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SAS/STAT® 9.2 User's Guide

The GENMOD Procedure

(Book Excerpt)

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Chapter 37

The GENMOD Procedure

Contents

Overview: GENMOD Procedure

The GENMOD procedure fits generalized linear models, as defined by Nelder and Wedderburn (1972). The class of generalized linear models is an extension of traditional linear models that allows the mean of a population to depend on a *linear predictor* through a nonlinear *link function* and allows the response probability distribution to be any member of an exponential family of distributions. Many widely used statistical models are generalized linear models. These include classical linear models with normal errors, logistic and probit models for binary data, and log-linear models for multinomial data. Many other useful statistical models can be formulated as generalized linear models by the selection of an appropriate link function and response probability distribution.

See McCullagh and Nelder (1989) for a discussion of statistical modeling using generalized linear models. The books by Aitkin et al. (1989) and Dobson (1990) are also excellent references with many examples of applications of generalized linear models. Firth (1991) provides an overview of generalized linear models.

The analysis of correlated data arising from repeated measurements when the measurements are assumed to be multivariate normal has been studied extensively. However, the normality assumption might not always be reasonable; for example, different methodology must be used in the data analysis when the responses are discrete and correlated. Generalized estimating equations (GEEs) provide a practical method with reasonable statistical efficiency to analyze such data.

Liang and Zeger (1986) introduced GEEs as a method of dealing with correlated data when, except for the correlation among responses, the data can be modeled as a generalized linear model. For example, correlated binary and count data in many cases can be modeled in this way.

The GENMOD procedure can fit models to correlated responses by the GEE method. You can use PROC GENMOD to fit models with most of the correlation structures from Liang and Zeger (1986) by using GEEs. See Hardin and Hilbe (2003), Diggle, Liang, and Zeger (1994), and Lipsitz et al. (1994) for more details on GEEs.

Bayesian analysis of generalized linear models can be requested by using the BAYES statement in the GENMOD procedure. In Bayesian analysis, the model parameters are treated as random variables, and inference about parameters is based on the posterior distribution of the parameters, given the data. The posterior distribution is obtained using Bayes' theorem as the likelihood function of the data weighted with a prior distribution. The prior distribution enables you to incorporate knowledge or experience of the likely range of values of the parameters of interest into the analysis. If you have no prior knowledge of the parameter values, you can use a noninformative prior distribution, and the results of the Bayesian analysis will be very similar to a classical analysis based on maximum likelihood. A closed form of the posterior distribution is often not feasible, and a Markov chain Monte Carlo method by Gibbs sampling is used to simulate samples from the posterior distribution. See Chapter 7, "Introduction to Bayesian Analysis Procedures," for an introduction to the basic concepts of Bayesian statistics. Also see the section "Bayesian Analysis: Advantages and Disadvantages" on page 149 for a discussion of the advantages and disadvantages of Bayesian analysis. See Ibrahim, Chen, and Sinha (2001) for a detailed description of Bayesian analysis.

In a Bayesian analysis, a Gibbs chain of samples from the posterior distribution is generated for the model parameters. Summary statistics (mean, standard deviation, quartiles, HPD and credible intervals, correlation matrix) and convergence diagnostics (autocorrelations; Gelman-Rubin, Geweke, Raftery-Lewis, and Heidelberger and Welch tests; the effective sample size; and Monte Carlo standard errors) are computed for each parameter, as well as the correlation matrix and the covariance matrix of the posterior sample. Trace plots, posterior density plots, and autocorrelation function plots that are created using ODS Graphics are also provided for each parameter.

The GENMOD procedure now uses ODS Graphics to create graphs as part of its output. For general information about ODS Graphics, see Chapter 21, "Statistical Graphics Using ODS."

What Is a Generalized Linear Model?

A traditional linear model is of the form

$$y_i = \mathbf{x}_i'\boldsymbol{\beta} + \varepsilon_i$$

where y_i is the response variable for the ith observation. The quantity $\mathbf{x}_i$ is a column vector of covariates, or explanatory variables, for observation i that is known from the experimental setting and is considered to be fixed, or nonrandom. The vector of unknown coefficients $\boldsymbol{\beta}$ is estimated by a least squares fit to the data $\mathbf{y}$. The ε_i are assumed to be independent, normal random variables with zero mean and constant variance. The expected value of y_i, denoted by μ_i, is

$$\mu_i = \mathbf{x}_i'\boldsymbol{\beta}$$

While traditional linear models are used extensively in statistical data analysis, there are types of problems such as the following for which they are not appropriate.

- It might not be reasonable to assume that data are normally distributed. For example, the normal distribution (which is continuous) might not be adequate for modeling counts or measured proportions that are considered to be discrete.
- If the mean of the data is naturally restricted to a range of values, the traditional linear model might not be appropriate, since the linear predictor $\mathbf{x}_i'\boldsymbol{\beta}$ can take on any value. For example, the mean of a measured proportion is between 0 and 1, but the linear predictor of the mean in a traditional linear model is not restricted to this range.
- It might not be realistic to assume that the variance of the data is constant for all observations. For example, it is not unusual to observe data where the variance increases with the mean of the data.

A generalized linear model extends the traditional linear model and is therefore applicable to a wider range of data analysis problems. A generalized linear model consists of the following components:

- The linear component is defined just as it is for traditional linear models:

  $$\eta_i = \mathbf{x}_i'\boldsymbol{\beta}$$

- A monotonic differentiable link function g describes how the expected value of y_i is related to the linear predictor η_i:

  $$g(\mu_i) = \mathbf{x}_i'\boldsymbol{\beta}$$

- The response variables y_i are independent for $i = 1, 2, \ldots$ and have a probability distribution from an exponential family. This implies that the variance of the response depends on the mean μ through a *variance function* V:

  $$var(y_i) = \frac{\phi V(\mu_i)}{w_i}$$

  where ϕ is a constant and w_i is a known weight for each observation. The *dispersion parameter* ϕ is either known (for example, for the binomial or Poisson distribution, $\phi = 1$) or must be estimated.

See the section "Response Probability Distributions" on page 1962 for the form of a probability distribution from the exponential family of distributions.

As in the case of traditional linear models, fitted generalized linear models can be summarized through statistics such as parameter estimates, their standard errors, and goodness-of-fit statistics. You can also make statistical inference about the parameters by using confidence intervals and hypothesis tests. However, specific inference procedures are usually based on asymptotic considerations, since exact distribution theory is not available or is not practical for all generalized linear models.

Examples of Generalized Linear Models

You construct a generalized linear model by deciding on response and explanatory variables for your data and choosing an appropriate link function and response probability distribution. Some examples of generalized linear models follow. Explanatory variables can be any combination of continuous variables, classification variables, and interactions.

Traditional Linear Model

- response variable: a continuous variable
- distribution: normal
- link function: identity $g(\mu) = \mu$

Logistic Regression

- response variable: a proportion
- distribution: binomial
- link function: logit $g(\mu) = \log\left(\frac{\mu}{1-\mu}\right)$

Poisson Regression in Log-Linear Model

- response variable: a count
- distribution: Poisson
- link function: log $g(\mu) = \log(\mu)$

Gamma Model with Log Link

- response variable: a positive, continuous variable

- distribution: gamma
- link function: $\log g(\mu) = \log(\mu)$

The GENMOD Procedure

The GENMOD procedure fits a generalized linear model to the data by maximum likelihood estimation of the parameter vector $\boldsymbol{\beta}$. There is, in general, no closed form solution for the maximum likelihood estimates of the parameters. The GENMOD procedure estimates the parameters of the model numerically through an iterative fitting process. The dispersion parameter ϕ is also estimated by maximum likelihood or, optionally, by the residual deviance or by Pearson's chi-square divided by the degrees of freedom. Covariances, standard errors, and p-values are computed for the estimated parameters based on the asymptotic normality of maximum likelihood estimators.

A number of popular link functions and probability distributions are available in the GENMOD procedure. The built-in link functions are as follows:

- identity: $g(\mu) = \mu$
- logit: $g(\mu) = \log(\mu/(1-\mu))$
- probit: $g(\mu) = \Phi^{-1}(\mu)$, where Φ is the standard normal cumulative distribution function
- power: $g(\mu) = \begin{cases} \mu^{\lambda} & \text{if } \lambda \neq 0 \\ \log(\mu) & \text{if } \lambda = 0 \end{cases}$
- log: $g(\mu) = \log(\mu)$
- complementary log-log: $g(\mu) = \log(-\log(1-\mu))$

The available distributions and associated variance functions are as follows:

- normal: $V(\mu) = 1$
- binomial (proportion): $V(\mu) = \mu(1-\mu)$
- Poisson: $V(\mu) = \mu$
- gamma: $V(\mu) = \mu^2$
- inverse Gaussian: $V(\mu) = \mu^3$
- negative binomial: $V(\mu) = \mu + k\mu^2$
- geometric: $V(\mu) = \mu + \mu^2$
- multinomial
- zero-inflated Poisson

The negative binomial is a distribution with an additional parameter k in the variance function. PROC GENMOD estimates k by maximum likelihood, or you can optionally set it to a constant value. See McCullagh and Nelder (1989), Hilbe (1994), or Lawless (1987) for discussions of the negative binomial distribution.

The multinomial distribution is sometimes used to model a response that can take values from a number of categories. The binomial is a special case of the multinomial with two categories. See the section "Multinomial Models" on page 1982 and McCullagh and Nelder (1989, Chapter 5) for a description of the multinomial distribution.

The zero-inflated Poisson is included in PROC GENMOD even though it is not a generalized linear model. It is a useful extension of generalized linear models. See the section "Zero-Inflated Poisson Models" on page 1983 for information about the zero-inflated Poisson.

In addition, you can easily define your own link functions or distributions through DATA step programming statements used within the procedure.

An important aspect of generalized linear modeling is the selection of explanatory variables in the model. Changes in goodness-of-fit statistics are often used to evaluate the contribution of subsets of explanatory variables to a particular model. The deviance, defined to be twice the difference between the maximum attainable log likelihood and the log likelihood of the model under consideration, is often used as a measure of goodness of fit. The maximum attainable log likelihood is achieved with a model that has a parameter for every observation. See the section "Goodness of Fit" on page 1968 for formulas for the deviance.

One strategy for variable selection is to fit a sequence of models, beginning with a simple model with only an intercept term, and then to include one additional explanatory variable in each successive model. You can measure the importance of the additional explanatory variable by the difference in deviances or fitted log likelihoods between successive models. Asymptotic tests computed by the GENMOD procedure enable you to assess the statistical significance of the additional term.

The GENMOD procedure enables you to fit a sequence of models, up through a maximum number of terms specified in a MODEL statement. A table summarizes twice the difference in log likelihoods between each successive pair of models. This is called a *Type 1* analysis in the GENMOD procedure, because it is analogous to Type I (sequential) sums of squares in the GLM procedure. As with the PROC GLM Type I sums of squares, the results from this process depend on the order in which the model terms are fit.

The GENMOD procedure also generates a *Type 3* analysis analogous to Type III sums of squares in the GLM procedure. A Type 3 analysis does not depend on the order in which the terms for the model are specified. A GENMOD procedure Type 3 analysis consists of specifying a model and computing likelihood ratio statistics for Type III contrasts for each term in the model. The contrasts are defined in the same way as they are in the GLM procedure. The GENMOD procedure optionally computes Wald statistics for Type III contrasts. This is computationally less expensive than likelihood ratio statistics, but it is thought to be less accurate because the specified significance level of hypothesis tests based on the Wald statistic might not be as close to the actual significance level as it is for likelihood ratio tests.

A Type 3 analysis generalizes the use of Type III estimable functions in linear models. Briefly, a Type III estimable function (contrast) for an effect is a linear function of the model parameters that involves the parameters of the effect and any interactions with that effect. A test of the hypothesis

that the Type III contrast for a main effect is equal to 0 is intended to test the significance of the main effect in the presence of interactions. See Chapter 39, "The GLM Procedure," and Chapter 15, "The Four Types of Estimable Functions," for more information about Type III estimable functions. Also refer to Littell, Freund, and Spector (1991).

Additional features of the GENMOD procedure include the following:

- likelihood ratio statistics for user-defined contrasts—that is, linear functions of the parameters and p-values based on their asymptotic chi-square distributions
- estimated values, standard errors, and confidence limits for user-defined contrasts and least squares means
- ability to create a SAS data set corresponding to most tables displayed by the procedure (see Table 37.4 and Table 37.5)
- confidence intervals for model parameters based on either the profile likelihood function or asymptotic normality
- syntax similar to that of PROC GLM for the specification of the response and model effects, including interaction terms and automatic coding of classification variables
- ability to fit GEE models for clustered response data
- ability to perform Bayesian analysis by Gibbs sampling

Getting Started: GENMOD Procedure

Poisson Regression

You can use the GENMOD procedure to fit a variety of statistical models. A typical use of PROC GENMOD is to perform Poisson regression.

You can use the Poisson distribution to model the distribution of cell counts in a multiway contingency table. Aitkin et al. (1989) have used this method to model insurance claims data. Suppose the following hypothetical insurance claims data are classified by two factors: age group (with two levels) and car type (with three levels).

```
data insure;
   input n c car$ age;
   ln = log(n);
   datalines;
500   42  small  1
1200  37  medium 1
100    1  large  1
400  101  small  2
500   73  medium 2
300   14  large  2
;
run;
```

In the preceding data set, the variable n represents the number of insurance policyholders and the variable c represents the number of insurance claims. The variable car is the type of car involved (classified into three groups) and the variable age is the age group of a policyholder (classified into two groups).

You can use PROC GENMOD to perform a Poisson regression analysis of these data with a log link function. This type of model is sometimes called a *log-linear model*.

Assume that the number of claims c has a Poisson probability distribution and that its mean, μ_i, is related to the factors car and age for observation i by

$$\begin{aligned}\log(\mu_i) &= \log(\mathsf{n}_i) + \mathbf{x}_i'\boldsymbol{\beta} \\ &= \log(\mathsf{n}_i) + \beta_0 + \\ &\quad \mathsf{car}_i(1)\beta_1 + \mathsf{car}_i(2)\beta_2 + \mathsf{car}_i(3)\beta_3 + \\ &\quad \mathsf{age}_i(1)\beta_4 + \mathsf{age}_i(2)\beta_5\end{aligned}$$

The indicator variables $\mathsf{car}_i(j)$ and $\mathsf{age}_i(j)$ are associated with the jth level of the variables car and age for observation i

$$\mathsf{car}_i(j) = \begin{cases} 1 & \text{if car} = j \\ 0 & \text{if car} \neq j \end{cases}$$

The βs are unknown parameters to be estimated by the procedure. The logarithm of the variable n is used as an *offset*—that is, a regression variable with a constant coefficient of 1 for each observation. A log-linear relationship between the mean and the factors car and age is specified by the log link function. The log link function ensures that the mean number of insurance claims for each car and age group predicted from the fitted model is positive.

The following statements invoke the GENMOD procedure to perform this analysis:

```
proc genmod data=insure;
   class car age;
   model c = car age / dist   = poisson
                       link   = log
                       offset = ln;
run;
```

The variables car and age are specified as CLASS variables so that PROC GENMOD automatically generates the indicator variables associated with car and age.

The MODEL statement specifies c as the response variable and car and age as explanatory variables. An intercept term is included by default. Thus, the model matrix $\mathbf{X}$ (the matrix that has as its ith row the transpose of the covariate vector for the ith observation) consists of a column of 1s representing the intercept term and columns of 0s and 1s derived from indicator variables representing the levels of the car and age variables.

That is, the model matrix is

$$\mathbf{X} = \left[\begin{array}{c|ccc|cc} 1 & 1 & 0 & 0 & 1 & 0 \\ 1 & 0 & 1 & 0 & 1 & 0 \\ 1 & 0 & 0 & 1 & 1 & 0 \\ 1 & 1 & 0 & 0 & 0 & 1 \\ 1 & 0 & 1 & 0 & 0 & 1 \\ 1 & 0 & 0 & 1 & 0 & 1 \end{array}\right]$$

where the first column corresponds to the intercept, the next three columns correspond to the variable car, and the last two columns correspond to the variable age.

The response distribution is specified as Poisson, and the link function is chosen to be log. That is, the Poisson mean parameter μ is related to the linear predictor by

$$\log(\mu) = \mathbf{x}_i'\boldsymbol{\beta}$$

The logarithm of n is specified as an offset variable, as is common in this type of analysis. In this case, the offset variable serves to normalize the fitted cell means to a per-policyholder basis, since the total number of claims, not individual policyholder claims, is observed.

PROC GENMOD produces the following default output from the preceding statements.

Figure 37.1 Model Information

```
                    The GENMOD Procedure

                     Model Information

Data Set                     WORK.INSURE
Distribution                     Poisson
Link Function                        Log
Dependent Variable                     c
Offset Variable                       ln
```

The "Model Information" table displayed in Figure 37.1 provides information about the specified model and the input data set.

Figure 37.2 Class Level Information

Class Level Information

Class	Levels	Values
car	3	large medium small
age	2	1 2

Figure 37.2 displays the "Class Level Information" table, which identifies the levels of the classification variables that are used in the model. Note that car is a character variable, and the values are sorted in alphabetical order. This is the default sort order, but you can select different sort orders with the ORDER= option in the PROC GENMOD statement.

Figure 37.3 Goodness of Fit

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	2	2.8207	1.4103
Scaled Deviance	2	2.8207	1.4103
Pearson Chi-Square	2	2.8416	1.4208
Scaled Pearson X2	2	2.8416	1.4208
Log Likelihood		837.4533	
Full Log Likelihood		-16.4638	
AIC (smaller is better)		40.9276	
AICC (smaller is better)		80.9276	
BIC (smaller is better)		40.0946	

The "Criteria For Assessing Goodness Of Fit" table displayed in Figure 37.3 contains statistics that summarize the fit of the specified model. These statistics are helpful in judging the adequacy of a model and in comparing it with other models under consideration. If you compare the deviance of 2.8207 with its asymptotic chi-square with 2 degrees of freedom distribution, you find that the p-value is 0.24. This indicates that the specified model fits the data reasonably well.

Figure 37.4 Analysis of Parameter Estimates

Analysis Of Maximum Likelihood Parameter Estimates

Parameter		DF	Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square
Intercept		1	−1.3168	0.0903	−1.4937	−1.1398	212.73
car	large	1	−1.7643	0.2724	−2.2981	−1.2304	41.96
car	medium	1	−0.6928	0.1282	−0.9441	−0.4414	29.18
car	small	0	0.0000	0.0000	0.0000	0.0000	.
age	1	1	−1.3199	0.1359	−1.5863	−1.0536	94.34
age	2	0	0.0000	0.0000	0.0000	0.0000	.
Scale		0	1.0000	0.0000	1.0000	1.0000	

Analysis Of Maximum Likelihood Parameter Estimates

Parameter		Pr > ChiSq
Intercept		<.0001
car	large	<.0001
car	medium	<.0001
car	small	.
age	1	<.0001
age	2	.
Scale		

NOTE: The scale parameter was held fixed.

Figure 37.4 displays the "Analysis Of Parameter Estimates" table, which summarizes the results of the iterative parameter estimation process. For each parameter in the model, PROC GENMOD displays columns with the parameter name, the degrees of freedom associated with the parameter, the estimated parameter value, the standard error of the parameter estimate, the confidence intervals, and the Wald chi-square statistic and associated p-value for testing the significance of the parameter to the model. If a column of the model matrix corresponding to a parameter is found to be linearly dependent, or *aliased*, with columns corresponding to parameters preceding it in the model, PROC GENMOD assigns it zero degrees of freedom and displays a value of zero for both the parameter estimate and its standard error.

This table includes a row for a scale parameter, even though there is no free scale parameter in the Poisson distribution. See the section "Response Probability Distributions" on page 1962 for the form of the Poisson probability distribution. PROC GENMOD allows the specification of a scale parameter to fit overdispersed Poisson and binomial distributions. In such cases, the SCALE row indicates the value of the overdispersion scale parameter used in adjusting output statistics. See the section "Overdispersion" on page 1971 for more about overdispersion and the meaning of the SCALE parameter output by the GENMOD procedure. PROC GENMOD displays a note indicating that the scale parameter is fixed—that is, not estimated by the iterative fitting process.

It is usually of interest to assess the importance of the main effects in the model. Type 1 and Type 3 analyses generate statistical tests for the significance of these effects. You can request these analyses with the TYPE1 and TYPE3 options in the MODEL statement, as follows:

```
proc genmod data=insure;
   class car age;
   model c = car age / dist   = poisson
                       link   = log
                       offset = ln
                       type1
                       type3;
run;
```

The results of these analyses are summarized in the figures that follow.

Figure 37.5 Type 1 Analysis

The GENMOD Procedure

LR Statistics For Type 1 Analysis

Source	Deviance	DF	Chi-Square	Pr > ChiSq
Intercept	175.1536			
car	107.4620	2	67.69	<.0001
age	2.8207	1	104.64	<.0001

In the table for Type 1 analysis displayed in Figure 37.5, each entry in the deviance column represents the deviance for the model containing the effect for that row and all effects preceding it in the table. For example, the deviance corresponding to car in the table is the deviance of the model containing an intercept and car. As more terms are included in the model, the deviance decreases.

Entries in the chi-square column are likelihood ratio statistics for testing the significance of the effect added to the model containing all the preceding effects. The chi-square value of 67.69 for car represents twice the difference in log likelihoods between fitting a model with only an intercept term and a model with an intercept and car. Since the scale parameter is set to 1 in this analysis, this is equal to the difference in deviances. Since two additional parameters are involved, this statistic can be compared with a chi-square distribution with two degrees of freedom. The resulting p-value (labeled Pr>Chi) of less than 0.0001 indicates that this variable is highly significant. Similarly, the chi-square value of 104.64 for age represents the difference in log likelihoods between the model with the intercept and car and the model with the intercept, car, and age. This effect is also highly significant, as indicated by the small p-value.

Figure 37.6 Type 3 Analysis

LR Statistics For Type 3 Analysis

Source	DF	Chi-Square	Pr > ChiSq
car	2	72.82	<.0001
age	1	104.64	<.0001

The Type 3 analysis results in the same conclusions as the Type 1 analysis. The Type 3 chi-square value for the car variable, for example, is twice the difference between the log likelihood for the model with the variables Intercept, car, and age included and the log likelihood for the model with the car variable excluded. The hypothesis tested in this case is the significance of the variable car given that the variable age is in the model. In other words, it tests the additional contribution of car in the model.

The values of the Type 3 likelihood ratio statistics for the car and age variables indicate that both of these factors are highly significant in determining the claims performance of the insurance policyholders.

Bayesian Analysis of a Linear Regression Model

Neter et al. (1996) describe a study of 54 patients undergoing a certain kind of liver operation in a surgical unit. The data set Surg contains survival time and certain covariates for each patient. Observations for the first 20 patients in the data set Surg are shown in Figure 37.7.

Figure 37.7 Surgical Unit Data

Obs	x1	x2	x3	x4	y	logy	Logx1
1	6.7	62	81	2.59	200	2.3010	1.90211
2	5.1	59	66	1.70	101	2.0043	1.62924
3	7.4	57	83	2.16	204	2.3096	2.00148
4	6.5	73	41	2.01	101	2.0043	1.87180
5	7.8	65	115	4.30	509	2.7067	2.05412
6	5.8	38	72	1.42	80	1.9031	1.75786
7	5.7	46	63	1.91	80	1.9031	1.74047
8	3.7	68	81	2.57	127	2.1038	1.30833
9	6.0	67	93	2.50	202	2.3054	1.79176
10	3.7	76	94	2.40	203	2.3075	1.30833
11	6.3	84	83	4.13	329	2.5172	1.84055
12	6.7	51	43	1.86	65	1.8129	1.90211
13	5.8	96	114	3.95	830	2.9191	1.75786
14	5.8	83	88	3.95	330	2.5185	1.75786
15	7.7	62	67	3.40	168	2.2253	2.04122
16	7.4	74	68	2.40	217	2.3365	2.00148
17	6.0	85	28	2.98	87	1.9395	1.79176
18	3.7	51	41	1.55	34	1.5315	1.30833
19	7.3	68	74	3.56	215	2.3324	1.98787
20	5.6	57	87	3.02	172	2.2355	1.72277

Consider the model

$$Y = \beta_0 + \beta_1 LogX1 + \beta_2 X2 + \beta_3 X3 + \beta_4 X4 + \epsilon$$

where Y is the survival time, LogX1 is log(blood-clotting score), X2 is a prognostic index, X3 is an enzyme function test score, X4 is a liver function test score, and ϵ is an $N(0, \sigma^2)$ error term.

A question of scientific interest is whether blood clotting score has a positive effect on survival time. Using PROC GENMOD, you can obtain a maximum likelihood estimate of the coefficient and construct a null point hypothesis to test whether β_1 is equal to 0. However, if you are interested in finding the probability that the coefficient is positive, Bayesian analysis offers a convenient alternative. You can use Bayesian analysis to directly estimate the conditional probability, $\Pr(\beta_1 > 0|\mathbf{Y})$, using the posterior distribution samples, which are produced as part of the output by PROC GENMOD.

The example that follows shows how to use PROC GENMOD to carry out a Bayesian analysis of the linear model with a normal error term. The SEED= option is specified to maintain reproducibility; no other options are specified in the BAYES statement. By default, a uniform prior distribution is assumed on the regression coefficients. The uniform prior is a flat prior on the real line with a distribution that reflects ignorance of the location of the parameter, placing equal likelihood on all possible values the regression coefficient can take. Using the uniform prior in the following example, you would expect the Bayesian estimates to resemble the classical results of maximizing the likelihood. If you can elicit an informative prior distribution for the regression coefficients, you should use the COEFFPRIOR= option to specify it. A default noninformative gamma prior is used for the scale parameter σ.

You should make sure that the posterior distribution samples have achieved convergence before using them for Bayesian inference. PROC GENMOD produces three convergence diagnostics by default. If ODS Graphics is enabled as specified in the following SAS statements, diagnostic plots are also displayed. See the section "Assessing Markov Chain Convergence" on page 156 for more information about convergence diagnostics and their interpretation.

Summary statistics of the posterior distribution samples are produced by default. However, these statistics might not be sufficient for carrying out your Bayesian inference, and further processing of the posterior samples might be necessary. The following SAS statements request the Bayesian analysis, and the OUTPOST= option saves the samples in the SAS data set PostSurg for further processing:

```
ods graphics on;
proc genmod data=Surg;
   model y = Logx1 X2 X3 X4 / dist=normal;
   bayes seed=1 OutPost=PostSurg;
run;
ods graphics off;
```

The results of this analysis are shown in the following figures.

The "Model Information" table in Figure 37.8 summarizes information about the model you fit and the size of the simulation.

Figure 37.8 Model Information

The GENMOD Procedure

Bayesian Analysis

Model Information

Data Set	WORK.SURG
Burn-In Size	2000
MC Sample Size	10000
Thinning	1
Distribution	Normal
Link Function	Identity
Dependent Variable	y Survival Time

The "Analysis of Maximum Likelihood Parameter Estimates" table in Figure 37.9 summarizes maximum likelihood estimates of the model parameters.

Figure 37.9 Maximum Likelihood Parameter Estimates

Analysis Of Maximum Likelihood Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald 95% Confidence Limits	
Intercept	1	-730.559	85.4333	-898.005	-563.112
Logx1	1	171.8758	38.2250	96.9561	246.7954
x2	1	4.3019	0.5566	3.2109	5.3929
x3	1	4.0309	0.4996	3.0517	5.0100
x4	1	18.1377	12.0721	-5.5232	41.7986
Scale	1	59.8591	5.7599	49.5705	72.2832

NOTE: The scale parameter was estimated by maximum likelihood.

Since no prior distributions for the regression coefficients were specified, the default noninformative uniform distributions shown in the "Uniform Prior for Regression Coefficients" table in Figure 37.10 are used. Noninformative priors are appropriate if you have no prior knowledge of the likely range of values of the parameters, and if you want to make probability statements about the parameters or functions of the parameters. See, for example, Ibrahim, Chen, and Sinha (2001) for more information about choosing prior distributions.

Figure 37.10 Regression Coefficient Priors

The GENMOD Procedure

Bayesian Analysis

Uniform Prior for Regression Coefficients

Parameter	Prior
Intercept	Constant
Logx1	Constant
x2	Constant
x3	Constant
x4	Constant

The default noninformative gamma prior distribution for the normal scale parameter is shown in the "Independent Prior Distributions for Model Parameters" table in Figure 37.11.

Figure 37.11 Scale Parameter Prior

Independent Prior Distributions for Model Parameters

		Hyperparameters	
Parameter	Prior Distribution	Shape	Inverse Scale
Scale	Gamma	0.001	0.001

By default, the maximum likelihood estimates of the regression parameters are used as the starting values for the simulation when noninformative prior distributions are used. These are listed in the "Initial Values and Seeds" table in Figure 37.12.

Figure 37.12 MCMC Initial Values and Seeds

Initial Values of the Chain

Chain	Seed	Intercept	Logx1	x2	x3	x4
1	1	-730.559	171.8758	4.301896	4.030878	18.1377

Initial Values of the Chain

Scale
59.26675

Summary statistics for the posterior sample are displayed in the "Fit Statistics," "Descriptive Statistics for the Posterior Sample," "Interval Statistics for the Posterior Sample," and "Posterior Correlation Matrix" tables in Figure 37.13, Figure 37.14, Figure 37.15, and Figure 37.16, respectively.

Figure 37.13 Fit Statistics

Fit Statistics

DIC (smaller is better)	607.406
pD (effective number of parameters)	5.912

Figure 37.14 Descriptive Statistics

The GENMOD Procedure

Bayesian Analysis

Posterior Summaries

Parameter	N	Mean	Standard Deviation	Percentiles 25%	50%	75%
Intercept	10000	-732.7	90.0925	-792.7	-732.2	-672.2
Logx1	10000	172.2	40.1142	145.5	171.7	198.6
x2	10000	4.3188	0.5924	3.9209	4.3166	4.7103
x3	10000	4.0477	0.5297	3.6923	4.0390	4.3966
x4	10000	17.8269	12.7611	9.3056	18.0202	26.3786
Scale	10000	63.6906	6.6360	59.0550	63.1311	67.7364

Figure 37.15 Interval Statistics

Posterior Intervals

Parameter	Alpha	Equal-Tail Interval		HPD Interval	
Intercept	0.050	-914.1	-558.4	-912.3	-557.7
Logx1	0.050	95.0527	253.0	93.5157	250.5
x2	0.050	3.1553	5.4898	3.1631	5.4928
x3	0.050	3.0250	5.1098	3.0256	5.1099
x4	0.050	-7.4580	42.6537	-7.3998	42.6693
Scale	0.050	52.3244	78.2094	51.2927	76.7926

Figure 37.16 Posterior Sample Correlation Matrix

Posterior Correlation Matrix

Parameter	Intercept	Logx1	x2	x3	x4	Scale
Intercept	1.000	-0.852	-0.575	-0.707	0.575	0.009
Logx1	-0.852	1.000	0.274	0.482	-0.637	-0.010
x2	-0.575	0.274	1.000	0.295	-0.473	0.004
x3	-0.707	0.482	0.295	1.000	-0.613	-0.000
x4	0.575	-0.637	-0.473	-0.613	1.000	-0.009
Scale	0.009	-0.010	0.004	-0.000	-0.009	1.000

Since noninformative prior distributions were used, the posterior sample means, standard deviations, and interval statistics shown in Figure 37.13 and Figure 37.14 are consistent with the maximum likelihood estimates shown in Figure 37.9.

By default, PROC GENMOD computes three convergence diagnostics: the lag1, lag5, lag10, and lag50 autocorrelations (Figure 37.17); Geweke diagnostic statistics (Figure 37.18); and effective sample sizes (Figure 37.19). There is no indication that the Markov chain has not converged. See the section "Assessing Markov Chain Convergence" on page 156 for more information about convergence diagnostics and their interpretation.

Figure 37.17 Posterior Sample Autocorrelations

The GENMOD Procedure

Bayesian Analysis

Posterior Autocorrelations

Parameter	Lag 1	Lag 5	Lag 10	Lag 50
Intercept	0.4525	0.0478	0.0104	−0.0083
Logx1	0.4226	0.0426	0.0078	−0.0052
x2	0.2328	0.0307	0.0123	−0.0057
x3	0.4020	0.0501	0.0009	−0.0034
x4	0.5906	0.0767	0.0124	0.0026
Scale	0.0941	0.0116	−0.0113	0.0050

Figure 37.18 Geweke Diagnostic Statistics

Geweke Diagnostics

Parameter	z	Pr > |z|
Intercept	−1.0049	0.3149
Logx1	1.2048	0.2283
x2	0.4330	0.6650
x3	0.8662	0.3864
x4	−0.9039	0.3661
Scale	−1.0094	0.3128

Figure 37.19 Effective Sample Sizes

Effective Sample Sizes

Parameter	ESS	Correlation Time	Efficiency
Intercept	3083.6	3.2430	0.3084
Logx1	3185.9	3.1389	0.3186
x2	5051.4	1.9797	0.5051
x3	3281.7	3.0472	0.3282
x4	2534.6	3.9454	0.2535
Scale	8107.8	1.2334	0.8108

Trace, autocorrelation, and density plots for the seven model parameters, shown in Figure 37.20 through Figure 37.25, are useful in diagnosing whether the Markov chain of posterior samples has converged. These plots show no evidence that the chain has not converged. See the section "Visual Analysis via Trace Plots" on page 156 for help with interpreting these diagnostic plots.

Figure 37.20 Diagnostic Plots for Intercept

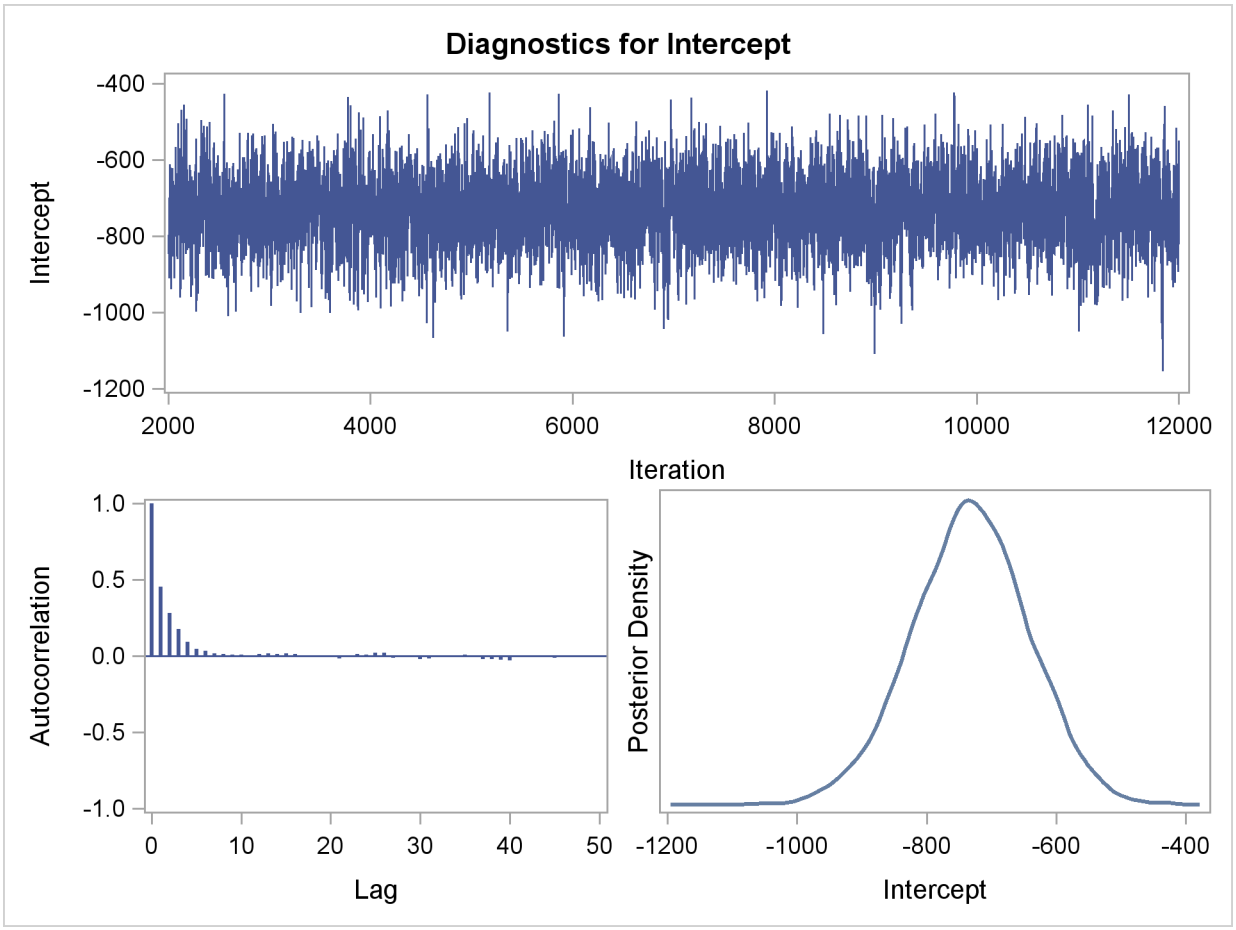


Figure 37.21 Diagnostic Plots for logX1

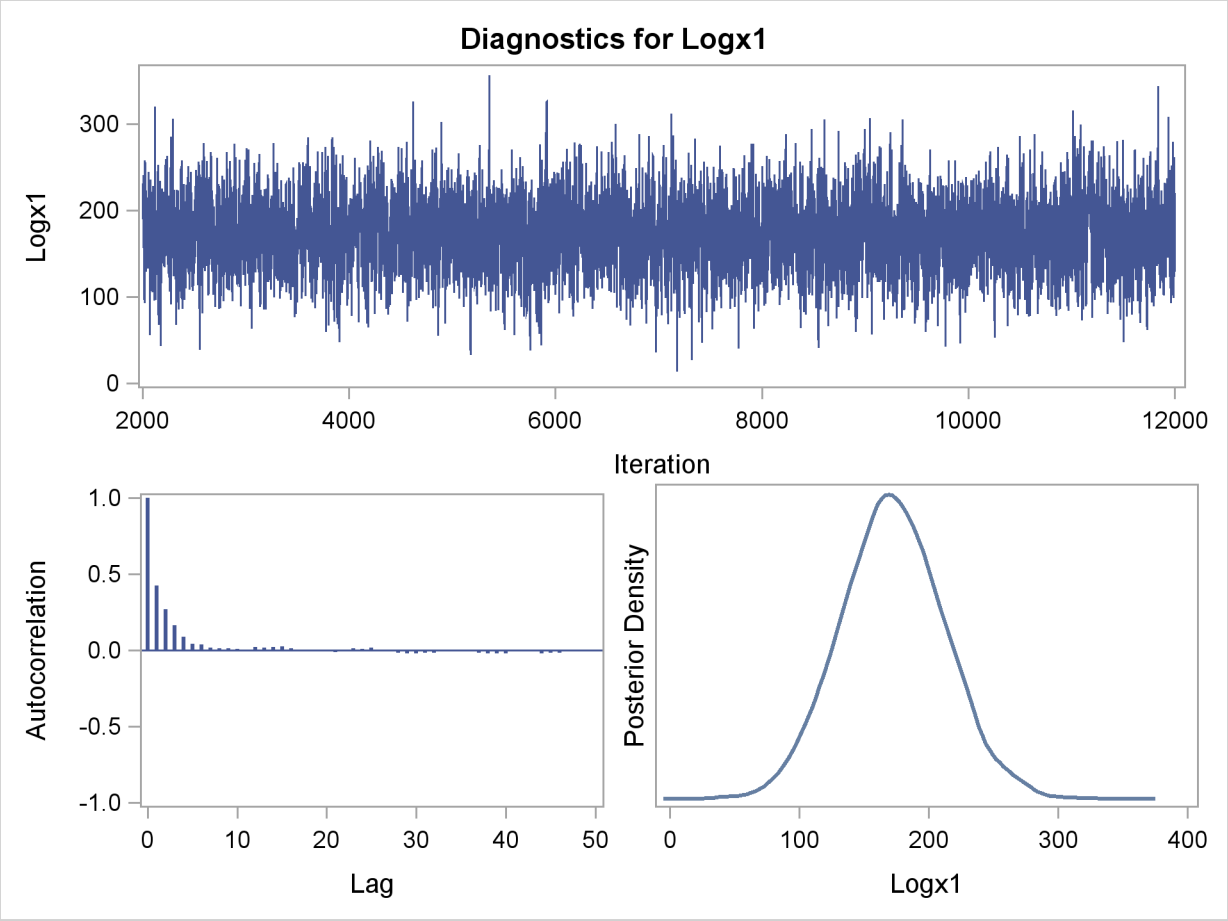


Figure 37.22 Diagnostic Plots for X2

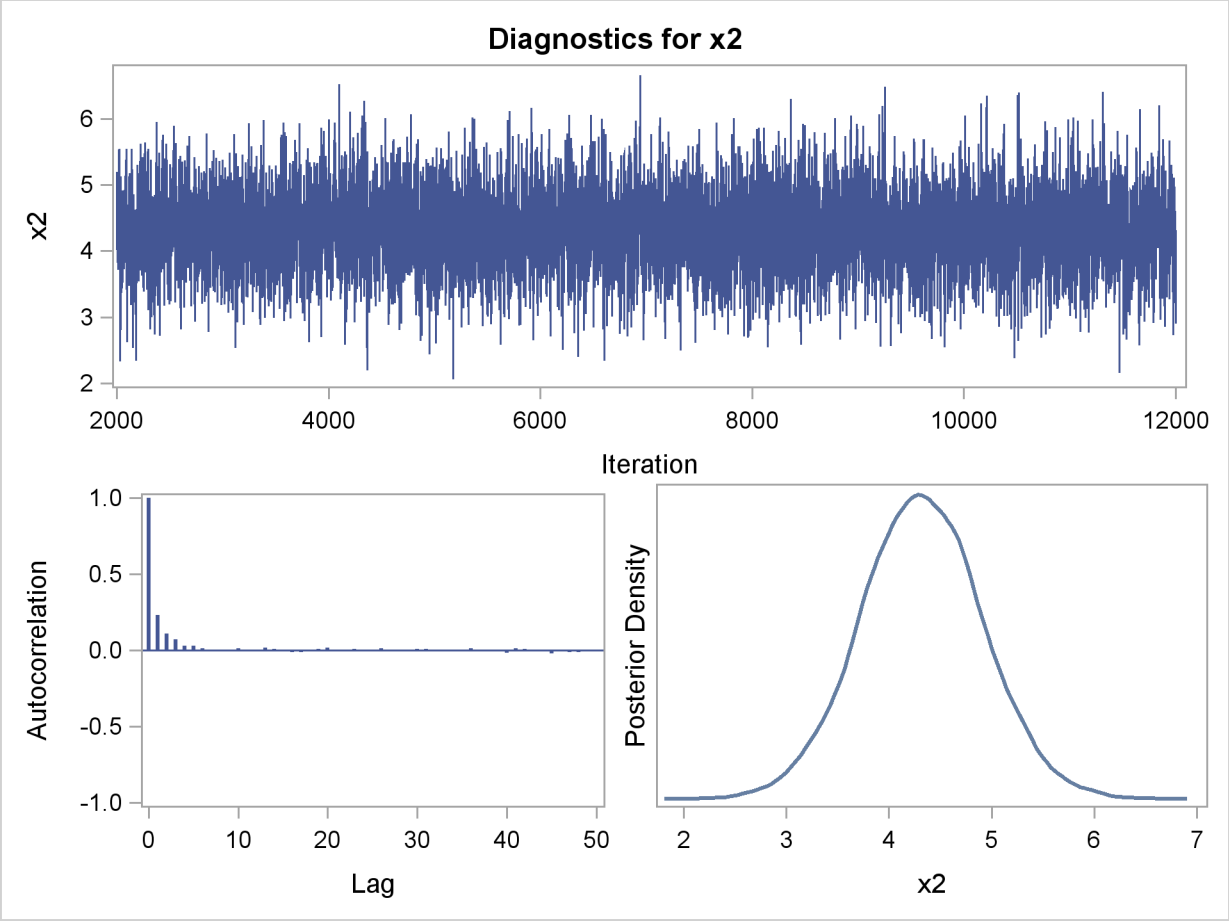


Figure 37.23 Diagnostic Plots for X3

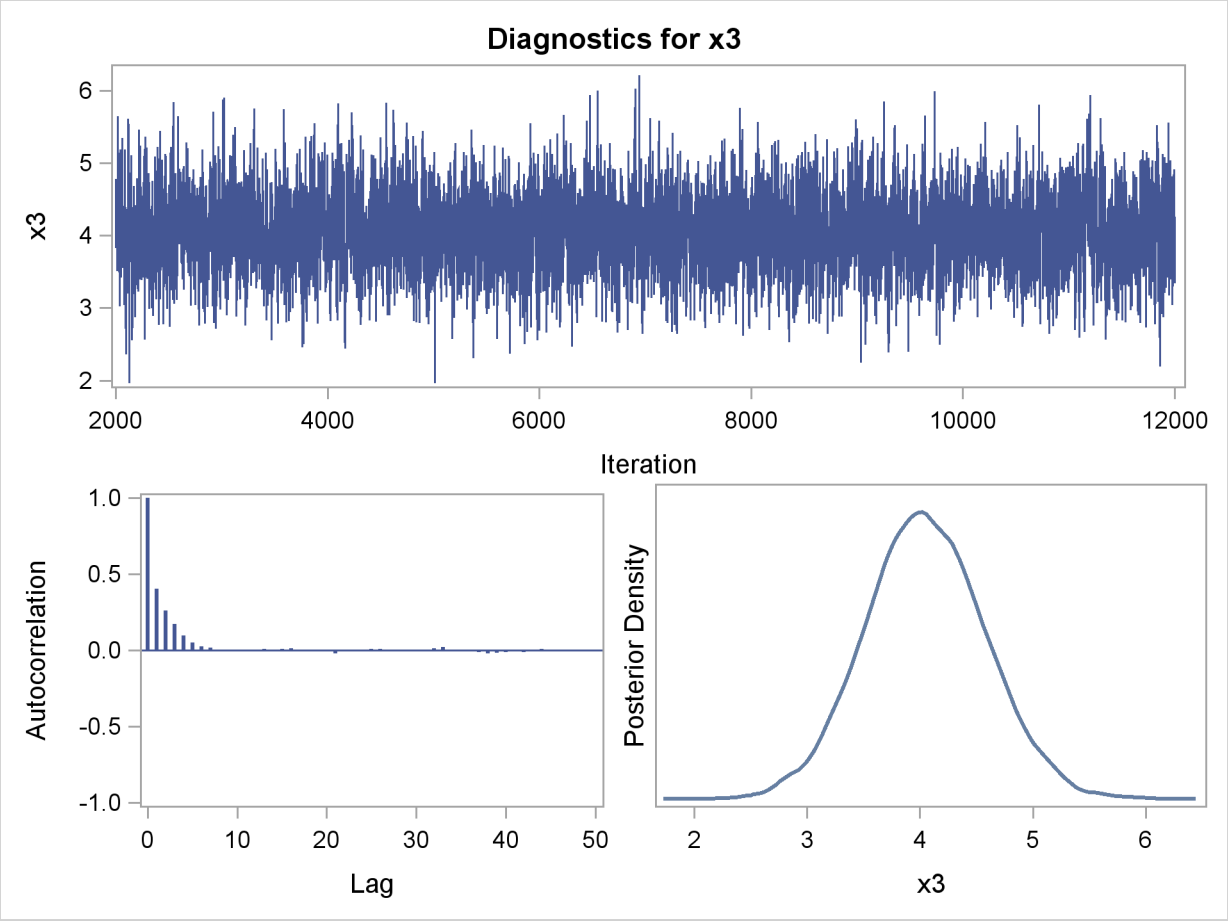


Figure 37.24 Diagnostic Plots for X4

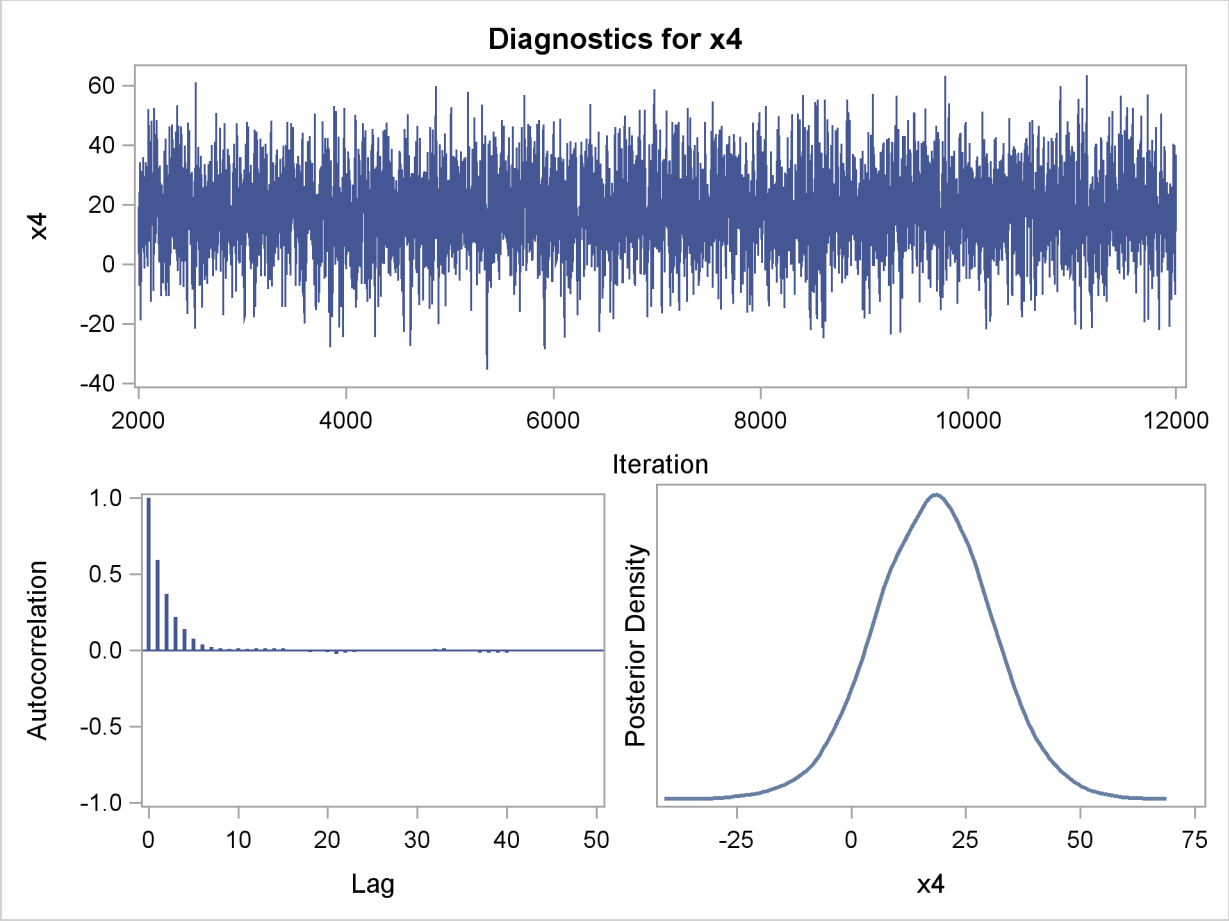
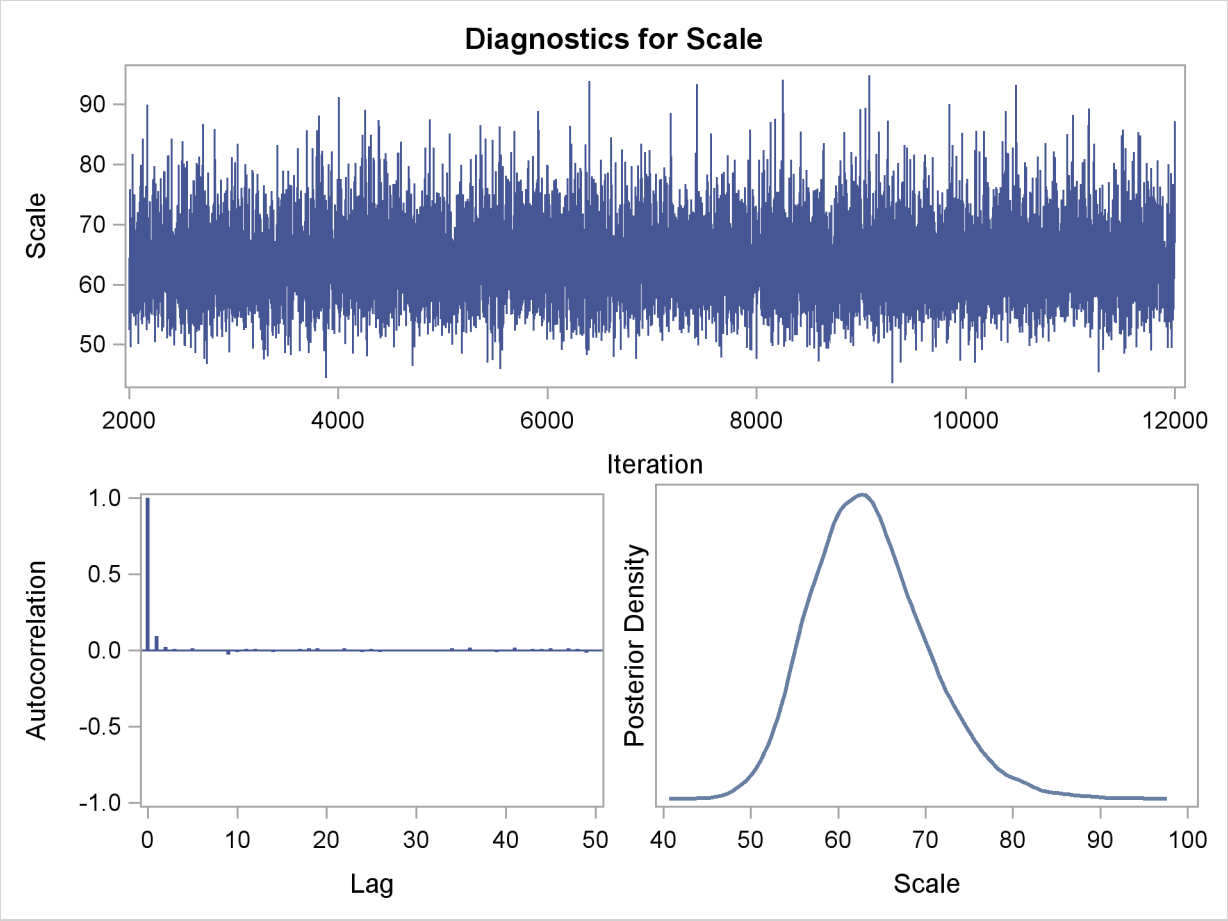


Figure 37.25 Diagnostic Plots for X5



Suppose, for illustration, a question of scientific interest is whether blood clotting score has a positive effect on survival time. Since the model parameters are regarded as random quantities in a Bayesian analysis, you can answer this question by estimating the conditional probability of β_1 being positive, given the data, $\Pr(\beta_1 > 0|\mathbf{Y})$, from the posterior distribution samples. The following SAS statements compute the estimate of the probability of β_1 being positive:

```
data Prob;
   set PostSurg;
   Indicator = (logX1 > 0);
   label Indicator= 'log(Blood Clotting Score) > 0';
run;

proc Means data = Prob(keep=Indicator) n mean;
run;
```

As shown in Figure 37.26, there is a 1.00 probability of a positive relationship between the logarithm of a blood clotting score and survival time, adjusted for the other covariates.

Figure 37.26 Probability That $\beta_1 > 0$

```
                          The MEANS Procedure

        Analysis Variable : Indicator log(Blood Clotting Score) > 0

                             N            Mean
                        ----------------------
                        10000       1.0000000
                        ----------------------
```

Generalized Estimating Equations

This section illustrates the use of the REPEATED statement to fit a GEE model, using repeated measures data from the "Six Cities" study of the health effects of air pollution (Ware et al. 1984). The data analyzed are the 16 selected cases in Lipsitz et al. (1994). The binary response is the wheezing status of 16 children at ages 9, 10, 11, and 12 years. The mean response is modeled as a logistic regression model by using the explanatory variables city of residence, age, and maternal smoking status at the particular age. The binary responses for individual children are assumed to be equally correlated, implying an exchangeable correlation structure.

The data set and SAS statements that fit the model by the GEE method are as follows:

```
data six;
   input case city$ @@;
   do i=1 to 4;
      input age smoke wheeze @@;
      output;
   end;
   datalines;
1 portage   9 0 1  10 0 1  11 0 1  12 0 0
2 kingston  9 1 1  10 2 1  11 2 0  12 2 0
3 kingston  9 0 1  10 0 0  11 1 0  12 1 0
4 portage   9 0 0  10 0 1  11 0 1  12 1 0
5 kingston  9 0 0  10 1 0  11 1 0  12 1 0
6 portage   9 0 0  10 1 0  11 1 0  12 1 0
7 kingston  9 1 0  10 1 0  11 0 0  12 0 0
8 portage   9 1 0  10 1 0  11 1 0  12 2 0
9 portage   9 2 1  10 2 0  11 1 0  12 1 0
10 kingston  9 0 0  10 0 0  11 0 0  12 1 0
11 kingston  9 1 1  10 0 0  11 0 1  12 0 1
12 portage   9 1 0  10 0 0  11 0 0  12 0 0
13 kingston  9 1 0  10 0 1  11 1 1  12 1 1
14 portage   9 1 0  10 2 0  11 1 0  12 2 1
15 kingston  9 1 0  10 1 0  11 1 0  12 2 1
16 portage   9 1 1  10 1 1  11 2 0  12 1 0
;
run;
```

```
proc genmod data=six ;
   class case city ;
   model  wheeze = city age smoke  /  dist=bin;
   repeated  subject=case / type=exch covb corrw;
run;
```

The CLASS statement and the MODEL statement specify the model for the mean of the wheeze variable response as a logistic regression with city, age, and smoke as independent variables, just as for an ordinary logistic regression.

The REPEATED statement invokes the GEE method, specifies the correlation structure, and controls the displayed output from the GEE model. The option SUBJECT=CASE specifies that individual subjects be identified in the input data set by the variable case. The SUBJECT= variable case must be listed in the CLASS statement. Measurements on individual subjects at ages 9, 10, 11, and 12 are in the proper order in the data set, so the WITHINSUBJECT= option is not required. The TYPE=EXCH option specifies an exchangeable working correlation structure, the COVB option specifies that the parameter estimate covariance matrix be displayed, and the CORRW option specifies that the final working correlation be displayed.

Initial parameter estimates for iterative fitting of the GEE model are computed as in an ordinary generalized linear model, as described previously. Results of the initial model fit displayed as part of the generated output are not shown here. Statistics for the initial model fit such as parameter estimates, standard errors, deviances, and Pearson chi-squares do not apply to the GEE model and are valid only for the initial model fit. The following figures display information that applies to the GEE model fit.

Figure 37.27 displays general information about the GEE model fit.

Figure 37.27 GEE Model Information

The GENMOD Procedure

GEE Model Information

Correlation Structure	Exchangeable
Subject Effect	case (16 levels)
Number of Clusters	16
Correlation Matrix Dimension	4
Maximum Cluster Size	4
Minimum Cluster Size	4

Figure 37.28 displays the parameter estimate covariance matrices specified by the COVB option. Both model-based and empirical covariances are produced.

Figure 37.28 GEE Parameter Estimate Covariance Matrices

Covariance Matrix (Model-Based)

	Prm1	Prm2	Prm4	Prm5
Prm1	5.74947	-0.22257	-0.53472	0.01655
Prm2	-0.22257	0.45478	-0.002410	0.01876
Prm4	-0.53472	-0.002410	0.05300	-0.01658
Prm5	0.01655	0.01876	-0.01658	0.19104

Covariance Matrix (Empirical)

	Prm1	Prm2	Prm4	Prm5
Prm1	9.33994	-0.85104	-0.83253	-0.16534
Prm2	-0.85104	0.47368	0.05736	0.04023
Prm4	-0.83253	0.05736	0.07778	-0.002364
Prm5	-0.16534	0.04023	-0.002364	0.13051

The exchangeable working correlation matrix specified by the CORRW option is displayed in Figure 37.29.

Figure 37.29 GEE Working Correlation Matrix

Working Correlation Matrix

	Col1	Col2	Col3	Col4
Row1	1.0000	0.1648	0.1648	0.1648
Row2	0.1648	1.0000	0.1648	0.1648
Row3	0.1648	0.1648	1.0000	0.1648
Row4	0.1648	0.1648	0.1648	1.0000

The parameter estimates table, displayed in Figure 37.30, contains parameter estimates, standard errors, confidence intervals, Z scores, and p-values for the parameter estimates. Empirical standard error estimates are used in this table. A table that displays model-based standard errors can be created by using the REPEATED statement option MODELSE.

Figure 37.30 GEE Parameter Estimates Table

Analysis Of GEE Parameter Estimates
Empirical Standard Error Estimates

Parameter		Estimate	Standard Error	95% Confidence Limits		Z	Pr > |Z|
Intercept		-1.2751	3.0561	-7.2650	4.7148	-0.42	0.6765
city	kingston	-0.1223	0.6882	-1.4713	1.2266	-0.18	0.8589
city	portage	0.0000	0.0000	0.0000	0.0000	.	.
age		0.2036	0.2789	-0.3431	0.7502	0.73	0.4655
smoke		0.0935	0.3613	-0.6145	0.8016	0.26	0.7957

Syntax: GENMOD Procedure

You can specify the following statements in the GENMOD procedure. Items within the <> are optional.

PROC GENMOD < *options* > ;
ASSESS | ASSESSMENT **keyword** / < *options* > ;
BAYES < *options* > ;
BY *variables* ;
CLASS *variables* ;
CONTRAST *'label' effect values* < . . . *effect values* > / < *options* > ;
DEVIANCE *variable = expression* ;
ESTIMATE *'label' effect values* < . . . *effect values* > / < *options* > ;
FREQ | FREQUENCY *variable* ;
FWDLINK *variable = expression* ;
INVLINK *variable = expression* ;
LSMEANS *effects* / < *options* > ;
MODEL *response = < effects > / < options >* ;
OUTPUT < **OUT=***SAS-data-set* >< **keyword=***name* . . . **keyword=***name* > ;
programming statements ;
REPEATED **SUBJECT=***subject-effect* / < *options* > ;
WEIGHT | SCWGT *variable* ;
VARIANCE *variable = expression* ;
ZEROMODEL < *effects* > / < *options* > ;

The PROC GENMOD statement invokes the procedure. All statements other than the MODEL statement are optional. The CLASS statement, if present, must precede the MODEL statement, and the CONTRAST statement must come after the MODEL statement.

PROC GENMOD Statement

PROC GENMOD < *options* > ;

The PROC GENMOD statement invokes the procedure. You can specify the following options.

DATA=*SAS-data-set*
specifies the SAS data set containing the data to be analyzed. If you omit the DATA= option, the procedure uses the most recently created SAS data set.

DESCENDING
DESCEND
DESC
specifies that the levels of the response variable for the ordinal multinomial model and the binomial model with single variable response syntax be sorted in the reverse of the default order. For example, if RORDER=FORMATTED (the default), the DESCENDING option

causes the levels to be sorted from highest to lowest instead of from lowest to highest. If RORDER=FREQ, the DESCENDING option causes the levels to be sorted from lowest frequency count to highest instead of from highest to lowest.

NAMELEN=*n*

specifies the length of effect names in tables and output data sets to be *n* characters long, where *n* is a value between 20 and 200 characters. The default length is 20 characters.

ORDER=*keyword*

specifies the sorting order for the levels of the classification variables (specified in the CLASS statement). This order determines which parameters in the model correspond to each level in the data, so the ORDER= option can be useful when you use the CONTRAST or ESTIMATE statement. Note that the ORDER= option applies to the levels for all classification variables. The exception is the default ORDER=FORMATTED for numeric variables for which you have supplied no explicit format. In this case, the levels are ordered by their internal value. Note that this represents a change from previous releases for how class levels are ordered. Before SAS 8, numeric class levels with no explicit format were ordered by their BEST12. formatted values, and to revert to the previous order you can specify this format explicitly for the affected classification variables. The change was implemented because the former default behavior for ORDER=FORMATTED often resulted in levels not being ordered numerically and usually required the user to intervene with an explicit format or ORDER=INTERNAL option to get the more natural order. The following table displays the valid *keywords* and describes how PROC GENMOD interprets them.

ORDER=*keyword*	**Levels Sorted by**
DATA	order of appearance in the input data set
FORMATTED	external formatted value, except for numeric variables with no explicit format, which are sorted by their unformatted (internal) value
FREQ	descending frequency count; levels with the most observations come first in the order
INTERNAL	unformatted value

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

For more information about sorting order, refer to the chapter on the SORT procedure in the *Base SAS Procedures Guide*.

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

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

specifies plots to be created using ODS Graphics. Many of the observational statistics in the output data set can be plotted using this option. You are not required to create an output data set in order to produce a plot. When you specify only one plot request, you can omit the parentheses around the plot request. Here are some examples:

```
PLOTS=ALL
PLOTS=PREDICTED
PLOTS=(PREDICTED RESCHI)
PLOTS(UNPACK)=DFBETA
```

You must enable ODS Graphics before requesting plots, for example, like this:

```
ods graphics on;

proc genmod plots=all;
   model y = x;
run;

ods graphics off;
```

Any specified global plot options apply to all plots that are specified with plot requests. The following global plot options are available.

CLUSTERLABEL
displays formatted levels of the SUBJECT= effect instead of plot symbols. This option applies only to diagnostic statistics for models fit by GEEs that are plotted against cluster number, and provides a way to identify cluster level names with corresponding ordered cluster numbers.

UNPACK
displays multiple plots individually. The default is to display related multiple plots in a panel.

See the section "OUTPUT Statement" on page 1952 for definitions of the statistics specified with the plot requests. The plot requests include the following:

ALL
produces all available plots.

COOKSD
DOBS
plots the Cook's distance statistic as a function of observation number.

DFBETA
plots the β deletion statistic as a function of observation number for each regression parameter in the model.

DFBETAS
plots the standardized β deletion statistic as a function of observation number for each regression parameter in the model.

LEVERAGE
plots the leverage as a function of observation number.

PREDICTED<(option)>
plots predicted values with confidence limits as a function of observation number. The PREDICTED plot request has the following option:

CLM
includes confidence limits in the predicted value plot.

RESCHI<(options)>
plots Pearson residuals. The RESCHI plot request has the following options:

INDEX
plots as a function of observation number.

XBETA
plots as a function of linear predictor.

If you do not specify an option, Pearson residuals are plotted as a function of observation number.

RESDEV< (options) >
plots deviance residuals. The RESDEV plot request has the following options:

INDEX
plots as a function of observation number.

XBETA
plots as a function of linear predictor.

If you do not specify an option, deviance residuals are plotted as a function of observation number.

RESLIK< (options) >
plots likelihood residuals. The RESLIK plot request has the following options:

INDEX
plots as a function of observation number.

XBETA
plots as a function of linear predictor.

If you do not specify an option, likelihood residuals are plotted as a function of observation number.

RESRAW< (options) >
plots raw residuals. The RESRAW plot request has the following options:

INDEX
plots as a function of observation number.

XBETA
plots as a function of linear predictor.

If you do not specify an option, raw residuals are plotted as a function of observation number.

STDRESCHI< (options) >
plots standardized Pearson residuals. The STDRESCHI plot request has the following options:

INDEX
plots as a function of observation number.

XBETA
plots as a function of linear predictor.

If you do not specify an option, standardized Pearson residuals are plotted as a function of observation number.

STDRESDEV< (options) >
plots standardized deviance residuals. The STDRESDEV plot request has the following options:

INDEX
plots as a function of observation number.

XBETA
plots as a function of linear predictor.

If you do not specify an option, standardized deviance residuals are plotted as a function of observation number.

If you fit a model by using generalized estimating equations (GEEs), the following additional plot requests are available:

CLEVERAGE
plots the cluster leverage as a function of ordered cluster.

CLUSTERCOOKSD
DCLS
plots the cluster Cook's distance statistic as a function of ordered cluster.

CLUSTERDFIT
MCLS
plots the studentized cluster Cook's distance statistic as a function of ordered cluster.

DFBETAC
plots the cluster deletion statistic as a function of ordered cluster for each regression parameter in the model.

DFBETACS
plots the standardized cluster deletion statistic as a function of ordered cluster for each regression parameter in the model.

RORDER=*keyword*
specifies the sorting order for the levels of the response variable. This order determines which intercept parameter in the model corresponds to each level in the data. If RORDER=FORMATTED for numeric variables for which you have supplied no explicit format, the levels are ordered by their internal values. Note that this represents a change from previous releases for how class levels are ordered. Before SAS 8, numeric class levels with no explicit format were ordered by their BEST12. formatted values, and to revert to the previous order you can specify this format explicitly for the response variable. The change was implemented because the former default behavior for RORDER=FORMATTED often resulted

in levels not being ordered numerically and usually required the user to intervene with an explicit format or RORDER=INTERNAL to get the more natural ordering. The following table displays the valid *keywords* and describes how PROC GENMOD interprets them.

RORDER=*keyword*	Levels Sorted by
DATA	order of appearance in the input data set
FORMATTED	external formatted value, except for numeric variables with no explicit format, which are sorted by their unformatted (internal) value
FREQ	descending frequency count; levels with the most observations come first in the order
INTERNAL	unformatted value

By default, RORDER=FORMATTED. For RORDER=FORMATTED and RORDER=INTERNAL, the sort order is machine dependent. The DESCENDING option in the PROC GENMOD statement causes the response variable to be sorted in the reverse of the order displayed in the previous table. For more information about sorting order, refer to the chapter on the SORT procedure in the *Base SAS Procedures Guide*.

The NOPRINT option, which suppresses displayed output in other SAS procedures, is not available in the PROC GENMOD statement. However, you can use the Output Delivery System (ODS) to suppress all displayed output, store all output on disk for further analysis, or create SAS data sets from selected output. You can suppress all displayed output with the statement **`ODS SELECT NONE;`** and turn displayed output back on with the statement **`ODS SELECT ALL;`**. See Table 37.4 and Table 37.5 for the names of output tables available from PROC GENMOD. For more information about ODS, see Chapter 20, "Using the Output Delivery System."

ASSESS Statement

ASSESS VAR=*(effect)* | **LINK** < / *options* > **;**

ASSESSMENT VAR=*(effect)* | **LINK** < / *options* > **;**

The ASSESS statement computes and plots, using ODS Graphics, model-checking statistics based on aggregates of residuals. See the section "Assessment of Models Based on Aggregates of Residuals" on page 1993 for details about the model assessment methods available in GENMOD.

The types of aggregates available are cumulative residuals, moving sums of residuals, and loess smoothed residuals. If you do not specify which aggregate to use, the assessments are based on cumulative sums. PROC GENMOD uses ODS Graphics for graphical displays. For specific information about the graphics available in PROC GENMOD, see the section "ODS Graphics" on page 2020.

You must specify either LINK or VAR= in order to create an analysis.

LINK requests the assessment of the link function by performing the analysis with respect to the linear predictor.

VAR=(*effect***)** specifies that the functional form of a covariate be checked by performing the analysis with respect to the variable identified by the effect. The effect must be specified in the MODEL statement and must contain only continuous variables (variables not listed in a CLASS statement).

You can specify the following options after the slash (/).

CRPANEL
requests that a plot with four panels showing just a few of the paths from the default aggregate plot to make it easier to compare simulated and observed paths. The plot in each panel contains aggregates of the observed residuals and two simulated curves (fewer if NPATHS= is less than 8).

LOESS<(*number***)>**

LOWESS<(*number***)>**
requests model assessment based on loess smoothed residuals with optional *number* the fraction of data used; *number* must be between zero and one. If *number* is not specified, the default value one-third is used.

NPATHS=*number*

NPATH=*number*

PATHS=*number*

PATH=*number*
specifies the number of simulated paths to plot in the default aggregate residuals plot. The default value of *number* is twenty.

RESAMPLE<=*number***>**

RESAMPLES<=*number***>**
specifies that a p-value be computed based on 1,000 simulated paths, or *number* paths, if *number* is specified.

SEED=*number*
specifies a seed for the normal random number generator used in creating simulated realizations of aggregates of residuals for plots and estimating p-values. Specifying a seed enables you to produce identical graphs and p-values from one run of the procedure to the next run. If a seed is not specified, or if *number* is negative or zero, a random number seed is derived from the time of day.

WINDOW<(*number***)>**
requests assessment based on a moving sum window of width *number*. If *number* is not specified, a value of one-half of the range of the x-coordinate is used.

BAYES Statement

BAYES < *options* > **;**

The BAYES statement requests a Bayesian analysis of the regression model by using Gibbs sampling. The Bayesian posterior samples (also known as the chain) for the regression parameters are not tabulated. The Bayesian posterior samples (also known as the chain) for the regression parameters can be output to a SAS data set. Table 37.1 summarizes the options available in the BAYES statement.

Table 37.1 BAYES Statement Options

Option	Description
Monte Carlo Options	
INITIAL=	specifies initial values of the chain
INITIALMLE	specifies that maximum likelihood estimates be used as initial values of the chain
METROPOLIS=	specifies the use of a Metropolis step
NBI=	specifies the number of burn-in iterations
NMC=	specifies the number of iterations after burn-in
SEED=	specifies the random number generator seed
THINNING=	controls the thinning of the Markov chain
Model and Prior Options	
COEFFPRIOR=	specifies the prior of the regression coefficients
DISPERSIONPRIOR=	specifies the prior of the dispersion parameter
PRECISIONPRIOR=	specifies the prior of the precision parameter
SCALEPRIOR=	specifies the prior of the scale parameter
Summary Statistics and Convergence Diagnostics	
DIAGNOSTICS=	displays convergence diagnostics
PLOTS=	displays diagnostic plots
STATISTICS=	displays summary statistics of the posterior samples
Posterior Samples	
OUTPOST=	names a SAS data set for the posterior samples

The following list describes these options and their suboptions.

COEFFPRIOR=JEFFREYS< *(option)* > | **NORMAL**< *(options)* > | **UNIFORM**

COEFF=JEFFREYS< *(options)* > | **NORMAL**< *(options)* > | **UNIFORM**

CPRIOR=JEFFREYS< *(options)* > | **NORMAL**< *(options)* > | **UNIFORM**

specifies the prior distribution for the regression coefficients. The default is COEFFPRIOR=UNIFORM, which specifies the noninformative and improper prior of a constant.

Jeffreys' prior is specified by COEFFPRIOR=JEFFREYS, which can be followed by the following option in parentheses. Jeffreys' prior is proportional to $|I(\boldsymbol{\beta})|^{\frac{1}{2}}$, where $I(\boldsymbol{\beta})$ is the

Fisher information matrix. See the section "Jeffreys' Prior" on page 2003 and Ibrahim and Laud (1991) for more details.

CONDITIONAL
specifies that the Jeffreys' prior, conditional on the current Markov chain value of the generalized linear model precision parameter τ, is proportional to $|\tau \mathbf{I}(\boldsymbol{\beta})|^{\frac{1}{2}}$.

The normal prior is specified by COEFFPRIOR=NORMAL, which can be followed by one of the following options enclosed in parentheses. However, if you do not specify an option, the normal prior $N(\mathbf{0}, 10^6\mathbf{I})$, where $\mathbf{I}$ is the identity matrix, is used. See the section "Normal Prior" on page 2003 for more details.

CONDITIONAL
specifies that the normal prior, conditional on the current Markov chain value of the generalized linear model precision parameter τ, is $N(\boldsymbol{\mu}, \tau^{-1}\boldsymbol{\Sigma})$, where $\boldsymbol{\mu}$ and $\boldsymbol{\Sigma}$ are the mean and covariance of the normal prior specified by other normal options.

INPUT=*SAS-data-set*
specifies a SAS data set containing the mean and covariance information of the normal prior. The data set must have a _TYPE_ variable to represent the type of each observation and a variable for each regression coefficient. If the data set also contains a _NAME_ variable, the values of this variable are used to identify the covariances for the _TYPE_='COV' observations; otherwise, the _TYPE_='COV' observations are assumed to be in the same order as the explanatory variables in the MODEL statement. PROC GENMOD reads the mean vector from the observation with _TYPE_='MEAN' and reads the covariance matrix from observations with _TYPE_='COV'. For an independent normal prior, the variances can be specified with _TYPE_='VAR'; alternatively, the precisions (inverse of the variances) can be specified with _TYPE_='PRECISION'.

RELVAR< *=c* **>**
specifies the normal prior $N(\mathbf{0}, c\mathbf{J})$, where $\mathbf{J}$ is a diagonal matrix with diagonal elements equal to the variances of the corresponding ML estimator. By default, $c = 10^6$.

VAR< *=c* **>**
specifies the normal prior $N(\mathbf{0}, c\mathbf{I})$, where $\mathbf{I}$ is the identity matrix.

DIAGNOSTICS=ALL | NONE | *(keyword-list)*
DIAG=ALL | NONE | *(keyword-list)*
controls the number of diagnostics produced. You can request all the following diagnostics by specifying DIAGNOSTICS=ALL. If you do not want any of these diagnostics, specify DIAGNOSTICS=NONE. If you want some but not all of the diagnostics, or if you want to change certain settings of these diagnostics, specify a subset of the following keywords. The default is DIAGNOSTICS=(AUTOCORR ESS GEWEKE).

AUTOCORR < (LAGS= *numeric-list***) >**
computes the autocorrelations of lags given by LAGS= list for each parameter. Elements in the list are truncated to integers and repeated values are removed. If the LAGS= option is not specified, autocorrelations of lags 1, 5, 10, and 50 are computed for each variable. See the section "Autocorrelations" on page 169 for details.

ESS

computes Carlin's estimate of the effective sample size, the correlation time, and the efficiency of the chain for each parameter. See the section "Effective Sample Size" on page 169 for details.

GELMAN < *(gelman-options)* >

computes the Gelman and Rubin convergence diagnostics. You can specify one or more of the following *gelman-options*:

NCHAIN | **N=***number*

specifies the number of parallel chains used to compute the diagnostic, and must be 2 or larger. The default is NCHAIN=3. If an INITIAL= data set is used, NCHAIN defaults to the number of rows in the INITIAL= data set. If any number other than this is specified with the NCHAIN= option, the NCHAIN= value is ignored.

ALPHA=*value*

specifies the significance level for the upper bound. The default is ALPHA=0.05, resulting in a 97.5% bound.

See the section "Gelman and Rubin Diagnostics" on page 161 for details.

GEWEKE < *(geweke-options)* >

computes the Geweke spectral density diagnostics, 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 163 for details.

HEIDELBERGER < *(heidel-options)* >

computes the Heidelberger and Welch diagnostic for each variable, which consists of a stationarity test of the null hypothesis that the sample values form a stationary process. If the stationarity test is not rejected, a halfwidth test is then carried out. Optionally, you can specify one or more of the following *heidel-options*:

SALPHA=*value*

specifies the α level ($0 < \alpha < 1$) for the stationarity test.

HALPHA=*value*

specifies the α level ($0 < \alpha < 1$) for the halfwidth test.

EPS=*value*

specifies a positive number ϵ such that if the halfwidth is less than ϵ times the sample mean of the retained iterates, the halfwidth test is passed.

See the section "Heidelberger and Welch Diagnostics" on page 165 for details.

MCERROR

MCSE

computes an estimate of the Monte Carlo standard error for each parameter. See the section "Standard Error of the Mean Estimate" on page 170 for details.

RAFTERY< *(raftery-options)* **>**

computes the Raftery and Lewis diagnostics that 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. A stopping criterion is 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, $\Pr(Q - R \leq \hat{P}_Q \leq Q + R) = S$. The following *raftery-options* enable you to specify Q, R, S, and a precision level ϵ for the test:

QUANTILE | Q=*value*

specifies the order (a value between 0 and 1) of the quantile of interest. The default is 0.025.

ACCURACY | R=*value*

specifies a small positive number as the margin of error for measuring the accuracy of estimation of the quantile. The default is 0.005.

PROBABILITY | S=*value*

specifies the probability of attaining the accuracy of the estimation of the quantile. The default is 0.95.

EPSILON | EPS=*value*

specifies the tolerance level (a small positive number) for the stationary test. The default is 0.001.

See the section "Raftery and Lewis Diagnostics" on page 166 for details.

DISPERSIONPRIOR=GAMMA< *(options)* **> | IGAMMA<** *(options)* **> | IMPROPER**

DPRIOR=GAMMA< *(options)* **> | IGAMMA<** *(options)* **> | IMPROPER**

specifies that Gibbs sampling be performed on the generalized linear model dispersion parameter and the prior distribution for the dispersion parameter, if there is a dispersion parameter in the model. For models that do not have a dispersion parameter (the Poisson and binomial), this option is ignored. Note that you can specify Gibbs sampling on either the dispersion parameter ϕ, the scale parameter $\sigma = \phi^{\frac{1}{2}}$, or the precision parameter $\tau = \phi^{-1}$, with the DPRIOR=, SPRIOR=, and PPRIOR= options, respectively. These three parameters are transformations of one another, and you should specify Gibbs sampling for only one of them.

A gamma prior $G(a,b)$ with density $f(t) = \frac{b(bt)^{a-1}\mathrm{e}^{-bt}}{\Gamma(a)}$ is specified by DISPERSIONPRIOR=GAMMA, which can be followed by one of the following *gamma-options* enclosed in parentheses. The hyperparameters a and b are the shape and inverse-scale parameters of the gamma distribution, respectively. See the section "Gamma Prior" on page 2002 for details. The default is $G(10^{-4}, 10^{-4})$.

RELSHAPE< =*c* >
specifies independent $G(c\hat{\phi}, c)$ distribution, where $\hat{\phi}$ is the MLE of the dispersion parameter. With this choice of hyperparameters, the mean of the prior distribution is $\hat{\phi}$ and the variance is $\frac{\hat{\phi}}{c}$. By default, *c*=10^{-4}.

SHAPE=*a*
and

ISCALE=*b*
specify the $G(a, b)$ prior.

SHAPE=*c*
specifies the $G(c, c)$ prior.

ISCALE=*c*
specifies the $G(c, c)$ prior.

An inverse gamma prior $IG(a, b)$ with density $f(t) = \frac{b^a}{\Gamma(a)} t^{-(a+1)} \mathrm{e}^{-b/t}$ is specified by DISPERSIONPRIOR=IGAMMA, which can be followed by one of the following *inverse gamma-options* enclosed in parentheses. The hyperparameters a and b are the shape and scale parameters of the inverse gamma distribution, respectively. See the section "Inverse Gamma Prior" on page 2002 for details. The default is $IG(2.001, 0.001)$.

RELSHAPE< =*c* >
specifies independent $IG(\frac{c+\hat{\phi}}{\hat{\phi}}, c)$ distribution, where $\hat{\phi}$ is the MLE of the dispersion parameter. With this choice of hyperparameters, the mean of the prior distribution is $\hat{\phi}$. By default, *c*=10^{-4}.

SHAPE=*a*
and

SCALE=*b*
specify the $IG(a, b)$ prior.

SHAPE=*c*
specifies the $IG(c, c)$ prior.

SCALE=*c*
specifies the $IG(c, c)$ prior.

An improper prior with density $f(t)$ proportional to t^{-1} is specified with DISPERSIONPRIOR=IMPROPER.

INITIAL=*SAS-data-set*
specifies the SAS data set that contains the initial values of the Markov chains. The INITIAL= data set must contain all the variables of the model. You can specify multiple rows as the initial values of the parallel chains for the Gelman-Rubin statistics, but posterior summaries, diagnostics, and plots are computed only for the first chain. If the data set also contains the variable _SEED_, the value of the _SEED_ variable is used as the seed of the random number generator for the corresponding chain.

INITIALMLE

specifies that maximum likelihood estimates of the model parameters be used as initial values of the Markov chain. If this option is not specified, estimates of the mode of the posterior distribution obtained by optimization are used as initial values.

METROPOLIS=YES

METROPOLIS=NO

specifies the use of a Metropolis step to generate Gibbs samples for posterior distributions that are not log concave. The default value is METROPOLIS=YES.

NBI=*number*

specifies the number of burn-in iterations before the chains are saved. The default is 2000.

NMC=*number*

specifies the number of iterations after the burn-in. The default is 10000.

OUTPOST=*SAS-data-set*

OUT=*SAS-data-set*

names the SAS data set that contains the posterior samples. See the section "OUTPOST= Output Data Set" on page 2005 for more information. Alternatively, you can create the output data set by specifying an ODS OUTPUT statement as follows:

ODS output posteriorsample = *SAS-data-set* **;**

PRECISIONPRIOR=GAMMA< *(options)* **>** | **IMPROPER**

PPRIOR=GAMMA< *(options)* **>** | **IMPROPER**

specifies that Gibbs sampling be performed on the generalized linear model precision parameter and the prior distribution for the precision parameter, if there is a precision parameter in the model. For models that do not have a precision parameter (the Poisson and binomial), this option is ignored. Note that you can specify Gibbs sampling on either the dispersion parameter ϕ, the scale parameter $\sigma = \phi^{\frac{1}{2}}$, or the precision parameter $\tau = \phi^{-1}$, with the DPRIOR=, SPRIOR=, and PPRIOR= options, respectively. These three parameters are transformations of one another, and you should specify Gibbs sampling for only one of them.

A gamma prior $G(a, b)$ with density $f(t) = \frac{b(bt)^{a-1}\mathrm{e}^{-bt}}{\Gamma(a)}$ is specified by PRECISIONPRIOR=GAMMA, which can be followed by one of the following *gamma-options* enclosed in parentheses. The hyperparameters a and b are the shape and inverse-scale parameters of the gamma distribution, respectively. See the section "Gamma Prior" on page 2002 for details. The default is $G(10^{-4}, 10^{-4})$.

RELSHAPE< =*c* **>**

specifies independent $G(c\hat{\tau}, c)$ distribution, where $\hat{\tau}$ is the MLE of the dispersion parameter. With this choice of hyperparameters, the mean of the prior distribution is $\hat{\tau}$ and the variance is $\frac{\hat{\tau}}{c}$. By default, $c = 10^{-4}$.

SHAPE=*a*

and

ISCALE=*b*

specify the $G(a, b)$ prior.

SHAPE=*c*
specifies the $G(c, c)$ prior.

ISCALE=*c*
specifies the $G(c, c)$ prior.

An improper prior with density $f(t)$ proportional to t^{-1} is specified with PRECISION-PRIOR=IMPROPER.

SCALEPRIOR=GAMMA< *(options)* **>** | **IMPROPER**

SPRIOR=GAMMA< *(options)* **>** | **IMPROPER**
specifies that Gibbs sampling be performed on the generalized linear model scale parameter and the prior distribution for the scale parameter, if there is a scale parameter in the model. For models that do not have a scale parameter (the Poisson and binomial), this option is ignored. Note that you can specify Gibbs sampling on either the dispersion parameter ϕ, the scale parameter $\sigma = \phi^{\frac{1}{2}}$, or the precision parameter $\tau = \phi^{-1}$, with the DPRIOR=, SPRIOR=, and PPRIOR= options, respectively. These three parameters are transformations of one another, and you should specify Gibbs sampling for only one of them.

A gamma prior $G(a, b)$ with density $f(t) = \frac{b(bt)^{a-1}\mathrm{e}^{-bt}}{\Gamma(a)}$ is specified by SCALEPRIOR=GAMMA, which can be followed by one of the following *gamma-options* enclosed in parentheses. The hyperparameters a and b are the shape and inverse-scale parameters of the gamma distribution, respectively. See the section "Gamma Prior" on page 2002 for details. The default is $G(10^{-4}, 10^{-4})$.

RELSHAPE< =*c* **>**
specifies independent $G(c\hat{\sigma}, c)$ distribution, where $\hat{\sigma}$ is the MLE of the dispersion parameter. With this choice of hyperparameters, the mean of the prior distribution is $\hat{\sigma}$ and the variance is $\frac{\hat{\sigma}}{c}$. By default, $c = 10^{-4}$.

SHAPE=*a*
and

ISCALE=*b*
specify the $G(a, b)$ prior.

SHAPE=*c*
specifies the $G(c, c)$ prior.

ISCALE=*c*
specifies the $G(c, c)$ prior.

An improper prior with density $f(t)$ proportional to t^{-1} is specified with SCALEPRIOR=IMPROPER.

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

PLOTS< *(global-plot-options)* **>=** *(plot-request < . . . plot-request>)*
controls the display of diagnostic plots. Three types of plots can be requested: trace plots, autocorrelation function plots, and kernel density plots. By default, the plots are displayed in panels unless the global plot option UNPACK is specified. Also, when you are specifying more than one type of plots, the plots are displayed by parameters unless the global plot

option GROUPBY is specified. When you specify only one plot request, you can omit the parentheses around the plot request. For example:

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

You must enable ODS Graphics before requesting plots. For example, the following SAS statements enable ODS Graphics:

```
ods graphics on;
proc genmod;
   model y=x;
   bayes plots=trace;
   run;
end;
ods graphics off;
```

The global plot options are as follows:

FRINGE
creates a fringe plot on the X axis of the density plot.

GROUPBY=PARAMETER

GROUPBY=TYPE
specifies how the plots are grouped when there is more than one type of plot.

GROUPBY=TYPE
specifies that the plots be grouped by type.

GROUPBY=PARAMETER
specifies that the plots be grouped by parameter.

GROUPBY=PARAMETER is the default.

LAGS=*n*
specifies that autocorrelations be plotted up to lag *n*. If this option is not specified, autocorrelations are plotted up to lag 50.

SMOOTH
displays a fitted penalized B-spline curve for each trace plot.

UNPACKPANEL

UNPACK
specifies that all paneled plots be unpacked, meaning that each plot in a panel is displayed separately.

The plot requests include the following:

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

AUTOCORR
displays the autocorrelation function plots for the parameters.

DENSITY
displays the kernel density plots for the parameters.

NONE
suppresses all diagnostic plots.

TRACE
displays the trace plots for the parameters. See the section "Visual Analysis via Trace Plots" on page 156 for details.

SEED=*number*
specifies an integer seed in the range 1 to $2^{31} - 1$ for the random number generator in the simulation. Specifying a seed enables you to reproduce identical Markov chains for the same specification. If the SEED= option is not specified, or if you specify a nonpositive seed, a random seed is derived from the time of day.

STATISTICS < *(global-options)* > = **ALL** | **NONE** | *keyword* | *(keyword-list)*
STATS < *(global-options)* > = **ALL** | **NONE** | *keyword* | *(keyword-list)*
controls the number of posterior statistics produced. Specifying STATISTICS=ALL is equivalent to specifying STATISTICS= (SUMMARY INTERVAL COV CORR). If you do not want any posterior statistics, you specify STATISTICS=NONE. The default is STATISTICS=(SUMMARY INTERVAL). See the section "Summary Statistics" on page 170 for details. The *global-options* include the following:

ALPHA=*numeric-list*
controls the probabilities of the 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 intervals for each parameters. The default is the value of the ALPHA= option in the MODEL statement, or 0.05 if that option is not specified (yielding the 95% credible intervals for each parameter).

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

The list of *keywords* includes the following:

CORR
produces the posterior correlation matrix.

COV
produces the posterior covariance matrix.

SUMMARY
produces the means, standard deviations, and percentile points for the posterior samples. The default is to produce the 25th, 50th, and 75th percentile points, but you can use the global PERCENT= option to request specific percentile points.

INTERVAL

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

THINNING=*number*

THIN=*number*

controls the thinning of the Markov chain. Only one in every k samples is used when THINNING=k, and if NBI=n_0 and NMC=n, the number of samples kept is

$$\left[\frac{n_0+n}{k}\right]-\left[\frac{n_0}{k}\right]$$

where $[a]$ represents the integer part of the number a. The default is THINNING=1.

BY Statement

BY *variables* **;**

You can specify a BY statement with PROC GENMOD to obtain separate analyses on observations in groups 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.

Since sorting the data changes the order in which PROC GENMOD reads the data, this can affect the sorting order for the levels of classification variables if you have specified ORDER=DATA in the PROC GENMOD statement. This in turn affects specifications in the CONTRAST statement.

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 BY statement option NOTSORTED or DESCENDING in the BY statement for the GENMOD 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.

For more information about the BY statement, see *SAS Language Reference: Concepts*. For more information about the DATASETS procedure, see the *Base SAS Procedures Guide*.

CLASS Statement

The CLASS statement names the classification variables to be used in the analysis. The CLASS statement must precede the MODEL statement. You can specify various *v-options* for each variable

by enclosing them in parentheses after the variable name. You can also specify global *v-options* for the CLASS statement by placing them after a slash (/). Global *v-options* are applied to all the variables specified in the CLASS statement. If you specify more than one CLASS statement, the global *v-options* specified in any one CLASS statement apply to all CLASS statements. However, individual CLASS variable *v-options* override the global *v-options*.

DESCENDING

DESC

reverses the sorting order of the classification variable.

MISSING

allows missing value ('.' for a numeric variable and blank for a character variable) as a valid value for the CLASS variable.

ORDER=DATA

ORDER=FORMATTED

ORDER=FREQ

ORDER=INTERNAL

specifies the sorting order for the levels of classification variables. This order determines which parameters in the model correspond to each level in the data, so the ORDER= option can be useful when you use the CONTRAST or ESTIMATE statement. If ORDER=FORMATTED for numeric variables for which you have supplied no explicit format, the levels are ordered by their internal values. Note that this represents a change from previous releases for how class levels are ordered. Before SAS 8, numeric class levels with no explicit format were ordered by their BEST12. formatted values, and to revert to the previous ordering you can specify this format explicitly for the affected classification variables. The change was implemented because the former default behavior for ORDER=FORMATTED often resulted in levels not being ordered numerically and usually required the user to intervene with an explicit format or ORDER=INTERNAL to get the more natural order. The following table shows how PROC GENMOD interprets values of the ORDER= option.

Value of ORDER=	Levels Sorted by
DATA	order of appearance in the input data set
FORMATTED	external formatted value, except for numeric variables with no explicit format, which are sorted by their unformatted (internal) value
FREQ	descending frequency count; levels with the most observations come first in the order
INTERNAL	unformatted value

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

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*.

PARAM=*keyword*

specifies the parameterization method for the classification variable or variables. Design matrix columns are created from CLASS variables according to the following coding schemes. The default is PARAM=GLM. If PARAM=ORTHPOLY or PARAM=POLY, and the CLASS levels are numeric, then the ORDER= option in the CLASS statement is ignored, and the internal, unformatted values are used. See the section "CLASS Variable Parameterization" on page 1973 for further details. You can use the following *keywords*:

EFFECT specifies effect coding.

GLM specifies less-than-full-rank, reference-cell coding; this option can be used only as a global option.

ORDINAL

THERMOMETER specifies the cumulative parameterization for an ordinal CLASS variable.

POLYNOMIAL

POLY specifies polynomial coding.

REFERENCE

REF specifies reference-cell coding.

ORTHEFFECT orthogonalizes PARAM=EFFECT.

ORTHORDINAL

ORTHOTHERM orthogonalizes PARAM=ORDINAL.

ORTHPOLY orthogonalizes PARAM=POLYNOMIAL.

ORTHREF orthogonalizes PARAM=REFERENCE.

The EFFECT, POLYNOMIAL, REFERENCE, and ORDINAL suboptions and their orthogonal parameterizations are full rank. The REF= option in the CLASS statement determines the reference level for the EFFECT and REFERENCE suboptions and their orthogonal parameterizations.

REF=*'level' | keyword*

specifies the reference level for PARAM=EFFECT, PARAM=REFERENCE, and their orthogonalizations. For an individual (but not a global) variable REF= *option*, you can specify the *level* of the variable to use as the reference level. For a global or individual variable REF= *option*, you can use one of the following *keywords*. The default is REF=LAST.

FIRST designates the first ordered level as reference.

LAST designates the last ordered level as reference.

TRUNCATE< *=n* >

specifies the length *n* of CLASS variable values to use in determining CLASS variable levels. If you specify TRUNCATE without the length *n*, the first 16 characters of the formatted values are used. When formatted values are longer than 16 characters, you can use this option to revert to the levels as determined in releases before SAS 9. The default is to use the full formatted length of the CLASS variable. The TRUNCATE option is available only as a global option.

CONTRAST Statement

CONTRAST *'label' contrast-specification* / < *options* > **;**

The CONTRAST statement provides a means of obtaining a test of a specified hypothesis concerning the model parameters. This is accomplished by specifying a matrix $\mathbf{L}$ for testing the hypothesis $\mathbf{L}'\boldsymbol{\beta} = 0$. You must be familiar with the details of the model parameterization that PROC GENMOD uses. For more information, see the section "Parameterization Used in PROC GENMOD" on page 1973 and the section "CLASS Variable Parameterization" on page 1973. Computed statistics are based on the asymptotic chi-square distribution of the likelihood ratio statistic, or the generalized score statistic for GEE models, with degrees of freedom determined by the number of linearly independent rows in the $\mathbf{L}'$ matrix. You can request Wald chi-square statistics with the Wald option in the CONTRAST statement.

There is no limit to the number of CONTRAST statements that you can specify, but they must appear after the MODEL statement and after the ZEROMODEL statement for zero-inflated Poisson models. Statistics for multiple CONTRAST statements are displayed in a single table.

The elements of the CONTRAST statement are as follows:

label identifies the contrast on the output. A label is required for every contrast specified. Labels can be up to 20 characters and must be enclosed in single quotes.

contrast-specification identifies the effects and their coefficients from which the $\mathbf{L}$ matrix is formed. The *contrast-specification* can be specified in two different ways. The first method applies to all models except the zero-inflated Poisson (ZIP) distribution, and the syntax is:

effect values <,... *effect values*>

The second method of specifying a contrast applies only to ZIP models, and the syntax is:

effect values <,... *effect values*> @*zero effect values* <,... *effect values*>

Specification of sets of *effect values* before the @*zero* separator results in a row of the $\mathbf{L}'$ matrix with coefficients for *effects* in the regression part of the model set to *values* and with the coefficients for the zero-inflation part of the model set to zero. Specification of sets of *effect values* after the @*zero* separator results in a row of the $\mathbf{L}$ matrix with the coefficients for the regression part of the model set to zero and with the coefficients of *effects* in the zero-inflation part of the model set to *values*.

For example, the statements

```
CLASS A;
MODEL y=A;
CONTRAST 'Label1' A 1 -1;
```

specify an $\mathbf{L}'$ matrix with one row with coefficients 1 for the first level of A and –1 for the second level of A.

The statements

```
CLASS A B;
MODEL y=A / Dist=ZIP;
ZEROMODEL B;
CONTRAST 'Label2' A 1 -1 @ZERO B 1 -1;
```

specify an $\mathbf{L}'$ matrix with two rows: the first row has coefficients 1 for the first level of A, –1 for the second level of A, and zeros for all levels of B; the second row has coefficients 0 for all levels of A, 1 for the first level of B, and –1 for the second level of B.

effect identifies an effect that appears in the MODEL statement. The value INTERCEPT or intercept can be used as an effect when an intercept is included in the model. You do not need to include all effects that are included in the MODEL statement.

values are constants that are elements of the $\mathbf{L}$ vector associated with the effect.

The rows of $\mathbf{L}'$ are specified in order and are separated by commas.

If you use the default less-than-full-rank PROC GLM CLASS variable parameterization, each row of the $\mathbf{L}'$ matrix is checked for estimability. If PROC GENMOD finds a contrast to be nonestimable, it displays missing values in corresponding rows in the results. See Searle (1971) for a discussion of estimable functions. If the elements of $\mathbf{L}'$ are not specified for an effect that contains a specified effect, then the elements of the specified effect are distributed over the levels of the higher-order effect just as the GLM procedure does for its CONTRAST and ESTIMATE statements. For example, suppose that the model contains effects A and B and their interaction A*B. If you specify a CONTRAST statement involving A alone, the $\mathbf{L}'$ matrix contains nonzero terms for both A and A*B, since A*B contains A.

When you use any of the full-rank PARAM= CLASS variable options, all parameters are directly estimable, and rows of $\mathbf{L}'$ are not checked for estimability.

If an effect is not specified in the CONTRAST statement, all of its coefficients in the $\mathbf{L}'$ matrix are set to 0. If too many values are specified for an effect, the extra ones are ignored. If too few values are specified, the remaining ones are set to 0.

PROC GENMOD handles missing level combinations of classification variables in the same manner as the GLM and MIXED procedures. Parameters corresponding to missing level combinations are not included in the model. This convention can affect the way in which you specify the $\mathbf{L}$ matrix in your CONTRAST statement.

If you specify the WALD option, the test of hypothesis is based on a Wald chi-square statistic. If you omit the WALD option, the test statistic computed depends on whether an ordinary generalized linear model or a GEE-type model is specified.

For an ordinary generalized linear model, the CONTRAST statement computes the likelihood ratio statistic. This is defined to be twice the difference between the log likelihood of the model unconstrained by the contrast and the log likelihood with the model fitted under the constraint that the linear function of the parameters defined by the contrast is equal to 0. A p-value is computed based on the asymptotic chi-square distribution of the chi-square statistic.

If you specify a GEE model with the REPEATED statement, the test is based on a score statistic. The GEE model is fit under the constraint that the linear function of the parameters defined by the contrast is equal to 0. The score chi-square statistic is computed based on the generalized score function. See the section "Generalized Score Statistics" on page 1993 for more information.

The degrees of freedom is the number of linearly independent constraints implied by the CONTRAST statement—that is, the rank of $\mathbf{L}$.

You can specify the following options after a slash (/).

E

requests that the $\mathbf{L}$ matrix be displayed.

SINGULAR=*number*

EPSILON=*number*

tunes the estimability checking. If $\mathbf{v}$ is a vector, define ABS($\mathbf{v}$) to be the absolute value of the element of $\mathbf{v}$ with the largest absolute value. Let $\mathbf{K}'$ be any row in the contrast matrix $\mathbf{L}$. Define C to be equal to ABS($\mathbf{K}'$) if ABS($\mathbf{K}'$) is greater than 0; otherwise, C equals 1. If ABS($\mathbf{K}' - \mathbf{K}'\mathbf{T}$) is greater than C$*$*number*, then $\mathbf{K}$ is declared nonestimable. $\mathbf{T}$ is the Hermite form matrix $(\mathbf{X}'\mathbf{X})^{-}(\mathbf{X}'\mathbf{X})$, and $(\mathbf{X}'\mathbf{X})^{-}$ represents a generalized inverse of the matrix $\mathbf{X}'\mathbf{X}$. The value for $number$ must be between 0 and 1; the default value is 1E−4. The SINGULAR= option in the MODEL statement affects the computation of the generalized inverse of the matrix $\mathbf{X}'\mathbf{X}$. It might also be necessary to adjust this value for some data.

WALD

requests that a Wald chi-square statistic be computed for the contrast rather than the default likelihood ratio or score statistic. The Wald statistic for testing $\mathbf{L}'\boldsymbol{\beta} = \mathbf{0}$ is defined by

$$S = (\mathbf{L}'\hat{\boldsymbol{\beta}})'(\mathbf{L}'\boldsymbol{\Sigma}\mathbf{L})^{-}(\mathbf{L}'\hat{\boldsymbol{\beta}})$$

where $\hat{\boldsymbol{\beta}}$ is the maximum likelihood estimate and $\boldsymbol{\Sigma}$ is its estimated covariance matrix. The asymptotic distribution of S is χ^2_r, where r is the rank of $\mathbf{L}$. Computed p-values are based on this distribution.

If you specify a GEE model with the REPEATED statement, $\boldsymbol{\Sigma}$ is the empirical covariance matrix estimate.

DEVIANCE Statement

DEVIANCE *variable = expression* **;**

You can specify a probability distribution other than those available in PROC GENMOD by using the DEVIANCE and VARIANCE statements. You do not need to specify the DEVIANCE or VARIANCE statement if you use the DIST= MODEL statement option to specify a probability distribution. The *variable* identifies the deviance contribution from a single observation to the procedure, and it must be a valid SAS variable name that does not appear in the input data set. The *expression* can be any arithmetic expression supported by the DATA step language, and it is used to define the functional dependence of the deviance on the mean and the response. You use the automatic variables _MEAN_ and _RESP_ to represent the mean and response in the *expression*.

Alternatively, the deviance function can be defined using programming statements (see the section "Programming Statements" on page 1955) and assigned to a variable, which is then listed as the *expression*. This form is convenient for using complex statements such as IF-THEN/ELSE clauses.

The DEVIANCE statement is ignored unless the VARIANCE statement is also specified.

ESTIMATE Statement

ESTIMATE *'label' effect values <,... effect values> </options>* **;**

The ESTIMATE statement is similar to a CONTRAST statement, except only one-row $\mathbf{L}'$ matrices are permitted.

In the case of zero-inflated Poisson (ZIP) models, the statement syntax is:

ESTIMATE *'label' effect values <,... effect values> @zero effect values <,... effect values> </options>* **;**

where sets of *effects values* before the *@zero* separator correspond to the regression part of the model, and *effects values* after the *@zero* separator correspond to the zero-inflation part of the model. In the case of ZIP models, a one-row $\mathbf{L}'$ matrix is created for the regression part of the model, another one-row $\mathbf{L}'$ matrix is created for the zero-inflation part of the model, and separate estimate estimates for the two $\mathbf{L}$ matrices are computed and displayed.

If you use the default less-than-full-rank GLM CLASS variable parameterization, each row is checked for estimability. If PROC GENMOD finds a contrast to be nonestimable, it displays missing values in corresponding rows in the results. See Searle (1971) for a discussion of estimable functions.

The actual estimate, $\mathbf{L}'\boldsymbol{\gamma}$, its approximate standard error, and its confidence limits are displayed. A Wald chi-square test that $\mathbf{L}'\boldsymbol{\beta} = 0$ is also displayed.

The approximate standard error of the estimate is computed as the square root of $\mathbf{L}'\hat{\boldsymbol{\Sigma}}\mathbf{L}$, where $\hat{\boldsymbol{\Sigma}}$ is the estimated covariance matrix of the parameter estimates. If you specify a GEE model in the REPEATED statement, $\hat{\boldsymbol{\Sigma}}$ is the empirical covariance matrix estimate.

If you specify the EXP option, then $\exp(\mathbf{L}'\boldsymbol{\beta})$, its standard error, and its confidence limits are also displayed.

The construction of the $\mathbf{L}$ vector and the checking for estimability for an ESTIMATE statement follow the same rules as listed under the CONTRAST statement.

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

ALPHA=*number*
: requests that a confidence interval be constructed with confidence level $1 - number$. The value of *number* must be between 0 and 1; the default value is 0.05.

E
: requests that the $\mathbf{L}$ matrix coefficients be displayed.

EXP
: requests that $\exp(\mathbf{L}'\boldsymbol{\beta})$, its standard error, and its confidence limits be computed. If you specify the EXP option, standard errors and confidence intervals are computed using the delta method.

SINGULAR=*number*

EPSILON=*number*

tunes the estimability checking as described for the CONTRAST statement.

FREQ Statement

FREQ *variable* **;**

FREQUENCY *variable* **;**

The *variable* in the FREQ statement identifies a variable in the input data set containing the frequency of occurrence of each observation. PROC GENMOD treats each observation as if it appears *n* times, where *n* 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 it is less than 1 or missing, the observation is not used. In the case of models fit with generalized estimating equations (GEEs), the frequencies apply to the subject/cluster and therefore must be the same for all observations within each subject.

FWDLINK Statement

FWDLINK *variable = expression* **;**

You can define a link function other than a built-in link function by using the FWDLINK statement. If you use the MODEL statement option LINK= to specify a link function, you do not need to use the FWDLINK statement. The *variable* identifies the link function to the procedure. The *expression* can be any arithmetic expression supported by the DATA step language, and it is used to define the functional dependence on the mean.

Alternatively, the link function can be defined by using programming statements (see the section "Programming Statements" on page 1955) and assigned to a variable, which is then listed as the *expression*. The second form is convenient for using complex statements such as IF-THEN/ELSE clauses. The GENMOD procedure automatically computes derivatives of the link function required for iterative fitting. You must specify the inverse of the link function in the INVLINK statement when you specify the FWDLINK statement to define the link function. You use the automatic variable _MEAN_ to represent the mean in the preceding *expression*.

INVLINK Statement

INVLINK *variable = expression* **;**

If you define a link function in the FWDLINK statement, then you must define the inverse link function by using the INVLINK statement. If you use the MODEL statement option LINK= to specify a link function, you do not need to use the INVLINK statement. The *variable* identifies the

inverse link function to the procedure. The *expression* can be any arithmetic expression supported by the DATA step language, and it is used to define the functional dependence on the linear predictor.

Alternatively, the inverse link function can be defined using programming statements (see the section "Programming Statements" on page 1955) and assigned to a variable, which is then listed as the *expression*. The second form is convenient for using complex statements such as IF-THEN/ELSE clauses. The automatic variable _XBETA_ represents the linear predictor in the preceding *expression*.

LSMEANS Statement

LSMEANS *effects* < / *options* > **;**

The LSMEANS statement computes least squares means (LS-means) corresponding to the specified effects for the linear predictor part of the model. The $\mathbf{L}$ matrix constructed to compute them is precisely the same as the one formed in PROC GLM.

The LSMEANS statement is not available for multinomial distribution models for ordinal response data.

Each LS-mean is computed as $\mathbf{L}'\hat{\boldsymbol{\beta}}$, where $\mathbf{L}$ is the coefficient matrix associated with the least squares mean and $\hat{\boldsymbol{\beta}}$ is the estimate of the parameter vector. The approximate standard errors for the LS-mean is computed as the square root of $\mathbf{L}'\hat{\boldsymbol{\Sigma}}\mathbf{L}$, where $\hat{\boldsymbol{\Sigma}}$ is the estimated covariance matrix of the parameter estimates. If you specify a GEE model in the REPEATED statement, $\hat{\boldsymbol{\Sigma}}$ is the empirical covariance matrix estimate.

LS-means can be computed for any effect in the MODEL statement that involves CLASS variables. You can specify multiple effects in one LSMEANS statement or multiple LSMEANS statements, and all LSMEANS statements must appear after the MODEL statement.

As in the ESTIMATE statement, the $\mathbf{L}$ matrix is tested for estimability, and if this test fails, PROC GENMOD displays "Non-est" for the LS-means entries.

Assuming the LS-mean is estimable, PROC GENMOD constructs a Wald chi-square test to test the null hypothesis that the associated population quantity equals zero.

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

ALPHA=*number*
: requests that a confidence interval be constructed for each of the LS-means with confidence level $(1 - number) \times 100\%$. The value of *number* must be between 0 and 1; the default value is 0.05, corresponding to a 95% confidence interval.

CL
: requests that confidence limits be constructed for each of the LS-means. The confidence level is 0.95 by default; this can be changed with the ALPHA= option.

CORR
: displays the estimated correlation matrix of the LS-means as part of the "Least Squares Means" table.

COV

displays the estimated covariance matrix of the LS-means as part of the "Least Squares Means" table.

DIFF

requests that differences of the LS-means be displayed. All possible differences of LS-means, standard errors, and a Wald chi-square test are computed. Confidence limits are computed if the CL option is also specified.

E

requests that the **L** matrix coefficients for all LSMEANS effects be displayed.

SINGULAR=*number*

EPSILON=*number*

tunes the estimability checking as described for the CONTRAST statement.

MODEL Statement

MODEL *response* = < *effects* > < */options* > **;**

MODEL *events/trials* = < *effects* > < */options* > **;**

The MODEL statement specifies the response, or dependent variable, and the effects, or explanatory variables. If you omit the explanatory variables, the procedure fits an intercept-only model. An intercept term is included in the model by default. The intercept can be removed with the NOINT option.

You can specify the response in the form of a single variable or in the form of a ratio of two variables denoted *events/trials*. The first form is applicable to all responses. The second form is applicable only to summarized binomial response data. When each observation in the input data set contains the number of events (for example, successes) and the number of trials from a set of binomial trials, use the *events/trials* syntax.

In the *events/trials* model syntax, you specify two variables that contain the event and trial counts. These two variables are separated by a slash (/). The values of both *events* and (*trials*−*events*) must be nonnegative, and the value of the *trials* variable must be greater than 0 for an observation to be valid. The variable *events* or *trials* can take noninteger values.

When each observation in the input data set contains a single trial from a binomial or multinomial experiment, use the first form of the preceding MODEL statements. The response variable can be numeric or character. The ordering of response levels is critical in these models. You can use the RORDER= option in the PROC GENMOD statement to specify the response level ordering.

Responses for the Poisson distribution must be all nonnegative, but they can be noninteger values.

The effects in the MODEL statement consist of an explanatory variable or combination of variables. Explanatory variables can be continuous or classification variables. Classification variables can be character or numeric. Explanatory variables representing nominal, or classification, data must be declared in a CLASS statement. Interactions between variables can also be included as effects.

Columns of the design matrix are automatically generated for classification variables and interactions. The syntax for specification of effects is the same as for the GLM procedure. See the section "Specification of Effects" on page 1972 for more information. Also refer to Chapter 39, "The GLM Procedure."

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

AGGREGATE= *(variable-list)*

AGGREGATE= *variable*

AGGREGATE

specifies the subpopulations on which the Pearson chi-square and the deviance are calculated. This option applies only to the multinomial distribution or the binomial distribution with binary (single trial syntax) response. It is ignored if specified for other cases. Observations with common values in the given list of variables are regarded as coming from the same subpopulation. This affects the computation of the deviance and Pearson chi-square statistics. Variables in the list can be any variables in the input data set. Specifying the AGGREGATE option is equivalent to specifying the AGGREGATE= option with a variable list that includes all explanatory variables in the MODEL statement. Pearson chi-square and deviance statistics are not computed for multinomial models unless this option is specified.

ALPHA=*number*

ALPH=*number*

A=*number*

sets the confidence coefficient for parameter confidence intervals to 1−*number*. The value of *number* must be between 0 and 1. The default value of *number* is 0.05.

CICONV=*number*

sets the convergence criterion for profile likelihood confidence intervals. See the section "Confidence Intervals for Parameters" on page 1978 for the definition of convergence. The value of *number* must be between 0 and 1. By default, CICONV=1E−4.

CL

requests that confidence limits for predicted values be displayed (see the OBSTATS option).

CODING=EFFECT

CODING=FULLRANK

specifies that effect coding be used for all classification variables in the model. This is the same as specifying PARAM=EFFECT as a CLASS statement option.

CONVERGE=*number*

sets the convergence criterion. The value of *number* must be between 0 and 1. The iterations are considered to have converged when the maximum change in the parameter estimates between iteration steps is less than the value specified. The change is a relative change if the parameter is greater than 0.01 in absolute value; otherwise, it is an absolute change. By default, CONVERGE=1E−4. This convergence criterion is used in parameter estimation for a single model fit, Type 1 statistics, and likelihood ratio statistics for Type 3 analyses and CONTRAST statements.

CONVH=*number*

sets the relative Hessian convergence criterion. The value of *number* must be between 0 and 1. After convergence is determined with the change in parameter criterion specified with the CONVERGE= option, the quantity $tc = \frac{\mathbf{g}'\mathbf{H}^{-1}\mathbf{g}}{|f|}$ is computed and compared to *number*, where $\mathbf{g}$ is the gradient vector, $\mathbf{H}$ is the Hessian matrix for the model parameters, and f is the log-likelihood function. If tc is greater than *number*, a warning that the relative Hessian convergence criterion has been exceeded is printed. This criterion detects the occasional case where the change in parameter convergence criterion is satisfied, but a maximum in the log-likelihood function has not been attained. By default, CONVH=1E−4.

CORRB

requests that the parameter estimate correlation matrix be displayed.

COVB

requests that the parameter estimate covariance matrix be displayed.

DIAGNOSTICS

INFLUENCE

requests that case deletion diagnostic statistics be displayed (see the OBSTATS option).

DIST=*keyword*

D=*keyword*

ERROR=*keyword*

ERR=*keyword*

specifies the built-in probability distribution to use in the model. If you specify the DIST= option and you omit a user-defined link function, a default link function is chosen as displayed in the following table. If you specify no distribution and no link function, then the GENMOD procedure defaults to the normal distribution with the identity link function.

DIST=	Distribution	Default Link Function
BINOMIAL | BIN | B	binomial	logit
GAMMA | GAM | G	gamma	inverse (power(−1))
GEOMETRIC | GEOM	geometric	log
IGAUSSIAN | IG	inverse Gaussian	inverse squared (power(−2))
MULTINOMIAL | MULT	multinomial	cumulative logit
NEGBIN | NB	negative binomial	log
NORMAL | NOR | N	normal	identity
POISSON | POI | P	Poisson	log
ZIP		

EXPECTED

requests that the expected Fisher information matrix be used to compute parameter estimate covariances and the associated statistics. The default action is to use the observed Fisher information matrix. This option does not affect the model fitting, only the way in which the covariance matrix is computed (see the SCORING= option.)

ID=*variable*

causes the values of *variable* in the input data set to be displayed in the OBSTATS table. If

an explicit format for *variable* has been defined, the formatted values are displayed. If the OBSTATS option is not specified, this option has no effect.

INITIAL=*numbers*

sets initial values for parameter estimates in the model. The default initial parameter values are weighted least squares estimates based on using the response data as the initial mean estimate. This option can be useful in case of convergence difficulty. The intercept parameter is initialized with the INTERCEPT= option and is not included here. The values are assigned to the variables in the MODEL statement in the same order in which they appear in the MODEL statement. The order of levels for CLASS variables is determined by the ORDER= option. Note that some levels of classification variables can be aliased; that is, they correspond to linearly dependent parameters that are not estimated by the procedure. Initial values must be assigned to all levels of classification variables, regardless of whether they are aliased or not. The procedure ignores initial values corresponding to parameters not being estimated. If you specify a BY statement, all classification variables must take on the same number of levels in each BY group. Otherwise, classification variables in some of the BY groups are assigned incorrect initial values. Types of INITIAL= specifications are illustrated in the following table.

Type of List	Specification
list separated by blanks	INITIAL = 3 4 5
list separated by commas	INITIAL = 3, 4, 5
x to y	INITIAL = 3 to 5
x to y by z	INITIAL = 3 to 5 by 1
combination of list types	INITIAL = 1, 3 to 5, 9

INTERCEPT=*number*

INTERCEPT=*number-list*

initializes the intercept term to *number* for parameter estimation. If you specify both the INTERCEPT= and the NOINT options, the intercept term is not estimated, but an intercept term of *number* is included in the model. If you specify a multinomial model for ordinal data, you can specify a *number-list* for the multiple intercepts in the model.

ITPRINT

displays the iteration history for all iterative processes: parameter estimation, fitting constrained models for contrasts and Type 3 analyses, and profile likelihood confidence intervals. The last evaluation of the gradient and the negative of the Hessian (second derivative) matrix are also displayed for parameter estimation. If you perform a Bayesian analysis by specifying the BAYES statement, the iteration history for computing the mode of the posterior distribution is also displayed.

This option might result in a large amount of displayed output, especially if some of the optional iterative processes are selected.

LINK=*keyword*

specifies the link function to use in the model. The keywords and their associated built-in link functions are as follows.

LINK=	Link Function
CUMCLL	
CCLL	cumulative complementary log-log
CUMLOGIT	
CLOGIT	cumulative logit
CUMPROBIT	
CPROBIT	cumulative probit
CLOGLOG	
CLL	complementary log-log
IDENTITY	
ID	identity
LOG	log
LOGIT	logit
PROBIT	probit
POWER(*number*) | POW(*number*)	power with λ= *number*

If no LINK= option is supplied and there is a user-defined link function, the user-defined link function is used. If you specify neither the LINK= option nor a user-defined link function, then the default canonical link function is used if you specify the DIST= option. Otherwise, if you omit the DIST= option, the identity link function is used.

The cumulative link functions are appropriate only for the multinomial distribution.

LRCI

requests that two-sided confidence intervals for all model parameters be computed based on the profile likelihood function. This is sometimes called the partially maximized likelihood function. See the section "Confidence Intervals for Parameters" on page 1978 for more information about the profile likelihood function. This computation is iterative and can consume a relatively large amount of CPU time. The confidence coefficient can be selected with the ALPHA=*number* option. The resulting confidence coefficient is 1−*number*. The default confidence coefficient is 0.95.

MAXITER=*number*

MAXIT=*number*

sets the maximum allowable number of iterations for all iterative computation processes in PROC GENMOD. By default, MAXITER=50.

NOINT

requests that no intercept term be included in the model. An intercept is included unless this option is specified.

NOSCALE

holds the scale parameter fixed. Otherwise, for the normal, inverse Gaussian, and gamma distributions, the scale parameter is estimated by maximum likelihood. If you omit the SCALE= option, the scale parameter is fixed at the value 1.

OBSTATS

specifies that an additional table of statistics be displayed. Formulas for the statistics are given in the section "Predicted Values of the Mean" on page 1980, the section "Residuals"

on page 1981, and the section "Case Deletion Diagnostic Statistics" on page 1997. Residuals and fit diagnostics are not computed for multinomial models.

For each observation, the following items are displayed:

- the value of the response variable (variables if the data are binomial), frequency, and weight variables
- the values of the regression variables
- predicted mean, $\hat{\mu} = g^{-1}(\eta)$, where $\eta = \mathbf{x}_i'\hat{\boldsymbol{\beta}}$ is the linear predictor and g is the link function. If there is an offset, it is included in $\mathbf{x}_i'\hat{\boldsymbol{\beta}}$.
- estimate of the linear predictor $\mathbf{x}_i'\hat{\boldsymbol{\beta}}$. If there is an offset, it is included in $\mathbf{x}_i'\hat{\boldsymbol{\beta}}$.
- standard error of the linear predictor $\mathbf{x}_i'\hat{\boldsymbol{\beta}}$
- the value of the Hessian weight at the final iteration
- lower confidence limit of the predicted value of the mean. The confidence coefficient is specified with the ALPHA= option. See the section "Confidence Intervals on Predicted Values" on page 1980 for the computational method.
- upper confidence limit of the predicted value of the mean
- raw residual, defined as $Y - \mu$
- Pearson, or chi residual, defined as the square root of the contribution for the observation to the Pearson chi-square—that is,

  $$\frac{Y - \mu}{\sqrt{V(\mu)/w}}$$

  where Y is the response, μ is the predicted mean, w is the value of the prior weight variable specified in a WEIGHT statement, and $\mathrm{V}(\mu)$ is the variance function evaluated at μ.
- the standardized Pearson residual
- deviance residual, defined as the square root of the deviance contribution for the observation, with sign equal to the sign of the raw residual
- the standardized deviance residual
- the likelihood residual
- a Cook distance type statistic for assessing the influence of individual observations on overall model fit
- observation leverage
- DFBETA, defined as an approximation to $\hat{\beta} - \hat{\beta_{[i]}}$ for each parameter estimate $\hat{\beta}$, where $\hat{\beta_{[i]}}$ is the parameter estimate with the ith observation deleted
- standardized DFBETA, defined as DFBETA, normalized by its standard deviation
- zero inflation probability for zero inflated models
- the mean of a zero inflated response

The following additional cluster deletion diagnostic statistics are created and displayed for each cluster if a REPEATED statement is specified:

- a Cook distance type statistic for assessing the influence of entire clusters on overall model fit
- a studentized Cook distance for assessing influence of clusters
- cluster leverage
- cluster DFBETA for assessing the influence of entire clusters on individual parameter estimates
- cluster DFBETA normalized by its standard deviation

If you specify the multinomial distribution, only regression variable values, response values, predicted values, confidence limits for the predicted values, and the linear predictor are displayed in the table. Residuals and other diagnostic statistics are not available for the multinomial distribution.

The RESIDUALS, DIAGNOSTICS | INFLUENCE, PREDICTED, XVARS, and CL options cause only subgroups of the observation statistics to be displayed. You can specify more than one of these options to include different subgroups of statistics.

The ID=*variable* option causes the values of *variable* in the input data set to be displayed in the table. If an explicit format for *variable* has been defined, the formatted values are displayed.

If a REPEATED statement is present, a table is displayed for the GEE model specified in the REPEATED statement. Regression variables, response values, predicted values, confidence limits for the predicted values, linear predictor, raw residuals, Pearson residuals for each observation in the input data set are available. Case deletion diagnostic statistics are available for each observation and for each cluster.

OFFSET=*variable*

specifies a variable in the input data set to be used as an offset variable. This variable cannot be a CLASS variable, and it cannot be the response variable or one of the explanatory variables.

PREDICTED

PRED

P

requests that predicted values, the linear predictor, its standard error, and the Hessian weight be displayed (see the OBSTATS option).

RESIDUALS

R

requests that residuals and standardized residuals be displayed. Residuals and other diagnostic statistics are not available for the multinomial distribution (see the OBSTATS option).

SCALE=*number*

SCALE=PEARSON

SCALE=P

PSCALE

SCALE=DEVIANCE

SCALE=D

DSCALE

sets the value used for the scale parameter where the NOSCALE option is used. For the binomial and Poisson distributions, which have no free scale parameter, this can be used to specify an *overdispersed* model. In this case, the parameter covariance matrix and the likelihood function are adjusted by the scale parameter. See the section "Dispersion Parameter" on page 1970 and the section "Overdispersion" on page 1971 for more information. If the NOSCALE option is not specified, then *number* is used as an initial estimate of the scale parameter.

Specifying SCALE=PEARSON or SCALE=P is the same as specifying the PSCALE option. This fixes the scale parameter at the value 1 in the estimation procedure. After the parameter estimates are determined, the exponential family dispersion parameter is assumed to be given by Pearson's chi-square statistic divided by the degrees of freedom, and all statistics such as standard errors and likelihood ratio statistics are adjusted appropriately.

Specifying SCALE=DEVIANCE or SCALE=D is the same as specifying the DSCALE option. This fixes the scale parameter at a value of 1 in the estimation procedure.

After the parameter estimates are determined, the exponential family dispersion parameter is assumed to be given by the deviance divided by the degrees of freedom. All statistics such as standard errors and likelihood ratio statistics are adjusted appropriately.

SCORING=*number*

requests that on iterations up to *number*, the Hessian matrix be computed using the Fisher scoring method. For further iterations, the full Hessian matrix is computed. The default value is 1. A value of 0 causes all iterations to use the full Hessian matrix, and a value greater than or equal to the value of the MAXITER option causes all iterations to use Fisher scoring. The value of the SCORING= option must be 0 or a positive integer.

SINGULAR=*number*

sets the tolerance for testing singularity of the information matrix and the crossproducts matrix. Roughly, the test requires that a pivot be at least this number times the original diagonal value. By default, *number* is 10^7 times the machine epsilon. The default *number* is approximately 10^{-9} on most machines. This value also controls the check on estimability for ESTIMATE and CONTRAST statements.

TYPE1

requests that a Type 1, or sequential, analysis be performed. This consists of sequentially fitting models, beginning with the null (intercept term only) model and continuing up to the model specified in the MODEL statement. The likelihood ratio statistic between each successive pair of models is computed and displayed in a table.

A Type 1 analysis is not available for GEE models, since there is no associated likelihood.

TYPE3

requests that statistics for Type 3 contrasts be computed for each effect specified in the MODEL statement. The default analysis is to compute likelihood ratio statistics for the contrasts or score statistics for GEEs. Wald statistics are computed if the WALD option is also specified.

WALD
requests Wald statistics for Type 3 contrasts. You must also specify the TYPE3 option in order to compute Type 3 Wald statistics.

WALDCI
requests that two-sided Wald confidence intervals for all model parameters be computed based on the asymptotic normality of the parameter estimators. This computation is not as time-consuming as the LRCI method, since it does not involve an iterative procedure. However, it is thought to be less accurate, especially for small sample sizes. The confidence coefficient can be selected with the ALPHA= option in the same way as for the LRCI option.

XVARS
requests that the regression variables be included in the OBSTATS table.

OUTPUT Statement

OUTPUT < **OUT=***SAS-data-set* > < *keyword=name . . . keyword=name* > **;**

The OUTPUT statement creates a new SAS data set that contains all the variables in the input data set and, optionally, the estimated linear predictors (XBETA) and their standard error estimates, the weights for the Hessian matrix, predicted values of the mean, confidence limits for predicted values, residuals, and case deletion diagnostics. Residuals and diagnostic statistics are not computed for multinomial models.

You can also request these statistics with the OBSTATS, PREDICTED, RESIDUALS, DIAGNOSTICS | INFLUENCE, CL, or XVARS option in the MODEL statement. You can then create a SAS data set containing them with ODS OUTPUT commands. You might prefer to specify the OUTPUT statement for requesting these statistics since the following are true:

- The OUTPUT statement produces no tabular output.
- The OUTPUT statement creates a SAS data set more efficiently than ODS. This can be an advantage for large data sets.
- You can specify the individual statistics to be included in the SAS data set.

If you use the multinomial distribution with one of the cumulative link functions for ordinal data, the data set also contains variables named _ORDER_ and _LEVEL_ that indicate the levels of the ordinal response variable and the values of the variable in the input data set corresponding to the sorted levels. These variables indicate that the predicted value for a given observation is the probability that the response variable is as large as the value of the Value variable. Residuals and other diagnostic statistics are not available for the multinomial distribution.

The estimated linear predictor, its standard error estimate, and the predicted values and their confidence intervals are computed for all observations in which the explanatory variables are all nonmissing, even if the response is missing. By adding observations with missing response values to the input data set, you can compute these statistics for new observations or for settings of the explanatory variables not present in the data without affecting the model fit.

The following list explains specifications in the OUTPUT statement.

OUT=*SAS-data-set*
specifies the output data set. If you omit the OUT=option, the output data set is created and given a default name that uses the DATA*n* convention.

keyword=name
specifies the statistics to be included in the output data set and names the new variables that contain the statistics. Specify a keyword for each desired statistic (see the following list of keywords), an equal sign, and the name of the new variable or variables to contain the statistic. You can list only one variable after the equal sign for all the statistics, except for the case deletion diagnostics for individual parameter estimates, DFBETA, DFBETAS, DFBETAC, and DFBETACS. You can list variables enclosed in parentheses to correspond to the variables in the model, or you can specify the keyword *_all_*, without parentheses, to include deletion diagnostics for all of the parameters in the model.

Although you can use the OUTPUT statement without any *keyword=name* specifications, the output data set then contains only the original variables and, possibly, the variables Level and Value (if you use the multinomial model with ordinal data). Note that the residuals and deletion diagnostics are not available for the multinomial model with ordinal data. Some of the case deletion diagnostic statistics apply only to models for correlated data specified with a REPEATED statement. If you request these statistics for ordinary generalized linear models, the values of the corresponding variables are set to missing in the output data set. Formulas for the statistics are given in the section "Predicted Values of the Mean" on page 1980, the section "Residuals" on page 1981, and the section "Case Deletion Diagnostic Statistics" on page 1997. The keywords allowed and the statistics they represent are as follows:

DFBETA | DBETA represents the effect of deleting an observation on parameter estimates. If you specify the keyword *_all_* after the equal sign, variables named DFBETA_*ParameterName* will be included in the output data set to contain the values of the diagnostic statistic to measure the influence of deleting a single observation on the individual parameter estimates. *ParameterName* is the name of the regression model parameter formed from the input variable names concatenated with the appropriate levels, if classification variables are involved.

DFBETAS | DBETAS represents the effect of deleting an observation on standardized parameter estimates. If you specify the keyword *_all_* after the equal sign, variables named DFBETAS_*ParameterName* will be included in the output data set to contain the values of the diagnostic statistic to measure the influence of deleting a single observation on the individual parameter estimates. *ParameterName* is the name of the regression model parameter formed from the input variable names concatenated with the appropriate levels, if classification variables are involved.

DOBS | COOKD | COOKSD represents the Cook distance type statistic to measure the influence of deleting a single observation on the overall model fit.

HESSWGT represents the diagonal element of the weight matrix used in computing the Hessian matrix.

H | LEVERAGE represents the leverage of a single observation.

LOWER | L represents the lower confidence limit for the predicted value of the mean, or the lower confidence limit for the probability that the response is less than or equal to the value of Level or Value. The confidence coefficient is determined by the ALPHA=$number$ option in the MODEL statement as $(1 - number) \times 100\%$. The default confidence coefficient is 95%.

PREDICTED | PRED | PROB | P represents the predicted value of the mean of the response or the predicted probability that the response variable is less than or equal to the value of Level or Value if the multinomial model for ordinal data is used (in other words, Pr(Y $\leq$ Value), where Y is the response variable).

PZERO represents the zero-inflation probability for zero-inflated models.

RESCHI represents the Pearson (chi) residual for identifying observations that are poorly accounted for by the model.

RESDEV represents the deviance residual for identifying poorly fitted observations.

RESLIK represents the likelihood residual for identifying poorly fitted observations.

RESRAW represents the raw residual for identifying poorly fitted observations.

STDRESCHI represents the standardized Pearson (chi) residual for identifying observations that are poorly accounted for by the model.

STDRESDEV represents the standardized deviance residual for identifying poorly fitted observations.

STDXBETA represents the standard error estimate of XBETA (see the XBETA keyword).

UPPER | U represents the upper confidence limit for the predicted value of the mean, or the upper confidence limit for the probability that the response is less than or equal to the value of Level or Value. The confidence coefficient is determined by the ALPHA=$number$ option in the MODEL statement as $(1 - number) \times 100\%$. The default confidence coefficient is 95%.

XBETA represents the estimate of the linear predictor $\mathbf{x}_i'\boldsymbol{\beta}$ for observation i, or $\alpha_j + \mathbf{x}_i'\boldsymbol{\beta}$, where j is the corresponding ordered value of the response variable for the multinomial model with ordinal data. If there is an offset, it is included in $\mathbf{x}_i'\boldsymbol{\beta}$.

The keywords in the following list apply only to models specified with a REPEATED statement, fit by generalized estimating equations (GEEs).

CH | CLUSTERH | CLEVERAGE represents the leverage of a cluster.

CLUSTER represents the numerical cluster index, in order of sorted clusters.

DCLS | CLUSTERCOOKD | CLUSTERCOOKSD represents the Cook distance type statistic to measure the influence of deleting an entire cluster on the overall model fit.

DFBETAC | DBETAC represents the effect of deleting an entire cluster on parameter estimates. If you specify the keyword *_all_* after the equal sign, variables named DFBETAC_*ParameterName* will be included in the output data set to contain the values of the diagnostic statistic to measure the influence of deleting the cluster on the individual parameter estimates. *ParameterName* is the name of the regression model parameter formed from the input variable names concatenated with the appropriate levels, if classification variables are involved.

DFBETACS | DBETACS represents the effect of deleting an entire cluster on normalized parameter estimates. If you specify the keyword *_all_* after the equal sign, variables named DFBETACS_*ParameterName* will be included in the output data set to contain the values of the diagnostic statistic to measure the influence of deleting the cluster on the individual parameter estimates, normalized by their standard errors. *ParameterName* is the name of the regression model parameter formed from the input variable names concatenated with the appropriate levels, if classification variables are involved.

MCLS | CLUSTERDFIT represents the studentized Cook distance type statistic to measure the influence of deleting an entire cluster on the overall model fit.

Programming Statements

Although the most commonly used link and probability distributions are available as built-in functions, the GENMOD procedure enables you to define your own link functions and response probability distributions by using the FWDLINK, INVLINK, VARIANCE, and DEVIANCE statements. The variables assigned in these statements can have values computed in programming statements. These programming statements can occur anywhere between the PROC GENMOD statement and the RUN statement. Variable names used in programming statements must be unique. Variables from the input data set can be referenced in programming statements. The mean, linear predictor, and response are represented by the automatic variables _MEAN_, _XBETA_, and _RESP_, respectively, which can be referenced in your programming statements. Programming statements are used to define the functional dependencies of the link function, the inverse link function, the variance function, and the deviance function on the mean, linear predictor, and response variable.

The following statements illustrate the use of programming statements. Even though you usually request the Poisson distribution by specifying DIST=POISSON as a MODEL statement option, you can define the variance and deviance functions for the Poisson distribution by using the VARIANCE and DEVIANCE statements. For example, the following statements perform the same analysis as the Poisson regression example in the section "Getting Started: GENMOD Procedure" on page 1898.

The statements must be in logical order for computation, just as in a DATA step.

```
proc genmod ;
   class car age;
   a = _MEAN_;
   y = _RESP_;
   d = 2 * ( y * log( y / a ) - ( y - a ) );
   variance var = a;
   deviance dev = d;
   model c = car age / link = log offset = ln;
run;
```

The variables var and dev are dummy variables used internally by the procedure to identify the variance and deviance functions. Any valid SAS variable names can be used.

Similarly, the log link function and its inverse could be defined with the FWDLINK and INVLINK statements, as follows:

```
fwdlink link = log(_MEAN_);
invlink ilink = exp(_XBETA_);
```

These statements are for illustration, and they work well for most Poisson regression problems. If, however, in the iterative fitting process, the mean parameter becomes too close to 0, or a 0 response value occurs, an error condition occurs when the procedure attempts to evaluate the log function. You can circumvent this kind of problem by using IF-THEN/ELSE clauses or other conditional statements to check for possible error conditions and appropriately define the functions for these cases.

Data set variables can be referenced in user definitions of the link function and response distributions by using programming statements and the FWDLINK, INVLINK, DEVIANCE, and VARIANCE statements.

See the DEVIANCE, VARIANCE, FWDLINK, and INVLINK statements for more information.

REPEATED Statement

REPEATED *SUBJECT= subject-effect < / options >* **;**

The REPEATED statement specifies the covariance structure of multivariate responses for GEE model fitting in the GENMOD procedure. In addition, the REPEATED statement controls the iterative fitting algorithm used in GEEs and specifies optional output. Other GENMOD procedure statements, such as the MODEL and CLASS statements, are used in the same way as they are for ordinary generalized linear models to specify the regression model for the mean of the responses.

SUBJECT=*subject-effect*

identifies subjects in the input data set. The *subject-effect* can be a single variable, an interaction effect, a nested effect, or a combination. Each distinct value, or level, of the effect identifies a different subject, or cluster. Responses from different subjects are assumed to be statistically independent, and responses within subjects are assumed to be correlated. A

subject-effect must be specified, and variables used in defining the *subject-effect* must be listed in the CLASS statement. The input data set does not need to be sorted by subject (see the SORTED option).

The *options* control how the model is fit and what output is produced. You can specify the following options after a slash (/).

ALPHAINIT=*numbers*
specifies initial values for log odds ratio regression parameters if the LOGOR= option is specified for binary data. If this option is not specified, an initial value of 0.01 is used for all the parameters.

CONVERGE=*number*
specifies the convergence criterion for GEE parameter estimation. If the maximum absolute difference between regression parameter estimates is less than the value of *number* on two successive iterations, convergence is declared. If the absolute value of a regression parameter estimate is greater than 0.08, then the absolute difference normalized by the regression parameter value is used instead of the absolute difference. The default value of *number* is 0.0001.

CORRW
displays the estimated working correlation matrix. If you specify an exchangeable working correlation structure with the CORR=EXCH option, the CORRW option is not needed to view the estimated correlation, since a table is printed by default that contains the single estimated correlation.

CORRB
displays the estimated regression parameter correlation matrix. Both model-based and empirical correlations are displayed.

COVB
displays the estimated regression parameter covariance matrix. Both model-based and empirical covariances are displayed.

ECORRB
displays the estimated regression parameter empirical correlation matrix.

ECOVB
displays the estimated regression parameter empirical covariance matrix.

INTERCEPT=*number*
specifies either an initial or a fixed value of the intercept regression parameter in the GEE model. If you specify the NOINT option in the MODEL statement, then the intercept is fixed at the value of *number*.

INITIAL=*numbers*
specifies initial values of the regression parameters estimation, other than the intercept parameter, for GEE estimation. If this option is not specified, the estimated regression parameters assuming independence for all responses are used for the initial values.

LOGOR=*log-odds-ratio-structure-keyword*

specifies the regression structure of the log odds ratio used to model the association of the responses from subjects for binary data. The response syntax must be of the single variable type, the distribution must be binomial, and the data must be binary. Table 37.2 displays the log odds ratio structure keywords and the corresponding log odds ratio regression structures. See the section "Alternating Logistic Regressions" on page 1988 for definitions of the log odds ratio types and examples of specifying log odds ratio models. You should specify either the LOGOR= or the TYPE= option, but not both.

Table 37.2 Log Odds Ratio Regression Structures

Keyword	Log Odds Ratio Regression Structure
EXCH	exchangeable
FULLCLUST	fully parameterized clusters
LOGORVAR(*variable*)	indicator variable for specifying block effects
NESTK	*k*-nested
NEST1	1-nested
ZFULL	fully specified *z*-matrix specified in ZDATA= data set
ZREP	single cluster specification for replicated *z*-matrix specified in ZDATA= data set
ZREP(matrix)	single cluster specification for replicated *z*-matrix

MAXITER=*number*

MAXIT=*number*

specifies the maximum number of iterations allowed in the iterative GEE estimation process. The default number is 50.

MCORRB

displays the estimated regression parameter model-based correlation matrix.

MCOVB

displays the estimated regression parameter model-based covariance matrix.

MODELSE

displays an analysis of parameter estimates table that uses model-based standard errors for inference. By default, an "Analysis of Parameter Estimates" table based on empirical standard errors is displayed.

PRINTMLE

displays an analysis of maximum likelihood parameter estimates table. The maximum likelihood estimates are not displayed unless this option is specified.

RUPDATE=*number*

specifies the number of iterations between updates of the working correlation matrix. For example, RUPDATE=5 specifies that the working correlation is updated once for every five regression parameter updates. The default value of *number* is 1; that is, the working correlation is updated every time the regression parameters are updated.

SORTED

specifies that the input data are grouped by subject and sorted within subject. If this option is not specified, then the procedure internally sorts by *subject-effect* and *within subject-effect*, if a *within subject-effect* is specified.

SUBCLUSTER=*variable*

SUBCLUST=*variable*

specifies a variable defining subclusters for the 1-nested or k-nested log odds ratio association modeling structures. This variable must be listed in the CLASS statement.

TYPE=*correlation-structure keyword*

CORR=*correlation-structure keyword*

specifies the structure of the working correlation matrix used to model the correlation of the responses from subjects. Table 37.3 displays the correlation structure keywords and the corresponding correlation structures. The default working correlation type is the independent (CORR=IND). See the section "Details: GENMOD Procedure" on page 1962 for definitions of the correlation matrix types. You should specify LOGOR= or TYPE= but not both.

Table 37.3 Correlation Structure Types

Keyword	Correlation Matrix Type
AR	
AR(1)	autoregressive(1)
EXCH	
CS	exchangeable
IND	independent
MDEP(number)	m-dependent with m=number
UNSTR	
UN	unstructured
USER	
FIXED (matrix)	fixed, user-specified correlation matrix

For example, you can specify a fixed 4×4 correlation matrix with the following option:

```
TYPE=USER( 1.0  0.9  0.8  0.6
           0.9  1.0  0.9  0.8
           0.8  0.9  1.0  0.9
           0.6  0.8  0.9  1.0 )
```

V6CORR

specifies that the SAS 'Version 6' method of computing the normalized Pearson chi-square be used for working correlation estimation and for model-based covariance matrix scale factor.

WITHINSUBJECT | WITHIN=*within subject-effect*

defines an effect specifying the order of measurements within subjects. Each distinct level of the *within subject-effect* defines a different response from the same subject. If the data are in proper order within each subject, you do not need to specify this option.

If some measurements do not appear in the data for some subjects, this option properly orders the existing measurements and treats the omitted measurements as missing values. If the WITHINSUBJECT= option is not used in this situation, measurements might be improperly ordered and missing values assumed for the last measurements in a cluster.

Variables used in defining the *within subject-effect* must be listed in the CLASS statement.

YPAIR=*variable-list*
specifies the variables in the ZDATA= data set corresponding to pairs of responses for log odds ratio association modeling.

ZDATA=*SAS-data-set*
specifies a SAS data set containing either the full z-matrix for log odds ratio association modeling or the z-matrix for a single complete cluster to be replicated for all clusters.

ZROW=*variable-list*
specifies the variables in the ZDATA= data set corresponding to rows of the z-matrix for log odds ratio association modeling.

VARIANCE Statement

VARIANCE *variable = expression* **;**

You can specify a probability distribution other than the built-in distributions by using the VARIANCE and DEVIANCE statements. The variable name *variable* identifies the variance function to the procedure. The *expression* is used to define the functional dependence on the mean, and it can be any arithmetic expression supported by the DATA step language. You use the automatic variable _MEAN_ to represent the mean in the expression.

Alternatively, you can define the variance function with programming statements, as detailed in the section "Programming Statements" on page 1955. This form is convenient for using complex statements such as IF-THEN/ELSE clauses. Derivatives of the variance function for use during optimization are computed automatically. The DEVIANCE statement must also appear when the VARIANCE statement is used to define the variance function.

WEIGHT Statement

WEIGHT | SCWGT *variable* **;**

The WEIGHT statement identifies a variable in the input data set to be used as the exponential family dispersion parameter weight for each observation. The exponential family dispersion parameter is divided by the WEIGHT variable value for each observation. This is true regardless of whether the parameter is estimated by the procedure or specified in the MODEL statement with the SCALE= option. It is also true for distributions such as the Poisson and binomial that are not

usually defined to have a dispersion parameter. For these distributions, a WEIGHT variable weights the overdispersion parameter, which has the default value of 1.

The WEIGHT variable does not have to be an integer; if it is less than or equal to 0 or if it is missing, the corresponding observation is not used.

ZEROMODEL Statement

ZEROMODEL *effects* < */options* > **;**

The effects in the ZEROMODEL statement consist of explanatory variables or combinations of variables for the zero-inflation probability regression model in a zero-inflated model. The same effects can be used in both the ZEROMODEL statement and the MODEL statement, or effects can be used in one statement or the other separately. Explanatory variables can be continuous or classification variables. Classification variables can be character or numeric. Explanatory variables representing nominal, or classification, data must be declared in a CLASS statement. Interactions between variables can also be included as effects. Columns of the design matrix are automatically generated for classification variables and interactions. The syntax for specification of effects is the same as for the GLM procedure. See the section "Specification of Effects" on page 1972 for more information. Also refer to Chapter 39, "The GLM Procedure."

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

LINK=*keyword*

specifies the link function to use in the model. The keywords and their associated link functions are as follows.

LINK=	Link Function
CLOGLOG	
CLL	complementary log-log
LOGIT	logit
PROBIT	probit

If no LINK= option is supplied, the LOGIT link is used. User-defined link functions are not allowed.

Details: GENMOD Procedure

Generalized Linear Models Theory

This is a brief introduction to the theory of generalized linear models.

Response Probability Distributions

In generalized linear models, the response is assumed to possess a probability distribution of the exponential form. That is, the probability density of the response Y for continuous response variables, or the probability function for discrete responses, can be expressed as

$$f(y) = \exp\left\{\frac{y\theta - b(\theta)}{a(\phi)} + c(y,\phi)\right\}$$

for some functions a, b, and c that determine the specific distribution. For fixed ϕ, this is a one-parameter exponential family of distributions. The functions a and c are such that $a(\phi) = \phi/w$ and $c = c(y, \phi/w)$, where w is a known weight for each observation. A variable representing w in the input data set can be specified in the WEIGHT statement. If no WEIGHT statement is specified, $w_i = 1$ for all observations.

Standard theory for this type of distribution gives expressions for the mean and variance of Y:

$$\begin{aligned} \mathrm{E}(Y) &= b'(\theta) \\ \mathrm{Var}(Y) &= \frac{b''(\theta)\phi}{w} \end{aligned}$$

where the primes denote derivatives with respect to θ. If μ represents the mean of Y, then the variance expressed as a function of the mean is

$$\mathrm{Var}(Y) = \frac{V(\mu)\phi}{w}$$

where V is the *variance function*.

Probability distributions of the response Y in generalized linear models are usually parameterized in terms of the mean μ and dispersion parameter ϕ instead of the *natural parameter* θ. The probability distributions that are available in the GENMOD procedure are shown in the following list. The zero-inflated Poisson distribution is not a generalized linear model. However, the zero-inflated Poisson is included in PROC GENMOD since it is a useful extension of generalized linear models. See Long (1997) for a discussion of the zero-inflated Poisson. The PROC GENMOD scale parameter and the variance of Y are also shown.

- Normal:

$$\begin{aligned} f(y) &= \frac{1}{\sqrt{2\pi}\sigma}\exp\left[-\frac{1}{2}\left(\frac{y-\mu}{\sigma}\right)^2\right] \quad \text{for } -\infty < y < \infty \\ \phi &= \sigma^2 \\ \text{scale} &= \sigma \\ \text{Var}(Y) &= \sigma^2 \end{aligned}$$

- Inverse Gaussian:

$$\begin{aligned} f(y) &= \frac{1}{\sqrt{2\pi y^3}\sigma}\exp\left[-\frac{1}{2y}\left(\frac{y-\mu}{\mu\sigma}\right)^2\right] \quad \text{for } 0 < y < \infty \\ \phi &= \sigma^2 \\ \text{scale} &= \sigma \\ \text{Var}(Y) &= \sigma^2\mu^3 \end{aligned}$$

- Gamma:

$$\begin{aligned} f(y) &= \frac{1}{\Gamma(\nu)y}\left(\frac{y\nu}{\mu}\right)^{\nu}\exp\left(-\frac{y\nu}{\mu}\right) \quad \text{for } 0 < y < \infty \\ \phi &= \nu^{-1} \\ \text{scale} &= \nu \\ \text{Var}(Y) &= \frac{\mu^2}{\nu} \end{aligned}$$

- Geometric: This is a special case of the negative binomial with $k = 1$.

$$\begin{aligned} f(y) &= \frac{(\mu)^y}{(1+\mu)^{y+1}} \quad \text{for } y = 0, 1, 2, \ldots \\ \phi &= 1 \\ \text{Var}(Y) &= \mu(1+\mu) \end{aligned}$$

- Negative binomial:

$$\begin{aligned} f(y) &= \frac{\Gamma(y+1/k)}{\Gamma(y+1)\Gamma(1/k)}\frac{(k\mu)^y}{(1+k\mu)^{y+1/k}} \quad \text{for } y = 0, 1, 2, \ldots \\ \text{dispersion} &= k \\ \text{Var}(Y) &= \mu + k\mu^2 \end{aligned}$$

- Poisson:

$$\begin{aligned} f(y) &= \frac{\mu^y \mathrm{e}^{-\mu}}{y!} \quad \text{for } y = 0, 1, 2, \ldots \\ \phi &= 1 \\ \mathrm{Var}(Y) &= \mu \end{aligned}$$

- Binomial:

$$\begin{aligned} f(y) &= \left(\begin{array}{c} n \\ r \end{array} \right) \mu^r (1-\mu)^{n-r} \quad \text{for } y = \frac{r}{n},\ r = 0, 1, 2, \ldots, n \\ \phi &= 1 \\ \mathrm{Var}(Y) &= \frac{\mu(1-\mu)}{n} \end{aligned}$$

- Multinomial:

$$\begin{aligned} f(y_1, y_2, \cdots, y_k) &= \frac{m!}{y_1! y_2! \cdots y_k!} p_1^{y_1} p_2^{y_2} \cdots p_k^{y_k} \\ \phi &= 1 \end{aligned}$$

- Zero-inflated Poisson:

$$\begin{aligned} f(y) &= \begin{cases} \omega + (1-\omega)\mathrm{e}^{-\lambda} & \text{for } y = 0 \\ (1-\omega)\frac{\lambda^y \mathrm{e}^{-\lambda}}{y!} & \text{for } y = 1, 2, \ldots \end{cases} \\ \phi &= 1 \\ \mu = \mathrm{E}(Y) &= (1-\omega)\lambda \\ \mathrm{Var}(Y) &= \mu + \frac{\omega}{1-\omega}\mu^2 \end{aligned}$$

The negative binomial distribution contains a parameter k, called the negative binomial dispersion parameter. This is not the same as the generalized linear model dispersion ϕ, but it is an additional distribution parameter that must be estimated or set to a fixed value.

For the binomial distribution, the response is the binomial proportion $Y = \textit{events}/\textit{trials}$. The variance function is $V(\mu) = \mu(1-\mu)$, and the binomial trials parameter n is regarded as a weight w.

If a weight variable is present, ϕ is replaced with ϕ/w, where w is the weight variable.

PROC GENMOD works with a scale parameter that is related to the exponential family dispersion parameter ϕ instead of working with ϕ itself. The scale parameters are related to the dispersion parameter as shown previously with the probability distribution definitions. Thus, the scale parameter output in the "Analysis of Parameter Estimates" table is related to the exponential family dispersion parameter. If you specify a constant scale parameter with the SCALE= option in the MODEL statement, it is also related to the exponential family dispersion parameter in the same way.

Link Function

The mean μ_i of the response in the ith observation is related to a linear predictor through a monotonic differentiable link function g.

$$g(\mu_i) = \mathbf{x}_i'\boldsymbol{\beta}$$

Here, $\mathbf{x}_i$ is a fixed known vector of explanatory variables, and $\boldsymbol{\beta}$ is a vector of unknown parameters.

Log-Likelihood Functions

Log-likelihood functions for the distributions that are available in the procedure are parameterized in terms of the means μ_i and the dispersion parameter ϕ. The term y_i represents the response for the ith observation, and w_i represents the known dispersion weight. The log-likelihood functions are of the form

$$L(\mathbf{y}, \boldsymbol{\mu}, \phi) = \sum_i \log\left(f(y_i, \mu_i, \phi)\right)$$

where the sum is over the observations. The forms of the individual contributions

$$l_i = \log\left(f(y_i, \mu_i, \phi)\right)$$

are shown in the following list; the parameterizations are expressed in terms of the mean and dispersion parameters.

For the discrete distributions (binomial, multinomial, negative binomial, and Poisson), the functions computed as the sum of the l_i terms are not proper log-likelihood functions, since terms involving binomial coefficients or factorials of the observed counts are dropped from the computation of the log likelihood, and a dispersion parameter ϕ is included in the computation. Deletion of factorial terms and inclusion of a dispersion parameter do not affect parameter estimates or their estimated covariances for these distributions, and this is the function used in maximum likelihood estimation. The value of ϕ used in computing the reported log-likelihood function is either the final estimated value, or the fixed value, if the dispersion parameter is fixed. Even though it is not a proper log-likelihood function in all cases, the function computed as the sum of the l_i terms is reported in the output as the *log likelihood*. The proper log-likelihood function is also computed as the sum of the ll_i terms in the following list, and it is reported as the *full log likelihood* in the output.

- Normal:

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

- Inverse Gaussian:

$$ll_i = l_i = -\frac{1}{2}\left[\frac{w_i(y_i - \mu_i)^2}{y_i\mu^2\phi} + \log\left(\frac{\phi y_i^3}{w_i}\right) + \log(2\pi)\right]$$

- Gamma:

$$ll_i = l_i = \frac{w_i}{\phi}\log\left(\frac{w_i y_i}{\phi\mu_i}\right) - \frac{w_i y_i}{\phi\mu_i} - \log(y_i) - \log\left(\Gamma\left(\frac{w_i}{\phi}\right)\right)$$

- Negative binomial:

$$l_i = y_i \log\left(\frac{k\mu}{w_i}\right) - (y_i + w_i/k)\log\left(1 + \frac{k\mu}{w_i}\right) + \log\left(\frac{\Gamma(y_i + w_i/k)}{\Gamma(w_i/k)}\right)$$

$$ll_i = y_i \log\left(\frac{k\mu}{w_i}\right) - (y_i + w_i/k)\log\left(1 + \frac{k\mu}{w_i}\right) + \log\left(\frac{\Gamma(y_i + w_i/k)}{\Gamma(y_i + 1)\Gamma(w_i/k)}\right)$$

- Poisson:

$$l_i = \frac{w_i}{\phi}[y_i \log(\mu_i) - \mu_i]$$

$$ll_i = w_i[y_i \log(\mu_i) - \mu_i - \log(y_i!)]$$

- Binomial:

$$l_i = \frac{w_i}{\phi}[r_i \log(p_i) + (n_i - r_i)\log(1 - p_i)]$$

$$ll_i = w_i[\log\left(\begin{array}{c} n_i \\ r_i \end{array}\right) + r_i \log(p_i) + (n_i - r_i)\log(1 - p_i)]$$

- Multinomial (k categories):

$$l_i = \frac{w_i}{\phi}\sum_{j=1}^{k} y_{ij} \log(\mu_{ij})$$

$$ll_i = w_i[\log(m_i!) + \sum_{j=1}^{k}(y_{ij} \log(\mu_{ij}) - \log(y_{ij}!))]$$

- Zero-inflated Poisson:

$$l_i = ll_i = \begin{cases} w_i \log[\omega_i + (1 - \omega_i)\exp(-\mu_i)] & y_i = 0 \\ w_i[\log(1 - \omega_i) + y_i \log(\mu_i) - \mu_i - \log(y_i!)] & y_i > 0 \end{cases}$$

Maximum Likelihood Fitting

The GENMOD procedure uses a ridge-stabilized Newton-Raphson algorithm to maximize the log-likelihood function $L(\mathbf{y}, \boldsymbol{\mu}, \phi)$ with respect to the regression parameters. By default, the procedure also produces maximum likelihood estimates of the scale parameter as defined in the section "Response Probability Distributions" on page 1962 for the normal, inverse Gaussian, negative binomial, and gamma distributions.

On the rth iteration, the algorithm updates the parameter vector $\boldsymbol{\beta}_r$ with

$$\boldsymbol{\beta}_{r+1} = \boldsymbol{\beta}_r - \mathbf{H}^{-1}\mathbf{s}$$

where $\mathbf{H}$ is the Hessian (second derivative) matrix, and $\mathbf{s}$ is the gradient (first derivative) vector of the log-likelihood function, both evaluated at the current value of the parameter vector. That is,

$$\mathbf{s} = [s_j] = \left[\frac{\partial L}{\partial \beta_j}\right]$$

and

$$\mathbf{H} = [h_{ij}] = \left[\frac{\partial^2 L}{\partial \beta_i \partial \beta_j}\right]$$

In some cases, the scale parameter is estimated by maximum likelihood. In these cases, elements corresponding to the scale parameter are computed and included in $\mathbf{s}$ and $\mathbf{H}$.

If $\eta_i = \mathbf{x}_i'\boldsymbol{\beta}$ is the linear predictor for observation i and g is the link function, then $\eta_i = g(\mu_i)$, so that $\mu_i = g^{-1}(\mathbf{x}_i'\boldsymbol{\beta})$ is an estimate of the mean of the ith observation, obtained from an estimate of the parameter vector $\boldsymbol{\beta}$.

The gradient vector and Hessian matrix for the regression parameters are given by

$$\begin{aligned} \mathbf{s} &= \sum_i \frac{w_i(y_i - \mu_i)\mathbf{x}_i}{V(\mu_i)g'(\mu_i)\phi} \\ \mathbf{H} &= -\mathbf{X}'\mathbf{W}_o\mathbf{X} \end{aligned}$$

where $\mathbf{X}$ is the design matrix, $\mathbf{x}_i$ is the transpose of the ith row of $\mathbf{X}$, and V is the variance function. The matrix $\mathbf{W}_o$ is diagonal with its ith diagonal element

$$w_{oi} = w_{ei} + w_i(y_i - \mu_i)\frac{V(\mu_i)g''(\mu_i) + V'(\mu_i)g'(\mu_i)}{(V(\mu_i))^2(g'(\mu_i))^3\phi}$$

where

$$w_{ei} = \frac{w_i}{\phi V(\mu_i)(g'(\mu_i))^2}$$

The primes denote derivatives of g and V with respect to μ. The negative of $\mathbf{H}$ is called the observed information matrix. The expected value of $\mathbf{W}_o$ is a diagonal matrix $\mathbf{W}_e$ with diagonal values w_{ei}. If you replace $\mathbf{W}_o$ with $\mathbf{W}_e$, then the negative of $\mathbf{H}$ is called the expected information matrix. $\mathbf{W}_e$ is the weight matrix for the Fisher scoring method of fitting. Either $\mathbf{W}_o$ or $\mathbf{W}_e$ can be used in the update equation. The GENMOD procedure uses Fisher scoring for iterations up to the number specified by the SCORING option in the MODEL statement, and it uses the observed information matrix on additional iterations.

Covariance and Correlation Matrix

The estimated covariance matrix of the parameter estimator is given by

$$\mathbf{\Sigma} = -\mathbf{H}^{-1}$$

where $\mathbf{H}$ is the Hessian matrix evaluated using the parameter estimates on the last iteration. Note that the dispersion parameter, whether estimated or specified, is incorporated into $\mathbf{H}$. Rows and columns corresponding to aliased parameters are not included in $\mathbf{\Sigma}$.

The correlation matrix is the normalized covariance matrix. That is, if σ_{ij} is an element of $\mathbf{\Sigma}$, then the corresponding element of the correlation matrix is $\sigma_{ij}/\sigma_i\sigma_j$, where $\sigma_i = \sqrt{\sigma_{ii}}$.

Goodness of Fit

Two statistics that are helpful in assessing the goodness of fit of a given generalized linear model are the scaled deviance and Pearson's chi-square statistic. For a fixed value of the dispersion parameter ϕ, the scaled deviance is defined to be twice the difference between the maximum achievable log likelihood and the log likelihood at the maximum likelihood estimates of the regression parameters.

Note that these statistics are not valid for GEE models.

If $l(\mathbf{y}, \boldsymbol{\mu})$ is the log-likelihood function expressed as a function of the predicted mean values $\boldsymbol{\mu}$ and the vector $\mathbf{y}$ of response values, then the scaled deviance is defined by

$$D^*(\mathbf{y}, \boldsymbol{\mu}) = 2(l(\mathbf{y}, \mathbf{y}) - l(\mathbf{y}, \boldsymbol{\mu}))$$

For specific distributions, this can be expressed as

$$D^*(\mathbf{y}, \boldsymbol{\mu}) = \frac{D(\mathbf{y}, \boldsymbol{\mu})}{\phi}$$

where D is the deviance. The following table displays the deviance for each of the probability distributions available in PROC GENMOD. The deviance cannot be directly calculated for the zero-inflated Poisson model. Twice the negative of the log likelihood is reported instead of the proper deviance for the zero-inflated Poisson.

Distribution	Deviance
normal	$\sum_i w_i(y_i - \mu_i)^2$
Poisson	$2\sum_i w_i \left[y_i \log\left(\frac{y_i}{\mu_i}\right) - (y_i - \mu_i) \right]$
binomial	$2\sum_i w_i m_i \left[y_i \log\left(\frac{y_i}{\mu_i}\right) + (1 - y_i) \log\left(\frac{1-y_i}{1-\mu_i}\right) \right]$
gamma	$2\sum_i w_i \left[-\log\left(\frac{y_i}{\mu_i}\right) + \frac{y_i - \mu_i}{\mu_i} \right]$
inverse Gaussian	$\sum_i \frac{w_i(y_i-\mu_i)^2}{\mu_i^2 y_i}$
multinomial	$\sum_i \sum_j w_i y_{ij} \log\left(\frac{y_{ij}}{p_{ij} m_i}\right)$
negative binomial	$2\sum_i \left[y \log(y/\mu) - (y + w_i/k) \log\left(\frac{y + w_i/k}{\mu + w_i/k}\right) \right]$
zero-inflated Poisson	$-2\sum_i \begin{cases} w_i \log[\omega_i + (1-\omega_i)\exp(-\mu_i)] & y_i = 0 \\ w_i[\log(1-\omega_i) + y_i \log(\mu_i) - \mu_i - \log(y_i!)] & y_i > 0 \end{cases}$

In the binomial case, $y_i = r_i/m_i$, where r_i is a binomial count and m_i is the binomial number of trials parameter.

In the multinomial case, y_{ij} refers to the observed number of occurrences of the jth category for the ith subpopulation defined by the AGGREGATE= variable, m_i is the total number in the ith subpopulation, and p_{ij} is the category probability.

Pearson's chi-square statistic is defined as

$$X^2 = \sum_i \frac{w_i(y_i - \mu_i)^2}{V(\mu_i)}$$

and the scaled Pearson's chi-square is X^2/ϕ.

The scaled version of both of these statistics, under certain regularity conditions, has a limiting chi-square distribution, with degrees of freedom equal to the number of observations minus the number of parameters estimated. The scaled version can be used as an approximate guide to the goodness of fit of a given model. Use caution before applying these statistics to ensure that all the conditions for the asymptotic distributions hold. McCullagh and Nelder (1989) advise that differences in deviances for nested models can be better approximated by chi-square distributions than the deviances can themselves.

In cases where the dispersion parameter is not known, an estimate can be used to obtain an approximation to the scaled deviance and Pearson's chi-square statistic. One strategy is to fit a model that contains a sufficient number of parameters so that all systematic variation is removed, estimate ϕ from this model, and then use this estimate in computing the scaled deviance of submodels. The deviance or Pearson's chi-square divided by its degrees of freedom is sometimes used as an estimate of the dispersion parameter ϕ. For example, since the limiting chi-square distribution of the scaled deviance $D^* = D/\phi$ has $n - p$ degrees of freedom, where n is the number of observations and p is the number of parameters, equating D^* to its mean and solving for ϕ yields $\hat{\phi} = D/(n - p)$. Similarly, an estimate of ϕ based on Pearson's chi-square X^2 is $\hat{\phi} = X^2/(n - p)$. Alternatively, a maximum likelihood estimate of ϕ can be computed by the procedure, if desired. See the discussion in the section "Type 1 Analysis" on page 1976 for more about the estimation of the dispersion parameter.

Other Fit Statistics

The Akaike information criterion (AIC) is a measure of goodness of model fit that balances model fit against model simplicity. AIC has the form

$$\text{AIC} = -2LL + 2p$$

where p is the number of parameters estimated in the model, and LL is the log likelihood evaluated at the value of the estimated parameters. An alternative form is the corrected AIC given by

$$\text{AICC} = -2LL + 2p\frac{n}{n - p - 1}$$

where n is the total number of observations used.

The Bayesian information criterion (BIC) is a similar measure. BIC is defined by

$$\text{BIC} = -2LL + p\log(n)$$

See Akaike (1981, 1979) for details of AIC and BIC. See Simonoff (2003) for a discussion of using AIC, AICC, and BIC with generalized linear models. These criteria are useful in selecting among regression models, with smaller values representing better model fit. PROC GENMOD uses the full log likelihoods defined in the section "Log-Likelihood Functions" on page 1965, with all terms included, for computing all of the criteria.

Dispersion Parameter

There are several options available in PROC GENMOD for handling the exponential distribution dispersion parameter. The NOSCALE and SCALE options in the MODEL statement affect the way in which the dispersion parameter is treated. If you specify the SCALE=DEVIANCE option, the dispersion parameter is estimated by the deviance divided by its degrees of freedom. If you specify the SCALE=PEARSON option, the dispersion parameter is estimated by Pearson's chi-square statistic divided by its degrees of freedom.

Otherwise, values of the SCALE and NOSCALE options and the resultant actions are displayed in the following table.

NOSCALE	**SCALE=*value***	**Action**
present	present	scale fixed at *value*
present	not present	scale fixed at 1
not present	not present	scale estimated by ML
not present	present	scale estimated by ML, starting point at *value*
present (negative binomial)	not present	k fixed at 0

The meaning of the scale parameter displayed in the "Analysis Of Parameter Estimates" table is different for the gamma distribution than for the other distributions. The relation of the scale parameter as used by PROC GENMOD to the exponential family dispersion parameter ϕ is displayed in the following table. For the binomial and Poisson distributions, ϕ is the overdispersion parameter, as defined in the "Overdispersion" section, which follows.

Distribution	**Scale**
normal	$\sqrt{\phi}$
inverse Gaussian	$\sqrt{\phi}$
gamma	$1/\phi$
binomial	$\sqrt{\phi}$
Poisson	$\sqrt{\phi}$

In the case of the negative binomial distribution, PROC GENMOD reports the "dispersion" parameter estimated by maximum likelihood. This is the negative binomial parameter k defined in the section "Response Probability Distributions" on page 1962.

Overdispersion

Overdispersion is a phenomenon that sometimes occurs in data that are modeled with the binomial or Poisson distributions. If the estimate of dispersion after fitting, as measured by the deviance or Pearson's chi-square, divided by the degrees of freedom, is not near 1, then the data might be *overdispersed* if the dispersion estimate is greater than 1 or *underdispersed* if the dispersion estimate is less than 1. A simple way to model this situation is to allow the variance functions of these distributions to have a multiplicative overdispersion factor ϕ:

- binomial: $V(\mu) = \phi\mu(1-\mu)$
- Poisson: $V(\mu) = \phi\mu$

An alternative method to allow for overdispersion in the Poisson distribution is to fit a negative binomial distribution, where $V(\mu) = \mu + k\mu^2$, instead of the Poisson. The parameter k can be estimated by maximum likelihood, thus allowing for overdispersion of a specific form. This is different from the multiplicative overdispersion factor ϕ, which can accommodate many forms of overdispersion.

The models are fit in the usual way, and the parameter estimates are not affected by the value of ϕ. The covariance matrix, however, is multiplied by ϕ, and the scaled deviance and log likelihoods used in likelihood ratio tests are divided by ϕ. The profile likelihood function used in computing confidence intervals is also divided by ϕ. If you specify a WEIGHT statement, ϕ is divided by the value of the WEIGHT variable for each observation. This has the effect of multiplying the contributions of the log-likelihood function, the gradient, and the Hessian by the value of the WEIGHT variable for each observation.

The SCALE= option in the MODEL statement enables you to specify a value of $\sigma = \sqrt{\phi}$ for the binomial and Poisson distributions. If you specify the SCALE=DEVIANCE option in the MODEL statement, the procedure uses the deviance divided by degrees of freedom as an estimate of ϕ, and all statistics are adjusted appropriately. You can use Pearson's chi-square instead of the deviance by specifying the SCALE=PEARSON option.

The function obtained by dividing a log-likelihood function for the binomial or Poisson distribution by a dispersion parameter is not a legitimate log-likelihood function. It is an example of a *quasi-likelihood* function. Most of the asymptotic theory for log likelihoods also applies to quasi-likelihoods, which justifies computing standard errors and likelihood ratio statistics by using quasi-likelihoods instead of proper log likelihoods. See McCullagh and Nelder (1989, Chapter 9), McCullagh (1983), and Hardin and Hilbe (2003) for details on quasi-likelihood functions.

Although the estimate of the dispersion parameter is often used to indicate overdispersion or underdispersion, this estimate might also indicate other problems such as an incorrectly specified model or outliers in the data. You should carefully assess whether this type of model is appropriate for your data.

Specification of Effects

Each term in a model is called an effect. Effects are specified in the MODEL statement. You specify effects with a special notation that uses variable names and operators. There are two types of variables, *classification* (or *CLASS*) variables and *continuous* variables. There are two primary types of operators, *crossing* and *nesting*. A third type, the *bar* operator, is used to simplify effect specification. Crossing is the type of operator most commonly used in generalized linear models.

Variables that identify classification levels are called *CLASS* variables in SAS and are identified in a CLASS statement. These might also be called *categorical, qualitative, discrete,* or *nominal* variables. CLASS variables can be either character or numeric. The values of CLASS variables are called *levels*. For example, the CLASS variable Sex could have the levels 'male' and 'female'.

In a model, an explanatory variable that is not declared in a CLASS statement is assumed to be continuous. Continuous variables must be numeric. For example, the heights and weights of subjects in an experiment are continuous variables.

The types of effects most useful in generalized linear models are shown in the following list. Assume that A, B, and C are classification variables and that X1 and X2 are continuous variables.

- Regressor effects are specified by writing continuous variables by themselves: X1, X2.
- Polynomial effects are specified by joining two or more continuous variables with asterisks: X1*X2.
- Main effects are specified by writing classification variables by themselves: A, B, C.
- Crossed effects (interactions) are specified by joining two or more classification variables with asterisks: A*B, B*C, A*B*C.
- Nested effects are specified by following a main effect or crossed effect with a classification variable or list of classification variables enclosed in parentheses: B(A), C(B A), A*B(C). In the preceding example, B(A) is "B nested within A."
- Combinations of continuous and classification variables can be specified in the same way by using the crossing and nesting operators.

The bar operator consists of two effects joined with a vertical bar (|). It is shorthand notation for including the left-hand side, the right-hand side, and the cross between them as effects in the model. For example, A | B is equivalent to A B A*B. The effects in the bar operator can be classification variables, continuous variables, or combinations of effects defined using operators. Multiple bars are permitted. For example, A | B | C means A B C A*B A*C B*C A*B*C.

You can specify the maximum number of variables in any effect that results from bar evaluation by specifying the maximum number, preceded by an @ sign. For example, A | B | C@2 results in effects that involve two or fewer variables: A B C A*B A*C B*C.

Parameterization Used in PROC GENMOD

Design Matrix

The linear predictor part of a generalized linear model is

$$\eta = \mathbf{X}\beta$$

where β is an unknown parameter vector and $\mathbf{X}$ is a known design matrix. By default, all models automatically contain an intercept term; that is, the first column of $\mathbf{X}$ contains all 1s. Additional columns of $\mathbf{X}$ are generated for classification variables, regression variables, and any interaction terms included in the model. It is important to understand the ordering of classification variable parameters when you use the ESTIMATE or CONTRAST statement. The ordering of these parameters is displayed in the "CLASS Level Information" table and in tables displaying the parameter estimates of the fitted model.

When you specify an overparameterized model with the PARAM=GLM option in the CLASS statement, some columns of $\mathbf{X}$ can be linearly dependent on other columns. For example, when you specify a model consisting of an intercept term and a classification variable, the column corresponding to any one of the levels of the classification variable is linearly dependent on the other columns of $\mathbf{X}$. The columns of $\mathbf{X}'\mathbf{X}$ are checked in the order in which the model is specified for dependence on preceding columns. If a dependency is found, the parameter corresponding to the dependent column is set to 0 along with its standard error to indicate that it is not estimated. The order in which the levels of a classification variable are checked for dependencies can be set by the ORDER= option in the PROC GENMOD statement or by the ORDER= option in the CLASS statement. For full-rank parameterizations, the columns of the $\mathbf{X}$ matrix are designed to be linearly independent.

You can exclude the intercept term from the model by specifying the NOINT option in the MODEL statement.

Missing Level Combinations

All levels of interaction terms involving classification variables might not be represented in the data. In that case, PROC GENMOD does not include parameters in the model for the missing levels.

CLASS Variable Parameterization

Consider a model with one CLASS variable A with four levels, 1, 2, 5, and 7. Details of the possible choices for the PARAM= option follow.

EFFECT — Three columns are created to indicate group membership of the nonreference levels. For the reference level, all three dummy variables have a value of -1. For instance, if the reference level is 7 (REF=7), the design matrix columns for A are as follows:

Effect Coding			
	Design Matrix		
A	A1	A2	A5
1	1	0	0
2	0	1	0
5	0	0	1
7	−1	−1	−1

Parameter estimates of CLASS main effects that use the effect coding scheme estimate the difference in the effect of each nonreference level compared to the average effect over all four levels.

GLM

As in PROC GLM, four columns are created to indicate group membership. The design matrix columns for A are as follows:

GLM Coding				
	Design Matrix			
A	A1	A2	A5	A7
1	1	0	0	0
2	0	1	0	0
5	0	0	1	0
7	0	0	0	1

Parameter estimates of CLASS main effects that use the GLM coding scheme estimate the difference in the effects of each level compared to the last level.

ORDINAL

THERMOMETER

Three columns are created to indicate group membership of the higher levels of the effect. For the first level of the effect (which for A is 1), all three dummy variables have a value of 0. The design matrix columns for A are as follows:

Ordinal Coding			
	Design Matrix		
A	A2	A5	A7
1	0	0	0
2	1	0	0
5	1	1	0
7	1	1	1

The first level of the effect is a control or baseline level. Parameter estimates of CLASS main effects that use the ORDINAL coding scheme estimate the effect on the response as the ordinal factor is set to each succeeding level. When the parameters for an ordinal main effect have the same sign, the response effect is monotonic across the levels.

POLYNOMIAL

POLY

Three columns are created. The first represents the linear term (x), the second represents the quadratic term (x^2), and the third represents the cubic term (x^3), where x is the level value. If the CLASS levels are not numeric, they are translated into 1, 2, 3, ... according to their sorting order. The design matrix columns for A are as follows:

Polynomial Coding			
	Design Matrix		
A	APOLY1	APOLY2	APOLY3
1	1	1	1
2	2	4	8
5	5	25	125
7	7	49	343

REFERENCE

REF Three columns are created to indicate group membership of the nonreference levels. For the reference level, all three dummy variables have a value of 0. For instance, if the reference level is 7 (REF=7), the design matrix columns for A are as follows:

Reference Coding			
	Design Matrix		
A	A1	A2	A5
1	1	0	0
2	0	1	0
5	0	0	1
7	0	0	0

Parameter estimates of CLASS main effects that use the reference coding scheme estimate the difference in the effect of each nonreference level compared to the effect of the reference level.

ORTHEFFECT The columns are obtained by applying the Gram-Schmidt orthogonalization to the columns for PARAM=EFFECT. The design matrix columns for A are as follows:

Orthogonal Effect Coding			
	Design Matrix		
A	AOEFF1	AOEFF2	AOEFF3
1	1.41421	−0.81650	−0.57735
2	0.00000	1.63299	−0.57735
5	0.00000	0.00000	1.73205
7	−1.41421	−0.81649	−0.57735

ORTHORDINAL

ORTHOTHERM The columns are obtained by applying the Gram-Schmidt orthogonalization to the columns for PARAM=ORDINAL. The design matrix columns for A are as follows:

Orthogonal Ordinal Coding			
	Design Matrix		
A	AOORD1	AOORD2	AOORD3
1	−1.73205	0.00000	0.00000
2	0.57735	−1.63299	0.00000
5	0.57735	0.81650	−1.41421
7	0.57735	0.81650	1.41421

ORTHPOLY The columns are obtained by applying the Gram-Schmidt orthogonalization to the columns for PARAM=POLY. The design matrix columns for A are as follows:

Orthogonal Polynomial Coding			
	Design Matrix		
A	AOPOLY1	AOPOLY2	AOPOLY5
1	−1.153	0.907	−0.921
2	−0.734	−0.540	1.473
5	0.524	−1.370	−0.921
7	1.363	1.004	0.368

ORTHREF The columns are obtained by applying the Gram-Schmidt orthogonalization to the columns for PARAM=REFERENCE. The design matrix columns for A are as follows:

Orthogonal Reference Coding			
	Design Matrix		
A	AOREF1	AOREF2	AOREF3
1	1.73205	0.00000	0.00000
2	−0.57735	1.63299	0.00000
5	−0.57735	−0.81650	1.41421
7	−0.57735	−0.81650	−1.41421

Type 1 Analysis

A Type 1 analysis consists of fitting a sequence of models, beginning with a simple model with only an intercept term, and continuing through a model of specified complexity, fitting one additional effect on each step. Likelihood ratio statistics—that is, twice the difference of the log likelihoods—are computed between successive models. This type of analysis is sometimes called an analysis of deviance since, if the dispersion parameter is held fixed for all models, it is equivalent to computing differences of scaled deviances. The asymptotic distribution of the likelihood ratio statistics, under the hypothesis that the additional parameters included in the model are equal to 0, is a chi-square with degrees of freedom equal to the difference in the number of parameters estimated in the successive models. Thus, these statistics can be used in a test of hypothesis of the significance of each additional term fit.

This type of analysis is not available for GEE models, since the deviance is not computed for this type of model.

If the dispersion parameter ϕ is known, it can be included in the models; if it is unknown, there are two strategies allowed by PROC GENMOD. The dispersion parameter can be estimated from a maximal model by the deviance or Pearson's chi-square divided by degrees of freedom, as discussed in the section "Goodness of Fit" on page 1968, and this value can be used in all models. An alternative is to consider the dispersion to be an additional unknown parameter for each model and estimate it by maximum likelihood on each step. By default, PROC GENMOD estimates scale by maximum likelihood at each step.

A table of likelihood ratio statistics is produced, along with associated p-values based on the asymptotic chi-square distributions.

If you specify either the SCALE=DEVIANCE or the SCALE=PEARSON option in the MODEL statement, the dispersion parameter is estimated using the deviance or Pearson's chi-square statistic, and F statistics are computed in addition to the chi-square statistics for assessing the significance of each additional term in the Type 1 analysis. See the section "*F* Statistics" on page 1979 for a definition of F statistics.

This Type 1 analysis has the general property that the results depend on the order in which the terms of the model are fitted. The terms are fitted in the order in which they are specified in the MODEL statement.

Type 3 Analysis

A Type 3 analysis is similar to the Type III sums of squares used in PROC GLM, except that likelihood ratios are used instead of sums of squares. First, a Type III estimable function is defined for an effect of interest in exactly the same way as in PROC GLM. Then maximum likelihood estimates are computed under the constraint that the Type III function of the parameters is equal to 0, by using constrained optimization. Let the resulting constrained parameter estimates be $\tilde{\boldsymbol{\beta}}$ and the log likelihood be $l(\tilde{\boldsymbol{\beta}})$. Then the likelihood ratio statistic

$$S = 2(l(\hat{\boldsymbol{\beta}}) - l(\tilde{\boldsymbol{\beta}}))$$

where $\hat{\boldsymbol{\beta}}$ is the unconstrained estimate, has an asymptotic chi-square distribution under the hypothesis that the Type III contrast is equal to 0, with degrees of freedom equal to the number of parameters associated with the effect.

When a Type 3 analysis is requested, PROC GENMOD produces a table that contains the likelihood ratio statistics, degrees of freedom, and p-values based on the limiting chi-square distributions for each effect in the model. If you specify either the DSCALE or PSCALE option in the MODEL statement, F statistics are also computed for each effect.

Options for handling the dispersion parameter are the same as for a Type 1 analysis. The dispersion parameter can be specified to be a known value, estimated from the deviance or Pearson's chi-square divided by degrees of freedom, or estimated by maximum likelihood individually for the unconstrained and constrained models. By default, PROC GENMOD estimates scale by maximum likelihood for each model fit.

The results of this type of analysis do not depend on the order in which the terms are specified in the MODEL statement.

A Type 3 analysis can consume considerable computation time since a constrained model is fitted for each effect. Wald statistics for Type 3 contrasts are computed if you specify the WALD option. Wald statistics for contrasts use less computation time than likelihood ratio statistics but might be less accurate indicators of the significance of the effect of interest. The Wald statistic for testing $\mathbf{L}'\boldsymbol{\beta} = \mathbf{0}$, where $\mathbf{L}$ is the contrast matrix, is defined by

$$S = (\mathbf{L}'\hat{\boldsymbol{\beta}})'(\mathbf{L}'\hat{\boldsymbol{\Sigma}}\mathbf{L})^{-}(\mathbf{L}'\hat{\boldsymbol{\beta}})$$

where $\boldsymbol{\beta}$ is the maximum likelihood estimate and $\boldsymbol{\Sigma}$ is its estimated covariance matrix. The asymptotic distribution of S is chi-square with r degrees of freedom, where r is the rank of $\mathbf{L}$.

See Chapter 39, "The GLM Procedure,"and Chapter 15, "The Four Types of Estimable Functions," for more information about Type III estimable functions. Also refer to Littell, Freund, and Spector (1991).

Generalized score tests for Type III contrasts are computed for GEE models if you specify the TYPE3 option in the MODEL statement when a REPEATED statement is also used. See the section "Generalized Score Statistics" on page 1993 for more information about generalized score statistics. Wald tests are also available with the Wald option in the CONTRAST statement. In this case, the robust covariance matrix estimate is used for $\mathbf{\Sigma}$ in the Wald statistic.

Confidence Intervals for Parameters

Likelihood Ratio-Based Confidence Intervals

PROC GENMOD produces likelihood ratio-based confidence intervals, also known as profile likelihood confidence intervals, for parameter estimates for generalized linear models. These are not computed for GEE models, since there is no likelihood for this type of model. Suppose that the parameter vector is $\boldsymbol{\beta} = [\beta_0, \beta_1, \ldots, \beta_p]'$ and that you want a confidence interval for β_j. The profile likelihood function for β_j is defined as

$$l^*(\beta_j) = \max_{\tilde{\boldsymbol{\beta}}} l(\boldsymbol{\beta})$$

where $\tilde{\boldsymbol{\beta}}$ is the vector $\boldsymbol{\beta}$ with the jth element fixed at β_j and l is the log-likelihood function. If $l = l(\hat{\boldsymbol{\beta}})$ is the log likelihood evaluated at the maximum likelihood estimate $\hat{\boldsymbol{\beta}}$, then $2(l - l^*(\beta_j))$ has a limiting chi-square distribution with one degree of freedom if β_j is the true parameter value. A $(1-\alpha)100\%$ confidence interval for β_j is

$$\{\beta_j : l^*(\beta_j) \geq l_0 = l - 0.5\chi^2_{1-\alpha,1}\}$$

where $\chi^2_{1-\alpha,1}$ is the $100(1-\alpha)$th percentile of the chi-square distribution with one degree of freedom. The endpoints of the confidence interval can be found by solving numerically for values of β_j that satisfy equality in the preceding relation. PROC GENMOD solves this by starting at the maximum likelihood estimate of $\boldsymbol{\beta}$. The log-likelihood function is approximated with a quadratic surface, for which an exact solution is possible. The process is iterated until convergence to an endpoint is attained. The process is repeated for the other endpoint.

Convergence is controlled by the CICONV= option in the MODEL statement. Suppose ϵ is the number specified in the CICONV= option. The default value of ϵ is 10^{-4}. Let the parameter of interest be β_j, and define $\mathbf{r} = \mathbf{u}_j$, the unit vector with a 1 in position j and 0s elsewhere. Convergence is declared on the current iteration if the following two conditions are satisfied:

$$|l^*(\beta_j) - l_0| \leq \epsilon$$
$$(\mathbf{s} + \lambda\mathbf{r})'\mathbf{H}^{-1}(\mathbf{s} + \lambda\mathbf{r}) \leq \epsilon$$

where $l^*(\beta_j)$, $\mathbf{s}$, and $\mathbf{H}$ are the log likelihood, the gradient, and the Hessian evaluated at the current parameter vector and λ is a constant computed by the procedure. The first condition for convergence means that the log-likelihood function must be within ϵ of the correct value, and the second condition means that the gradient vector must be proportional to the restriction vector $\mathbf{r}$.

When you specify the LRCI option in the MODEL statement, PROC GENMOD computes profile likelihood confidence intervals for all parameters in the model, including the scale parameter, if there is one. The interval endpoints are displayed in a table as well as the values of the remaining parameters at the solution.

Wald Confidence Intervals

You can request that PROC GENMOD produce Wald confidence intervals for the parameters. The $(1-\alpha)100\%$ Wald confidence interval for a parameter β is defined as

$$\hat{\beta} \pm z_{1-\alpha/2}\hat{\sigma}$$

where z_p is the $100p$th percentile of the standard normal distribution, $\hat{\beta}$ is the parameter estimate, and $\hat{\sigma}$ is the estimate of its standard error.

F Statistics

Suppose that D_0 is the deviance resulting from fitting a generalized linear model and that D_1 is the deviance from fitting a submodel. Then, under appropriate regularity conditions, the asymptotic distribution of $(D_1-D_0)/\phi$ is chi-square with r degrees of freedom, where r is the difference in the number of parameters between the two models and ϕ is the dispersion parameter. If ϕ is unknown, and $\hat{\phi}$ is an estimate of ϕ based on the deviance or Pearson's chi-square divided by degrees of freedom, then, under regularity conditions, $(n-p)\hat{\phi}/\phi$ has an asymptotic chi-square distribution with $n-p$ degrees of freedom. Here, n is the number of observations and p is the number of parameters in the model that is used to estimate ϕ. Thus, the asymptotic distribution of

$$F = \frac{D_1 - D_0}{r\hat{\phi}}$$

is the F distribution with r and $n-p$ degrees of freedom, assuming that $(D_1-D_0)/\phi$ and $(n-p)\hat{\phi}/\phi$ are approximately independent.

This F statistic is computed for the Type 1 analysis, Type 3 analysis, and hypothesis tests specified in CONTRAST statements when the dispersion parameter is estimated by either the deviance or Pearson's chi-square divided by degrees of freedom, as specified by the DSCALE or PSCALE option in the MODEL statement. In the case of a Type 1 analysis, model 0 is the higher-order model obtained by including one additional effect in model 1. For a Type 3 analysis and hypothesis tests, model 0 is the full specified model and model 1 is the submodel obtained from constraining the Type III contrast or the user-specified contrast to be 0.

Lagrange Multiplier Statistics

When you select the NOINT or NOSCALE option, restrictions are placed on the intercept or scale parameters. Lagrange multiplier, or score, statistics are computed in these cases. These statistics

assess the validity of the restrictions, and they are computed as

$$\chi^2 = \frac{s^2}{V}$$

where s is the component of the score vector evaluated at the restricted maximum corresponding to the restricted parameter and $V = \mathbf{I}_{11} - \mathbf{I}_{12}\mathbf{I}_{22}^{-1}\mathbf{I}_{21}$. The matrix $\mathbf{I}$ is the information matrix, 1 refers to the restricted parameter, and 2 refers to the rest of the parameters.

Under regularity conditions, this statistic has an asymptotic chi-square distribution with one degree of freedom, and p-values are computed based on this limiting distribution.

If you set $k = 0$ in a negative binomial model, s is the score statistic of Cameron and Trivedi (1998) for testing for overdispersion in a Poisson model against alternatives of the form $V(\mu) = \mu + k\mu^2$.

See Rao (1973, p. 417) for more details.

Predicted Values of the Mean

Predicted Values

A predicted value, or fitted value, of the mean μ_i corresponding to the vector of covariates $\mathbf{x}_i$ is given by

$$\hat{\mu_i} = g^{-1}(\mathbf{x}_i'\hat{\boldsymbol{\beta}})$$

where g is the link function, regardless of whether $\mathbf{x}_i$ corresponds to an observation or not. That is, the response variable can be missing and the predicted value is still computed for valid $\mathbf{x}_i$. In the case where $\mathbf{x}_i$ does not correspond to a valid observation, $\mathbf{x}_i$ is not checked for estimability. You should check the estimability of $\mathbf{x}_i$ in this case in order to ensure the uniqueness of the predicted value of the mean. If there is an offset, it is included in the predicted value computation.

Confidence Intervals on Predicted Values

Approximate confidence intervals for predicted values of the mean can be computed as follows. The variance of the linear predictor $\eta_i = \mathbf{x}_i'\hat{\boldsymbol{\beta}}$ is estimated by

$$\sigma_x^2 = \mathbf{x}_i'\boldsymbol{\Sigma}\mathbf{x}_i$$

where $\boldsymbol{\Sigma}$ is the estimated covariance of $\hat{\boldsymbol{\beta}}$. The robust estimate of the covariance is used for $\boldsymbol{\Sigma}$ in the case of models fit with GEEs.

Approximate $100(1-\alpha)\%$ confidence intervals are computed as

$$g^{-1}\left(\mathbf{x}_i'\hat{\beta} \pm z_{1-\alpha/2}\sigma_x\right)$$

where z_p is the $100p$th percentile of the standard normal distribution and g is the link function. If either endpoint in the argument is outside the valid range of arguments for the inverse link function, the corresponding confidence interval endpoint is set to missing.

Residuals

The GENMOD procedure computes three kinds of residuals. Residuals are available for all generalized linear models except multinomial models for ordinal response data, for which residuals are not available. Raw residuals and Pearson residuals are available for models fit with generalized estimating equations (GEEs).

The raw residual is defined as

$$r_i = y_i - \mu_i$$

where y_i is the ith response and μ_i is the corresponding predicted mean. You can request raw residuals in an output data set with the keyword RESRAW in the OUTPUT statement.

The Pearson residual is the square root of the ith contribution to the Pearson's chi-square:

$$r_{Pi} = (y_i - \mu_i)\sqrt{\frac{w_i}{V(\mu_i)}}$$

You can request Pearson residuals in an output data set with the keyword RESCHI in the OUTPUT statement.

Finally, the deviance residual is defined as the square root of the contribution of the ith observation to the deviance, with the sign of the raw residual:

$$r_{Di} = \sqrt{d_i}(\text{sign}(y_i - \mu_i))$$

You can request deviance residuals in an output data set with the keyword RESDEV in the OUTPUT statement.

The adjusted Pearson, deviance, and likelihood residuals are defined by Agresti (2002), Williams (1987), and Davison and Snell (1991). These residuals are useful for outlier detection and for assessing the influence of single observations on the fitted model.

For the generalized linear model, the variance of the ith individual observation is given by

$$v_i = \frac{\phi V(\mu_i)}{w_i}$$

where ϕ is the dispersion parameter, w_i is a user-specified prior weight (if not specified, $w_i = 1$), μ_i is the mean, and $V(\mu_i)$ is the variance function. Let

$$w_{ei} = v_i^{-1}(g'(\mu_i))^{-2}$$

for the ith observation, where $g'(\mu_i)$ is the derivative of the link function, evaluated at μ_i. Let $\mathbf{W}_e$ be the diagonal matrix with w_{ei} denoting the ith diagonal element. The weight matrix $\mathbf{W}_e$ is used in computing the expected information matrix.

Define h_i as the ith diagonal element of the matrix

$$\mathbf{W}_e^{\frac{1}{2}}\mathbf{X}(\mathbf{X}'\mathbf{W}_e\mathbf{X})^{-1}\mathbf{X}'\mathbf{W}_e^{\frac{1}{2}}$$

The Pearson residuals, standardized to have unit asymptotic variance, are given by

$$r_{Pi} = \frac{y_i - \mu_i}{\sqrt{v_i(1-h_i)}}$$

You can request standardized Pearson residuals in an output data set with the keyword STDRESCHI in the OUTPUT statement. The deviance residuals, standardized to have unit asymptotic variance, are given by

$$r_{Di} = \frac{\text{sign}(y_i - \mu_i)\sqrt{d_i}}{\sqrt{\phi(1-h_i)}}$$

where d_i is the contribution to the total deviance from observation i, and $\text{sign}(y_i - \mu_i)$ is 1 if $y_i - \mu_i$ is positive and -1 if $y_i - \mu_i$ is negative. You can request standardized deviance residuals in an output data set with the keyword STDRESDEV in the OUTPUT statement. The likelihood residuals are defined by

$$r_{Gi} = \text{sign}(y_i - \mu_i)\sqrt{(1-h_i)r_{Di}^2 + h_i r_{Pi}^2}$$

You can request likelihood residuals in an output data set with the keyword RESLIK in the OUTPUT statement.

Multinomial Models

This type of model applies to cases where an observation can fall into one of k categories. Binary data occur in the special case where $k = 2$. If there are m_i observations in a subpopulation i, then the probability distribution of the number falling into the k categories $\mathbf{y}_i = (y_{i1}, y_{i2}, \cdots y_{ik})$ can be modeled by the multinomial distribution, defined in the section "Response Probability Distributions" on page 1962, with $\sum_j y_{ij} = m_i$. The multinomial model is an *ordinal* model if the categories have a natural order.

Residuals are not available in the OBSTATS table or the output data set for multinomial models.

By default, and consistently with binomial models, the GENMOD procedure orders the response categories for ordinal multinomial models from lowest to highest and models the probabilities of the lower response levels. You can change the way PROC GENMOD orders the response levels with the RORDER= option in the PROC GENMOD statement. The order that PROC GENMOD uses is shown in the "Response Profiles" output table described in the section "Response Profile" on page 2006.

The GENMOD procedure supports only the ordinal multinomial model. If $(p_{i1}, p_{i2}, \cdots p_{ik})$ are the category probabilities, the cumulative category probabilities are modeled with the same link functions used for binomial data. Let $P_{ir} = \sum_{j=1}^{r} p_{ij}$, $r = 1, 2, \cdots, k-1$, be the cumulative category probabilities (note that $P_{ik} = 1$). The ordinal model is

$$g(P_{ir}) = \mu_r + \mathbf{x}'\boldsymbol{\beta} \quad \text{for} \quad r = 1, 2, \cdots k-1$$

where $\mu_1, \mu_2, \cdots \mu_{k-1}$ are intercept terms that depend only on the categories and $\mathbf{x}_i$ is a vector of covariates that does not include an intercept term. The logit, probit, and complementary log-log link functions g are available. These are obtained by specifying the MODEL statement options

DIST=MULTINOMIAL and LINK=CUMLOGIT (cumulative logit), LINK=CUMPROBIT (cumulative probit), or LINK=CUMCLL (cumulative complementary log-log). Alternatively,

$$P_{ir} = \mathrm{F}(\mu_r + \mathbf{x}'\boldsymbol{\beta}) \quad \text{for} \quad r = 1, 2, \cdots k-1$$

where $\mathrm{F} = g^{-1}$ is a cumulative distribution function for the logistic, normal, or extreme-value distribution.

PROC GENMOD estimates the intercept parameters $\mu_1, \mu_2, \cdots \mu_{k-1}$ and regression parameters $\boldsymbol{\beta}$ by maximum likelihood.

The subpopulations i are defined by constant values of the AGGREGATE= variable. This has no effect on the parameter estimates, but it does affect the deviance and Pearson chi-square statistics; it also affects parameter estimate standard errors if you specify the SCALE=DEVIANCE or SCALE=PEARSON option.

Zero-Inflated Poisson Models

Count data that have an incidence of zero counts greater than expected for the Poisson distribution can be modeled with the zero-inflated Poisson distribution. See Long (1997) and Cameron and Trivedi (1998) for more information about zero-inflated Poisson models. The population is considered to consist of two types of individuals. The first type gives Poisson distributed counts, which might contain zeros. The second type always gives a zero count. Let λ be the Poisson mean and ω be the probability of an individual being of the second type. The parameter ω is called here the *zero-inflation probability*, and is the probability of zero counts in excess of the frequency predicted by the Poisson distribution. You can request that the zero inflation probability be displayed in an output data set with the PZERO keyword. The probability distribution of a zero-inflated random variable Y is given by

$$\Pr(\mathrm{Y} = y) = \begin{cases} \omega + (1-\omega)\mathrm{e}^{-\lambda} & \text{for } y = 0 \\ (1-\omega)\frac{\lambda^y \mathrm{e}^{-\lambda}}{y!} & \text{for } y = 1, 2, \ldots \end{cases}$$

You can model the parameters ω and λ in GENMOD with the regression models:

$$\begin{aligned} h(\omega_i) &= \mathbf{z}_i'\boldsymbol{\gamma} \\ g(\lambda_i) &= \mathbf{x}_i'\boldsymbol{\beta} \end{aligned}$$

where h is one of the binary link functions: logit, probit, or complementary log-log. The link function h is the logit link by default, or the link function option specified in the ZEROMODEL statement. The link function for the Poisson part of the model, g, is the log link function by default, or the link function specified in the MODEL statement. The covariates $\mathbf{z}_i$ for observation i are determined by the model specified in the ZEROMODEL statement, and the covariates $\mathbf{x}_i$ are determined by the model specified in the MODEL statement. The regression parameters $\boldsymbol{\gamma}$ and $\boldsymbol{\beta}$ are estimated by maximum likelihood.

The mean and variance of Y are given by

$$\begin{aligned} \mathrm{E}(Y) &= \mu = (1-\omega)\lambda \\ \mathrm{Var}(Y) &= \mu + \frac{\omega}{1-\omega}\mu^2 \end{aligned}$$

You can request that the mean of Y be displayed for each observation in an output data set with the PRED keyword.

Generalized Estimating Equations

Let y_{ij}, $j = 1, \ldots, n_i$, $i = 1, \ldots, K$, represent the jth measurement on the ith subject. There are n_i measurements on subject i and $\sum_{i=1}^{K} n_i$ total measurements.

Correlated data are modeled using the same link function and linear predictor setup (systematic component) as the independence case. The random component is described by the same variance functions as in the independence case, but the covariance structure of the correlated measurements must also be modeled. Let the vector of measurements on the ith subject be $\mathbf{Y}_i = [y_{i1}, \ldots, y_{in_i}]'$ with corresponding vector of means $\boldsymbol{\mu}_i = [\mu_{i1}, \ldots, \mu_{in_i}]'$, and let $\mathbf{V}_i$ be the covariance matrix of $\mathbf{Y}_i$. Let the vector of independent, or explanatory, variables for the jth measurement on the ith subject be

$$\mathbf{x}_{ij} = [x_{ij1}, \ldots, x_{ijp}]'$$

The generalized estimating equation of Liang and Zeger (1986) for estimating the $p \times 1$ vector of regression parameters $\boldsymbol{\beta}$ is an extension of the independence estimating equation to correlated data and is given by

$$\mathbf{S}(\boldsymbol{\beta}) = \sum_{i=1}^{K} \mathbf{D}_i' \mathbf{V}_i^{-1} (\mathbf{Y}_i - \boldsymbol{\mu}_i(\boldsymbol{\beta})) = \mathbf{0}$$

where

$$\mathbf{D}_i = \frac{\partial \boldsymbol{\mu}_i}{\partial \boldsymbol{\beta}}$$

Since

$$g(\mu_{ij}) = \mathbf{x}_{ij}{}'\boldsymbol{\beta}$$

where g is the link function, the $p \times n_i$ matrix of partial derivatives of the mean with respect to the regression parameters for the ith subject is given by

$$\mathbf{D}_i' = \frac{\partial \boldsymbol{\mu}_i'}{\partial \boldsymbol{\beta}} = \begin{bmatrix} \frac{x_{i11}}{g'(\mu_{i1})} & \cdots & \frac{x_{in_i1}}{g'(\mu_{in_i})} \\ \vdots & & \vdots \\ \frac{x_{i1p}}{g'(\mu_{i1})} & \cdots & \frac{x_{in_ip}}{g'(\mu_{in_i})} \end{bmatrix}$$

Working Correlation Matrix

Let $\mathbf{R}_i(\boldsymbol{\alpha})$ be an $n_i \times n_i$ "working" correlation matrix that is fully specified by the vector of parameters $\boldsymbol{\alpha}$. The covariance matrix of $\mathbf{Y}_i$ is modeled as

$$\mathbf{V}_i = \phi \mathbf{A}_i^{\frac{1}{2}} \mathbf{W}_i^{-\frac{1}{2}} \mathbf{R}(\boldsymbol{\alpha}) \mathbf{W}_i^{-\frac{1}{2}} \mathbf{A}_i^{\frac{1}{2}}$$

where $\mathbf{A}_i$ is an $n_i \times n_i$ diagonal matrix with $v(\mu_{ij})$ as the jth diagonal element and $\mathbf{W}_i$ is an $n_i \times n_i$ diagonal matrix with w_{ij} as the jth diagonal, where w_{ij} is a weight specified with the WEIGHT statement. If there is no WEIGHT statement, $w_{ij} = 1$ for all i and j. If $\mathbf{R}_i(\boldsymbol{\alpha})$ is the true correlation matrix of $\mathbf{Y}_i$, then $\mathbf{V}_i$ is the true covariance matrix of $\mathbf{Y}_i$.

The working correlation matrix is usually unknown and must be estimated. It is estimated in the iterative fitting process by using the current value of the parameter vector $\boldsymbol{\beta}$ to compute appropriate functions of the Pearson residual

$$e_{ij} = \frac{y_{ij} - \mu_{ij}}{\sqrt{v(\mu_{ij})/w_{ij}}}$$

If you specify the working correlation as $\mathbf{R_0} = \mathbf{I}$, which is the identity matrix, the GEE reduces to the independence estimating equation.

Following are the structures of the working correlation supported by the GENMOD procedure and the estimators used to estimate the working correlations.

Working Correlation Structure	Estimator
Fixed $\text{Corr}(Y_{ij}, Y_{ik}) = r_{jk}$ where r_{jk} is the jkth element of a constant, user-specified correlation matrix $\mathbf{R}_0$.	The working correlation is not estimated in this case.
Independent $\text{Corr}(Y_{ij}, Y_{ik}) = \begin{cases} 1 & j = k \\ 0 & j \neq k \end{cases}$	The working correlation is not estimated in this case.
***m*-dependent** $\text{Corr}(Y_{ij}, Y_{i,j+t}) = \begin{cases} 1 & t = 0 \\ \alpha_t & t = 1, 2, \ldots, m \\ 0 & t > m \end{cases}$	$\hat{\alpha}_t = \frac{1}{(K_t - p)\phi} \sum_{i=1}^{K} \sum_{j \leq n_i - t} e_{ij} e_{i,j+t}$ $K_t = \sum_{i=1}^{K} (n_i - t)$
Exchangeable $\text{Corr}(Y_{ij}, Y_{ik}) = \begin{cases} 1 & j = k \\ \alpha & j \neq k \end{cases}$	$\hat{\alpha} = \frac{1}{(N^* - p)\phi} \sum_{i=1}^{K} \sum_{j<k} e_{ij} e_{ik}$ $N^* = 0.5 \sum_{i=1}^{K} n_i (n_i - 1)$
Unstructured $\text{Corr}(Y_{ij}, Y_{ik}) = \begin{cases} 1 & j = k \\ \alpha_{jk} & j \neq k \end{cases}$	$\hat{\alpha}_{jk} = \frac{1}{(K - p)\phi} \sum_{i=1}^{K} e_{ij} e_{ik}$
Autoregressive **AR(1)** $\text{Corr}(Y_{ij}, Y_{i,j+t}) = \alpha^t$ for $t = 0, 1, 2, \ldots, n_i - j$	$\hat{\alpha} = \frac{1}{(K_1 - p)\phi} \sum_{i=1}^{K} \sum_{j \leq n_i - 1} e_{ij} e_{i,j+1}$ $K_1 = \sum_{i=1}^{K} (n_i - 1)$

Dispersion Parameter

The dispersion parameter ϕ is estimated by

$$\hat{\phi} = \frac{1}{N - p} \sum_{i=1}^{K} \sum_{j=1}^{n_i} e_{ij}^2$$

where $N = \sum_{i=1}^{K} n_i$ is the total number of measurements and p is the number of regression parameters.

The square root of $\hat{\phi}$ is reported by PROC GENMOD as the scale parameter in the "Analysis of GEE Parameter Estimates Model-Based Standard Error Estimates" output table. If a fixed scale parameter is specified with the NOSCALE option in the MODEL statement, then the fixed value is used in estimating the model-based covariance matrix and standard errors.

Fitting Algorithm

The following is an algorithm for fitting the specified model by using GEEs. Note that this is not in general a likelihood-based method of estimation, so that inferences based on likelihoods are not possible for GEE methods.

1. Compute an initial estimate of $\boldsymbol{\beta}$ with an ordinary generalized linear model assuming independence.
2. Compute the working correlations $\mathbf{R}$ based on the standardized residuals, the current $\boldsymbol{\beta}$, and the assumed structure of $\mathbf{R}$.
3. Compute an estimate of the covariance:

$$\mathbf{V}_i = \phi \mathbf{A}_i^{\frac{1}{2}} \mathbf{W}_i^{-\frac{1}{2}} \hat{\mathbf{R}}(\boldsymbol{\alpha}) \mathbf{W}_i^{-\frac{1}{2}} \mathbf{A}_i^{\frac{1}{2}}$$

4. Update $\boldsymbol{\beta}$:

$$\boldsymbol{\beta}_{r+1} = \boldsymbol{\beta}_r + \left[\sum_{i=1}^{K} \frac{\partial \boldsymbol{\mu}_i}{\partial \boldsymbol{\beta}}' \mathbf{V}_i^{-1} \frac{\partial \boldsymbol{\mu}_i}{\partial \boldsymbol{\beta}} \right]^{-1} \left[\sum_{i=1}^{K} \frac{\partial \boldsymbol{\mu}_i}{\partial \boldsymbol{\beta}}' \mathbf{V}_i^{-1} (\mathbf{Y}_i - \boldsymbol{\mu}_i) \right]$$

5. Repeat steps 2-4 until convergence.

Missing Data

See Diggle, Liang, and Zeger (1994, Chapter 11) for a discussion of missing values in longitudinal data. Suppose that you intend to take measurements $Y_{i1}, \ldots, Y_{in}$ for the ith unit. Missing values for which Y_{ij} are missing whenever Y_{ik} is missing for all $j \geq k$ are called *dropouts*. Otherwise, missing values that occur intermixed with nonmissing values are *intermittent* missing values. The GENMOD procedure can estimate the working correlation from data containing both types of missing values by using the *all available pairs* method, in which all nonmissing pairs of data are used in the moment estimators of the working correlation parameters defined previously. The resulting covariances and standard errors are valid under the missing completely at random (MCAR) assumption.

For example, for the unstructured working correlation model,

$$\hat{\alpha}_{jk} = \frac{1}{(K' - p)\phi} \sum e_{ij} e_{ik}$$

where the sum is over the units that have nonmissing measurements at times j and k, and K' is the number of units with nonmissing measurements at j and k. Estimates of the parameters for other working correlation types are computed in a similar manner, using available nonmissing pairs in the appropriate moment estimators.

The contribution of the ith unit to the parameter update equation is computed by omitting the elements of $(\mathbf{Y}_i - \boldsymbol{\mu}_i)$, the columns of $\mathbf{D}_i' = \frac{\partial \boldsymbol{\mu}}{\partial \boldsymbol{\beta}}'$, and the rows and columns of $\mathbf{V}_i$ corresponding to missing measurements.

Parameter Estimate Covariances

The *model-based* estimator of $\mathrm{Cov}(\hat{\boldsymbol{\beta}})$ is given by

$$\boldsymbol{\Sigma}_m(\hat{\boldsymbol{\beta}}) = \mathbf{I}_0^{-1}$$

where

$$\mathbf{I}_0 = \sum_{i=1}^{K} \frac{\partial \boldsymbol{\mu}_i}{\partial \boldsymbol{\beta}}' \mathbf{V}_i^{-1} \frac{\partial \boldsymbol{\mu}_i}{\partial \boldsymbol{\beta}}$$

This is the GEE equivalent of the inverse of the Fisher information matrix that is often used in generalized linear models as an estimator of the covariance estimate of the maximum likelihood estimator of $\boldsymbol{\beta}$. It is a consistent estimator of the covariance matrix of $\hat{\boldsymbol{\beta}}$ if the mean model and the working correlation matrix are correctly specified.

The estimator

$$\boldsymbol{\Sigma}_e = \mathbf{I}_0^{-1}\mathbf{I}_1\mathbf{I}_0^{-1}$$

is called the *empirical*, or *robust*, estimator of the covariance matrix of $\hat{\boldsymbol{\beta}}$, where

$$\mathbf{I}_1 = \sum_{i=1}^{K} \frac{\partial \boldsymbol{\mu}_i}{\partial \boldsymbol{\beta}}' \mathbf{V}_i^{-1}\mathrm{Cov}(\mathbf{Y}_i)\mathbf{V}_i^{-1} \frac{\partial \boldsymbol{\mu}_i}{\partial \boldsymbol{\beta}}$$

It has the property of being a consistent estimator of the covariance matrix of $\hat{\boldsymbol{\beta}}$, even if the working correlation matrix is misspecified—that is, if $\mathrm{Cov}(\mathbf{Y}_i) \neq \mathbf{V}_i$. See Zeger, Liang, and Albert (1988)), Royall (1986), and White (1982) for further information about the robust variance estimate. In computing $\boldsymbol{\Sigma}_e$, $\boldsymbol{\beta}$ and ϕ are replaced by estimates, and $\mathrm{Cov}(\mathbf{Y}_i)$ is replaced by the estimate

$$(\mathbf{Y}_i - \boldsymbol{\mu}_i(\hat{\boldsymbol{\beta}}))(\mathbf{Y}_i - \boldsymbol{\mu}_i(\hat{\boldsymbol{\beta}}))'$$

Multinomial GEEs

Lipsitz, Kim, and Zhao (1994) and Miller, Davis, and Landis (1993) describe how to extend GEEs to multinomial data. Currently, only the independent working correlation is available for multinomial models in PROC GENMOD.

Alternating Logistic Regressions

If the responses are binary (that is, they take only two values), then there is an alternative method to account for the association among the measurements. The alternating logistic regressions (ALR) algorithm of Carey, Zeger, and Diggle (1993) models the association between pairs of responses with log odds ratios, instead of with correlations, as ordinary GEEs do.

For binary data, the correlation between the jth and kth response is, by definition,

$$\mathrm{Corr}(Y_{ij}, Y_{ik}) = \frac{\Pr(Y_{ij} = 1, Y_{ik} = 1) - \mu_{ij}\mu_{ik}}{\sqrt{\mu_{ij}(1-\mu_{ij})\mu_{ik}(1-\mu_{ik})}}$$

The joint probability in the numerator satisfies the following bounds, by elementary properties of probability, since $\mu_{ij} = \Pr(Y_{ij} = 1)$:

$$\max(0, \mu_{ij} + \mu_{ik} - 1) \leq \Pr(Y_{ij} = 1, Y_{ik} = 1) \leq \min(\mu_{ij}, \mu_{ik})$$

The correlation, therefore, is constrained to be within limits that depend in a complicated way on the means of the data.

The odds ratio, defined as

$$\mathrm{OR}(Y_{ij}, Y_{ik}) = \frac{\Pr(Y_{ij} = 1, Y_{ik} = 1)\Pr(Y_{ij} = 0, Y_{ik} = 0)}{\Pr(Y_{ij} = 1, Y_{ik} = 0)\Pr(Y_{ij} = 0, Y_{ik} = 1)}$$

is not constrained by the means and is preferred, in some cases, to correlations for binary data.

The ALR algorithm seeks to model the logarithm of the odds ratio, $\gamma_{ijk} = \log(\mathrm{OR}(Y_{ij}, Y_{ik}))$, as

$$\gamma_{ijk} = \mathbf{z}'_{ijk}\boldsymbol{\alpha}$$

where $\boldsymbol{\alpha}$ is a $q \times 1$ vector of regression parameters and $\mathbf{z}_{ijk}$ is a fixed, specified vector of coefficients.

The parameter γ_{ijk} can take any value in $(-\infty, \infty)$ with $\gamma_{ijk} = 0$ corresponding to no association.

The log odds ratio, when modeled in this way with a regression model, can take different values in subgroups defined by $\mathbf{z}_{ijk}$. For example, $\mathbf{z}_{ijk}$ can define subgroups within clusters, or it can define "block effects" between clusters.

You specify a GEE model for binary data that uses log odds ratios by specifying a model for the mean, as in ordinary GEEs, and a model for the log odds ratios. You can use any of the link functions appropriate for binary data in the model for the mean, such as logistic, probit, or complementary log-log. The ALR algorithm alternates between a GEE step to update the model for the mean and a logistic regression step to update the log odds ratio model. Upon convergence, the ALR algorithm provides estimates of the regression parameters for the mean, $\boldsymbol{\beta}$, the regression parameters for the log odds ratios, $\boldsymbol{\alpha}$, their standard errors, and their covariances.

Specifying Log Odds Ratio Models

Specifying a regression model for the log odds ratio requires you to specify rows of the z-matrix $\mathbf{z}_{ijk}$ for each cluster i and each unique within-cluster pair (j, k). The GENMOD procedure provides several methods of specifying $\mathbf{z}_{ijk}$. These are controlled by the LOGOR=*keyword* and associated options in the REPEATED statement. The supported keywords and the resulting log odds ratio models are described as follows.

EXCH — specifies exchangeable log odds ratios. In this model, the log odds ratio is a constant for all clusters i and pairs (j, k). The parameter α is the common log odds ratio.

$$\mathbf{z}_{ijk} = 1 \quad \text{for all} \quad i, j, k$$

FULLCLUST — specifies fully parameterized clusters. Each cluster is parameterized in the same way, and there is a parameter for each unique pair within clusters. If a complete cluster is of size n, then there are $\frac{n(n-1)}{2}$ parameters

in the vector $\boldsymbol{\alpha}$. For example, if a full cluster is of size 4, then there are $\frac{4\times3}{2} = 6$ parameters, and the z-matrix is of the form

$$Z = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

The elements of $\boldsymbol{\alpha}$ correspond to log odds ratios for cluster pairs in the following order:

Pair	Parameter
(1,2)	Alpha1
(1,3)	Alpha2
(1,4)	Alpha3
(2.3)	Alpha4
(2,4)	Alpha5
(3,4)	Alpha6

LOGORVAR(*variable*) specifies log odds ratios by cluster. The argument *variable* is a variable name that defines the "block effects" between clusters. The log odds ratios are constant within clusters, but they take a different value for each different value of the *variable*. For example, if Center is a variable in the input data set taking a different value for k treatment centers, then specifying LOGOR=LOGORVAR(Center) requests a model with different log odds ratios for each of the k centers, constant within center.

NESTK specifies k-nested log odds ratios. You must also specify the SUBCLUST=*variable* option to define subclusters within clusters. Within each cluster, PROC GENMOD computes a log odds ratio parameter for pairs having the same value of *variable* for both members of the pair and one log odds ratio parameter for each unique combination of different values of *variable*.

NEST1 specifies 1-nested log odds ratios. You must also specify the SUBCLUST=*variable* option to define subclusters within clusters. There are two log odds ratio parameters for this model. Pairs having the same value of *variable* correspond to one parameter; pairs having different values of *variable* correspond to the other parameter. For example, if clusters are hospitals and subclusters are wards within hospitals, then patients within the same ward have one log odds ratio parameter, and patients from different wards have the other parameter.

ZFULL specifies the full z-matrix. You must also specify a SAS data set containing the z-matrix with the ZDATA=*data-set-name* option. Each observation in the data set corresponds to one row of the z-matrix. You must specify the ZDATA data set as if all clusters are complete—that is, as if all clusters are the same size and there are no missing observations. The ZDATA data set has $K[n_{max}(n_{max} - 1)/2]$ observations, where K is the number of clusters and n_{max} is the maximum

cluster size. If the members of cluster i are ordered as $1, 2, \cdots, n$, then the rows of the z-matrix must be specified for pairs in the order $(1,2), (1,3), \cdots, (1,n), (2,3), \cdots, (2,n), \cdots, (n-1,n)$. The variables specified in the REPEATED statement for the SUBJECT effect must also be present in the ZDATA= data set to identify clusters. You must specify variables in the data set that define the columns of the z-matrix by the ZROW=*variable-list* option. If there are q columns (q variables in *variable-list*), then there are q log odds ratio parameters. You can optionally specify variables indicating the cluster pairs corresponding to each row of the z-matrix with the YPAIR=(*variable1, variable2*) option. If you specify this option, the data from the ZDATA data set are sorted within each cluster by *variable1* and *variable2*. See Example 37.6 for an example of specifying a full z-matrix.

ZREP

specifies a replicated z-matrix. You specify z-matrix data exactly as you do for the ZFULL case, except that you specify only one complete cluster. The z-matrix for the one cluster is replicated for each cluster. The number of observations in the ZDATA data set is $\frac{n_{max}(n_{max}-1)}{2}$, where n_{max} is the size of a complete cluster (a cluster with no missing observations).

ZREP(matrix)

specifies direct input of the replicated z-matrix. You specify the z-matrix for one cluster with the syntax LOGOR=ZREP ($(y_1 \;\; y_2) z_1 \;\; z_2 \cdots z_q, \cdots$), where y_1 and y_2 are numbers representing a pair of observations and the values $z_1, z_2, \cdots, z_q$ make up the corresponding row of the z-matrix. The number of rows specified is $\frac{n_{max}(n_{max}-1)}{2}$, where n_{max} is the size of a complete cluster (a cluster with no missing observations). For example,

```
LOGOR =  ZREP((1 2) 1 0,
              (1 3) 1 0,
              (1 4) 1 0,
              (2 3) 1 1,
              (2 4) 1 1,
              (3 4) 1 1)
```

specifies the $\frac{4\times3}{2} = 6$ rows of the z-matrix for a cluster of size 4 with $q = 2$ log odds ratio parameters. The log odds ratio for the pairs (1 2), (1 3), (1 4) is α_1, and the log odds ratio for the pairs (2 3), (2 4), (3 4) is $\alpha_1 + \alpha_2$.

Quasi-likelihood Information Criterion

The quasi-likelihood information criterion (QIC) was developed by Pan (2001) as a modification of the Akaike information criterion (AIC) to apply to models fit by GEEs.

Define the quasi-likelihood under the independence working correlation assumption, evaluated with the parameter estimates under the working correlation of interest as

$$Q(\hat{\boldsymbol{\beta}}(R), \phi) = \sum_{i=1}^{K} \sum_{j=1}^{n_i} Q(\hat{\boldsymbol{\beta}}(R), \phi; (Y_{ij}, \mathbf{X}_{ij}))$$

where the quasi-likelihood contribution of the jth observation in the ith cluster is defined in the section "Quasi-likelihood Functions" on page 1992 and $\hat{\boldsymbol{\beta}}(R)$ are the parameter estimates obtained from GEEs with the working correlation of interest R.

QIC is defined as

$$QIC(R) = -2Q(\hat{\boldsymbol{\beta}}(R), \phi) + 2\text{trace}(\hat{\Omega}_I \hat{V}_R)$$

where $\hat{V}_R$ is the robust covariance estimate and $\hat{\Omega}_I$ is the inverse of the model-based covariance estimate under the independent working correlation assumption, evaluated at $\hat{\boldsymbol{\beta}}(R)$, the parameter estimates obtained from GEEs with the working correlation of interest R.

PROC GENMOD also computes an approximation to $QIC(R)$ defined by Pan (2001) as

$$QIC_u(R) = -2Q(\hat{\boldsymbol{\beta}}(R), \phi) + 2p$$

where p is the number of regression parameters.

Pan (2001) notes that QIC is appropriate for selecting regression models and working correlations, whereas QIC_u is appropriate only for selecting regression models.

Quasi-likelihood Functions

See McCullagh and Nelder (1989) and Hardin and Hilbe (2003) for discussions of quasi-likelihood functions. The contribution of observation j in cluster i to the quasi-likelihood function evaluated at the regression parameters $\boldsymbol{\beta}$ is given by $Q(\boldsymbol{\beta}, \phi; (Y_{ij}, \mathbf{X}_{ij})) = \frac{Q_{ij}}{\phi}$, where Q_{ij} is defined in the following list. These are used in the computation of the quasi-likelihood information criteria (QIC) for goodness of fit of models fit with GEEs. The w_{ij} are prior weights, if any, specified with the WEIGHT or FREQ statements. Note that the definition of the quasi-likelihood for the negative binomial differs from that given in McCullagh and Nelder (1989). The definition used here allows the negative binomial quasi-likelihood to approach the Poisson as $k \to 0$.

- Normal:

$$Q_{ij} = -\frac{1}{2} w_{ij} (y_{ij} - \mu_{ij})^2$$

- Inverse Gaussian:

$$Q_{ij} = \frac{w_{ij}(\mu_{ij} - .5y_{ij})}{\mu_{ij}^2}$$

- Gamma:

$$Q_{ij} = -w_{ij} \left[\frac{y_{ij}}{\mu_{ij}} + \log(\mu_{ij}) \right]$$

- Negative binomial:

$$Q_{ij} = w_{ij} [\log \Gamma(y_{ij} + \frac{1}{k}) - \log \Gamma(\frac{1}{k}) + y_{ij} \log \left(\frac{k\mu_{ij}}{1 + k\mu_{ij}} \right) + \frac{1}{k} \log \left(\frac{1}{1 + k\mu_{ij}} \right)]$$

- Poisson:

$$Q_{ij} = w_{ij}(y_{ij}\log(\mu_{ij}) - \mu_{ij})$$

- Binomial:

$$Q_{ij} = w_{ij}[r_{ij}\log(p_{ij}) + (n_{ij} - r_{ij})\log(1 - p_{ij})]$$

- Multinomial (s categories):

$$Q_{ij} = w_{ij}\sum_{k=1}^{s} y_{ijk}\log(\mu_{ijk})$$

Generalized Score Statistics

Boos (1992) and Rotnitzky and Jewell (1990) describe score tests applicable to testing $\mathbf{L}'\boldsymbol{\beta} = \mathbf{0}$ in GEEs, where $\mathbf{L}'$ is a user-specified $r \times p$ contrast matrix or a contrast for a Type 3 test of hypothesis.

Let $\tilde{\boldsymbol{\beta}}$ be the regression parameters resulting from solving the GEE under the restricted model $\mathbf{L}'\boldsymbol{\beta} = \mathbf{0}$, and let $\mathbf{S}(\tilde{\boldsymbol{\beta}})$ be the generalized estimating equation values at $\tilde{\boldsymbol{\beta}}$.

The generalized score statistic is

$$T = \mathbf{S}(\tilde{\boldsymbol{\beta}})'\boldsymbol{\Sigma}_m\mathbf{L}(\mathbf{L}'\boldsymbol{\Sigma}_e\mathbf{L})^{-1}\mathbf{L}'\boldsymbol{\Sigma}_m\mathbf{S}(\tilde{\boldsymbol{\beta}})$$

where $\boldsymbol{\Sigma}_m$ is the model-based covariance estimate and $\boldsymbol{\Sigma}_e$ is the empirical covariance estimate. The p-values for T are computed based on the chi-square distribution with r degrees of freedom.

Assessment of Models Based on Aggregates of Residuals

Lin, Wei, and Ying (2002) present graphical and numerical methods for model assessment based on the cumulative sums of residuals over certain coordinates (such as covariates or linear predictors) or some related aggregates of residuals. The distributions of these stochastic processes under the assumed model can be approximated by the distributions of certain zero-mean Gaussian processes whose realizations can be generated by simulation. Each observed residual pattern can then be compared, both graphically and numerically, with a number of realizations from the null distribution. Such comparisons enable you to assess objectively whether the observed residual pattern reflects anything beyond random fluctuation. These procedures are useful in determining appropriate functional forms of covariates and link function. You use the ASSESS|ASSESSMENT statement to perform this kind of model-checking with cumulative sums of residuals, moving sums of residuals, or LOESS smoothed residuals. See Example 37.8 and Example 37.9 for examples of model assessment.

Let the model for the mean be

$$g(\mu_i) = \mathbf{x}_i'\boldsymbol{\beta}$$

where μ_i is the mean of the response y_i and $\mathbf{x}_i$ is the vector of covariates for the ith observation. Denote the raw residual resulting from fitting the model as

$$e_i = y_i - \hat{\mu}_i$$

and let x_{ij} be the value of the jth covariate in the model for observation i. Then to check the functional form of the jth covariate, consider the cumulative sum of residuals with respect to x_{ij},

$$W_j(x) = \frac{1}{\sqrt{n}} \sum_{i=1}^{n} I(x_{ij} \leq x) e_i$$

where $I()$ is the indicator function. For any x, $W_j(x)$ is the sum of the residuals with values of x_j less than or equal to x.

Denote the score, or gradient vector, by

$$U(\boldsymbol{\beta}) = \sum_{i=1}^{n} h(\mathbf{x}'\boldsymbol{\beta}) \mathbf{x}_i (y_i - \nu(\mathbf{x}'\boldsymbol{\beta}))$$

where $\nu(r) = g^{-1}(r)$, and

$$h(r) = \frac{1}{g'(\nu(r)) V(\nu(r))}$$

Let J be the Fisher information matrix

$$J(\boldsymbol{\beta}) = -\frac{\partial U(\boldsymbol{\beta})}{\partial \boldsymbol{\beta}'}$$

Define

$$\hat{W}_j(x) = \frac{1}{\sqrt{n}} \sum_{i=1}^{n} [I(x_{ij} \leq x) + \boldsymbol{\eta}'(x; \hat{\boldsymbol{\beta}}) J^{-1}(\hat{\boldsymbol{\beta}}) \mathbf{x}_i h(\mathbf{x}'\hat{\boldsymbol{\beta}})] e_i Z_i$$

where

$$\boldsymbol{\eta}(x; \boldsymbol{\beta}) = -\sum_{i=1}^{n} I(x_{ij} \leq x) \frac{\partial \nu(\mathbf{x}_i'\boldsymbol{\beta})}{\partial \boldsymbol{\beta}}$$

and Z_i are independent $N(0, 1)$ random variables. Then the conditional distribution of $\hat{W}_j(x)$, given $(y_i, \mathbf{x}_i), i = 1, \ldots, n$, under the null hypothesis H_0 that the model for the mean is correct, is the same asymptotically as $n \to \infty$ as the unconditional distribution of $W_j(x)$ (Lin, Wei, and Ying 2002).

You can approximate realizations from the null hypothesis distribution of $W_j(x)$ by repeatedly generating normal samples $Z_i, i = 1, \ldots, n$, while holding $(y_i, \mathbf{x}_i), i = 1, \ldots, n$, at their observed values and computing $\hat{W}_j(x)$ for each sample.

You can assess the functional form of covariate j by plotting a few realizations of $\hat{W}_j(x)$ on the same plot as the observed $W_j(x)$ and visually comparing to see how typical the observed $W_j(x)$ is of the null distribution samples.

You can supplement the graphical inspection method with a Kolmogorov-type supremum test. Let s_j be the observed value of $S_j = \sup_x |W_j(x)|$. The p-value $\Pr[S_j \geq s_j]$ is approximated by $\Pr[\hat{S}_j \geq s_j]$, where $\hat{S}_j = \sup_x |\hat{W}_j(x)|$. $\Pr[\hat{S}_j \geq s_j]$ is estimated by generating realizations of $\hat{W}_j(.)$ (1,000 is the default number of realizations).

You can check the link function instead of the jth covariate by using values of the linear predictor $\mathbf{x}_i'\hat{\boldsymbol{\beta}}$ in place of values of the jth covariate x_{ij}. The graphical and numerical methods described previously are then sensitive to inadequacies in the link function.

An alternative aggregate of residuals is the moving sum statistic

$$W_j(x,b) = \frac{1}{\sqrt{n}} \sum_{i=1}^{n} I(x - b \leq x_{ij} \leq x) e_i$$

If you specify the keyword WINDOW(b), then the moving sum statistic with window size b is used instead of the cumulative sum of residuals, with $I(x - b \leq x_{ij} \leq x)$ replacing $I(x_{ij} \leq x)$ in the earlier equation.

If you specify the keyword LOESS(f), loess smoothed residuals are used in the preceding formulas, where f is the fraction of the data to be used at a given point. If f is not specified, $f = \frac{1}{3}$ is used. For data $(Y_i, X_i), i = 1, \ldots, n$, define r as the nearest integer to nf and h as the rth smallest among $|X_i - x|, i = 1, \ldots, n$. Let

$$K_i(x) = K\left(\frac{X_i - x}{h}\right)$$

where

$$K(t) = \frac{70}{81}(1 - |t|^3)^3 I(-1 \leq t \leq 1)$$

Define

$$w_i(x) = K_i(x)[S_2(x) - (X_i - x)S_1(x)]$$

where

$$S_1(x) = \sum_{i=1}^{n} K_i(x)(X_i - x)$$

$$S_2(x) = \sum_{i=1}^{n} K_i(x)(X_i - x)^2$$

Then the loess estimate of Y at x is defined by

$$\hat{Y}(x) = \sum_{i=1}^{n} \frac{w_i(x)}{\sum_{i=1}^{n} w_i(x)} Y_i$$

Loess smoothed residuals for checking the functional form of the jth covariate are defined by replacing Y_i with e_i and X_i with x_{ij}. To implement the graphical and numerical assessment methods, $I(x_{ij} \le x)$ is replaced with $\frac{w_i(x)}{\sum_{i=1}^{n} w_i(x)}$ in the formulas for $W_j(x)$ and $\hat{W}_j(x)$.

You can perform the model checking described earlier for marginal models for dependent responses fit by generalized estimating equations (GEEs). Let y_{ik} denote the kth measurement on the ith cluster, $i = 1, \ldots, K$, $k = 1, \ldots, n_i$, and let $\mathbf{x}_{ik}$ denote the corresponding vector of covariates. The marginal mean of the response $\mu_{ik} = \mathrm{E}(y_{ik})$ is assumed to depend on the covariate vector by

$$g(\mu_{ik}) = \mathbf{x}_{ik}'\boldsymbol{\beta}$$

where g is the link function.

Define the vector of residuals for the ith cluster as

$$\mathbf{e}_i = (e_{i1}, \ldots, e_{in_i})' = (y_{i1} - \hat{\mu}_{i1}, \ldots, y_{in_i} - \hat{\mu}_{in_i})'$$

You use the following extension of $W_j(x)$ defined earlier to check the functional form of the jth covariate:

$$W_j(x) = \frac{1}{\sqrt{K}} \sum_{i=1}^{K} \sum_{k=1}^{n_i} I(x_{ikj} \le x) e_{ik}$$

where x_{ikj} is the jth component of $\mathbf{x}_{ik}$.

The null distribution of $W_j(x)$ can be approximated by the conditional distribution of

$$\hat{W}_j(x) = \frac{1}{\sqrt{K}} \sum_{i=1}^{K} \left\{ \sum_{k=1}^{n_i} I(x_{ikj} \le x) e_{ik} + \boldsymbol{\eta}'(x, \hat{\boldsymbol{\beta}}) \mathbf{I}_0^{-1} \hat{\mathbf{D}}_i' \hat{\mathbf{V}}_i^{-1} \mathbf{e}_i \right\} Z_i$$

where $\hat{\mathbf{D}}_i$ and $\hat{\mathbf{V}}_i$ are defined as in the section "Generalized Estimating Equations" on page 1984 with the unknown parameters replaced by their estimated values,

$$\boldsymbol{\eta}(x, \boldsymbol{\beta}) = -\sum_{i=1}^{K} \sum_{k=1}^{n_i} I(x_{ikj} \le x) \frac{\partial \mu_{ik}}{\partial \boldsymbol{\beta}}$$

$$\mathbf{I}_0 = \sum_{i=1}^{K} \hat{\mathbf{D}}_i' \hat{\mathbf{V}}_i^{-1} \hat{\mathbf{D}}_i$$

and $Z_i, i = 1, \ldots, K$, are independent $N(0, 1)$ random variables. You replace x_{ikj} with the linear predictor $\mathbf{x}_{ik}'\hat{\boldsymbol{\beta}}$ in the preceding formulas to check the link function.

Case Deletion Diagnostic Statistics

For ordinary generalized linear models, regression diagnostic statistics developed by Williams (1987) can be requested in an output data set or in the OBSTATS table by specifying the DIAGNOSTICS | INFLUENCE option in the MODEL statement. These diagnostics measure the influence of an individual observation on model fit, and generalize the one-step diagnostics developed by Pregibon (1981) for the logistic regression model for binary data.

Preisser and Qaqish (1996) further generalize regression diagnostics to apply to models for correlated data fit by generalized estimating equations (GEEs), where the influence of entire clusters of correlated observations is measured. These diagnostic statistics can be requested in an output data set or in the OBSTATS table if a model for correlated data is specified with a REPEATED statement.

The next two sections use the following notation:

- $\hat{\boldsymbol{\beta}}$ is the maximum likelihood estimate of the regression parameters $\boldsymbol{\beta}$, or, in the case of correlated data, the solution of the GEEs.
- $\hat{\boldsymbol{\beta}}_{[i]}$ is the corresponding estimate evaluated with the ith observation deleted, or, in the case of correlated data, with the ith cluster deleted.
- p is the dimension of the regression parameter vector $\boldsymbol{\beta}$.
- r_{pi} is the standardized Pearson residual $\frac{y_i-\mu_i}{\sqrt{v_i(1-h_i)}}$, where v_i is the variance of the ith response and h_i is the leverage defined in the section "H | LEVERAGE" on page 1998.
- v_i is the variance of response i, $\text{var}(Y_i) = \phi V(\mu_i)$, where $V(\mu)$ is the variance function and ϕ is the dispersion parameter.
- w_i is the prior weight of the ith observation specified with the WEIGHT statement. If there is no WEIGHT statement, $w_i = 1$ for all i.

All unknown quantities are replaced by their estimated values in the following two sections.

Diagnostics for Ordinary Generalized Linear Models

The following statistics are available for generalized linear models.

DFBETA

The DFBETA statistic for measuring the influence of the ith observation is defined as the one-step approximation to the difference in the MLE of the regression parameter vector and the MLE of the regression parameter vector without the ith observation. This one-step approximation assumes a Fisher scoring step, and is given by

$$\hat{\boldsymbol{\beta}} - \hat{\boldsymbol{\beta}}_{[i]} \approx DFBETA_i = (X'WX)^{-1}X_i'W_i^{\frac{1}{2}}(1-h_i)^{-\frac{1}{2}}r_{pi}$$

where h_i is the leverage defined in the section "H | LEVERAGE" on page 1998.

DFBETAS

The standardized DFBETA statistic for assessing the influence of the ith observation on the jth regression parameter is defined as the DFBETA statistic for the jth parameter divided by its estimated standard deviation, where the standard deviation is estimated from all the data.

$$DFBETAS_{ij} = DFBETA_{ij}/\hat{\sigma}(\beta_j)$$

DOBS | COOKD | COOKSD

In normal linear regression, the influence of observation i can be measured by Cook's distance (Cook and Weisberg 1982). A measure of influence of observation i for generalized linear models that is equivalent to Cook's distance for normal linear regression is given by

$$DOBS_i = p^{-1}h_i(1-h_i)^{-1}r_{pi}^2$$

where h_i is the leverage defined in the section "H | LEVERAGE" on page 1998. This measure is the one-step approximation to $2p^{-1}[L(\hat{\boldsymbol{\beta}}) - L(\hat{\boldsymbol{\beta}}_{[i]})]$, where $L(\boldsymbol{\beta})$ is the log likelihood evaluated at $\boldsymbol{\beta}$.

H | LEVERAGE

The Fisher scores, or expected, weight for observation i is $w_{ei} = \frac{w_i}{\phi V(\mu_i)(g'(\mu_i))^2}$. Let W be the diagonal matrix with w_{ei} as the ith diagonal. The leverage h_i of the ith observation is defined as the ith diagonal element of the hat matrix

$$H = W^{\frac{1}{2}}(X'WX)^{-1}W^{\frac{1}{2}}$$

Diagnostics for Models Fit by Generalized Estimating Equations (GEEs)

The diagnostic statistics in this section were developed by Preisser and Qaqish (1996). See the section "Generalized Estimating Equations" on page 1984 for further information and notation for generalized estimating equations (GEEs). The following additional notation is used in this section.

Partition the design matrix $\mathbf{X}$ and response vector $\mathbf{Y}$ by cluster; that is, let $\mathbf{X} = (X_1', \ldots, X_K')'$, and $\mathbf{Y} = (Y_1', \ldots, Y_K')'$ corresponding to the K clusters.

Let n_i be the number of responses for cluster i, and denote by $N = \sum_{i=1}^{K} n_i$ the total number of observations. Denote by A_i the $n_i \times n_i$ diagonal matrix with $V(\mu_{ij})$ as the jth diagonal element. If there is a WEIGHT statement, the diagonal element of A_i is $V(\mu_{ij})/w_{ij}$, where w_{ij} is the specified weight of the jth observation in the ith cluster. Let B the $N \times N$ diagonal matrix with $g'(\mu_{ij})$ as diagonal elements, $i = 1, \ldots, K$, $j = 1, \ldots, n_i$. Let B_i the $n_i \times n_i$ diagonal matrix corresponding to cluster i with $g'(\mu_{ij})$ as the jth diagonal element.

Let W be the $N \times N$ block diagonal weight matrix whose ith block, corresponding to the ith cluster, is the $n_i \times n_i$ matrix

$$W_{ei} = B_i^{-1}A_i^{-\frac{1}{2}}R_i^{-1}(\hat{\boldsymbol{\alpha}})A_i^{-\frac{1}{2}}B_i^{-1}$$

where R_i is the working correlation matrix for cluster i.

Let

$$Q_i = X_i(X'WX)^{-1}X_i'$$

where X_i is the $n_i \times p$ design matrix corresponding to cluster i.

Define the adjusted residual vector as

$$E = B(\mathbf{Y} - \hat{\boldsymbol{\mu}})$$

and $E_i = B_i(\mathbf{Y}_i - \hat{\boldsymbol{\mu}}_i)$, the estimated residual for the ith cluster.

Let the subscript $[i]$ denote estimates evaluated without the ith cluster, $[it]$ estimates evaluated using all the data except the tth observation of the ith cluster, and let $i[t]$ denote matrices corresponding to the ith cluster without the tth observation.

The following statistics are available for generalized estimating equation models.

CH | CLUSTERH | CLEVERAGE

The leverage of cluster i is contained in the matrix $H_i = Q_i W_{ei}$, and is summarized by the trace of H_i,

$$ch_i = tr(H_i)$$

The leverage h_i of the tth observation in the ith cluster is the tth diagonal element of H_i.

DFBETAC

The effect of deleting cluster i on the estimated parameter vector is given by the following one-step approximation for $\hat{\boldsymbol{\beta}} - \hat{\boldsymbol{\beta}}_{[i]}$:

$$DBETAC_i = (X'WX)^{-1}X_i'(W_{ei}^{-1} - Q_i)^{-1}E_i$$

DFBETACS

The cluster deletion statistic DFBETAC can be standardized using the variances of $\hat{\boldsymbol{\beta}}$ based on the complete data. The standardized one-step approximation for the change in $\hat{\beta}_j$ due to deletion of cluster i is

$$DBETACS_{ij} = \frac{DBETAC_{ij}}{\hat{\phi}[(X'WX)^{-1}]_{jj}^{\frac{1}{2}}}$$

DFBETAO

Partition the matrices W_{ei} and V_i as

$$W_{ei} = \begin{pmatrix} W_{eit} & W_{eit[t]} \\ W_{ei[t]t} & W_{ei[t]} \end{pmatrix}$$

$$V_i = W_{ei}^{-1} = \begin{pmatrix} V_{it} & V_{it[t]} \\ V_{i[t]t} & V_{i[t]} \end{pmatrix}$$

and let $E_{it} = B_{it}(Y_{it} - \hat{\mu}_{it})$ and $E_{i[t]} = B_{i[t]}(Y_{i[t]} - \hat{\mu}_{i[t]})$.

The effect of deleting the tth observation from the ith cluster is given by the following one-step approximation to $\hat{\boldsymbol{\beta}} - \hat{\boldsymbol{\beta}}_{[it]}$:

$$DBETAO_{it} = (X'WX)^{-1}\tilde{X}'_{it}\frac{\tilde{E}_{it}}{W_{eit}^{-1} - \tilde{Q}_{it}}$$

where $\tilde{X}_{it} = X_{it} - V_{it[t]}V_{i[t]}^{-1}X_{i[t]}$, $\tilde{Q}_{it} = \tilde{X}_{it}(X'WX)^{-1}\tilde{X}'_{it}$, and $\tilde{E}_{it} = E_{it} - V_{it[t]}V_{i[t]}^{-1}E_{i[t]}$. Note that W_{eit}, $\tilde{Q}_{it}$, and $\tilde{E}_{it}$ are scalars.

DFBETAOS

The observation deletion statistic DFBETAO can be standardized using the variances of $\hat{\boldsymbol{\beta}}$ based on the complete data. The standardized one-step approximation for the change in $\hat{\beta}_j$ due to deletion of observation t in cluster i is

$$DBETAOS_{itj} = \frac{DBETAO_{itj}}{\hat{\phi}[(X'WX)^{-1}]_{jj}^{\frac{1}{2}}}$$

DCLS | CLUSTERCOOKD | CLUSTERCOOKSD

A measure of the standardized influence of the subset m of observations on the overall fit is $(\hat{\boldsymbol{\beta}} - \hat{\boldsymbol{\beta}}_{[m]})'(X'WX)(\hat{\boldsymbol{\beta}} - \hat{\boldsymbol{\beta}}_{[m]})/p\hat{\phi}$. For deletion of cluster i, this is approximated by

$$DCLS_i = E_i'(W_{ei}^{-1} - Q_i)^{-1})Q_i(W_{ei}^{-1} - Q_i)^{-1})E_i/p\hat{\phi}$$

DOBS | COOKD | COOKSD

The measure of overall fit in the section "DCLS | CLUSTERCOOKD | CLUSTERCOOKSD" on page 2000 for the deletion of the tth observation in the ith cluster is approximated by

$$DOBS_{it} = \frac{\tilde{E}_{it}^2\tilde{Q}_{it}}{p\hat{\phi}(W_{eit}^{-1} - \tilde{Q}_{it})^2}$$

where $\tilde{E}_{it}$, $\tilde{Q}_{it}$, and W_{eit} are defined in the section "DFBETAO" on page 1999. In the case of the independence working correlation, this is equal to the measure for ordinary generalized linear models defined in the section "DOBS | COOKD | COOKSD" on page 1998.

MCLS | CLUSTERDFIT

A studentized distance measure of the type defined in the section "DCLS | CLUSTERCOOKD | CLUSTERCOOKSD" on page 2000 of the influence of the ith cluster is given by

$$MCLS_i = E_i'(W_{ei}^{-1} - Q_i)^{-1}H_iE_i/p\hat{\phi}$$

Bayesian Analysis

Gibbs Sampling

This section provides details for Bayesian analysis by Gibbs sampling in generalized linear models. See the section "Gibbs Sampler" on page 154 for a general discussion of Gibbs sampling. See Gilks, Richardson, and Spiegelhalter (1996) for a discussion of applications of Gibbs sampling to a number of different models, including generalized linear models. In generalized linear models, the response has a probability distribution from a family of distributions of the exponential form. That is, the probability density of the response Y for continuous response variables, or the probability function for discrete responses, can be expressed as

$$f(y) = \exp\left\{\frac{y\theta - b(\theta)}{a(\phi)} + c(y,\phi)\right\}$$

for some functions a, b, and c that determine the specific distribution. The canonical parameters θ depend only on the means of the response μ_i, which are related to the regression parameters β through the link function $g(\mu_i) = x'\beta$. The additional parameter ϕ is the dispersion parameter. The GENMOD procedure estimates the regression parameters and the scale parameter $\sigma = \phi^{\frac{1}{2}}$ by maximum likelihood. However, the GENMOD procedure can also provide Bayesian estimates of the regression parameters and either the scale σ, the dispersion ϕ, or the precision $\tau = \phi^{-1}$ by Gibbs sampling. Except where noted, the following discussion applies to either σ, ϕ, or τ, although ϕ is used to illustrate the formulas. Note that the Poisson and binomial distributions do not have a dispersion parameter, and the dispersion is considered to be fixed at $\phi = 1$. The ASSESS, CONTRAST, ESTIMATE, OUTPUT, and REPEATED statements, if specified, are ignored. Also ignored are the PLOTS= option in the PROC GENMOD statement and the following options in the MODEL statement: ALPHA=, CORRB, COVB, TYPE1, TYPE3, SCALE=DEVIANCE (DSCALE), SCALE=PEARSON (PSCALE), OBSTATS, RESIDUALS, XVARS, PREDICTED, DIAGNOSTICS, and SCALE= for Poisson and binomial distributions. The multinomial and zero-inflated Poisson distributions are not available for Bayesian analysis.

Let $\boldsymbol{\theta} = (\theta_1, \ldots, \theta_k)'$ be the parameter vector. For generalized linear models, the θ_is are the regression coefficients β_is and the dispersion parameter ϕ. Let $L(D|\boldsymbol{\theta})$ be the likelihood function, where D is the observed data. Let $\pi(\boldsymbol{\theta})$ be the prior distribution. The full conditional distribution of $[\theta_i|\theta_j, i \neq j]$ is proportional to the joint distribution; that is,

$$\pi(\theta_i|\theta_j, i \neq j, D) \propto L(D|\boldsymbol{\theta})p(\boldsymbol{\theta})$$

For instance, the one-dimensional conditional distribution of θ_1 given $\theta_j = \theta_j^*, 2 \leq j \leq k$, is computed as

$$\pi(\theta_1|\theta_j = \theta_j^*, 2 \leq j \leq k, D) = L(D|(\boldsymbol{\theta} = (\theta_1, \theta_2^*, \ldots, \theta_k^*)')p(\boldsymbol{\theta} = (\theta_1, \theta_2^*, \ldots, \theta_k^*)')$$

Suppose you have a set of arbitrary starting values $\{\theta_1^{(0)}, \ldots, \theta_k^{(0)}\}$. Using the ARMS (adaptive rejection Metropolis sampling) algorithm of Gilks and Wild (1992) and Gilks, Best, and Tan (1995), you can do the following:

draw $\theta_1^{(1)}$ from $[\theta_1|\theta_2^{(0)}, \ldots, \theta_k^{(0)}]$

draw $\theta_2^{(1)}$ from $[\theta_2|\theta_1^{(1)}, \theta_3^{(0)}, \ldots, \theta_k^{(0)}]$

...

draw $\theta_k^{(1)}$ from $[\theta_k|\theta_1^{(1)}, \ldots, \theta_{k-1}^{(1)}]$

This completes one iteration of the Gibbs sampler. After one iteration, you have $\{\theta_1^{(1)}, \ldots, \theta_k^{(1)}\}$. After n iterations, you have $\{\theta_1^{(n)}, \ldots, \theta_k^{(n)}\}$. PROC GENMOD implements the ARMS algorithm provided by Gilks (2003) to draw a sample from a full conditional distribution. See the section "Assessing Markov Chain Convergence" on page 156 for information about assessing the convergence of the chain of posterior samples.

You can output these posterior samples into a SAS data set through ODS. The following SAS statement outputs the posterior samples into the SAS data set Post:

```
OUTPOST=Post
```

The data set also includes the variable LogPost, representing the log of the posterior log likelihood.

Priors for Model Parameters

The model parameters are the regression coefficients and the dispersion parameter (or the precision or scale), if the model has one. The priors for the dispersion parameter and the priors for the regression coefficients are assumed to be independent, while you can have a joint multivariate normal prior for the regression coefficients.

Dispersion, Precision, or Scale Parameter

Gamma Prior The gamma distribution $G(a, b)$ has a PDF

$$f(u) = \frac{b(bu)^{a-1}e^{-bu}}{\Gamma(a)}, \qquad u > 0$$

where a is the shape parameter and b is the inverse-scale parameter. The mean is $\frac{a}{b}$ and the variance is $\frac{a}{b^2}$.

Improper Prior The joint prior density is given by

$$p(u) \propto u^{-1}, \qquad u > 0$$

Inverse Gamma Prior The inverse gamma distribution $IG(a, b)$ has a PDF

$$f(u) = \frac{b^a}{\Gamma(a)} u^{-(a+1)} e^{-b/u}, \qquad u > 0$$

where a is the shape parameter and b is the scale parameter. The mean is $\frac{b}{a-1}$ if $a > 1$, and the variance is $\frac{b^2}{(a-1)^2(a-2)}$ if $a > 2$.

Regression Coefficients

Let $\boldsymbol{\beta}$ be the regression coefficients.

Jeffreys' Prior The joint prior density is given by

$$p(\boldsymbol{\beta}) \propto |\mathbf{I}(\boldsymbol{\beta})|^{\frac{1}{2}}$$

where $\mathbf{I}(\boldsymbol{\beta})$ is the Fisher information matrix for the model. If the underlying model has a scale parameter (for example, a normal linear regression model), then the Fisher information matrix is computed with the scale parameter set to a fixed value of one.

If you specify the CONDITIONAL option, then Jeffreys' prior, conditional on the current Markov chain value of the generalized linear model precision parameter τ, is given by

$$|\tau\mathbf{I}(\boldsymbol{\beta})|^{\frac{1}{2}}$$

where τ is the model precision parameter.

See Ibrahim and Laud (1991) for a full discussion, with examples, of Jeffreys' prior for generalized linear models.

Normal Prior Assume $\boldsymbol{\beta}$ has a multivariate normal prior with mean vector $\boldsymbol{\beta}_0$ and covariance matrix $\boldsymbol{\Sigma}_0$. The joint prior density is given by

$$p(\boldsymbol{\beta}) \propto \mathrm{e}^{-\frac{1}{2}(\boldsymbol{\beta}-\boldsymbol{\beta}_0)'\boldsymbol{\Sigma}_0^{-1}(\boldsymbol{\beta}-\boldsymbol{\beta}_0)}$$

If you specify the CONDITIONAL option, then, conditional on the current Markov chain value of the generalized linear model precision parameter τ, the joint prior density is given by

$$p(\boldsymbol{\beta}) \propto \mathrm{e}^{-\frac{1}{2}(\boldsymbol{\beta}-\boldsymbol{\beta}_0)'\tau\boldsymbol{\Sigma}_0^{-1}(\boldsymbol{\beta}-\boldsymbol{\beta}_0)}$$

Uniform Prior The joint prior density is given by

$$p(\boldsymbol{\beta}) \propto 1$$

Deviance Information Criterion

Let θ_i be the model parameters at iteration i of the Gibbs sampler and let $\mathrm{LL}(\theta_i)$ be the corresponding model log likelihood. PROC GENMOD computes the following fit statistics defined by Spiegelhalter et al. (2002):

- Effective number of parameters:

$$p_D = \overline{\mathrm{LL}(\theta)} - \mathrm{LL}(\bar{\theta})$$

- Deviance information criterion (DIC):

$$\mathrm{DIC} = \overline{\mathrm{LL}(\theta)} + p_D$$

where

$$\overline{\mathrm{LL}(\theta)} = \frac{1}{n}\sum_{i=1}^{n}\mathrm{LL}(\theta_i)$$

$$\bar{\theta} = \frac{1}{n}\sum_{i=1}^{n}\theta_i$$

PROC GENMOD uses the full log likelihoods defined in the section "Log-Likelihood Functions" on page 1965, with all terms included, for computing the DIC.

Posterior Distribution

Denote the observed data by D.

The posterior distribution is

$$\pi(\boldsymbol{\beta}|D) \propto L_P(D|\boldsymbol{\beta})p(\boldsymbol{\beta})$$

where $L_P(D|\boldsymbol{\beta})$ is the likelihood function with regression coefficients $\boldsymbol{\beta}$ as parameters.

Starting Values of the Markov Chains

When the BAYES statement is specified, PROC GENMOD generates one Markov chain containing the approximate posterior samples of the model parameters. Additional chains are produced when the Gelman-Rubin diagnostics are requested. Starting values (or initial values) can be specified in the INITIAL= data set in the BAYES statement. If INITIAL= option is not specified, PROC GENMOD picks its own initial values for the chains.

Denote $[x]$ as the integral value of x. Denote $\hat{s}(X)$ as the estimated standard error of the estimator X.

Regression Coefficients

For the first chain that the summary statistics and regression diagnostics are based on, the default initial values are estimates of the mode of the posterior distribution. If the INITIALMLE option is specified, the initial values are the maximum likelihood estimates; that is,

$$\beta_i^{(0)} = \hat{\beta}_i$$

Initial values for the rth chain ($r \geq 2$) are given by

$$\beta_i^{(0)} = \hat{\beta}_i \pm \left(2 + \left[\frac{r}{2}\right]\right)\hat{s}(\hat{\beta}_i)$$

with the plus sign for odd r and minus sign for even r.

Dispersion, Scale, or Precision Parameter λ

Let λ be the generalized linear model parameter you choose to sample, either the dispersion, scale, or precision parameter. Note that the Poisson and binomial distributions do not have this additional parameter.

For the first chain that the summary statistics and regression diagnostics are based on, the default initial values are estimates of the mode of the posterior distribution. If the INITIALMLE option is specified, the initial values are the maximum likelihood estimates; that is,

$$\lambda^{(0)} = \hat{\lambda}$$

The initial values of the rth chain ($r \geq 2$) are given by

$$\lambda^{(0)} = \hat{\lambda} e^{\pm\left([\frac{r}{2}]+2\right)\hat{s}(\hat{\lambda})}$$

with the plus sign for odd r and minus sign for even r.

OUTPOST= Output Data Set

The OUTPOST= data set contains the generated posterior samples. There are 2+n variables, where n is the number of model parameters. The variable Iteration represents the iteration number and the variable LogPost contains the log posterior likelihood values. The other n variables represent the draws of the Markov chain for the model parameters.

Missing Values

For generalized linear models, PROC GENMOD ignores any observation with a missing value for any variable involved in the model. You can score an observation in an output data set by setting only the response value to missing. For models fit with generalized estimating equations (GEEs), observations with missing values within a cluster are not used, and all available pairs are used in estimating the working correlation matrix. Clusters with fewer observations than the full cluster size are treated as having missing observations occurring at the end of the cluster. You can specify the order of missing observations with the WITHINSUBJECT= option. See the section "Missing Data" on page 1987 for more information about missing values in GEEs.

Displayed Output for Classical Analysis

The following output is produced by the GENMOD procedure. Note that some of the tables are optional and appear only in conjunction with the REPEATED statement and its options or with options in the MODEL statement. For details, see the section "ODS Table Names" on page 2017.

Model Information

The "Model Information" table displays the two-level data set name, the response distribution, the link function, the response variable name, the offset variable name, the frequency variable name, the scale weight variable name, the number of observations used, the number of events if events/trials format is used for response, the number of trials if events/trials format is used for response, the sum of frequency weights, the number of missing values in data set, and the number of invalid observations (for example, negative or 0 response values with gamma distribution or number of observations with events greater than trials with binomial distribution).

Class Level Information

If you use classification variables in the model, PROC GENMOD displays the levels of classification variables specified in the CLASS statement and in the MODEL statement. The levels are displayed in the same sorted order used to generate columns in the design matrix.

Response Profile

If you specify an ordinal model for the multinomial distribution, a table titled "Response Profile" is displayed containing the ordered values of the response variable and the number of occurrences of the values used in the model.

Iteration History for Parameter Estimates

If you specify the ITPRINT model option, PROC GENMOD displays a table containing the following for each iteration in the Newton-Raphson procedure for model fitting: the iteration number, the ridge value, the log likelihood, and values of all parameters in the model.

Criteria for Assessing Goodness of Fit

In the "Criteria for Assessing Goodness of Fit" table, PROC GENMOD displays the degrees of freedom for deviance and Pearson's chi-square, equal to the number of observations minus the number of regression parameters estimated, the deviance, the deviance divided by degrees of freedom, the scaled deviance, the scaled deviance divided by degrees of freedom, Pearson's chi-square, Pearson's chi-square divided by degrees of freedom, the scaled Pearson's chi-square, the scaled Pearson's chi-square divided by degrees of freedom, the log likelihood (excludes factorial terms) the full log likelihood, the Akaike information criterion, the corrected Akaike information criterion, and the Bayesian information criterion. The information in this table is valid only for maximum likelihood model fitting, and the table is not printed if the REPEATED statement is specified.

Last Evaluation of the Gradient

If you specify the model option ITPRINT, the GENMOD procedure displays the last evaluation of the gradient vector.

Last Evaluation of the Hessian

If you specify the model option ITPRINT, the GENMOD procedure displays the last evaluation of the Hessian matrix.

Analysis of (Initial) Parameter Estimates

The "Analysis of (Initial) Parameter Estimates" table contains the results from fitting a generalized linear model to the data. If you specify the REPEATED statement, these GLM parameter estimates are used as initial values for the GEE solution, and are displayed only if the PRINTMLE option in the REPEATED statement is specified. For each parameter in the model, PROC GENMOD displays the parameter name, as follows:

- the variable name for continuous regression variables
- the variable name and level for classification variables and interactions involving classification variables
- SCALE for the scale variable related to the dispersion parameter

In addition, PROC GENMOD displays the degrees of freedom for the parameter, the estimate value, the standard error, the Wald chi-square value, the p-value based on the chi-square distribution, and the confidence limits (Wald or profile likelihood) for parameters.

Lagrange Multiplier Statistics

If you specify that either the model intercept or the scale parameter is fixed, for those distributions that have a distribution scale parameter, the GENMOD procedure displays a table of Lagrange multiplier, or score, statistics for testing the validity of the constrained parameter that contains the test statistic, and the p-value.

Estimated Covariance Matrix

If you specify the model option COVB, the GENMOD procedure displays the estimated covariance matrix, defined as the inverse of the information matrix at the final iteration. This is based on the expected information matrix if the EXPECTED option is specified in the MODEL statement. Otherwise, it is based on the Hessian matrix used at the final iteration. This is, by default, the observed Hessian unless altered by the SCORING option in the MODEL statement.

Estimated Correlation Matrix

If you specify the CORRB model option, PROC GENMOD displays the estimated correlation matrix. This is based on the expected information matrix if the EXPECTED option is specified in the MODEL statement. Otherwise, it is based on the Hessian matrix used at the final iteration. This is, by default, the observed Hessian unless altered by the SCORING option in the MODEL statement.

Iteration History for LR Confidence Intervals

If you specify the ITPRINT and LRCI model options, PROC GENMOD displays an iteration history table for profile likelihood-based confidence intervals. For each parameter in the model, PROC GENMOD displays the parameter identification number, the iteration number, the log-likelihood value, parameter values.

Likelihood Ratio-Based Confidence Intervals for Parameters

If you specify the LRCI and the ITPRINT options in the MODEL statement, a table is displayed that summarizes profile likelihood-based confidence intervals for all parameters. For each parameter in the model, the table displays the confidence coefficient, the parameter identification number, lower and upper endpoints of confidence intervals for the parameter, and values of all other parameters at the solution.

LR Statistics for Type 1 Analysis

If you specify the TYPE1 model option, a table is displayed that contains the name of the effect, the deviance for the model including the effect and all previous effects, the degrees of freedom for the effect, the likelihood ratio statistic for testing the significance of the effect, and the p-value computed from the chi-square distribution with the effect's degrees of freedom.

If you specify either the SCALE=DEVIANCE or SCALE=PEARSON option in the MODEL statement, columns are displayed that contain the name of the effect, the deviance for the model including the effect and all previous effects, the numerator degrees of freedom, the denominator degrees of freedom, the chi-square statistic for testing the significance of the effect, the p-value computed from the chi-square distribution with numerator degrees of freedom, the F statistic for testing the significance of the effect, and the p-value based on the F distribution.

Iteration History for Type 3 Contrasts

If you specify the model options ITPRINT and TYPE3, an iteration history table is displayed for fitting the model with Type 3 contrast constraints for each effect that contains the effect name, the iteration number, the ridge value, the log likelihood, and values of all parameters.

LR Statistics for Type 3 Analysis

If you specify the TYPE3 model option, a table is displayed that contains, for each effect in the model, the name of the effect, the likelihood ratio statistic for testing the significance of the effect, the degrees of freedom for the effect, and the p-value computed from the chi-square distribution.

If you specify either the SCALE=DEVIANCE or SCALE=PEARSON option in the MODEL statement, columns are displayed that contain the name of the effect, the likelihood ratio statistic for testing the significance of the effect, the F statistic for testing the significance of the effect, the numerator degrees of freedom, the denominator degrees of freedom, the p-value based on the F distribution, and the p-value computed from the chi-square distribution with the numerator's degrees of freedom.

Wald Statistics for Type 3 Analysis

If you specify the TYPE3 and WALD model options, a table is displayed that contains the name of the effect, the degrees of freedom of the effect, the Wald statistic for testing the significance of the effect, and the p-value computed from the chi-square distribution.

Parameter Information

If you specify the ITPRINT, COVB, CORRB, WALDCI, or LRCI option in the MODEL statement, or if you specify a CONTRAST statement, a table is displayed that identifies parameters with numbers, rather than names, for use in tables and matrices where a compact identifier for parameters is helpful. For each parameter, the table contains an index number that identifies the parameter, and the parameter name, including level information for effects containing classification variables.

Observation Statistics

If you specify the OBSTATS option in the MODEL statement, PROC GENMOD displays a table containing miscellaneous statistics. Residuals and case deletion diagnostic statistics are not available for the multinomial distribution. Case deletion diagnostics are not available for zero-inflated models.

For each observation in the input data set, the following are displayed:

- the value of the response variable
- the predicted value of the mean
- the value of the linear predictor The value of an OFFSET variable is added to the linear predictor.
- the estimated standard error of the linear predictor

- the value of the negative of the weight in the Hessian matrix at the final iteration. This is the expected weight if the EXPECTED option is specified in the MODEL statement. Otherwise, it is the weight used in the final iteration. That is, it is the observed weight unless the SCORING= option has been specified.
- approximate lower and upper endpoints for a confidence interval for the predicted value of the mean
- raw residual
- Pearson residual
- deviance residual
- standardized Pearson residual
- standardized deviance residual
- likelihood residual
- leverage
- Cook's distance statistic
- DFBETA statistic, for each parameter
- standardized DFBETA statistic, for each parameter
- zero-inflation probability for zero-inflated models
- response mean for zero-inflated models

ESTIMATE Statement Results

If you specify a REPEATED statement, the ESTIMATE statement results apply to the specified GEE model. Otherwise, they apply to the specified generalized linear model.

For each ESTIMATE statement, the table contains the contrast label, the estimated value of the contrast, the standard error of the estimate, the significance level α, $(1 - \alpha) \times 100\%$ confidence intervals for contrast, the Wald chi-square statistic for the contrast, and the p-value computed from the chi-square distribution.

If you specify the EXP option, an additional row is displayed with statistics for the exponentiated value of the contrast.

CONTRAST Coefficients

If you specify the CONTRAST or ESTIMATE statement and you specify the E option, a table titled "Coefficients For Contrast *label*" is displayed, where *label* is the label specified in the CONTRAST statement. The table contains the contrast label, and the rows of the contrast matrix.

Iteration History for Contrasts

If you specify the ITPRINT option, an iteration history table is displayed for fitting the model with contrast constraints for each effect. The table contains the contrast label, the iteration number, the ridge value, the log likelihood, and values of all parameters.

CONTRAST Statement Results

If you specify a REPEATED statement, the CONTRAST statement results apply to the specified GEE model. Otherwise, they apply to the specified generalized linear model.

A table is displayed that contains the contrast label, the degrees of freedom for the contrast, and the likelihood ratio, score, or Wald statistic for testing the significance of the contrast. Score statistics are used in GEE models, likelihood ratio statistics are used in generalized linear models, and Wald statistics are used in both. Also displayed are the p-value computed from the chi-square distribution, and the type of statistic computed for this contrast: Wald, LR, or score.

If you specify either the SCALE=DEVIANCE or SCALE=PEARSON option for generalized linear models, columns are displayed that contain the contrast label, the likelihood ratio statistic for testing the significance of the contrast, the F statistic for testing the significance of the contrast, the numerator degrees of freedom, the denominator degrees of freedom, the p-value based on the F distribution, and the p-value computed from the chi-square distribution with numerator degrees of freedom.

LSMEANS Coefficients

If you specify the LSMEANS statement and you specify the E option, the "Coefficients for *effect* Least Squares Means" table is displayed, where *effect* is the effect specified in the LSMEANS statement. The table contains the effect names and the rows of least squares means coefficients.

Least Squares Means

If you specify the LSMEANS statement, the "Least Squares Means" table is displayed. The table contains for each effect the following: the effect name, and for each level of each effect the following:

- the least squares mean estimate
- standard error
- chi-square value
- p-value computed from the chi-square distribution

If you specify the DIFF option, a table titled "Differences of Least Squares Means" is displayed containing corresponding statistics for the differences between the least squares means for the levels of each effect.

GEE Model Information

If you specify the REPEATED statement, the "GEE Model Information" table displays the correlation structure of the working correlation matrix or the log odds ratio structure, the within-subject effect, the subject effect, the number of clusters, the correlation matrix dimension, and the minimum and maximum cluster size.

Log Odds Ratio Parameter Information

If you specify the REPEATED statement and specify a log odds ratio model for binary data with the LOGOR= option, then the "Log Odds Ratio Parameter Information" table is displayed showing the correspondence between data pairs and log odds ratio model parameters.

Iteration History for GEE Parameter Estimates

If you specify the REPEATED statement and the MODEL statement option ITPRINT, the "Iteration History For GEE Parameter Estimates" table is displayed. The table contains the parameter identification number, the iteration number, and values of all parameters.

Last Evaluation of the Generalized Gradient and Hessian

If you specify the REPEATED statement and select ITPRINT as a model option, PROC GENMOD displays the "Last Evaluation Of The Generalized Gradient And Hessian" table.

GEE Parameter Estimate Covariance Matrices

If you specify the REPEATED statement and the COVB option, PROC GENMOD displays the "Covariance Matrix (Model-Based)" and "Covariance Matrix (Empirical)" tables.

GEE Parameter Estimate Correlation Matrices

If you specify the REPEATED statement and the CORRB option, PROC GENMOD displays the "Correlation Matrix (Model-Based)" and "Correlation Matrix (Empirical)" tables.

GEE Working Correlation Matrix

If you specify the REPEATED statement and the CORRW option, PROC GENMOD displays the "Working Correlation Matrix" table.

GEE Fit Criteria

If you specify the REPEATED statement, PROC GENMOD displays the quasi-likelihood information criteria for model fit QIC and QIC_u in the "GEE Fit Criteria" table.

Analysis of GEE Parameter Estimates

If you specify the REPEATED statement, PROC GENMOD uses empirical standard error estimates to compute and display the "Analysis Of GEE Parameter Estimates Empirical Standard Error Estimates" table that contains the parameter names as follows:

- the variable name for continuous regression variables
- the variable name and level for classification variables and interactions involving classification variables
- "Scale" for the scale variable related to the dispersion parameter

In addition, the parameter estimate, the empirical standard error, a 95% confidence interval, and the Z score and p-value are displayed for each parameter.

If you specify the MODELSE option in the REPEATED statement, the "Analysis Of GEE Parameter Estimates Model-Based Standard Error Estimates" table based on model-based standard errors is also produced.

GEE Observation Statistics

If you specify the OBSTATS option in the REPEATED statement, PROC GENMOD displays a table containing miscellaneous statistics. For each observation in the input data set, the following are displayed:

- the value of the response variable and all other variables in the model, denoted by the variable names
- the predicted value of the mean
- the value of the linear predictor
- the standard error of the linear predictor
- confidence limits for the predicted values
- raw residual
- Pearson residual
- cluster number
- leverage

- cluster leverage
- cluster Cook's distance statistic
- studentized cluster Cook's distance statistic
- individual observation Cook's distance statistic
- cluster DFBETA statistic for each parameter
- cluster standardized DFBETA statistic for each parameter
- individual observation DFBETA statistic for each parameter
- individual observation standardized DFBETA statistic for each parameter

Displayed Output for Bayesian Analysis

If a Bayesian analysis is requested with a BAYES statement, the displayed output includes the following.

Model Information

The "Model Information" table displays the two-level data set name, the number of burn-in iterations, the number of iterations after the burn-in, the number of thinning iterations, the response distribution, the link function, the response variable name, the offset variable name, the frequency variable name, the scale weight variable name, the number of observations used, the number of events if events/trials format is used for response, the number of trials if events/trials format is used for response, the sum of frequency weights, the number of missing values in data set, and the number of invalid observations (for example, negative or 0 response values with gamma distribution or number of observations with events greater than trials with binomial distribution).

Class Level Information

The "Class Level Information" table displays the levels of classification variables if you specify a CLASS statement.

Maximum Likelihood Estimates

The "Analysis of Maximum Likelihood Parameter Estimates" table displays the maximum likelihood estimate of each parameter, the estimated standard error of the parameter estimator, and confidence limits for each parameter.

Coefficient Prior

The "Coefficient Prior" table displays the prior distribution of the regression coefficients.

Independent Prior Distributions for Model Parameters

The "Independent Prior Distributions for Model Parameters" table displays the prior distributions of additional model parameters (scale, exponential scale, Weibull scale, Weibull shape, gamma shape).

Initial Values and Seeds

The "Initial Values and Seeds" table displays the initial values and random number generator seeds for the Gibbs chains.

Fit Statistics

The "Fit Statistics" table displays the deviance information criterion (DIC) and the effective number of parameters.

Descriptive Statistics of the Posterior Samples

The "Descriptive Statistics of the Posterior Sample" table contains the size of the sample, the mean, the standard deviation, and the quartiles for each model parameter.

Interval Estimates for Posterior Sample

The "Interval Estimates for Posterior Sample" table contains the HPD intervals and the credible intervals for each model parameter.

Correlation Matrix of the Posterior Samples

The "Correlation Matrix of the Posterior Samples" table is produced if you include the CORR suboption in the SUMMARY= option in the BAYES statement. This table displays the sample correlation of the posterior samples.

Covariance Matrix of the Posterior Samples

The "Covariance Matrix of the Posterior Samples" table is produced if you include the COV suboption in the SUMMARY= option in the BAYES statement. This table displays the sample covariance of the posterior samples.

Autocorrelations of the Posterior Samples

The "Autocorrelations of the Posterior Samples" table displays the lag1, lag5, lag10, and lag50 autocorrelations for each parameter.

Gelman and Rubin Diagnostics

The "Gelman and Rubin Diagnostics" table is produced if you include the GELMAN suboption in the DIAGNOSTIC= option in the BAYES statement. This table displays the estimate of the potential scale reduction factor and its 97.5% upper confidence limit for each parameter.

Geweke Diagnostics

The "Geweke Diagnostics" table displays the Geweke statistic and its p-value for each parameter.

Raftery and Lewis Diagnostics

The "Raftery Diagnostics" tables is produced if you include the RAFTERY suboption in the DIAGNOSTIC= option in the BAYES statement. This table displays the Raftery and Lewis diagnostics for each variable.

Heidelberger and Welch Diagnostics

The "Heidelberger and Welch Diagnostics" table is displayed if you include the HEIDELBERGER suboption in the DIAGNOSTIC= option in the BAYES statement. This table shows the results of a stationary test and a halfwidth test for each parameter.

Effective Sample Size

The "Effective Sample Size" table displays, for each parameter, the effective sample size, the correlation time, and the efficiency.

Monte Carlo Standard Errors

The "Monte Carlo Standard Errors" table displays, for each parameter, the Monte Carlo standard error, the posterior sample standard deviation, and the ratio of the two.

ODS Table Names

PROC GENMOD assigns a name to each table that it creates. You can use these names to reference the table when using the Output Delivery System (ODS) to select tables and create output data sets. These names are listed separately in Table 37.4 for a maximum likelihood analysis and in Table 37.5 for a Bayesian analysis. For more information about ODS, see Chapter 20, "Using the Output Delivery System."

Table 37.4 ODS Tables Produced in PROC GENMOD for a Classical Analysis

ODS Table Name	Description	Statement	Option
AssessmentSummary	Model assessment summary	ASSESS	default
ClassLevels	Classification variable levels	CLASS	default
Contrasts	Tests of contrasts	CONTRAST	default
ContrastCoef	Contrast coefficients	CONTRAST	E
ConvergenceStatus	Convergence status	MODEL	default
CorrB	Parameter estimate correlation matrix	MODEL	CORRB
CovB	Parameter estimate covariance matrix	MODEL	COVB
Estimates	Estimates of contrasts	ESTIMATE	default
EstimateCoef	Contrast coefficients	ESTIMATE	E
GEEEmpPEst	GEE parameter estimates with empirical standard errors	REPEATED	default
GEEFitCriteria	GEE QIC fit criteria	REPEATED	default
GEELogORInfo	GEE log odds ratio model information	REPEATED	LOGOR=
GEEModInfo	GEE model information	REPEATED	default
GEEModPEst	GEE parameter estimates with model-based standard errors	REPEATED	MODELSE
GEENCorr	GEE model-based correlation matrix	REPEATED	MCORRB
GEENCov	GEE model-based covariance matrix	REPEATED	MCOVB
GEERCorr	GEE empirical correlation matrix	REPEATED	ECORRB
GEERCov	GEE empirical covariance matrix	REPEATED	ECOVB
GEEWCorr	GEE working correlation matrix	REPEATED	CORRW
IterContrasts	Iteration history for contrasts	MODEL CONTRAST	ITPRINT

Table 37.4 *continued*

ODS Table Name	Description	Statement	Option
IterLRCI	Iteration history for likelihood ratio confidence intervals	MODEL	LRCI ITPRINT
IterParms	Iteration history for parameter estimates	MODEL	ITPRINT
IterParmsGEE	Iteration history for GEE parameter estimates	MODEL REPEATED	ITPRINT
IterType3	Iteration history for Type 3 statistics	MODEL	TYPE3 ITPRINT
LRCI	Likelihood ratio confidence intervals	MODEL	LRCI ITPRINT
LSMeanCoef	Coefficients for least squares means	LSMEANS	E
LSMeanDiffs	Least squares means differences	LSMEANS	DIFF
LSMeans	Least squares means	LSMEANS	default
LagrangeStatistics	Lagrange statistics	MODEL	NOINT | NOSCALE
LastGEEGrad	Last evaluation of the generalized gradient and Hessian	MODEL REPEATED	ITPRINT
LastGradHess	Last evaluation of the gradient and Hessian	MODEL	ITPRINT
LinDep	Linearly dependent rows of contrasts	CONTRAST	default
ModelInfo	Model information	MODEL	default
Modelfit	Goodness-of-fit statistics	MODEL	default
NObs	Number of observations summary		default
NonEst	Nonestimable rows of contrasts	CONTRAST	default
ObStats	Observation-wise statistics	MODEL	OBSTATS | CL | PREDICTED | RESIDUALS | XVARS
ParameterEstimates	Parameter estimates	MODEL	default
ParmInfo	Parameter indices	MODEL	default
ResponseProfiles	Frequency counts for multinomial and binary models	MODEL	DIST=MULTINOMIAL | DIST=BINOMIAL
Type1	Type 1 tests	MODEL	TYPE1
Type3	Type 3 tests	MODEL	TYPE3
ZeroParameterEstimates	Parameter estimates for zero-inflated model	ZEROMODEL	default

Table 37.5 ODS Tables Produced in PROC GENMOD for a Bayesian Analysis

ODS Table Name	Description	Statement	Option
AutoCorr	Autocorrelations of the posterior samples	BAYES	default
ClassLevels	Classification variable levels	CLASS	default
CoeffPrior	Prior distribution of the regression coefficients	BAYES	default
ConvergenceStatus	Convergence status of maximum likelihood estimation	MODEL	default
Corr	Correlation matrix of the posterior samples	BAYES	SUMMARY=CORR
ESS	Effective sample size	BAYES	default
FitStatistics	Fit statistics	BAYES	default
Gelman	Gelman and Rubin convergence diagnostics	BAYES	DIAG=GELMAN
Geweke	Geweke convergence diagnostics	BAYES	default
Heidelberger	Heidelberger and Welch convergence diagnostics	BAYES	DIAG=HEIDELBERGER
InitialValues	Initial values of the Markov chains	BAYES	default
IterParms	Iteration history for parameter estimates	MODEL	ITPRINT
LastGradHess	Last evaluation of the gradient and Hessian for maximum likelihood estimation	MODEL	ITPRINT
ModelInfo	Model information	PROC	default
NObs	Number of observations		default
ParameterEstimates	Maximum likelihood estimates of model parameters	MODEL	default
ParmInfo	Parameter indices	MODEL	default
ParmPrior	Prior distribution for scale and shape	BAYES	default
PostIntervals	HPD and equal-tail intervals of the posterior samples	BAYES	default
PosteriorSample	Posterior samples (for ODS output data set only)	BAYES	
PostSummaries	Summary statistics of the posterior samples	BAYES	default
Raftery	Raftery and Lewis convergence diagnostics	BAYES	DIAG=RAFTERY

ODS Graphics

To request graphics with PROC GENMOD, you must first enable ODS Graphics by specifying the **ods graphics on** statement. See Chapter 21, "Statistical Graphics Using ODS," for more information. Some graphs are produced by default; other graphs are produced by using statements and options. You can reference every graph produced through ODS Graphics with a name. The names of the graphs that PROC GENMOD generates are listed in Table 37.6, along with the required statements and options.

ODS Graph Names

PROC GENMOD assigns a name to each graph it creates using ODS. You can use these names to reference the graphs when using ODS. The names are listed in Table 37.6.

To request these graphs, you must specify the **ods graphics on** statement in addition to the options indicated in Table 37.6.

Table 37.6 ODS Graphics Produced by PROC GENMOD

ODS Graph Name	Description	Statement	Option
ADPanel	Autocorrelation function and density panel	BAYES	PLOTS=(AUTOCORR DENSITY)
AutocorrPanel	Autocorrelation function panel	BAYES	PLOTS= AUTOCORR
AutocorrPlot	Autocorrelation function plot	BAYES	PLOTS(UNPACK)=AUTOCORR
ClusterCooksDPlot	Cluster Cook's *D* by cluster number	PROC	PLOTS=
ClusterDFFITPlot	Cluster DFFIT by cluster number	PROC	PLOTS=
ClusterLeveragePlot	Cluster leverage by cluster number	PROC	PLOTS=
CooksDPlot	Cook's distance	PROC	PLOTS=
CumResidPanel	Panel of aggregates of residuals	ASSESS	CRPANEL
CumulativeResiduals	Model assessment based on aggregates of residuals	ASSESS	default
DevianceResidByXBeta	Deviance residuals by linear predictor	PROC	PLOTS=
DevianceResidualPlot	Deviance values	PROC	PLOTS=
DFBETAByCluster	Cluster DFBeta by cluster number	PROC	PLOTS=
DFBETAPlot	DFBeta	PROC	PLOTS=

Table 37.6 *continued*

ODS Table Name	Description	Statement	Option
DiagnosticPlot	Panel of residuals, influence, and diagnostic statistics	PROC MODEL REPEATED	PLOTS=
LeveragePlot	Leverage	PROC	PLOTS=
LikeResidByXBeta	Likelihood residuals by linear predictor	PROC	PLOTS=
LikeResidualPlot	Likelihood residuals	PROC	PLOTS=
PearsonResidByXBeta	Pearson residuals by linear predictor	PROC	PLOTS=
PearsonResidualPlot	Pearson residuals	PROC	PLOTS=
PredictedByObservation	Predicted values	PROC	PLOTS=
RawResidByXBeta	Raw residuals by linear predictor	PROC	PLOTS=
RawResidualPlot	Raw residuals	PROC	PLOTS=
StdDevianceResidByXBeta	Standardized deviance residuals by linear predictor	PROC	PLOTS=
StdDevianceResidualPlot	Standardized deviance residuals	PROC	PLOTS=
StdDFBETAByCluster	Standardized cluster DFBeta by cluster number	PROC	PLOTS=
StdDFBETAPlot	Standardized DFBeta	PROC	PLOTS=
StdPearsonResidByXBeta	Standardized Pearson residuals by linear predictor	PROC	PLOTS=
StdPearsonResidualPlot	Standardized Pearson residuals	PROC	PLOTS=
TAPanel	Trace and autocorrelation function panel	BAYES	PLOTS=(TRACE AUTOCORR)
TADPanel	Trace, autocorrelation, and density function panel	BAYES	default
TDPanel	Trace and density panel	BAYES	PLOTS=(TRACE DENSITY)
TracePanel	Trace panel	BAYES	PLOTS=TRACE
TracePlot	Trace plot	BAYES	PLOTS(UNPACK)=TRACE
ZeroInflationProbPlot	Zero-inflation probabilities	PROC	PLOTS=

Examples: GENMOD Procedure

The following examples illustrate some of the capabilities of the GENMOD procedure. These are not intended to represent definitive analyses of the data sets presented here. You should refer to the texts cited in the references for guidance on complete analysis of data by using generalized linear models.

Example 37.1: Logistic Regression

In an experiment comparing the effects of five different drugs, each drug is tested on a number of different subjects. The outcome of each experiment is the presence or absence of a positive response in a subject. The following artificial data represent the number of responses r in the n subjects for the five different drugs, labeled A through E. The response is measured for different levels of a continuous covariate x for each drug. The drug type and the continuous covariate x are explanatory variables in this experiment. The number of responses r is modeled as a binomial random variable for each combination of the explanatory variable values, with the binomial number of trials parameter equal to the number of subjects n and the binomial probability equal to the probability of a response.

The following DATA step creates the data set:

```
data drug;
   input drug$ x r n @@;
   datalines;
A  .1   1  10   A  .23  2  12   A  .67  1   9
B  .2   3  13   B  .3   4  15   B  .45  5  16   B  .78  5  13
C  .04  0  10   C  .15  0  11   C  .56  1  12   C  .7   2  12
D  .34  5  10   D  .6   5   9   D  .7   8  10
E  .2  12  20   E  .34 15  20   E  .56 13  15   E  .8  17  20
;
run;
```

A logistic regression for these data is a generalized linear model with response equal to the binomial proportion r/n. The probability distribution is binomial, and the link function is logit. For these data, drug and x are explanatory variables. The probit and the complementary log-log link functions are also appropriate for binomial data.

PROC GENMOD performs a logistic regression on the data in the following SAS statements:

```
proc genmod data=drug;
   class drug;
   model r/n = x drug / dist = bin
                        link = logit
                        lrci;
run;
```

Since these data are binomial, you use the events/trials syntax to specify the response in the MODEL statement. Profile likelihood confidence intervals for the regression parameters are computed using the LRCI option.

General model and data information is produced in Output 37.1.1.

Output 37.1.1 Model Information

The GENMOD Procedure

Model Information

Data Set	WORK.DRUG
Distribution	Binomial
Link Function	Logit
Response Variable (Events)	r
Response Variable (Trials)	n

The five levels of the CLASS variable DRUG are displayed in Output 37.1.2.

Output 37.1.2 CLASS Variable Levels

Class Level Information

Class	Levels	Values
drug	5	A B C D E

In the "Criteria For Assessing Goodness Of Fit" table displayed in Output 37.1.3, the value of the deviance divided by its degrees of freedom is less than 1. A p-value is not computed for the deviance; however, a deviance that is approximately equal to its degrees of freedom is a possible indication of a good model fit. Asymptotic distribution theory applies to binomial data as the number of binomial trials parameter n becomes large for each combination of explanatory variables. McCullagh and Nelder (1989) caution against the use of the deviance alone to assess model fit. The model fit for each observation should be assessed by examination of residuals. The OBSTATS option in the MODEL statement produces a table of residuals and other useful statistics for each observation.

Output 37.1.3 Goodness-of-Fit Criteria

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	12	5.2751	0.4396
Scaled Deviance	12	5.2751	0.4396
Pearson Chi-Square	12	4.5133	0.3761
Scaled Pearson X2	12	4.5133	0.3761
Log Likelihood		-114.7732	
Full Log Likelihood		-23.7343	
AIC (smaller is better)		59.4686	
AICC (smaller is better)		67.1050	
BIC (smaller is better)		64.8109	

In the "Analysis Of Parameter Estimates" table displayed in Output 37.1.4, chi-square values for the explanatory variables indicate that the parameter values other than the intercept term are all significant. The scale parameter is set to 1 for the binomial distribution. When you perform an overdispersion analysis, the value of the overdispersion parameter is indicated here. See the section "Overdispersion" on page 1971 for a discussion of overdispersion.

Output 37.1.4 Parameter Estimates

Analysis Of Maximum Likelihood Parameter Estimates

Parameter		DF	Estimate	Standard Error	Likelihood Ratio 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
Intercept		1	0.2792	0.4196	-0.5336	1.1190	0.44	0.5057
x		1	1.9794	0.7660	0.5038	3.5206	6.68	0.0098
drug	A	1	-2.8955	0.6092	-4.2280	-1.7909	22.59	<.0001
drug	B	1	-2.0162	0.4052	-2.8375	-1.2435	24.76	<.0001
drug	C	1	-3.7952	0.6655	-5.3111	-2.6261	32.53	<.0001
drug	D	1	-0.8548	0.4838	-1.8072	0.1028	3.12	0.0773
drug	E	0	0.0000	0.0000	0.0000	0.0000	.	.
Scale		0	1.0000	0.0000	1.0000	1.0000		

NOTE: The scale parameter was held fixed.

The preceding table contains the profile likelihood confidence intervals for the explanatory variable parameters requested with the LRCI option. Wald confidence intervals are displayed by default. Profile likelihood confidence intervals are considered to be more accurate than Wald intervals (see Aitkin et al. (1989)), especially with small sample sizes. You can specify the confidence coefficient with the ALPHA= option in the MODEL statement. The default value of 0.05, corresponding to 95% confidence limits, is used here. See the section "Confidence Intervals for Parameters" on page 1978 for a discussion of profile likelihood confidence intervals.

Example 37.2: Normal Regression, Log Link

Consider the following data, where x is an explanatory variable and y is the response variable. It appears that y varies nonlinearly with x and that the variance is approximately constant. A normal distribution with a log link function is chosen to model these data; that is, $\log(\mu_i) = \mathbf{x}_i'\boldsymbol{\beta}$ so that $\mu_i = \exp(\mathbf{x}_i'\boldsymbol{\beta})$.

```
data nor;
   input x y;
   datalines;
0 5
0 7
0 9
1 7
1 10
1 8
2 11
2 9
3 16
3 13
3 14
4 25
4 24
5 34
5 32
5 30
;
run;
```

The following SAS statements produce the analysis with the normal distribution and log link:

```
proc genmod data=nor;
   model y = x / dist = normal
                 link = log;
   output out       = Residuals
          pred      = Pred
          resraw    = Resraw
          reschi    = Reschi
          resdev    = Resdev
          stdreschi = Stdreschi
          stdresdev = Stdresdev
          reslik    = Reslik;
run;
```

The OUTPUT statement is specified to produce a data set that contains predicted values and residuals for each observation. This data set can be useful for further analysis, such as residual plotting.

The results from these statements are displayed in Output 37.2.1.

Output 37.2.1 Log-Linked Normal Regression

The GENMOD Procedure

Model Information

Data Set	WORK.NOR
Distribution	Normal
Link Function	Log
Dependent Variable	y

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	14	52.3000	3.7357
Scaled Deviance	14	16.0000	1.1429
Pearson Chi-Square	14	52.3000	3.7357
Scaled Pearson X2	14	16.0000	1.1429
Log Likelihood		-32.1783	
Full Log Likelihood		-32.1783	
AIC (smaller is better)		70.3566	
AICC (smaller is better)		72.3566	
BIC (smaller is better)		72.6743	

Analysis Of Maximum Likelihood Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
Intercept	1	1.7214	0.0894	1.5461	1.8966	370.76	<.0001
x	1	0.3496	0.0206	0.3091	0.3901	286.64	<.0001
Scale	1	1.8080	0.3196	1.2786	2.5566		

NOTE: The scale parameter was estimated by maximum likelihood.

The PROC GENMOD scale parameter, in the case of the normal distribution, is the standard deviation. By default, the scale parameter is estimated by maximum likelihood. You can specify a fixed standard deviation by using the NOSCALE and SCALE= options in the MODEL statement.

```
proc print data=Residuals ;
run;
```

Output 37.2.2 Data Set of Predicted Values and Residuals

Obs	x	y	Pred	Reschi	Resraw	Resdev	Stdreschi	Stdresdev	Reslik
1	0	5	5.5921	-0.59212	-0.59212	-0.59212	-0.34036	-0.34036	-0.34036
2	0	7	5.5921	1.40788	1.40788	1.40788	0.80928	0.80928	0.80928
3	0	9	5.5921	3.40788	3.40788	3.40788	1.95892	1.95892	1.95892
4	1	7	7.9324	-0.93243	-0.93243	-0.93243	-0.54093	-0.54093	-0.54093
5	1	10	7.9324	2.06757	2.06757	2.06757	1.19947	1.19947	1.19947
6	1	8	7.9324	0.06757	0.06757	0.06757	0.03920	0.03920	0.03920
7	2	11	11.2522	-0.25217	-0.25217	-0.25217	-0.14686	-0.14686	-0.14686
8	2	9	11.2522	-2.25217	-2.25217	-2.25217	-1.31166	-1.31166	-1.31166
9	3	16	15.9612	0.03878	0.03878	0.03878	0.02249	0.02249	0.02249
10	3	13	15.9612	-2.96122	-2.96122	-2.96122	-1.71738	-1.71738	-1.71738
11	3	14	15.9612	-1.96122	-1.96122	-1.96122	-1.13743	-1.13743	-1.13743
12	4	25	22.6410	2.35897	2.35897	2.35897	1.37252	1.37252	1.37252
13	4	24	22.6410	1.35897	1.35897	1.35897	0.79069	0.79069	0.79069
14	5	34	32.1163	1.88366	1.88366	1.88366	1.22914	1.22914	1.22914
15	5	32	32.1163	-0.11634	-0.11634	-0.11634	-0.07592	-0.07592	-0.07592
16	5	30	32.1163	-2.11634	-2.11634	-2.11634	-1.38098	-1.38098	-1.38098

The data set of predicted values and residuals (Output 37.2.2) is created by the OUTPUT statement. You can use the PLOTS= option in the PROC GENMOD statement to create plots of predicted values and residuals. Note that raw, Pearson, and deviance residuals are equal in this example. This is a characteristic of the normal distribution and is not true in general for other distributions.

Example 37.3: Gamma Distribution Applied to Life Data

Life data are sometimes modeled with the gamma distribution. Although PROC GENMOD does not analyze censored data or provide other useful lifetime distributions such as the Weibull or log-normal, it can be used for modeling complete (uncensored) data with the gamma distribution, and it can provide a statistical test for the exponential distribution against other gamma distribution alternatives. See Lawless (2003) or Nelson (1982) for applications of the gamma distribution to life data.

The following data represent failure times of machine parts, some of which are manufactured by manufacturer A and some by manufacturer B.

```
data A;
   input lifetime@@ ;
   mfg = 'A';
   datalines;
620  470  260  89   388  242
103  100  39   460  284  1285
218  393  106  158  152  477
403  103  69   158  818  947
399  1274 32   12   134  660
548  381  203  871  193  531
317  85   1410 250  41   1101
```

```
32   421  32   343  376  1512
1792 47   95   76   515  72
1585 253  6    860  89   1055
537  101  385  176  11   565
164  16   1267 352  160  195
1279 356  751  500  803  560
151  24   689  1119 1733 2194
763  555  14   45   776  1
;
run;

data B;
   input lifetime@@ ;
   mfg = 'B';
   datalines;
1747 945  12   1453 14   150
20   41   35   69   195  89
1090 1868 294  96   618  44
142  892  1307 310  230  30
403  860  23   406  1054 1935
561  348  130  13   230  250
317  304  79   1793 536  12
9    256  201  733  510  660
122  27   273  1231 182  289
667  761  1096 43   44   87
405  998  1409 61   278  407
113  25   940  28   848  41
646  575  219  303  304  38
195  1061 174  377  388  10
246  323  198  234  39   308
55   729  813  1216 1618 539
6    1566 459  946  764  794
35   181  147  116  141  19
380  609  546
;
run;

data lifdat;
   set A B;
run;
```

The following SAS statements use PROC GENMOD to compute Type 3 statistics to test for differences between the two manufacturers in machine part life. Type 3 statistics are identical to Type 1 statistics in this case, since there is only one effect in the model. The log link function is selected to ensure that the mean is positive.

```
proc genmod data = lifdat;
   class mfg;
   model lifetime = mfg / dist=gamma
                          link=log
                          type3;
run;
```

The output from these statements is displayed in Output 37.3.1.

Output 37.3.1 Gamma Model of Life Data

The GENMOD Procedure

Model Information

Data Set	WORK.LIFDAT
Distribution	Gamma
Link Function	Log
Dependent Variable	lifetime

Class Level Information

Class	Levels	Values
mfg	2	A B

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	199	287.0591	1.4425
Scaled Deviance	199	237.5335	1.1936
Pearson Chi-Square	199	211.6870	1.0638
Scaled Pearson X2	199	175.1652	0.8802
Log Likelihood		-1432.4177	
Full Log Likelihood		-1432.4177	
AIC (smaller is better)		2870.8353	
AICC (smaller is better)		2870.9572	
BIC (smaller is better)		2880.7453	

Analysis Of Maximum Likelihood Parameter Estimates

Parameter		DF	Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
Intercept		1	6.1302	0.1043	5.9257	6.3347	3451.61	<.0001
mfg	A	1	0.0199	0.1559	-0.2857	0.3255	0.02	0.8985
mfg	B	0	0.0000	0.0000	0.0000	0.0000	.	.
Scale		1	0.8275	0.0714	0.6987	0.9800		

NOTE: The scale parameter was estimated by maximum likelihood.

LR Statistics For Type 3 Analysis

Source	DF	Chi-Square	Pr > ChiSq
mfg	1	0.02	0.8985

The p-value of 0.8985 for the chi-square statistic in the Type 3 table indicates that there is no significant difference in the part life between the two manufacturers.

Using the following statements, you can refit the model without using the manufacturer as an effect. The LRCI option in the MODEL statement is specified to compute profile likelihood confidence intervals for the mean life and scale parameters.

```
proc genmod data = lifdat;
   model lifetime = / dist=gamma
                      link=log
                      lrci;
run;
```

Output 37.3.2 displays the results of fitting the model with the mfg effect omitted.

Output 37.3.2 Refitting of the Gamma Model: Omitting the mfg Effect

The GENMOD Procedure

Analysis Of Maximum Likelihood Parameter Estimates

Parameter	DF	Estimate	Standard Error	Likelihood Ratio 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
Intercept	1	6.1391	0.0775	5.9904	6.2956	6268.10	<.0001
Scale	1	0.8274	0.0714	0.6959	0.9762		

NOTE: The scale parameter was estimated by maximum likelihood.

The intercept is the estimated log mean of the fitted gamma distribution, so that the mean life of the parts is

$$\mu = \exp(\text{INTERCEPT}) = \exp(6.1391) = 463.64$$

The SCALE parameter used in PROC GENMOD is the inverse of the gamma dispersion parameter, and it is sometimes called the gamma *index parameter*. See the section "Response Probability Distributions" on page 1962 for the definition of the gamma probability density function. A value of 1 for the index parameter corresponds to the exponential distribution . The estimated value of the scale parameter is 0.8274. The 95% profile likelihood confidence interval for the scale parameter is (0.6959, 0.9762), which does not contain 1. The hypothesis of an exponential distribution for the data is, therefore, rejected at the 0.05 level. A confidence interval for the mean life is

$$(\exp(5.99), \exp(6.30)) = (399.57, 542.18)$$

Example 37.4: Ordinal Model for Multinomial Data

This example illustrates how you can use the GENMOD procedure to fit a model to data measured on an ordinal scale. The following statements create a SAS data set called Icecream. The data set contains the results of a hypothetical taste test of three brands of ice cream. The three brands are rated for taste on a five-point scale from very good (vg) to very bad (vb). An analysis is performed

to assess the differences in the ratings of the three brands. The variable taste contains the ratings, and the variable brand contains the brands tested. The variable count contains the number of testers rating each brand in each category.

The following statements create the Icecream data set:

```
data Icecream;
   input count brand$ taste$;
   datalines;
70  ice1 vg
71  ice1 g
151 ice1 m
30  ice1 b
46  ice1 vb
20  ice2 vg
36  ice2 g
130 ice2 m
74  ice2 b
70  ice2 vb
50  ice3 vg
55  ice3 g
140 ice3 m
52  ice3 b
50  ice3 vb
;
run;
```

The following statements fit a cumulative logit model to the ordinal data with the variable taste as the response and the variable brand as a covariate. The variable count is used as a FREQ variable.

```
proc genmod data=Icecream rorder=data;
   freq count;
   class brand;
   model taste = brand / dist=multinomial
                         link=cumlogit
                         aggregate=brand
                         type1;
   estimate 'LogOR12' brand 1 -1 / exp;
   estimate 'LogOR13' brand 1  0  -1 / exp;
   estimate 'LogOR23' brand 0  1  -1 / exp;
run;
```

The AGGREGATE=BRAND option in the MODEL statement specifies the variable brand as defining multinomial populations for computing deviances and Pearson chi-squares. The RORDER=DATA option specifies that the taste variable levels be ordered by their order of appearance in the input data set—that is, from very good (vg) to very bad (vb). By default, the response is sorted in increasing ASCII order. Always check the "Response Profiles" table to verify that response levels are appropriately ordered. The TYPE1 option requests a Type 1 test for the significance of the covariate brand.

If $\gamma_j(\mathbf{x}) = \Pr(\text{taste} \leq j)$ is the cumulative probability of the jth or lower taste category, then the odds ratio comparing $\mathbf{x}_1$ to $\mathbf{x}_2$ is as follows:

$$\frac{\gamma_j(\mathbf{x}_1)/(1-\gamma_j(\mathbf{x}_1))}{\gamma_j(\mathbf{x}_2)/(1-\gamma_j(\mathbf{x}_2))} = \exp[(\mathbf{x}_1-\mathbf{x}_2)'\boldsymbol{\beta}]$$

See McCullagh and Nelder (1989, Chapter 5) for details on the cumulative logit model. The ESTIMATE statements compute log odds ratios comparing each of brands. The EXP option in the ESTIMATE statements exponentiates the log odds ratios to form odds ratio estimates. Standard errors and confidence intervals are also computed.

Output 37.4.1 displays general information about the model and data, the levels of the CLASS variable brand, and the total number of occurrences of the ordered levels of the response variable taste.

Output 37.4.1 Ordinal Model Information

The GENMOD Procedure

Model Information

Data Set	WORK.ICECREAM
Distribution	Multinomial
Link Function	Cumulative Logit
Dependent Variable	taste
Frequency Weight Variable	count

Class Level Information

Class	Levels	Values
brand	3	ice1 ice2 ice3

Response Profile

Ordered Value	taste	Total Frequency
1	vg	140
2	g	162
3	m	421
4	b	156
5	vb	166

Output 37.4.2 displays estimates of the intercept terms and covariates and associated statistics. The intercept terms correspond to the four cumulative logits defined on the taste categories in the order shown in Output 37.4.1. That is, Intercept1 is the intercept for the first cumulative logit, $\log(\frac{p_1}{1-p_1})$, Intercept2 is the intercept for the second cumulative logit, $\log(\frac{p_1+p_2}{1-(p_1+p_2)})$, and so forth.

Output 37.4.2 Parameter Estimates

Analysis Of Maximum Likelihood Parameter Estimates

Parameter		DF	Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square
Intercept1		1	−1.8578	0.1219	−2.0967	−1.6189	232.35
Intercept2		1	−0.8646	0.1056	−1.0716	−0.6576	67.02
Intercept3		1	0.9231	0.1060	0.7154	1.1308	75.87
Intercept4		1	1.8078	0.1191	1.5743	2.0413	230.32
brand	ice1	1	0.3847	0.1370	0.1162	0.6532	7.89
brand	ice2	1	−0.6457	0.1397	−0.9196	−0.3719	21.36
brand	ice3	0	0.0000	0.0000	0.0000	0.0000	.
Scale		0	1.0000	0.0000	1.0000	1.0000	

Analysis Of Maximum Likelihood Parameter Estimates

Parameter		Pr > ChiSq
Intercept1		<.0001
Intercept2		<.0001
Intercept3		<.0001
Intercept4		<.0001
brand	ice1	0.0050
brand	ice2	<.0001
brand	ice3	.
Scale		

NOTE: The scale parameter was held fixed.

The Type 1 test displayed in Output 37.4.3 indicates that Brand is highly significant; that is, there are significant differences among the brands. The log odds ratios and odds ratios in the "ESTIMATE Statement Results" table indicate the relative differences among the brands. For example, the odds ratio of 2.8 in the "Exp(LogOR12)" row indicates that the odds of brand 1 being in lower taste categories is 2.8 times the odds of brand 2 being in lower taste categories. Since, in this ordering, the lower categories represent the more favorable taste results, this indicates that brand 1 scored significantly better than brand 2. This is also apparent from the data in this example.

Output 37.4.3 Type 1 Tests and Odds Ratios

LR Statistics For Type 1 Analysis

Source	Deviance	DF	Chi-Square	Pr > ChiSq
Intercepts	65.9576			
brand	9.8654	2	56.09	<.0001

Output 37.4.3 *continued*

Contrast Estimate Results

Label	Mean Estimate	Mean Confidence Limits		L'Beta Estimate	Standard Error	Alpha
LogOR12	0.7370	0.6805	0.7867	1.0305	0.1401	0.05
Exp(LogOR12)				2.8024	0.3926	0.05
LogOR13	0.5950	0.5290	0.6577	0.3847	0.1370	0.05
Exp(LogOR13)				1.4692	0.2013	0.05
LogOR23	0.3439	0.2850	0.4081	-0.6457	0.1397	0.05
Exp(LogOR23)				0.5243	0.0733	0.05

Contrast Estimate Results

Label	L'Beta Confidence Limits		Chi-Square	Pr > ChiSq
LogOR12	0.7559	1.3050	54.11	<.0001
Exp(LogOR12)	2.1295	3.6878		
LogOR13	0.1162	0.6532	7.89	0.0050
Exp(LogOR13)	1.1233	1.9217		
LogOR23	-0.9196	-0.3719	21.36	<.0001
Exp(LogOR23)	0.3987	0.6894		

Example 37.5: GEE for Binary Data with Logit Link Function

Output 37.5.1 displays a partial listing of a SAS data set of clinical trial data comparing two treatments for a respiratory disorder. See "Gee Model for Binary Data" in the SAS/STAT Sample Program Library for the complete data set. These data are from Stokes, Davis, and Koch (2000).

Patients in each of two centers are randomly assigned to groups receiving the active treatment or a placebo. During treatment, respiratory status, represented by the variable outcome (coded here as 0=poor, 1=good), is determined for each of four visits. The variables center, treatment, sex, and baseline (baseline respiratory status) are classification variables with two levels. The variable age (age at time of entry into the study) is a continuous variable.

Explanatory variables in the model are Intercept (x_{ij1}), treatment (x_{ij2}), center (x_{ij3}), sex (x_{ij4}), age (x_{ij5}), and baseline (x_{ij6}), so that $x' = [x_{ij1}, x_{ij2}, \ldots, x_{ij6}]$ is the vector of explanatory variables. Indicator variables for the classification explanatory variables can be automatically generated by listing them in the CLASS statement in PROC GENMOD. To be consistent with the analysis in Stokes, Davis, and Koch (2000), the four classification explanatory variables are coded as follows via options in the CLASS statement:

$$x_{ij2} = \begin{cases} 0 \text{ placebo} \\ 1 \text{ active} \end{cases} \qquad x_{ij3} = \begin{cases} 0 \text{ center 1} \\ 1 \text{ center 2} \end{cases}$$

$$x_{ij4} = \begin{cases} 0 \text{ male} \\ 1 \text{ female} \end{cases} \qquad x_{ij6} = \begin{cases} 0\ 0 \\ 1\ 1 \end{cases}$$

Suppose y_{ij} represents the respiratory status of patient i at the jth visit, $j = 1, \ldots, 4$, and $\mu_{ij} = \mathrm{E}(y_{ij})$ represents the mean of the respiratory status. Since the response data are binary, you can use the variance function for the binomial distribution $v(\mu_{ij}) = \mu_{ij}(1-\mu_{ij})$ and the logit link function $g(\mu_{ij}) = \log(\mu_{ij}/(1-\mu_{ij}))$. The model for the mean is $g(\mu_{ij}) = \mathbf{x}_{ij}'\boldsymbol{\beta}$, where $\boldsymbol{\beta}$ is a vector of regression parameters to be estimated.

Output 37.5.1 Respiratory Disorder Data

Obs	center	id	treatment	sex	age	baseline	visit1	visit2	visit3	visit4	visit	outcome
1	1	1	P	M	46	0	0	0	0	0	1	0
2	1	1	P	M	46	0	0	0	0	0	2	0
3	1	1	P	M	46	0	0	0	0	0	3	0
4	1	1	P	M	46	0	0	0	0	0	4	0
5	1	2	P	M	28	0	0	0	0	0	1	0
6	1	2	P	M	28	0	0	0	0	0	2	0
7	1	2	P	M	28	0	0	0	0	0	3	0
8	1	2	P	M	28	0	0	0	0	0	4	0
9	1	3	A	M	23	1	1	1	1	1	1	1
10	1	3	A	M	23	1	1	1	1	1	2	1
11	1	3	A	M	23	1	1	1	1	1	3	1
12	1	3	A	M	23	1	1	1	1	1	4	1
13	1	4	P	M	44	1	1	1	1	0	1	1
14	1	4	P	M	44	1	1	1	1	0	2	1
15	1	4	P	M	44	1	1	1	1	0	3	1
16	1	4	P	M	44	1	1	1	1	0	4	0
17	1	5	P	F	13	1	1	1	1	1	1	1
18	1	5	P	F	13	1	1	1	1	1	2	1
19	1	5	P	F	13	1	1	1	1	1	3	1
20	1	5	P	F	13	1	1	1	1	1	4	1

The GEE solution is requested with the REPEATED statement in the GENMOD procedure. The option SUBJECT=ID(CENTER) specifies that the observations in a single cluster be uniquely identified by center and id within center. The option TYPE=UNSTR specifies the unstructured working correlation structure. The MODEL statement specifies the regression model for the mean with the binomial distribution variance function. The following SAS statements perform the GEE model fit:

```
proc genmod data=resp descend;
   class id treatment(ref="P") center(ref="1") sex(ref="M")
      baseline(ref="0") / param=ref;
   model outcome=treatment center sex age baseline / dist=bin;
   repeated subject=id(center) / corr=unstr corrw;
run;
```

These statements first fit the generalized linear (GLM) model specified in the MODEL statement. The parameter estimates from the generalized linear model fit are not shown in the output, but they are used as initial values for the GEE solution. The DESCEND option in the PROC GENMOD statement specifies that the probability that outcome $= 1$ be modeled. If the DESCEND option had not been specified, the probability that outcome $= 0$ would be modeled by default.

Information about the GEE model is displayed in Output 37.5.2. The results of GEE model fitting are displayed in Output 37.5.3. Model goodness-of-fit criteria are displayed in Output 37.5.4. If you specify no other options, the standard errors, confidence intervals, Z scores, and p-values are based on empirical standard error estimates. You can specify the MODELSE option in the REPEATED statement to create a table based on model-based standard error estimates.

Output 37.5.2 Model Fitting Information

The GENMOD Procedure

GEE Model Information

Correlation Structure	Unstructured
Subject Effect	id(center) (111 levels)
Number of Clusters	111
Correlation Matrix Dimension	4
Maximum Cluster Size	4
Minimum Cluster Size	4

Output 37.5.3 Results of Model Fitting

Working Correlation Matrix

	Col1	Col2	Col3	Col4
Row1	1.0000	0.3351	0.2140	0.2953
Row2	0.3351	1.0000	0.4429	0.3581
Row3	0.2140	0.4429	1.0000	0.3964
Row4	0.2953	0.3581	0.3964	1.0000

Output 37.5.3 *continued*

Analysis Of GEE Parameter Estimates
Empirical Standard Error Estimates

Parameter		Estimate	Standard Error	95% Confidence Limits		Z	Pr > |Z|
Intercept		−0.8882	0.4568	−1.7835	0.0071	−1.94	0.0519
treatment	A	1.2442	0.3455	0.5669	1.9214	3.60	0.0003
center	2	0.6558	0.3512	−0.0326	1.3442	1.87	0.0619
sex	F	0.1128	0.4408	−0.7512	0.9768	0.26	0.7981
age		−0.0175	0.0129	−0.0427	0.0077	−1.36	0.1728
baseline	1	1.8981	0.3441	1.2237	2.5725	5.52	<.0001

Output 37.5.4 Model Fit Criteria

GEE Fit Criteria

QIC	512.3416
QICu	499.6081

The nonsignificance of age and sex make them candidates for omission from the model.

Example 37.6: Log Odds Ratios and the ALR Algorithm

Since the respiratory data in Example 37.5 are binary, you can use the ALR algorithm to model the log odds ratios instead of using working correlations to model associations. In this example, a "fully parameterized cluster" model for the log odds ratio is fit. That is, there is a log odds ratio parameter for each unique pair of responses within clusters, and all clusters are parameterized identically. The following statements fit the same regression model for the mean as in Example 37.5 but use a regression model for the log odds ratios instead of a working correlation. The LOGOR=FULLCLUST option specifies a fully parameterized log odds ratio model.

```
proc genmod data=resp descend;
   class id treatment(ref="P") center(ref="1") sex(ref="M")
      baseline(ref="0") / param=ref;
   model outcome=treatment center sex age baseline / dist=bin;
   repeated  subject=id(center) / logor=fullclust;
run;
```

The results of fitting the model are displayed in Output 37.6.1 along with a table that shows the correspondence between the log odds ratio parameters and the within-cluster pairs. Model goodness-of-fit criteria are shown in Output 37.6.2. The QIC for the ALR model shown in Output 37.6.2 is 511.86, whereas the QIC for the unstructured working correlation model shown in Output 37.5.4 is 512.34, indicating that the ALR model is a slightly better fit.

Output 37.6.1 Results of Model Fitting

The GENMOD Procedure

Log Odds Ratio
Parameter Information

Parameter	Group
Alpha1	(1, 2)
Alpha2	(1, 3)
Alpha3	(1, 4)
Alpha4	(2, 3)
Alpha5	(2, 4)
Alpha6	(3, 4)

Analysis Of GEE Parameter Estimates
Empirical Standard Error Estimates

Parameter		Estimate	Standard Error	95% Confidence Limits		Z	Pr > |Z|
Intercept		-0.9266	0.4513	-1.8111	-0.0421	-2.05	0.0400
treatment	A	1.2611	0.3406	0.5934	1.9287	3.70	0.0002
center	2	0.6287	0.3486	-0.0545	1.3119	1.80	0.0713
sex	F	0.1024	0.4362	-0.7526	0.9575	0.23	0.8144
age		-0.0162	0.0125	-0.0407	0.0084	-1.29	0.1977
baseline	1	1.8980	0.3404	1.2308	2.5652	5.58	<.0001
Alpha1		1.6109	0.4892	0.6522	2.5696	3.29	0.0010
Alpha2		1.0771	0.4834	0.1297	2.0246	2.23	0.0259
Alpha3		1.5875	0.4735	0.6594	2.5155	3.35	0.0008
Alpha4		2.1224	0.5022	1.1381	3.1068	4.23	<.0001
Alpha5		1.8818	0.4686	0.9634	2.8001	4.02	<.0001
Alpha6		2.1046	0.4949	1.1347	3.0745	4.25	<.0001

Output 37.6.2 Model Fit Criteria

GEE Fit Criteria

QIC	511.8589
QICu	499.6516

You can fit the same model by fully specifying the z-matrix. The following statements create a data set containing the full z-matrix:

```
data zin;
   keep id center z1-z6 y1 y2;
   array zin(6) z1-z6;
   set resp ;
   by center id;
   if first.id
      then do;
         t = 0;
         do m = 1 to 4;
            do n = m+1 to 4;
               do j = 1 to 6;
                  zin(j) = 0;
               end;
            y1 = m;
            y2 = n;
            t + 1;
            zin(t) = 1;
            output;
            end;
         end;
      end;
run;

proc print data=zin (obs=12);
```

Output 37.6.3 displays the full z-matrix for the first two clusters. The z-matrix is identical for all clusters in this example.

Output 37.6.3 Full z-Matrix Data Set

Obs	z1	z2	z3	z4	z5	z6	center	id	y1	y2
1	1	0	0	0	0	0	1	1	1	2
2	0	1	0	0	0	0	1	1	1	3
3	0	0	1	0	0	0	1	1	1	4
4	0	0	0	1	0	0	1	1	2	3
5	0	0	0	0	1	0	1	1	2	4
6	0	0	0	0	0	1	1	1	3	4
7	1	0	0	0	0	0	1	2	1	2
8	0	1	0	0	0	0	1	2	1	3
9	0	0	1	0	0	0	1	2	1	4
10	0	0	0	1	0	0	1	2	2	3
11	0	0	0	0	1	0	1	2	2	4
12	0	0	0	0	0	1	1	2	3	4

The following statements fit the model for fully parameterized clusters by fully specifying the z-matrix. The results are identical to those shown previously.

```
proc genmod data=resp descend;
   class id treatment(ref="P") center(ref="1") sex(ref="M")
      baseline(ref="0") / param=ref;
   model outcome=treatment center sex age baseline / dist=bin;
   repeated  subject=id(center) / logor=zfull
                                  zdata=zin
                                  zrow =(z1-z6)
                                  ypair=(y1 y2) ;
run;
```

Example 37.7: Log-Linear Model for Count Data

In this example the data, from Thall and Vail (1990), concern the treatment of people suffering from epileptic seizure episodes. These data are also analyzed in Diggle, Liang, and Zeger (1994). The data consist of the number of epileptic seizures in an eight-week baseline period, before any treatment, and in each of four two-week treatment periods, in which patients received either a placebo or the drug Progabide in addition to other therapy. A portion of the data is displayed in Table 37.7. See "Gee Model for Count Data, Exchangeable Correlation" in the SAS/STAT Sample Program Library for the complete data set.

Table 37.7 Epileptic Seizure Data

Patient ID	Treatment	Baseline	Visit1	Visit2	Visit3	Visit4
104	Placebo	11	5	3	3	3
106	Placebo	11	3	5	3	3
107	Placebo	6	2	4	0	5
.						
.						
.						
101	Progabide	76	11	14	9	8
102	Progabide	38	8	7	9	4
103	Progabide	19	0	4	3	0
.						
.						
.						

Model the data as a log-linear model with $V(\mu) = \mu$ (the Poisson variance function) and

$$\log(E(Y_{ij})) = \beta_0 + x_{i1}\beta_1 + x_{i2}\beta_2 + x_{i1}x_{i2}\beta_3 + \log(t_{ij})$$

where

Y_{ij} = number of epileptic seizures in interval j

t_{ij} = length of interval j

$$x_{i1} = \begin{cases} 1: & \text{weeks 8–16 (treatment)} \\ 0: & \text{weeks 0–8 (baseline)} \end{cases}$$

$$x_{i2} = \begin{cases} 1: & \text{progabide group} \\ 0: & \text{placebo group} \end{cases}$$

The correlations between the counts are modeled as $r_{ij} = \alpha, i \neq j$ (exchangeable correlations). For comparison, the correlations are also modeled as independent (identity correlation matrix). In this model, the regression parameters have the interpretation in terms of the log seizure rate displayed in Table 37.8.

Table 37.8 Interpretation of Regression Parameters

Treatment	Visit	$\log(E(Y_{ij})/t_{ij})$
Placebo	Baseline	β_0
	1–4	$\beta_0 + \beta_1$
Progabide	Baseline	$\beta_0 + \beta_2$
	1–4	$\beta_0 + \beta_1 + \beta_2 + \beta_3$

The difference between the log seizure rates in the pretreatment (baseline) period and the treatment periods is β_1 for the placebo group and $\beta_1 + \beta_3$ for the Progabide group. A value of $\beta_3 < 0$ indicates a reduction in the seizure rate.

Output 37.7.1 lists the first 14 observations of the data, which are arranged as one visit per observation:

Output 37.7.1 Partial Listing of the Seizure Data

Obs	id	y	visit	trt	bline	age
1	104	5	1	0	11	31
2	104	3	2	0	11	31
3	104	3	3	0	11	31
4	104	3	4	0	11	31
5	106	3	1	0	11	30
6	106	5	2	0	11	30
7	106	3	3	0	11	30
8	106	3	4	0	11	30
9	107	2	1	0	6	25
10	107	4	2	0	6	25
11	107	0	3	0	6	25
12	107	5	4	0	6	25
13	114	4	1	0	8	36
14	114	4	2	0	8	36

Some further data manipulations create an observation for the baseline measures, a log time interval variable for use as an offset, and an indicator variable for whether the observation is for a baseline measurement or a visit measurement. Patient 207 is deleted as an outlier, as in the Diggle, Liang, and Zeger (1994) analysis. The following statements prepare the data for analysis with PROC GENMOD:

```
data new;
   set thall;
   output;
   if visit=1 then do;
      y=bline;
      visit=0;
      output;
   end;
run;

data new;
   set new;
   if id ne 207;
   if visit=0 then do;
      x1=0;
      ltime=log(8);
   end;
   else do;
      x1=1;
      ltime=log(2);
   end;
run;
```

For comparison with the GEE results, an ordinary Poisson regression is first fit. The results are shown in Output 37.7.2.

Output 37.7.2 Maximum Likelihood Estimates

The GENMOD Procedure

Analysis Of Maximum Likelihood Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
Intercept	1	1.3476	0.0341	1.2809	1.4144	1565.44	<.0001
x1	1	0.1108	0.0469	0.0189	0.2027	5.58	0.0181
trt	1	-0.1080	0.0486	-0.2034	-0.0127	4.93	0.0264
x1*trt	1	-0.3016	0.0697	-0.4383	-0.1649	18.70	<.0001
Scale	0	1.0000	0.0000	1.0000	1.0000		

NOTE: The scale parameter was held fixed.

The GEE solution is requested with the REPEATED statement in the GENMOD procedure. The SUBJECT=ID option indicates that the variable id describes the observations for a single cluster, and the CORRW option displays the working correlation matrix. The TYPE= option specifies the correlation structure; the value EXCH indicates the exchangeable structure.

The following statements perform the analysis:

```
proc genmod data=new;
   class id;
   model y=x1 | trt / d=poisson offset=ltime;
   repeated subject=id / corrw covb type=exch;
run;
```

These statements first fit a generalized linear model (GLM) to these data by maximum likelihood. The estimates are not shown in the output, but are used as initial values for the GEE solution.

Information about the GEE model is displayed in Output 37.7.3. The results of fitting the model are displayed in Output 37.7.4. Compare these with the model of independence displayed in Output 37.7.2. The parameter estimates are nearly identical, but the standard errors for the independence case are underestimated. The coefficient of the interaction term, β_3, is highly significant under the independence model and marginally significant with the exchangeable correlations model.

Output 37.7.3 GEE Model Information

The GENMOD Procedure

GEE Model Information

Correlation Structure	Exchangeable
Subject Effect	id (58 levels)
Number of Clusters	58
Correlation Matrix Dimension	5
Maximum Cluster Size	5
Minimum Cluster Size	5

Output 37.7.4 GEE Parameter Estimates

Analysis Of GEE Parameter Estimates
Empirical Standard Error Estimates

Parameter	Estimate	Standard Error	95% Confidence Limits		Z	Pr > |Z|
Intercept	1.3476	0.1574	1.0392	1.6560	8.56	<.0001
x1	0.1108	0.1161	-0.1168	0.3383	0.95	0.3399
trt	-0.1080	0.1937	-0.4876	0.2716	-0.56	0.5770
x1*trt	-0.3016	0.1712	-0.6371	0.0339	-1.76	0.0781

Table 37.9 displays the regression coefficients, standard errors, and normalized coefficients that result from fitting the model with independent and exchangeable working correlation matrices.

Table 37.9 Results of Model Fitting

Variable	Correlation Structure	Coef.	Std. Error	Coef./S.E.
Intercept	Exchangeable	1.35	0.16	8.56
	Independent	1.35	0.03	39.52
Visit (x_1)	Exchangeable	0.11	0.12	0.95
	Independent	0.11	0.05	2.36
Treat (x_2)	Exchangeable	−0.11	0.19	−0.56
	Independent	−0.11	0.05	−2.22
$x_1 * x_2$	Exchangeable	−0.30	0.17	−1.76
	Independent	−0.30	0.07	−4.32

The fitted exchangeable correlation matrix is specified with the CORRW option and is displayed in Output 37.7.5.

Output 37.7.5 Working Correlation Matrix

Working Correlation Matrix

	Col1	Col2	Col3	Col4	Col5
Row1	1.0000	0.5941	0.5941	0.5941	0.5941
Row2	0.5941	1.0000	0.5941	0.5941	0.5941
Row3	0.5941	0.5941	1.0000	0.5941	0.5941
Row4	0.5941	0.5941	0.5941	1.0000	0.5941
Row5	0.5941	0.5941	0.5941	0.5941	1.0000

If you specify the COVB option, you produce both the model-based (naive) and the empirical (robust) covariance matrices. Output 37.7.6 contains these estimates.

Output 37.7.6 Covariance Matrices

Covariance Matrix (Model-Based)

	Prm1	Prm2	Prm3	Prm4
Prm1	0.01223	0.001520	-0.01223	-0.001520
Prm2	0.001520	0.01519	-0.001520	-0.01519
Prm3	-0.01223	-0.001520	0.02495	0.005427
Prm4	-0.001520	-0.01519	0.005427	0.03748

Covariance Matrix (Empirical)

	Prm1	Prm2	Prm3	Prm4
Prm1	0.02476	-0.001152	-0.02476	0.001152
Prm2	-0.001152	0.01348	0.001152	-0.01348
Prm3	-0.02476	0.001152	0.03751	-0.002999
Prm4	0.001152	-0.01348	-0.002999	0.02931

The two covariance estimates are similar, indicating an adequate correlation model.

Example 37.8: Model Assessment of Multiple Regression Using Aggregates of Residuals

This example illustrates the use of cumulative residuals to assess the adequacy of a normal linear regression model. Neter et al. (1996, Section 8.2) describe a study of 54 patients undergoing a certain kind of liver operation in a surgical unit. The data consist of the survival time and certain covariates. After a model selection procedure, they arrived at the following model:

$$Y = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \epsilon$$

where Y is the logarithm (base 10) of the survival time; X_1, X_2, X_3 are *blood-clotting score*, *prognostic index*, and *enzyme function*, respectively; and ϵ is a normal error term. A listing of the SAS data set containing the data is shown in Output 37.8.1. The variables Y, X1, X2, and X3 correspond to Y, X_1, X_2, and X_3, and LogX1 is $\log(X_1)$. The PROC GENMOD fit of the model is shown in Output 37.8.2. The analysis first focuses on the adequacy of the functional form of X_1, *blood-clotting score*.

Output 37.8.1 Surgical Unit Example Data

Obs	Y	X1	X2	X3	LogX1
1	2.3010	6.7	62	81	0.82607
2	2.0043	5.1	59	66	0.70757
3	2.3096	7.4	57	83	0.86923
4	2.0043	6.5	73	41	0.81291
5	2.7067	7.8	65	115	0.89209
6	1.9031	5.8	38	72	0.76343
7	1.9031	5.7	46	63	0.75587
8	2.1038	3.7	68	81	0.56820
9	2.3054	6.0	67	93	0.77815
10	2.3075	3.7	76	94	0.56820
11	2.5172	6.3	84	83	0.79934
12	1.8129	6.7	51	43	0.82607
13	2.9191	5.8	96	114	0.76343
14	2.5185	5.8	83	88	0.76343
15	2.2253	7.7	62	67	0.88649
16	2.3365	7.4	74	68	0.86923
17	1.9395	6.0	85	28	0.77815
18	1.5315	3.7	51	41	0.56820
19	2.3324	7.3	68	74	0.86332
20	2.2355	5.6	57	87	0.74819
21	2.0374	5.2	52	76	0.71600
22	2.1335	3.4	83	53	0.53148
23	1.8451	6.7	26	68	0.82607
24	2.3424	5.8	67	86	0.76343
25	2.4409	6.3	59	100	0.79934
26	2.1584	5.8	61	73	0.76343
27	2.2577	5.2	52	86	0.71600
28	2.7589	11.2	76	90	1.04922
29	1.8573	5.2	54	56	0.71600
30	2.2504	5.8	76	59	0.76343
31	1.8513	3.2	64	65	0.50515
32	1.7634	8.7	45	23	0.93952
33	2.0645	5.0	59	73	0.69897
34	2.4698	5.8	72	93	0.76343
35	2.0607	5.4	58	70	0.73239
36	2.2648	5.3	51	99	0.72428
37	2.0719	2.6	74	86	0.41497
38	2.0792	4.3	8	119	0.63347
39	2.1790	4.8	61	76	0.68124
40	2.1703	5.4	52	88	0.73239
41	1.9777	5.2	49	72	0.71600
42	1.8751	3.6	28	99	0.55630
43	2.6840	8.8	86	88	0.94448
44	2.1847	6.5	56	77	0.81291
45	2.2810	3.4	77	93	0.53148
46	2.0899	6.5	40	84	0.81291
47	2.4928	4.5	73	106	0.65321
48	2.5999	4.8	86	101	0.68124
49	2.1987	5.1	67	77	0.70757
50	2.4914	3.9	82	103	0.59106
51	2.0934	6.6	77	46	0.81954
52	2.0969	6.4	85	40	0.80618
53	2.2967	6.4	59	85	0.80618
54	2.4955	8.8	78	72	0.94448

In order to assess the adequacy of the fitted multiple regression model, the ASSESS statement in the following SAS statements is used to create the plots of cumulative residuals against X1 shown in Output 37.8.3 and Output 37.8.4 and the summary table in Output 37.8.5:

```
ods graphics on;
proc genmod data=Surg;
   model Y = X1 X2 X3 / scale=Pearson;
   assess var=(X1) / resample=10000
                     seed=603708000
                     crpanel ;
run;
ods graphics off;
```

Output 37.8.2 Regression Model for Linear X1

The GENMOD Procedure

Analysis Of Maximum Likelihood Parameter Estimates

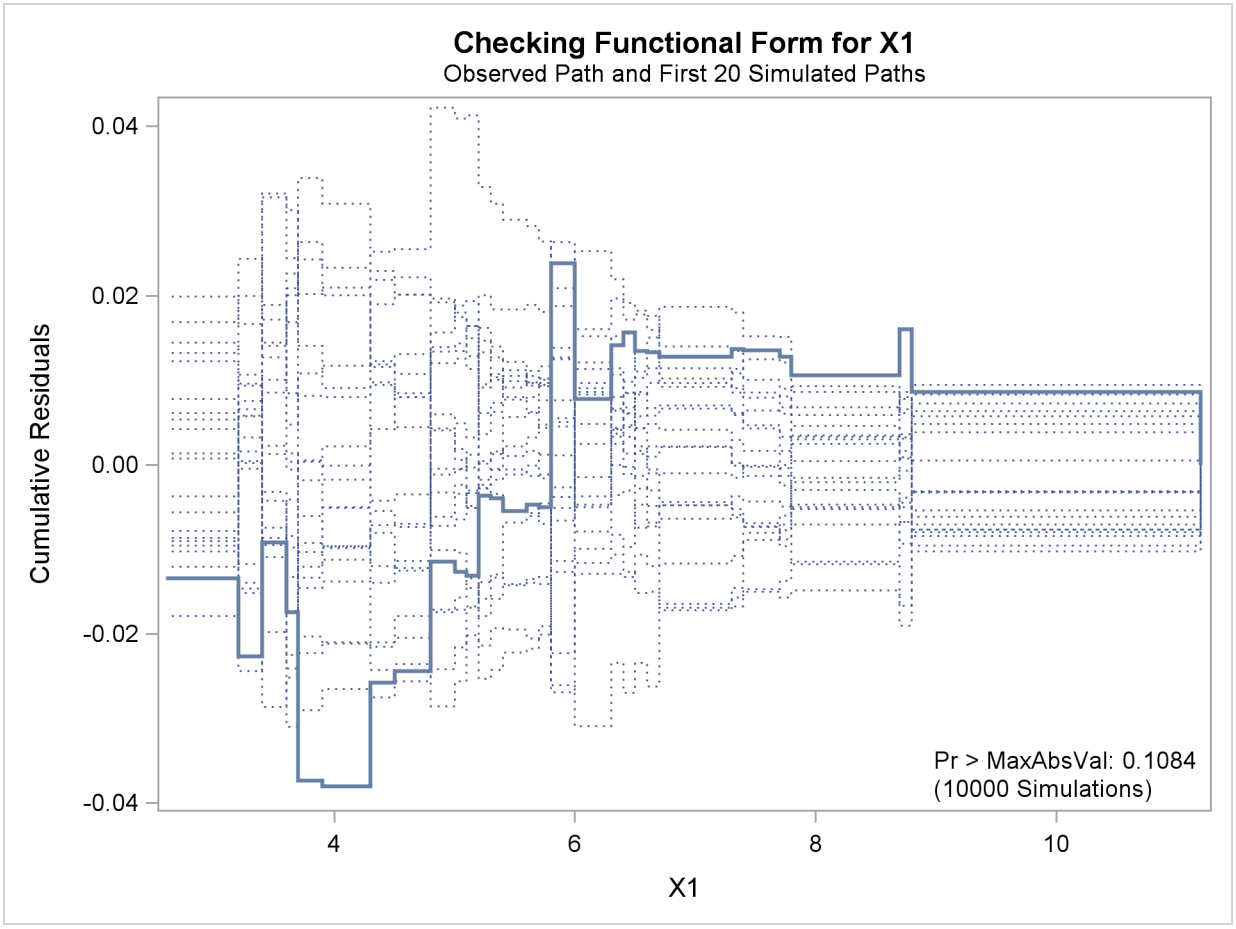
Parameter	DF	Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
Intercept	1	0.4836	0.0426	0.4001	0.5672	128.71	<.0001
X1	1	0.0692	0.0041	0.0612	0.0772	288.17	<.0001
X2	1	0.0093	0.0004	0.0085	0.0100	590.45	<.0001
X3	1	0.0095	0.0003	0.0089	0.0101	966.07	<.0001
Scale	0	0.0469	0.0000	0.0469	0.0469		

NOTE: The scale parameter was estimated by the square root of Pearson's Chi-Square/DOF.

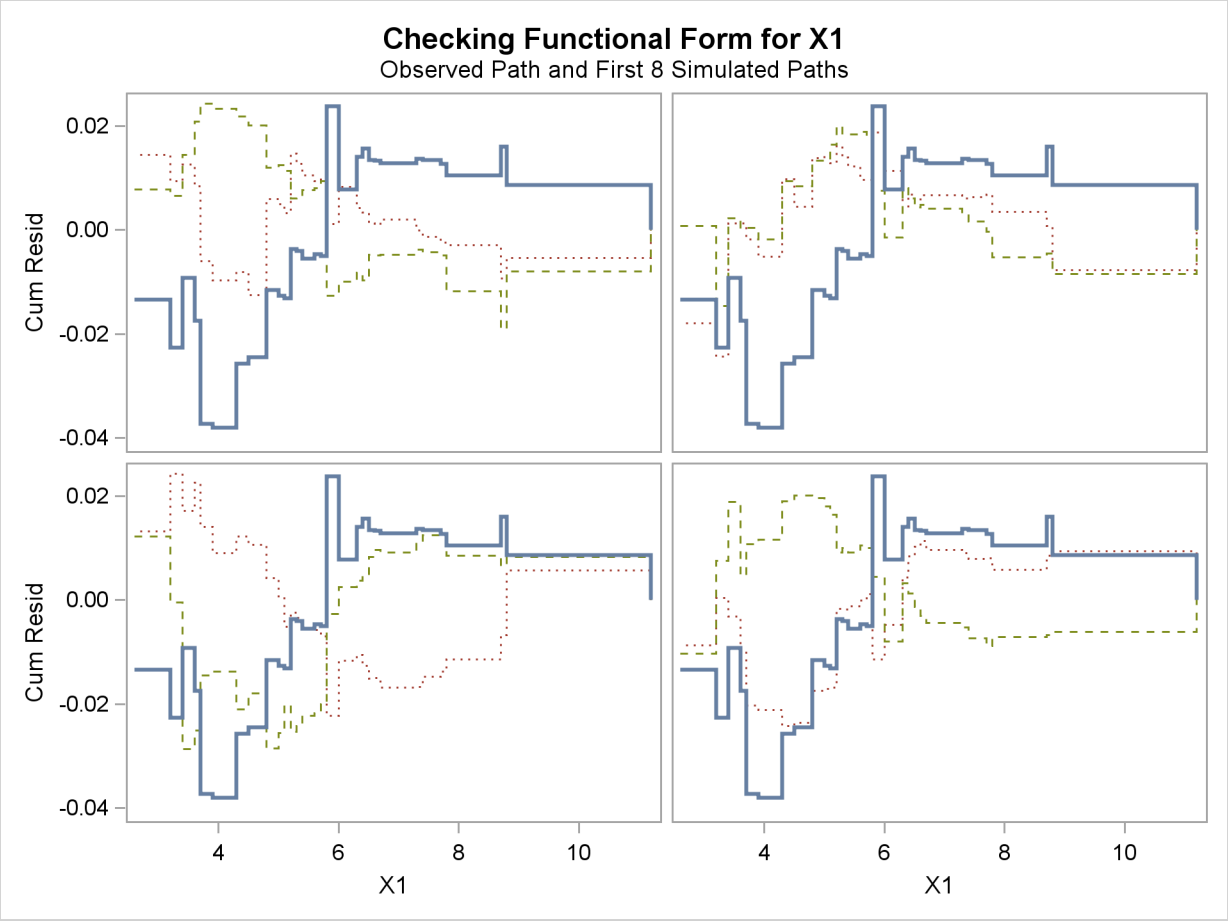
See Lin, Wei, and Ying (2002) for details about model assessment that uses cumulative residual plots. The RESAMPLE= keyword specifies that a p-value be computed based on a sample of 10,000 simulated residual paths. A random number seed is specified by the SEED= keyword for reproducibility. If you do not specify the seed, one is derived from the time of day. The keyword CRPANEL specifies that the panel of four cumulative residual plots shown in Output 37.8.4 be created, each with two simulated paths. The single residual plot with 20 simulated paths in Output 37.8.3 is created by default.

These graphical displays are requested by specifying the ODS GRAPHICS statement and the ASSESS statement. For general information about ODS Graphics, see Chapter 21, "Statistical Graphics Using ODS." For specific information about the graphics available in the GENMOD procedure, see the section "ODS Graphics" on page 2020.

Output 37.8.3 Cumulative Residual Plot for Linear X1 Fit



Output 37.8.4 Cumulative Residual Panel Plot for Linear X1 Fit



Output 37.8.5 Summary of Model Assessment

Assessment Summary

Assessment Variable	Maximum Absolute Value	Replications	Seed	Pr > MaxAbsVal
X1	0.0380	10000	603708000	0.1084

The p-value of 0.1084 reported on Output 37.8.3 and Output 37.8.5 suggests that a more adequate model might be possible. The observed cumulative residuals in Output 37.8.3 and Output 37.8.4, represented by the heavy lines, seem atypical of the simulated curves, represented by the light lines, reinforcing the conclusion that a more appropriate functional form for X1 is possible.

The cumulative residual plots in Output 37.8.6 provide guidance in determining a more appropriate functional form. The four curves were created from simple forms of model misspecification by using simulated data. The mean models of the data and the fitted model are shown in Table 37.10.

Output 37.8.6 Typical Cumulative Residual Patterns

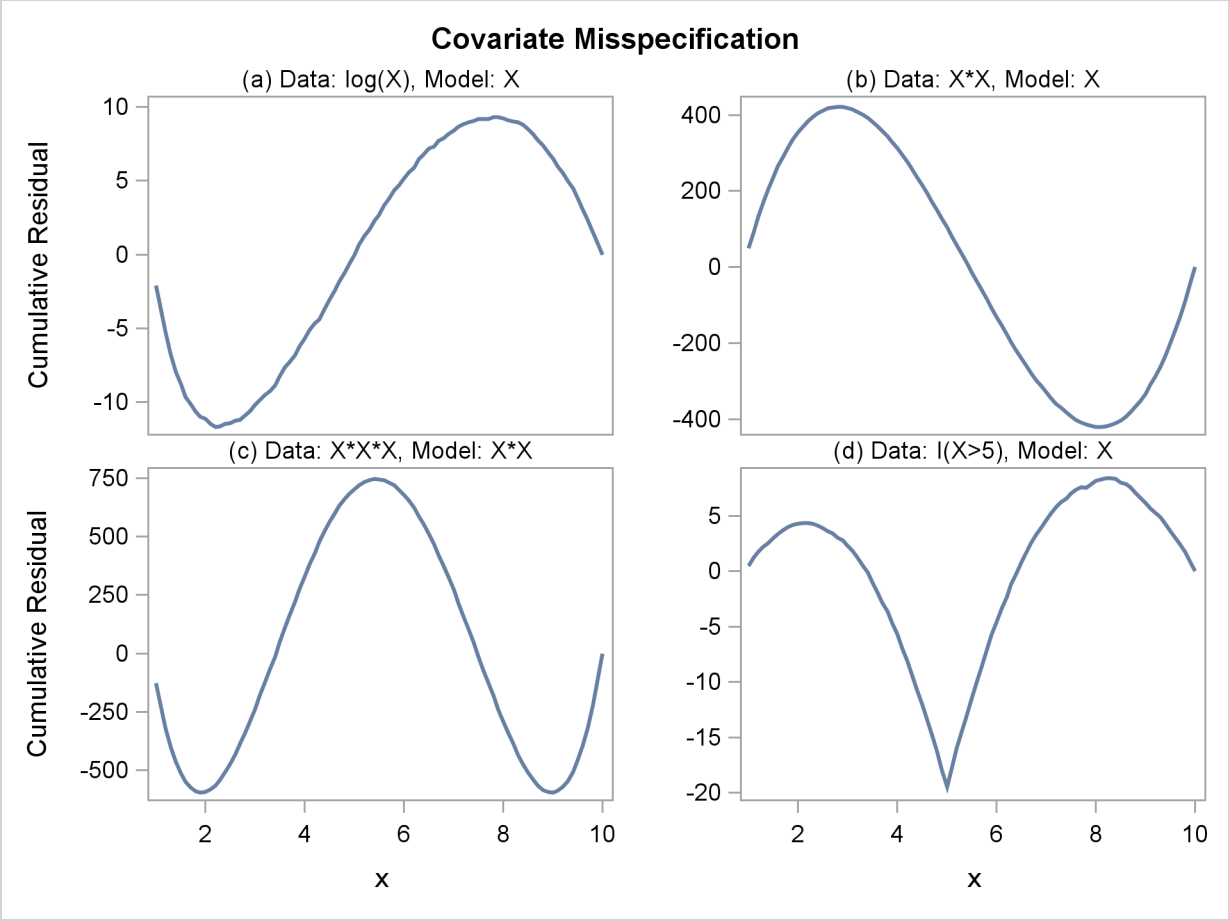


Table 37.10 Model Misspecifications

Plot	Data E(Y)	Fitted Model E(Y)
(a)	$\log(X)$	X
(b)	$X + X^2$	X
(c)	$X + X^2 + X^3$	$X + X^2$
(d)	$I(X > 5)$	X

The observed cumulative residual pattern in Output 37.8.3 and Output 37.8.4 most resembles the behavior of the curve in plot (a) of Output 37.8.6, indicating that $\log(X_1)$ might be a more appropriate term in the model than X_1.

The following SAS statements fit a model with LogX1 in place of X1 and request a model assessment:

```
proc genmod data=Surg;
ods graphics on;
   model Y = LogX1 X2 X3 / scale=Pearson;
   assess var=(LogX1) / resample=10000
                        seed=603708000;
run;
ods graphics off;
```

The revised model fit is shown in Output 37.8.7, the p-value from the simulation is 0.4777, and the cumulative residuals plotted in Output 37.8.8 show no systematic trend. The log transformation for X1 is more appropriate. Under the revised model, the p-values for testing the functional forms of X2 and X3 are 0.20 and 0.63, respectively; and the p-value for testing the linearity of the model is 0.65. Thus, the revised model seems reasonable.

Output 37.8.7 Multiple Regression Model with Log(X1)

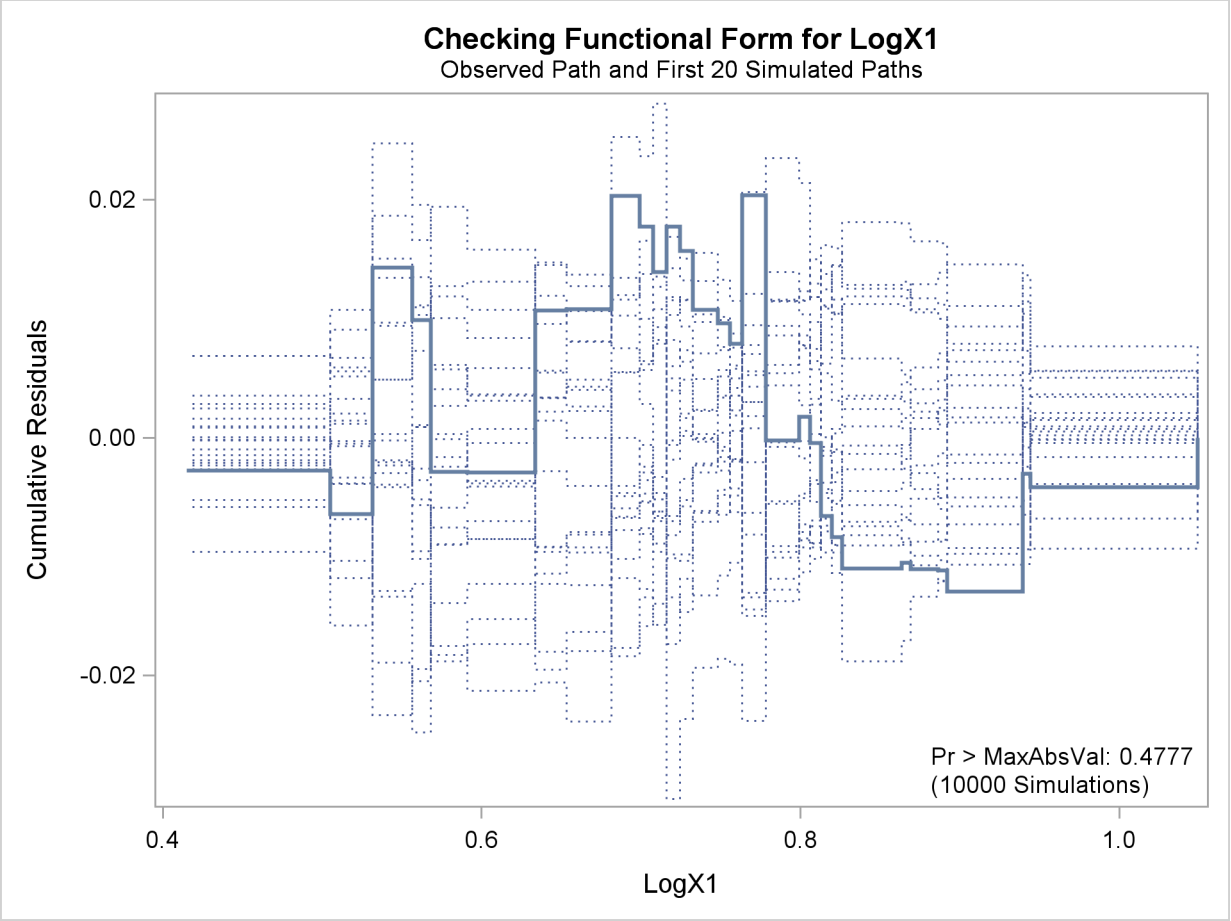
The GENMOD Procedure

Analysis Of Maximum Likelihood Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
Intercept	1	0.1844	0.0504	0.0857	0.2832	13.41	0.0003
LogX1	1	0.9121	0.0491	0.8158	1.0083	345.05	<.0001
X2	1	0.0095	0.0004	0.0088	0.0102	728.62	<.0001
X3	1	0.0096	0.0003	0.0090	0.0101	1139.73	<.0001
Scale	0	0.0434	0.0000	0.0434	0.0434		

NOTE: The scale parameter was estimated by the square root of Pearson's Chi-Square/DOF.

Output 37.8.8 Cumulative Residual Plot with Log(X1)



Example 37.9: Assessment of a Marginal Model for Dependent Data

This example illustrates the use of cumulative residuals to assess the adequacy of a marginal model for dependent data fit by generalized estimating equations (GEEs). The assessment methods are applied to CD4 count data from an AIDS clinical trial reported by Fischl, Richman, and Hansen (1990) and reanalyzed by Lin, Wei, and Ying (2002). The study randomly assigned 360 HIV patients to the drug AZT and 351 patients to placebo. CD4 counts were measured repeatedly over the course of the study. The data used here are the 4328 measurements taken in the first 40 weeks of the study.

The analysis focuses on the time trend of the response. The first model considered is

$$E(y_{ik}) = \beta_0 + \beta_1 T_{ik} + \beta_2 T_{ik}^2 + \beta_3 R_i T_{ik} + \beta_4 R_i T_{ik}^2$$

where T_{ik} is the time (in weeks) of the kth measurement on the ith patient, y_{ik} is the CD4 count at T_{ik} for the ith patient, and R_i is the indicator of AZT for the ith patient. Normal errors and an independent working correlation are assumed.

The following statements create the SAS data set cd4:

```
data cd4;
   input Id Y Time Time2 TrtTime TrtTime2;
   Time3 = Time2 * Time;
   TrtTime3 = TrtTime2 * Time;
   datalines;
1     264.00024       -0.28571        0.08163       -0.28571        0.08163
1     175.00070        4.14286       17.16327        4.14286       17.16327
1     306.00150        8.14286       66.30612        8.14286       66.30612
1     331.99835       12.14286      147.44898       12.14286      147.44898
1     309.99929       16.14286      260.59184       16.14286      260.59184
1     185.00077       28.71429      824.51020       28.71429      824.51020
1     175.00070       40.14286     1611.44898       40.14286     1611.44898

... more lines ...

711     488.00224       12.14286      147.44898       12.14286      147.44898
711     240.00026       18.14286      329.16327       18.14286      329.16327
;
run;
```

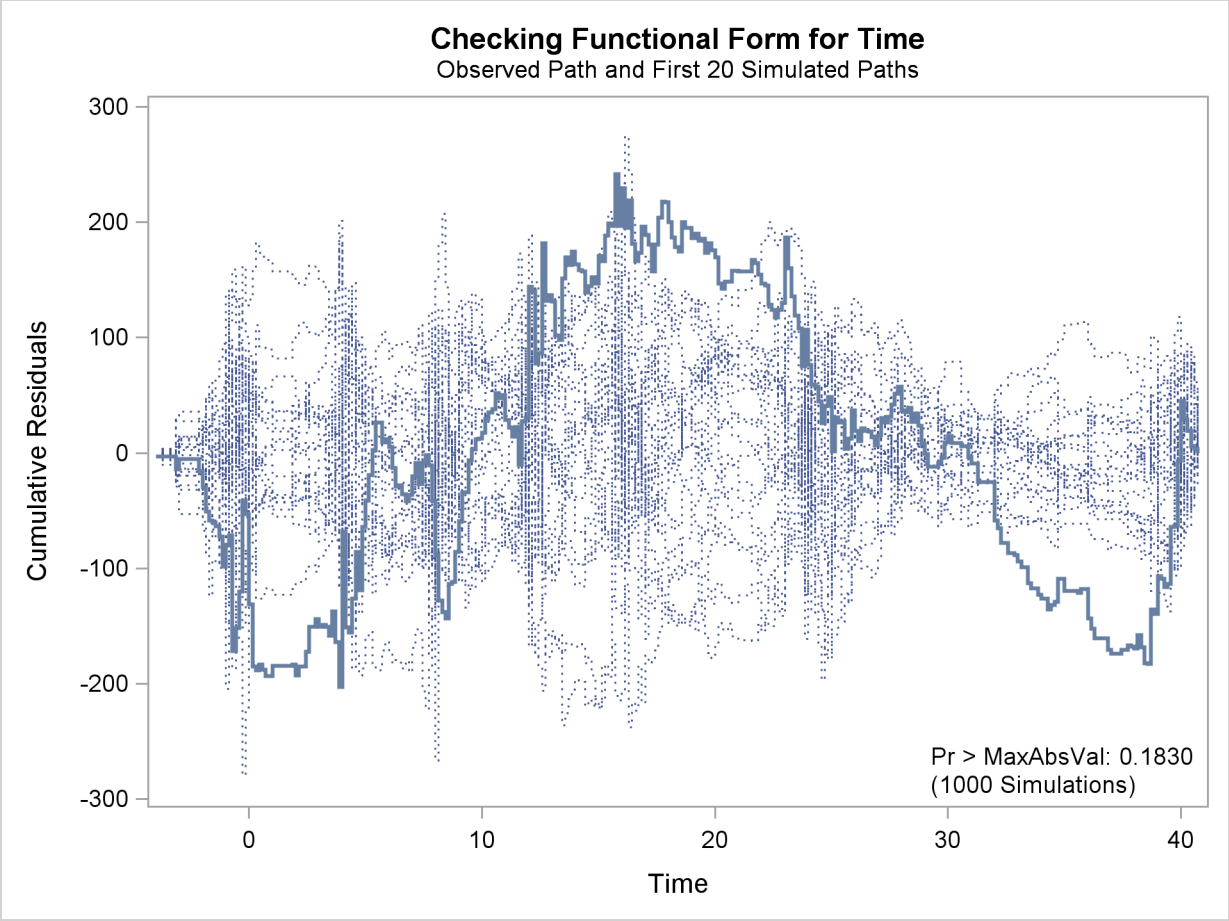
The following SAS statements fit the preceding model, create the cumulative residual plot in Output 37.9.1, and compute a p-value for the model.

These graphical displays are requested by specifying the ODS GRAPHICS statement and the ASSESS statement. For general information about ODS Graphics, see Chapter 21, "Statistical Graphics Using ODS." For specific information about the graphics available in the GENMOD procedure, see the section "ODS Graphics" on page 2020.

Here, the SAS data set variables Time, Time2, TrtTime, and TrtTime2 correspond to T_{ik}, T_{ik}^2, $R_i T_{ik}$, and $R_i T_{ik}^2$, respectively. The variable Id identifies individual patients.

```
ods graphics on;
proc genmod data=cd4;
   class Id;
   model Y = Time Time2 TrtTime TrtTime2;
   repeated sub=Id;
   assess var=(Time) / resample
                       seed=603708000;
run;
ods graphics off;
```

Output 37.9.1 Cumulative Residual Plot for Quadratic Time Fit

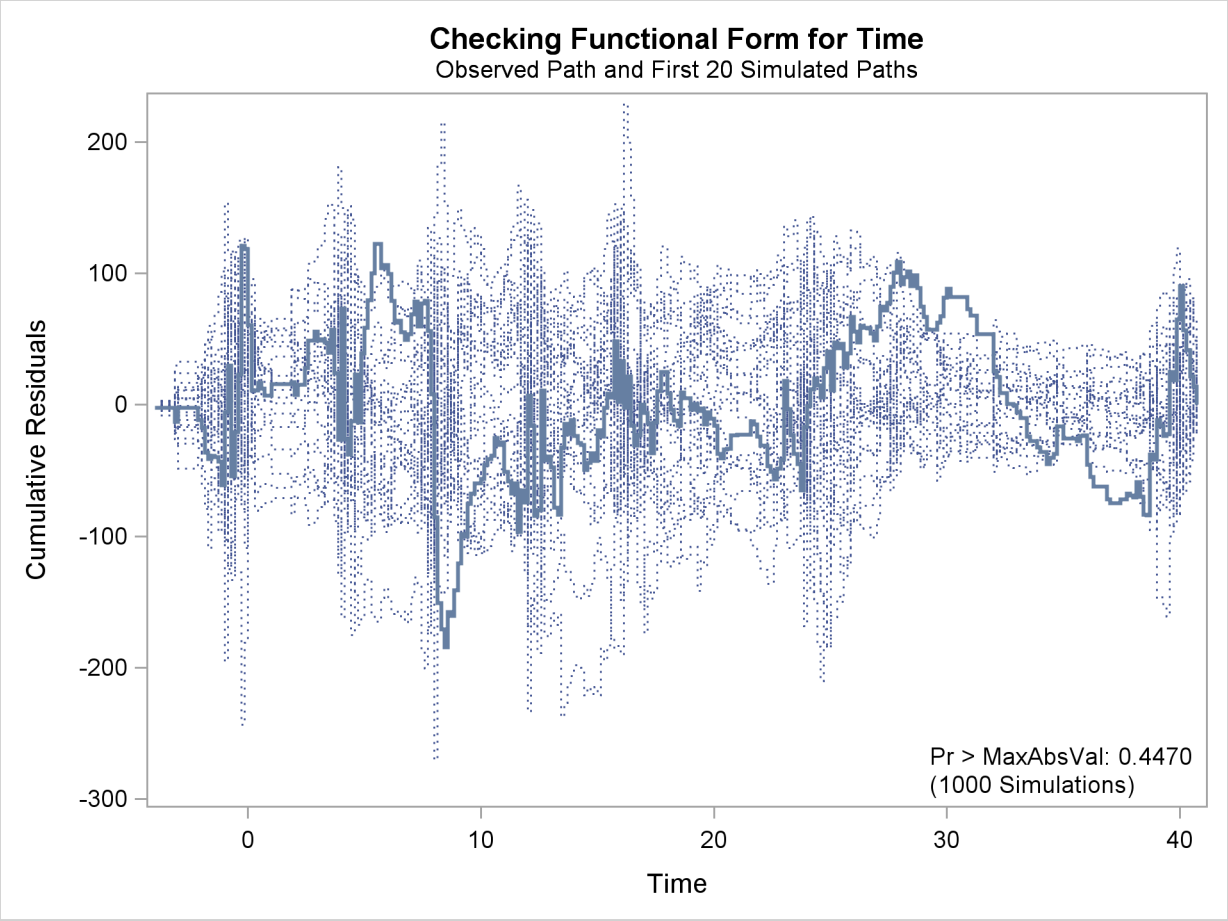


The cumulative residual plot in Output 37.9.1 displays cumulative residuals versus time for the model and 20 simulated realizations. The associated p-value, also shown in Output 37.9.1, is 0.18. These results indicate that a more satisfactory model might be possible. The observed cumulative residual pattern most resembles plot (c) in Output 37.8.6, suggesting cubic time trends.

The following SAS statements fit the model, create the plot in Output 37.9.2, and compute a p-value for a model with the additional terms T_{ik}^3 and $R_i T_{ik}^3$:

```
ods graphics on;
proc genmod data=cd4;
   class Id;
   model Y = Time Time2 Time3 TrtTime TrtTime2 TrtTime3;
   repeated sub=Id;
   assess var=(Time) / resample
                       seed=603708000;
run;
ods graphics off;
```

Output 37.9.2 Cumulative Residual Plot for Cubic Time Fit



The observed cumulative residual pattern appears more typical of the simulated realizations, and the p-value is 0.45, indicating that the model with cubic time trends is more appropriate.

Example 37.10: Bayesian Analysis of a Poisson Regression Model

This example illustrates a Bayesian analysis of a log-linear Poisson regression model. Consider the following data on patients from clinical trials. The data set is a subset of the data described in Ibrahim, Chen, and Lipsitz (1999).

```
data Liver;
input X1-X6 Y;
datalines;
19.1358    50.0110     51.000      0        0       1        3
23.5970    18.4959      3.429      0        0       1        9
20.0474    56.7699      3.429      1        1       0        6
28.0277    59.7836      4.000      0        0       1        6
28.6851    74.1589      5.714      1        0       1        1
18.8092    31.0630      2.286      0        1       1       61
28.7201    52.9178     37.286      1        0       1        6
21.3669    61.6603     54.143      0        1       1        6
23.7332    42.2904      0.571      1        0       1       21

... more lines ...

19.1327    65.3425      2.571      1        0       0        1
17.3010    51.4493      4.429      1        0       0        6
;
run;
```

The primary interest is in prediction of the number of cancerous liver nodes when a patient enters the trials, by using six other baseline characteristics. The number of nodes is modeled by a Poisson regression model with the six baseline characteristics as covariates. The response and regression variables are as follows:

Y	Number of Cancerous Liver Nodes
X1	Body Mass Index
X2	Age, in Years
X3	Time Since Diagnosis of Disease, in Weeks
X4	Two Biochemical Markers (each classified as normal=1 or abnormal=0)
X5	Anti Hepatitis B Antigen
X6	Associated Jaundice (yes=1, no=0)

Two analyses are performed using PROC GENMOD. The first analysis uses noninformative normal prior distributions, and the second analysis uses an informative normal prior for one of the regression parameters.

In the following BAYES statement, COEFFPRIOR=NORMAL specifies a noninformative independent normal prior distribution with zero mean and variance 10^6 for each parameter.

The initial analysis is performed using PROC GENMOD to obtain Bayesian estimates of the regression coefficients by using the following SAS statements:

```
ods graphics ON;
proc genmod data=Liver;
   model Y = X1-X6 / dist=Poisson link=log;
   bayes seed=1 coeffprior=normal;
run;
```

Maximum likelihood estimates of the model parameters are computed by default. These are shown in the "Analysis of Maximum Likelihood Parameter Estimates" table in Output 37.10.1.

Output 37.10.1 Maximum Likelihood Parameter Estimates

The GENMOD Procedure

Bayesian Analysis

Analysis Of Maximum Likelihood Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald 95% Confidence Limits	
Intercept	1	2.4508	0.2284	2.0032	2.8984
X1	1	-0.0044	0.0080	-0.0201	0.0114
X2	1	-0.0135	0.0024	-0.0181	-0.0088
X3	1	-0.0029	0.0022	-0.0072	0.0014
X4	1	-0.2715	0.0795	-0.4272	-0.1157
X5	1	0.3215	0.0832	0.1585	0.4845
X6	1	0.2077	0.0827	0.0456	0.3698
Scale	0	1.0000	0.0000	1.0000	1.0000

NOTE: The scale parameter was held fixed.

Noninformative independent normal prior distributions with zero means and variances of 10^6 were used in the initial analysis. These are shown in Output 37.10.2.

Output 37.10.2 Regression Coefficient Priors

The GENMOD Procedure

Bayesian Analysis

Independent Normal Prior for Regression Coefficients

Parameter	Mean	Precision
Intercept	0	1E-6
X1	0	1E-6
X2	0	1E-6
X3	0	1E-6
X4	0	1E-6
X5	0	1E-6
X6	0	1E-6

Initial values for the Markov chain are listed in the "Initial Values and Seeds" table in Output 37.10.3. The random number seed is also listed so that you can reproduce the analysis. Since no seed was specified, the seed shown was derived from the time of day.

Output 37.10.3 MCMC Initial Values and Seeds

Initial Values of the Chain

Chain	Seed	Intercept	X1	X2	X3	X4
1	1	2.450813	-0.00435	-0.01347	-0.00291	-0.27149

Initial Values of the Chain

X5	X6
0.321507	0.207713

Summary statistics for the posterior sample are displayed in the "Fit Statistics," "Descriptive Statistics for the Posterior Sample," "Interval Statistics for the Posterior Sample," and "Posterior Correlation Matrix" tables in Output 37.10.4, Output 37.10.5, Output 37.10.6, and Output 37.10.7, respectively. Since noninformative prior distributions for the regression coefficients were used, the mean and standard deviations of the posterior distributions for the model parameters are close to the maximum likelihood estimates and standard errors.

Output 37.10.4 Fit Statistics

Fit Statistics

DIC (smaller is better)	829.729
pD (effective number of parameters)	6.966

Output 37.10.5 Descriptive Statistics

The GENMOD Procedure

Bayesian Analysis

Posterior Summaries

Parameter	N	Mean	Standard Deviation	Percentiles 25%	50%	75%
Intercept	10000	2.4520	0.2268	2.2997	2.4521	2.6053
X1	10000	-0.00473	0.00801	-0.0100	-0.00465	0.000759
X2	10000	-0.0134	0.00236	-0.0150	-0.0134	-0.0118
X3	10000	-0.00309	0.00220	-0.00455	-0.00305	-0.00158
X4	10000	-0.2705	0.0792	-0.3241	-0.2697	-0.2172
X5	10000	0.3193	0.0834	0.2629	0.3180	0.3762
X6	10000	0.2095	0.0834	0.1538	0.2086	0.2653

Output 37.10.6 Interval Statistics

Posterior Intervals

Parameter	Alpha	Equal-Tail Interval		HPD Interval	
Intercept	0.050	2.0169	2.9056	2.0069	2.8923
X1	0.050	−0.0210	0.0106	−0.0212	0.0103
X2	0.050	−0.0181	−0.00878	−0.0181	−0.00885
X3	0.050	−0.00757	0.00109	−0.00764	0.000989
X4	0.050	−0.4250	−0.1132	−0.4232	−0.1119
X5	0.050	0.1552	0.4821	0.1647	0.4905
X6	0.050	0.0477	0.3749	0.0490	0.3758

Output 37.10.7 Posterior Sample Correlation Matrix

Posterior Correlation Matrix

Parameter	Intercept	X1	X2	X3	X4	X5	X6
Intercept	1.000	−0.705	−0.430	−0.046	−0.225	−0.180	−0.415
X1	−0.705	1.000	−0.211	−0.013	−0.068	0.067	0.128
X2	−0.430	−0.211	1.000	−0.006	0.070	0.057	0.118
X3	−0.046	−0.013	−0.006	1.000	0.016	−0.055	−0.089
X4	−0.225	−0.068	0.070	0.016	1.000	−0.011	0.089
X5	−0.180	0.067	0.057	−0.055	−0.011	1.000	−0.042
X6	−0.415	0.128	0.118	−0.089	0.089	−0.042	1.000

Posterior sample autocorrelations for each model parameter are shown in Output 37.10.8. The autocorrelation after 10 lags is negligible for all parameters, indicating good mixing in the Markov chain.

Output 37.10.8 Posterior Sample Autocorrelations

The GENMOD Procedure

Bayesian Analysis

Posterior Autocorrelations

Parameter	Lag 1	Lag 5	Lag 10	Lag 50
Intercept	0.0551	−0.0134	−0.0101	0.0012
X1	0.0894	−0.0054	−0.0080	0.0019
X2	0.1197	−0.0170	0.0061	0.0006
X3	0.0324	−0.0036	−0.0033	−0.0160
X4	0.0309	0.0056	0.0053	0.0115
X5	0.0402	0.0015	−0.0111	0.0123
X6	0.0696	−0.0047	−0.0024	0.0006

The *p*-values for the Geweke test statistics shown in Output 37.10.9 all indicate convergence of the MCMC. See the section "Assessing Markov Chain Convergence" on page 156 for more information about convergence diagnostics and their interpretation.

Output 37.10.9 Geweke Diagnostic Statistics

Geweke Diagnostics

Parameter	z	Pr > |z|
Intercept	0.9855	0.3244
X1	−1.0835	0.2786
X2	−0.3847	0.7005
X3	0.6715	0.5019
X4	0.1328	0.8943
X5	1.0698	0.2847
X6	−0.1647	0.8692

The effective sample sizes for each parameter are shown in Output 37.10.10.

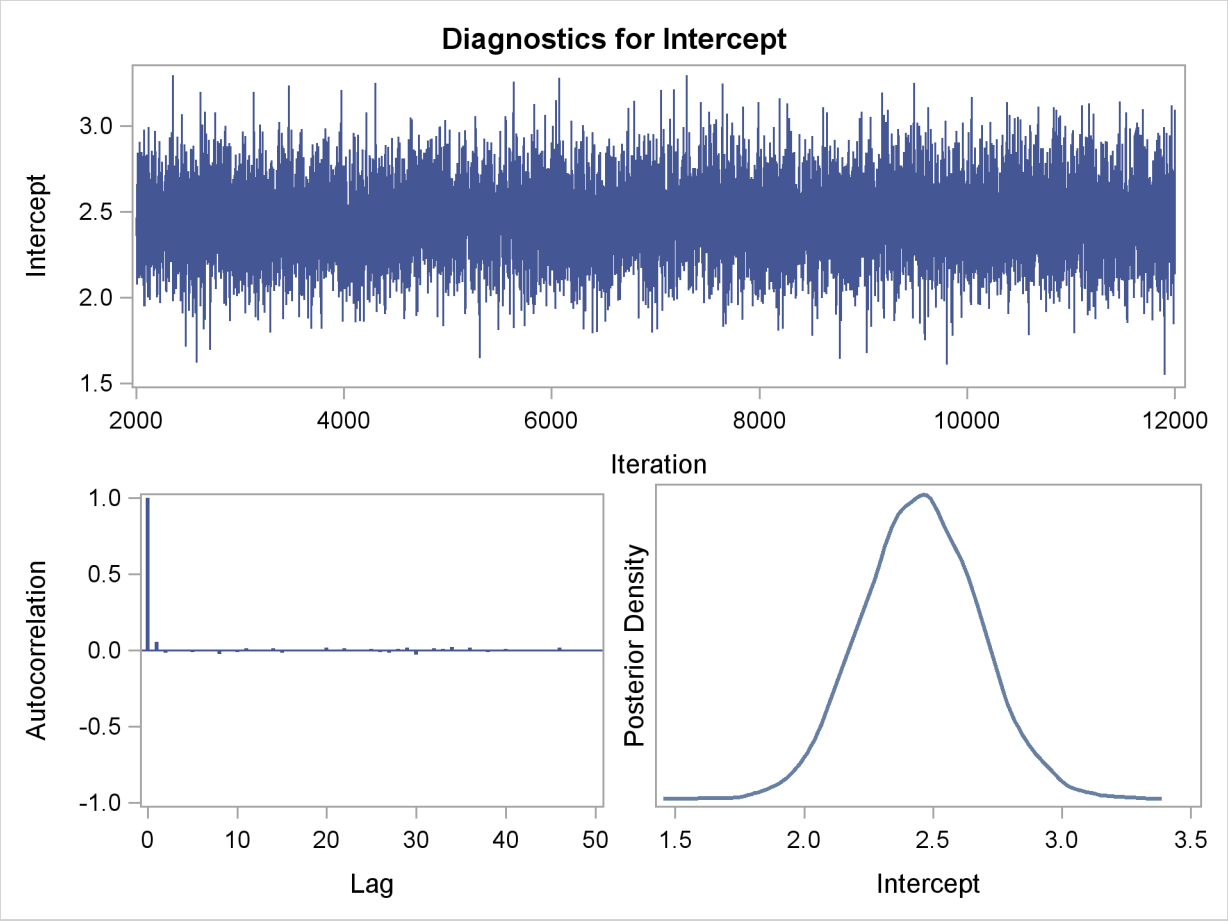
Output 37.10.10 Effective Sample Sizes

Effective Sample Sizes

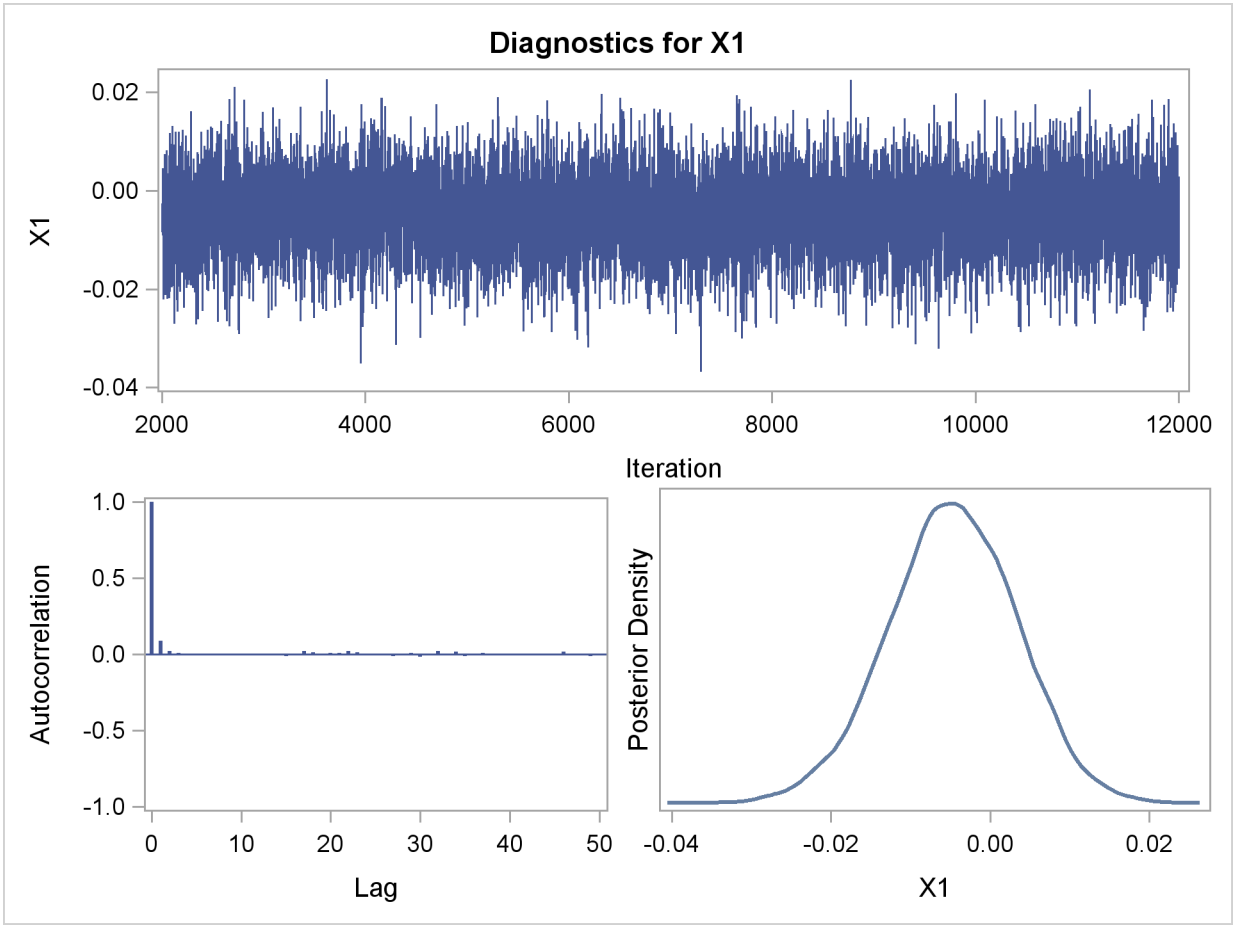
Parameter	ESS	Correlation Time	Efficiency
Intercept	9245.8	1.0816	0.9246
X1	8179.5	1.2226	0.8179
X2	8067.8	1.2395	0.8068
X3	9390.6	1.0649	0.9391
X4	9157.6	1.0920	0.9158
X5	9665.2	1.0346	0.9665
X6	8778.7	1.1391	0.8779

Trace, autocorrelation, and density plots for the seven model parameters are shown in Output 37.10.11 through Output 37.10.17. All indicate satisfactory convergence of the Markov chain.

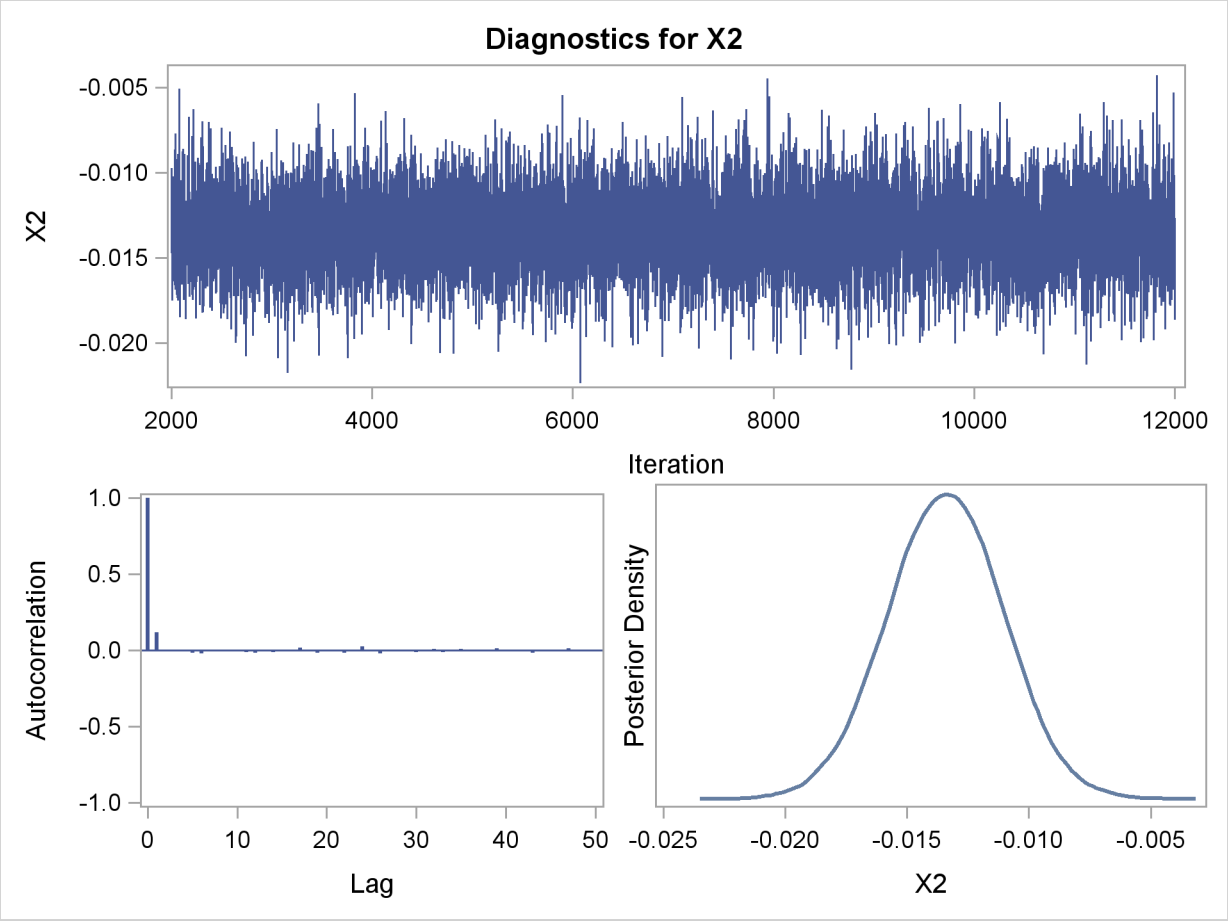
Output 37.10.11 Diagnostic Plots for Intercept



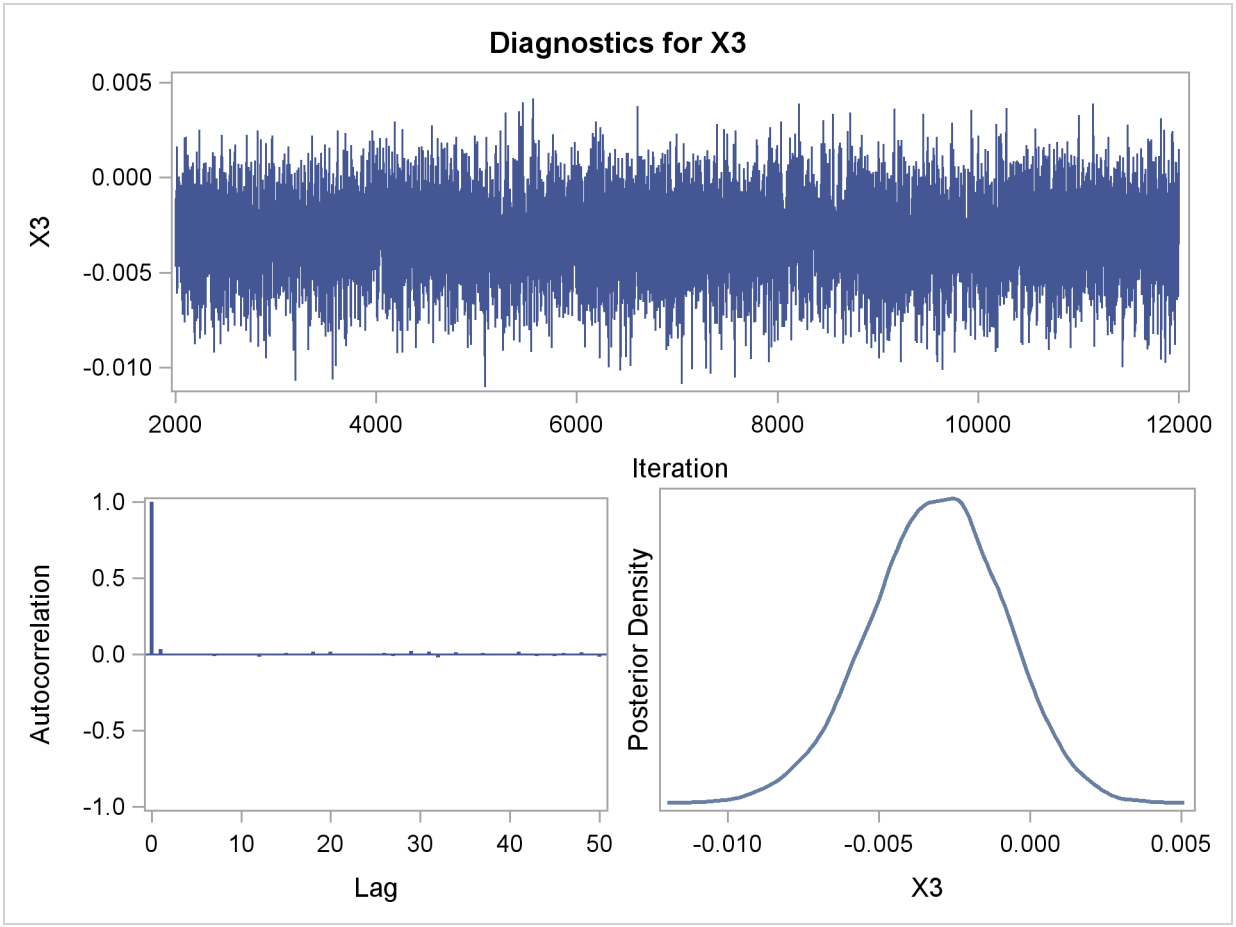
Output 37.10.12 Diagnostic Plots for X1



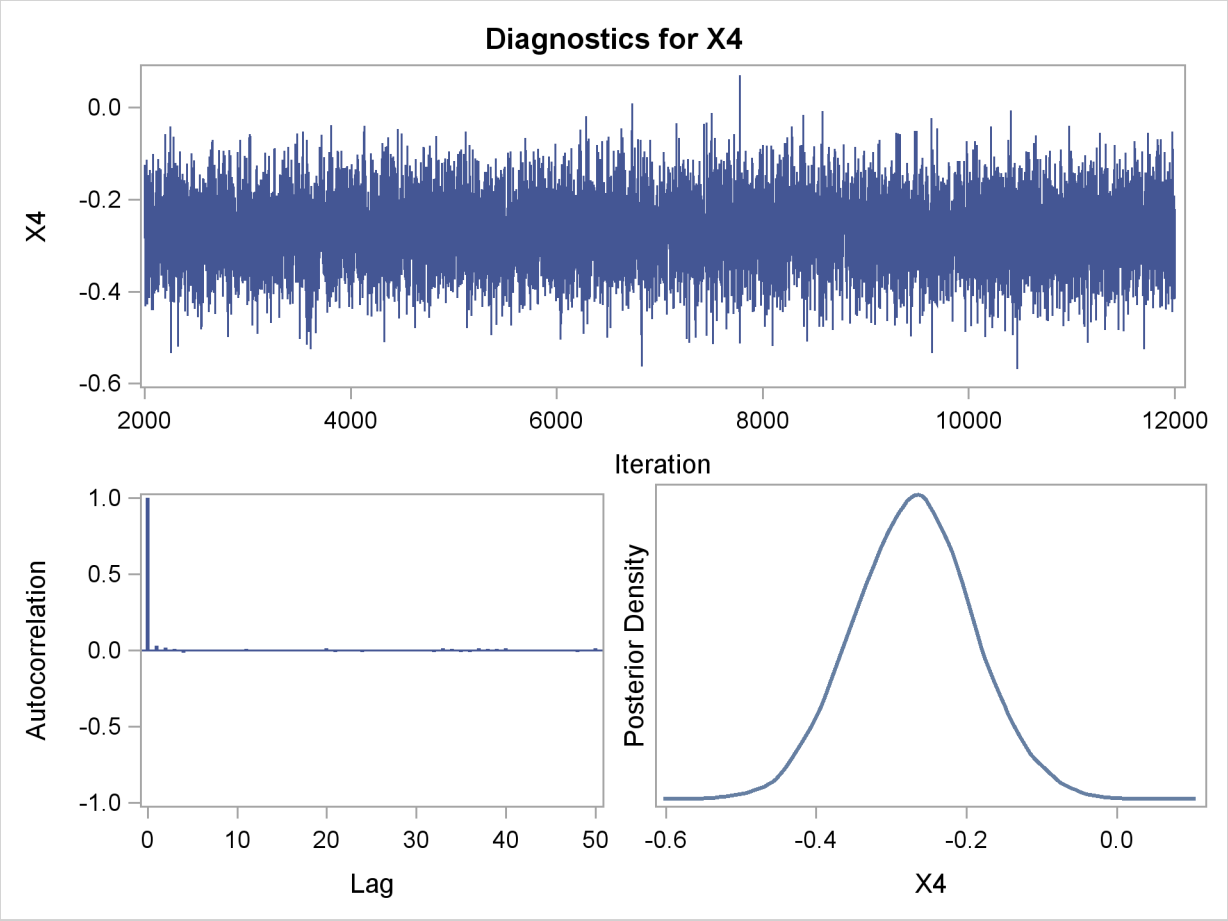
Output 37.10.13 Diagnostic Plots for X2



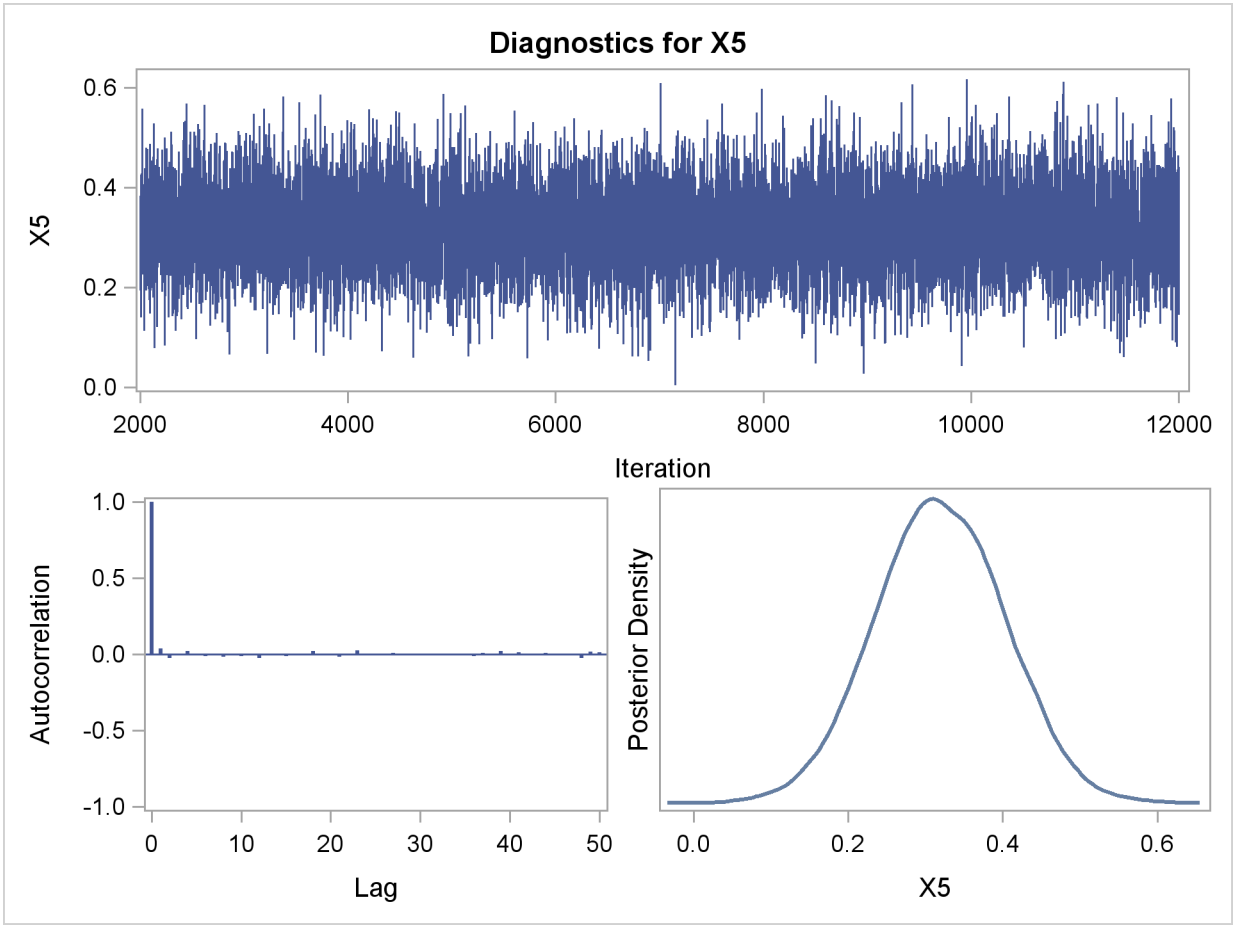
Output 37.10.14 Diagnostic Plots for X3



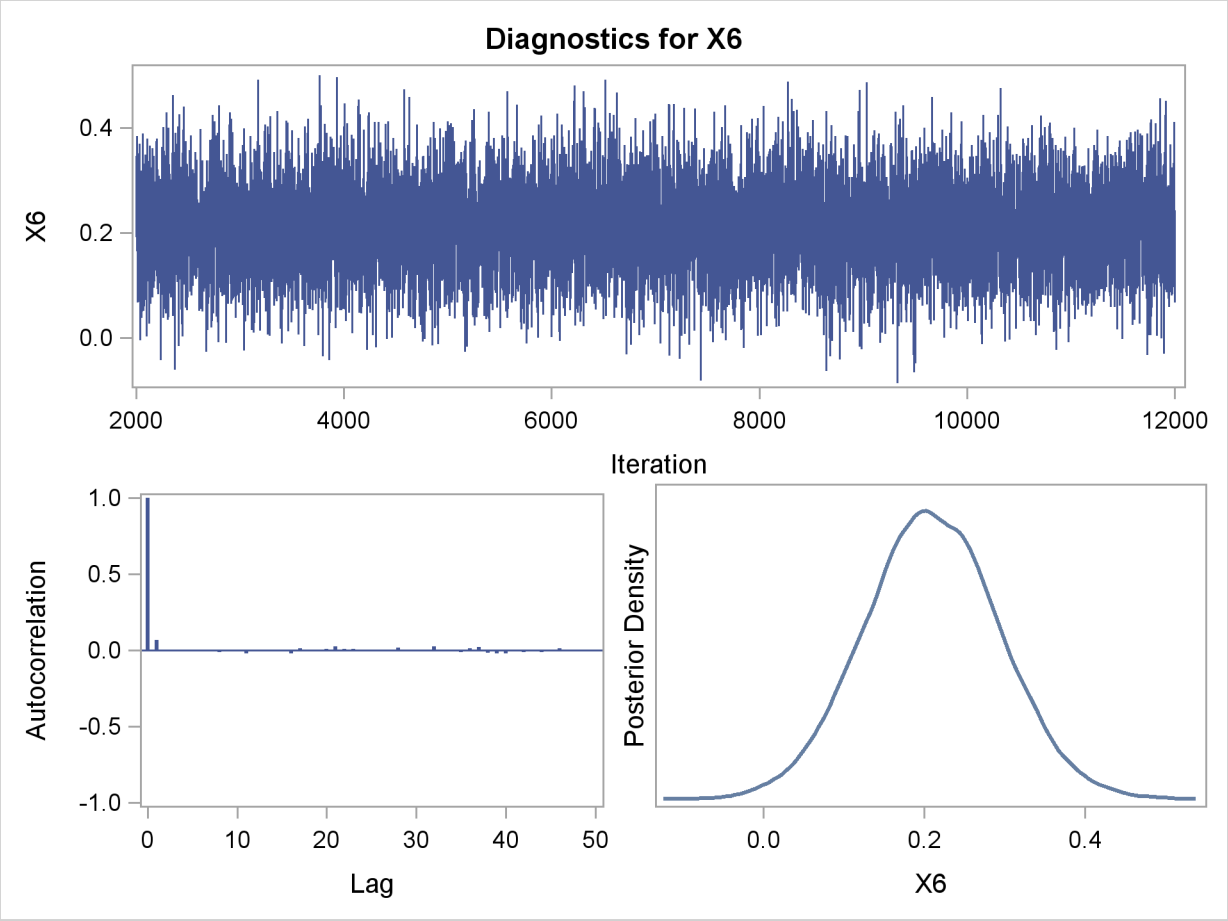
Output 37.10.15 Diagnostic Plots for X4



Output 37.10.16 Diagnostic Plots for X5



Output 37.10.17 Diagnostic Plots for X6



In order to illustrate the use of an informative prior distribution, suppose that researchers expect that a unit increase in body mass index (X1) will be associated with an increase in the mean number of nodes of between 10% and 20%, and they want to incorporate this prior knowledge in the Bayesian analysis. For log-linear models, the mean and linear predictor are related by $\log(\mu_i) = \boldsymbol{x}_i'\boldsymbol{\beta}$. If $\mathrm{X1}_1$ and $\mathrm{X1}_2$ are two values of body mass index, μ_1 and μ_2 are the two mean values, and all other covariates remain equal for the two values of X1, then

$$\frac{\mu_1}{\mu_2} = \exp(\beta(X1_1 - X1_2))$$

so that for a unit change in X1,

$$\frac{\mu_1}{\mu_2} = \exp(\beta)$$

If $1.1 \leq \frac{\mu_1}{\mu_2} \leq 1.2$, then $1.1 \leq \exp(\beta) \leq 1.2$, or $0.095 \leq \beta \leq 0.182$. This gives you guidance in specifying a prior distribution for the β for body mass index. Taking the mean of the prior normal

distribution to be the midrange of the values of β, and taking $\mu \pm 2\sigma$ to be the extremes of the range, an $N(0.1385, 0.0005)$ is the resulting prior distribution. The second analysis uses this informative normal prior distribution for the coefficient of $X1$ and uses independent noninformative normal priors with zero means and variances equal to 10^6 for the remaining model regression parameters.

In the following BAYES statement, COEFFPRIOR=NORMAL(INPUT=NormalPrior) specifies the normal prior distribution for the regression coefficients with means and variances contained in the data set NormalPrior.

An analysis is performed using PROC GENMOD to obtain Bayesian estimates of the regression coefficients by using the following SAS statements:

```
data NormalPrior;
  input _type_ $ Intercept X1-X6;
  datalines;
Var  1e6   0.0005      1e6      1e6      1e6      1e6      1e6
Mean 0.0   0.1385      0.0      0.0      0.0      0.0      0.0
;
run;

proc genmod data=Liver;
   model Y = X1-X6 / dist=Poisson link=log;
   bayes seed=1 plots=none coeffprior=normal(input=NormalPrior) ;
run;
ods graphics off;
```

The prior distributions for the regression parameters are shown in Output 37.10.18.

Output 37.10.18 Regression Coefficient Priors

The GENMOD Procedure

Bayesian Analysis

Independent Normal Prior for Regression Coefficients

Parameter	Mean	Precision
Intercept	0	1E-6
X1	0.1385	2000
X2	0	1E-6
X3	0	1E-6
X4	0	1E-6
X5	0	1E-6
X6	0	1E-6

Initial values for the MCMC are shown in Output 37.10.19. The initial values of the covariates are joint estimates of their posterior modes. The prior distribution for X1 is informative, so the initial value of X1 is further from the MLE than the rest of the covariates. Initial values for the rest of the covariates are close to their MLEs, since noninformative prior distributions were specified for them.

Output 37.10.19 MCMC Initial Values and Seeds

Initial Values of the Chain

Chain	Seed	Intercept	X1	X2	X3	X4
1	1	2.14282	0.010595	−0.01434	−0.00301	−0.28062

Initial Values of the Chain

X5	X6
0.334983	0.231213

Goodness-of-fit, summary, and interval statistics are shown in Output 37.10.20. Except for X1, the statistics shown in Output 37.10.20 are very similar to the previous statistics for noninformative priors shown in Output 37.10.4 through Output 37.10.7. The point estimate for X1 is now positive. This is expected because the prior distribution on β_1 is quite informative. The distribution reflects the belief that the coefficient is positive. The $N(0.1385, 0.0005)$ distribution places the majority of its probability density on positive values. As a result, the posterior density of β_1 places more likelihood on positive values than in the noninformative case.

Output 37.10.20 Fit Statistics

Fit Statistics

DIC (smaller is better)	833.134
pD (effective number of parameters)	6.861

The GENMOD Procedure

Bayesian Analysis

Posterior Summaries

Parameter	N	Mean	Standard Deviation	Percentiles 25%	50%	75%
Intercept	10000	2.1393	0.2160	1.9929	2.1417	2.2845
X1	10000	0.0104	0.00685	0.00583	0.0106	0.0151
X2	10000	−0.0143	0.00236	−0.0159	−0.0143	−0.0127
X3	10000	−0.00318	0.00218	−0.00463	−0.00313	−0.00170
X4	10000	−0.2801	0.0798	−0.3342	−0.2807	−0.2258
X5	10000	0.3336	0.0834	0.2772	0.3337	0.3902
X6	10000	0.2333	0.0822	0.1791	0.2327	0.2892

Output 37.10.20 *continued*

Posterior Intervals					
Parameter	Alpha	Equal-Tail Interval		HPD Interval	
Intercept	0.050	1.7161	2.5599	1.7075	2.5507
X1	0.050	-0.00323	0.0236	-0.00264	0.0241
X2	0.050	-0.0189	-0.00960	-0.0189	-0.00972
X3	0.050	-0.00754	0.00101	-0.00754	0.000963
X4	0.050	-0.4348	-0.1223	-0.4311	-0.1196
X5	0.050	0.1705	0.4970	0.1661	0.4915
X6	0.050	0.0696	0.3968	0.0655	0.3904

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