
\Pr(Y = y) = \pi p_1 + (1 - \pi) p_2(y, \mu)
\]

\[
p_1 = \begin{cases} 
1 & y = 0 \\
0 & \text{otherwise} 
\end{cases}
\]

where \(p_2(y, \mu)\) is a standard count model with mean \(\mu\) and support \(y \in \{0, 1, 2, \cdots\}\).

The following data illustrates the use of a zero-inflated model. In a survey of park attendees, randomly selected individuals were asked about the number of fish they caught in the last six months. Along with that count, the gender and age of each sampled individual was recorded. The following DATA step displays the data for the analysis:

```plaintext
data catch;
  input gender $ age count @@;
  datalines;
  F 54 18 M 37 0 F 48 12 M 27 0
  M 55 0 M 32 0 F 49 12 F 45 11
  M 39 0 F 34 1 F 50 0 M 52 4
  M 33 0 M 32 0 F 23 1 F 17 0
  F 44 5 M 44 0 F 26 0 F 30 0
  F 38 0 F 38 0 F 52 18 M 23 1
  F 23 0 M 32 0 F 33 3 M 26 0
  F 46 8 M 45 5 M 51 10 F 48 5
  F 31 2 F 25 1 M 22 0 M 41 0
  M 19 0 M 23 0 M 31 1 M 17 0
  F 21 0 F 44 7 M 28 0 M 47 3
  M 23 0 F 29 3 F 24 0 M 34 1
  F 19 0 F 35 2 M 39 0 M 43 6
;```

At first glance, the prevalence of zeros in the DATA set is apparent. Many park attendees did not catch any fish. These zero counts are made up of two populations: attendees who do not fish and attendees who fish poorly. A zero-inflation mechanism thus appears reasonable for this application since a zero count can be produced by two separate distributions.

The following statements fit a standard Poisson regression model to these data. A common intercept is assumed for men and women, and the regression slope varies with gender.

```sas
proc fmm data=catch;
   class gender;
   model count = gender*age / dist=Poisson;
run;
```

Figure 37.7 displays information about the model and data set. The “Model Information” table conveys that the model is a single-component Poisson model (a Poisson GLM) and that parameters are estimated by maximum likelihood. There are two levels in the CLASS variable gender, with females preceding males.

![Figure 37.7 Model Information and Class Levels in Poisson Regression](image)

The “Fit Statistics” and “Parameter Estimates” tables from the maximum likelihood estimation of the Poisson GLM are shown in Figure 37.8. If the model is not overdispersed, the Pearson statistic should roughly equal the number of observations in the data set minus the number of parameters. With $n = 52$, there is evidence of overdispersion in these data.
Suppose that the cause of overdispersion is zero-inflation of the count data. The following statements fit a zero-inflated Poisson model.

```plaintext
proc fmm data=catch;
  class gender;
  model count = gender*age / dist=Poisson ;
  model + / dist=Constant;
run;
```

There are two MODEL statements, one for each component of the mixture. Because the distributions are different for the components, you cannot specify the mixture model with a single MODEL statement. The first MODEL statement identifies the response variable for the model (count) and defines a Poisson model with intercept and gender-specific slopes. The second MODEL statement uses the continuation operator (“+”) and adds a model with a degenerate distribution by using DIST=CONSTANT. Because the mass of the constant is placed by default at zero, the second MODEL statement adds a zero-inflation component to the model. It is sufficient to specify the response variable in one of the MODEL statements; you use the “=” sign in that statement to separate the response variable from the model effects.

Figure 37.9 displays the “Model Information” and “Optimization Information” tables for this run of the FMM procedure. The model is now identified as a zero-inflated Poisson (ZIP) model with two components, and the parameters continue to be estimated by maximum likelihood. The “Optimization Information” table shows that there are four parameters in the optimization (compared to three parameters in the Poisson GLM model). The four parameters correspond to three parameters in the mean function (intercept and two gender-specific slopes) and the mixing probability.
Chapter 37: The FMM Procedure (Experimental)

Figure 37.9 Model and Optimization Information in the ZIP Model

The FMM Procedure

Model Information

Data Set WORK.CATCH
Response Variable count
Type of Model Zero-inflated Poisson
Components 2
Estimation Method Maximum Likelihood

Optimization Information

Optimization Technique Dual Quasi-Newton
Parameters in Optimization 4
Mean Function Parameters 3
Scale Parameters 0
Mixing Prob Parameters 1
Number of Threads 2

Results from fitting the ZIP model by maximum likelihood are shown in Figure 37.10. The $-2 \log$ likelihood and the information criteria suggest a much-improved fit over the single-component Poisson model (compare Figure 37.10 to Figure 37.8). The Pearson statistic is reduced by factor 2 compared to the Poisson model and suggests a better fit than the standard Poisson model.

Figure 37.10 Maximum Likelihood Results for the ZIP model

Fit Statistics

-2 Log Likelihood 145.6
AIC (smaller is better) 153.6
AICC (smaller is better) 154.5
BIC (smaller is better) 161.4
Pearson Statistic 43.4467
Effective Parameters 4
Effective Components 2

Parameter Estimates for 'Poisson' Model

| Component | Effect | gender | Estimate | Error | z Value | Pr > |z| |
|-----------|--------|--------|----------|-------|---------|-------|
| 1         | Intercept |       | -3.5215  | 0.6448 | -5.46   | <.0001|
| 1         | age*gender | F      | 0.1216  | 0.01344 | 9.04   | <.0001|
| 1         | age*gender | M      | 0.1056  | 0.01394 | 7.58   | <.0001|

Parameter Estimates for Mixing Probabilities

| Effect | Estimate | Error | z Value | Pr > |z| | Probability |
|--------|----------|-------|---------|-------|----------------|-------------|
| Intercept | 0.8342  | 0.4768 | 1.75  | 0.0802 | 0.6972 |
The number of effective parameters and components shown in Figure 37.8 equals the values from Figure 37.9. This is not always the case because components can collapse (for example, when the mixing probability approaches zero or when two components have identical parameter estimates). In this example, both components and all four parameters are identifiable. The Poisson regression and the zero process mix, with a probability of approximately 0.6972 attributed to the Poisson component.

The FMM procedure enables you to fit some mixture models by Bayesian techniques. The following statements add the BAYES statement to the previous PROC FMM statements:

```plaintext
proc fmm data=catch seed=12345;
   class gender;
   model count = gender*age / dist=Poisson;
   model + / dist=constant;
   performance cpucount=2;
   bayes;
run;
```

The “Model Information” table indicates that the model parameters are estimated by Markov chain Monte Carlo techniques, and it displays the random number seed (Figure 37.11). This is useful if you did not specify a seed to identify the seed value that reproduces the current analysis. The “Bayes Information” table provides basic information about the Monte Carlo sampling scheme. The sampling method uses a data augmentation scheme to impute component membership and then the Gamerman (1997) algorithm to sample the component-specific parameters. The 2,000 burn-in samples are followed by 10,000 Monte Carlo samples without thinning.

**Figure 37.11** Model, Bayes, and Prior Information in the ZIP Model

<table>
<thead>
<tr>
<th>The FMM Procedure</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model Information</td>
</tr>
</tbody>
</table>

- **Data Set**: WORK.CATCH
- **Response Variable**: count
- **Type of Model**: Zero-inflated Poisson
- **Components**: 2
- **Estimation Method**: Markov Chain Monte Carlo
- **Random Number Seed**: 12345

<table>
<thead>
<tr>
<th>Bayes Information</th>
</tr>
</thead>
</table>

- **Sampling Algorithm**: Gamerman
- **Data Augmentation**: Latent Variable
- **Initial Values of Chain**: ML Estimates
- **Burn-In Size**: 2000
- **MC Sample Size**: 10000
- **MC Thinning**: 1
- **Parameters in Sampling**: 4
- **Mean Function Parameters**: 3
- **Scale Parameters**: 0
- **Mixing Prob Parameters**: 1
- **Number of Threads**: 2
The “Prior Distributions” table identifies the prior distributions, their parameters for the sampled quantities, and their initial values. The prior distribution of parameters associated with model effects is a normal distribution with mean 0 and variance 1,000. The prior distribution for the mixing probability is a Dirichlet(1,1), which is identical to a uniform distribution (Figure 37.11). Since the second mixture component is a degeneracy at zero with no associated parameters, it does not appear in the “Prior Distributions” table in Figure 37.11.

Figure 37.12 displays descriptive statistics about the 10,000 posterior samples. Recall from Figure 37.10 that the maximum likelihood estimates were -3.5215, 0.1216, 0.1056, and 0.6972, respectively. With this choice of prior, the means of the posterior samples are generally close to the MLEs in this example. The “Posterior Intervals” table displays 95% intervals of equal-tail probability and 95% intervals of highest posterior density (HPD) intervals.
You can generate trace plots for the posterior parameter estimates by enabling ODS Graphics:

```plaintext
ods graphics on;
ods select TADPanel;
proc fmm data=catch seed=12345;
    class gender;
    model count = gender*age / dist=Poisson;
    model + / dist=constant;
    performance cpucount=2;
    bayes;
run;
ods graphics off;
```

A separate trace panel is produced for each sampled parameter, and the panels for the gender-specific slopes are shown in Figure 37.13. There is good mixing in the chains: the modest autocorrelation that diminishes after about 10 successive samples. By default, the FMM procedure transfers the credible intervals for each parameter from the “Posterior Intervals” table to the trace plot and the density plot in the trace panel.
Figure 37.13  Trace Panels for Gender-Specific Slopes
Mixture modeling is essentially a generalized form of one-dimensional cluster analysis. The following example shows how you can use PROC FMM to explore the number and nature of Gaussian clusters in univariate data.

Roeder (1990) presents data from the Corona Borealis sky survey with the velocities of 82 galaxies in a narrow slice of the sky. Cosmological theory suggests that the observed velocity of each galaxy is proportional to its distance from the observer. Thus, the presence of multiple modes in the density of these velocities could indicate a clustering of the galaxies at different distances.

The following DATA step recreates the data set in Roeder (1990). The computed variable \( v \) represents the measured velocity in thousands of kilometers per second.
title "FMM Analysis of Galaxies Data";
data galaxies;
   input velocity @@;
   v = velocity / 1000;
datalines;
9172  9350  9483  9558  9775  10227  10406  16084  16170  18419
18552 18600 18927 19052 19330 19343 19349 19440 19473
19529 19541 19547 19663 19846 19856 19863 19914 19918 19973
19989 20166 20175 20179 20196 20215 20221 20415 20629 20795
20821 20846 20875 20986 21137 21492 21701 21814 21921 21960
22185 22209 22242 22314 22374 22495 22746 22747 22888
22914 23206 23241 23263 23484 23538 23542 23666 23706 23711
24129 24285 24289 24366 24717 24990 25633 26960 26995 32065
32789 34279
;
run;

Analysis of potentially multimodal data is a natural application of finite mixture models. In this case, the modeling is complicated by the question of the variance for each of the components. Using identical variances for each component could obscure underlying structure, but the additional flexibility granted by component-specific variances might introduce spurious features.

You can use PROC FMM to prepare analyses for equal and unequal variances and use one of the available fit statistics to compare the resulting models. You can use the model selection facility to explore models with varying numbers of mixture components—say, from three to seven as investigated in Roeder (1990). The following statements select the best unequal-variance model using Akaike's information criterion (AIC), which has a built-in penalty for model complexity:

    title2 "Three to Seven Components, Unequal Variances";
    ods graphics on;
    ods select DensityPlot;
    proc fmm data=galaxies criterion=AIC;
       model v = / kmin=3 kmax=7;
            ods exclude IterHistory OptInfo ComponentInfo;
    run;

The KMIN= and KMAX= options indicate the smallest and largest number of components to consider. The ODS GRAPHICS and ODS SELECT statements request a density plot. The output for unequal variances is shown in Figure 37.14 and Figure 37.15.
Figure 37.14 Model Selection for Galaxy Data Assuming Unequal Variances

<table>
<thead>
<tr>
<th>Model ID</th>
<th>Components</th>
<th>Parameters</th>
<th>-2 Log L</th>
<th>AIC</th>
<th>AICC</th>
<th>BIC</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>3</td>
<td>8</td>
<td>406.96</td>
<td>422.96</td>
<td>424.94</td>
<td>442.22</td>
</tr>
<tr>
<td>2</td>
<td>4</td>
<td>11</td>
<td>406.96</td>
<td>428.96</td>
<td>432.74</td>
<td>455.44</td>
</tr>
<tr>
<td>3</td>
<td>5</td>
<td>14</td>
<td>406.96</td>
<td>434.96</td>
<td>441.23</td>
<td>468.66</td>
</tr>
<tr>
<td>4</td>
<td>6</td>
<td>17</td>
<td>406.96</td>
<td>440.96</td>
<td>450.53</td>
<td>481.88</td>
</tr>
<tr>
<td>5</td>
<td>7</td>
<td>20</td>
<td>406.96</td>
<td>446.96</td>
<td>460.73</td>
<td>495.10</td>
</tr>
</tbody>
</table>

The model with 3 components (ID=1) was selected as 'best' based on the AIC statistic.

Fit Statistics

-2 Log Likelihood 407.0
AIC (smaller is better) 423.0
AICC (smaller is better) 424.9
BIC (smaller is better) 442.2
Pearson Statistic 82.0002
Effective Parameters 8
Effective Components 3
### Parameter Estimates for 'Normal' Model

| Component | Parameter | Estimate | Error | z Value | Pr > |z| |
|-----------|-----------|----------|-------|---------|-------|-----|
| 1         | Intercept | 9.7101   | 0.1597| 60.80   | <.0001|
| 2         | Intercept | 33.0444  | 0.5322| 62.09   | <.0001|
| 3         | Intercept | 21.4039  | 0.2597| 82.41   | <.0001|
| 1         | Variance  | 0.1785   | 0.09542|        |       |
| 2         | Variance  | 0.8496   | 0.6937|         |       |
| 3         | Variance  | 4.8567   | 0.8098|         |       |

### Parameter Estimates for Mixing Probabilities

| Component | Parameter  | Estimate | Error | z Value | Pr > |z| | Probability |
|-----------|------------|----------|-------|---------|-------|-----|-------------|
| 1         | Probability| -2.3308  | 0.3959| -5.89   | <.0001| 0.0854|
| 2         | Probability| -3.1781  | 0.5893| -5.39   | <.0001| 0.0366|
To require that the separate components have identical variances, add the `EQUATE=SCALE` option in the `MODEL` statement:

```plaintext
title2 "Three to Seven Components, Equal Variances";
ods select DensityPlot;
proc fmm data=galaxies criterion=AIC gconv=0;
    model v = / kmin=3 kmax=7 equate=scale;
    ods exclude IterHistory OptInfo ComponentInfo;
run;
```

The `GCONV=` convergence criterion is turned off in this PROC FMM run to avoid the early stoppage of the iterations when the relative gradient changes little between iterations. Turning the criterion off usually ensures that convergence is achieved with a small absolute gradient of the objective function.

The output for equal variances is shown in Figure 37.16 and Figure 37.17.
**Figure 37.16** Model Selection for Galaxy Data Assuming Equal Variances

<table>
<thead>
<tr>
<th>Model</th>
<th>Components</th>
<th>Parameters</th>
<th>-2 Log L</th>
<th>AIC</th>
<th>AICC</th>
<th>BIC</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>3</td>
<td>6</td>
<td>478.74</td>
<td>490.74</td>
<td>491.86</td>
<td>505.18</td>
</tr>
<tr>
<td>2</td>
<td>4</td>
<td>8</td>
<td>416.49</td>
<td>432.49</td>
<td>434.47</td>
<td>451.75</td>
</tr>
<tr>
<td>3</td>
<td>5</td>
<td>10</td>
<td>416.49</td>
<td>436.49</td>
<td>439.59</td>
<td>460.56</td>
</tr>
<tr>
<td>4</td>
<td>6</td>
<td>12</td>
<td>416.49</td>
<td>440.49</td>
<td>445.02</td>
<td>469.37</td>
</tr>
<tr>
<td>5</td>
<td>7</td>
<td>14</td>
<td>416.49</td>
<td>444.49</td>
<td>450.76</td>
<td>478.19</td>
</tr>
</tbody>
</table>

The model with 4 components (ID=2) was selected as 'best' based on the AIC statistic.

**Fit Statistics**

- -2 Log Likelihood: 416.5
- AIC (smaller is better): 432.5
- AICC (smaller is better): 434.5
- BIC (smaller is better): 451.7
- Pearson Statistic: 82.0000
- Effective Parameters: 8
- Effective Components: 4
### Parameter Estimates for 'Normal' Model

| Component | Parameter | Estimate | Error | z Value | Pr > |z| |
|-----------|-----------|----------|-------|---------|-------|---|
| 1         | Intercept | 23.5058  | 0.3460| 67.93   | <.0001|
| 2         | Intercept | 33.0440  | 0.7610| 43.42   | <.0001|
| 3         | Intercept | 20.0086  | 0.3029| 66.06   | <.0001|
| 4         | Intercept | 9.7103   | 0.4981| 19.50   | <.0001|
| 1         | Variance  | 1.7354   | 0.3905|         |       |
| 2         | Variance  | 1.7354   | 0.3905|         |       |
| 3         | Variance  | 1.7354   | 0.3905|         |       |
| 4         | Variance  | 1.7354   | 0.3905|         |       |

### Parameter Estimates for Mixing Probabilities

| Component | Parameter | Estimate | Error | z Value | Pr > |z| Probability |
|-----------|-----------|----------|-------|---------|-------|-------------|
| 1         | Probability | 1.4118  | 0.4497| 3.14    | 0.0017| 0.3503      |
| 2         | Probability | -0.8473 | 0.6901| -1.23   | 0.2195| 0.0366      |
| 3         | Probability | 1.8216  | 0.4205| 4.33    | <.0001| 0.5277      |
Not surprisingly, the two variance specifications produce different optimal models. The unequal variance specification favors a three-component model while the equal variance specification favors a four-component model. Comparison of the AIC fit statistics, 423.0 and 432.5, indicates that the three-component, unequal variance model provides the best overall fit.

**Comparison with Roeder's Method**

It is important to note that Roeder’s original analysis proceeds in a different manner than the finite mixture modeling presented here. The technique presented by Roeder first develops a “best” range of scale parameters based on a specific criterion. Roeder then uses fixed scale parameters taken from this range to develop optimal equal-scale Gaussian mixture models.

You can reproduce Roeder’s point estimate for the density by specifying a five-component Gaussian mixture. In addition, use the EQUATE=SCALE option in the MODEL statement and a RESTRICT statement fixing the first component’s scale parameter at 0.9025 (Roeder’s $h = 0.95$, scale= $h^2$). The combination of these options produces a mixture of five Gaussian components, each with variance 0.9025. The following statements conduct this analysis:
Looking for Multiple Modes: Are Galaxies Clustered?

```sas
proc fmm data=galaxies;
  model v = / K=5 equate=scale;
  restrict int 0 (scale 1) = 0.9025;
  ods exclude IterHistory OptInfo ComponentInfo;
run;
ods graphics off;
```

The output is shown in Figure 37.18 and Figure 37.19.

**Figure 37.18** Reproduction of Roeder’s Five-Component Analysis of Galaxy Data

<table>
<thead>
<tr>
<th>FMM Analysis of Galaxies Data</th>
</tr>
</thead>
<tbody>
<tr>
<td>Five Components, Equal Variances = 0.9025</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Model Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Set WORK.GALAXIES</td>
</tr>
<tr>
<td>Response Variable v</td>
</tr>
<tr>
<td>Type of Model Homogeneous Mixture</td>
</tr>
<tr>
<td>Distribution Normal</td>
</tr>
<tr>
<td>Components 5</td>
</tr>
<tr>
<td>Link Function Identity</td>
</tr>
<tr>
<td>Estimation Method Maximum Likelihood</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Fit Statistics</th>
</tr>
</thead>
<tbody>
<tr>
<td>-2 Log Likelihood 412.2</td>
</tr>
<tr>
<td>AIC (smaller is better) 430.2</td>
</tr>
<tr>
<td>AICC (smaller is better) 432.7</td>
</tr>
<tr>
<td>BIC (smaller is better) 451.9</td>
</tr>
<tr>
<td>Pearson Statistic 82.5549</td>
</tr>
<tr>
<td>Effective Parameters 9</td>
</tr>
<tr>
<td>Effective Components 5</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Linear Constraints at Solution</th>
</tr>
</thead>
<tbody>
<tr>
<td>Constraint k = 1 Active</td>
</tr>
<tr>
<td>Variance = 0.90 Yes</td>
</tr>
</tbody>
</table>

### Parameter Estimates for 'Normal' Model

| Component | Parameter | Estimate | Error | z Value | Pr > |z| |
|-----------|-----------|----------|-------|---------|-------|
| 1 | Intercept | 26.3266  | 0.7778 | 33.85   | <.0001 |
| 2 | Intercept | 33.0443  | 0.5485 | 60.25   | <.0001 |
| 3 | Intercept | 9.7101   | 0.3591 | 27.04   | <.0001 |
| 4 | Intercept | 23.0295  | 0.2294 | 100.38  | <.0001 |
| 5 | Intercept | 19.7187  | 0.1784 | 110.55  | <.0001 |
| 1 | Variance  | 0.9025   | 0      |         |       |
| 2 | Variance  | 0.9025   | 0      |         |       |
| 3 | Variance  | 0.9025   | 0      |         |       |
| 4 | Variance  | 0.9025   | 0      |         |       |
| 5 | Variance  | 0.9025   | 0      |         |       |

Parameter Estimates for Mixing Probabilities

| Component | Parameter   | Estimate | Error  | z Value | Pr > |z| | Probability |
|-----------|-------------|----------|--------|---------|-------|-------------|
| 1 | Probability | -2.4739  | 0.7084 | -3.49   | 0.0005| 0.0397      |
| 2 | Probability | -2.5544  | 0.6016 | -4.25   | <.0001| 0.0366      |
| 3 | Probability | -1.7071  | 0.4141 | -4.12   | <.0001| 0.0854      |
| 4 | Probability | -0.2466  | 0.2699 | -0.91   | 0.3609| 0.3678      |

---

Figure 37.18 continued
Figure 37.19  Density Plot for Roeder's Analysis

Distribution and Estimated Density for \( v \)

With Estimated Component Densities

- Mixture
- 1: Normal(26.3, 0.9)
- 2: Normal(33.0, 0.9)
- 3: Normal(9.71, 0.9)
- 4: Normal(23.0, 0.9)
- 5: Normal(19.7, 0.9)
Syntax: FMM Procedure

You can specify the following statements in the FMM procedure:

```
PROC FMM < options > ;
   BAYES bayes-options ;
   BY variables ;
   CLASS variables < / TRUNCATE > ;
   FREQ variable ;
   ID variables ;
   MODEL response < (response-options) >= < effects > < / model-options > ;
   MODEL events/trials = < effects > < / model-options > ;
   OUTPUT < OUT=SAS-data-set >
       < keyword < (keyword-options) > <=name>=... 
       < keyword < (keyword-options) > <=name>= < / options > ;
   PERFORMANCE performance-options ;
   PROBMODEL < effects > < / probmodel-options > ;
   RESTRICT < 'label' > constraint-specification < , ... , constraint-specification >
       < operator < value >= < / option > ;
   WEIGHT variable ;
```

The PROC FMM statement and at least one MODEL statement is required. The CLASS, RESTRICT and
MODEL statements can appear multiple times. If a CLASS statement is specified, it must precede the
MODEL statements. The RESTRICT statements must appear after the MODEL statements.

PROC FMM Statement

```
PROC FMM < options > ;
```

The PROC FMM statement invokes the procedure. Table 37.2 summarizes important options in the PROC
FMM statement by function. These and other options in the PROC FMM statement are then described fully
in alphabetical order.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Basic Options</strong></td>
<td></td>
</tr>
<tr>
<td>DATA=</td>
<td>Specifies the input data set</td>
</tr>
<tr>
<td>EXCLUSION=</td>
<td>Specifies how the procedure responds to support violations in the data</td>
</tr>
<tr>
<td>NAMELEN=</td>
<td>Specifies the length of effect names</td>
</tr>
<tr>
<td>ORDER=</td>
<td>Determines the sort order of CLASS variables</td>
</tr>
<tr>
<td>SEED=</td>
<td>Specifies the random number seed for analyses that require random number draws</td>
</tr>
<tr>
<td>Option</td>
<td>Description</td>
</tr>
<tr>
<td>---------------------</td>
<td>---------------------------------------------------------------------------------------------------------------------------------------------</td>
</tr>
<tr>
<td><strong>Displayed Output</strong></td>
<td></td>
</tr>
<tr>
<td>COMPONENTINFO</td>
<td>Displays information about the mixture components</td>
</tr>
<tr>
<td>CORR</td>
<td>Displays the asymptotic correlation matrix of the maximum likelihood parameter estimates or the empirical correlation matrix of the Bayesian posterior estimates</td>
</tr>
<tr>
<td>COV</td>
<td>Displays the asymptotic covariance matrix of the maximum likelihood parameter estimates or the empirical covariance matrix of the Bayesian posterior estimates</td>
</tr>
<tr>
<td>COVI</td>
<td>Displays the inverse of the covariance matrix of the parameter estimates</td>
</tr>
<tr>
<td>FITDETAILS</td>
<td>Displays fit information for all examined models</td>
</tr>
<tr>
<td>ITDETAILS</td>
<td>Adds estimates and gradients to the “Iteration History” table</td>
</tr>
<tr>
<td>NOCLPRINT</td>
<td>Suppresses the “Class Level Information” table completely or partially</td>
</tr>
<tr>
<td>NOITPRINT</td>
<td>Suppresses the “Iteration History Information” table</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses tabular and graphical output</td>
</tr>
<tr>
<td>PARMSTYLE=</td>
<td>Specifies how parameters are displayed in ODS tables</td>
</tr>
<tr>
<td>PLOTS</td>
<td>Produces ODS statistical graphics</td>
</tr>
<tr>
<td><strong>Computational Options</strong></td>
<td></td>
</tr>
<tr>
<td>CRITERION=</td>
<td>Specifies the criterion used in model selection</td>
</tr>
<tr>
<td>NOCENTER</td>
<td>Prevents centering and scaling of the regressor variables</td>
</tr>
<tr>
<td>PARTIAL=</td>
<td>Specifies a variable that defines a partial classification</td>
</tr>
<tr>
<td><strong>Options Related to Optimization</strong></td>
<td></td>
</tr>
<tr>
<td>ABSCONV=</td>
<td>Tunes an absolute function convergence criterion</td>
</tr>
<tr>
<td>ABSFCOVN=</td>
<td>Tunes an absolute function difference convergence criterion</td>
</tr>
<tr>
<td>ABSGCONV=</td>
<td>Tunes the absolute gradient convergence criterion</td>
</tr>
<tr>
<td>FCONV=</td>
<td>Tunes the relative function convergence criterion</td>
</tr>
<tr>
<td>GCONV=</td>
<td>Tunes the relative gradient convergence criterion</td>
</tr>
<tr>
<td>MAXITER=</td>
<td>Specifies the maximum number of iterations in any optimization</td>
</tr>
<tr>
<td>MAXFUNC=</td>
<td>Specifies the maximum number of function evaluations in any optimization</td>
</tr>
<tr>
<td>MAXTIME=</td>
<td>Specifies the upper limit of CPU time in seconds for any optimization</td>
</tr>
<tr>
<td>MINITER=</td>
<td>Specifies the minimum number of iterations in any optimization</td>
</tr>
<tr>
<td>TECHNIQUE=</td>
<td>Selects the optimization technique</td>
</tr>
<tr>
<td><strong>Singularity Tolerances</strong></td>
<td></td>
</tr>
<tr>
<td>INVALIDLOGL=</td>
<td>Tunes the value assigned to an invalid component log likelihood</td>
</tr>
<tr>
<td>SINGCHOL=</td>
<td>Tunes singularity for Cholesky decompositions</td>
</tr>
<tr>
<td>SINGRES=</td>
<td>Tunes singularity for the residual variance</td>
</tr>
<tr>
<td>SINGULAR=</td>
<td>Tunes general singularity criterion</td>
</tr>
</tbody>
</table>
You can specify the following options in the PROC FMM statement.

**ABSCONV=r**

**ABSTOL=r**

specifies an absolute function convergence criterion. For minimization, termination requires $f(\psi^{(k)}) \leq r$, where $\psi$ is the vector of parameters in the optimization and $f(\cdot)$ is the objective function. The default value of $r$ is the negative square root of the largest double-precision value, which serves only as a protection against overflows.

**ABSFCONV=r <n>**

**ABSFTOL=r <n>**

specifies an absolute function difference convergence criterion. For all techniques except NMSIMP, termination requires a small change of the function value in successive iterations:

$$|f(\psi^{(k-1)}) - f(\psi^{(k)})| \leq r$$

Here, $\psi$ denotes the vector of parameters that participate in the optimization, and $f(\cdot)$ is the objective function. The same formula is used for the NMSIMP technique, but $\psi^{(k)}$ is defined as the vertex with the lowest function value, and $\psi^{(k-1)}$ is defined as the vertex with the highest function value in the simplex. The default value is $r = 0$. The optional integer value $n$ specifies the number of successive iterations for which the criterion must be satisfied before the process can be terminated.

**ABSGCONV=r <n>**

**ABSGTOL=r <n>**

specifies an absolute gradient convergence criterion. Termination requires the maximum absolute gradient element to be small:

$$\max_j |g_j(\psi^{(k)})| \leq r$$

Here, $\psi$ denotes the vector of parameters that participate in the optimization, and $g_j(\cdot)$ is the gradient of the objective function with respect to the $j$th parameter. This criterion is not used by the NMSIMP technique. The default value is $r = 1E-5$. The optional integer value $n$ specifies the number of successive iterations for which the criterion must be satisfied before the process can be terminated.

**COMPONENTINFO**

**COMPINFO**

**CINFO**

produces a table with additional details about the fitted model components.

**COV**

produces the covariance matrix of the parameter estimates. For maximum likelihood estimation, this matrix is based on the inverse (projected) Hessian matrix. For Bayesian estimation, it is the empirical covariance matrix of the posterior estimates. The covariance matrix is shown for all parameters, even if they did not participate in the optimization or sampling.

**COVI**

produces the inverse of the covariance matrix of the parameter estimates. For maximum likelihood estimation, the covariance matrix is based on the inverse (projected) Hessian matrix. For Bayesian estimation, it is the empirical covariance matrix of the posterior estimates. This matrix is then inverted by sweeping, and rows and columns that correspond to linear dependencies or singularities are zeroed.
CORR produces the correlation matrix of the parameter estimates. For maximum likelihood estimation this matrix is based on the inverse (projected) Hessian matrix. For Bayesian estimation, it is based on the empirical covariance matrix of the posterior estimates.

**CRITERION=** *keyword*

**CRIT=** *keyword*

specifies the criterion by which the FMM procedure ranks models when multiple models are evaluated during maximum likelihood estimation. You can choose from the following keywords to rank models:

- **LOGL | LL** based on the mixture log likelihood
- **AIC** based on Akaike’s information criterion
- **AICC** based on the bias-corrected AIC criterion
- **BIC** based on the Bayesian information criterion
- **PEARSON** based on the Pearson statistic
- **GRADIENT** based on the largest element of the gradient (in absolute value)

The default is CRITERION=LOGL.

**DATA=** *SAS-data-set*

names the SAS data set to be used by PROC FMM. The default is the most recently created data set.

**EXCLUSION=** *NONE | ANY | ALL*

**EXCLUDE=** *NONE | ANY | ALL*

specifies how the FMM procedure handles support violations of observations. For example, in a mixture of two Poisson variables, negative response values are not possible. However, in a mixture of a Poisson and a normal variable, negative values are possible, and their likelihood contribution to the Poisson component is zero. An observation that violates the support of one component distribution of the model might be a valid response with respect to one or more other component distributions. This requires some nuanced handling of support violations in mixture models.

The default exclusion technique, EXCLUSION=ALL, removes an observation from the analysis only if it violates the support of all component distributions. The other extreme, EXCLUSION=NONE, permits an observation into the analysis regardless of support violations. EXCLUSION=ANY removes observations from the analysis if the response violates the support of any component distributions. In the single-component case, EXCLUSION=ALL and EXCLUSION=ANY are identical.

**FCONV=** \( r \) \( < n > \)

**FTOL=** \( r \) \( < n > \)

specifies a relative function convergence criterion. For all techniques except NMSIMP, termination requires a small relative change of the function value in successive iterations,

\[
\frac{|f(\psi^{(k)}) - f(\psi^{(k-1)})|}{|f(\psi^{(k-1)})|} \leq r
\]

Here, \( \psi \) denotes the vector of parameters that participate in the optimization, and \( f(\cdot) \) is the objective function. The same formula is used for the NMSIMP technique, but \( \psi^{(k)} \) is defined as the vertex with
the lowest function value, and \( \psi^{(k-1)} \) is defined as the vertex with the highest function value in the simplex. The default is \( r = 10^{-\text{FDIGITS}} \), where FDIGITS is by default \(-\log_{10}\epsilon\), and \( \epsilon \) is the machine precision. The optional integer value \( n \) specifies the number of successive iterations for which the criterion must be satisfied before the process can terminate.

**FITDETAILS**
requests that the “Optimization Information,” “Iteration History,” and “Fit Statistics” tables be produced for all optimizations when models with different number of components are evaluated. For example, the following statements fit a binomial regression model with up to three components and produces fit and optimization information for all three:

```plaintext
proc fmm fitdetails;
   model y/n = x / kmax=3;
run;
```
Without the FITDETAILS option, only the “Fit Statistics” table for the selected model is displayed.

**GCONV=r**<\( n \)>
**GTOL=r**<\( n \)>
specifies a relative gradient convergence criterion. For all techniques except CONGRA and NMSIMP, termination requires that the normalized predicted function reduction be small,

\[
\frac{g(\psi^{(k)})' [H^{(k)}]^{-1} g(\psi^{(k)})}{|f(\psi^{(k)})|} \leq r
\]
Here, \( \psi \) denotes the vector of parameters that participate in the optimization, \( f(\cdot) \) is the objective function, and \( g(\cdot) \) is the gradient. For the CONGRA technique (where a reliable Hessian estimate \( H \) is not available), the following criterion is used:

\[
\frac{\| g(\psi^{(k)}) \|_2^2}{\| g(\psi^{(k)}) - g(\psi^{(k-1)}) \|_2 |f(\psi^{(k)})|} \leq r
\]
This criterion is not used by the NMSIMP technique. The default value is \( r = 1E-8 \). The optional integer value \( n \) specifies the number of successive iterations for which the criterion must be satisfied before the process can terminate.

**HESSIAN**
displays the Hessian matrix of the model. This option is not available for Bayesian estimation.

**INVALIDLOGL=r**
specifies the value assumed by the FMM procedure if a log likelihood cannot be computed (for example, because the value of the response variable falls outside of the response distribution’s support). The default value is \(-1E20\).

**ITDETAILS**
adds parameter estimates and gradients to the “Iteration History” table. If the FMM procedure centers or scales the model variables (or both), the parameter estimates and gradients reported during the iteration refer to that scale. You can suppress centering and scaling with the NOCENTER option.
**MAXFUNC=**<i>n</i>

**MAXFU=**<i>n</i>

specifies the maximum number of function calls in the optimization process. The default values are as follows, depending on the optimization technique:

- TRUREG, NRRIDG, and NEWRAP: 125
- QUANEW and DBLDOG: 500
- CONGRA: 1000
- NMSIMP: 3000

The optimization can terminate only after completing a full iteration. Therefore, the number of function calls that are actually performed can exceed the number that is specified by the MAXFUNC= option. You can choose the optimization technique with the TECHNIQUE= option.

**MAXITER=**<i>n</i>

**MAXIT=**<i>n</i>

specifies the maximum number of iterations in the optimization process. The default values are as follows, depending on the optimization technique:

- TRUREG, NRRIDG, and NEWRAP: 50
- QUANEW and DBLDOG: 200
- CONGRA: 400
- NMSIMP: 1000

These default values also apply when <i>n</i> is specified as a missing value. You can choose the optimization technique with the TECHNIQUE= option.

**MAXTIME=**<i>r</i>

specifies an upper limit of <i>r</i> seconds of CPU time for the optimization process. The default value is the largest floating-point double representation of your computer. The time specified by the MAXTIME= option is checked only once at the end of each iteration. Therefore, the actual running time can be longer than that specified by the MAXTIME= option.

**MINITER=**<i>n</i>

**MINIT=**<i>n</i>

specifies the minimum number of iterations. The default value is 0. If you request more iterations than are actually needed for convergence to a stationary point, the optimization algorithms can behave strangely. For example, the effect of rounding errors can prevent the algorithm from continuing for the required number of iterations.

**NAMELEN=**<i>number</i>

specifies the length to which long effect names are shortened. The default and minimum value is 20.

**NOCENTER**

requests that regressor variables not be centered or scaled. By default the FMM procedure centers and scales columns of the <i>X</i> matrix if the models contain intercepts. If NOINT options in MODEL statements are in effect, the columns of <i>X</i> are scaled but not centered. Centering and scaling can help
with the stability of estimation and sampling algorithms. The FMM procedure does not produce a
table of the centered and scaled coefficients and provides no user control over the type of centering
and scaling that is applied. The NOCENTER option turns any centering and scaling off and processes
the raw values of the continuous variables.

`NOCLPRINT< =number>`
suppresses the display of the “Class Level Information” table if you do not specify `number`. If you
specify `number`, the values of the classification variables are displayed for only those variables whose
number of levels is less than `number`. Specifying a `number` helps to reduce the size of the “Class
Level Information” table if some classification variables have a large number of levels.

`NOITPRINT`
suppresses the display of the “Iteration History Information” table.

`NOPRINT`
suppresses the normal display of tabular and graphical results. The NOPRINT option is useful when
you want to create only one or more output data sets with the procedure. This option temporarily
disables the Output Delivery System (ODS); see Chapter 20, “Using the Output Delivery System,”
for more information.

`ORDER=order-type`
specifies the sorting order for the levels of CLASS variables. This ordering determines which param-
eters in the model correspond to each level in the data.

You can specify the following values for `order-type`:

`DATA`
sorts the levels by order of appearance in the input data set.

`FORMATTED`
sorts the levels by external formatted value, except for numeric variables with no explicit format,
which are sorted by their unformatted (internal) value.

`FREQ`
sorts the levels by descending frequency count; levels with the most observations come first in
the order.

`INTERNAL`
sorts the levels by unformatted value.

`FREQDATA`
sorts the levels by order of descending frequency count, and within counts by order of appear-
ance in the input data set when counts are tied.

`FREQFORMATTED`
sorts the levels by order of descending frequency count, and within counts by formatted value
(as above) when counts are tied.

`FREQINTERNAL`
sorts the levels by order of descending frequency count, and within counts by unformatted value
when counts are tied.
When the default ORDER=FORMATTED is in effect for numeric variables for which you have supplied no explicit format, the levels are ordered by their internal values. To order numeric class levels with no explicit format by their BEST12. formatted values, you can specify this format explicitly for the CLASS variables.

When FORMATTED and INTERNAL values are involved, the sort order is machine-dependent.

When the response variable appears in a CLASS statement, the ORDER= option in the PROC FMM statement applies to its sort order. For example, in the following statements the sort order of the wheeze variable is determined by the order of appearance in the input data set because the response variable appears in the CLASS statement:

```plaintext
proc fmm order=data;
  class city wheeze;
  model wheeze = city age / dist=binary s;
run;
```

However, in the following statements the sort order of the wheeze variable is determined by the formatted value (the default response-option in the MODEL statement):

```plaintext
proc fmm order=data;
  class city;
  model wheeze = city age / dist=binary s;
run;
```

The ORDER= option in the PROC FMM statement has no effect on the sort order of the wheeze variable because it does not appear in the CLASS statement.

When you specify a response-option in the MODEL statement, it overrides the ORDER= option in the PROC FMM statement.

For more information about sorting order, see the chapter on the SORT procedure in the Base SAS Procedures Guide and the discussion of BY-group processing in SAS Language Reference: Concepts.

**PARMSTYLE=EFFECT | LABEL**

specifies the display style for parameters and effects. The FMM procedure can display parameters in two styles:

- The EFFECT style (which is used by the MIXED and GLIMMIX procedure, for example) identifies a parameter with an “Effect” column and adds separate columns for the CLASS variables in the model.
- The LABEL style creates one column, named Parameter, that combines the relevant information about a parameter into a single column. If your model contains multiple CLASS variables, the LABEL style might use space more economically.

The EFFECT style is the default for models that contain effects; otherwise the LABEL style is used (for example, in homogeneous mixtures). You can change the display style with the PARMSTYLE= option. Regardless of the display style, ODS output data sets that contain information about parameter estimates contain columns for both styles.
PARTIAL=variable

MEMBERSHIP=variable

specifies a variable in the input data set that identifies component membership. You can specify missing values for observations whose component membership is undetermined; this is known as a partial classification (McLachlan and Peel 2000, p. 75). For observations with known membership, the likelihood contribution is no longer a mixture. If observation \( i \) is known to be a member of component \( m \), then its log likelihood contribution is

\[
\log \left\{ \pi_m(z, \alpha_m) p_m(y; x'_m \beta_m, \phi_m) \right\}
\]

Otherwise, if membership is underdetermined, it is

\[
\log \left\{ \sum_{j=1}^{k} \pi_j(z, \alpha_j) p_j(y; x'_j \beta_j, \phi_j) \right\}
\]

The variable specified in the PARTIAL= option can be numeric or character. In case of a character variable, the variable must appear in the CLASS statement. If the PARTIAL= variable appears in the CLASS statement, the membership assignment is made based on the levelized values of the variable, as shown in the “Class Level Information” table. Invalid values of the PARTIAL= variable are ignored.

In a model in which label switching is a problem, the switching can sometimes be avoided by assigning just a few observations to categories. For example, in a three-component model, switches might be prevented by assigning the observation with the smallest response value to the first component and the observation with the largest response value to the last component.

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

controls the plots produced through ODS Graphics.

ODS Graphics must be enabled before requesting plots. For example:

```r
ods graphics on;
proc fmm data=yeast seed=12345;
  model count/n = / k=2;
    freq f;
    performance cpucount=2;
    bayes;
run;
ods graphics off;
```

For more information about enabling and disabling ODS Graphics, see the section “Enabling and Disabling ODS Graphics” on page 609 in Chapter 21, “Statistical Graphics Using ODS.”

Global Plot Options

The global-plot-options apply to all relevant plots generated by the FMM procedure. The global-plot-options supported by the FMM procedure are as follows:
UNPACKPANEL
UNPACK

breaks a graphic that is otherwise paneled into individual component plots.

ONLY

produces only the specified plots. This option is useful if you do not want the procedure to generate all default graphics, but only the ones specified.

Specific Plot Options

The following listing describes the specific plots and their options.

ALL

requests that all plots appropriate for the analysis be produced.

NONE

requests that no ODS graphics be produced.

DENSITY < (density-options) >

requests a plot of the data histogram and mixture density function. This graphic is a default graphic in models without effects in the MODEL statements and is available only in these models. Furthermore, all distributions involved in the mixture must be continuous. You can specify the following density-options to modify the plot:

CUMULATIVE

CDF
displays the histogram and densities in cumulative form.

NBINS=n

BINS=n

specifies the number of bins in the histogram; n is greater than or equal to 0. By default, the FMM procedure computes a suitable bin width and number of bins, based on the range of the response and the number of usable observations. The option has no effect for binary data.

NOCOMPONENTS
NOCOMP

suppresses the component densities from the plot. If the component densities are displayed, they are scaled so that their sum equals the mixture density at any point on the graph. In single-component models, this option has no effect.

NODENSITY
NODENS

suppresses the computation of the mixture density (and the component densities if the COMPONENTS suboption is specified). If you specify the NOHISTOGRAM and the NODENSITY option, no graphic is produced.
NOLABEL
suppresses the component identification with labels. By default, the FMM procedure
labels component densities in the legend of the plot. If you do not specify a model label
with the LABEL= option in the MODEL statement, an identifying label is constructed
from the parameter estimates that are associated with the component. In this case the
parameter values are not necessarily the mean and variance of the distribution; the values
used to identify the densities on the plot are chosen to simplify linking between graphical
and tabular results.

NOHISTOGRAM
NOHIST
suppresses the computation of the histogram of the raw values. If you specify the NO-
HISTOGRAM and the NODENSITY option, no graphic is produced.

NPOINTS=n
N=n
specifies the number of values used to compute the density functions; n is greater than or
equal to 0. The default is N=200.

WIDTH=value
BINWIDTH=value
specifies the bin width for the histogram. The value is specified in units of the response
variable and must be positive. The option has no effect for binary data.

TRACE < (tadpanel-options) >
requests a trace panel with posterior diagnostics for a Bayesian analysis. If a BAYES statement
is present, the trace panel plots are generated by default, one for each sampled parameter. You
can specify the following tadpanel-options to modify the graphic:

BOX
BOXPLOT
replaces the autocorrelation plot with a box plot of the posterior sample.

SMOOTH=None | MEAN | SPLINE
adds a reference estimate to the trace plot. By default, SMOOTH=None. SMOOTH=MEAN uses the arithmetic mean of the trace as the reference. SMOOTH=SPLINE adds a penalized B-spline.

REFERENCE= reference-style
adds vertical reference lines to the density plot, trace plot, and box plot. The available
options for the reference-style are:

NONE suppresses the reference lines
EQT requests equal-tail intervals
HPD requests intervals of highest posterior density. The level for the credible or HPD intervals is chosen based on the “Posterior Interval Statistics” table.
PERCENTILES (or PERC) for percentiles. Up to three percentiles can be displayed, as based on the “Posterior Summary Statistics” table.

The default is REFERENCE=CREDIBLE.

UNPACK
unpacks the panel graphic and displays its elements as separate plots.

SEED=n

determines the random number seed for analyses that depend on a random number stream. If you do not specify a seed or if you specify a value less than or equal to zero, the seed is generated from reading the time of day from the computer clock. The largest possible value for the seed is $2^{31} - 1$. The seed value is reported in the “Model Information” table.

You can use the SYSRANDOM and SYSRANEND macro variables after a PROC FMM run to query the initial and final seed values. However, using the final seed value as the starting seed for a subsequent analysis does not continue the random number stream where the previous analysis left off. The SYSRANEND macro variable provides a mechanism to pass on seed values to ensure that the sequence of random numbers is the same every time you run an entire program.

Analyses that use the same (nonzero) seed are not completely reproducible if they are executed with a different number of threads since the random number streams in separate threads are independent. You can control the number of threads used by the FMM procedure with system options or through the PERFORMANCE statement in the FMM procedure.

SINGCHOL=number

tunes the singularity criterion in Cholesky decompositions. The default is 1E4 times the machine epsilon; this product is approximately 1E−12 on most computers.

SINGRES=number
sets the tolerance for which the residual variance or scale parameter is considered to be zero. The default is 1E4 times the machine epsilon; this product is approximately 1E−12 on most computers.

SINGULAR=number

tunes the general singularity criterion applied by the FMM procedure in sweeps and inversions. The default is 1E4 times the machine epsilon; this product is approximately 1E−12 on most computers.

TECHNIQUE=keyword
TECH=keyword

specifies the optimization technique to obtain maximum likelihood estimates. You can choose from the following techniques by specifying the appropriate keyword:

    CONGRA performs a conjugate-gradient optimization.
    DBLDOG performs a version of double-dogleg optimization.
    NEWRAP performs a Newton-Raphson optimization combining a line-search algorithm with ridging.
    NMSIMP performs a Nelder-Mead simplex optimization.
    NONE performs no optimization.
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NRRIDG performs a Newton-Raphson optimization with ridging.
QUANEW performs a dual quasi-Newton optimization.
TRUREG performs a trust-region optimization.

The default is TECH=QUANEW.

For more details about these optimization methods, see the section “Choosing an Optimization Algorithm” on page 505 of Chapter 19, “Shared Concepts and Topics.”

---

BAYES Statement

**BAYES bayes-options ;**

The BAYES statement requests that the parameters of the model be estimated by Markov chain Monte Carlo sampling techniques. The FMM procedure can estimate by maximum likelihood the parameters of all models supported by the procedure. Bayes estimation, on the other hand, is available for only a subset of these models.

In Bayesian analysis, it is essential to examine the convergence of the Markov chains before you proceed with posterior inference. With ODS Graphics turned on, the FMM procedure produces graphs at the end of the procedure output; these graphs enable you to visually examine the convergence of the chain. Inferences cannot be made if the Markov chain has not converged.

The output produced for a Bayesian analysis is markedly different from that for a frequentist (maximum likelihood) analysis for the following reasons:

- Parameter estimates do not have the same interpretation in the two analyses. Parameters are fixed unknown constants in the frequentist context and random variables in a Bayesian analysis.
- The results of a Bayesian analysis are summarized through chain diagnostics and posterior summary statistics and intervals.
- The FMM procedure samples the mixing probabilities in Bayesian models directly, rather than mapping them onto a logistic (or other) scale.

The FMM procedure applies highly specialized sampling algorithms in Bayesian models. For single-component models without effects, a conjugate sampling algorithm is used where possible. For models in the exponential family that contain effects, the sampling algorithm is based on Gamerman (1997). For the normal and \( t \) distributions, a conjugate sampler is the default sampling algorithm for models with and without effects. In multi-component models, the sampling algorithm is based on latent variable sampling through data augmentation (Frühwirth-Schnatter 2006) and the Gamerman or conjugate sampler. Because of this specialization, the options for controlling the prior distributions of the parameters are limited.

Table 37.3 summarizes important **bayes-options** in the BAYES statement by function. The full assortment of options is then described in alphabetical order.
You can specify the following options in the BAYES statement.

**BETAPRIORPARMS**=

**BETAPRIORPARMS**(pair-specification … pair-specification)

specifies the parameters for the normal prior distribution of the parameters that are associated with model effects ($\beta$s). The pair-specification is of the form $(a, b)$, and the values $a$ and $b$ are the mean and variance of the normal distribution, respectively.

The form of the BETAPRIORPARMS with an equal sign and a single pair is used to specify one pair of prior parameters that applies to all components in the mixture. In the following example, the two intercepts and the two regression coefficients all have a $N(0, 100)$ prior distribution:

```plaintext
proc fmm;
   model y = x / k=2;
   bayes betapriorparms=(0,100);
run;
```
You can also provide a list of pairs to specify different sets of prior parameters for the various regression parameters and components. For example:

```
proc fmm;
  model y = x/ k=2;
  bayes betapriorparms( (0,10) (0,20) (. .) (3,100) );
run;
```

The simple linear regression in the first component has a $N(0,10)$ prior for the intercept and a $N(0,20)$ prior for the slope. The prior for the intercept in the second component uses the FMM default, whereas the prior for the slope is $N(3,100)$.

**DIAGNOSTICS=ALL | NONE | (keyword-list)** controls the computation of diagnostics for the posterior chain. You can request all posterior diagnostics by specifying DIAGNOSTICS=ALL or suppress the computation of posterior diagnostics by specifying DIAGNOSTICS=NONE. The following keywords enable you to select subsets of posterior diagnostics; the default is DIAGNOSTICS=(AUTOCORR).

- **AUTOCORR <(LAGS= numeric-list)>** computes for each sampled parameter the autocorrelations of lags specified in the LAGS= list. Elements in the list are truncated to integers, and repeated values are removed. If the LAGS= option is not specified, autocorrelations are computed by default for lags 1, 5, 10, and 50. See the section “Autocorrelations” on page 156 for details.

- **ESS** computes an estimate of the effective sample size (Kass et al. 1998), the correlation time, and the efficiency of the chain for each parameter. See the section “Effective Sample Size” on page 156 for details.

- **GEWEKE <(geweke-options)>** computes the Geweke spectral density diagnostics (Geweke 1992), which are essentially a two-sample $t$ test between the first $f_1$ portion and the last $f_2$ portion of the chain. The default is $f_1 = 0.1$ and $f_2 = 0.5$, but you can choose other fractions by using the following geweke-options:

  - **FRAC1=value** specifies the fraction $f_1$ for the first window.

  - **FRAC2=value** specifies the fraction $f_2$ for the second window.

  See the section “Geweke Diagnostics” on page 150 for details.

- **HEIDELBERGER <(Heidel-options)>** computes the Heidelberger and Welch diagnostic (which consists of a stationarity test and a half-width 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 half-width test is then carried out. See the section “Heidelberger and Welch Diagnostics” on page 152 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 $\alpha$ level ($0 < \alpha < 1$) for the stationarity test. By default, SALPHA=0.05.

HALPHA=value

specifies the $\alpha$ level ($0 < \alpha < 1$) for the half-width test. By default, HALPHA=0.05.

EPS=value

specifies a small positive number $\epsilon$ such that if the half-width is less than $\epsilon$ times the sample mean of the retaining iterates, the half-width test is passed. By default, EPS=0.1.

MCERROR

computes an estimate of the Monte Carlo standard error for each sampled parameter. See the section “Standard Error of the Mean Estimate” on page 157 for details.

MAXLAG=n

specifies the largest lag used in computing the effective sample size and the Monte Carlo standard error. Specifying this option implies the ESS and MCERROR options. The default is MAXLAG=250.

RAFTERY < (Raftery-options) >

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 153 for more details. The Raftery-options enable you to specify $Q$, $R$, $S$, and a precision level $\epsilon$ for a stationary test.

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

QUANTILE=value

specifies the order (a value between 0 and 1) of the quantile of interest. By default, QUANTILE=0.025.
ACCURACY=value
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=value
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 between 0 and 1) for the stationary test. By default, EPS=0.001.

MIXPRIORPARMS=K
MIXPRIORPARMS(value-list)

specifies the parameters used in constructing the Dirichlet prior distribution for the mixing parameters. If you specify MIXPRIORPARMS=K, the parameters of the \( k \)-dimensional Dirichlet distribution are a vector that contains the number of components in the model \( k \), whatever that might be. You can specify an explicit list of parameters in value-list. If the MIXPRIORPARMS option is not specified, the default Dirichlet parameter vector is a vector of length \( k \) of ones. This results in a uniform prior over the unit simplex; for \( k = 2 \), this is the uniform distribution. See the section “Prior Distributions” on page 2500 for the distribution function of the Dirichlet as used by the FMM procedure.

ESTIMATE=MEAN | MAP

determines which overall estimate is used, based on the posterior sample, in the computation of OUT-PUT statistics and certain ODS graphics. By default, the arithmetic average of the (thinned) posterior sample is used. If you specify ESTIMATE=MAP, the parameter vector is used that corresponds to the maximum log posterior density in the posterior sample. In any event, a message is written to the SAS log if postprocessing results depend on a summary estimate of the posterior sample.

INITIAL=DATA | MLE | MODE | RANDOM

determines how initial values for the Markov chain are obtained. The default when a conjugate sampler is used is INITIAL=DATA, in which case the FMM procedure uses the same algorithm to obtain data-dependent starting values as it uses for maximum likelihood estimation. If no conjugate sampler is available or if you use the METROPOLIS option to explicitly request that it not be used, then the default is INITIAL=MLE, in which case the maximum likelihood estimates are used as the initial values. If the maximum likelihood optimization fails, the FMM procedure switches to the default INITIAL=DATA.

The options INITIAL=MODE and INITIAL=RANDOM use the mode and random draws from the prior distribution, respectively, to obtain initial values. If the mode does not exist or if it falls on the boundary of the parameter space, the prior mean is used instead.

METROPOLIS

requests that the FMM procedure use the Metropolis-Hastings sampling algorithm based on Gamerman (1997), even in situations where a conjugate sampler is available.
MUPRIORPARMS=\textit{pair-specification}

\textbf{MUPRIORPARMS}( \textit{pair-specification} \ldots \textit{pair-specification})

specifies the parameters for the means in homogeneous mixtures without regression coefficients. The \textit{pair-specification} is of the form \((a, b)\), where \(a\) and \(b\) are the two parameters of the prior distribution, optionally delimited with a comma. The actual distribution of the parameter is implied by the distribution selected in the \textbf{MODEL} statement. For example, it is a normal distribution for a mixture of normals, a gamma distribution for a mixture of Poisson variables, a beta distribution for a mixture of binary variables, and an inverse gamma distribution for a mixture of exponential variables. The parameters correspond as follows:

\begin{itemize}
  \item \textbf{Beta:} The parameters correspond to the \(\alpha\) and \(\beta\) parameters of the beta prior distribution such that its mean is \(\mu = \alpha / (\alpha + \beta)\) and its variance is \(\mu(1 - \mu) / (\alpha + \beta + 1)\).
  \item \textbf{Normal:} The parameters correspond to the mean and variance of the normal prior distribution.
  \item \textbf{Gamma:} The parameters correspond to the \(\alpha\) and \(\beta\) parameters of the gamma prior distribution such that its mean is \(\mu = \alpha / \beta\) and its variance is \(\alpha / \beta^2\).
  \item \textbf{Inverse gamma:} The parameters correspond to the \(\alpha\) and \(\beta\) parameters of the inverse gamma prior distribution such that its mean is \(\mu = \beta / (\alpha - 1)\) and its variance is \(\mu^2 / (\alpha - 2)\).
\end{itemize}

The two techniques for specifying the prior parameters with the MUPRIORPARMS option are as follows:

\begin{itemize}
  \item Specify an equal sign and a single pair of values:

    \begin{verbatim}
    proc fmm seed=12345;
      model y = / k=2;
      bayes mupriorparms=(0,50);
    run;
    \end{verbatim}

  \item Specify a list of parameter pairs within parentheses:

    \begin{verbatim}
    proc fmm seed=12345;
      model y = / k=2;
      bayes mupriorparms( (.), (.1,10.5));
    run;
    \end{verbatim}
\end{itemize}

If you specify an invalid value (outside of the parameter space for the prior distribution), the FMM procedure chooses the default value and writes a message to the SAS log. If you want to use the default values for a particular parameter, you can also specify missing values in the \textit{pair-specification}. For example, the preceding list specification assigns default values for the first component and uses the values 1.4 and 10.5 for the mean and variance of the normal prior distribution in the second component. The first example assigns a \(N(0, 50)\) prior distribution to the means in both components.

NBI=\textit{n}

specifies the number of burn-in samples. During the burn-in phase, chains are not saved. The default is NBI=2000.
NMC=n
SAMPLE=n

specifies the number of Monte Carlo samples after the burn-in. Samples after the burn-in phase are saved unless they are thinned with the THIN= option. The default is NMC=10000.

OUTPOST<(outpost-options)>=data-set

requests that the posterior sample be saved to a SAS data set. In addition to variables that contain log likelihood and log posterior values, the OUTPOST data set contains variables for the parameters. The variable names for the parameters are generic (Parm_1, Parm_2, ..., Parm_p). The labels of the parameters are descriptive and correspond to the “Parameter Mapping” table that is produced when the OUTPOST= option is in effect.

You can specify the following outpost-options in parentheses:

LOGPRIOR
adds the value of the log prior distribution to the data set.

NONSINGULAR | NONSING | COMPRESS
eliminates parameters that correspond to singular columns in the design matrix (and were not sampled) from the posterior data set. This is the default.

SINGULAR | SING
adds columns of zeros to the data set in positions that correspond to singularities in the model or to parameters that were not sampled for other reasons. By default, these columns of zeros are not written to the posterior data set.

PHIPRIORPARMS=pair-specification

PHIPRIORPARMS( pair-specification ... pair-specification)

specifies the parameters for the inverse gamma prior distribution of the scale parameters (φ’s) in the model. The pair-specification is of the form (a, b), and the values are chosen such that the prior distribution has mean \( \mu = b/(a - 1) \) and variance \( \mu^2/(a - 2) \).

The form of the PHIPRIORPARMS with an equal sign and a single pair is used to specify one pair of prior parameters that applies to all components in the mixture. For example:

```
proc fmm seed=12345;
  model y = / k=2;
    bayes phipriorparms=(2.001,1.001);
run;
```

The form with a list of pairs is used to specify different prior parameters for the scale parameters in different components. For example:

```
proc fmm seed=12345;
  model y = / k=2;
    bayes phipriorparms( (.,1.001) (3.001,2.001) );
run;
```
If you specify an invalid value (outside of the parameter space for the prior distribution), the FMM procedure chooses the default value and writes a message to the SAS log. If you want to use the default values for a particular parameter, you can also specify missing values in the *pair-specification*. For example, the preceding list specification assigns default values for the first component $a$ prior parameter and uses the value 1.001 for the $b$ prior parameter. The second pair assigns 3.001 and 2.001 for the $a$ and $b$ prior parameters, respectively.

**PRIOROPTIONS** $<$ = >(*prior-options*)

**PRIOROPTS** $<$ = >(*prior-options*)

specifies options related to the construction of the prior distribution and the choice of their parameters. Some *prior-options* apply only in particular models.

You can specify the following *prior-options*:

**CONDITIONAL | COND**

chooses a conditional prior specification for the homogeneous normal and $t$ distribution response components. The default prior specification in these models is an independence prior where the mean of the $h$th component has prior $\mu_h \sim N(a, b)$. The conditional prior is characterized by $\mu_h \sim N(a, \sigma^2_h/b)$.

**DEPENDENT | DEP**

chooses a data-dependent prior for the homogeneous models without effects. The prior parameters $a$ and $b$ are chosen as follows, based on the distribution in the **MODEL** statement:

- Binary and binomial: $a = \bar{y}/(1 - \bar{y})$, $b = 1$, and the prior distribution for the success probability is beta($a$, $b$).
- Poisson: $a = 1$, $b = 1/\bar{y}$, and the prior distribution for $\mu$ is gamma($a$, $b$). See Frühwirth-Schnatter (2006, p. 280) and Viallefont, Richardson, and Greene (2002).
- Exponential: $a = 3$, $b = 2\bar{y}$, and the prior distribution for $\mu$ is inverse gamma with parameters $a$ and $b$.
- Normal and $t$: Under the default independence prior, the prior distribution for $\mu$ is $N(\bar{y}, f s^2)$ where $f$ is the variance factor from the **VAR=** option and

$$s^2 = \frac{1}{n} \sum_{i=1}^{n} (y_i - \bar{y})^2$$

Under the default conditional prior specification, the prior for $\mu_h$ is $N(a, \sigma^2_h/b)$ where $a = \bar{y}$ and $b = 2.6/(\max\{y\} - \min\{y\})$. The prior for the scale parameter is inverse gamma with parameters 1.28 and 0.36$s^2$. For further details, see Raftery (1996) and Frühwirth-Schnatter (2006, p. 179).

**VAR=**$ackslash f$

specifies the variance for normal prior distributions. The default is VAR=1000. This factor is used, for example, in determining the prior variance of regression coefficients or in determining the prior variance of means in homogeneous mixtures of $t$ or normal distributions (unless a data-dependent prior is used).
MLE=$r$ specifies that the prior distribution for regression variables be based on a multivariate normal distribution centered at the MLEs and whose dispersion is a multiple $r$ of the asymptotic MLE covariance matrix. The default is MLE=10. In other words, if you specify PRIOROPTS(\textit{MLE}), the FMM procedure chooses the prior distribution for the regression variables as $N(\hat{\beta}, 10\text{Var}[\hat{\beta}])$ where $\hat{\beta}$ is the vector of maximum likelihood estimates. The prior for the scale parameter is inverse gamma with parameters 1.28 and 0.36$s^2$ where

$$s^2 = \frac{1}{n} \sum_{i=1}^{n} (y_i - \bar{y})^2$$

For further details, see Raftery (1996) and Frühwirth-Schnatter (2006, p. 179).

The MLE option is not available for mixture models in which the parameters are estimated directly on the data scale, such as homogeneous mixture models or mixtures of distributions without model effects for which a conjugate sampler is available. By using the METROPOLIS option, you can always force the FMM procedure to abandon a conjugate sampler in favor of a Metropolis-Hastings sampling algorithm to which the MLE option applies.

\textbf{STATISTICS} < (\textit{global-options})> = ALL | NONE | keyword | (keyword-list)

\textbf{SUMMARIES} < (\textit{global-options})> = ALL | NONE | keyword | (keyword-list)

controls the number of posterior statistics produced. Specifying STATISTICS=ALL is equivalent to specifying STATISTICS=(SUMMARY INTERVAL). To suppress the computation of posterior statistics, specify STATISTICS=NONE. The default is STATISTICS=(SUMMARY INTERVAL). See the section “Summary Statistics” on page 157 for more details.

The global-options include the following:

\textbf{ALPHA=numeric-list}

controls the coverage levels of the equal-tail credible intervals and the credible intervals of highest posterior density (HPD) credible intervals. The ALPHA= values must be between 0 and 1. Each ALPHA= value produces a pair of $100(1 - \alpha)\%$ equal-tail and HPD credible intervals for each sampled parameter. The default is ALPHA=0.05, which results in 95\% credible intervals for the parameters.

\textbf{PERCENT=numeric-list}

requests the percentile points of the posterior samples. The values in numeric-list must be between 0 and 100. The default is PERCENT=(25 50 75), which yields for each parameter the 25th, 50th, and 75th percentiles, respectively.

The list of keywords includes the following:

\textbf{SUMMARY}

produces the means, standard deviations, and percentile points for the posterior samples. The default is to produce the 25th, 50th, and 75th percentiles; you can modify this list with the global PERCENT= option.

\textbf{INTERVAL}

produces equal-tail and HPD credible intervals. The default is to produce the 95\% equal-tail credible intervals and 95\% HPD credible intervals, but you can use the ALPHA= global-option to request credible intervals for any probabilities.
BY Statement

BY variables;

You can specify a BY statement with PROC FMM to obtain separate analyses on 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 FMM 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).

Because sorting the data changes the order in which PROC FMM reads observations, the sorting order for the levels of the CLASS variable might be affected if you have specified ORDER=DATA in the PROC FMM statement.

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.

**THIN=n**

**THINNING=n**

controls the thinning of the Markov chain after the burn-in. Only one in every $k$ samples is used when THIN=$k$, and if NB1=$n_0$ and NMC=$n$, the number of samples kept is

$$\left\lfloor \frac{n_0 + n}{k} \right\rfloor - \left\lfloor \frac{n_0}{k} \right\rfloor$$

where $[a]$ represents the integer part of the number $a$. The default is THIN=1—that is, all samples are kept after the burn-in phase.

**TIMEINC=n**

specifies a time interval in seconds to report progress during the burn-in and sampling phase. The time interval is approximate, since the minimum time interval in which the FMM procedure can respond depends on the multithreading configuration.
CLASS Statement

```plaintext
CLASS variables < / TRUNCATE > ;
```

The CLASS statement names the classification variables to be used in the model. Typical classification variables are Treatment, Sex, Race, Group, and Replication. If you use the CLASS statement, it must appear before the MODEL statement.

Classification variables can be either character or numeric. By default, class levels are determined from the entire set of formatted values of the CLASS variables.

**NOTE:** Prior to SAS 9, class levels were determined by using no more than the first 16 characters of the formatted values. To revert to this previous behavior, you can use the TRUNCATE option in the CLASS statement.

In any case, you can use formats to group values into levels. See the discussion of the FORMAT procedure in the *Base SAS Procedures Guide* and the discussions of the FORMAT statement and SAS formats in *SAS Formats and Informats: Reference*. You can adjust the order of CLASS variable levels with the ORDER= option in the PROC FMM statement. You can specify the following option in the CLASS statement after a slash (/):

TRUNCATE specifies that class levels should be determined by using only up to the first 16 characters of the formatted values of CLASS variables. When formatted values are longer than 16 characters, you can use this option to revert to the levels as determined in releases prior to SAS 9.

FREQ Statement

```plaintext
FREQ variable ;
```

The variable in the FREQ statement identifies a numeric variable in the data set that contains the frequency of occurrence for each observation. PROC FMM treats each observation as if it appears \( f \) times, where \( f \) is the value of the FREQ variable for the observation. If it is not an integer, the frequency value is truncated to an integer. If the frequency value is less than 1 or missing, the observation is not used in the analysis. When the FREQ statement is not specified, each observation is assigned a frequency of 1.

ID Statement

```plaintext
ID variables ;
```

The ID statement specifies a list of variables that are included in the OUT= data set of the OUTPUT statement. If no ID statement is specified, all variables from the input data set are copied into the output data set.
The MODEL statement defines elements of the mixture model, such as the model effects, the distribution, and the link function. At least one MODEL statement is required. You can specify more than one MODEL statement. Each MODEL statement identifies one or more components of a mixture. For example, if components differ in their distributions, link functions, or regressor variables, then you can use separate MODEL statements to define the components. If the finite mixture model is homogeneous—in the sense that all components share the same regressors, distribution, and link function—then you can specify the mixture model with a single MODEL statement by using the K= option.

An intercept is included in each model by default. It can be removed with the NOINT option.

The dependent variable can be specified by using either the response syntax or the events/trials syntax. The events/trials syntax is specific to models for binomial-type data. A binomial(n, π) variable is the sum of n independent Bernoulli trials with event probability π. Each Bernoulli trial results in either an event or a nonevent (with probability 1 − π). The value of the second variable, trials, gives the number n of Bernoulli trials. The value of the first variable, events, is the number of events out of n. The values of both events and (trials−events) must be nonnegative, and the value of trials must be positive. Other distributions that allow the events/trials syntax are the beta-binomial distribution and the binomial cluster model.

If the events/trials syntax is used, the FMM procedure defaults to the binomial distribution. If you use the response syntax, the procedure defaults to the normal distribution unless the response variable is a character variable or listed in the CLASS statement.

The FMM procedure supports a continuation-style syntax in MODEL statements. Since a mixture has only one response variable, it is sufficient to specify the response variable in one MODEL statement. Other MODEL statements can use the continuation symbol “+” before the specification of effects. For example, the following statements fit a three-component binomial mixture model:

```plaintext
class A;
model y/n = x / k=2;
model + A;
```

The first MODEL statement uses the “=” sign to separate response from effect information and specifies the response variable by using the events/trials syntax. This determines the distribution as binomial. This MODEL statement adds two components to the mixture models with different intercepts and regression slopes. The second MODEL statement adds another component to the mixture where the mean is a function of the classification main effect for variable A. The response is also binomial; it is a continuation from the previous MODEL statement.

There are two sets of options in the MODEL statement. The response-options determine how the FMM procedure models probabilities for binary data. The model-options control other aspects of model formation and inference. Table 37.4 summarizes important response-options and model-options. These are subsequently discussed in detail in alphabetical order by option category.
### Table 37.4  Summary of Important MODEL Statement Options

<table>
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<th>Option</th>
<th>Description</th>
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<td></td>
</tr>
<tr>
<td>DESCENDING</td>
<td>Reverses the order of response categories</td>
</tr>
<tr>
<td>EVENT=</td>
<td>Specifies the event category in binary models</td>
</tr>
<tr>
<td>ORDER=</td>
<td>Specifies the sort order for the response variable</td>
</tr>
<tr>
<td>REFERENCE=</td>
<td>Specifies the reference category in categorical models</td>
</tr>
<tr>
<td><strong>Model Building</strong></td>
<td></td>
</tr>
<tr>
<td>DIST=</td>
<td>Specifies the response distribution</td>
</tr>
<tr>
<td>LINK=</td>
<td>Specifies the link function</td>
</tr>
<tr>
<td>K=</td>
<td>Specifies the number of mixture components</td>
</tr>
<tr>
<td>KMAX=</td>
<td>Specifies the maximum number of mixture components</td>
</tr>
<tr>
<td>KMIN=</td>
<td>Specifies the minimum number of mixture components</td>
</tr>
<tr>
<td>NOINT</td>
<td>Excludes fixed-effect intercept from model</td>
</tr>
<tr>
<td>OFFSET=</td>
<td>Specifies the offset variable for linear predictor</td>
</tr>
<tr>
<td><strong>Statistical Computations and Output</strong></td>
<td></td>
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<tr>
<td>ALPHA=(\alpha)</td>
<td>Determines the confidence level (1 - \alpha)</td>
</tr>
<tr>
<td>CL</td>
<td>Displays confidence limits for fixed-effects parameter estimates</td>
</tr>
<tr>
<td>EQUATE=</td>
<td>Imposes simple equality constraints on parameters in this model</td>
</tr>
<tr>
<td>LABEL=</td>
<td>Identifies the model</td>
</tr>
<tr>
<td>PARMS</td>
<td>Provides starting values for the parameters in this model</td>
</tr>
</tbody>
</table>

### Response Variable Options

Response variable options determine how the FMM procedure models probabilities for binary data.

You can specify the following *response-options* by enclosing them in parentheses after the *response* variable. The default is ORDER=FORMATTED.

**DESCENDING**

**DESC** reverses the order of the response categories. If both the DESCENDING and ORDER= options are specified, PROC FMM orders the response categories according to the ORDER= option and then reverses that order.

**EVENT=’category’ | keyword**

specifies the event category for the binary response model. PROC FMM models the probability of the event category. You can specify the value (formatted, if a format is applied) of the event category in quotes, or you can specify one of the following keywords:

**FIRST**

designates the first ordered category as the event. This is the default.
LAST
designates the last ordered category as the event.

ORDER=order-type
specifies the sort order for the levels of the response variable. You can specify the following values for order-type:

DATA
sorts the levels by order of appearance in the input data set.

FORMATTED
sorts the levels by external formatted value, except for numeric variables with no explicit format, which are sorted by their unformatted (internal) value.

FREQ
sorts the levels by descending frequency count; levels with the most observations come first in the order.

INTERNAL
sorts the levels by unformatted value.

FREQDATA
sorts the levels by order of descending frequency count, and within counts by order of appearance in the input data set when counts are tied.

FREQFORMATTED
sorts the levels by order of descending frequency count, and within counts by formatted value (as above) when counts are tied.

FREQINTERNAL
sorts the levels by order of descending frequency count, and within counts by unformatted value when counts are tied.

When ORDER=FORMATTED (the default) for numeric variables for which you have supplied no explicit format (that is, for which there is no corresponding FORMAT statement in the current PROC FMM run or in the DATA step that created the data set), the levels are ordered by their internal (numeric) value. If you specify the ORDER= option in the MODEL statement and the ORDER= option in the PROC FMM statement, the former takes precedence.

By default, ORDER=FORMATTED. For the FORMATTED and INTERNAL values, the sort order is machine-dependent.

For more information about sort order, see the chapter on the SORT procedure in the **Base SAS Procedures Guide** and the discussion of BY-group processing in **SAS Language Reference: Concepts**.

REFERENCE='category' | keyword
REF='category' | keyword
specifies the reference category for categorical models. For the binary response model, specifying one response category as the reference is the same as specifying the other response category as the event category. You can specify the value (formatted if a format is applied) of the reference category in quotes, or you can specify one of the following keywords:
FIRST
designates the first ordered category as the reference category.

LAST
designates the last ordered category as the reference category. This is the default.

Model Options

**ALPHA=**`number`
requests that confidence intervals be constructed for each of the parameters with confidence level $1 - number$. The value of `number` must be between 0 and 1; the default is 0.05.

**CL**
requests that confidence limits be constructed for each of the parameter estimates. The confidence level is 0.95 by default; this can be changed with the **ALPHA=** option.

**DISTRIBUTION=**`keyword`
**DIST=**`keyword`
specifies the probability distribution for a mixture component.

If you specify the DIST= option and you do not specify a link function with the LINK= option, a default link function is chosen according to Table 37.5. If you do not specify a distribution, the FMM procedure defaults to the normal distribution for continuous response variables and to the binary distribution for classification or character variables, unless the `events/trial` syntax is used in the MODEL statement. If you choose the `events/trial` syntax, the FMM procedure defaults to the binomial distribution.

Table 37.5 lists the values of the DIST= option and the corresponding default link functions. For the case of generalized linear models with these distributions, you can find expressions for the log-likelihood functions in the section “Log-Likelihood Functions for Response Distributions” on page 2493.

<table>
<thead>
<tr>
<th>DIST=</th>
<th>Alias</th>
<th>Distribution</th>
<th>Default Link Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>BETA</td>
<td></td>
<td>Beta</td>
<td>Logit</td>
</tr>
<tr>
<td>BETABINOMIAL</td>
<td>BETABIN</td>
<td>Beta-binomial</td>
<td>Logit</td>
</tr>
<tr>
<td>BINARY</td>
<td>BERNOULLI</td>
<td>Binary</td>
<td>Logit</td>
</tr>
<tr>
<td>BINOMIAL</td>
<td>BIN</td>
<td>Binomial</td>
<td>Logit</td>
</tr>
<tr>
<td>BINOMCLUSTER</td>
<td>BINOMCLUS</td>
<td>Binomial cluster</td>
<td>Logit</td>
</tr>
<tr>
<td>CONSTANT</td>
<td>DEGENERATE</td>
<td>Degenerate</td>
<td>N/A</td>
</tr>
<tr>
<td>EXPONENTIAL</td>
<td>EXPO</td>
<td>Exponential</td>
<td>Log</td>
</tr>
<tr>
<td>FOLDEDNORMAL</td>
<td>FNORMAL</td>
<td>Folded normal</td>
<td>Identity</td>
</tr>
<tr>
<td>GAMMA</td>
<td>GAM</td>
<td>Gamma</td>
<td>Log</td>
</tr>
<tr>
<td>GAUSSIAN</td>
<td>NORMAL</td>
<td>Normal</td>
<td>Identity</td>
</tr>
<tr>
<td>GENPOISSON</td>
<td>GPOISSON</td>
<td>Generalized Poisson</td>
<td>Log</td>
</tr>
<tr>
<td>GEOMETRIC</td>
<td>GEOM</td>
<td>Geometric</td>
<td>Log</td>
</tr>
</tbody>
</table>
Table 37.5  continued

<table>
<thead>
<tr>
<th>DIST=</th>
<th>Alias</th>
<th>Distribution</th>
<th>Default Link Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>INVGAUSS</td>
<td>IG, IGAUSSIAN</td>
<td>Inverse Gaussian</td>
<td>Inverse squared (power(−2))</td>
</tr>
<tr>
<td>LOGNORMAL</td>
<td>LOGN</td>
<td>Lognormal</td>
<td>Identity</td>
</tr>
<tr>
<td>NEGBINOMIAL</td>
<td>NEGBIN, NB</td>
<td>Negative binomial</td>
<td>Log</td>
</tr>
<tr>
<td>POISSON</td>
<td>POI</td>
<td>Poisson</td>
<td>Log</td>
</tr>
<tr>
<td>T</td>
<td>STUDENT</td>
<td>t</td>
<td>Identity</td>
</tr>
<tr>
<td>TRUNCPOISSON</td>
<td>TPOISSON, TPOI</td>
<td>Truncated Poisson</td>
<td>Log</td>
</tr>
<tr>
<td>UNIFORM</td>
<td>UNIF</td>
<td>Uniform</td>
<td>N/A</td>
</tr>
<tr>
<td>WEIBULL</td>
<td></td>
<td>Weibull</td>
<td>Log</td>
</tr>
</tbody>
</table>

Note that the PROC FMM default link for the gamma or exponential distribution is not the canonical link (the reciprocal link).

The binomial cluster model is a two-component model described in Morel and Nagaraj (1993), Morel and Neerchal (1997), and Neerchal and Morel (1998). See Example 37.1 for an application of the binomial cluster model in a teratological experiment.

If the `events/trials` syntax is used, the default distribution is the binomial and only the following choices are available: `DIST=BINOMIAL`, `DIST=BETABINOMIAL`, and `DIST=BINOMCLUSTER`. The `trials` variable is ignored for all other distributions. This enables you to fit models in which some components have a binomial or binomial-like distribution. For example, suppose that variable `n` is a binomial denominator and variable `logn` is its logarithm. Then the following statements model a two-component mixture of a binomial and Poisson count model:

```plaintext
model y/n = ;
model + / dist=Poisson offset=logn;
```

The `OFFSET=` option is used in the second `MODEL` statement to specify that the Poisson counts refer to different base counts, since the trial variable `n` is ignored in the second model.

If `DIST=BINOMIAL` is specified without the `events/trials` syntax, then `n=1` is used for the default number of trials.

For several distributional specifications you can provide additional parameters to further define the distribution. These optional parameters are listed in the following:

- `DIST=CONSTANT<(c)>` The number `c` specifies the value where the mass is concentrated. The default is `DIST=CONSTANT(0)`, so that adding a `MODEL` statement with `DIST=CONSTANT` can be used to add zero-inflation to any model.

- `DIST=T<(v)>` The number `v` specifies the degrees of freedom for the (shifted) `t` distribution. The default is `DIST=T(3)`, and this leads to a heavy-tailed distribution for which the variance is defined. See the section “Log-Likelihood Functions for Response Distributions” on page 2493 for the density function of the shifted `tv` distribution.
DIST=UNIFORM<(a,b)>  The values a and b define the support of the uniform distribution, a < b.
By default, a = 0 and b = 1.

EQUATE=MEAN | SCALE | NONE

EQUATE=EFFECTS(effect-list)
specifies simple sets of parameter constraints across the components in a MODEL statement; the
default is EQUATE=NONE. This option is available only for maximum likelihood estimation. If
you specify EQUATE=MEAN, the parameters that determine the mean are reduced to a single set
that is applicable to all components in the MODEL statement. If you specify EQUATE=SCALE,
a single parameter represents the common scale for all components in the MODEL statement. The
EFFECTS option enables you to force the parameters for the chosen model effects to be equal across
components; however, the number of parameters is unaffected.

For example, the following statements fit a two-component multiple regression model in which the
coefficients for variable logd vary by component and the intercepts and coefficients for variable dose
are the same for the two components:

```plaintext
proc fmm;
   model num = dose logd / equate=effects(int dose) k=2;
run;
```

To fix all coefficients across the two components, you can write the MODEL statement as

```plaintext
model num = dose logd / equate=effects(int dose logd) k=2;
```
or

```plaintext
model num = dose logd / equate=mean k=2;
```

If you restrict all parameters in a k-component MODEL statement to be equal, the FMM procedure
reduces the model to k = 1.

K=n
NUMBER=n
specifies the number of components the MODEL statement contributes to the overall mixture. For the
binomial cluster model, this option is not available, since this model is a two-component model by
definition.

KMAX=n
specifies the maximum number of components the MODEL statement contributes to the overall mix-

If the maximum number of components in the mixture, as determined by all KMAX= options, is
larger than the minimum number of components, the FMM procedure fits all possible models and
displays summary fit information for the sequence of evaluated models. The “best” model according
to the CRITERION= option in the PROC FMM statement is then chosen, and the remaining output
and analyses performed by PROC FMM pertain to this “best” model.
The KMAX= option is available only for maximum likelihood estimation. When you estimate the parameters of a mixture by MCMC methods, you need to ensure that the chain for a given value of $k$ has converged; otherwise, comparisons among models with varying number of components might not be meaningful.

\textbf{KMIN=}$n$

specifies the minimum number of components the MODEL statement contributes to the overall mixture. This option is available only for maximum likelihood estimation. When you estimate the parameters of a mixture by MCMC methods, you need to ensure that the chain for a given value of $k$ has converged; otherwise comparisons among models with varying number of components might not be meaningful.

\textbf{LABEL='label'}

specifies an optional label for the model that is used to identify the model in printed output, on graphics, and in data sets created from ODS tables.

\textbf{LINK=}$\text{keyword}$

specifies the link function in the model. The keywords and expressions for the associated link functions are shown in Table 37.6.

\begin{table}[h]
\centering
\begin{tabular}{lll}
\hline
\textbf{LINK=} & \textbf{Alias} & \textbf{Function} \\
\hline
CLOGLOG & CLL & Complementary log-log $g(\mu) = \log(- \log(1 - \mu))$

IDENTITY & ID & Identity $\mu$

LOG & Log & $\log(\mu)$

LOGIT & Logit & $\log(\mu/(1 - \mu))$

LOGLOG & Log-log & $- \log(- \log(\mu))$

PROBIT & NORMIT & Probit $\Phi^{-1}(\mu)$

POWER($\lambda$) & POW($\lambda$) & Power with exponent $\lambda = \text{number}$

\{ $\mu^\lambda$ if $\lambda \neq 0$

\{ $\log(\mu)$ if $\lambda = 0$

POWERMINUS2 & & $1/\mu^2$

RECIPIROCAL & INVERSE & Reciprocal $1/\mu$

\hline
\end{tabular}
\caption{Link Functions in MODEL Statement of the FMM Procedure}
\end{table}

The default link functions for the various distributions are shown in Table 37.5.

\textbf{NOINT}

requests that no intercept be included in the model. An intercept is included by default, unless the distribution is DIST=CONSTANT or DIST=UNIFORM.

\textbf{OFFSET=}$\text{variable}$

specifies the offset variable function for the linear predictor in the model. An offset variable can be thought of as a regressor variable whose regression coefficient is known to be 1. For example, you can use an offset in a Poisson model when counts have been obtained in time intervals of different lengths. With a log link function, you can model the counts as Poisson variables with the logarithm of the time interval as the offset variable.
PARAMETERS(\texttt{parameter-specification})

PARMS(\texttt{parameter-specification}) specifies starting values for the model parameters. If no PARMS option is given, the FMM procedure determines starting values by a data-dependent algorithm. To determine initial values for the Markov chain with Bayes estimation, see also the INITIAL= option in the BAYES statement. The specification of the parameters takes the following form: parameters in the mean function precede the scale parameters, and parameters for different components are separated by commas.

The following statements specify starting parameters for a two-component normal model. The initial values for the intercepts are 1 and $-3$; the initial values for the variances are $0.5$ and $4$.

```sas
proc fmm;
  model y = / k=2 parms(1 0.5, -3 4);
run;
```

You can specify missing values for parameters whose starting values are to be determined by the default method. Only values for parameters that participate in the optimization are specified. The values for model effects are specified on the linear (linked) scale.

---

**OUTPUT Statement**

```
OUTPUT < OUT=SAS-data-set>
  \texttt{keyword}\langle \texttt{keyword-options}\rangle \texttt{name}\ldots
  \texttt{keyword}\langle \texttt{keyword-options}\rangle \texttt{name}\langle \texttt{/ options}\rangle ;
```

The OUTPUT statement creates a data set that contains observationwise statistics that are computed after fitting the model. By default, all variables in the original data set are included in the output data set. You can use the ID statement to limit the variables copied from the input data set to the output data set.

The output statistics are computed based on the parameter estimates of the converged model if the parameters are estimated by maximum likelihood. If a Bayesian analysis is performed, the output statistics are computed based on the arithmetic mean in the posterior sample. You can change to the maximum posterior estimate with the ESTIMATE=MAP option in the BAYES statement.

You can specify the following syntax elements in the OUTPUT statement before the slash (/).

**OUT=SAS-data-set**

**DATA=SAS-data-set** specifies the name of the output data set. If the OUT= (or DATA=) option is omitted, the procedure uses the DATA_n convention to name the output data set.

**keyword\langle \texttt{keyword-options}\rangle \texttt{name}** specifies a statistic to include in the output data set and optionally assigns the variable the name name. If you do not provide a name, the FMM procedure assigns a default name based on the type of statistic requested. If you provide a name for a statistic that leads to multiple output statistics, the name is modified to index the associated component number.
You can use the `keyword-options` to control which type of a particular statistic is computed. The following are valid values for `keyword` and `keyword-options`:

**PREDICTED< (COMPONENT | OVERALL) >**
**PRED< (COMPONENT | OVERALL) >**
**MEAN< (COMPONENT | OVERALL) >**
requests predicted values (predicted means) for the response variable. The predictions in the output data set are mapped onto the data scale. For example, if the response is binomial or binary, the predictions are probabilities. The default is to compute the predicted value for the mixture (OVERALL). You can request predictions for the means of the component distributions by adding the COMPONENT suboption in parentheses. The predicted values for some distributions are not identical to the parameter modeled as $\mu$. For example, in the lognormal distribution the predicted mean is $\exp\{\mu + 0.5\phi\}$ where $\mu$ and $\phi$ are the parameters of an underlying normal process; see the section “Log-Likelihood Functions for Response Distributions” on page 2493 for details.

**RESIDUAL< (COMPONENT | OVERALL) >**
**RESID< (COMPONENT | OVERALL) >**
requests residuals for the response or residuals in the component distributions. Only “raw” residuals on the data scale are computed (observed minus predicted).

**VARIANCE< (COMPONENT | OVERALL) >**
**VAR< (COMPONENT | OVERALL) >**
requests variances for the mixture or the component distributions.

**LOGLIKE< (COMPONENT | OVERALL) >**
**LOGL< (COMPONENT | OVERALL) >**
requests values of the log-likelihood function for the mixture or the components. For observations used in the analysis, the overall computed value is the observations’ contribution to the log likelihood; if a FREQ statement is present, the frequency is accounted for in the computed value. In other words, if all observations in the input data set have been used in the analysis, adding the value of the log-likelihood contributions in the OUTPUT data set produces the negative of the final objective function value in the “Iteration History” table. By default, the log-likelihood contribution to the mixture is computed. You can request the individual mixture component contributions with the COMPONENT suboption.

**MIXPROBS< (COMPONENT | MAX) >**
**MIXPROB< (COMPONENT | MAX) >**
**PRIOR< (COMPONENT | MAX) >**
**MIXWEIGHTS< (COMPONENT | MAX) >**
requests that the prior weights $\pi_j(z, \alpha_j)$ be added to the OUTPUT data set. By default, the probabilities are output for all components. You can limit the output to a single statistic, the largest mixing probability, with the MAX suboption.

**NOTE:** The keyword “prior” is used here because of long-standing practice to refer to the mixing probabilities as prior weights. This must not be confused with the prior distribution and its parameters in a Bayesian analysis.
requests that the posterior weights

\[
\frac{\pi_j(z, \alpha_j) p_j(y; x_j' \beta_j, \phi_j)}{\sum_{j=1}^{k} \pi_j(z, \alpha_j) p_j(y; x_j' \beta_j, \phi_j)}
\]

be added to the OUTPUT data set. By default, the probabilities are output for all components. You can limit the output to a single statistic, the largest posterior probability, with the MAX suboption.

**NOTE:** The keyword “posterior” is used here because of long-standing practice to refer to these probabilities as posterior probabilities. This must not be confused with the posterior distribution in a Bayesian analysis.

**LINP**

**XBETA**

requests that the linear predictors for the models be added to the OUTPUT data set.

**CLASS | CATEGORY | GROUP**

adds the estimated component membership to the OUTPUT data set. An observation is associated with the component that has the highest posterior probability.

**MAXPOST | MAXPROB**

adds the highest posterior probability to the OUTPUT data set.

A **keyword** can appear multiple times. For example, the following OUTPUT statement requests predicted values for the mixture in addition to the predicted means in the individual components:

```
output out=fmmout pred=MixtureMean pred(component)=CompMean;
```

In a three-component model, this produces four variables in the fmmout data set: MixtureMean, CompMean_1, CompMean_2, and CompMean_3.

You can specify the following **options** in the OUTPUT statement after a slash (/).

**ALLSTATS**

requests that all statistics are computed. If you do not use a keyword to assign a name, the FMM procedure uses the default name.

**NOVAR**

requests that variables from the input data set not be added to the output data set. This option does not apply to variables listed in the **BY** statement or to variables listed in the **ID** statement.
PERFORMANCE Statement

PERFORMANCE <performance-options> ;

The PERFORMANCE statement enables you to control the performance characteristics of the FMM procedure (for example, the number of CPUs, the number of threads for multithreading, and so on). By default, the FMM procedure performs many analyses in multiple threads, and the number of threads equals the number of CPUs. Certain system and configuration options also can control the number of CPUs available to a SAS session or whether multithreaded computations are permissible. For example, you can set the number of available processors to two with

   options cpucount=2;

The FMM procedure then acts as though two processors were available, regardless of the number of physically available processors.

The FMM procedure applies multithreading to the following analytical tasks:

**Starting values:** all starting value computations that require a pass through the data.

**Optimization:** all evaluations of objective function, gradient, and Hessian; computation of covariance matrix.

**Bayesian analysis:** all sample passes through the data, formation of cross-product matrices, sampling of latent variables, and posterior diagnostics.

**Scoring and ODS Graphics:** computation of all output statistics and statistics for the construction of graphics that require passes through the data.

You can specify the following performance-options:

**CPUCOUNT=n**

**CPUCOUNT=ACTUAL**

specifies the number of processors available to the FMM procedure; the number $n$ must be between 1 and 1024. CPUCOUNT=ACTUAL sets the number of available processors equal to the number of physical processors.

**DETAILS**

requests a table with timing detail for the tasks performed by the FMM procedure.

**NOTHREADS**

disables multithreaded computations.

**THREADS=YES**

**THREADS=NO**

enables or disables multithreaded processing. The number of threads used by the FMM procedure is displayed in the “Bayes Information” or “Optimization Information” table. It typically equals the number of available CPUs, which can be different from the number of physical CPUs, and can be modified with the global CPUCOUNT SAS option or with the CPUCOUNT= option in the PERFORMANCE statement.
**PROBMODEL Statement**

```
PROBMODEL <effects> < / probmodel-options> ;
```

The PROBMODEL statement defines the model effects for the mixing probabilities and their link function. By default, the FMM procedure models mixing probabilities on the logit scale for two-component models and as generalized logit models in situations with more than two components. The PROBMODEL statement is not required, and it is not supported with Bayesian estimation.

The generalized logit model with \( k \) categories has a common vector of regressor or design variables, \( z, k - 1 \) parameter vectors that vary with category, and one linear predictor whose value is constant. The constant linear predictor is assigned by the FMM procedure to the last component in the model, and its value is zero (\( \alpha_k = 0 \)). The probability of observing category \( 1 \leq j \leq k \) is then

\[
\pi_j(z, \alpha_j) = \frac{\exp\{z'\alpha_j\}}{\sum_{i=1}^{k} \exp\{z'\alpha_i\}}
\]

For \( k = 2 \), the generalized logit model reduces to a model with the logit link (a logistic model); hence the attribute generalized logit.

By default, an intercept is included in the model for the mixing probabilities. If you suppress the intercept with the NOINT option, you must specify at least one effect in the statement.

You can specify the following `probmodel-options` in the PROBMODEL statement after the slash (/):

- **ALPHA=number**
  requests that confidence intervals be constructed for the parameters in the probability model with confidence level \( 1 - \text{number} \). The value of `number` must be between 0 and 1; the default is 0.05. If the probability model is simple—that is, it does not contain any effects, the confidence intervals are produced for the estimated parameters (on the logit scale) as well as for the mixing probabilities.

- **CL**
  requests that confidence limits be constructed for each of the parameter estimates. The confidence level is 0.95 by default; this can be changed with the `ALPHA=` option.

- **LINK=keyword**
  specifies the link function in the model for the mixing probabilities. The default is a logit link for models with two components. For models with more than two components, only the generalized logit link is available. The keywords and expressions for the associated link functions for two-component models are shown in Table 37.7.

---

**Table 37.7** Link Functions in the PROBMODEL Statement

<table>
<thead>
<tr>
<th>LINK=</th>
<th>Function</th>
<th>( g(\mu) = \eta = )</th>
</tr>
</thead>
<tbody>
<tr>
<td>CLOGLOG</td>
<td>Complementary log-log</td>
<td>( \log(-\log(1 - \mu)) )</td>
</tr>
<tr>
<td>LOGIT</td>
<td>Logit</td>
<td>( \log(\mu/(1 - \mu)) )</td>
</tr>
<tr>
<td>LOGLOG</td>
<td>Log-log</td>
<td>( -\log(-\log(\mu)) )</td>
</tr>
<tr>
<td>PROBIT</td>
<td>Probit</td>
<td>( \Phi^{-1}(\mu) )</td>
</tr>
</tbody>
</table>
requests that no intercept be included in the model for the mixing probabilities. An intercept is included by default. If you suppress the intercept with the NOINT option, you must specify at least one other effect for the mixing probabilities—since an empty probability model is not meaningful.

PARAMETERS(parameter-specification)
PARMS(parameter-specification)
specifies starting values for the parameters. The specification of the parameters takes the following form: parameters in the mean function appear in a list, and parameters for different components are separated by commas. Starting values are given on the linked scale, not in terms of probabilities. Also, you need to specify starting values for only up to the first \( k - 1 \) components in a \( k \)-component model. The linear predictor for the last component is always assumed to be zero.

The following statements specify a three-component mixture of multiple regression models. The PROBMODEL statement does not list any effects, a standard “intercept-only” generalized logit model is used to model the mixing probabilities.

```sas
proc fmm;
  model y = x1 x2 / k=3;
  probmodel / parms(2, 1);
run;
```

There are three linear predictors in the model for the mixing probabilities, \( \alpha_1 \), \( \alpha_2 \), and \( \alpha_3 \). With starting values of \( \alpha_1 = 2 \), \( \alpha_2 = 1 \), and \( \alpha_3 = 0 \), this leads to initial mixing probabilities of

\[
\pi_1 = \frac{e^2}{e^2 + e^1 + e^0} = 0.24 \\
\pi_2 = \frac{e^1}{e^2 + e^1 + e^0} = 0.66 \\
\pi_3 = \frac{e^0}{e^2 + e^1 + e^0} = 0.1
\]

You can specify missing values for parameters whose starting values are to be determined by the default method.

---

RESTRICT Statement

```
RESTRICT < 'label'> constraint-specification < , . . . , constraint-specification >
  < operator < value > > < / option > ;
```

The RESTRICT statement enables you to specify linear equality or inequality constraints among the parameters of a mixture model. These restrictions are incorporated into the maximum likelihood analysis. The RESTRICT statement is not available for a Bayesian analysis with the FMM procedure.

Following are reasons why you might want to place constraints and restrictions on the model parameters:
• to fix a parameter at a particular value
• to equate parameters in different components in a mixture
• to impose order conditions on the parameters in a model
• to specify contrasts among the parameters that the fitted model should honor

A restriction is composed of a left-hand side and a right-hand side, separated by an operator. If the operator and right-hand side are not specified, the restriction is assumed to be an equality constraint against zero. If the right-hand side is not specified, the value is assumed to be zero.

An individual constraint-specification is written in (nearly) the same form as estimable linear functions are specified in the ESTIMATE statement of the GLM, MIXED, or GLIMMIX procedure. The constraint-specification takes the form

\[
\text{model-effect value-list} < \ldots \text{model-effect value-list} > < (\text{SCALE} = \text{value})>
\]

At least one model-effect must be specified followed by one or more values in the value-list. The values in the list correspond to the multipliers of the corresponding parameter that is associated with the position in the model effect. If you specify more values in the value-list than the model-effect occupies in the model design matrix, the extra coefficients are ignored.

To specify restrictions for effects in specific components in the model, separate the constraint-specification by commas. The following statements provide an example:

```plaintext
proc fmm;
  class A;
  model y/n = A x / k = 2;
  restrict A 1 0 -1;
  restrict x 2, x -1 >= 0.5;
run;
```

The linear predictors for this two-component model can be written as

\[
\begin{align*}
\eta_1 &= \beta_{10} + \alpha_{11} A_1 + \cdots + \alpha_{1a} A_a + x\beta_{11} \\
\eta_2 &= \beta_{20} + \alpha_{21} A_1 + \cdots + \alpha_{2a} A_a + x\beta_{21}
\end{align*}
\]

where \(A_k\) is the binary variable associated with the \(k\)th level of \(A\).

The first RESTRICT statement applies only to the first component and specifies that the parameter estimates that are associated with the first and third level of the \(A\) effect are identical. In terms of the linear predictor, the restriction can be written as

\[
\alpha_{11} - \alpha_{13} = 0
\]

Now suppose that \(A\) has only two levels. Then the FMM procedure ignores the value \(-1\) in the first RESTRICT statement and imposes the restriction

\[
\alpha_{11} = 0
\]

on the fitted model.
The second RESTRICT statement involves parameters in two different components of the model. In terms of the linear predictors, the restriction can be written as

\[ 2\beta_{11} - \beta_{21} \geq \frac{1}{2} \]

When restrictions are specified explicitly through the RESTRICT statement or implied through the EQUATE=EFFECTS option in the MODEL statement, the FMM procedure lists all restrictions after the model fit in a table of linear constraints and indicates whether a particular constraint is active at the converged solution.

The following operators can be specified to separate the left- and right-hand sides of the restriction: =, >, <, >=, <=. You can also use the alternate EQ, GT, LT, GE, and LE, respectively.

Some distributions involve scale parameters (the parameter \( \phi \) in the expressions of the log likelihood) and you can also use the constraint specification to involve a component’s scale parameter in a constraint. To this end, assign a value to the keyword SCALE, separated from the model effects and value lists with parentheses. The following statements fit a two-component normal model and restrict the component variances to be equal:

```plaintext
proc fmm;
  model y = / k=2;
  restrict int 0 (scale 1),
          int 0 (scale -1);
run;
```

The intercept specification is necessary because each constraint specification requires at least one model effect. The zero coefficient ensures that the intercepts are not involved in the restriction. Instead, the RESTRICT statement leads to \( \phi_1 - \phi_2 = 0 \).

You can specify the following option in the RESTRICT statement after a slash (/).

**DIVISOR=value**

specifies a value by which all coefficients on the right-hand side and left-hand side of the restriction are divided.

---

**WEIGHT Statement**

**WEIGHT variable;**

The WEIGHT statement is used to perform a weighted analysis. Consult the section “Log-Likelihood Functions for Response Distributions” on page 2493 for expressions on how weight variables are included in the log-likelihood functions. Because the probability structure of a mixture model is different from that of a classical statistical model, the presence of a weight variable in a mixture model cannot be interpreted as altering the variance of an observation.

Observations with nonpositive or missing weights are not included in the PROC FMM analysis. If a WEIGHT statement is not included, all observations used in the analysis are assigned a weight of 1.
A Gentle Introduction to Finite Mixture Models

The Form of the Finite Mixture Model

Suppose that you observe realizations of a random variable $Y$, the distribution of which depends on an unobservable random variable $S$ that has a discrete distribution. $S$ can occupy one of $k$ states, the number of which might be unknown but is at least known to be finite. Since $S$ is not observable, it is frequently referred to as a latent variable.

Let $\pi_j$ denote the probability that $S$ takes on state $j$. Conditional on $S = j$, the distribution of the response $Y$ is assumed to be $f_j(y; \alpha_j, \beta_j|S = j)$. In other words, each distinct state $j$ of the random variable $S$ leads to a particular distributional form $f_j$ and set of parameters $\{\alpha_j, \beta_j\}$ for $Y$.

Let $\{\alpha, \beta\}$ denote the collection of $\alpha_j$ and $\beta_j$ parameters across all $j = 1$ to $k$. The marginal distribution of $Y$ is obtained by summing the joint distribution of $Y$ and $S$ over the states in the support of $S$:

$$f(y; \alpha, \beta) = \sum_{j=1}^{k} \Pr(S = j) f(y; \alpha_j, \beta_j|S = j)$$

$$= \sum_{j=1}^{k} \pi_j f(y; \alpha_j, \beta_j|S = j)$$

This is a mixture of distributions, and the $\pi_j$ are called the mixture (or prior) probabilities. Because the number of states $k$ of the latent variable $S$ is finite, the entire model is termed a finite mixture (of distributions) model.

The finite mixture model can be expressed in a more general form by representing $\alpha$ and $\beta$ in terms of regressor variables and parameters with optional additional scale parameters for $\beta$. The section “Notation for the Finite Mixture Model” on page 2424 develops this in detail.

Mixture Models Contrasted with Mixing and Mixed Models: Untangling the Terminology Web

Statistical terminology can have its limitations. The terms mixture, mixing, and mixed models are sometimes used interchangeably, causing confusion. Even worse, the terms arise in related situations. One application needs to be eliminated from the discussion in this documentation: mixture experiments, where design factors are the proportions with which components contribute to a blend, are not mixture models and do not fall under the purview of the FMM procedure. However, the data from a mixture experiment might be analyzed with a mixture model, a mixing model, or a mixed model, besides other types of statistical models.

Suppose that you observe realizations of random variable $Y$ and assume that $Y$ follows some distribution $f(y; \alpha, \beta)$ that depends on parameters $\alpha$ and $\beta$. Furthermore, suppose that the model is found to be deficient
in the sense that the variability implied by the fitted model is less than the observed variability in the data, a condition known as overdispersion (see the section “Overdispersion” on page 2492). To tackle the problem the statistical model needs to be modified to allow for more variability. Clearly, one way of doing this is to introduce additional random variables into the process. Mixture, mixing, and mixed models are simply different ways of adding such random variables. The section “The Form of the Finite Mixture Model” on page 2490 explains how mixture models add a discrete state variable $S$. The following two subsections explain how mixing and mixed models instead assume variation for a natural parameter or in the mean function.

**Mixing Models**

Suppose that the model is modified to allow for some random quantity $U$, which might be one of the parameters of the model or a quantity related to the parameters. Now there are two distributions to cope with: the conditional distribution of the response given the random effect $U$,

$$f(y; \alpha, \beta | u)$$

and the marginal distribution of the data. If $U$ is continuous, the marginal distribution is obtained by integration:

$$f(y; \alpha, \beta) = \int f(y; \alpha, \beta | u) \ f(u) \ du$$

Otherwise, it is obtained by summation over the support of $U$:

$$f(y; \alpha, \beta) = \sum_u \Pr(U = u) \ f(y; \alpha, \beta | u)$$

The important entity for statistical estimation is the marginal distribution $f(y; \alpha, \beta)$; the conditional distribution is often important for model description, genesis, and interpretation.

In a mixing model the marginal distribution is known and is typically of a well-known form. For example, if $Y | n$ has a binomial$(n, \mu)$ distribution and $n$ follows a Poisson distribution, then the marginal distribution of $Y$ is Poisson. The preceding operation is called mixing a binomial distribution with a Poisson distribution. Similarly, when mixing a Poisson($\lambda$) distribution with a gamma($a, b$) distribution for $\lambda$, a negative binomial distribution results as the marginal distribution. Other important mixing models involve mixing a binomial$(n, \mu)$ random variable with a beta($a, b$) distribution for the binomial success probability $\mu$. This results in a distribution known as the beta-binomial.

The finite mixtures have in common with the mixing models the introduction of random effects into the model to vary some or all of the parameters at random.

**Mixed Models**

The difference between a mixing and a mixed model is that the conditional distribution is not that important in the mixing model. It matters to motivate the overdispersed reference model and to arrive at the marginal distribution. Inferences with respect to the conditional distribution, such as predicting the random variable $U$, are not performed in mixing models. In a mixed model the random variable $U$ typically follows a continuous distribution—almost always a normal distribution. The random effects usually do not model the natural parameters of the distribution; instead, they are involved in linear predictors that relate to the
conditional mean. For example, a linear mixed model is a model in which the response and the random
effects are normally distributed, and the random effects enter the conditional mean function linearly:

\[ Y = X\beta + ZU + \epsilon \]
\[ U \sim N(0, G) \]
\[ \epsilon \sim N(0, R) \]
\[ \text{Cov}[U, \epsilon] = 0 \]

The conditional and marginal distributions are then

\[ Y|U \sim N(X\beta + ZU + \epsilon, R) \]
\[ Y \sim N(X\beta, ZGZ' + R) \]

For this model, because of the linearity in the mean and the normality of the random effects, you could also
refer to mixing the normal vector \( Y \) with the normal vector \( U \), since the marginal distribution is known. The
linear mixed model can be fit with the MIXED procedure. When the conditional distribution is not normal
and the random effects are normal, the marginal distribution does not have a closed form. In this class of
mixed models, called generalized linear mixed models, model approximations and numerical integration
methods are commonly used in model fitting; see for example, those models fit by the GLIMMIX and
NLMIXED procedures. Chapter 6, “Introduction to Mixed Modeling Procedures,” contains details about
the various classes of mixed models and about the relevant SAS/STAT procedures.

The previous expression for the marginal variance in the linear mixed model, \( \text{var}[Y] = ZGZ' + R \), empha-
sizes again that the variability in the marginal distribution of a model that contains random effects exceeds
the variability in a model without the random effects (\( R \)).

The finite mixtures have in common with the mixed models that the marginal distribution is not necessarily
a well-known model, but is expressed through a formal integration over the random-effects distribution. In
contrast to the mixed models, in particular those involving nonnormal distributions or nonlinear elements,
this integration is rather trivial; it reduces to a weighted and finite sum of densities or mass functions.

**Overdispersion**

Overdispersion is the condition by which the data are more dispersed than is permissible under a reference
model. Overdispersion arises only if the variability a model can capture is limited (for example, because
of a functional relationship between mean and variance). For example, a model for normal data can never
be overdispersed in this sense, although the reasons that lead to overdispersion also negatively affect a mis-
specified model for normal data. For example, omitted variables increase the residual variance estimate
because variability that should have been modeled through changes in the mean is now “picked up” as error
variability.

Overdispersion is important because an overdispersed model can lead to misleading inferences and conclu-
sions. However, diagnosing and remedying overdispersion is complicated. In order to handle it appropriately,
the source of overdispersion must be identified. For example, overdispersion can arise from any of the
following conditions alone or in combination:

- omitted variables and model effects
• omitted random effects (a source of random variation is not being modeled or is modeled as a fixed effect)

• correlation among the observations

• incorrect distributional assumptions

• incorrectly specified mean-variance relationships

• outliers in the data

As discussed in the previous section, introducing randomness into a system increases its variability. Mixture, mixed, and mixing models have thus been popular in modeling data that appear overdispersed. Finite mixture models are particularly powerful in this regard, because even low-order mixtures of basic, symmetric distributions (such as two- or three-component mixtures of normal or \( t \) distributions) enable you to model data with multiple modes, heavy tails, and skewness. In addition, the latent variable \( S \) provides a natural way to accommodate omitted, unobservable variables into the model.

One approach to remedy overdispersion is to apply simple modifications of the variance function of the reference model. For example, with binomial-type data this approach replaces the variance of the binomial count variable \( Y \sim \text{Binomial}(n, \mu) \), \( \text{Var}[Y] = n \times \mu(1 - \mu) \) with a scaled version, \( \phi n \times \mu(1 - \mu) \), where \( \phi \) is called an overdispersion parameter, \( \phi > 0 \).

In addressing overdispersion problems, it is important to tackle the problem at its root. A missing scale factor on the variance function is hardly ever the root cause of overdispersion; it is only the easiest remedy.

---

**Log-Likelihood Functions for Response Distributions**

The FMM procedure calculates the log likelihood that corresponds to a particular response distribution according to the following formulas. The response distribution is the distribution specified (or chosen by default) through the DIST= option in the MODEL statement. The parameterizations used for log-likelihood functions of these distributions were chosen to facilitate expressions in terms of mean parameters that are modeled through an (inverse) link functions and in terms of scale parameters. These are not necessarily the parameterizations in which parameters of prior distributions are specified in a Bayesian analysis of homogeneous mixtures. See the section “Prior Distributions” on page 2500 for details about the parameterizations of prior distributions.

The FMM procedure includes all constant terms in the computation of densities or mass functions. In the expressions that follow, \( l \) denotes the log-likelihood function, \( \phi \) denotes a general scale parameter, \( \mu_i \) is the “mean”, and \( w_i \) is a weight from the use of a WEIGHT statement.

For some distributions \( \mu_i \) is not the mean of the distribution (for example, the Weibull distribution). The parameter \( \mu_i \) is the quantity that is modeled as \( g^{-1}(x'\beta) \), where \( g^{-1}(\cdot) \) is the inverse link function and the \( x \) vector is constructed based on the effects in the MODEL statement. Situations in which the parameter \( \mu \) does not represent the mean of the distribution are explicitly mentioned in the list that follows.

The parameter \( \phi \) is frequently labeled as “Scale” parameter in output from the FMM procedure. It is not necessarily the scale parameter of the particular distribution.
Beta($\mu, \phi$)

\[ l(\mu_i, \phi; y_i, w_i) = \log\left\{ \frac{\Gamma(\phi/w_i)}{\Gamma(\mu_i\phi/w_i)\Gamma((1-\mu_i)\phi/w_i)} \right\} \]

\[ + (\mu_i\phi/w_i - 1) \log\{y_i\} \]

\[ + ((1-\mu_i)\phi/w_i - 1) \log\{1 - y_i\} \]

This parameterization of the beta distribution is due to Ferrari and Cribari-Neto (2004) and has properties $E[Y] = \mu$, $\text{Var}[Y] = \mu(1-\mu)/(1+\phi)$, $\phi > 0$.

Beta-binomial($n; \mu, \phi$)

\[ \phi = (1 - \rho^2)/\rho^2 \]

\[ l(\mu_i, \rho; y_i) = \log\{\Gamma(n_i + 1)\} - \log\{\Gamma(y_i + 1)\} \]

\[ - \log\{\Gamma(n_i - y_i + 1)\} \]

\[ + \log\{\Gamma(\phi)\} - \log\{\Gamma(n_i + \phi)\} + \log\{\Gamma(y_i + \phi\mu_i)\} \]

\[ + \log\{\Gamma(n_i - y_i + \phi(1 - \mu_i))\} - \log\{\Gamma(\phi\mu_i)\} \]

\[ - \log\{\Gamma(\phi(1 - \mu_i))\} \]

\[ l(\mu_i, \rho; y_i, w_i) = w_i l(\mu_i, \rho; y_i) \]

where $y_i$ and $n_i$ are the events and trials in the events/trials syntax and $0 < \rho < 1$. This parameterization of the beta-binomial model presents the distribution as a special case of the Dirichlet-Multinomial distribution—see, for example, Neerchal and Morel (1998). In this parameterization, $E[Y] = n\mu$ and $\text{Var}[Y] = n\mu(1-\mu)(1+(n-1)/(\phi+1))$. $0 \leq \rho \leq 1$. The FMM procedure models the parameter $\phi$ and labels it “Scale” on the procedure output. For other parameterizations of the beta-binomial model, see Griffiths (1973) or Williams (1975).

Binomial($n; \mu$)

\[ l(\mu_i; y_i) = y_i \log\{\mu_i\} + (n_i - y_i) \log\{1 - \mu_i\} \]

\[ + \log\{\Gamma(n_i + 1)\} - \log\{\Gamma(y_i + 1)\} \]

\[ - \log\{\Gamma(n_i - y_i + 1)\} \]

\[ l(\mu_i; y_i, w_i) = w_i l(\mu_i; y_i) \]

where $y_i$ and $n_i$ are the events and trials in the events/trials syntax and $0 < \mu < 1$. In this parameterization $E[Y] = n\mu$, $\text{Var}[Y] = n\mu(1 - \mu)$.

Binomial cluster($n; \mu, \pi$)

\[ z = \log\{\Gamma(n_i + 1)\} - \log\{\Gamma(y_i + 1)\} - \log\{\Gamma(n_i - y_i + 1)\} \]

\[ \mu^*_i = (1 - \mu_i)\pi \]

\[ l(\mu_i, \pi; y_i) = \log\{\pi\} + z + y_i \log\{\mu^*_i + \mu_i\} \]

\[ + (n_i - y_i) \log\{1 - \mu^*_i - \mu_i\} \]

\[ + \log\{1 - \pi\} + z + y_i \log\{\mu^*_i\} \]

\[ + (n_i - y_i) \log\{1 - \mu^*_i\} \]

\[ l(\mu_i, \pi; y_i, w_i) = w_i l(\mu_i, \pi; y_i) \]
In this parameterization, $E[Y] = n \pi$ and $\text{Var}[Y] = n \pi (1 - \pi) \{1 + \mu^2 (n - 1)\}$. The binomial cluster model is a two-component mixture of a binomial($n, \mu^* + \mu$) and a binomial($n, \mu^*$) random variable. This mixture is unusual in that it fixes the number of components and because the mixing probability $\pi$ appears in the moments of the mixture components. For further details, see Morel and Nagaraj (1993), Morel and Neerchal (1997), Neerchal and Morel (1998), and Example 37.1 in this chapter. The expressions for the mean and variance in the binomial cluster model are identical to those of the beta-binomial model shown previously, with $\pi_{bc} = \mu_{bb}$, $\mu_{bc} = \rho_{bb}$.

The FMM procedure models the parameter $\mu$ through the MODEL statement and the parameter $\pi$ through the PROBMODEL statement.

**Constant($c$)**

$$l(y_i) = \begin{cases} 0 & y_i = c \\ -1E20 & y_i \neq c \end{cases}$$

The extreme value when $y_i \neq c$ is chosen so that $\exp\{l(y_i)\}$ yields a likelihood of zero. You can change this value with the INVALIDLOGL= option in the PROC FMM statement. The constant distribution is useful for modeling overdispersion due to zero-inflation (or inflation of the process at support $c$).

**Exponential($\mu$)**

$$l(\mu_i; y_i, w_i) = \begin{cases} -\log\{\mu_i\} - y_i / \mu_i & w_i = 1 \\ w_i \log\left\{w_i y_i / \mu_i\right\} - w_i y_i / \mu_i - \log\{y_i \Gamma(w_i)\} & w_i \neq 1 \end{cases}$$

In this parameterization, $E[Y] = \mu$ and $\text{Var}[Y] = \mu^2$.

**Folded normal($\mu, \phi$)**

$$l(\mu_i, \phi; y_i, w_i) = -\frac{1}{2} \log\{2\pi\} - \frac{1}{2} \log\{\phi / w_i\} + \log\left\{\exp\left\{-w_i (y_i - \mu_i)^2 / 2\phi\right\} + \exp\left\{-w_i (y_i + \mu_i)^2 / 2\phi\right\}\right\}$$

If $X$ has a normal distribution with mean $\mu$ and variance $\phi$, then $Y = |X|$ has a folded normal distribution and log-likelihood function $l(\mu, \phi; y, w)$ for $y \geq 0$. The folded normal distribution arises, for example, when normally distributed measurements are observed, but their signs are not observed. The mean and variance of the folded normal in terms of the underlying $N(\mu, \phi)$ distribution are

$$E[Y] = \frac{1}{\sqrt{2\pi\phi}} \exp\left\{-\frac{\mu^2}{2\phi}\right\} + \mu \left(1 - 2\Phi\left(-\frac{\mu}{\sqrt{\phi}}\right)\right)$$

$$\text{Var}[Y] = \phi + \mu^2 - E[Y]^2$$

The FMM procedure models the folded normal distribution through the mean $\mu$ and variance $\phi$ of the underlying normal distribution. When the FMM procedure computes output statistics for the response variable (for example when you use the OUTPUT statement), the mean and variance of the response $Y$ are reported. Similarly, the fit statistics apply to the distribution of $Y = |X|$, not the distribution of $X$. When you model a folded normal variable, the response input variable should be positive; the FMM procedure treats negative values of $Y$ as a support violation.
**Gamma(μ, φ)**

$$l(\mu_i, \phi; y_i, w_i) = w_i \phi \log \left( \frac{w_i y_i \phi}{\mu_i} \right) - \frac{w_i y_i \phi}{\mu_i} - \log \{y_i\} - \log \{\Gamma(w_i \phi)\}$$

In this parameterization, $E[Y] = \mu$ and $\text{Var}[Y] = \mu^2 / \phi$. $\phi > 0$. This parameterization of the gamma distribution differs from that in the GLIMMIX procedure, which expresses the log-likelihood function in terms of $1/\phi$ in order to achieve a variance function suitable for mixed model analysis.

**Geometric(μ)**

$$l(\mu_i; y_i, w_i) = y_i \log \left( \frac{\mu_i}{w_i} \right) - (y_i + w_i) \log \left( 1 + \frac{\mu_i}{w_i} \right)$$

$$+ \log \left( \frac{\Gamma(y_i + w_i)}{\Gamma(w_i) \Gamma(y_i + 1)} \right)$$

In this parameterization, $E[Y] = \mu$ and $\text{Var}[Y] = \mu + \mu^2$. The exponential distribution is a special case of the negative binomial distribution with $\phi = 0$.

**Generalized Poisson(μ, φ)**

$$\xi_i = \frac{(1 - \exp\{-\phi\})}{\phi}$$

$$\mu_i^* = \mu_i - \xi_i \phi$$

$$l(\mu_i^*; \xi_i; y_i; w_i) = \log \{\mu_i^* - \xi_i \phi \} + (y_i - 1) \log \{\mu_i^* \}$$

$$- \mu_i^* - \log \{\Gamma(y_i + 1)\}$$

In this parameterization, $E[Y] = \mu$, $\text{Var}[Y] = \mu / (1 - \xi)^2$, and $\phi \geq 0$. The FMM procedure models the mean $\mu$ through the effects in the MODEL statement and applies a log link by default. The generalized Poisson distribution provides an overdispersed alternative to the Poisson distribution; $\phi = \xi_i = 0$ produces the mass function of a regular Poisson random variable. For details about the generalized Poisson distribution and a comparison with the negative binomial distribution, see Joe and Zhu (2005).

**Inverse Gaussian(μ, φ)**

$$l(\mu_i, \phi; y_i, w_i) = -\frac{1}{2} \left[ \frac{w_i (y_i - \mu_i)^2}{y_i \phi \mu_i^2} + \log \left( \frac{\phi y_i^2}{w_i} \right) + \log \{2\pi\} \right]$$

The variance is $\text{Var}[Y] = \phi \mu^3$. $\phi > 0$.

**Lognormal(μ, φ)**

$$z_i = \log \{y_i\} - \mu_i$$

$$l(\mu_i, \phi; y_i, w_i) = -\frac{1}{2} \left( 2 \log \{y_i\} + \log \left( \frac{\phi}{w_i} \right) + \log \{2\pi\} + \frac{w_i z_i^2}{\phi} \right)$$

If $X = \log \{Y\}$ has a normal distribution with mean $\mu$ and variance $\phi$, then $Y$ has the log-likelihood function $l(\mu_i, \phi; y_i, w_i)$. The FMM procedure models the lognormal distribution and not the “shortcut” version you can obtain by taking the logarithm of a random variable and modeling that as normally distributed. The two approaches are not
equivalent, and the approach taken by PROC FMM is the actual lognormal distribution. Although the lognormal model is a member of the exponential family of distributions, it is not in the “natural” exponential family because it cannot be written in canonical form. In terms of the parameters $\mu$ and $\phi$ of the underlying normal process for $X$, the mean and variance of $Y$ are $E[Y] = \exp(\mu)\sqrt{\omega}$ and $\text{Var}[Y] = \exp(2\mu)\omega(\omega - 1)$, respectively, where $\omega = \exp(\phi)$. When you request predicted values with the OUTPUT statement, the FMM procedure computes $E[Y]$ and not $\mu$.

**Negative binomial ($\mu, \phi$)**

$$l(\mu_i, \phi; y_i, w_i) = y_i \log \left( \frac{\phi \mu_i}{w_i} \right) - (y_i + w_i/\phi) \log \left( 1 + \frac{\phi \mu_i}{w_i} \right) + \log \left( \frac{\Gamma(y_i + w_i/\phi)}{\Gamma(w_i/\phi) \Gamma(y_i + 1)} \right)$$

The variance is $\text{Var}[Y] = \mu + \phi \mu^2$, $\phi > 0$.

For a given $\phi$, the negative binomial distribution is a member of the exponential family. The parameter $\phi$ is related to the scale of the data because it is part of the variance function. However, it cannot be factored from the variance, as is the case with the $\phi$ parameter in many other distributions.

**Normal ($\mu, \phi$)**

$$l(\mu_i, \phi; y_i, w_i) = -\frac{1}{2} \left[ \frac{w_i (y_i - \mu_i)^2}{\phi} + \log \left( \frac{\phi}{w_i} \right) + \log(2\pi) \right]$$

The mean and variance are $E[Y] = \mu$ and $\text{Var}[Y] = \phi$, respectively, $\phi > 0$.

**Poisson ($\mu$)**

$$l(\mu_i; y_i, w_i) = w_i (y_i \log \{\mu_i\} - \mu_i - \log \{\Gamma(y_i + 1)\})$$

The mean and variance are $E[Y] = \mu$ and $\text{Var}[Y] = \mu$.

**Shifted $T(v; \mu, \phi$)**

$$z_i = -0.5 \log \left( \frac{\phi}{\sqrt{w_i}} \right) + \log \{\Gamma(0.5v + 1)\} - \log \{\Gamma(0.5v)\} - 0.5 \times \log \{\pi v\}$$

$$l(\mu_i, \phi; y_i, w_i) = -\left( \frac{v + 1}{2} \right) \log \left( 1 + \frac{w_i (y_i - \mu_i)^2}{v \phi} \right) + z_i$$

In this parameterization $E[Y] = \mu$ and $\text{Var}[Y] = \phi v/(v - 2)$, $\phi > 0, v > 0$. Note that this form of the $t$ distribution is not a non-central distribution, but that of a shifted central $t$ random variable.

**Uniform ($a, b$)**

$$l(\mu_i; y_i, w_i) = -\log\{b - a\}$$

The mean and variance are $E[Y] = 0.5(a + b)$ and $\text{Var}[Y] = (b - a)^2/12$. 

---

*Log-Likelihood Functions for Response Distributions*
Weibull($\mu, \phi$)

\[
l(\mu, \phi; y_i) = -\frac{\phi - 1}{\phi} \log \left\{ \frac{y_i}{\mu_i} \right\} - \log \{\mu, \phi\}
- \exp \left\{ \log \left\{ \frac{y_i}{\mu_i} \right\} / \phi \right\}
\]

In this particular parameterization of the two-parameter Weibull distribution, the mean and variance of the random variable $Y$ are $E[Y] = \mu \Gamma(1 + \phi)$ and $\text{Var}[Y] = \mu^2 \left\{ \Gamma(1 + 2\phi) - \Gamma^2(1 + \phi) \right\}$.

---

Bayesian Analysis

Conjugate Sampling

The FMM procedure uses Bayesian analysis via a conjugate Gibbs sampler if the model belongs to a small class of mixture models for which a conjugate sampler is available. See the section “Gibbs Sampler” on page 140 for a general discussion of Gibbs sampling. Table 37.8 summarizes the models for which conjugate and Metropolis-Hastings samplers are available.

<table>
<thead>
<tr>
<th>Effects (exclusive of intercept)</th>
<th>Distributions</th>
<th>Available Samplers</th>
</tr>
</thead>
<tbody>
<tr>
<td>No</td>
<td>Normal or T</td>
<td>Conjugate or Metropolis-Hastings</td>
</tr>
<tr>
<td>Yes</td>
<td>Normal or T</td>
<td>Conjugate or Metropolis-Hastings</td>
</tr>
<tr>
<td>No</td>
<td>Binomial, binary, Poisson, exponential</td>
<td>Conjugate or Metropolis-Hastings</td>
</tr>
<tr>
<td>Yes</td>
<td>Binominal, binary, Poisson, exponential</td>
<td>Metropolis-Hastings only</td>
</tr>
</tbody>
</table>

The conjugate sampler enjoys greater efficiency than the Metropolis-Hastings sampler and has the advantage of sampling in terms of the natural parameters of the distribution.

You can always switch to the Metropolis-Hastings sampling algorithm in any model by adding the METROPOLIS option in the BAYES statement.

Metropolis-Hastings Algorithm

If Metropolis-Hastings is the only sampler available for the specified model (see Table 37.8) or if the METROPOLIS option is specified in the BAYES statement, PROC FMM uses the Metropolis-Hastings approach of Gamerman (1997). See the section “Metropolis and Metropolis-Hastings Algorithms” on page 139 for a general discussion of the Metropolis-Hastings algorithm.

The Gamerman (1997) algorithm derives a specific density that is used to generate proposals for the component-specific parameters $\beta_j$. The form of this proposal density is multivariate normal, with mean $m_j$ and covariance matrix $C_j$ derived as follows.
Suppose $\mathbf{\beta}_j$ is the vector of model coefficients in the $j$th component and suppose that $\mathbf{\beta}_j$ has prior distribution $N(\mathbf{a}, \mathbf{R})$. Consider a generalized linear model (GLM) with link function $g(\mu) = \eta = \mathbf{x}'\mathbf{\beta}$ and variance function $a(\mu)$. The pseudo-response and weight in the GLM for a weighted least squares step are

$$y^* = \eta + (y - \mu)/\partial \mu / \partial \eta$$
$$w = \partial \mu / \partial \eta / a(\mu)$$

If the model contains offsets or FREQ or WEIGHT statements, or if a trials variable is involved, suitable adjustments are made to these quantities.

In each component, $j = 1, \cdots, k$, form an adjusted cross-product matrix with a “pseudo” border

$$\begin{bmatrix}
X_j' W_j X_j + \mathbf{R}^{-1} & X_j' W_j y_j^* + \mathbf{R}^{-1} a \\
y_j W_j X_j + a \mathbf{R}^{-1} & c
\end{bmatrix}$$

where $W_j$ is a diagonal matrix formed from the pseudo-weights $w$, $y^*$ is a vector of pseudo-responses, and $c$ is arbitrary. This is basically a system of normal equations with ridging, and the degree of ridging is governed by the precision and mean of the normal prior distribution of the coefficients. Sweeping on the leading partition leads to

$$C_j = \left( X_j' W_j X_j + \mathbf{R}^{-1} \right)^{-1}$$

$$m_j = C_j \left( X_j' W_j y_j^* + \mathbf{R}^{-1} a \right)$$

where the generalized inverse is a reflexive, $g_2$-inverse (see the section “Linear Model Theory” on page 54 of Chapter 3, “Introduction to Statistical Modeling with SAS/STAT Software,” for details).

PROC FMM then generates a proposed parameter vector from the resulting multivariate normal distribution, and then accepts or rejects this proposal according to the appropriate Metropolis-Hastings thresholds.

**Latent Variables via Data Augmentation**

In order to fit finite Bayesian mixture models, the FMM procedure treats the mixture model as a missing data problem and introduces an assignment variable $S$ as in Dempster, Laird, and Rubin (1977). Since $S$ is not observable, it is frequently referred to as a latent variable. The unobservable variable $S$ assigns an observation to a component in the mixture model. The number of states, $k$, might be unknown, but it is known to be finite. Conditioning on the latent variable $S$, the component memberships of each observation is assumed to be known, and Bayesian estimation is straightforward for each component in the finite mixture model. That is, conditional on $S = j$, the distribution of the response is now assumed to be $f(y; \alpha_j, \mathbf{\beta}_j | S = j)$. In other words, each distinct state of the random variable $S$ leads to a distinct set of parameters. The parameters in each component individually are then updated using a conjugate Gibbs sampler (where available) or a Metropolis-Hastings sampling algorithm.

The FMM procedure assumes that the random variable $S$ has a discrete multinomial distribution with probability $\pi_j$ of belonging to a component $j$; it can occupy one of $k$ states. The distribution for the latent variable $S$ is

$$f(S_i = j | \pi_1, \ldots, \pi_k) = \text{multinomial}(1, \pi_1, \ldots, \pi_k)$$
where \( f(\cdot|\cdot) \) denotes a conditional probability density. The parameters in the density \( \pi_j \) denote the probability that \( S \) takes on state \( j \).

The FMM procedure assumes a conjugate Dirichlet prior distribution on the mixture proportions \( \pi_j \) written as:

\[
p(\pi) = \text{Dirichlet}(a_1, \ldots, a_k)
\]

where \( p(\cdot) \) indicates a prior distribution.

Using Bayes’ theorem, the likelihood function and prior distributions determine a conditionally conjugate posterior distribution of \( S \) and \( \pi \) from the multinomial distribution and Dirichlet distribution, respectively.

### Prior Distributions

The following list displays the parameterization of prior distributions for situations in which the FMM procedure uses a conjugate sampler in mixture models without model effects and certain basic distributions (binary, binomial, exponential, Poisson, normal, and \( t \)). You specify the parameters \( a \) and \( b \) in the formulas below in the MUPRIORPARMS and PHIPRIORPARMS options in the BAYES statement in these models.

**Beta** \((a, b)\)

\[
f(y) = \frac{\Gamma(a + b)}{\Gamma(a)\Gamma(b)} y^{a-1} (1 - y)^{b-1}
\]

where \( a > 0, b > 0 \). In this parameterization, the mean and variance of the distribution are \( \mu = \frac{a}{a + b} \) and \( \mu(1 - \mu)/(a + b + 1) \), respectively. The beta distribution is the prior distribution for the success probability in binary and binomial distributions when conjugate sampling is used.

**Dirichlet** \((a_1, \ldots, a_k)\)

\[
f(y) = \frac{\Gamma\left(\sum_{i=1}^{k} a_i\right)}{\prod_{i=1}^{k} \Gamma(a_i)} y_1^{a_1-1} \cdots y_k^{a_k-1}
\]

where \( \sum_{i=1}^{k} y_i = 1 \) and the parameters \( a_i > 0 \). If any \( a_i \) were zero, an improper density would result. The Dirichlet density is the prior distribution for the mixture probabilities. You can affect the choice of the \( a_i \) through the MIXPRIORPARMS option in the BAYES statement. If \( k = 2 \), the Dirichlet is the same as the beta\((a, b)\) distribution.

**Gamma** \((a, b)\)

\[
f(y) = \frac{b^a}{\Gamma(a)} y^{a-1} \exp\{-by\}
\]

where \( a > 0, b > 0 \). In this parameterization, the mean and variance of the distribution are \( \mu = a/b \) and \( \mu/b \), respectively. The gamma distribution is the prior distribution for the mean parameter of the Poisson distribution when conjugate sampling is used.
Inverse gamma \((a, b)\)

\[
f(y) = \frac{ba}{\Gamma(a)} y^{-a-1} \exp\left\{-\frac{y}{b}\right\}
\]

where \(a > 0, b > 0\). In this parameterization, the mean and variance of the distribution are \(\mu = \frac{b}{a-1}\) if \(a > 1\) and \(\mu^2/(a-2)\) if \(a > 2\), respectively. The inverse gamma distribution is the prior distribution for the mean parameter of the exponential distribution when conjugate sampling is used. It is also the prior distribution for the scale parameter \(\phi\) in all models.

Multinomial \((1, \pi_1, \cdots, \pi_k)\)

\[
f(y) = \frac{1}{y_1! \cdots y_k!} \pi_1^{y_1} \cdots \pi_k^{y_k}
\]

where \(\sum_{j=1}^{k} y_j = n, y_j \geq 0, \sum_{j=1}^{k} \pi_j = 1,\) and \(n\) is the number of observations included in the analysis. The multinomial density is the prior distribution for the mixture proportions. The mean and variance of \(Y_j\) are \(\mu_j = \pi_j\) and \(\mu_j(1-\pi_j)\), respectively.

Normal \((a, b)\)

\[
f(y) = \frac{a}{\sqrt{2\pi b}} \exp\left\{-\frac{1}{2} \left(\frac{y-a}{b}\right)^2\right\}
\]

where \(b > 0\). The mean and variance of the distribution are \(\mu = a\) and \(b\), respectively. The normal distribution is the prior distribution for the mean parameter of the normal and \(t\) distribution when conjugate sampling is used.

When a MODEL statement contains effects or if you specify the METROPOLIS option, the prior distribution for the regression parameters is multivariate normal, and you can specify the means and variances of the parameters in the BETAPRIORPARMS option in the BAYES statement.

---

Parameterization of Model Effects

PROC FMM constructs a finite mixture model according to the specifications in the CLASS, MODEL, and PROBMODEL statements. Each effect in the MODEL statement generates one or more columns in the matrix \(X\) for that model. The same \(X\) matrix applies to all components that are associated with the MODEL statement. Each effect in the PROBMODEL statement generates one or more columns in the matrix \(Z\) from which the linear predictors in the model for the mixture probability models is formed. The same \(Z\) matrix applies to all components.

The formation of effects from continuous and classification variables in the FMM procedure follows the same general rules and techniques as for other linear modeling procedures. See the section “GLM Parameterization of Classification Variables and Effects” on page 394 of Chapter 19, “Shared Concepts and Topics.”
Default Output

The following sections describe the output that PROC FMM produces by default. The output is organized into various tables, which are discussed in the order of appearance for maximum likelihood and Bayes estimation, respectively.

Model Information

The “Model Information” table displays basic information about the model, such as the response variable, frequency variable, link function, and the model category that the FMM procedure determined based on your input and options. The “Model Information” table is one of a few tables that are produced irrespective of estimation technique. Most other tables are specific to Bayes or maximum likelihood estimation.

If the analysis depends on generated random numbers, the “Model Information” table also displays the random number seed used to initialize the random number generators. If you repeat the analysis and pass this seed value in the SEED= option in the PROC FMM statement, an identical stream of random numbers results.

Class Level Information

The “Class Level Information” table lists the levels of every variable specified in the CLASS statement. You should check this information to make sure that the data are correct. You can adjust the order of the CLASS variable levels with the ORDER= option in the PROC FMM statement. You can suppress the “Class Level Information” table completely or partially with the NOCLPRINT option in the PROC FMM statement.

Number of Observations

The “Number of Observations” table displays the number of observations read from the input data set and the number of observations used in the analysis. If you specify a FREQ statement, the table also displays the sum of frequencies read and used. If the events/trials syntax is used for the response, the table also displays the number of events and trials used in the analysis.

Note that the number of observations “used” in the analysis is not unambiguous in a mixture model. An observation that is “unused” for one component distribution (because the response value is outside of the support of the distribution) might still be usable in the mixture model when the response value is in the support of another component distribution. You can affect the way in which PROC FMM handles exclusion of observations due to support violations with the EXCLUSION= option in the PROC FMM statement.

Response Profile

For binary data, the “Response Profile” table displays the ordered value from which the FMM procedure determines the probability being modeled as an event for binary data. For each response category level, the frequency used in the analysis is reported.
Default Output for Maximum Likelihood

Optimization Information
The “Optimization Information” table displays basic information about the optimization setup to determine the maximum likelihood estimates, such as the optimization technique, the parameters that participate in the optimization, and the number of threads used for the calculations.

Iteration History
The “Iteration History” table displays for each iteration of the optimization the number of function evaluations (including gradient and Hessian evaluations), the value of the objective function, the change in the objective function from the previous iteration, and the absolute value of the largest (projected) gradient element. The objective function used in the optimization in the FMM procedure is the negative of the mixture log likelihood; consequently, PROC FMM performs a minimization.

Convergence Status
The convergence status table is a small ODS table that follows the “Iteration History” table in the default output. In the listing, it appears as a message that identifies whether the optimization succeeded and which convergence criterion was met. If the optimization fails, the message indicates the reason for the failure. If you save the “Convergence Status” table to an output data set, a numeric Status variable is added that allows you to assess convergence programmatically. The values of the Status variable encode the following:

0 Convergence was achieved or an optimization was not performed (because of TECHNIQUE=NONE).

1 The objective function could not be improved.

2 Convergence was not achieved because of a user interrupt or because a limit was exceeded, such as the maximum number of iterations or the maximum number of function evaluations. To modify these limits, see the MAXITER=, MAXFUNC=, and MAXTIME= options in the PROC FMM statement.

3 Optimization failed to converge because function or derivative evaluations failed at the starting values or during the iterations or because a feasible point that satisfies the parameter constraints could not be found in the parameter space.

Fit Statistics
The “Fit Statistics” table displays a variety of fit measures based on the mixture log likelihood in addition to the Pearson statistic. All statistics are presented in “smaller is better” form. If you are fitting a single-component normal, gamma, or inverse gaussian model, the table also contains the unscaled Pearson statistic. If you are fitting a mixture model or the model has been fitted under restrictions, the table also contains the number of effective components and the number of effective parameters.

The calculation of the information criteria uses the following formulas, where \( p \) denotes the number of effective parameters, \( n \) denotes the number of observations used (or the sum of the frequencies used if a
FREQ statement is present), and $l$ is the log likelihood of the mixture evaluated at the converged estimates:

\[
\text{AIC} = -2l + 2p \\
\text{AICC} = \begin{cases} 
-2l + 2pn/(n - p - 1) & n > p + 2 \\
-2l + 2(p + 2) & \text{otherwise}
\end{cases} \\
\text{BIC} = -2l + p \log(n)
\]

The Pearson statistic is computed simply as

\[
\text{Pearson statistic} = \sum_{i=1}^{n} f_i \frac{(y_i - \hat{\mu}_i)^2}{\text{Var}[Y_i]}
\]

where $n$ denotes the number of observations used in the analysis, $f_i$ is the frequency associated with the $i$th observation (or 1 if no frequency is specified), $\mu_i$ is the mean of the mixture, and the denominator is the variance of the $i$th observation in the mixture. Note that the mean and variance in this expression are not those of the component distributions, but the mean and variance of the mixture:

\[
\mu_i = \mathbb{E}[Y_i] = \sum_{j=1}^{k} \pi_{ij} \mu_{ij} \\
\text{Var}[Y_i] = -\mu_i^2 + \sum_{j=1}^{k} \pi_{ij} \left( \sigma_{ij}^2 + \mu_{ij}^2 \right)
\]

where $\mu_{ij}$ and $\sigma_{ij}^2$ are the mean and variance, respectively, for observation $i$ in the $j$th component distribution and $\pi_{ij}$ is the mixing probability for observation $i$ in component $j$.

The unscaled Pearson statistic is computed with the same expression as the Pearson statistic with $n$, $f_i$, and $\mu_i$ as previously defined, but the scale parameter $\phi$ is set to 1 in the $\text{Var}[Y_i]$ expression.

The number of effective components and the number of effective parameters are determined by examining the converged solution for the parameters that are associated with model effects and the mixing probabilities. For example, if a component has an estimated mixing probability of zero, the values of its parameter estimates are immaterial. You might argue that all parameters should be counted towards the penalty in the information criteria. But a component with zero mixing probability in a $k$-component model effectively reduces the model to a $(k - 1)$-component model. A situation of an overfit model, for which a parameter penalty needs to be taken when calculating the information criteria, is a different situation; here the mixing probability might be small, possibly close to zero.

**Parameter Estimates**

The parameter estimates, their estimated (asymptotic) standard errors, and $p$-values for the hypothesis that the parameter is zero are presented in the “Parameter Estimates” table. A separate table is produced for each MODEL statement, and the components that are associated with a MODEL statement are identified with an overall component count variable that counts across MODEL statements. If you assign a label to a model with the LABEL= option in the MODEL statement, the label appears in the title of the “Parameter Estimates” table. Otherwise, the internal label generated by the FMM procedure is used.

If the MODEL statement does not contain effects and the link function is not the identity, the inversely linked estimate is also displayed in the table. For many distributions, the inverse linked estimate is the
estimated mean on the data scale. For example, in a binomial or binary model, it represents the estimated probability of an event. For some distributions (for example, the Weibull distribution), the inverse linked estimate is not the component distribution mean.

If you request confidence intervals with the CL or ALPHA= option in the MODEL statement, confidence limits are produced for the estimate on the linear scale. If the inverse linked estimate is displayed, confidence intervals for that estimate are also produced by inversely linking the confidence bounds on the linear scale.

**Mixing Probabilities**

If you fit a model with more than one component, the table of mixing probabilities is produced. If there are no effects in the PROBMODEL statement or if there is no PROBMODEL statement, the parameters are reported on the linear scale and as mixing probabilities. If model effects are present, only the linear parameters (on the scale of the logit, generalized logit, probit, and so on) are displayed.

**Default Output for Bayes Estimation**

**Bayes Information**

This table provides basic information about the sampling algorithm. The FMM procedure uses either a conjugate sampler or a Metropolis-Hastings sampling algorithm based on Gamerman (1997). The table reveals, for example, how many model parameters are sampled, how many parameters associated with mixing probabilities are sampled, and how many threads are used to perform multithreaded analysis.

**Prior Distributions**

The “Prior Distributions” table lists for each sampled parameter the prior distribution and its parameters. The mean and variance (if they exist) for those values of the parameters are also displayed, along with the initial value for the parameter in the Markov chain. The Component column in this table identifies the mixture component to which a particular parameter belongs. You can control how the FMM procedure determines initial values with the INITIAL= option in the BAYES statement.

**Posterior Summaries**

The arithmetic mean, standard deviation, and percentiles of the posterior distribution of the parameter estimates are displayed in the “Posterior Summaries” table. By default, the FMM procedure computes the 25th, 50th (median), and 75th percentiles of the sampling distribution. You can modify the percentiles through suboptions of the STATISTICS option in the BAYES statement. If a parameter corresponds to a singularity in the design and was removed from sampling for that purpose, it is also displayed in the table of posterior summaries (and in other tables that relate to output from the BAYES statement). The posterior sample size for such a parameter is shown as N = 0.

**Posterior Intervals**

The table of “Posterior Intervals” displays equal-tail intervals and intervals of highest posterior density for each parameter. By default, intervals are computed for an α-level of 0.05, which corresponds to 95%
intervals. You can modify this confidence level by providing one or more $\alpha$ values in the ALPHA= suboption of the STATISTICS option in the BAYES statement. The computation of these intervals is detailed in section “Summary Statistics” on page 157 of Chapter 7, “Introduction to Bayesian Analysis Procedures.”

**Posterior Autocorrelations**

Autocorrelations for the posterior estimates are computed by default for autocorrelation lags 1, 5, 10, and 50, provided that a sufficient number of posterior samples is available. See the section “Assessing Markov Chain Convergence” on page 143 of Chapter 7, “Introduction to Bayesian Analysis Procedures,” for the computation of posterior autocorrelations and their utility in diagnosing convergence of Markov chains. You can modify the list of lags for which posterior autocorrelations are calculated with the AUTOCORR suboption of the DIAGNOSTICS option in the BAYES statement.

**ODS Table Names**

Each table created by PROC FMM has a name associated with it, and you must use this name to reference the table when you use ODS statements. These names are listed in Table 37.9.

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Required Statement / Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>Autocorr</td>
<td>Autocorrelation among posterior estimates</td>
<td>BAYES</td>
</tr>
<tr>
<td>BayesInfo</td>
<td>Basic information about Bayesian estimation</td>
<td>BAYES</td>
</tr>
<tr>
<td>ClassLevels</td>
<td>Level information from the CLASS statement</td>
<td>CLASS</td>
</tr>
<tr>
<td>CompDescription</td>
<td>Component description in models with varying number of components</td>
<td>KMAX= in MODEL with ML estimation</td>
</tr>
<tr>
<td>CompEvaluation</td>
<td>Comparison of mixture models with varying number of components</td>
<td>KMAX= in MODEL with ML estimation</td>
</tr>
<tr>
<td>CompInfo</td>
<td>Component information</td>
<td>COMPONENTINFO option in PROC FMM statement</td>
</tr>
<tr>
<td>ConvergenceStatus</td>
<td>Status of optimization at conclusion of optimization</td>
<td>Default output</td>
</tr>
<tr>
<td>Constraints</td>
<td>Linear equality and inequality constraints</td>
<td>RESTRICT statement or EQUATE=EFFECTS option in MODEL statement</td>
</tr>
<tr>
<td>Corr</td>
<td>Asymptotic correlation matrix of parameter estimates (ML) or empirical correlation matrix of the Bayesian posterior estimates</td>
<td>CORR option in PROC FMM statement</td>
</tr>
<tr>
<td>Table Name</td>
<td>Description</td>
<td>Required Statement / Option</td>
</tr>
<tr>
<td>-------------</td>
<td>-----------------------------------------------------------------------------</td>
<td>------------------------------------------------------------------</td>
</tr>
<tr>
<td>Cov</td>
<td>Asymptotic covariance matrix of parameter estimates (ML) or empirical covariance matrix of the Bayesian posterior estimates</td>
<td>COV option in PROC FMM statement</td>
</tr>
<tr>
<td>CovI</td>
<td>Inverse of the covariance matrix of the parameter estimates</td>
<td>COVI option in PROC FMM statement</td>
</tr>
<tr>
<td>ESS</td>
<td>Effective sample size</td>
<td>DIAG=ESS option in BAYES statement</td>
</tr>
<tr>
<td>FitStatistics</td>
<td>Fit statistics</td>
<td>Default output</td>
</tr>
<tr>
<td>Geweke</td>
<td>Geweke diagnostics (Geweke 1992) for Markov chain</td>
<td>DIAG=GEWEKE option in BAYES statement</td>
</tr>
<tr>
<td>Hessian</td>
<td>Hessian matrix from the maximum likelihood optimization, evaluated at the converged estimates</td>
<td>HESSIAN</td>
</tr>
<tr>
<td>IterHistory</td>
<td>Iteration history</td>
<td>Default output for ML estimation</td>
</tr>
<tr>
<td>MCSE</td>
<td>Monte Carlo standard errors</td>
<td>DIAG=MCERROR in BAYES statement</td>
</tr>
<tr>
<td>MixingProbs</td>
<td>Solutions for the parameter estimates associated with effects in PROBMODEL statements</td>
<td>Default output for ML estimation if number of components is greater than 1</td>
</tr>
<tr>
<td>ModelInfo</td>
<td>Model information</td>
<td>Default output</td>
</tr>
<tr>
<td>NObs</td>
<td>Number of observations read and used, number of trials and events</td>
<td>Default output</td>
</tr>
<tr>
<td>OptInfo</td>
<td>Optimization information</td>
<td>Default output for ML estimation</td>
</tr>
<tr>
<td>ParameterEstimates</td>
<td>Solutions for the parameter estimates associated with effects in MODEL statements</td>
<td>Default output for ML estimation</td>
</tr>
<tr>
<td>ParameterMap</td>
<td>Mapping of parameter names to OUTPOST= data set</td>
<td>OUTPOST= option in BAYES statement</td>
</tr>
<tr>
<td>PriorInfo</td>
<td>Prior distributions and initial value of Markov chain</td>
<td>BAYES</td>
</tr>
<tr>
<td>PostSummaries</td>
<td>Summary statistics for posterior estimates</td>
<td>BAYES</td>
</tr>
<tr>
<td>PostIntervals</td>
<td>Equal-tail and highest posterior density intervals for posterior estimates</td>
<td>BAYES</td>
</tr>
<tr>
<td>ResponseProfile</td>
<td>Response categories and category modeled</td>
<td>Default output in models with binary response</td>
</tr>
</tbody>
</table>
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, with the ODS GRAPHICS ON statement). For more information about enabling and disabling ODS Graphics, see the section “Enabling and Disabling ODS Graphics” on page 609 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 608 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 FMM generates are listed in Table 37.10, along with the required statements and options.

<table>
<thead>
<tr>
<th>ODS Graph Name</th>
<th>Plot Description</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>TADPanel</td>
<td>Panel of diagnostic graphics to assess convergence of Markov chains</td>
<td>BAYES</td>
</tr>
<tr>
<td>DensityPlot</td>
<td>Histogram and density with component distributions</td>
<td></td>
</tr>
</tbody>
</table>

Examples: FMM Procedure

Example 37.1: Modeling Mixing Probabilities: All Mice Are Created Equal, but Some Are More Equal

This example demonstrates how you can model the means and mixture proportions separately in a binomial cluster model. It also compares the binomial cluster model to the beta-binomial model.

In a typical teratological experiment, the offspring of animals that were exposed to a toxin during pregnancy are studied for malformation. If you count the number of malformed offspring in a litter of size \( n \), then this count is typically not binomially distributed. The responses of the offspring from the same litter are not independent; hence their sum does not constitute a binomial random variable. Relative to a binomial model, data from teratological experiments exhibit overdispersion because ignoring positive correlation among the responses tends to overstate the precision of the parameter estimates. Oversdispersion mechanisms are briefly discussed in the section “Overdispersion” on page 2492.

In this application, the focus is on mixtures and models that involve a mixing mechanism. The mixing
Example 37.1: Modeling Mixing Probabilities: All Mice Are Created Equal, but Some Are More Equal

approach, considered in Williams (1975) and Haseman and Kupper (1979), supposes that the binomial success probability is a random variable that follows a beta($\alpha, \beta$) distribution:

\[
Y | \mu \sim \text{Binomial}(n, \mu) \\
\mu \sim \text{Beta}(\alpha, \beta) \\
Y \sim \text{Beta-binomial}(n, \mu, \phi) \\
E[Y] = n\pi \\
\text{Var}[Y] = n\pi(1 - \pi) \left\{ 1 + \mu^2(n - 1) \right\}
\]

If $\mu = 0$, then the beta-binomial distribution reduces to a standard binomial model with success probability $\pi$. The parameterization of the beta-binomial distribution used by the FMM procedure is based on Neerchal and Morel (1998); see the section “Log-Likelihood Functions for Response Distributions” on page 2493 for details.

Morel and Nagaraj (1993), Morel and Neerchal (1997), and Neerchal and Morel (1998) propose a different model to capture dependency within binomial clusters. Their model is a two-component mixture that gives rise to the same mean and variance function as the beta-binomial model. The genesis is different, however. In the binomial cluster model of Morel and Neerchal, suppose there is a cluster of $n$ Bernoulli outcomes with success probability $\pi$. The number of responses in the cluster decomposes into $N \leq n$ outcomes that all respond with either “success” or “failure”; the important aspect is that they all respond identically. The remaining $n - N$ Bernoulli outcomes respond independently, so the sum of successes in this group is a binomial($n - N, \pi$) random variable. Denote the probability with which cluster members fall into the group of identical respondents as $C$. Then $1 - C$ is the probability that a response belongs to the group of independent Bernoulli outcomes.

It is easy to see how this process of dividing the individual Bernoulli outcomes creates clustering. The binomial cluster model can be written as the two-component mixture

\[
\Pr(Y = y) = \pi \Pr(U = y) + (1 - \pi) \Pr(V = y)
\]

where $U \sim \text{Binomial}(n, \mu^* + \mu)$, $V \sim \text{Binomial}(n, \mu^*)$, and $\mu^* = (1 - \mu)\pi$. This mixture model is somewhat unusual because the mixing probability $\pi$ appears as a parameter in the component distributions. The two probabilities involved, $\pi$ and $\mu$, have the following interpretation: $\pi$ is the unconditional probability of success for any observation, and $\mu$ is the probability with which the Bernoulli observations respond identically. The complement of this probability, $1 - \mu$, is the probability with which the Bernoulli outcomes respond independently. If $\mu = 0$, then the two-component mixture reduces to a standard Binomial model with success probability $\pi$. Since both $\pi$ and $\mu$ are involved in the success probabilities of the two Binomial variables in the mixture, you can affect these binomial means by specifying effects in the PROBMODEL statement (for the $\pi$s) or the MODEL statement (for the $\mu$s). In a “straight” two-component Binomial mixture,

\[
\pi \text{Binomial}(n, \mu_1) + (1 - \pi) \text{Binomial}(n, \mu_2)
\]

you would vary the success probabilities $\mu_1$ and $\mu_2$ through the MODEL statement.

With the FMM procedure, you can fit the beta-binomial model by specifying DIST=BETABIN and the binomial cluster model by specifying DIST=BINOMCLUS in the MODEL statement.

Morel and Neerchal (1997) report data from a completely randomized design that studies the teratogenicity of phenytoin in 81 pregnant mice. The treatment structure of the experiment is an augmented factorial. In
addition to an untreated control, mice received 60 mg/kg of phenytoin (PHT), 100 mg/kg of trichloropropene oxide (TCPO), and their combination. The design was augmented with a control group that was treated with water. As in Morel and Neerchal (1997), the two control groups are combined here into a single group.

The following DATA step creates the data for this analysis as displayed in Table 1 of Morel and Neerchal (1997). The second DATA step creates continuous variables x1–x3 to match the parameterization of these authors.

```plaintext
data ossi;
  length tx $8;
  input tx$ n @@;
  do i=1 to n;
    input y m @@;
    output;
  end;
  drop i;
  datalines;
Control 18 8 9 9 7 9 0 5 3 3 5 8 9 10 5 8 5 8 1 6 0 5
  8 8 9 10 5 5 4 7 9 10 6 6 3 5
Control 17 8 9 7 10 10 1 6 6 6 1 9 8 9 6 7 5 5 7 9
  2 5 5 6 2 8 1 8 0 2 7 8 5 7
PHT 19 1 9 4 9 3 7 4 7 0 7 0 4 1 8 1 7 2 7 2 8 1 7
  0 2 3 1 0 3 7 2 7 0 8 0 8 1 1 0 1 1
TCPO 16 0 5 7 10 4 4 8 11 6 10 6 9 3 4 2 8 0 6 0 9
  3 6 2 9 7 9 1 1 0 8 8 6 9
PHT+TCPO 11 2 2 0 7 1 8 7 8 0 10 0 4 0 6 0 7 6 6 1 6 1 7;

data ossi;
  set ossi;
  array xx{3} x1-x3;
  do i=1 to 3; xx(i)=0; end;
  pht = 0;
  tcpo = 0;
  if (tx='TCPO') then do;
    xx(1) = 1;
    tcpo = 100;
  end; else if (tx='PHT') then do;
    xx(2) = 1;
    pht = 60;
  end; else if (tx='PHT+TCPO') then do;
    pht = 60;
    tcpo = 100;
    xx(1) = 1; xx(2) = 1; xx(3)=1;
  end;
run;
```

The FMM procedure models the mean parameters $\mu$ through the MODEL statement and the mixing proportions $\pi$ through the PROBMODEL statement. In the binomial cluster model, you can place a regression structure on either set of probabilities, and the regression structure does not need to be the same. In the following statements, the unconditional probability of ossification is modeled as a two-way factorial, whereas the intralitter effect—the propensity to group within a cluster—is assumed to be constant:
proc fmm data=ossi;
    class pht tcpo;
    model y/m = / dist=binomcluster;
    probmodel pht tcpo pht*tcpo;
run;

The CLASS statement declares the PHT and TCPO variables as classification variables. They affect the analysis through their levels, not through their numeric values. The MODEL statement declares the distribution of the data to follow a binomial cluster model. The FMM procedure then automatically assumes that the model is a two-component mixture. An intercept is included by default. The PROBMODEL statement declares the effect structure for the mixing probabilities. The unconditional probability of ossification of a fetus depends on the main effects and the interaction in the factorial.

The “Model Information” table displays important details about the model fit with the FMM procedure (Output 37.1.1). Although no K= option was specified in the MODEL statement, the FMM procedure recognizes the model as a two-component model. The “Class Level Information” table displays the levels and values of the PHT and TCPO variables. Eighty-one observations are read from the data and are used in the analysis. These observations comprise 287 events and 585 total outcomes.

**Output 37.1.1** Model Information in Binomial Cluster Model with Constant Clustering Probability

<table>
<thead>
<tr>
<th>The FMM Procedure</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model Information</td>
</tr>
<tr>
<td>Data Set</td>
</tr>
<tr>
<td>Response Variable (Events)</td>
</tr>
<tr>
<td>Response Variable (Trials)</td>
</tr>
<tr>
<td>Type of Model</td>
</tr>
<tr>
<td>Distribution</td>
</tr>
<tr>
<td>Components</td>
</tr>
<tr>
<td>Link Function</td>
</tr>
<tr>
<td>Estimation Method</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Class Level Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Class</td>
</tr>
<tr>
<td>---------</td>
</tr>
<tr>
<td>pht</td>
</tr>
<tr>
<td>tcpo</td>
</tr>
</tbody>
</table>

| Number of Observations Read       | 81 |
| Number of Observations Used       | 81 |
| Number of Events                  | 287|
| Number of Trials                  | 585|

The “Optimization Information” table in **Output 37.1.2** gives details about the maximum likelihood optimization. By default, the FMM procedure uses a quasi-Newton algorithm. The model contains five parameters, four of which are part of the model for the mixing probabilities. The fifth parameter is the intercept in the model for $\mu$. 
Output 37.1.2 Optimization in Binomial Cluster Model with Constant Clustering Probability

Optimization Information

<table>
<thead>
<tr>
<th>Optimization Technique</th>
<th>Dual Quasi-Newton</th>
</tr>
</thead>
<tbody>
<tr>
<td>Parameters in Optimization</td>
<td>5</td>
</tr>
<tr>
<td>Mean Function Parameters</td>
<td>1</td>
</tr>
<tr>
<td>Scale Parameters</td>
<td>0</td>
</tr>
<tr>
<td>Mixing Prob Parameters</td>
<td>4</td>
</tr>
<tr>
<td>Number of Threads</td>
<td>2</td>
</tr>
</tbody>
</table>

Iteration History

<table>
<thead>
<tr>
<th>Iteration</th>
<th>Evaluations</th>
<th>Objective Function</th>
<th>Change</th>
<th>Gradient</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>5</td>
<td>174.92723892</td>
<td></td>
<td>43.78769</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>154.13180744</td>
<td>20.79543149</td>
<td>11.2346</td>
</tr>
<tr>
<td>2</td>
<td>3</td>
<td>153.26693611</td>
<td>0.86487133</td>
<td>6.888215</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>152.84974281</td>
<td>0.41719329</td>
<td>3.541977</td>
</tr>
<tr>
<td>4</td>
<td>3</td>
<td>152.61756033</td>
<td>0.23218248</td>
<td>2.783556</td>
</tr>
<tr>
<td>5</td>
<td>3</td>
<td>152.54795303</td>
<td>0.06960730</td>
<td>1.146807</td>
</tr>
<tr>
<td>6</td>
<td>3</td>
<td>152.52684929</td>
<td>0.02110374</td>
<td>0.034367</td>
</tr>
<tr>
<td>7</td>
<td>3</td>
<td>152.52671214</td>
<td>0.00013715</td>
<td>0.011511</td>
</tr>
<tr>
<td>8</td>
<td>3</td>
<td>152.52670799</td>
<td>0.00000415</td>
<td>0.000202</td>
</tr>
<tr>
<td>9</td>
<td>3</td>
<td>152.52670799</td>
<td>0.00000000</td>
<td>4.001E-6</td>
</tr>
</tbody>
</table>

Convergence criterion (GCONV=1E-8) satisfied.

Fit Statistics

<table>
<thead>
<tr>
<th>Fit Statistic</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>-2 Log Likelihood</td>
<td>305.1</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
<td>315.1</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
<td>315.9</td>
</tr>
<tr>
<td>BIC (smaller is better)</td>
<td>327.0</td>
</tr>
<tr>
<td>Pearson Statistic</td>
<td>89.2077</td>
</tr>
<tr>
<td>Effective Parameters</td>
<td>5</td>
</tr>
<tr>
<td>Effective Components</td>
<td>2</td>
</tr>
</tbody>
</table>

After nine iterations, the iterative optimization converges. The \(-2\) log likelihood at the converged solution is 305.1, and the Pearson statistic is 89.2077. The FMM procedure computes the Pearson statistic as a general goodness-of-fit measure that expresses the closeness of the fitted model to the data.

The estimates of the parameters in the conditional probability \(\mu\) and in the unconditional probability \(\pi\) are given in Output 37.1.3. The intercept estimate in the model for \(\mu\) is 0.3356. Since the default link in the binomial cluster model is the logit link, the estimate of the conditional probability is

\[
\hat{\mu} = \frac{1}{1 + \exp\{-0.3356\}} = 0.5831
\]

This value is displayed in the “Inverse Linked Estimate” column. There is greater than a 50% chance that the individual fetuses in a litter provide the same response. The clustering tendency is substantial.
Example 37.1: Modeling Mixing Probabilities: All Mice Are Created Equal, but Some Are More Equal

Output 37.1.3 Parameter Estimates in Binomial Cluster Model with Constant Clustering Probability

| Component | Effect | Estimate | Standard Error | z Value | Pr > |z| | Inverse Linked Estimate |
|-----------|--------|----------|----------------|---------|-------|-----------------------|------------------------|
| 1         | Intercept | 0.3356   | 0.1714         | 1.96    | 0.0503 | 0.5831                |

Parameter Estimates for Mixing Probabilities

| Effect | pht | tcpo | Estimate | Standard Error | z Value | Pr > |z| |
|--------|-----|------|----------|----------------|---------|-------|-------|
| Intercept | -1.2194 | 0.4690 | -2.60 | 0.0093 |
| pht      | 0   | 0.9129 | 0.5608 | 1.63 | 0.1036 |
| tcpo     | 60  | 0     | 0.3295 | 0.5534 | 0.60 | 0.5516 |
| pht*tcpo | 0   | 0     | 0.6162 | 0.6678 | 0.92 | 0.3561 |
| pht*tcpo | 100 | 0     | 0       | 0.3065 | 0.4240 |
| pht*tcpo | 0   | 0     | 0       | 0.2280 |

The “Mixing Probabilities” table displays the estimates of the parameters in the model for \( \pi \) on the logit scale (Output 37.1.3). Table 37.11 constructs the estimates of the unconditional probabilities of ossification.

Table 37.11 Estimates of Ossification Probabilities

<table>
<thead>
<tr>
<th>PHT</th>
<th>TCPO</th>
<th>( \hat{\eta} )</th>
<th>( \hat{\pi} )</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>0</td>
<td>( -1.2194+0.9129+0.3295+0.6162=0.6392 )</td>
<td>0.6546</td>
</tr>
<tr>
<td>60</td>
<td>0</td>
<td>( -1.2194+0.3295=-0.8899 )</td>
<td>0.2911</td>
</tr>
<tr>
<td>0</td>
<td>100</td>
<td>( -1.2194+0.9129=-0.3065 )</td>
<td>0.4240</td>
</tr>
<tr>
<td>60</td>
<td>100</td>
<td>( -1.2194 )</td>
<td>0.2280</td>
</tr>
</tbody>
</table>

Morel and Neerchal (1997) considered a model in which the intralitter effects also depend on the treatments. This model is fit with the FMM procedure with the following statements:

```plaintext
proc fmm data=ossi;
  class pht tcpo;
  model y/m = pht tcpo pht*tcpo / dist=binomcluster;
  probmodel pht tcpo pht*tcpo;
run;
```

The \(-2\) log likelihood of this model is much reduced compared to the previous model with constant conditional probability (compare 287.8 in Output 37.1.4 with 305.1 in Output 37.1.2). The likelihood-ratio statistic of 17.3 is significant, \( Pr(\chi^2_3 > 17.3 = 0.0006) \). Varying the conditional probabilities by treatment improved the model fit significantly.
Output 37.1.4  Fit Statistics and Parameter Estimates in Binomial Cluster Model

The FMM Procedure

Fit Statistics
-2 Log Likelihood  287.8
AIC (smaller is better)  303.8
AICC (smaller is better)  305.8
BIC (smaller is better)  323.0
Pearson Statistic  85.5998
Effective Parameters  8
Effective Components  2

Parameter Estimates for 'Binomial Cluster' Model

| Component | Effect | Effect | pht  | tcpo | Estimate | Error | z Value | Pr > |z| |
|-----------|--------|--------|------|------|----------|-------|---------|-------|
| 1         | Intercept  | 1.8213 | 0.5889 | 3.09 | 0.0020 |
| 1         | pht  | 0 | -1.4962 | 0.6630 | -2.26 | 0.0240 |
| 1         | pht  | 60 | 0 | . | . |
| 1         | tcpo | 0 | -3.1828 | 1.1261 | -2.83 | 0.0047 |
| 1         | tcpo | 100 | 0 | . | . |
| 1         | pht*tcpo | 0 | 0 | 3.3736 | 1.1953 | 2.82 | 0.0048 |
| 1         | pht*tcpo | 0 | 100 | 0 | . | . |
| 1         | pht*tcpo | 60 | 0 | 0 | . | . |
| 1         | pht*tcpo | 60 | 100 | 0 | . | . |

Parameter Estimates for Mixing Probabilities

| Effect | pht  | tcpo | Estimate | Error | z Value | Pr > |z| |
|--------|------|------|----------|-------|---------|-------|
| Intercept | -0.7394 | 0.5395 | -1.37 | 0.1705 |
| pht  | 0 | 0.4351 | 0.6203 | 0.70 | 0.4830 |
| pht  | 60 | 0 | . | . |
| tcpo | 0 | -0.5342 | 0.5893 | -0.91 | 0.3646 |
| tcpo | 100 | 0 | . | . |
| pht*tcpo | 0 | 1.4055 | 0.7080 | 1.99 | 0.0471 |
| pht*tcpo | 0 | 100 | 0 | . | . |
| pht*tcpo | 60 | 0 | 0 | . | . |
| pht*tcpo | 60 | 100 | 0 | . | . |

Table 37.12 computes the conditional probabilities in the four treatment groups. Recall that the previous model estimated a constant clustering probability of 0.5831.

Table 37.12  Estimates of Clustering Probabilities

<table>
<thead>
<tr>
<th>PHT</th>
<th>TCPO</th>
<th>$\hat{\eta}$</th>
<th>$\hat{\mu}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>0</td>
<td>1.8213–1.4962–3.1828+3.3736=0.5159</td>
<td>0.6262</td>
</tr>
<tr>
<td>60</td>
<td>0</td>
<td>1.8213–3.1828= -1.3615</td>
<td>0.2040</td>
</tr>
<tr>
<td>0</td>
<td>100</td>
<td>1.8213–1.4962=0.3251</td>
<td>0.5806</td>
</tr>
<tr>
<td>60</td>
<td>100</td>
<td>1.8213</td>
<td>0.8607</td>
</tr>
</tbody>
</table>
Example 37.1: Modeling Mixing Probabilities: All Mice Are Created Equal, but Some Are More Equal

The presence of phenytoin alone reduces the probability of response clustering within the litter. The presence of trichloropropene oxide alone does not have a strong effect on the clustering. The simultaneous presence of both agents substantially increases the probability of clustering.

The following statements fit the binomial cluster model in the parameterization of Morel and Neerchal (1997).

```
proc fmm data=ossi;
  model y/m = x1-x3 / dist=binomcluster;
  probmodel x1-x3;
run;
```

The model fit is the same as in the previous model (compare the “Fit Statistics” tables in Output 37.1.5 and Output 37.1.4). The parameter estimates change due to the reparameterization of the treatment effects and match the results in Table III of Morel and Neerchal (1997).

Output 37.1.5 Fit Statistics and Estimates (Morel and Neerchal Parameterization)

| Component | Effect | Estimate | Error | z Value | Pr > |z| |
|-----------|--------|----------|-------|---------|-------|
| 1         | Intercept | 0.5159 | 0.2603 | 1.98 | 0.0475 |
| 1         | x1 | -0.1908 | 0.4006 | -0.48 | 0.6339 |
| 1         | x2 | -1.8774 | 0.9946 | -1.89 | 0.0591 |
| 1         | x3 | 3.3736 | 1.1953 | 2.82 | 0.0048 |

| Effect | Estimate | Error | z Value | Pr > |z| |
|--------|----------|-------|---------|-------|
| Intercept | 0.5669 | 0.2455 | 2.31 | 0.0209 |
| x1 | -0.8712 | 0.3924 | -2.22 | 0.0264 |
| x2 | -1.8405 | 0.3413 | -5.39 | <.0001 |
| x3 | 1.4055 | 0.7080 | 1.99 | 0.0471 |

The following sets of statements fit the binomial and beta-binomial models, respectively, as single-component mixtures in the parameterization akin to the first binomial cluster model. Note that the model effects that affect the underlying Bernoulli success probabilities are specified in the MODELL statement, in contrast to the binomial cluster model.
The Pearson statistic for the beta-binomial model (Output 37.1.6) indicates a much better fit compared to the single-component binomial model (Output 37.1.7). This is not surprising since these data are obviously overdispersed relative to a binomial model because the Bernoulli outcomes are not independent. The difference between the binomial cluster and the beta-binomial model lies in the mechanism by which the correlations are induced:

- a mixing mechanism in the beta-binomial model that leads to a common shared random effect among all offspring in a cluster
- a mixture specification in the binomial cluster model that divides the offspring in a litter into identical and independent responders

**Output 37.1.6** Fit Statistics in Binomial Model

<table>
<thead>
<tr>
<th>The FMM Procedure</th>
<th>Fit Statistics</th>
</tr>
</thead>
<tbody>
<tr>
<td>-2 Log Likelihood</td>
<td>401.8</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
<td>409.8</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
<td>410.3</td>
</tr>
<tr>
<td>BIC (smaller is better)</td>
<td>419.4</td>
</tr>
<tr>
<td>Pearson Statistic</td>
<td>252.1</td>
</tr>
</tbody>
</table>

**Output 37.1.7** Fit Statistics in Beta-Binomial Model

<table>
<thead>
<tr>
<th>The FMM Procedure</th>
<th>Fit Statistics</th>
</tr>
</thead>
<tbody>
<tr>
<td>-2 Log Likelihood</td>
<td>306.6</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
<td>316.6</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
<td>317.4</td>
</tr>
<tr>
<td>BIC (smaller is better)</td>
<td>328.5</td>
</tr>
<tr>
<td>Pearson Statistic</td>
<td>87.5379</td>
</tr>
</tbody>
</table>
Example 37.2: The Usefulness of Custom Starting Values: When Do Cows Eat?

This example with a mixture of normal and Weibull distributions illustrates the benefits of specifying starting values for some of the components.

The data for this example were generously provided by Dr. Luciano A. Gonzalez of the Lethbridge Research Centre of Agriculture and Agri-Food Canada and his collaborator, Dr. Bert Tolkamp, from the Scottish Agricultural College.

The outcome variable of interest is the logarithm of a time interval between consecutive visits by cattle to feeders. The intervals fall into three categories:

- short breaks within meals—such as when an animal stops eating for a moment and resumes shortly thereafter
- somewhat longer breaks when eating is interrupted to go have a drink of water
- long breaks between meals

Modeling such time interval data is important to understand the feeding behavior and biology of the animals and to derive other biological parameters such as the probability of an animal to stop eating after it has consumed a certain amount of a given food. Because there are three distinct biological categories, data of this nature are frequently modeled as three-component mixtures. The point at which the second and third components cross over is used to separate feeding events into meals.

The original data set comprises 141,414 observations of log feeding intervals. For the purpose of presentation in this document, where space is limited, the data have been rounded to precision 0.05 and grouped by frequency. The following DATA step displays the modified data used in this example. A comparison with the raw data and the results obtained in a full analysis of the original data show that the grouping does not alter the presentation or conclusions in a way that matters for the purpose of this example.

data cattle;
  input LogInt Count @@;
datalines;
0.70 195 1.10 233 1.40 355 1.60 563
1.80 822 1.95 926 2.10 1018 2.20 1712
2.30 3190 2.40 2212 2.50 1692 2.55 1558
2.65 1622 2.70 1637 2.75 1568 2.85 1599
2.90 1575 2.95 1526 3.00 1537 3.05 1561
3.10 1555 3.15 1427 3.20 2852 3.25 1396
3.30 1343 3.35 2473 3.40 1310 3.45 2453
3.50 1168 3.55 2300 3.60 2174 3.65 2050
3.70 1926 3.75 1849 3.80 1687 3.85 2416
3.90 1449 3.95 2095 4.00 1278 4.05 1864
4.10 1672 4.15 2104 4.20 1443 4.25 1341
4.30 1685 4.35 1445 4.40 1369 4.45 1284
4.50 1523 4.55 1367 4.60 1027 4.65 1491
4.70 1057 4.75 1155 4.80 1095 4.85 1019
4.90 1158 4.95 1088 5.00 1075 5.05 912
If you scan the columns for the Count variable in the DATA step, the prevalence of values between 2 and 5 units of LogInt is apparent, as is a long right tail. To explore these data graphically, the following statements produce a histogram of the data and a kernel density estimate of the density of the LogInt variable.

```r
ods graphics on;
proc kde data=cattle;
  univar LogInt / bwm=4;
  freq count;
run;
```
Output 37.2.1 Histogram and Kernel Density for LogInt

Two modes are clearly visible in Output 37.2.1. Given the biological background, one would expect that three components contribute to the mixture. The histogram would suggest either a two-component mixture with modes near 4 and 9, or a three-component mixture with modes near 3, 5, and 9.

Following Dr. Gonzalez’ suggestion, the process is modeled as a three-component mixture of two normal distributions and a Weibull distribution. The Weibull distribution is chosen because it can have long left and right tails and it is popular in modeling data that relate to time intervals.

```
proc fmm data=cattle gconv=0;
  model LogInt = / dist=normal k=2 parms(3 1, 5 1);
  model + / dist=weibull;
  freq count;
run;
```

The GCONV= convergence criterion is turned off in this PROC FMM run to avoid the early stoppage of the iterations when the relative gradient changes little between iterations. Turning the criterion off usually ensures that convergence is achieved with a small absolute gradient of the objective function. The PARMS option in the first MODEL statement provides starting values for the means and variances for the parameters of the normal distributions. The means for the two components are started at \( \mu = 3 \) and \( \mu = 5 \), respectively. Specifying starting values is generally not necessary. However, the choice of starting values can play an
important role in modeling finite mixture models; the importance of the choice of starting values in this example is discussed further below.

The “Model Information” table shows that the model is a three-component mixture and that the FMM procedure considers the estimation of a density to be the purpose of modeling. The procedure draws this conclusion from the absence of effects in the MODEL statements. There are 187 observations in the data set, but these actually represent 141,414 measurements (Output 37.2.2).

**Output 37.2.2** Model Information and Number of Observations

<table>
<thead>
<tr>
<th>The FMM Procedure</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model Information</td>
</tr>
<tr>
<td>Data Set WORK.CATTLE</td>
</tr>
<tr>
<td>Response Variable LogInt</td>
</tr>
<tr>
<td>Frequency Variable Count</td>
</tr>
<tr>
<td>Type of Model Density Estimation</td>
</tr>
<tr>
<td>Components 3</td>
</tr>
<tr>
<td>Estimation Method Maximum Likelihood</td>
</tr>
<tr>
<td>Number of Observations Read 187</td>
</tr>
<tr>
<td>Number of Observations Used 187</td>
</tr>
<tr>
<td>Sum of Frequencies Read 141414</td>
</tr>
<tr>
<td>Sum of Frequencies Used 141414</td>
</tr>
</tbody>
</table>

There are eight parameters in the optimization: the means and variances of the two normal distributions, the $\mu$ and $\phi$ parameter of the Weibull distribution, and the two mixing probabilities (Output 37.2.3). At the converged solution, the $-2 \log$ likelihood is 563,153 and all parameters and components are effective—that is, the model is not overspecified in the sense that components have collapsed during the model fitting. The Pearson statistic is close to the number of observations in the data set, indicating a good fit.

**Output 37.2.3** Optimization Information and Fit Statistics

<table>
<thead>
<tr>
<th>Optimization Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Optimization Technique Dual Quasi-Newton</td>
</tr>
<tr>
<td>Parameters in Optimization 8</td>
</tr>
<tr>
<td>Mean Function Parameters 3</td>
</tr>
<tr>
<td>Scale Parameters 3</td>
</tr>
<tr>
<td>Mixing Prob Parameters 2</td>
</tr>
<tr>
<td>Lower Boundaries 3</td>
</tr>
<tr>
<td>Upper Boundaries 0</td>
</tr>
<tr>
<td>Number of Threads 2</td>
</tr>
</tbody>
</table>
**Example 37.2: The Usefulness of Custom Starting Values: When Do Cows Eat?**

**Output 37.2.3 continued**

<table>
<thead>
<tr>
<th>Fit Statistics</th>
</tr>
</thead>
<tbody>
<tr>
<td>-2 Log Likelihood</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
</tr>
<tr>
<td>BIC (smaller is better)</td>
</tr>
<tr>
<td>Pearson Statistic</td>
</tr>
<tr>
<td>Effective Parameters</td>
</tr>
<tr>
<td>Effective Components</td>
</tr>
</tbody>
</table>

Output 37.2.4 displays the parameter estimates for the three models and for the mixing probabilities. The order in which the “Parameter Estimates” tables appear in the output corresponds to the order in which the MODEL statements were specified.

**Output 37.2.4 Optimization Information and Fit Statistics**

<table>
<thead>
<tr>
<th>Parameter Estimates for 'Normal' Model</th>
</tr>
</thead>
<tbody>
<tr>
<td>Component</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>2</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>2</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Parameter Estimates for 'Weibull' Model</th>
</tr>
</thead>
<tbody>
<tr>
<td>Component</td>
</tr>
<tr>
<td>3</td>
</tr>
<tr>
<td>3</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Parameter Estimates for Mixing Probabilities</th>
</tr>
</thead>
<tbody>
<tr>
<td>Component</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>2</td>
</tr>
</tbody>
</table>

The estimated means of the two normal components are 3.3415 and 4.8940, respectively. Note that the means are displayed here as Intercept. The inverse linked estimate is not produced because the default link for the normal distribution is the identity link; hence the Estimate column represents the means of the component distributions. The parameter estimates in the Weibull model are \( \hat{\beta}_0 = 2.2531 \), \( \hat{\phi} = 0.06848 \), and \( \hat{\mu} = \exp(\hat{\beta}_0) = 9.5174 \). In the Weibull distribution, the \( \mu \) parameter does not estimate the mean of the distribution, the maximum likelihood estimate of the distribution’s mean is \( \hat{\mu} \Gamma(\hat{\phi} + 1) = 9.1828 \).
The estimated mixing probabilities are $\hat{\pi}_1 = 0.4545$, $\hat{\pi}_2 = 0.3435$, and $\hat{\pi}_3 = 1 - \hat{\pi}_1 - \hat{\pi}_2 = 0.2020$. In other words, the estimated distribution of log feeding intervals is a 45:35:20 mixture of an $\text{N}(3.3415, 0.6718)$, a $\text{N}(4.8940, 1.4497)$, and a Weibull$(9.5174, 0.06848)$ distribution.

You can obtain a graphical display of the observed and estimated distribution of these data by enabling ODS Graphics. The PLOTS option in the PROC FMM statement modifies the default density plot by adding the densities of the mixture components:

```plaintext
ods select DensityPlot;
proc fmm data=cattle gconv=0;
   model LogInt = / dist=normal k=2 parms(3 1, 5 1);
   model + / dist=weibull;
   freq count;
run;
```

**Output 37.2.5** Observed and Estimated Densities in the Three-Component Model

The estimated mixture density matches the histogram of the observed data closely (Output 37.2.5). The component densities are displayed in such a way that, at each point in the support of the LogInt variable, their sum combines to the overall mixture density. The three components in the mixtures are well separated.

The excellent quality of the fit is even more evident when the distributions are displayed cumulatively by
adding the CUMULATIVE option in the DENSITY option (Output 37.2.6):

```
ods select DensityPlot;
proc fmm data=cattle plot=density(cumulative) gconv=0;
   model LogInt = / dist=normal k=2 parms(3 1, 5 1);
   model + / dist=weibull;
   freq count;
run;
```

The component cumulative distribution functions are again scaled so that their sum produces the overall mixture cumulative distribution function. Because of this scaling, the percentage reached at the maximum value of LogInt corresponds to the mixing probabilities in Output 37.2.4.

**Output 37.2.6** Observed and Estimated Cumulative Densities in the Three-Component Model

![Empirical and Estimated Cumulative Density for LogInt](image)

The importance of starting values for the parameter estimates was mentioned previously. Suppose that different starting values are selected for the three components (for example, the default starting values).

```
proc fmm data=cattle gconv=0;
   model LogInt = / dist=normal k=2;
   model + / dist=weibull;
   freq count;
run;
ods graphics off;
```
The fit statistics and parameter estimates from this run are displayed in Output 37.2.7, and the density plot is shown in Output 37.2.8.

**Output 37.2.7** Fit Statistics and Parameter Estimates

```
| Component | Parameter | Estimate | Error  | z Value | Pr > |z| |
|-----------|-----------|----------|--------|---------|-------|--------|
| 1         | Intercept | 4.9106   | 0.02604| 188.56  | <.0001|
| 2         | Intercept | 9.2883   | 0.005031| 1846.28| <.0001|
| 1         | Variance  | 1.7410   | 0.02753 |         |       |
| 2         | Variance  | 0.4158   | 0.005086|         |       |
```

Parameter Estimates for 'Normal' Model

Parameter Estimates for 'Weibull' Model

```
| Component | Parameter | Standard Estimate | Error  | z Value | Pr > |z| Estimate |
|-----------|-----------|-------------------|--------|---------|-------|---------|
| 3         | Intercept | 1.2908            | 0.002790| 462.71  | <.0001| 3.6358  |
| 3         | Scale     | 0.2093            | 0.001311|         |       |         |
```

Parameter Estimates for Mixing Probabilities

```
| Component | Parameter | Standard Estimate | Error  | z Value | Pr > |z| Probability |
|-----------|-----------|-------------------|--------|---------|-------|-------------|
| 1         | Probability | -0.1505       | 0.03678| -4.09   | <.0001| 0.3745     |
| 2         | Probability | -0.8280       | 0.01922| -43.08  | <.0001| 0.1902     |
```

All components are active; no collapsing of components occurred. However, a closer look at the “Parameter Estimates” tables in Output 37.2.7 shows an important difference from the tables in Output 37.2.4. The means of the two normal distributions are now 4.9106 and 9.2883. Previously, the means were 3.3415 and 4.8940. The “position” of the Weibull distribution has moved from right to left, and the third component is now modeled by a symmetric normal distribution (Output 37.2.8). The mixture probabilities have also changed—in particular, for the first and third component.
Such switching is not uncommon in mixture modeling. As judged by the information criteria, the model in which the Weibull distribution is the component with the smallest mean does not fit the data as well as the first model in which the specification of the starting values guided the optimization towards placing the normal distributions first. The converged solution found in the last FMM run represents a local minimum of the log-likelihood surface. There are other local minima—for example, when components are removed from the model, which is tantamount to estimating the associated mixture probabilities as zero.

**Example 37.3: Enforcing Homogeneity Constraints: Count and Dispersion—It Is All Over!**

The following example demonstrates how you can use either the EQUATE= option in the MODEL statement or the RESTRICT statement to impose homogeneity constraints on chosen model effects.

The data for this example were presented by Margolin, Kaplan, and Zeiger (1981) and analyzed by various authors applying a number of techniques. The following DATA step shows the number of revertant
salmonella colonies (variable `num`) at six levels of quinoline dosing (variable `dose`). There are three replicate plates at each dose of quinoline.

```sas
data assay;
  label dose = 'Dose of quinoline (microg/plate)'
     num = 'Observed number of colonies';
  input dose @;
  logd = log(dose+10);
  do i=1 to 3; input num@; output; end;
  datalines;
  0 15 21 29
  10 16 18 21
  33 16 26 33
  100 27 41 60
  333 33 38 41
  1000 20 27 42
;
```

The basic notion is that the data are overdispersed relative to a Poisson distribution in which the logarithm of the mean count is modeled as a linear regression in dose (in $\mu g$/plate) and in the derived variable $\log(dose + 10)$ (Lawless 1987). The log of the expected count of revertants is thus

$$\beta_0 + \beta_1 dose + \beta_2 \log(dose + 10)$$

The following statements fit a standard Poisson regression model to these data:

```sas
proc fmm data=assay;
  model num = dose logd / dist=Poisson;
run;
```

The Pearson statistic for this model is rather large compared to the number of degrees of freedom ($18 - 3 = 15$). The ratio 46.2707/15 = 3.08 indicates an overdispersion problem in the Poisson model (Output 37.3.1).

**Output 37.3.1 Result of Fitting Poisson Regression Models**

<table>
<thead>
<tr>
<th>The FMM Procedure</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Observations Read</td>
</tr>
<tr>
<td>Number of Observations Used</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Fit Statistics</th>
</tr>
</thead>
<tbody>
<tr>
<td>-2 Log Likelihood</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
</tr>
<tr>
<td>BIC (smaller is better)</td>
</tr>
<tr>
<td>Pearson Statistic</td>
</tr>
</tbody>
</table>
Example 37.3: Enforcing Homogeneity Constraints: Count and Dispersion—It Is All Over!

Output 37.3.1 continued

| Parameter Estimates for 'Poisson' Model |
|-----------------|--------|---------|--------|--------|
| Effect          | Estimate | Standard Error | z Value | Pr > |z|
| Intercept       | 2.1728  | 0.2184   | 9.95   | <.0001|
| dose            | -0.00101| 0.000245 | -4.13  | <.0001|
| logd            | 0.3198  | 0.05700  | 5.61   | <.0001|

Breslow (1984) accounts for overdispersion by including a random effect in the predictor for the log rate and applying a quasi-likelihood technique to estimate the parameters. Wang et al. (1996) examine these data using mixtures of Poisson regression models. They fit several two- and three-component Poisson regression mixtures. Examining the log likelihoods, AIC, and BIC criteria, they eventually settle on a two-component model in which the intercepts vary by category and the regression coefficients are the same. This mixture model can be written as

\[
\begin{align*}
  f(y) &= \pi \frac{1}{y!} \lambda_1^y \exp\{-\lambda_1\} + (1 - \pi) \frac{1}{y!} \lambda_2^y \exp\{-\lambda_2\} \\
  \lambda_1 &= \exp\{\beta_{01} + \beta_1 \text{dose} + \beta_2 \log\{\text{dose} + 10\}\} \\
  \lambda_2 &= \exp\{\beta_{02} + \beta_1 \text{dose} + \beta_2 \log\{\text{dose} + 10\}\}
\end{align*}
\]

This model is fit with the FMM procedure with the following statements:

```plaintext
proc fmm data=assay;
  model num = dose logd / dist=Poisson k=2
              equate=effects(dose logd);
run;
```

The `EQUATE=` option in the `MODEL` statement places constraints on the optimization and makes the coefficients for `dose` and `logd` homogeneous across components in the model. Output 37.3.2 displays the “Fit Statistics” and parameter estimates in the mixture. The Pearson statistic is drastically reduced compared to the Poisson regression model in Output 37.3.1. With \(18 - 5 = 13\) degrees of freedom, the ratio of the Pearson and the degrees of freedom is now \(16.1573/13 = 1.2429\). Note that the effective number of parameters was used to compute the degrees of freedom, not the total number of parameters, because of the equality constraints.
Output 37.3.2 Result for Two-Component Poisson Regression Mixture

The FMM Procedure

Fit Statistics

-2 Log Likelihood 121.8
AIC (smaller is better) 131.8
AICC (smaller is better) 136.8
BIC (smaller is better) 136.3
Pearson Statistic 16.1573
Effective Parameters 5
Effective Components 2

Parameter Estimates for 'Poisson' Model

| Component | Effect | Estimate | Error  | z Value | Pr > |z| |
|-----------|--------|----------|--------|---------|-------|---|
| 1         | Intercept | 1.9097  | 0.2654  | 7.20     | <.0001 |
| 1         | dose     | -0.00126| 0.000273| -4.62    | <.0001 |
| 1         | logd     | 0.3639  | 0.06602 | 5.51     | <.0001 |
| 2         | Intercept | 2.4770  | 0.2731  | 9.07     | <.0001 |
| 2         | dose     | -0.00126| 0.000273| -4.62    | <.0001 |
| 2         | logd     | 0.3639  | 0.06602 | 5.51     | <.0001 |

Parameter Estimates for Mixing Probabilities

---------------Linked Scale---------------

| Effect | Estimate | Error  | z Value | Pr > |z| Probability |
|--------|----------|--------|---------|-------|--------------|
| Intercept | 1.4984  | 0.6875 | 2.18    | 0.0293 | 0.8173       |

You could also have used RESTRICT statements to impose the homogeneity constraints on the model fit, as shown in the following statements:

```
proc fmm data=assay;
  model num = dose logd / dist=Poisson k=2;
  restrict 'common dose' dose 1, dose -1;
  restrict 'common logd' logd 1, logd -1;
run;
```

The first RESTRICT statement equates the coefficients for the dose variable in the two components, and the second RESTRICT statement accomplishes the same for the coefficients of the logd variable. If the right-hand side of a restriction is not specified, PROC FMM defaults to equating the left-hand side of the restriction to zero. The “Linear Constraints” table in Output 37.3.3 shows that both linear equality constraints are active. The parameter estimates match the previous FMM run.
Example 37.3: Enforcing Homogeneity Constraints: Count and Dispersion—It Is All Over!

Output 37.3.3 Result for Two-Component Mixture with RESTRICT Statements

The FMM Procedure
Linear Constraints at Solution

<table>
<thead>
<tr>
<th>k = 1</th>
<th>k = 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Label</td>
<td>Constraint</td>
</tr>
<tr>
<td>common dose</td>
<td>dose - dose = 0</td>
</tr>
<tr>
<td>common logd</td>
<td>logd - logd = 0</td>
</tr>
</tbody>
</table>

Parameter Estimates for 'Poisson' Model

| Component | Effect  | Estimate | Error | z Value | Pr > |z| |
|-----------|---------|----------|-------|---------|-------|
| 1 Intercept | 1.9097 | 0.2654 | 7.20 | <.0001 |
| 1 dose | -0.00126 | 0.000273 | -4.62 | <.0001 |
| 1 logd | 0.3639 | 0.06602 | 5.51 | <.0001 |
| 2 Intercept | 2.4770 | 0.2731 | 9.07 | <.0001 |
| 2 dose | -0.00126 | 0.000273 | -4.62 | <.0001 |
| 2 logd | 0.3639 | 0.06602 | 5.51 | <.0001 |

Parameter Estimates for Mixing Probabilities

| Effect | Estimate | Error | z Value | Pr > |z| Probability |
|--------|----------|-------|---------|-------|-------------|
| Intercept | 1.4984 | 0.6875 | 2.18 | 0.0293 | 0.8173 |

Wang et al. (1996) note that observation 12 with a revertant colony count of 60 is comparably high. The following statements remove the observation from the analysis and fit their selected model:

```plaintext
proc fmm data=assay(where=(num ne 60));
  model num = dose logd / dist=Poisson k=2
    equate=effects(dose logd);
run;
```

Output 37.3.4 Result for Two-Component Model without Outlier

The FMM Procedure
Fit Statistics

| Effect | Estimate | Error | z Value | Pr > |z| Probability |
|--------|----------|-------|---------|-------|-------------|
| Intercept | 1.4984 | 0.6875 | 2.18 | 0.0293 | 0.8173 |
The ratio of Pearson Statistic over degrees of freedom (12) is only slightly worse than in the previous model; the loss of 5% of the observations carries a price (Output 37.3.4). The parameter estimates for the two intercepts are now fairly close. If the intercepts were identical, then the two-component model would collapse to the Poisson regression model:

```plaintext
proc fmm data=assay(where=(num ne 60));
   model num = dose logd / dist=Poisson;
run;
```

**Output 37.3.5** Result of Fitting Poisson Regression Model without Outlier
Compared to the same model applied to the full data, the Pearson statistic is much reduced (compare 46.2707 in Output 37.3.1 to 27.8008 in Output 37.3.5). The outlier—or overcount, if you will—induces at least some of the overdispersion.

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