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SAS/STAT[®] 9.22 User's Guide
The LIFEREG Procedure
(Book Excerpt)



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Chapter 48

The LIFEREG Procedure

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Overview: LIFEREG Procedure

The LIFEREG procedure fits parametric models to failure time data that can be uncensored, right censored, left censored, or interval censored. The models for the response variable consist of a linear effect composed of the covariates and a random disturbance term. The distribution of the random disturbance can be taken from a class of distributions that includes the extreme value, normal, logistic, and, by using a log transformation, the exponential, Weibull, lognormal, log-logistic, and three-parameter gamma distributions.

The model assumed for the response y is

$$y = \mathbf{X}\boldsymbol{\beta} + \sigma\epsilon$$

where y is a vector of response values, often the log of the failure times, \mathbf{X} is a matrix of covariates or independent variables (usually including an intercept term), $\boldsymbol{\beta}$ is a vector of unknown regression parameters, σ is an unknown scale parameter, and ϵ is a vector of errors assumed to come from a known distribution (such as the standard normal distribution). If an offset variable O is specified, the form of the model is $y = \mathbf{X}\boldsymbol{\beta} + O + \sigma\epsilon$, where O is a vector of values of the offset variable O . The distribution might also depend on additional shape parameters. These models are equivalent to accelerated failure time models when the log of the response is the quantity being modeled. The effect of the covariates in an accelerated failure time model is to change the scale, and not the location, of a baseline distribution of failure times.

The LIFEREG procedure estimates the parameters by maximum likelihood with a Newton-Raphson algorithm. PROC LIFEREG estimates the standard errors of the parameter estimates from the inverse of the observed information matrix.

The accelerated failure time model assumes that the effect of independent variables on an event time distribution is multiplicative on the event time. Usually, the scale function is $\exp(\mathbf{x}'_c\boldsymbol{\beta}_c)$, where \mathbf{x}_c is the vector of covariate values (not including the intercept term) and $\boldsymbol{\beta}_c$ is a vector of unknown parameters. Thus, if T_0 is an event time sampled from the baseline distribution corresponding to values of zero for the covariates, then the accelerated failure time model specifies that, if the vector of covariates is \mathbf{x}_c , the event time is $T = \exp(\mathbf{x}'_c\boldsymbol{\beta}_c)T_0$. If $y = \log(T)$ and $y_0 = \log(T_0)$, then

$$y = \mathbf{x}'_c\boldsymbol{\beta}_c + y_0$$

This is a linear model with y_0 as the error term.

In terms of survival or exceedance probabilities, this model is

$$\Pr(T > t \mid \mathbf{x}_c) = \Pr(T_0 > \exp(-\mathbf{x}'_c \boldsymbol{\beta}_c)t)$$

The probability on the left-hand side of the equal sign is evaluated given the value \mathbf{x}_c for the covariates, and the right-hand side is computed using the baseline probability distribution but at a scaled value of the argument. The right-hand side of the equation represents the value of the baseline survival function evaluated at $\exp(-\mathbf{x}'_c \boldsymbol{\beta}_c)t$.

Models usually have an intercept parameter and a scale parameter. In terms of the original untransformed event times, the effects of the intercept term and the scale term are to scale the event time and to raise the event time to a power, respectively. That is, if

$$\log(T_0) = \mu + \sigma \log(T_\epsilon)$$

then

$$T_0 = \exp(\mu)T_\epsilon^\sigma$$

Although it is possible to fit these models to the original response variable by using the NOLOG option, it is more common to model the log of the response variable. Because of this log transformation, zero values for the observed failure times are not allowed unless the NOLOG option is specified. Similarly, small values for the observed failure times lead to large negative values for the transformed response. The NOLOG option should be used only if you want to fit a distribution appropriate for the untransformed response, such as the extreme value instead of the Weibull. If you specify the normal or logistic distributions, the responses are not log transformed; that is, the NOLOG option is implicitly assumed.

Parameter estimates for the normal distribution are sensitive to large negative values, and care must be taken that the fitted model is not unduly influenced by them. Large negative values for the normal distribution can occur when fitting the lognormal distribution by log transforming the response, and some response values are near zero. Likewise, values that are extremely large after the log transformation have a strong influence in fitting the Weibull distribution (that is, the extreme value distribution for log responses). You should examine the residuals and check the effects of removing observations with large residuals or extreme values of covariates on the model parameters. The logistic distribution gives robust parameter estimates in the sense that the estimates have a bounded influence function.

The standard errors of the parameter estimates are computed from large sample normal approximations by using the observed information matrix. In small samples, these approximations might be poor. Refer to Lawless (2003) for additional discussion and references. You can sometimes construct better confidence intervals by transforming the parameters. For example, large sample theory is often more accurate for $\log(\sigma)$ than σ . Therefore, it might be more accurate to construct confidence intervals for $\log(\sigma)$ and transform these into confidence intervals for σ . The parameter estimates and their estimated covariance matrix are available in an output SAS data set and can be used to construct additional tests or confidence intervals for the parameters. Alternatively, tests of parameters can be based on log-likelihood ratios. Refer to Cox and Oakes (1984) for a discussion of the merits of some possible test methods including score, Wald, and likelihood ratio tests. Likelihood ratio tests are generally more reliable for small samples than tests based on the information matrix.

The log-likelihood function is computed using the log of the failure time as a response. This log likelihood differs from the log likelihood obtained using the failure time as the response by an additive term of $\sum \log(t_i)$, where the sum is over the uncensored failure times. This term does not depend on the unknown parameters and does not affect parameter or standard error estimates. However, many published values of log likelihoods use the failure time as the basic response variable and, hence, differ by the additive term from the value computed by the LIFEREG procedure.

The classic Tobit model also fits into this class of models but with data usually censored on the left. The data considered by Tobin (1958) in his original paper came from a survey of consumers where the response variable is the ratio of expenditures on durable goods to the total disposable income. The two explanatory variables are the age of the head of household and the ratio of liquid assets to total disposable income. Because many observations in this data set have a value of zero for the response variable, the model fit by Tobin is

$$y = \max(\mathbf{x}'\boldsymbol{\beta} + \epsilon, 0)$$

which is a regression model with left censoring, where $\mathbf{x}' = (1, \mathbf{x}'_c)$.

Bayesian analysis of parametric survival models can be requested by using the BAYES statement in the LIFEREG 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 147 for a discussion of the advantages and disadvantages of Bayesian analysis. Refer to Ibrahim, Chen, and Sinha (2001) and Gilks, Richardson, and Spiegelhalter (1996) for more information about Bayesian analysis, including guidance in choosing prior distributions.

For Bayesian analysis, PROC LIFEREG generates a Gibbs chain for the posterior distribution of 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; and the effective sample size) are computed for each parameter, as well as the correlation 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 LIFEREG 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](#)."

Getting Started: LIFEREG Procedure

The following examples demonstrate how you can use the LIFEREG procedure to fit a parametric model to failure time data.

Suppose you have a response variable y that represents failure time; a binary variable, `sensor`, with `sensor=0` indicating censored values; and two linearly independent variables, x_1 and x_2 . The following statements perform a typical accelerated failure time model analysis. Higher-order effects such as interactions and nested effects are allowed in the independent variables list, but they are not shown in this example.

```
proc lifereg;  
  model y*censor(0) = x1 x2;  
run;
```

PROC LIFEREG can fit models to interval-censored data. The syntax for specifying interval-censored data is as follows:

```
proc lifereg;  
  model (begin, end) = x1 x2;  
run;
```

You can also model binomial data by using the *events/trials* syntax for the response, as illustrated in the following statements:

```
proc lifereg;  
  model r/n=x1 x2;  
run;
```

The variable n represents the number of trials, and the variable r represents the number of events.

Modeling Right-Censored Failure Time Data

The following example demonstrates how you can use the LIFEREG procedure to fit a model to right-censored failure time data.

Suppose you conduct a study of two headache pain relievers. You divide patients into two groups, with each group receiving a different type of pain reliever. You record the time taken (in minutes) for each patient to report headache relief. Because some of the patients never report relief for the entire study, some of the observations are censored.

The following DATA step creates the SAS data set `headache`:

```

data Headache;
  input Minutes Group Censor @@;
  datalines;
11 1 0 12 1 0 19 1 0 19 1 0
19 1 0 19 1 0 21 1 0 20 1 0
21 1 0 21 1 0 20 1 0 21 1 0
20 1 0 21 1 0 25 1 0 27 1 0
30 1 0 21 1 1 24 1 1 14 2 0
16 2 0 16 2 0 21 2 0 21 2 0
23 2 0 23 2 0 23 2 0 23 2 0
25 2 1 23 2 0 24 2 0 24 2 0
26 2 1 32 2 1 30 2 1 30 2 0
32 2 1 20 2 1
;

```

The data set `Headache` contains the variable `Minutes`, which represents the reported time to headache relief; the variable `Group`, the group to which the patient is assigned; and the variable `Censor`, a binary variable indicating whether the observation is censored. Valid values of the variable `Censor` are 0 (no) and 1 (yes). [Figure 48.1](#) shows the first five records of the data set `Headache`.

Figure 48.1 Headache Data

	Obs	Minutes	Group	Censor
	1	11	1	0
	2	12	1	0
	3	19	1	0
	4	19	1	0
	5	19	1	0

The following statements invoke the LIFEREG procedure:

```

proc lifereg data=Headache;
  class Group;
  model Minutes*Censor(1)=Group;
  output out=New cdf=Prob;
run;

```

The `CLASS` statement specifies the variable `Group` as the classification variable. The `MODEL` statement syntax indicates that the response variable `Minutes` is right censored when the variable `Censor` takes the value 1. The `MODEL` statement specifies the variable `Group` as the single explanatory variable. Because the `MODEL` statement does not specify the `DISTRIBUTION=` option, the LIFEREG procedure fits the default type 1 extreme-value distribution by using $\log(\text{Minutes})$ as the response. This is equivalent to fitting the Weibull distribution.

The `OUTPUT` statement creates the output data set `New`. In addition to containing the variables in the original data set `Headache`, the SAS data set `New` also contains the variable `Prob`. This new variable is created by the `CDF=` option to contain the estimates of the cumulative distribution function evaluated at the observed response.

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

Figure 48.2 Model Fitting Information from the LIFEREG Procedure

The LIFEREG Procedure		
Model Information		
Data Set	WORK.HEADACHE	
Dependent Variable	Log(Minutes)	
Censoring Variable	Censor	
Censoring Value(s)	1	
Number of Observations	38	
Noncensored Values	30	
Right Censored Values	8	
Left Censored Values	0	
Interval Censored Values	0	
Number of Parameters	3	
Name of Distribution	Weibull	
Log Likelihood	-9.37930239	
Class Level Information		
Name	Levels	Values
Group	2	1 2

Figure 48.2 displays the class level information and model fitting information. There are 30 uncensored observations and 8 right-censored observations. The log likelihood for the Weibull distribution is -9.3793 . The log-likelihood value can be used to compare the goodness of fit for nested models with different covariates, but with the same distribution.

Figure 48.3 Model Fit Statistics from the LIFEREG Procedure

Fit Statistics	
-2 Log Likelihood	18.759
AIC (smaller is better)	24.759
AICC (smaller is better)	25.464
BIC (smaller is better)	29.671
Fit Statistics (Unlogged Response)	
-2 Log Likelihood	199.747
Weibull AIC (smaller is better)	205.747
Weibull AICC (smaller is better)	206.453
Weibull BIC (smaller is better)	210.660

Figure 48.3 displays fit statistics for the model. The “Fit Statistics” table displays statistics based on the maximum extreme-value log likelihood fit by using $\log(\text{Minutes})$ as the response. These statistics are useful in comparing the fit of a different model when the fit criteria from the model that you compare is also based on the log likelihood using $\log(\text{Minutes})$ as the response.

The “Fit Statistics (Unlogged Response)” table is based on the maximum Weibull log likelihood using Minutes as the response. The AIC, BIC, and AICC statistics in this table can be used to compare models with different covariates, in addition to models with different distributions, as long as the fit statistics for the models that you compare use Minutes as the response.

Figure 48.4 Model Parameter Estimates from the LIFEREG Procedure

Analysis of Maximum Likelihood Parameter Estimates							
Parameter	DF	Estimate	Standard Error	95% Confidence Limits		Chi-Square	Pr > ChiSq
Intercept	1	3.3091	0.0589	3.1938	3.4245	3161.70	<.0001
Group	1 1	-0.1933	0.0786	-0.3473	-0.0393	6.05	0.0139
Group	2 0	0.0000
Scale	1	0.2122	0.0304	0.1603	0.2809		
Weibull Shape	1	4.7128	0.6742	3.5604	6.2381		

The table of parameter estimates is displayed in [Figure 48.4](#). Both the intercept and the slope parameter for the variable group are significantly different from 0 at the 0.05 level. Because the variable group has only one degree of freedom, parameter estimates are given for only one level of the variable group (group=1). However, the estimate for the intercept parameter provides a baseline for group=2.

The resulting model is as follows:

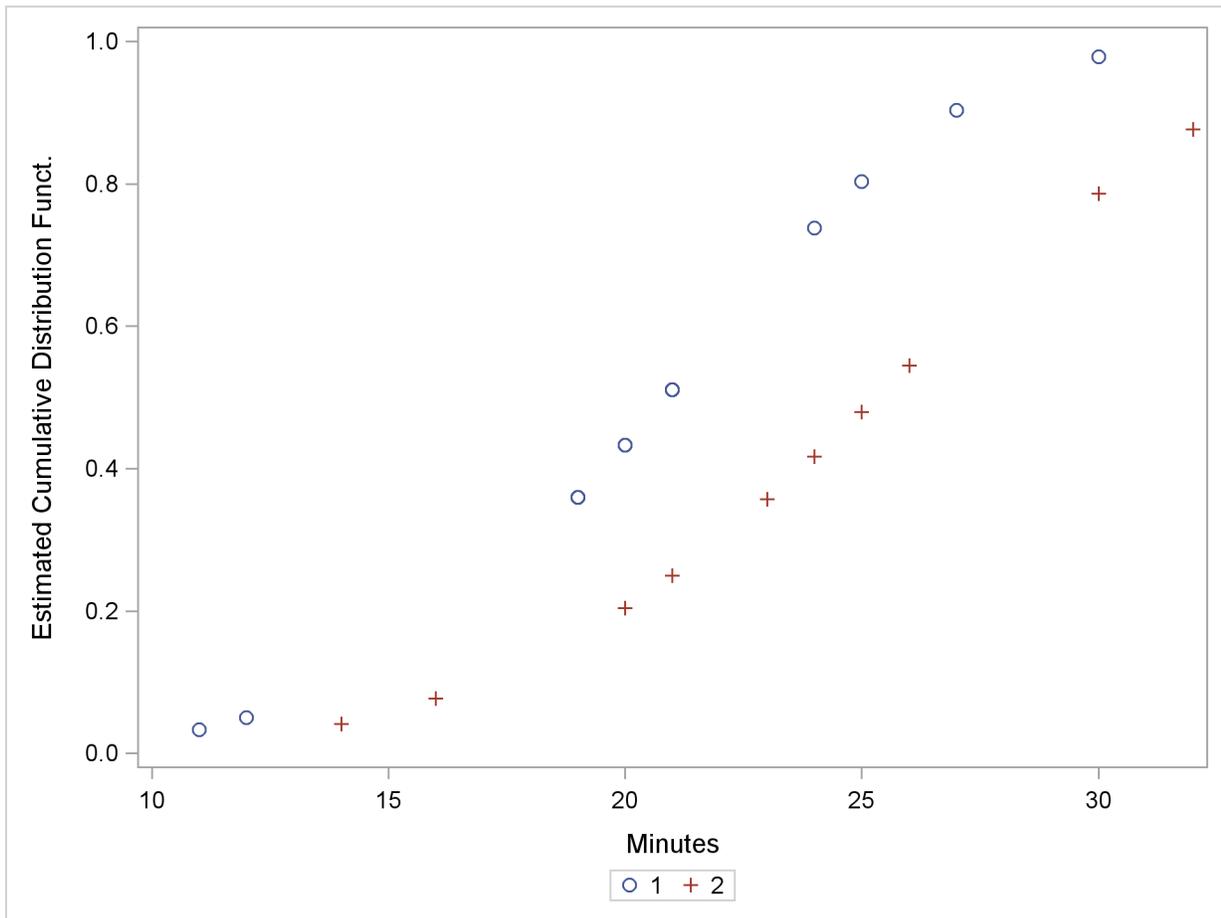
$$\log(\text{minutes}) = \begin{cases} 3.30911843 - 0.1933025 & \text{for group} = 1 \\ 3.30911843 & \text{for group} = 2 \end{cases}$$

Note that the Weibull shape parameter for this model is the reciprocal of the extreme-value scale parameter estimate shown in [Figure 48.4](#) ($1/0.21219 = 4.7128$).

The following statements produce a graph of the cumulative distribution values versus the variable Minutes.

```
proc sgplot data=New;
  scatter x=Minutes y=Prob / group=Group;
  discretelegend;
run;
```

[Figure 48.5](#) displays the estimated cumulative distribution function values contained in the output data set New for each group.

Figure 48.5 Plot of the Estimated Cumulative Distribution Function

Bayesian Analysis of Right-Censored Data

Nelson (1982) describes a study of the lifetimes of locomotive engine fans. This example shows how to use PROC LIFEREG to carry out a Bayesian analysis of the engine fan data. In this example, a lognormal distribution is used to model the engine lifetimes, but other survival time distributions, such as the Weibull, can also be used.

The following SAS statements create the SAS data set Fan. This data set contains a censoring indicator variable and right-censored survival times for the 70 locomotive engine fans in the study.

```

data Fan;
  input Lifetime Censor@@;
  datalines;
  450 0    460 1    1150 0    1150 0    1560 1
  1600 0    1660 1    1850 1    1850 1    1850 1
  1850 1    1850 1    2030 1    2030 1    2030 1
  2070 0    2070 0    2080 0    2200 1    3000 1
  3000 1    3000 1    3000 1    3100 0    3200 1
  3450 0    3750 1    3750 1    4150 1    4150 1
  4150 1    4150 1    4300 1    4300 1    4300 1
  4300 1    4600 0    4850 1    4850 1    4850 1
  4850 1    5000 1    5000 1    5000 1    6100 1
  6100 0    6100 1    6100 1    6300 1    6450 1
  6450 1    6700 1    7450 1    7800 1    7800 1
  8100 1    8100 1    8200 1    8500 1    8500 1
  8500 1    8750 1    8750 0    8750 1    9400 1
  9900 1    10100 1    10100 1    10100 1    11500 1
;
run;

```

Some of the fans had not failed at the time the data were collected, and the unfailed units have right-censored lifetimes. The variable `Lifetime` represents either a failure time or a censoring time. The variable `Censor` is equal to 0 if the value of `Lifetime` is a failure time, and it is equal to 1 if the value is a censoring time.

The following SAS statements specify a Bayesian analysis that uses a lognormal model for the engine lifetimes. There are no covariates, so the model is an intercept-only model. The `OUTPOST=` option saves the samples from the posterior distribution in the SAS data set `Post` for further processing.

```

ods graphics on;
proc lifereg data=Fan;
  model Lifetime*Censor( 1 )= / dist=lognormal;
  bayes seed=1 outpost=Post;
run;
ods graphics off;

```

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 for the intercept coefficient. 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 probability 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 on the regression coefficients, you should use the `COEFFPRIOR=` option to specify it. A default noninformative gamma prior is used for the lognormal scale parameter σ .

You should make sure that the posterior distribution samples have achieved convergence before using them for Bayesian inference. If you do not specify additional options, `PROC LIFEREG` produces by default three convergence diagnostics: autocorrelations of the posterior sample, effective sample size, and the Geweke statistic. See the section “[Assessing Markov Chain Convergence](#)” on page 155 for information about assessing the convergence of the chain of posterior samples. Trace plots, posterior density plots, and autocorrelation function plots that are created using `ODS Graphics` are

also provided for each parameter. See the section “Visual Analysis via Trace Plots” on page 155 for help in interpreting these plots.

The “Analysis of Maximum Likelihood Parameter Estimates” table in Figure 48.6 summarizes maximum likelihood estimates of the lognormal intercept and scale parameters.

Figure 48.6 Maximum Likelihood Estimates from the LIFEREG Procedure

The LIFEREG Procedure					
Bayesian Analysis					
Analysis of Maximum Likelihood Parameter Estimates					
Parameter	DF	Estimate	Standard Error	95% Confidence Limits	
Intercept	1	10.1432	0.5211	9.1219	11.1646
Scale	1	1.6796	0.3893	1.0664	2.6453

Since no prior distribution for the intercept was specified, the default uniform improper distribution shown in the “Uniform Prior for Regression Coefficients” table in Figure 48.7 is used.

Noninformative prior distributions 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. Refer, for example, to Ibrahim, Chen, and Sinha (2001) for more information about choosing prior distributions.

The default noninformative gamma prior distribution for the lognormal scale parameter is shown in the “Independent Prior Distributions for Model Parameters” table in Figure 48.7.

Figure 48.7 Noninformative Prior Distributions

The LIFEREG Procedure					
Bayesian Analysis					
Uniform Prior for Regression Coefficients					
Parameter	Prior				
Intercept	Constant				
Independent Prior Distributions for Model Parameters					
Parameter	Prior Distribution	Hyperparameters			
Scale	Gamma	Shape	0.001	Inverse Scale	0.001

By default, posterior mode estimates of the model parameters are used as the starting value for the simulation. These are listed in the “Initial Values of the Chain” table in Figure 48.8.

Figure 48.8 Markov Chain Initial Values

Initial Values of the Chain			
Chain	Seed	Intercept	Scale
1	1	10.0501	1.59544

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 48.9](#). Since noninformative prior distributions were used, these results are consistent with the maximum likelihood estimates shown in [Figure 48.6](#).

Figure 48.9 Posterior Sample Summary Statistics

Fit Statistics						
DIC (smaller is better)		87.245				
pD (effective number of parameters)		1.823				
The LIFEREG Procedure						
Bayesian Analysis						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
Intercept	10000	10.4196	0.6172	9.9670	10.3259	10.7959
Scale	10000	1.9196	0.4809	1.5675	1.8476	2.1931
Posterior Intervals						
Parameter	Alpha	Equal-Tail Interval		HPD Interval		
Intercept	0.050	9.4477	11.8994	9.3216	11.6752	
Scale	0.050	1.1906	3.0570	1.1104	2.8834	
Posterior Correlation Matrix						
Parameter	Intercept		Scale			
Intercept	1.0000		0.8297			
Scale	0.8297		1.0000			

By default, PROC LIFEREG computes three convergence diagnostics: the lag1, lag5, lag10, and lag50 autocorrelations; the Geweke diagnostic; and the effective sample size. These are displayed in [Figure 48.10](#). There is no indication that the Markov chain has not converged. See the section “[Assessing Markov Chain Convergence](#)” on page 155 for more information about convergence diagnostics and their interpretation.

Figure 48.10 Posterior Sample Summary Statistics

The LIFEREG Procedure				
Bayesian Analysis				
Posterior Autocorrelations				
Parameter	Lag 1	Lag 5	Lag 10	Lag 50
Intercept	0.6973	0.1765	0.0190	-0.0017
Scale	0.6955	0.1713	0.0172	-0.0002
Geweke Diagnostics				
Parameter	z	Pr > z		
Intercept	-0.9183	0.3585		
Scale	-0.9233	0.3559		
Effective Sample Sizes				
Parameter	ESS	Autocorrelation Time	Efficiency	
Intercept	1772.8	5.6408	0.1773	
Scale	1805.0	5.5400	0.1805	

Summary statistics of the posterior distribution samples are produced by default. However, these statistics might not be sufficient for carrying out your Bayesian inference. The samples from the posterior distribution saved in the SAS data set `Post` created with the `OUTPOST=` option can be used for further analysis.

Trace, autocorrelation, and density plots for the three model parameters shown in [Figure 48.11](#) and [Figure 48.12](#) 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 155 for more information about interpreting these types of diagnostic plots.

Figure 48.11 Diagnostic Plots

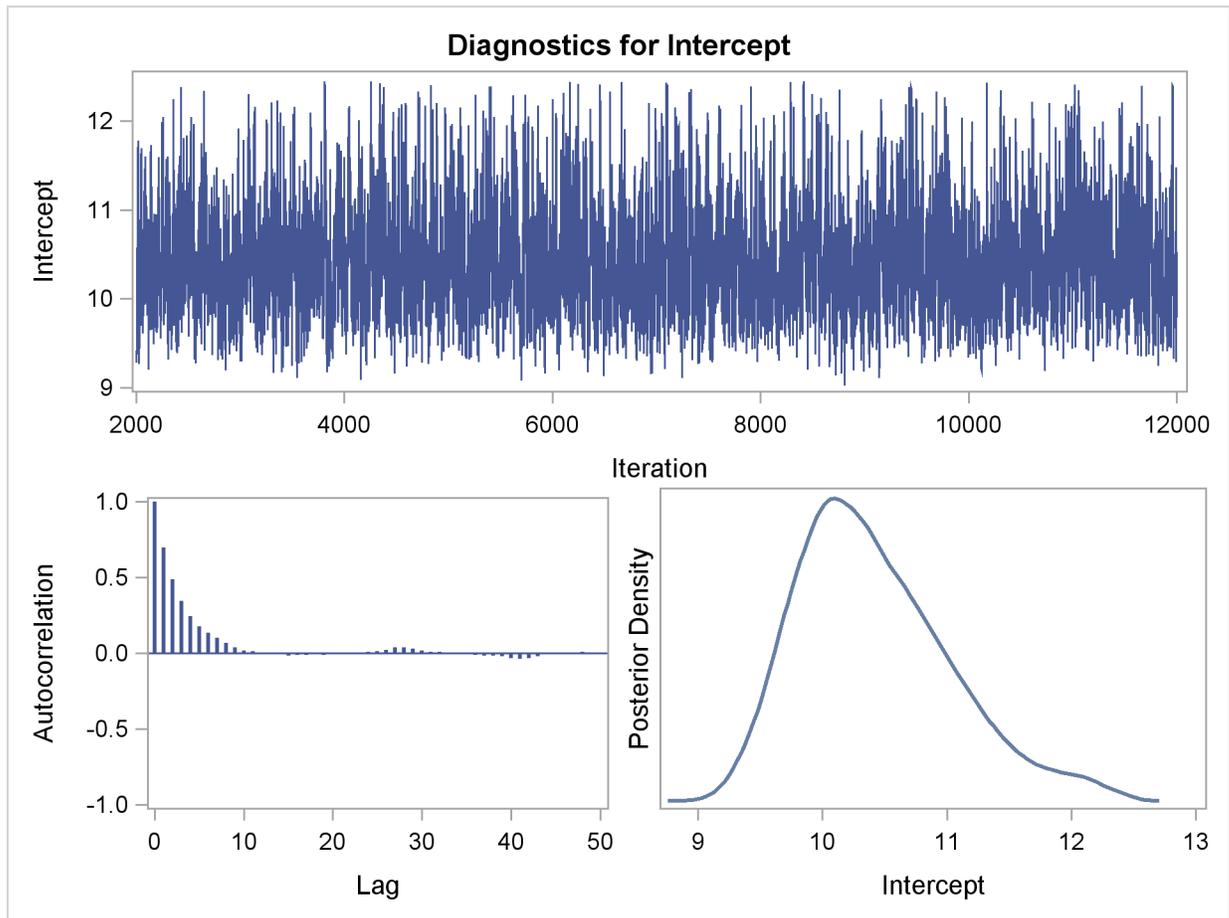
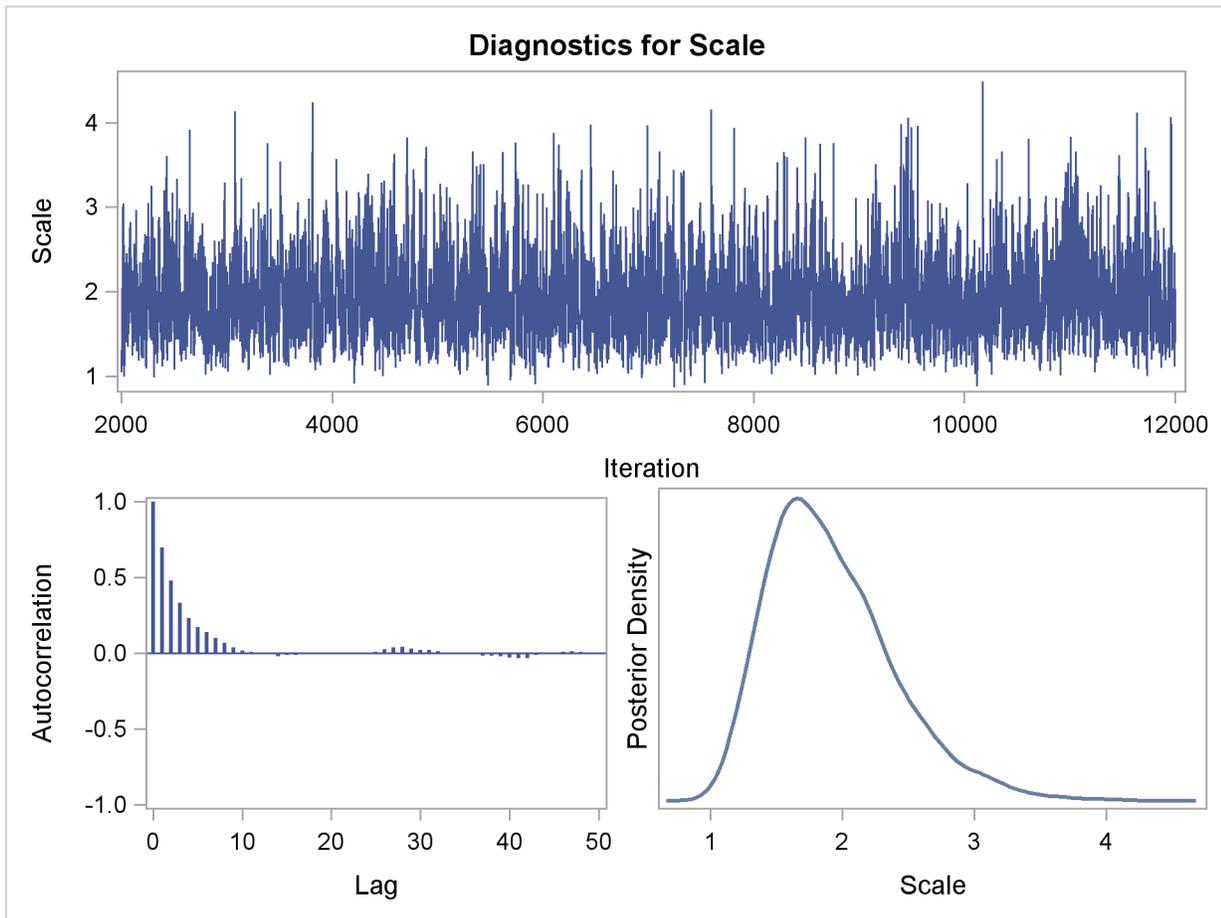


Figure 48.12 Diagnostic Plots



The fraction failing in the first 8000 hours of operation might be a quantity of interest. This kind of information could be useful, for example, in determining whether to improve the reliability of the engine components due to warranty considerations. The following SAS statements compute the mean and percentiles of the distribution of the fraction failing in the first 8000 hours from the posterior sample data set Post:

```
data Prob;
  set Post;
  Frac = ProbNorm(( log(8000) - Intercept ) / Scale );
  label Frac= 'Fraction Failing in 8000 Hours';
run;

proc means data = Prob(keep=Frac) n mean p10 p25 p50 p75 p90;
run;
```

The mean fraction of failures in the first 8000 hours, shown in Figure 48.13, is about 0.24, which could be used in further analysis of warranty costs. The 10th percentile is about 0.16 and the 90th percentile is about 0.32, which gives an assessment of the probable range of the fraction failing in the first 8000 hours.

Figure 48.13 Fraction Failing in 8000 Hours

The MEANS Procedure					
Analysis Variable : Frac Fraction Failing in 8000 Hours					
N	Mean	10th Pctl	25th Pctl	50th Pctl	75th Pctl
10000	0.2381467	0.1628591	0.1953691	0.2336756	0.2766051
Analysis Variable : Frac Fraction Failing in 8000 Hours					
			90th Pctl		

			0.3190883		

Syntax: LIFEREG Procedure

The following statements are available in PROC LIFEREG:

```

PROC LIFEREG < options > ;
  BY variables ;
  CLASS variables ;
  INSET < keyword-list > < / options > ;
  MODEL response=< effects > < / options > ;
  OUTPUT < OUT=SAS-data-set > < keyword=name ... keyword=name > < options > ;
  PROBPLOT < / options > ;
  WEIGHT variable ;

```

The PROC LIFEREG statement invokes the procedure. The MODEL statement is required and specifies the variables used in the regression part of the model as well as the distribution used for the error, or random, component of the model. Only a single MODEL statement can be used with one invocation of the LIFEREG procedure. If multiple MODEL statements are present, only the last is used. Main effects and interaction terms can be specified in the MODEL statement, as in the GLM procedure. Initial values can be specified in the MODEL statement or in an INEST= data set. If no initial values are specified, the starting estimates are obtained by ordinary least squares. The CLASS statement determines which explanatory variables are treated as categorical. The WEIGHT statement identifies a variable with values that are used to weight the observations. Observations with zero or negative weights are not used to fit the model, although predicted values can be computed for them. The OUTPUT statement creates an output data set containing predicted values and residuals.

PROC LIFEREG Statement

PROC LIFEREG < options > ;

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

COVOUT

writes the estimated covariance matrix to the OUTEST= data set if convergence is attained.

DATA=SAS-data-set

specifies the input SAS data set used by PROC LIFEREG. By default, the most recently created SAS data set is used.

GOUT=graphics-catalog

specifies a graphics catalog in which to save graphics output.

INEST=SAS-data-set

specifies an input SAS data set that contains initial estimates for all the parameters in the model. See the section “[INEST= Data Set](#)” on page 3656 for a detailed description of the contents of the INEST= data set.

NAMELEN=*n*

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

NOPRINT

suppresses the display of the output. Note that this option temporarily disables the Output Delivery System (ODS). For more information, see Chapter 20, “[Using the Output Delivery System](#).”

ORDER=DATA | FORMATTED | FREQ | INTERNAL

specifies the order in which to sort the levels of the classification variables (which are specified in the [CLASS](#) statement). This option applies to the levels for all classification variables, except when you use the (default) ORDER=FORMATTED option with numeric classification variables that have no explicit format. With this option, the levels of such variables are ordered by their internal value.

The ORDER= option can take the following values:

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

Table 48.0 *continued*

Value of ORDER=	Levels Sorted By
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*.

OUTEST=SAS-data-set

specifies an output SAS data set containing the parameter estimates, the maximized log likelihood, and, if the COVOUT option is specified, the estimated covariance matrix. See the section “OUTEST= Data Set” on page 3656 for a detailed description of the contents of the OUTEST= data set.

PLOTS=NONE | PROBPLOT

specifies the following graphics options:

- NONE suppresses any graphics specified in other LIFEREG statements, such as the BAYES or PROBPLOT statement.
- PROBPLOT creates a default probability plot based on information in the MODEL statement. If a PROBPLOT option is also specified, the probability plot specified in the PROBPLOT statement is created, and this option is ignored.

XDATA=SAS-data-set

specifies an input SAS data set that contains values for all the independent variables in the MODEL statement and variables in the CLASS statement for probability plotting. If there are covariates specified in a MODEL statement and a probability plot is requested with a PROBPLOT statement, you specify fixed values for the effects in the MODEL statement with the XDATA= data set. See the section “XDATA= Data Set” on page 3657 for a detailed description of the contents of the XDATA= data set.

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 model parameters can be output to a SAS data set.

Table 48.1 summarizes the options available in the BAYES statement.

Table 48.1 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
EXPONENTIALSCALEPRIOR=	Specifies the prior of the exponential scale parameter
GAMMASHAPEPRIOR=	Specifies the prior of the three-parameter gamma shape parameter
SCALEPRIOR=	Specifies the prior of the scale parameter
WEIBULLSCALEPRIOR=	Specifies the prior of the Weibull scale parameter
WEIBULLSHAPEPRIOR=	Specifies the prior of the Weibull shape 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=UNIFORM | NORMAL <(normal-options)>

CPRIOR=UNIFORM | NORMAL <(option)>

COEFF=UNIFORM | NORMAL <(option)>

specifies the prior distribution for the regression coefficients. The default is COEFFPRIOR=UNIFORM. The available prior distributions are as follows:

NORMAL<(normal-option)>

specifies a normal distribution. The *normal-options* include the following:

CONDITIONAL

specifies that the normal prior, conditional on the current Markov chain value of the location-scale model precision parameter $\tau = \frac{1}{\sigma^2}$, 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 that contains 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 LIFEREG 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.

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 3660 for more details.

UNIFORM

specifies a flat prior—that is, the prior that is proportional to a constant ($p(\beta_1, \dots, \beta_k) \propto 1$ for all $-\infty < \beta_i < \infty$).

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 168 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 168 for details.

GELMAN <(gelman-options)>

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

NCHAIN=number

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 160 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 162 for details.

HEIDELBERGER <(heidel-options)>

computes the Heidelberg 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 “[Heidelberg and Welch Diagnostics](#)” on page 164 for details.

MCSE

MCERROR

computes the Monte Carlo standard error for each parameter. The Monte Carlo standard error, which measures the simulation accuracy, is the standard error of the posterior mean estimate and is calculated as the posterior standard deviation divided by the square

root of the effective sample size. See the section “Standard Error of the Mean Estimate” on page 169 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 165 for details.

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

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

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

specifies that Gibbs sampling be performed on the exponential distribution scale parameter and the prior distribution for the scale parameter. This prior distribution applies only when the exponential distribution and no covariates are specified.

A gamma prior $G(a, b)$ with density $f(t) = \frac{b(bt)^{a-1}e^{-bt}}{\Gamma(a)}$ is specified by **EXPSCALEPRIOR=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 3660 for more details. The default is $G(10^{-4}, 10^{-4})$.

RELSHAPE< =*c* >

specifies independent $G(c\hat{\alpha}, c)$ distribution, where $\hat{\alpha}$ is the MLE of the exponential scale parameter. With this choice of hyperparameters, the mean of the prior distribution is $\hat{\alpha}$ and the variance is $\frac{\hat{\alpha}}{c^2}$. By default, $c=10^{-4}$.

SHAPE=*a*

ISCALE=*b*

when both specified, results in a $G(a, b)$ prior.

SHAPE=*c*

when specified alone, results in a $G(c, c)$ prior.

ISCALE=*c*

when specified alone, results in a $G(c, c)$ prior.

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

GAMMASHAPEPRIOR=NORMAL<(options)>**GAMASHAPEPRIOR=NORMAL<(options)>****SHAPE1PRIOR=NORMAL<(options)>**

specifies the prior distribution for the gamma distribution shape parameter. If you do not specify any options in a gamma model, the $N(0, 10^6)$ prior for the shape is used. You can specify `MEAN=` and `VAR=` or `RELVAR=` options, either alone or together, to specify the mean and variance of the normal prior for the gamma shape parameter.

MEAN=*a*

specifies a normal prior $N(a, 10^6)$. By default, $a=0$.

RELVAR=<*b*>

specifies the normal prior $N(0, bJ)$, where J is the variance of the MLE of the shape parameter. By default, $b=10^6$.

VAR=*c*

specifies the normal prior $N(0, c)$. By default, $c=10^6$.

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 3662 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 ;
```

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 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 lifereg;
  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 155 for details.

SCALEPRIOR=GAMMA<(options)>

specifies that Gibbs sampling be performed on the location-scale model scale parameter and the prior distribution for the scale parameter.

A gamma prior $G(a, b)$ with density $f(t) = \frac{b(bt)^{a-1}e^{-bt}}{\Gamma(a)}$ 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 3660 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 scale 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***ISCALE=*b***

when both specified, results in a $G(a, b)$ prior.

SHAPE=*c*

when specified alone, results in a $G(c, c)$ prior.

ISCALE=*c*

when specified alone, results in a $G(c, c)$ prior.

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-statoptions)> = 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 169 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 $100(1-\text{ALPHA})\%$ equal-tail and HPD intervals for each parameters. The default is ALPHA=0.05, which yields 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 yields 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 default 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.

NONE

suppresses printing all summary statistics.

THINNING=number**THIN=number**

controls the thinning of the Markov chain. Only one in every k samples is used when $\text{THINNING}=k$, and if $\text{NBI}=n_0$ and $\text{NMC}=n$, 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 $\text{THINNING}=1$.

WEIBULLSCALEPRIOR=GAMMA<(options)>**WSCALEPRIOR=GAMMA<(options)>****WSCPRIOR=GAMMA<(options)>**

specifies that Gibbs sampling be performed on the Weibull model scale parameter and the prior distribution for the scale parameter. This option applies only when a Weibull distribution and no covariates are specified. When this option is specified, PROC LIFEREG performs Gibbs sampling on the Weibull scale parameter, which is defined as $\exp(\mu)$, where μ is the intercept term.

A gamma prior $G(a, b)$ is specified by $\text{WEIBULLSCALEPRIOR=GAMMA}$, which can be followed by one of the following *gamma-options* enclosed in parentheses. The gamma probability density is given by $g(t) = \frac{b(bt)^{a-1}e^{-bt}}{\Gamma(a)}$. The hyperparameters a and b are the shape and inverse-scale parameters of the gamma distribution, respectively. See the section “Gamma Prior” on page 3660 for details about the gamma prior. The default is $G(10^{-4}, 10^{-4})$.

RELSHAPE<=c>

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

SHAPE=a**ISCALE=b**

when both specified, results in a $G(a, b)$ prior.

SHAPE=c

when specified alone, results in a $G(c, c)$ prior.

ISCALE=c

when specified alone, results in a $G(c, c)$ prior.

WEIBULLSHAPEPRIOR=GAMMA<(options)>**WSHAPEPRIOR=GAMMA<(options)>****WSHPRIOR=GAMMA<(options)>**

specifies that Gibbs sampling be performed on the Weibull model shape parameter and the prior distribution for the shape parameter. When this option is specified, PROC LIFEREG

performs Gibbs sampling on the Weibull shape parameter, which is defined as σ^{-1} , where σ is the location-scale model scale parameter.

A gamma prior $G(a, b)$ with density $f(t) = \frac{b(bt)^{a-1}e^{-bt}}{\Gamma(a)}$ is specified by WEIBULL-SHAPEPRIOR=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 3660 for details about the gamma prior. The default is $G(10^{-4}, 10^{-4})$.

RELSHAPE<=c>

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

SHAPE<=a>

ISCALE=b

when both specified, results in a $G(a, b)$ prior.

SHAPE=c

when specified alone, results in a $G(c, c)$ prior.

ISCALE=c

when specified alone, results in a $G(c, c)$ prior.

BY Statement

BY variables ;

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

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

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

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

CLASS Statement

CLASS *variables* </ TRUNCATE > ;

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

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

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

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

TRUNCATE

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

INSET Statement

INSET < *keyword-list* > </ options > ;

The box or table of summary information produced on plots made with the PROBLOT statement is called an *inset*. You can use the INSET statement to customize the information that is displayed in the inset box as well as to customize the appearance of the inset box. To supply the information that is displayed in the inset box, you specify *keywords* corresponding to the information that you want shown. For example, the following statements produce a probability plot with the number of observations, the number of right-censored observations, the name of the distribution, and the estimated Weibull shape parameter in the inset:

```
proc lifereg data=epidemic;
  model life = dose / dist = Weibull;
  probplot ;
  inset nobs right dist shape;
run;
```

By default, inset entries are identified with appropriate labels. However, you can provide a customized label by specifying the *keyword* for that entry followed by the equal sign (=) and the label in quotes.

For example, the following INSET statement produces an inset containing the number of observations and the name of the distribution, labeled “Sample Size” and “Distribution” in the inset:

```
inset nobs='Sample Size' dist='Distribution';
```

If you specify a keyword that does not apply to the plot you are creating, then the keyword is ignored.

If you specify more than one INSET statement, only the first one is used.

Table 48.2 lists keywords available in the INSET statement to display summary statistics, distribution parameters, and distribution fitting information.

Table 48.2 INSET Statement Keywords

Keyword	Description
CONFIDENCE	Confidence coefficient for all confidence intervals
DIST	Name of the distribution
INTERVAL	Number of interval-censored observations
LEFT	Number of left-censored observations
NOBS	Number of observations
NMISS	Number of observations with missing values
RIGHT	Number of right-censored observations
SCALE	Value of the scale parameter
SHAPE	Value of the shape parameter
UNCENSORED	Number of uncensored observations

The following *options* control the appearance of the box when you use traditional graphics. These options are not available if ODS Graphics is enabled. All *options* are specified after the slash (/) in the INSET statement.

CFILL=*color*

specifies the color for the filling box.

CFILLH=*color*

specifies the color for the filling box header.

CFRAME=*color*

specifies the color for the frame.

CHEADER=*color*

specifies the color for text in the header.

CTEXT=*color*

specifies the color for the text.

FONT=font

specifies the software font for the text.

HEIGHT=value

specifies the height of the text.

HEADER='quoted string'

specifies the text for the header or box title.

NOFRAME

omits the frame around the box.

POS=value < DATA | PERCENT >

determines the position of the inset. The *value* can be a compass point (N, NE, E, SE, S, SW, W, NW) or a pair of coordinates (x, y) enclosed in parentheses. The coordinates can be specified in screen percentage units or axis data units. The default is screen percentage units.

REFPOINT=name

specifies the reference point for an inset that is positioned by a pair of coordinates with the POS= option. You use the REFPOINT= option in conjunction with the POS= coordinates. The REFPOINT= option specifies which corner of the inset frame you have specified with coordinates (x, y), and it can take the value of BR (bottom right), BL (bottom left), TR (top right), or TL (top left). The default is REFPOINT=BL. If the inset position is specified as a compass point, then the REFPOINT= option is ignored.

MODEL Statement

<label:> MODEL response< *censor(list)>=effects </ options > ;

<label:> MODEL (lower,upper)=effects </ options > ;

<label:> MODEL events/trials=effects </ options > ;

Only a single MODEL statement can be used with one invocation of the LIFEREG procedure. If multiple MODEL statements are present, only the last is used. The optional *label* is used to label the model estimates in the output SAS data set and OUTEST= data set.

The first MODEL syntax is appropriate for right censoring. The variable *response* is possibly right censored. If the *response* variable can be right censored, then a second variable, denoted *censor*, must appear after the *response* variable with a list of parenthesized values, separated by commas or blanks, to indicate censoring. That is, if the *censor* variable takes on a value given in the list, the *response* is a right-censored value; otherwise, it is an observed value.

The second MODEL syntax specifies two variables, *lower* and *upper*, that contain values of the endpoints of the censoring interval. If the two values are the same (and not missing), it is assumed that there is no censoring and the actual response value is observed. If the lower value is missing, then the upper value is used as a left-censored value. If the upper value is missing, then the lower value is taken as a right-censored value. If both values are present and the lower value is less than the

upper value, it is assumed that the values specify a censoring interval. If the lower value is greater than the upper value or both values are missing, then the observation is not used in the analysis, although predicted values can still be obtained if none of the covariates are missing. The following table summarizes the ways of specifying censoring.

<i>lower</i>	<i>upper</i>	Comparison	Interpretation
Not missing	Not missing	Equal	No censoring
Not missing	Not missing	Lower < upper	Censoring interval
Missing	Not missing		Upper used as left-censoring value
Not missing	Missing		Lower used as right-censoring value
Not missing	Not missing	Lower > upper	Observation not used
Missing	Missing		Observation not used

The third MODEL syntax specifies two variables that contain count data for a binary response. The value of the first variable, *events*, is the number of successes. The value of the second variable, *trials*, is the number of tries. The values of both *events* and (*trials-events*) must be nonnegative, and *trials* must be positive for the response to be valid. The values of the two variables do not need to be integers and are not modified to be integers.

The *effects* following the equal sign are the covariates in the model. Higher-order effects, such as interactions and nested terms, are allowed in the list, similar to the GLM procedure. Variable names and combinations of variable names representing higher-order terms are allowed to appear in this list. Classification, or CLASS, variables can be used as effects, and indicator variables are generated for the class levels. If you do not specify any covariates following the equal sign, an intercept-only model is fit.

Examples of three valid MODEL statements follow:

```
a: model time*flag(1,3)=temp;
```

```
b: model (start, finish)=;
```

```
c: model r/n=dose;
```

MODEL statement a indicates that the response is contained in a variable named time and that, if the variable flag takes on the values 1 or 3, the observation is right censored. The explanatory variable is temp, which could be a CLASS variable. MODEL statement b indicates that the response is known to be in the interval between the values of the variables start and finish and that there are no covariates except for a default intercept term. MODEL statement c indicates a binary response, with the variable r containing the number of responses and the variable n containing the number of trials.

The following options can appear in the MODEL statement.

Task	Option
Model specification	
Sets the significance level	ALPHA=
Specifies the distribution type for failure time	DISTRIBUTION=
Requests no log transformation of response	NOLOG
Initial estimate for intercept term	INTERCEPT=
Holds the intercept term fixed	NOINT
Initial estimates for regression parameters	INITIAL=
Initializes the scale parameter	SCALE=
Holds the scale parameter fixed	NOSCALE
Initializes the first shape parameter	SHAPE1=
Holds the first shape parameter fixed	NOSHAPE1
Model fitting	
Sets the convergence criterion	CONVERGE=
Sets the maximum number of iterations	MAXITER=
Sets the tolerance for testing singularity	SINGULAR=
Output	
Displays the estimated correlation matrix	CORRB
Displays the estimated covariance matrix	COVB
Displays the iteration history, final gradient, and second derivative matrix	ITPRINT

ALPHA=*value*

sets the significance level for the confidence intervals for regression parameters and estimated survival probabilities. The value must be between 0 and 1. By default, ALPHA=0.05.

CONVERGE=*value*

sets the convergence criterion. Convergence is declared when the maximum change in the parameter estimates between Newton-Raphson 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-8.

CONVG=*value*

sets the relative Hessian convergence criterion; *value* 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 *value*, 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 *value*, a warning that the relative Hessian convergence criterion has been exceeded is displayed. 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, CONVG=1E-4.

CORRB

produces the estimated correlation matrix of the parameter estimates.

COVB

produces the estimated covariance matrix of the parameter estimates.

DISTRIBUTION=*distribution-type*

DIST=*distribution-type*

D=*distribution-type*

specifies the distribution type assumed for the failure time. By default, PROC LIFEREG fits a type 1 extreme-value distribution to the log of the response. This is equivalent to fitting the Weibull distribution, since the scale parameter for the extreme-value distribution is related to a Weibull shape parameter and the intercept is related to the Weibull scale parameter in this case. When the NOLOG option is specified, PROC LIFEREG models the untransformed response with a type 1 extreme-value distribution as the default. See the section “Supported Distributions” on page 3644 for descriptions of the distributions. The following are valid values for *distribution-type*:

EXPONENTIAL	the exponential distribution, which is treated as a restricted Weibull distribution
GAMMA	a generalized gamma distribution (Lawless 2003, p. 240). The standard two-parameter gamma distribution is not available in PROC LIFEREG.
LLOGISTIC	a log-logistic distribution
LNORMAL	a lognormal distribution
LOGISTIC	a logistic distribution (equivalent to LLOGISTIC when the NOLOG option is specified)
NORMAL	a normal distribution (equivalent to LNORMAL when the NOLOG option is specified)
WEIBULL	a Weibull distribution. If NOLOG is specified, it fits a type 1 extreme-value distribution to the raw, untransformed data.

By default, PROC LIFEREG transforms the response with the natural logarithm before fitting the specified model when you specify the GAMMA, LLOGISTIC, LNORMAL, or WEIBULL option. You can suppress the log transformation with the NOLOG option. The following table summarizes the resulting distributions when the preceding distribution options are used in combination with the NOLOG option.

DISTRIBUTION=	NOLOG Specified?	Resulting Distribution
EXPONENTIAL	No	Exponential
EXPONENTIAL	Yes	One-parameter extreme value
GAMMA	No	Generalized log-gamma using the log of the response. (This is the same as fitting the generalized gamma using the untransformed response.)
GAMMA	Yes	Generalized log-gamma with untransformed responses
LOGISTIC	No	Logistic
LOGISTIC	Yes	Logistic (NOLOG has no effect)
LLOGISTIC	No	Log-logistic
LLOGISTIC	Yes	Logistic
LNORMAL	No	Lognormal
LNORMAL	Yes	Normal
NORMAL	No	Normal
NORMAL	Yes	Normal (NOLOG has no effect)
WEIBULL	No	Weibull
WEIBULL	Yes	Extreme value

INITIAL=values

sets initial values for the regression parameters. This option can be helpful in the case of convergence difficulty. Specified values are used to initialize the regression coefficients for the covariates specified in the MODEL statement. 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 are listed in the MODEL statement. Note that a CLASS variable requires $k - 1$ values when the CLASS variable takes on k different levels. The order of the CLASS levels is determined by the ORDER= option. If there is no intercept term, the first CLASS variable requires k initial values. If a BY statement is used, all CLASS variables must take on the same number of levels in each BY group or no meaningful initial values can be specified. The INITIAL= option can be specified as follows.

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 methods	initial=1,3 to 5,9

By default, PROC LIFEREG computes initial estimates with ordinary least squares. See the section “[Computational Method](#)” on page 3642 for details.

NOTE: The INITIAL= option is overwritten by the INEST= option. See the section “[INEST= Data Set](#)” on page 3656 for details.

INTERCEPT=value

initializes the intercept term to *value*. By default, the intercept is initialized by an ordinary least squares estimate.

ITPRINT

displays the iteration history for computing maximum likelihood estimates, the final evaluation of the gradient, and the final evaluation of the negative of the second derivative matrix—that is, the negative of the Hessian. 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.

MAXITER=*n*

sets the maximum allowable number of iterations during the model estimation. By default, MAXITER=50.

NOINT

holds the intercept term fixed. Because of the usual log transformation of the response, the intercept parameter is usually a scale parameter for the untransformed response, or a location parameter for a transformed response.

NOLOG

requests that no log transformation of the response variable be performed. By default, PROC LIFEREG models the log of the response variable for the GAMMA, LLOGISTIC, LOGNORMAL, and WEIBULL distribution options. NOLOG is implicitly assumed for the NORMAL and LOGISTIC distribution options.

NOSCALE

holds the scale parameter fixed. Note that if the log transformation has been applied to the response, the effect of the scale parameter is a power transformation of the original response. If no SCALE= value is specified, the scale parameter is fixed at the value 1.

NOSHAPE1

holds the first shape parameter, SHAPE1, fixed. If no SHAPE1= value is specified, SHAPE1 is fixed at a value that depends on the DISTRIBUTION type.

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.

SCALE=*value*

initializes the scale parameter to *value*. If the Weibull distribution is specified, this scale parameter is the scale parameter of the type 1 extreme-value distribution, not the Weibull scale parameter. Note that, with a log transformation, the exponential model is the same as a Weibull model with the scale parameter fixed at the value 1.

SHAPE1=*value*

initializes the first shape parameter to *value*. If the specified distribution does not depend on this parameter, then this option has no effect. The only distribution that depends on this shape parameter is the generalized gamma distribution. See the section “Supported Distributions” on page 3644 for descriptions of the parameterizations of the distributions.

SINGULAR=*value*

sets the tolerance for testing singularity of the information matrix and the crossproducts matrix for the initial least squares estimates. Roughly, the test requires that a pivot be at least this value times the original diagonal value. By default, SINGULAR=1E-12.

OUTPUT Statement

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

The OUTPUT statement creates a new SAS data set containing statistics calculated after fitting the model. At least one specification of the form *keyword=name* is required.

All variables in the original data set are included in the new data set, along with the variables created as options for the OUTPUT statement. These new variables contain fitted values and estimated quantiles. If you want to create a permanent SAS data set, you must specify a two-level name (see *SAS Language Reference: Concepts* for more information about permanent SAS data sets). Each OUTPUT statement applies to the preceding MODEL statement. See [Example 48.1](#) for illustrations of the OUTPUT statement.

The following specifications can appear in the OUTPUT statement:

OUT=SAS-data-set specifies the new data set. By default, the procedure uses the *DATA*n** convention to name the new data set.

keyword=name specifies the statistics to include in the output data set and gives names to the new variables. Specify a keyword for each desired statistic (see the following list of keywords), an equal sign, and the variable to contain the statistic.

The keywords allowed and the statistics they represent are as follows:

CENSORED specifies an indicator variable to signal censoring. The variable takes on the value 1 if the observation is censored; otherwise, it is 0.

CDF specifies a variable to contain the estimates of the cumulative distribution function evaluated at the observed response. See the section “[Predicted Values](#)” on page 3648 for more information.

CONTROL specifies a variable in the input data set to control the estimation of quantiles. See [Example 48.1](#) for an illustration. If the specified variable has the value 1, estimates for all the values listed in the **QUANTILE=** list are computed for that observation in the input data set; otherwise, no estimates are computed. If no **CONTROL=** variable is specified, all quantiles are estimated for all observations. If the response variable in the MODEL statement is binomial, then this option has no effect.

CRESIDUAL | CRES specifies a variable to contain the Cox-Snell residuals

$$-\log(S(u_i))$$

where S is the standard survival function and

$$u_i = \frac{y_i - \mathbf{x}_i' \mathbf{b}}{\sigma}$$

If the response variable in the corresponding model statement is binomial, then the residuals are not computed, and this variable contains missing values.

SRESIDUAL | SRES specifies a variable to contain the standardized residuals

$$\frac{y_i - \mathbf{x}'_i \mathbf{b}}{\sigma}$$

If the response variable in the corresponding model statement is binomial, then the residuals are not computed, and this variable contains missing values.

PREDICTED | P specifies a variable to contain the quantile estimates. If the response variable in the corresponding model statement is binomial, then this variable contains the estimated probabilities, $1 - F(-\mathbf{x}'\mathbf{b})$.

QUANTILES | QUANTILE | Q gives a list of values for which quantiles are calculated. The values must be between 0 and 1, noninclusive. For each value, a corresponding quantile is estimated. This option is not used if the response variable in the corresponding MODEL statement is binomial. The QUANTILES option can be specified as follows.

Type of List	Specification
List separated by blanks	.2 .4 .6 .8
List separated by commas	.2, .4, .6, .8
x to y	.2 to .8
x to y by z	.2 to .8 by .1
Combination of methods	.1, .2 to .8 by .2

By default, QUANTILES=0.5. When the response is not binomial, a numeric variable, _PROB_, is added to the OUTPUT data set whenever the QUANTILES= option is specified. The variable _PROB_ gives the probability value for the quantile estimates. These are the values taken from the QUANTILES= list and are given as values between 0 and 1, not as values between 0 and 100.

STD_ERR | STD specifies a variable to contain the estimates of the standard errors of the estimated quantiles or $\mathbf{x}'\mathbf{b}$. If the response used in the MODEL statement is a binomial response, then these are the standard errors of $\mathbf{x}'\mathbf{b}$. Otherwise, they are the standard errors of the quantile estimates. These estimates can be used to compute confidence intervals for the quantiles. However, if the model is fit to the log of the event time, better confidence intervals can usually be computed by transforming the confidence intervals for the log response. See [Example 48.1](#) for such a transformation.

XBETA specifies a variable to contain the computed value of $\mathbf{x}'\mathbf{b}$, where \mathbf{x} is the covariate vector and \mathbf{b} is the vector of parameter estimates.

PROBPLOT Statement

PROBPLOT | PLOT *</ options>* ;

You can use the PROBPLOT statement to create a probability plot from lifetime data. The data can be uncensored, right censored, or arbitrarily censored. You can specify any number of PROBPLOT statements after a MODEL statement. The syntax used for the response in the MODEL statement determines the type of censoring assumed in creating the probability plot. The model fit with the MODEL statement is plotted along with the data. If there are covariates in the model, they are set to constant values specified in the XDATA= data set when creating the probability plot. If no XDATA= data set is specified, continuous variables are set to their overall mean values and categorical variables specified in the CLASS statement are set to their highest levels.

You can specify the following options to control the content, layout, and appearance of a probability plot.

Traditional Graphics

The following options are available if you use traditional graphics—that is, if ODS Graphics is not enabled.

ANNOTATE=*SAS-data-set*

ANNO=*SAS-data-set*

specifies an Annotate data set, as described in *SAS/GRAPH Software: Reference*, that enables you to add features to the probability plot. The data set you specify with the ANNOTATE= option in the PROBPLOT statement provides the Annotate data set for all plots created by the statement.

CAXIS=*color*

CAXES=*color*

specifies the color used for the axes and tick marks. This option overrides any COLOR= specifications in an AXIS statement. The default is the first color in the device color list.

CCENSOR=*color*

specifies the color for filling the censor plot area. The default is the first color in the device color list.

CENBIN

plots censored data as frequency counts (rounding for noninteger frequency) rather than as individual points.

CENCOLOR=*color*

specifies the color for the censor symbol. The default is the first color in the device color list.

CENSYMBOL=*symbol* | (*symbol list*)

specifies symbols for censored values. The *symbol* is one of the symbol names (plus, star, square, diamond, triangle, hash, paw, point, dot, and circle) or a letter (A–Z). If you do not

specify the CENSYMBOL= option, the symbol used for censored values is the same as for failures.

CFIT=*color*

specifies the color for the fitted probability line and confidence curves. The default is the first color in the device color list.

CFRAME=*color***CFR=***color*

specifies the color for the area enclosed by the axes and frame. This area is not shaded by default.

CGRID=*color*

specifies the color for grid lines. The default is the first color in the device color list.

CHREF=*color***CH=***color*

specifies the color for lines requested by the HREF= option. The default is the first color in the device color list.

CTEXT=*color*

specifies the color for tick mark values and axis labels. The default is the color specified for the CTEXT= option in the most recent GOPTIONS statement.

CVREF=*color***CV=***color*

specifies the color for lines requested by the VREF= option. The default is the first color in the device color list.

DESCRIPTION='*string*'**DES=**'*string*'

specifies a description, up to 40 characters, that appears in the PROC GREPLAY master menu. The default is the variable name.

FONT=*font*

specifies a software font for reference line and axis labels. You can also specify fonts for axis labels in an AXIS statement. The FONT= font takes precedence over the FTEXT= font specified in the most recent GOPTIONS statement. Hardware characters are used by default.

HCL

computes and draws confidence limits for the predicted probabilities in the horizontal direction.

HEIGHT=*value*

specifies the height of text used outside framed areas. The default value is 3.846 (in percentage).

HLOWER=*value*

specifies the lower limit on the lifetime axis scale. The HLOWER= option specifies *value* as the lower lifetime axis tick mark. The tick mark interval and the upper axis limit are determined automatically.

HOFFSET=*value*

specifies the offset for the horizontal axis. The default value is 1.

HUPPER=*value*

specifies *value* as the upper lifetime axis tick mark. The tick mark interval and the lower axis limit are determined automatically.

HREF < (INTERSECT) > =*value-list*

requests reference lines perpendicular to the horizontal axis. If (INTERSECT) is specified, a second reference line perpendicular to the vertical axis is drawn that intersects the fit line at the same point as the horizontal axis reference line. If a horizontal axis reference line label is specified, the intersecting vertical axis reference line is labeled with the vertical axis value. See also the CHREF=, HREFLABELS=, and LHREF= options.

HREFLABELS='*label1*' ... '*labeln*'**HREFLABEL=**'*label1*' ... '*labeln*'**HREFLAB=**'*label1*' ... '*labeln*'

specifies labels for the lines requested by the HREF= option. The number of labels must equal the number of lines. Enclose each label in quotes. Labels can be up to 16 characters.

HREFLABPOS=*n*

specifies the vertical position of labels for HREF= lines. The following table shows the valid values for *n* and the corresponding label placements.

<i>n</i>	Label Placement
1	Top
2	Staggered from top
3	Bottom
4	Staggered from bottom
5	Alternating from top
6	Alternating from bottom

INBORDER

requests a border around probability plots.

INTERTILE=*value*

specifies the distance between tiles.

ITPRINTEM

displays the iteration history for the Turnbull algorithm.

JITTER=*value*

specifies the amount to jitter overlaying plot symbols, in units of symbol width.

LFIT=*linetype*

specifies a line style for fitted curves and confidence limits. By default, fitted curves are drawn by connecting solid lines (*linetype* = 1), and confidence limits are drawn by connecting dashed lines (*linetype* = 3).

LGRID=*linetype*

specifies a line style for all grid lines; *linetype* is between 1 and 46. The default is 35.

LHREF=*linetype***LH=***linetype*

specifies the line type for lines requested by the HREF= option. The default is 2, which produces a dashed line.

LVREF=*linetype***LV=***linetype*

specifies the line type for lines requested by the VREF= option. The default is 2, which produces a dashed line.

MAXITEM=*n1 <,n2> n1*

specifies the maximum number of iterations allowed for the Turnbull algorithm. Iteration history will be displayed in increments of *n2* if requested with the ITPRINTEM option. See the section “Arbitrarily Censored Data” on page 3654 for details.

NAME=*'string'*

specifies a name for the plot, up to eight characters, that appears in the PROC GREPLAY master menu. The default is 'LIFEREG'.

NOCENPLOT

suppresses the plotting of censored data points.

NOCONF

suppresses the default confidence bands on the probability plot.

NODATA

suppresses plotting of the estimated empirical probability plot.

NOFIT

suppresses the fitted probability (percentile) line and confidence bands.

NOFRAME

suppresses the frame around plotting areas.

NOGRID

suppresses grid lines.

NOHLABEL

suppresses horizontal labels.

NOHTICK

suppresses horizontal tick marks.

NOPOLISH

suppresses setting small interval probabilities to zero in the Turnbull algorithm.

NOVLABEL

suppresses vertical labels.

NOVTICK

suppresses vertical tick marks.

NPINTERVALS=*interval type*

specifies one of the two kinds of confidence limits for the estimated cumulative probabilities, pointwise (NPINTERVALS=POINT) or simultaneous (NPINTERVALS=SIMUL), requested by the PPOUT option to be displayed in the tabular output.

PCTLIST=*value-list*

specifies the list of percentages for which to compute percentile estimates; *value-list* must be a list of values separated by blanks or commas. Each value in the list must be between 0 and 100.

PLOWER=*value*

specifies the lower limit on the probability axis scale. The PLOWER= option specifies *value* as the lower probability axis tick mark. The tick mark interval and the upper axis limit are determined automatically.

PRINTPROBS

displays intervals and associated probabilities for the Turnbull algorithm.

PUPPER=*value*

specifies the upper limit on the probability axis scale. The PUPPER= option specifies *value* as the upper probability axis tick mark. The tick mark interval and the lower axis limit are determined automatically.

PPOS=*character-list*

specifies the plotting position type. See the section “[Probability Plotting](#)” on page 3651 for details.

PPOS	Method
EXPRANK	Expected ranks
MEDRANK	Median ranks
MEDRANK1	Median ranks (exact formula)
KM	Kaplan-Meier
MKM	Modified Kaplan-Meier (default)

PPOUT

specifies that a table of the cumulative probabilities plotted on the probability plot be displayed. Kaplan-Meier estimates of the cumulative probabilities are also displayed, along with standard errors and confidence limits. The confidence limits can be pointwise or simultaneous, as specified by the NPINTERVALS= option.

PROBLIST=*value-list*

specifies the list of initial values for the Turnbull algorithm.

ROTATE

requests probability plots with probability scale on the horizontal axis.

SQUARE

makes the layout of the probability plots square.

TOLLIKE=*value*

specifies the criterion for convergence in the Turnbull algorithm.

TOLPROB=*value*

specifies the criterion for setting the interval probability to zero in the Turnbull algorithm.

VAXISLABEL='*string*'

specifies a label for the vertical axis.

VREF=*value-list*

requests reference lines perpendicular to the vertical axis. If (INTERSECT) is specified, a second reference line perpendicular to the horizontal axis is drawn that intersects the fit line at the same point as the vertical axis reference line. If a vertical axis reference line label is specified, the intersecting horizontal axis reference line is labeled with the horizontal axis value. See also the entries for the CVREF=, LVREF=, and VREFLABELS= options.

VREFLABELS='*label1*' ... '*labeln*'**VREFLABEL=**'*label1*' ... '*labeln*'**VREFLAB=**'*label1*' ... '*labeln*'

specifies labels for the lines requested by the VREF= option. The number of labels must equal the number of lines. Enclose each label in quotes. Labels can be up to 16 characters.

VREFLABPOS=*n*specifies the horizontal position of labels for VREF= lines. The valid values for *n* and the corresponding label placements are shown in the following table.

<i>n</i>	Label Placement
1	Left
2	Right

WAXIS=*n*

specifies line thickness for axes and frame. The default value is 1.

WFIT=*n*

specifies line thickness for fitted curves. The default value is 1.

WGRID=*n*

specifies line thickness for grids. The default value is 1.

WREFL=*n*

specifies line thickness for reference lines. The default value is 1.

ODS Graphics

The following options are available if ODS Graphics is enabled.

HCL

computes and draws confidence limits for the predicted probabilities in the horizontal direction.

HLOWER=*value*specifies the lower limit on the lifetime axis scale. The HLOWER= option specifies *value* as the lower lifetime axis tick mark. The tick mark interval and the upper axis limit are determined automatically.

HUPPER=*value*

specifies *value* as the upper lifetime axis tick mark. The tick mark interval and the lower axis limit are determined automatically.

HREF <(INTERSECT)> =*value-list*

requests reference lines perpendicular to the horizontal axis. If (INTERSECT) is specified, a second reference line perpendicular to the vertical axis is drawn that intersects the fit line at the same point as the horizontal axis reference line. If a horizontal axis reference line label is specified, the intersecting vertical axis reference line is labeled with the vertical axis value. See also the CHREF=, HREFLABELS=, and LHREF= options.

HREFLABELS='label1' ... 'labeln'**HREFLABEL='label1' ... 'labeln'****HREFLAB='label1' ... 'labeln'**

specifies labels for the lines requested by the HREF= option. The number of labels must equal the number of lines. Enclose each label in quotes. Labels can be up to 16 characters.

ITPRINTEM

displays the iteration history for the Turnbull algorithm.

MAXITEM=*n1* < ,*n2*> *n1*

specifies the maximum number of iterations allowed for the Turnbull algorithm. Iteration history will be displayed in increments of *n2* if requested with the ITPRINTEM option. See the section “[Arbitrarily Censored Data](#)” on page 3654 for details.

NOCENPLOT

suppresses the plotting of censored data points.

NOCONF

suppresses the default confidence bands on the probability plot.

NODATA

suppresses plotting of the estimated empirical probability plot.

NOFIT

suppresses the fitted probability (percentile) line and confidence bands.

NOFRAME

suppresses the frame around plotting areas.

NOGRID

suppresses grid lines.

NOPOLISH

suppresses setting small interval probabilities to zero in the Turnbull algorithm.

NPINTERVALS=*interval type*

specifies one of the two kinds of confidence limits for the estimated cumulative probabilities, pointwise (NPINTERVALS=POINT) or simultaneous (NPINTERVALS=SIMUL), requested by the PPOUT option to be displayed in the tabular output.

PCTLIST=*value-list*

specifies the list of percentages for which to compute percentile estimates; *value-list* must be a list of values separated by blanks or commas. Each value in the list must be between 0 and 100.

PLOWER=*value*

specifies the lower limit on the probability axis scale. The PLOWER= option specifies *value* as the lower probability axis tick mark. The tick mark interval and the upper axis limit are determined automatically.

PRINTPROBS

displays intervals and associated probabilities for the Turnbull algorithm.

PUPPER=*value*

specifies the upper limit on the probability axis scale. The PUPPER= option specifies *value* as the upper probability axis tick mark. The tick mark interval and the lower axis limit are determined automatically.

PPOS=*plotting-position-type*

specifies the plotting position type. See the section “Probability Plotting” on page 3651 for details.

PPOS	Method
EXPRANK	Expected ranks
MEDRANK	Median ranks
MEDRANK1	Median ranks (exact formula)
KM	Kaplan-Meier
MKM	Modified Kaplan-Meier (default)

PPOUT

specifies that a table of the cumulative probabilities plotted on the probability plot be displayed. Kaplan-Meier estimates of the cumulative probabilities are also displayed, along with standard errors and confidence limits. The confidence limits can be pointwise or simultaneous, as specified by the NPINTERVALS= option.

PROBLIST=*value-list*

specifies the list of initial values for the Turnbull algorithm.

ROTATE

requests probability plots with probability scale on the horizontal axis.

SQUARE

makes the layout of the probability plots square.

TOLLIKE=*value*

specifies the criterion for convergence in the Turnbull algorithm.

TOLPROB=*value*

specifies the criterion for setting the interval probability to zero in the Turnbull algorithm.

VREF=*value-list*

requests reference lines perpendicular to the vertical axis. If (INTERSECT) is specified, a second reference line perpendicular to the horizontal axis is drawn that intersects the fit line at the same point as the vertical axis reference line. If a vertical axis reference line label is specified, the intersecting horizontal axis reference line is labeled with the horizontal axis value. See also the entries for the CVREF=, LVREF=, and VREFLABELS= options.

VREFLABELS='label1' ... 'labeln'**VREFLABEL=**'label1' ... 'labeln'**VREFLAB=**'label1' ... 'labeln'

specifies labels for the lines requested by the VREF= option. The number of labels must equal the number of lines. Enclose each label in quotes. Labels can be up to 16 characters.

WEIGHT Statement

WEIGHT *variable* ;

If you want to use weights for each observation in the input data set, place the weights in a variable in the data set and specify the name in a WEIGHT statement. The values of the WEIGHT variable can be nonintegral and are not truncated. Observations with nonpositive or missing values for the weight variable do not contribute to the fit of the model. The WEIGHT variable multiplies the contribution to the log likelihood for each observation.

Details: LIFEREG Procedure

Missing Values

Any observation with missing values for the dependent variable is not used in the model estimation unless it is one and only one of the values in an interval specification. Also, if one of the explanatory variables or the censoring variable is missing, the observation is not used. For any observation to be used in the estimation of a model, only the variables needed in that model have to be nonmissing. Predicted values are computed for all observations with no missing explanatory variable values. If the censoring variable is missing, the CENSORED= variable in the OUT= SAS data set is also missing.

Model Specification

Main effects as well as interaction terms are allowed in the model specification, similar to the GLM procedure. For numeric variables, a main effect is a linear term equal to the value of the variable unless the variable appears in the CLASS statement. For variables listed in the CLASS statement, PROC LIFEREG creates indicator variables (variables taking the values zero or one) for every level of the variable except the last level. If there is no intercept term, the first CLASS variable has indicator variables created for all levels including the last level. The levels are ordered according to the ORDER= option. Estimates of a main effect depend upon other effects in the model and, therefore, are adjusted for the presence of other effects in the model.

Computational Method

By default, the LIFEREG procedure computes initial values for the parameters by using ordinary least squares (OLS) and ignoring censoring. This might not be the best set of starting values for a given set of data. For example, if there are extreme values in your data, the OLS fit might be excessively influenced by the extreme observations, causing an overflow or convergence problems. See [Example 48.3](#) for one way to deal with convergence problems.

You can specify the INITIAL= option in the MODEL statement to override these starting values. You can also specify the INTERCEPT=, SCALE=, and SHAPE= options to set initial values of the intercept, scale, and shape parameters. For models with multilevel interaction effects, it is a little difficult to use the INITIAL= option to provide starting values for all parameters. In this case, you can use the INEST= data set. See the section “[INEST= Data Set](#)” on page 3656 for details. The INEST= data set overrides all previous specifications for starting values of parameters.

The rank of the design matrix \mathbf{X} is estimated before the model is fit. Columns of \mathbf{X} that are judged linearly dependent on other columns have the corresponding parameters set to zero. The test for linear dependence is controlled by the SINGULAR= option in the MODEL statement. Variables are included in the model in the order in which they are listed in the MODEL statement with the continuous variables included in the model before any classification variables.

The log-likelihood function is maximized by means of a ridge-stabilized Newton-Raphson algorithm. The maximized value of the log likelihood can take positive or negative values, depending on the specified model and the values of the maximum likelihood estimates of the model parameters.

If convergence of the maximum likelihood estimates is attained, a Type III chi-square test statistic is computed for each effect, testing whether there is any contribution from any of the levels of the effect. This statistic is computed as a quadratic form in the appropriate parameter estimates by using the corresponding submatrix of the asymptotic covariance matrix estimate. See Chapter 39, “[The GLM Procedure](#),” and Chapter 15, “[The Four Types of Estimable Functions](#),” for more information about Type III estimable functions. The asymptotic covariance matrix is computed as the inverse of the observed information matrix. Note that if the NOINT option is specified and CLASS variables are used, the first CLASS variable contains a contribution from an intercept term. The results are displayed in an ODS table named “Type3Analysis.”

Chi-square tests for individual parameters are Wald tests based on the observed information matrix and the parameter estimates. If an effect has a single degree of freedom in the parameter estimates table, the chi-square test for this parameter is equivalent to the Type III test for this effect.

Before SAS 8.2, a multiple-degree-of-freedom statistic was computed for each effect to test for contribution from any level of the effect. In general, the Type III test statistic in a main-effect-only model (no interaction terms) will be equal to the previously computed effect statistic, unless there are collinearities among the effects. If there are collinearities, the Type III statistic will adjust for them, and the value of the Type III statistic and the number of degrees of freedom might not be equal to those of the previous effect statistic.

Suppose there are n observations from the model $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \sigma\boldsymbol{\epsilon}$ (or $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{O} + \sigma\boldsymbol{\epsilon}$ if there is an offset variable), where \mathbf{X} is an $n \times k$ matrix of covariate values (including the intercept), \mathbf{y} is a vector of responses, \mathbf{O} is a vector of offset variable values, and $\boldsymbol{\epsilon}$ is a vector of errors with survival function S , cumulative distribution function F , and probability density function f . That is, $S(t) = \Pr(\epsilon_i > t)$, $F(t) = \Pr(\epsilon_i \leq t)$, and $f(t) = dF(t)/dt$, where ϵ_i is a component of the error vector. Then, if all the responses are observed, the log likelihood, L , can be written as

$$L = \sum \log \left(\frac{f(u_i)}{\sigma} \right)$$

where $u_i = \frac{1}{\sigma}(y_i - \mathbf{x}'_i\boldsymbol{\beta})$.

If some of the responses are left, right, or interval censored, the log likelihood can be written as

$$L = \sum \log \left(\frac{f(u_i)}{\sigma} \right) + \sum \log(S(u_i)) + \sum \log(F(u_i)) + \sum \log(F(u_i) - F(v_i))$$

with the first sum over uncensored observations, the second sum over right-censored observations, the third sum over left-censored observations, the last sum over interval-censored observations, and

$$v_i = \frac{1}{\sigma}(z_i - \mathbf{x}'_i\boldsymbol{\beta})$$

where z_i is the lower end of a censoring interval.

If the response is specified in the binomial format, *events/trials*, then the log-likelihood function is

$$L = \sum r_i \log(P_i) + (n_i - r_i) \log(1 - P_i)$$

where r_i is the number of events and n_i is the number of trials for the i th observation. In this case, $P_i = 1 - F(-\mathbf{x}'_i\boldsymbol{\beta})$. For the symmetric distributions, logistic and normal, this is the same as $F(\mathbf{x}'_i\boldsymbol{\beta})$. Additional information about censored and limited dependent variable models can be found in Kalbfleisch and Prentice (1980) and Maddala (1983).

The estimated covariance matrix of the parameter estimates is computed as the negative inverse of \mathbf{I} , which is the information matrix of second derivatives of L with respect to the parameters evaluated at the final parameter estimates. If \mathbf{I} is not positive definite, a positive-definite submatrix of \mathbf{I} is inverted, and the remaining rows and columns of the inverse are set to zero. If some of the parameters, such as the scale and intercept, are restricted, the corresponding elements of the estimated covariance matrix are set to zero. The standard error estimates for the parameter estimates are taken as the square roots of the corresponding diagonal elements.

For restrictions placed on the intercept, scale, and shape parameters, one-degree-of-freedom Lagrange multiplier test statistics are computed. These statistics are computed as

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

where g is the derivative of the log likelihood with respect to the restricted parameter at the restricted maximum and

$$V = \mathbf{I}_{11} - \mathbf{I}_{12}\mathbf{I}_{22}^{-1}\mathbf{I}_{21}$$

where the 1 subscripts refer to the restricted parameter and the 2 subscripts refer to the unrestricted parameters. The information matrix is evaluated at the restricted maximum. These statistics are asymptotically distributed as chi-squares with one degree of freedom under the null hypothesis that the restrictions are valid, provided that some regularity conditions are satisfied. Refer to Rao (1973, p. 418) for a more complete discussion. It is possible for these statistics to be missing if the observed information matrix is not positive definite. Higher-degree-of-freedom tests for multiple restrictions are not currently computed.

A Lagrange multiplier test statistic is computed to test this constraint. Notice that this test statistic is comparable to the Wald test statistic for testing that the scale is one. The Wald statistic is the result of squaring the difference of the estimate of the scale parameter from one and dividing this by the square of its estimated standard error.

Supported Distributions

For most distributions, the baseline survival function (S) and the probability density function (f) are listed for the additive random disturbance (y_0 or $\log(T_0)$) with location parameter μ and scale parameter σ . See the section “[Overview: LIFEREG Procedure](#)” on page 3596 for more information. These distributions apply when the log of the response is modeled (this is the default analysis). The corresponding survival function (G) and its density function (g) are given for the untransformed baseline distribution (T_0).

For the normal and logistic distributions, the response is not log transformed by PROC LIFEREG, and the survival functions and probability density functions listed apply to the untransformed response.

For example, for the WEIBULL distribution, $S(w)$ and $f(w)$ are the survival function and the probability density function for the extreme-value distribution (distribution of the log of the response), while $G(t)$ and $g(t)$ are the survival function and the probability density function of a Weibull distribution (using the untransformed response).

The chosen baseline functions define the meaning of the intercept, scale, and shape parameters. Only the gamma distribution has a free shape parameter in the following parameterizations. Notice that some of the distributions do not have mean zero and that σ is not, in general, the standard deviation of the baseline distribution.

For the Weibull distribution, the accelerated failure time model is also a proportional-hazards model. However, the parameterization for the covariates differs by a multiple of the scale parameter from the parameterization commonly used for the proportional hazards model.

The distributions supported in the LIFEREG procedure follow. If there are no covariates in the model, $\mu = \text{Intercept}$ in the output; otherwise, $\mu = \mathbf{x}'\boldsymbol{\beta}$. $\sigma = \text{Scale}$ in the output.

Exponential

$$\begin{aligned} S(w) &= \exp(-\exp(w - \mu)) \\ f(w) &= \exp(w - \mu) \exp(-\exp(w - \mu)) \\ G(t) &= \exp(-\alpha t) \\ g(t) &= \alpha \exp(-\alpha t) \end{aligned}$$

where $\exp(-\mu) = \alpha$.

Generalized Gamma

$S(w) = S'(u)$, $f(w) = \sigma^{-1} f'(u)$, $G(t) = G'(v)$, $g(t) = \frac{v}{t\sigma} g'(v)$, $u = \frac{w-\mu}{\sigma}$, $v = \exp(\frac{\log(t)-\mu}{\sigma})$, and

$$\begin{aligned} S'(u) &= \begin{cases} 1 - \frac{\Gamma(\delta^{-2}, \delta^{-2} \exp(\delta u))}{\Gamma(\delta^{-2})} & \text{if } \delta > 0 \\ \frac{\Gamma(\delta^{-2}, \delta^{-2} \exp(\delta u))}{\Gamma(\delta^{-2})} & \text{if } \delta < 0 \end{cases} \\ f'(u) &= \frac{|\delta|}{\Gamma(\delta^{-2})} (\delta^{-2} \exp(\delta u))^{\delta^{-2}} \exp(-\exp(\delta u) \delta^{-2}) \\ G'(v) &= \begin{cases} 1 - \frac{\Gamma(\delta^{-2}, \delta^{-2} v^\delta)}{\Gamma(\delta^{-2})} & \text{if } \delta > 0 \\ \frac{\Gamma(\delta^{-2}, \delta^{-2} v^\delta)}{\Gamma(\delta^{-2})} & \text{if } \delta < 0 \end{cases} \\ g'(v) &= \frac{|\delta|}{v\Gamma(\delta^{-2})} (\delta^{-2} v^\delta)^{\delta^{-2}} \exp(-v^\delta \delta^{-2}) \end{aligned}$$

where $\Gamma(a)$ denotes the complete gamma function, $\Gamma(a, z)$ denotes the incomplete gamma function, and δ is a free shape parameter. The δ parameter is called Shape by PROC LIFEREG. See Lawless (2003, p. 240), and Klein and Moeschberger (1997, p. 386) for a description of the generalized gamma distribution.

Logistic

$$S(w) = \left(1 + \exp\left(\frac{w - \mu}{\sigma}\right)\right)^{-1}$$

$$f(w) = \frac{\exp\left(\frac{w - \mu}{\sigma}\right)}{\sigma \left(1 + \exp\left(\frac{w - \mu}{\sigma}\right)\right)^2}$$

Log-Logistic

$$S(w) = \left(1 + \exp\left(\frac{w - \mu}{\sigma}\right)\right)^{-1}$$

$$f(w) = \frac{\exp\left(\frac{w - \mu}{\sigma}\right)}{\sigma \left(1 + \exp\left(\frac{w - \mu}{\sigma}\right)\right)^2}$$

$$G(t) = \frac{1}{1 + \alpha t^\gamma}$$

$$g(t) = \frac{\alpha \gamma t^{\gamma-1}}{(1 + \alpha t^\gamma)^2}$$

where $\gamma = 1/\sigma$ and $\alpha = \exp(-\mu/\sigma)$.

Lognormal

$$S(w) = 1 - \Phi\left(\frac{w - \mu}{\sigma}\right)$$

$$f(w) = \frac{1}{\sqrt{2\pi}\sigma} \exp\left(-\frac{1}{2}\left(\frac{w - \mu}{\sigma}\right)^2\right)$$

$$G(t) = 1 - \Phi\left(\frac{\log(t) - \mu}{\sigma}\right)$$

$$g(t) = \frac{1}{\sqrt{2\pi}\sigma t} \exp\left(-\frac{1}{2}\left(\frac{\log(t) - \mu}{\sigma}\right)^2\right)$$

where Φ is the cumulative distribution function for the normal distribution.

Normal

$$S(w) = 1 - \Phi\left(\frac{w - \mu}{\sigma}\right)$$

$$f(w) = \frac{1}{\sqrt{2\pi}\sigma} \exp\left(-\frac{1}{2}\left(\frac{w - \mu}{\sigma}\right)^2\right)$$

where Φ is the cumulative distribution function for the normal distribution.

Weibull

$$S(w) = \exp\left(-\exp\left(\frac{w - \mu}{\sigma}\right)\right)$$

$$f(w) = \frac{1}{\sigma} \exp\left(\frac{w - \mu}{\sigma}\right) \exp\left(-\exp\left(\frac{w - \mu}{\sigma}\right)\right)$$

$$G(t) = \exp(-\alpha t^\gamma)$$

$$g(t) = \gamma \alpha t^{\gamma-1} \exp(-\alpha t^\gamma)$$

where $\sigma = 1/\gamma$ and $\alpha = \exp(-\mu/\sigma)$.

If your parameterization is different from the ones shown here, you can still use the procedure to fit your model. For example, a common parameterization for the Weibull distribution is

$$g(t; \lambda, \beta) = \left(\frac{\beta}{\lambda}\right) \left(\frac{t}{\lambda}\right)^{\beta-1} \exp\left(-\left(\frac{t}{\lambda}\right)^\beta\right)$$

$$G(t; \lambda, \beta) = \exp\left(-\left(\frac{t}{\lambda}\right)^\beta\right)$$

so that $\lambda = \exp(\mu)$ and $\beta = 1/\sigma$.

Again note that the expected value of the baseline log response is, in general, not zero and that the distributions are not symmetric in all cases. Thus, for a given set of covariates, \mathbf{x} , the expected value of the log response is not always $\mathbf{x}'\boldsymbol{\beta}$.

Some relations among the distributions are as follows:

- The gamma with Shape=1 is a Weibull distribution.

- The gamma with Shape=0 is a lognormal distribution.
- The Weibull with Scale=1 is an exponential distribution.

Predicted Values

For a given set of covariates, \mathbf{x} (including the intercept term), the p th quantile of the log response, y_p , is given by

$$y_p = \mathbf{x}'\boldsymbol{\beta} + \sigma u_p$$

if no offset variable has been specified, or

$$y_p = \mathbf{x}'\boldsymbol{\beta} + o + \sigma u_p$$

for a given value o of an offset variable, where u_p is the p th quantile of the baseline distribution. The estimated quantile is computed by replacing the unknown parameters with their estimates, including any shape parameters on which the baseline distribution might depend. The estimated quantile of the original response is obtained by taking the exponential of the estimated log quantile unless the NOLOG option is specified in the preceding MODEL statement.

The following table shows how u_p is computed from the baseline distribution $F(u)$:

Table 48.3 Baseline Probability Functions and u_p

Distribution	$F(u)$	u_p
Exponential	$1 - \exp(-\exp(u))$	$\log(-\log(1 - p))$
Generalized Gamma	$\begin{cases} \frac{\Gamma(\delta^{-2}, \delta^{-2} \exp(\delta u))}{\Gamma(\delta^{-2})} & \text{if } \delta > 0 \\ 1 - \frac{\Gamma(\delta^{-2}, \delta^{-2} \exp(\delta u))}{\Gamma(\delta^{-2})} & \text{if } \delta < 0 \end{cases}$	$F^{-1}(p)$
Logistic	$1 - (1 + \exp(u))^{-1}$	$\log(p/(1 - p))$
Log-logistic	$1 - (1 + \exp(u))^{-1}$	$\log(p/(1 - p))$
Lognormal	$\Phi(u)$	$\Phi^{-1}(p)$
Normal	$\Phi(u)$	$\Phi^{-1}(p)$
Weibull	$1 - \exp(-\exp(u))$	$\log(-\log(1 - p))$

For the generalized gamma distribution, u_p is computed numerically.

The standard errors of the quantile estimates are computed using the estimated covariance matrix of the parameter estimates and a Taylor series expansion of the quantile estimate. The standard error is computed as

$$\text{STD} = \sqrt{\mathbf{z}'\mathbf{V}\mathbf{z}}$$

where \mathbf{V} is the estimated covariance matrix of the parameter vector $(\boldsymbol{\beta}', \sigma, \delta)'$, and \mathbf{z} is the vector

$$\mathbf{z} = \begin{bmatrix} \mathbf{x} \\ \hat{u}_p \\ \hat{\sigma} \frac{\partial u_p}{\partial \delta} \end{bmatrix}$$

where δ is the vector of the shape parameters. Unless the NOLOG option is specified, this standard error estimate is converted into a standard error estimate for $\exp(y_p)$ as $\exp(\hat{y}_p)\text{STD}$. It might be more desirable to compute confidence limits for the log response and convert them back to the original response variable than to use the standard error estimates for $\exp(y_p)$ directly. See [Example 48.1](#) for a 90% confidence interval of the response constructed by exponentiating a confidence interval for the log response.

The variable CDF is computed as

$$\text{CDF}_i = F(u_i)$$

where the residual is defined by

$$u_i = \left(\frac{y_i - \mathbf{x}'_i \mathbf{b}}{\hat{\sigma}} \right)$$

and F is the baseline cumulative distribution function.

Confidence Intervals

Confidence intervals are computed for all model parameters and are reported in the “Analysis of Parameter Estimates” table. The confidence coefficient can be specified with the ALPHA= α MODEL statement option, resulting in a $(1 - \alpha) \times 100\%$ two-sided confidence coefficient. The default confidence coefficient is 95%, corresponding to $\alpha = 0.05$.

Regression Parameters

A two-sided $(1 - \alpha) \times 100\%$ confidence interval $[\beta_{iL}, \beta_{iU}]$ for the regression parameter β_i is based on the asymptotic normality of the maximum likelihood estimator $\hat{\beta}_i$ and is computed by

$$\beta_{iL} = \hat{\beta}_i - z_{1-\alpha/2}(\text{SE}_{\hat{\beta}_i})$$

$$\beta_{iU} = \hat{\beta}_i + z_{1-\alpha/2}(\text{SE}_{\hat{\beta}_i})$$

where $\text{SE}_{\hat{\beta}_i}$ is the estimated standard error of $\hat{\beta}_i$, and z_p is the $p \times 100\%$ percentile of the standard normal distribution.

Scale Parameter

A two-sided $(1 - \alpha) \times 100\%$ confidence interval $[\sigma_L, \sigma_U]$ for the scale parameter σ in the location-scale model is based on the asymptotic normality of the logarithm of the maximum likelihood estimator $\log(\hat{\sigma})$, and is computed by

$$\sigma_L = \hat{\sigma} / \exp[z_{1-\alpha/2}(\text{SE}_{\hat{\sigma}})/\hat{\sigma}]$$

$$\sigma_U = \hat{\sigma} \exp[z_{1-\alpha/2}(\text{SE}_{\hat{\sigma}})/\hat{\sigma}]$$

Refer to Meeker and Escobar (1998) for more information.

Weibull Scale and Shape Parameters

The Weibull distribution scale parameter η and shape parameter β are obtained by transforming the extreme-value location parameter μ and scale parameter σ :

$$\eta = \exp(\mu)$$

$$\beta = 1/\sigma$$

Consequently, two-sided $(1 - \alpha) \times 100\%$ confidence intervals for the Weibull scale and shape parameters are computed as

$$[\eta_L, \eta_U] = [\exp(\mu_L), \exp(\mu_U)]$$

$$[\beta_L, \beta_U] = [1/\sigma_U, 1/\sigma_L]$$

Gamma Shape Parameter

A two-sided $(1 - \alpha) \times 100\%$ confidence interval for the three-parameter gamma shape parameter δ is computed by

$$[\delta_L, \delta_U] = [\hat{\delta} - z_{1-\alpha/2}(\text{SE}_{\hat{\delta}}), \hat{\delta} + z_{1-\alpha/2}(\text{SE}_{\hat{\delta}})]$$

Fit Statistics

Suppose that the model contains p parameters and that n observations are used in model fitting. The fit criteria displayed by the LIFEREG procedure are calculated as follows:

- $-2 \log$ likelihood:

$$-2\log(L)$$

where L is the maximized likelihood for the model.

- Akaike's information criterion:

$$\text{AIC} = -2\log(L) + 2p$$

- corrected Akaike's information criterion:

$$\text{AICC} = \text{AIC} + \frac{2p(p+1)}{n-p-1}$$

- Bayesian information criterion:

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

If you specify the Weibull, exponential, lognormal, log-logistic, or gamma distribution, then maximum likelihood estimates of model parameters are computed by maximizing the log likelihood of the distribution of the logarithm of the response. This is equivalent to computing maximum likelihood parameter estimates based on the response on the original, rather than log, scale. If you specify the Weibull, exponential, lognormal, log-logistic, or gamma distribution, then fit statistics based on the maximized log likelihood $\log(L)$ of the log of the response are reported in the "Fit Statistics" table. Fit criteria computed in this way cannot be meaningfully compared with fit criteria that are based on the log likelihood of the unlogged response. If you specify the normal or logistic distribution, or if you specify the NOLOG option in the MODEL statement, then the fit criteria reported in the "Fit Statistics" table are based on the response on the original, rather than log, scale.

In addition to the "Fit Statistics" table described previously, if you specify the Weibull, exponential, lognormal, log-logistic, or gamma distribution, fit criteria that are based on the distribution of the response on the original scale, rather than the log of the response, are reported in the "Fit Statistics (Unlogged Response)" table.

When comparing models, you should compare fit criteria based on the log likelihood that is computed by using the response on the same scale, either always based on the log of the response or always based on the response on the original scale.

Refer to Akaike (1981, 1979) for details of AIC and BIC. Refer to Simonoff (2003) for a discussion of using AIC, AICC, and BIC in statistical modeling.

Probability Plotting

Probability plots are useful tools for the display and analysis of lifetime data. Probability plots use an inverse distribution scale so that a cumulative distribution function (CDF) plots as a straight line. A nonparametric estimate of the CDF of the lifetime data will plot approximately as a straight line, thus providing a visual assessment of goodness of fit.

You can use the PROBLOT statement in PROC LIFEREG to create probability plots of data that are complete, right censored, interval censored, or a combination of censoring types (arbitrarily censored). A line representing the maximum likelihood fit from the MODEL statement and pointwise parametric confidence bands for the cumulative probabilities are also included in the plot.

A random variable Y belongs to a *location-scale* family of distributions if its CDF F is of the form

$$Pr\{Y \leq y\} = F(y) = G\left(\frac{y - \mu}{\sigma}\right)$$

where μ is the location parameter and σ is the scale parameter. Here, G is a CDF that cannot depend on any unknown parameters, and G is the CDF of Y if $\mu = 0$ and $\sigma = 1$. For example, if Y is a normal random variable with mean μ and standard deviation σ ,

$$G(u) = \Phi(u) = \int_{-\infty}^u \frac{1}{\sqrt{2\pi}} \exp\left(-\frac{u^2}{2}\right) du$$

and

$$F(y) = \Phi\left(\frac{y - \mu}{\sigma}\right)$$

The normal, extreme-value, and logistic distributions are location-scale models. The three-parameter gamma distribution is a location-scale model if the shape parameter δ is fixed. If T has a lognormal, Weibull, or log-logistic distribution, then $\log(T)$ has a distribution that is a location-scale model. Probability plots are constructed for lognormal, Weibull, and log-logistic distributions by using $\log(T)$ instead of T in the plots.

Let $y_{(1)} \leq y_{(2)} \leq \dots \leq y_{(n)}$ be ordered observations of a random sample with distribution function $F(y)$. A probability plot is a plot of the points $y_{(i)}$ against $m_i = G^{-1}(a_i)$, where $a_i = \hat{F}(y_{(i)})$ is an estimate of the CDF $F(y_{(i)}) = G\left(\frac{y_{(i)} - \mu}{\sigma}\right)$. The nonparametric CDF estimates a_i are sometimes called *plotting positions*. The axis on which the points m_i are plotted is usually labeled with a probability scale (the scale of a_i).

If F is one of the location-scale distributions, then y is the lifetime; otherwise, the log of the lifetime is used to transform the distribution to a location-scale model.

If the data actually have the stated distribution, then $\hat{F} \approx F$,

$$m_i = G^{-1}(\hat{F}(y_{(i)})) \approx G^{-1}\left(G\left(\frac{y_{(i)} - \mu}{\sigma}\right)\right) = \frac{y_{(i)} - \mu}{\sigma}$$

and points $(y_{(i)}, m_i)$ should fall approximately in a straight line.

There are several ways to compute the nonparametric CDF estimates used in probability plots from lifetime data. These are discussed in the next two sections.

Complete and Right-Censored Data

The censoring times must be taken into account when you compute plotting positions for right-censored data. The modified Kaplan-Meier method described in the following section is the default method for computing nonparametric CDF estimates for display on probability plots. Refer to Abernethy (1996), Meeker and Escobar (1998), and Nelson (1982) for discussions of the methods described in the following sections.

Expected Ranks, Kaplan-Meier, and Modified Kaplan-Meier Methods

Let $y_{(1)} \leq y_{(2)} \leq \dots \leq y_{(n)}$ be ordered observations of a random sample including failure times and censor times. Order the data in increasing order. Label all the data with reverse ranks r_i , with $r_1 = n, \dots, r_n = 1$. For the lifetime (not censoring time) corresponding to reverse rank r_i , compute the survival function estimate

$$S_i = \left[\frac{r_i}{r_i + 1} \right] S_{i-1}$$

with $S_0 = 1$. The expected rank plotting position is computed as $a_i = 1 - S_i$. The option PPOS=EXPRANK specifies the expected rank plotting position.

For the Kaplan-Meier method,

$$S_i = \left[\frac{r_i - 1}{r_i} \right] S_{i-1}$$

The Kaplan-Meier plotting position is then computed as $a'_i = 1 - S_i$. The option PPOS=KM specifies the Kaplan-Meier plotting position.

For the modified Kaplan-Meier method, use

$$S'_i = \frac{S_i + S_{i-1}}{2}$$

where S_i is computed from the Kaplan-Meier formula with $S_0 = 1$. The plotting position is then computed as $a''_i = 1 - S'_i$. The option PPOS=MKM specifies the modified Kaplan-Meier plotting position. If the PPOS option is not specified, the modified Kaplan-Meier plotting position is used as the default method.

For complete samples, $a_i = i/(n + 1)$ for the expected rank method, $a'_i = i/n$ for the Kaplan-Meier method, and $a''_i = (i - 0.5)/n$ for the modified Kaplan-Meier method. If the largest observation is a failure for the Kaplan-Meier estimator, then $F_n = 1$ and the point is not plotted.

Median Ranks

Let $y_{(1)} \leq y_{(2)} \leq \dots \leq y_{(n)}$ be ordered observations of a random sample including failure times and censor times. A failure order number j_i is assigned to the i th failure: $j_i = j_{i-1} + \Delta$, where $j_0 = 0$. The increment Δ is initially 1 and is modified when a censoring time is encountered in the ordered sample. The new increment is computed as

$$\Delta = \frac{(n + 1) - \text{previous failure order number}}{1 + \text{number of items beyond previous censored item}}$$

The plotting position is computed for the i th failure time as

$$a_i = \frac{j_i - 0.3}{n + 0.4}$$

For complete samples, the failure order number j_i is equal to i , the order of the failure in the sample. In this case, the preceding equation for a_i is an approximation of the median plotting position computed as the median of the i th-order statistic from the uniform distribution on $(0, 1)$. In the censored case, j_i is not necessarily an integer, but the preceding equation still provides an approximation to the median plotting position. The PPOS=MEDRANK option specifies the median rank plotting position.

Arbitrarily Censored Data

The LIFEREG procedure can create probability plots for data that consist of combinations of exact, left-censored, right-censored, and interval-censored lifetimes—that is, arbitrarily censored data. The LIFEREG procedure uses an iterative algorithm developed by Turnbull (1976) to compute a nonparametric maximum likelihood estimate of the cumulative distribution function for the data. Since the technique is maximum likelihood, standard errors of the cumulative probability estimates are computed from the inverse of the associated Fisher information matrix. This algorithm is an example of the expectation-maximization (EM) algorithm. The default initial estimate assigns equal probabilities to each interval. You can specify different initial values with the PROBLIST= option. Convergence is determined if the change in the log likelihood between two successive iterations is less than delta, where the default value of delta is 10^{-8} . You can specify a different value for delta with the TOLLIKE= option. Iterations will be terminated if the algorithm does not converge after a fixed number of iterations. The default maximum number of iterations is 1000. Some data might require more iterations for convergence. You can specify the maximum allowed number of iterations with the MAXITEM= option in the PROBLOT statement. The iteration history of the log likelihood is displayed if you specify the ITPRINTEM option. The iteration history of the estimated interval probabilities are also displayed if you specify both options ITPRINTEM and PRINTPROBS.

If an interval probability is smaller than a tolerance (10^{-6} by default) after convergence, the probability is set to zero, the interval probabilities are renormalized so that they add to one, and iterations are restarted. Usually the algorithm converges in just a few more iterations. You can change the default value of the tolerance with the TOLPROB= option. You can specify the NOPOLISH option to avoid setting small probabilities to zero and restarting the algorithm.

If you specify the ITPRINTEM option, a table summarizing the Turnbull estimate of the interval probabilities is displayed. The columns labeled “Reduced Gradient” and “Lagrange Multiplier” are used in checking final convergence of the maximum likelihood estimate. The Lagrange multipliers must all be greater than or equal to zero, or the solution is not maximum likelihood. Refer to Gentleman and Geyer (1994) for more details of the convergence checking. Also refer to Meeker and Escobar (1998, Chapter 3) for more information.

See [Example 48.6](#) for an illustration.

Nonparametric Confidence Intervals

You can use the PPOUT option in the PROBLOT statement to create a table containing the nonparametric CDF estimates computed by the selected method, Kaplan-Meier CDF estimates, standard errors of the Kaplan-Meier estimator, and nonparametric confidence limits for the CDF. The confidence limits are either pointwise or simultaneous, depending on the value of the NPINTERVALS= option in the PROBLOT statement. The method used in the LIFEREG procedure for computation of approximate pointwise and simultaneous confidence intervals for cumulative failure probabilities relies on the Kaplan-Meier estimator of the cumulative distribution function of failure time and approximate standard deviation of the Kaplan-Meier estimator. For the case of arbitrarily censored data, the Turnbull algorithm, discussed previously, provides an extension of the Kaplan-Meier estimator. Both the Kaplan-Meier and the Turnbull estimators provide an estimate of the standard error of the CDF estimator, $se_{\hat{F}}$, that is used in computing confidence intervals.

Pointwise Confidence Intervals

Approximate $(1 - \alpha)100\%$ pointwise confidence intervals are computed as in Meeker and Escobar (1998, Section 3.6) as

$$[F_L, F_U] = \left[\frac{\hat{F}}{\hat{F} + (1 - \hat{F})w}, \frac{\hat{F}}{\hat{F} + (1 - \hat{F})/w} \right]$$

where

$$w = \exp \left[\frac{z_{1-\alpha/2} \text{se}_{\hat{F}}}{(\hat{F}(1 - \hat{F}))} \right]$$

where z_p is the p th quantile of the standard normal distribution.

Simultaneous Confidence Intervals

Approximate $(1 - \alpha)100\%$ simultaneous confidence bands valid over the lifetime interval (t_a, t_b) are computed as the “Equal Precision” case of Nair (1984) and Meeker and Escobar (1998, Section 3.8) as

$$[F_L, F_U] = \left[\frac{\hat{F}}{\hat{F} + (1 - \hat{F})w}, \frac{\hat{F}}{\hat{F} + (1 - \hat{F})/w} \right]$$

where

$$w = \exp \left[\frac{e_{a,b,1-\alpha/2} \text{se}_{\hat{F}}}{(\hat{F}(1 - \hat{F}))} \right]$$

where the factor $x = e_{a,b,1-\alpha/2}$ is the solution of

$$x \exp(-x^2/2) \log \left[\frac{(1-a)b}{(1-b)a} \right] / \sqrt{8\pi} = \alpha/2$$

The time interval (t_a, t_b) over which the bands are valid depends in a complicated way on the constants a and b defined in Nair (1984), $0 < a < b < 1$. The constants a and b are chosen by default so that the confidence bands are valid between the lowest and highest times corresponding to failures in the case of multiply censored data, or to the lowest and highest intervals for which probabilities are computed for arbitrarily censored data. You can optionally specify a and b directly with the NPINTERVALS=SIMULTANEOUS(a, b) option in the PROBLOT statement.

INEST= Data Set

If specified, the INEST= data set specifies initial estimates for all the parameters in the model. The INEST= data set must contain the intercept variable (named Intercept) and all independent variables in the MODEL statement.

If BY processing is used, the INEST= data set should also include the BY variables, and there must be at least one observation for each BY group. If there is more than one observation in one BY group, the first observation read is used for that BY group.

If the INEST= data set also contains the `_TYPE_` variable, only observations with `_TYPE_` value 'PARMS' are used as starting values. Combining the INEST= data set and the MAXITER= option in the MODEL statement, partial scoring can be done, such as predicting on a validation data set by using the model built from a training data set.

You can specify starting values for the iterative algorithm in the INEST= data set. This data set overwrites the INITIAL= option in the MODEL statement, which is a little difficult to use for models including multilevel interaction effects. The INEST= data set has the same structure as the OUTEST= data set but is not required to have all the variables or observations that appear in the OUTEST= data set. One simple use of the INEST= option is passing the previous OUTEST= data set directly to the next model as an INEST= data set, assuming that the two models have the same parameterization. See [Example 48.3](#) for an illustration.

OUTEST= Data Set

The OUTEST= data set contains parameter estimates and the log likelihood for the model. You can specify a label in the MODEL statement to distinguish between the estimates for different models fit with the LIFEREG procedure. If the COVOUT option is specified, the OUTEST= data set also contains the estimated covariance matrix of the parameter estimates. Note that, if the LIFEREG procedure does not converge, the parameter estimates are set to missing in the OUTEST data set.

The OUTEST= data set contains all variables specified in the MODEL statement and the BY statement. One observation consists of parameter values for the model with the dependent variable having the value -1 . If the COVOUT option is specified, there are additional observations containing the rows of the estimated covariance matrix. For these observations, the dependent variable contains the parameter estimate for the corresponding row variable. The following variables are also added to the data set:

<code>_MODEL_</code>	a character variable containing the label of the MODEL statement, if present. Otherwise, the variable's value is blank.
<code>_NAME_</code>	a character variable containing the name of the dependent variable for the parameter estimates observations or the name of the row for the covariance matrix estimates
<code>_TYPE_</code>	a character variable containing the type of the observation, either PARMS for parameter estimates or COV for covariance estimates

<code>_DIST_</code>	a character variable containing the name of the distribution modeled
<code>_LNLIKE_</code>	a numeric variable containing the last computed value of the log likelihood
<code>INTERCEPT</code>	a numeric variable containing the intercept parameter estimates and covariances
<code>_SCALE_</code>	a numeric variable containing the scale parameter estimates and covariances
<code>_SHAPE1_</code>	a numeric variable containing the first shape parameter estimates and covariances if the specified distribution has additional shape parameters

Any BY variables specified are also added to the OUTEST= data set.

XDATA= Data Set

The XDATA= data set is used for plotting the predicted probability when there are covariates specified in a MODEL statement and a probability plot is specified with a PROBPLOT statement. See [Example 48.4](#) for an illustration.

The XDATA= data set is an input SAS data set that contains values for all the independent variables in the MODEL statement and variables in the CLASS statement. The XDATA= data set has the same structure as the DATA= data set but is not required to have all the variables or observations that appear in the DATA= data set.

The XDATA= data set must contain all the independent variables in the MODEL statement and variables in the CLASS statement. Even though variables in the CLASS statement might not be used, valid values are required for these variables in the XDATA= data set. Missing values are not allowed. Missing values are not allowed in the XDATA= data set for any of the independent variables, either. Missing values are allowed for the dependent variables and other variables if they are included in the XDATA= data set.

If BY processing is used, the XDATA= data set should also include the BY variables, and there must be at least one valid observation for each BY group. If there is more than one valid observation in a BY group, the last one read is used for that BY group.

If there is no XDATA= data set in the PROC LIFEREG statement, by default, the LIFEREG procedure will use the overall mean for effects containing a continuous variable (or variables) and the highest level of a single classification variable as reference level. The rules are summarized as follows:

- If the effect contains a continuous variable (or variables), the overall mean of this effect (not the variables) is used.
- If the effect is a single classification variable, the highest level of the variable is used.

Computational Resources

Let p be the number of parameters estimated in the model. The minimum working space (in bytes) needed is

$$16p^2 + 100p$$

However, if sufficient space is available, the input data set is also kept in memory; otherwise, the input data set is reread for each evaluation of the likelihood function and its derivatives, with the resulting execution time of the procedure substantially increased.

Let n be the number of observations used in the model estimation. Each evaluation of the likelihood function and its first and second derivatives requires $O(np^2)$ multiplications and additions, n individual function evaluations for the log density or log distribution function, and n evaluations of the first and second derivatives of the function. The calculation of each updating step from the gradient and Hessian requires $O(p^3)$ multiplications and additions. The $O(v)$ notation means that, for large values of the argument, v , $O(v)$ is approximately a constant times v .

Bayesian Analysis

Gibbs Sampling

This section provides details about Bayesian analysis by Gibbs sampling in the location-scale models for survival data available in PROC LIFEREG. See the section “[Gibbs Sampler](#)” on page 151 for a general discussion of Gibbs sampling. PROC LIFEREG fits parametric location-scale survival models. That is, the probability density of the response Y can be expressed in the general form

$$f(y) = g\left(\frac{y - \mu}{\sigma}\right)$$

where $Y = \log(T)$ for lifetimes T . The function g determines the specific distribution. The location parameter μ_i is modeled through regression parameters as $\mu_i = \mathbf{x}_i' \boldsymbol{\beta}$. The LIFEREG procedure can provide Bayesian estimates of the regression parameters and σ . The OUTPUT and PROBPLOT statements, if specified, are ignored. The PLOTS=PROBPLOT option in the PROC LIFEREG statement and the CORRB and COVB options in the MODEL statement are also ignored.

For the Weibull distribution, you can specify that Gibbs sampling be performed on the Weibull shape parameter $\beta = \sigma^{-1}$ instead of the scale parameter σ by specifying a prior distribution for the shape parameter with the WEIBULLSHAPEPRIOR= option. In addition, if there are no covariates in the model, you can specify Gibbs sampling on the Weibull scale parameter $\alpha = \exp(\mu)$, where μ is the intercept term, with the WEIBULLSCALEPRIOR= option.

In the case of the exponential distribution with no covariates, you can specify Gibbs sampling on the exponential scale parameter $\alpha = \exp(\mu)$, where μ is the intercept term, with the EXPSCALEPRIOR= option.

Let $\boldsymbol{\theta} = (\theta_1, \dots, \theta_k)'$ be the parameter vector. For location-scale models, the θ_i 's are the regression coefficients β_i 's and the scale parameter σ . In the case of the three-parameter gamma distribution, there is an additional gamma shape parameter τ . 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

$$\pi(\theta_1|\theta_j = \theta_j^*, 2 \leq j \leq k, D) = L(D|(\boldsymbol{\theta} = (\theta_1, \theta_2^*, \dots, \theta_k^*)'))p(\boldsymbol{\theta} = (\theta_1, \theta_2^*, \dots, \theta_k^*)')$$

Suppose you have a set of arbitrary starting values $\{\theta_1^{(0)}, \dots, \theta_k^{(0)}\}$. 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  $[\theta_1|\theta_2^{(0)}, \dots, \theta_k^{(0)}]$ 
draw  $\theta_2^{(1)}$  from  $[\theta_2|\theta_1^{(1)}, \theta_3^{(0)}, \dots, \theta_k^{(0)}]$ 
...
draw  $\theta_k^{(1)}$  from  $[\theta_k|\theta_1^{(1)}, \dots, \theta_{k-1}^{(1)}]$ 
```

This completes one iteration of the Gibbs sampler. After one iteration, you have $\{\theta_1^{(1)}, \dots, \theta_k^{(1)}\}$. After n iterations, you have $\{\theta_1^{(n)}, \dots, \theta_k^{(n)}\}$. PROC LIFEREG implements the ARMS algorithm based on a program provided by Gilks (2003) to draw a sample from a full conditional distribution. See the section “[Assessing Markov Chain Convergence](#)” on page 155 for information about assessing the convergence of the chain of posterior samples.

You can output these posterior samples into a SAS data set. The following option in the BAYES statement outputs the posterior samples into the SAS data set Post:

OUTPOST= Post ;

The data set also includes the variables LogPost and LogLike, which represent the log of the posterior distribution and the log of the likelihood, respectively.

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.

Scale and Shape Parameters

Gamma Prior The gamma distribution $G(a, b)$ has a pdf

$$f_{a,b}(u) = \frac{b(bu)^{a-1}e^{-bu}}{\Gamma(a)}, \quad u > 0$$

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

$$p(u) \propto u^{-1}, \quad u > 0$$

Regression Coefficients

Let β be the regression coefficients.

Normal Prior Assume β has a multivariate normal prior with mean vector β_0 and covariance matrix Σ_0 . The joint prior density is given by

$$p(\beta) \propto e^{-\frac{1}{2}(\beta - \beta_0)' \Sigma_0^{-1} (\beta - \beta_0)}$$

Uniform Prior The joint prior density is given by

$$p(\beta) \propto 1$$

Posterior Distribution

Denote the observed data by D .

The posterior distribution is

$$\pi(\theta|D) \propto L_P(D|\theta)p(\theta)$$

where $L_P(D|\theta)$ is the likelihood function with regression coefficients and any additional parameters, such as scale or shape, θ as parameters; and $p(\theta)$ is the joint prior distribution of the parameters.

Deviance Information Criterion

Let θ_i be the model parameters at iteration i of the Gibbs sampler, and let $LL(\theta_i)$ be the corresponding model log likelihood. PROC LIFEREG computes the following fit statistics defined by Spiegelhalter et al. (2002):

- effective number of parameters:

$$p_D = \overline{LL(\theta)} - LL(\bar{\theta})$$

- deviance information criterion (DIC):

$$\text{DIC} = \overline{\text{LL}(\boldsymbol{\theta})} + p_D$$

where

$$\overline{\text{LL}(\boldsymbol{\theta})} = \frac{1}{n} \sum_{i=1}^n \text{LL}(\boldsymbol{\theta}_i)$$

$$\bar{\boldsymbol{\theta}} = \frac{1}{n} \sum_{i=1}^n \boldsymbol{\theta}_i$$

and n is the number of Gibbs samples.

Starting Values of the Markov Chains

When the BAYES statement is specified, PROC LIFEREG 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 LIFEREG 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 and Gamma Shape 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,

$$\beta_i^{(0)} = \hat{\beta}_i$$

Initial values for the r th 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 .

Scale, Exponential Scale, Weibull Scale, or Weibull Shape Parameter λ

Let λ be the parameter sampled.

For the first chain that the summary statistics and diagnostics are based on, the initial values are estimates of the mode of the posterior distribution; or the maximum likelihood estimates if the INITIALMLE option is specified; that is,

$$\lambda^{(0)} = \hat{\lambda}$$

The initial values of the r th chain ($r \geq 2$) are given by

$$\lambda^{(0)} = \hat{\lambda} e^{\pm \binom{r}{2} + 2} \hat{s}(\hat{\lambda})$$

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.

Displayed Output for Classical Analysis

For each model, PROC LIFEREG displays the following.

Model Information

The “Model Information” table displays the two-level name of the input data set, the distribution name, and the name and label of the dependent variable; the name and label of the censor indicator variable, for right-censored data; if you specify the WEIGHT statement, the name and label of the weight variable; and the maximum value of the log likelihood.

Number of Observations

The “Number of Observations” table displays the number of observations read from the input data set, and the number of observations used in the analysis.

Class Level Information

The “Class Level Information” table displays the levels of classification variables if you specify a CLASS statement.

Fit Statistics

The “Fit Statistics” table displays the negative of twice the log likelihood, Akaike’s information criterion (AIC), the corrected Akaike’s information criterion (AICC), and the Bayesian information criterion (BIC). If the specified distribution is Weibull, lognormal, log-logistic, or gamma, the fit criteria are based on the log likelihood for the log of the response, rather than for the response on the original scale.

Fit Statistics (Unlogged Response)

If the specified distribution is Weibull, lognormal, log-logistic, or gamma, the “Fit Statistics (Unlogged Response)” table displays fit criteria that are based on the log likelihood for the response on the original, rather than log, scale. The negative of twice the log likelihood, Akaike’s information criterion (AIC), the corrected Akaike’s information criterion (AICC), and the Bayesian information criterion (BIC) are displayed.

Type III Analysis of Effects

The “Type III Analysis of Effects” table displays, for each effect in the model, the effect name, the degrees of freedom associated with the type III contrast for the effect, the chi-square statistic for the contrast, and the p -value for the statistic.

Analysis of Maximum Likelihood Parameter Estimates

The “Analysis of Maximum Likelihood Parameter Estimates” table displays the parameter name, the degrees of freedom for each parameter, the maximum likelihood estimate of each parameter, the estimated standard error of the parameter estimator, confidence limits for each parameter, a chi-square statistic for testing whether the parameter is zero, and the associated p -value for the statistic.

Lagrange Multiplier Statistics

If there are constrained parameters in the model, such as the scale or intercept, then the “Lagrange Multiplier Statistics” table displays a Lagrange multiplier test for the constraint.

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 name of the input data set, the number of burn-in iterations, the number of iterations after the burn-in, the number of thinning iterations, the distribution name, and the name and label of the dependent variable; the name and label of the censor indicator variable, for right-censored data; if you specify the WEIGHT statement, the name and label of the weight variable; and the maximum value of the log likelihood.

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.

Posterior Summaries

The “Posterior Summaries” table contains the size of the sample, the mean, the standard deviation, and the quartiles for each model parameter.

Posterior Intervals

The “Posterior Intervals” 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 LIFEREG assigns a name to each table 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 48.4](#) for a maximum likelihood analysis and in [Table 48.5](#) for a Bayesian analysis. For more information about ODS, see Chapter 20, “Using the Output Delivery System.”

Table 48.4 ODS Tables Produced in PROC LIFEREG for a Classical Analysis

ODS Table Name	Description	Statement	Option
ClassLevels	Classification variable levels	CLASS	Default*
ConvergenceStatus	Convergence status	MODEL	Default
CorrB	Parameter estimate correlation matrix	MODEL	CORRB
CovB	Parameter estimate covariance matrix	MODEL	COVB
IterEM	Iteration history for Turnbull algorithm	PROBPLOT	ITPRINTEM
FitStatistics	Fit statistics	MODEL	Default
FitStatisticsUL	Fit statistics for unlogged response	MODEL	DISTRIBUTION=WEIBULL, LOGNORMAL, LLO- GISTIC, or GAMMA
IterHistory	Iteration history	MODEL	ITPRINT
LagrangeStatistics	Lagrange statistics	MODEL	NOINT NOSCALE
LastGrad	Last evaluation of the gradient	MODEL	ITPRINT
LastHess	Last evaluation of the Hessian	MODEL	ITPRINT
ModelInfo	Model information	MODEL	Default
NObs	Number of observations	MODEL	Default
ParameterEstimates	Parameter estimates	MODEL	Default
ParmInfo	Parameter indices	MODEL	Default
ProbabilityEstimates	Nonparametric CDF estimates	PROBPLOT	PPOUT
TConvergenceStatus	Convergence status for Turnbull algorithm	PROBPLOT	Default
Turnbull	Probability estimates from Turnbull algorithm	PROBPLOT	ITPRINTEM
Type3Analysis	Type 3 tests	MODEL	Default*

* Depends on data.

Table 48.5 ODS Tables Produced in PROC LIFEREG 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
MCErr	Monte Carlo standard errors	BAYES	DIAG=MCSE
ModelInfo	Model information	MODEL	Default
NObs	Number of observations	MODEL	Default
ParameterEstimates	Maximum likelihood estimates of model parameters	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 output data set only)	BAYES	
PostSummaries	Summary statistics of the posterior samples	BAYES	Default
Raftery	Raftery and Lewis convergence diagnostics	BAYES	DIAG=RAFTERY

* Depends on data.

ODS Graphics

To request graphics with PROC LIFEREG, 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 LIFEREG generates are listed in Table 48.6, along with the required statements and options.

ODS Graph Names

PROC LIFEREG 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 48.6.

To request these graphs, you must specify the ODS GRAPHICS ON; statement in addition to the options indicated in Table 48.6.

Table 48.6 ODS Graphics Produced by PROC LIFEREG

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
ProbPlot	Probability plot	PROBPLOT	Default
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

Examples: LIFEREG Procedure

Example 48.1: Motorette Failure

This example fits a Weibull model and a lognormal model to the example given in Kalbfleisch and Prentice (1980, p. 5). An output data set called models is specified to contain the parameter estimates. By default, the natural log of the variable time is used by the procedure as the response. After this log transformation, the Weibull model is fit using the extreme-value baseline distribution, and the lognormal is fit using the normal baseline distribution.

Since the extreme-value and normal distributions do not contain any shape parameters, the variable SHAPE1 is missing in the models data set. An additional output data set, out, is created that contains

the predicted quantiles and their standard errors for values of the covariate corresponding to temp=130 and temp=150. This is done with the control variable, which is set to 1 for only two observations.

Using the standard error estimates obtained from the output data set, approximate 90% confidence limits for the predicted quantities are then created in a subsequent DATA step for the log response. The logs of the predicted values are obtained because the values of the P= variable in the OUT= data set are in the same units as the original response variable, time. The standard errors of the quantiles of log(time) are approximated (using a Taylor series approximation) by the standard deviation of time divided by the mean value of time. These confidence limits are then converted back to the original scale by the exponential function.

The following statements produce [Output 48.1.1](#):

```

title 'Motorette Failures With Operating Temperature as a Covariate';
data motors;
  input time censor temp @@;
  if _N_=1 then
    do;
      temp=130;
      time=.;
      control=1;
      z=1000/(273.2+temp);
      output;
      temp=150;
      time=.;
      control=1;
      z=1000/(273.2+temp);
      output;
    end;
  if temp>150;
  control=0;
  z=1000/(273.2+temp);
  output;
  datalines;
8064 0 150 8064 0 150 8064 0 150 8064 0 150 8064 0 150
8064 0 150 8064 0 150 8064 0 150 8064 0 150 8064 0 150
1764 1 170 2772 1 170 3444 1 170 3542 1 170 3780 1 170
4860 1 170 5196 1 170 5448 0 170 5448 0 170 5448 0 170
  408 1 190  408 1 190 1344 1 190 1344 1 190 1440 1 190
1680 0 190 1680 0 190 1680 0 190 1680 0 190 1680 0 190
  408 1 220  408 1 220  504 1 220  504 1 220  504 1 220
  528 0 220  528 0 220  528 0 220  528 0 220  528 0 220
;
run;

proc print data=motors;
run;

```

Output 48.1.1 Motorette Failure Data

Motorette Failures With Operating Temperature as a Covariate					
Obs	time	censor	temp	control	z
1	.	0	130	1	2.48016
2	.	0	150	1	2.36295
3	1764	1	170	0	2.25632
4	2772	1	170	0	2.25632
5	3444	1	170	0	2.25632
6	3542	1	170	0	2.25632
7	3780	1	170	0	2.25632
8	4860	1	170	0	2.25632
9	5196	1	170	0	2.25632
10	5448	0	170	0	2.25632
11	5448	0	170	0	2.25632
12	5448	0	170	0	2.25632
13	408	1	190	0	2.15889
14	408	1	190	0	2.15889
15	1344	1	190	0	2.15889
16	1344	1	190	0	2.15889
17	1440	1	190	0	2.15889
18	1680	0	190	0	2.15889
19	1680	0	190	0	2.15889
20	1680	0	190	0	2.15889
21	1680	0	190	0	2.15889
22	1680	0	190	0	2.15889
23	408	1	220	0	2.02758
24	408	1	220	0	2.02758
25	504	1	220	0	2.02758
26	504	1	220	0	2.02758
27	504	1	220	0	2.02758
28	528	0	220	0	2.02758
29	528	0	220	0	2.02758
30	528	0	220	0	2.02758
31	528	0	220	0	2.02758
32	528	0	220	0	2.02758

The following statements produce [Output 48.1.2](#) and [Output 48.1.3](#):

```
proc lifereg data=motors outest=modela covout;
  a: model time*censor(0)=z;
      output out=outa quantiles=.1 .5 .9 std=std p=predtime
            control=control;
run;

proc lifereg data=motors outest=modelb covout;
  b: model time*censor(0)=z / dist=lnormal;
      output out=outb quantiles=.1 .5 .9 std=std p=predtime
            control=control;
run;
```

Output 48.1.2 Motorette Failure: Model A

Motorette Failures With Operating Temperature as a Covariate							
The LIFEREG Procedure							
Model Information							
Data Set	WORK.MOTORS						
Dependent Variable	Log(time)						
Censoring Variable	censor						
Censoring Value(s)	0						
Number of Observations	30						
Noncensored Values	17						
Right Censored Values	13						
Left Censored Values	0						
Interval Censored Values	0						
Number of Parameters	3						
Name of Distribution	Weibull						
Log Likelihood	-22.95148315						
Type III Analysis of Effects							
Effect	DF	Wald					
		Chi-Square	Pr > ChiSq				
z	1	99.5239	<.0001				
Analysis of Maximum Likelihood Parameter Estimates							
Parameter	DF	Estimate	Standard Error	95% Confidence Limits		Chi-Square	Pr > ChiSq
Intercept	1	-11.8912	1.9655	-15.7435	-8.0389	36.60	<.0001
z	1	9.0383	0.9060	7.2626	10.8141	99.52	<.0001
Scale	1	0.3613	0.0795	0.2347	0.5561		
Weibull Shape	1	2.7679	0.6091	1.7982	4.2605		

Output 48.1.3 Motorette Failure: Model B

Motorette Failures With Operating Temperature as a Covariate							
The LIFEREG Procedure							
Model Information							
Data Set	WORK.MOTORS						
Dependent Variable	Log(time)						
Censoring Variable	censor						
Censoring Value(s)	0						
Number of Observations	30						
Noncensored Values	17						
Right Censored Values	13						
Left Censored Values	0						
Interval Censored Values	0						
Number of Parameters	3						
Name of Distribution	Lognormal						
Log Likelihood	-24.47381031						
Type III Analysis of Effects							
Effect	DF	Wald					
		Chi-Square	Pr >	ChiSq			
z	1	42.0001	<.0001				
Analysis of Maximum Likelihood Parameter Estimates							
Parameter	DF	Estimate	Standard Error	95% Confidence Limits		Chi-Square	Pr > ChiSq
Intercept	1	-10.4706	2.7719	-15.9034	-5.0377	14.27	0.0002
z	1	8.3221	1.2841	5.8052	10.8389	42.00	<.0001
Scale	1	0.6040	0.1107	0.4217	0.8652		

The following statements produce [Output 48.1.4](#):

```
data models;
  set modela modelb;
run;
proc print data=models;
  id _model_;
  title 'fitted models';
run;
```

Output 48.1.4 Motorette Failure: Fitted Models

fitted models					
<u>MODEL</u>	<u>NAME</u>	<u>TYPE</u>	<u>DIST</u>	<u>STATUS</u>	<u>LNLIKE</u>
a	time	PARMS	Weibull	0 Converged	-22.9515
a	Intercept	COV	Weibull	0 Converged	-22.9515
a	z	COV	Weibull	0 Converged	-22.9515
a	Scale	COV	Weibull	0 Converged	-22.9515
b	time	PARMS	Lognormal	0 Converged	-24.4738
b	Intercept	COV	Lognormal	0 Converged	-24.4738
b	z	COV	Lognormal	0 Converged	-24.4738
b	Scale	COV	Lognormal	0 Converged	-24.4738

<u>MODEL</u>	<u>time</u>	<u>Intercept</u>	<u>z</u>	<u>SCALE</u>
a	-1.0000	-11.8912	9.03834	0.36128
a	-11.8912	3.8632	-1.77878	0.03448
a	9.0383	-1.7788	0.82082	-0.01488
a	0.3613	0.0345	-0.01488	0.00632
b	-1.0000	-10.4706	8.32208	0.60403
b	-10.4706	7.6835	-3.55566	0.03267
b	8.3221	-3.5557	1.64897	-0.01285
b	0.6040	0.0327	-0.01285	0.01226

The following statements produce [Output 48.1.5](#):

```

data out;
  set outa outb;
run;

data out1;
  set out;
  ltime=log(predtime);
  stde=std/predtime;
  upper=exp(ltime+1.64*stde);
  lower=exp(ltime-1.64*stde);
run;

title 'quantile estimates and confidence limits';
proc print data=out1;
  id temp;
run;
title;

```

Output 48.1.5 Motorette Failure: Quantile Estimates and Confidence Limits

quantile estimates and confidence limits									
c		P		l		u		l	
c o		r		t		p		o	
e n		e		s		e		w	
t t n t	R	t	s	t	s	p	e	w	e
e i s r	O	i	t	m	d	e	e	r	r
m m o o	B	m	t	e	e	r	r	r	r
p e r l	z	e	d	e	e	r	r	r	r
130	. 0 1	2.48016	0.1	16519.27	5999.85	9.7123	0.36320	29969.51	9105.47
130	. 0 1	2.48016	0.5	32626.65	9874.33	10.3929	0.30265	53595.71	19861.63
130	. 0 1	2.48016	0.9	50343.22	15044.35	10.8266	0.29884	82183.49	30838.80
150	. 0 1	2.36295	0.1	5726.74	1569.34	8.6529	0.27404	8976.12	3653.64
150	. 0 1	2.36295	0.5	11310.68	2299.92	9.3335	0.20334	15787.62	8103.28
150	. 0 1	2.36295	0.9	17452.49	3629.28	9.7672	0.20795	24545.37	12409.24
130	. 0 1	2.48016	0.1	12033.19	5482.34	9.3954	0.45560	25402.68	5700.09
130	. 0 1	2.48016	0.5	26095.68	11359.45	10.1695	0.43530	53285.36	12779.95
130	. 0 1	2.48016	0.9	56592.19	26036.90	10.9436	0.46008	120349.65	26611.42
150	. 0 1	2.36295	0.1	4536.88	1443.07	8.4200	0.31808	7643.71	2692.83
150	. 0 1	2.36295	0.5	9838.86	2901.15	9.1941	0.29487	15957.38	6066.36
150	. 0 1	2.36295	0.9	21336.97	7172.34	9.9682	0.33615	37029.72	12294.62

Example 48.2: Computing Predicted Values for a Tobit Model

The LIFEREG procedure can be used to perform a Tobit analysis. The Tobit model, described by Tobin (1958), is a regression model for left-censored data assuming a normally distributed error term. The model parameters are estimated by maximum likelihood. PROC LIFEREG provides estimates of the parameters of the distribution of the *uncensored* data. See Greene (1993) and Maddala (1983) for a more complete discussion of censored normal data and related distributions. This example shows how you can use PROC LIFEREG and the DATA step to compute two of the three types of predicted values discussed there.

Consider a continuous random variable Y and a constant C . If you were to sample from the distribution of Y but discard values less than (greater than) C , the distribution of the remaining observations would be *truncated* on the left (right). If you were to sample from the distribution of Y and report values less than (greater than) C as C , the distribution of the sample would be left (right) *censored*.

The probability density function of the truncated random variable Y' is given by

$$f_{Y'}(y) = \frac{f_Y(y)}{\Pr(Y > C)} \text{ for } y > C$$

where $f_Y(y)$ is the probability density function of Y . PROC LIFEREG cannot compute the proper likelihood function to estimate parameters or predicted values for a truncated distribution. Suppose the model being fit is specified as follows:

$$Y_i^* = \mathbf{x}_i' \boldsymbol{\beta} + \epsilon_i$$

where ϵ_i is a normal error term with zero mean and standard deviation σ .

Define the censored random variable Y_i as

$$\begin{aligned} Y_i &= 0 \text{ if } Y_i^* \leq 0 \\ Y_i &= Y_i^* \text{ if } Y_i^* > 0 \end{aligned}$$

This is the Tobit model for left-censored normal data. Y_i^* is sometimes called the *latent variable*. PROC LIFEREG estimates parameters of the distribution of Y_i^* by maximum likelihood.

You can use the LIFEREG procedure to compute predicted values based on the mean functions of the latent and observed variables. The mean of the latent variable Y_i^* is $\mathbf{x}'_i\boldsymbol{\beta}$, and you can compute values of the mean for different settings of \mathbf{x}_i by specifying `XBETA=variable-name` in an OUTPUT statement. Estimates of $\mathbf{x}'_i\boldsymbol{\beta}$ for each observation will be written to the `OUT=` data set. Predicted values of the observed variable Y_i can be computed based on the mean

$$E(Y_i) = \Phi\left(\frac{\mathbf{x}'_i\boldsymbol{\beta}}{\sigma}\right) (\mathbf{x}'_i\boldsymbol{\beta} + \sigma\lambda_i)$$

where

$$\lambda_i = \frac{\phi(\mathbf{x}'_i\boldsymbol{\beta}/\sigma)}{\Phi(\mathbf{x}'_i\boldsymbol{\beta}/\sigma)}$$

ϕ and Φ represent the normal probability density and cumulative distribution functions.

Although the distribution of ϵ_i in the Tobit model is often assumed normal, you can use other distributions for the Tobit model in the LIFEREG procedure by specifying a distribution with the `DISTRIBUTION=` option in the MODEL statement. One distribution that should be mentioned is the logistic distribution. For this distribution, the MLE has bounded influence function with respect to the response variable, but not the design variables. If you believe your data have outliers in the response direction, you might try this distribution for some robust estimation of the Tobit model.

With the logistic distribution, the predicted values of the observed variable Y_i can be computed based on the mean of Y_i^* ,

$$E(Y_i) = \sigma \ln(1 + \exp(\mathbf{x}'_i\boldsymbol{\beta}/\sigma))$$

The following table shows a subset of the Mroz (1987) data set. In these data, Hours is the number of hours the wife worked outside the household in a given year, Yrs_Ed is the years of education, and Yrs_Exp is the years of work experience. A Tobit model will be fit to the hours worked with years of education and experience as covariates.

Hours	Yrs_Ed	Yrs_Exp
0	8	9
0	8	12
0	9	10
0	10	15
0	11	4
0	11	6
1000	12	1
1960	12	29
0	13	3
2100	13	36
3686	14	11
1920	14	38
0	15	14
1728	16	3
1568	16	19
1316	17	7
0	17	15

If the wife was not employed (worked 0 hours), her hours worked will be left censored at zero. In order to accommodate left censoring in PROC LIFEREG, you need two variables to indicate censoring status of observations. You can think of these variables as lower and upper endpoints of interval censoring. If there is no censoring, set both variables to the observed value of Hours. To indicate left censoring, set the lower endpoint to missing and the upper endpoint to the censored value, zero in this case.

The following statements create a SAS data set with the variables Hours, Yrs_Ed, and Yrs_Exp from the preceding data. A new variable, Lower, is created such that Lower=. if Hours=0 and Lower=Hours if Hours>0.

```

data subset;
  input Hours Yrs_Ed Yrs_Exp @@;
  if Hours eq 0
    then Lower=.;
    else Lower=Hours;
datalines;
0 8 9 0 8 12 0 9 10 0 10 15 0 11 4 0 11 6
1000 12 1 1960 12 29 0 13 3 2100 13 36
3686 14 11 1920 14 38 0 15 14 1728 16 3
1568 16 19 1316 17 7 0 17 15
;
run;

```

The following statements fit a normal regression model to the left-censored Hours data with Yrs_Ed and Yrs_Exp as covariates. You need the estimated standard deviation of the normal distribution to compute the predicted values of the censored distribution from the preceding formulas. The data set OUTEST contains the standard deviation estimate in a variable named `_SCALE_`. You also need estimates of $\mathbf{x}'_i\boldsymbol{\beta}$. These are contained in the data set OUT as the variable Xbeta.

```
proc lifereg data=subset outest=OUTEST(keep=_scale_);
  model (lower, hours) = yrs_ed yrs_exp / d=normal;
  output out=OUT xbeta=Xbeta;
run;
```

Output 48.2.1 shows the results of the model fit. These tables show parameter estimates for the uncensored, or latent variable, distribution.

Output 48.2.1 Parameter Estimates from PROC LIFEREG

The LIFEREG Procedure							
Model Information							
Data Set							WORK.SUBSET
Dependent Variable							Lower
Dependent Variable							Hours
Number of Observations							17
Noncensored Values							8
Right Censored Values							0
Left Censored Values							9
Interval Censored Values							0
Number of Parameters							4
Name of Distribution							Normal
Log Likelihood							-74.9369977
Analysis of Maximum Likelihood Parameter Estimates							
Parameter	DF	Estimate	Standard Error	95% Confidence Limits		Chi-Square	Pr > ChiSq
Intercept	1	-5598.64	2850.248	-11185.0	-12.2553	3.86	0.0495
Yrs_Ed	1	373.1477	191.8872	-2.9442	749.2397	3.78	0.0518
Yrs_Exp	1	63.3371	38.3632	-11.8533	138.5276	2.73	0.0987
Scale	1	1582.870	442.6732	914.9433	2738.397		

The following statements combine the two data sets created by PROC LIFEREG to compute predicted values for the censored distribution. The OUTEST= data set contains the estimate of the standard deviation from the uncensored distribution, and the OUT= data set contains estimates of $x_i'\beta$.

```
data predict;
  drop lambda _scale_ _prob_;
  set out;
  if _n_ eq 1 then set outest;
  lambda = pdf('NORMAL', Xbeta/_scale_)
          / cdf('NORMAL', Xbeta/_scale_);
  Predict = cdf('NORMAL', Xbeta/_scale_)
           * (Xbeta + _scale_*lambda);
  label Xbeta='MEAN OF UNCENSORED VARIABLE'
        Predict = 'MEAN OF CENSORED VARIABLE';
run;
```

Output 48.2.2 shows the original variables, the predicted means of the uncensored distribution, and the predicted means of the censored distribution.

Output 48.2.2 Predicted Means from PROC LIFEREG

Hours	Lower	Yrs_Ed	Yrs_Exp	MEAN OF UNCENSORED VARIABLE	MEAN OF CENSORED VARIABLE
0	.	8	9	-2043.42	73.46
0	.	8	12	-1853.41	94.23
0	.	9	10	-1606.94	128.10
0	.	10	15	-917.10	276.04
0	.	11	4	-1240.67	195.76
0	.	11	6	-1113.99	224.72
1000	1000	12	1	-1057.53	238.63
1960	1960	12	29	715.91	1052.94
0	.	13	3	-557.71	391.42
2100	2100	13	36	1532.42	1672.50
3686	3686	14	11	322.14	805.58
1920	1920	14	38	2032.24	2106.81
0	.	15	14	885.30	1170.39
1728	1728	16	3	561.74	951.69
1568	1568	16	19	1575.13	1708.24
1316	1316	17	7	1188.23	1395.61
0	.	17	15	1694.93	1809.97

Example 48.3: Overcoming Convergence Problems by Specifying Initial Values

This example illustrates the use of parameter initial value specification to help overcome convergence difficulties.

The following statements create a SAS data set.

```
data raw;
  input censor x c1 @@;
  datalines;
0 16 0.00  0 17 0.00  0 18 0.00
0 17 0.04  0 18 0.04  0 18 0.04
0 23 0.40  0 22 0.40  0 22 0.40
0 33 4.00  0 34 4.00  0 35 4.00
1 54 40.00  1 54 40.00  1 54 40.00
1 54 400.00 1 54 400.00 1 54 400.00
;
run;
```

Output 48.3.1 shows the contents of the data set raw.

Output 48.3.1 Contents of the Data Set

Obs	sensor	x	c1
1	0	16	0.00
2	0	17	0.00
3	0	18	0.00
4	0	17	0.04
5	0	18	0.04
6	0	18	0.04
7	0	23	0.40
8	0	22	0.40
9	0	22	0.40
10	0	33	4.00
11	0	34	4.00
12	0	35	4.00
13	1	54	40.00
14	1	54	40.00
15	1	54	40.00
16	1	54	400.00
17	1	54	400.00
18	1	54	400.00

The following SAS statements request that a Weibull regression model be fit to the data:

```

title 'OLS (default) initial values';
proc lifereg data=raw;
  model x*sensor(1) = c1 / distribution = Weibull itprint;
run;

```

Convergence was not attained in 50 iterations for this model, as the following messages to the log indicate:

```

WARNING: Convergence was not attained in 50 iterations. You might want to
increase the maximum number of iterations (MAXITER= option) or
change the convergence criteria (CONVERGE = value) in the MODEL
statement.
WARNING: The procedure is continuing in spite of the above warning. Results
shown are based on the last maximum likelihood iteration. Validity
of the model fit is questionable.

```

The first line (iter=0) of the iteration history table, shown in [Output 48.3.2](#), shows the default initial ordinary least squares (OLS) estimates of the parameters.

Output 48.3.2 Initial Least Squares

OLS (default) initial values					
The LIFEREG Procedure					
Iteration History for Parameter Estimates					
Iter	Ridge	Loglikelihood	Intercept	c1	Scale
0	0	-22.891088	3.2324769714	0.0020664542	0.3995754195
1	0	-16.427074	3.5337141598	0.0028713635	0.3283544365
2	0	-13.216768	3.4480787541	0.0052801225	0.3816964358
3	0	-5.0786635	3.1966395335	0.0191439929	0.2325418958
4	0	-2.0018885	3.1848047525	0.0275425402	0.1963590539
5	0	-0.1814984	3.1478989655	0.0374731819	0.2103607621
6	0	2.90712131	3.0858183316	0.0659946149	0.1818245261
7	0.063	2.9991781	3.1014479187	0.0661096622	0.1648677081
8	0.063	3.01557837	3.0995493638	0.0662333056	0.1670552505
9	0.063	3.0301815	3.0992317977	0.0663580659	0.1669529486
10	0.063	3.0448013	3.0989901232	0.0664827053	0.1667371524
11	0.063	3.05941254	3.0987507448	0.0666071514	0.1665197313
12	0.063	3.07401474	3.0985118143	0.0667314052	0.1663026517
13	0.063	3.08860788	3.0982732928	0.066855467	0.1660859472
14	0.063	3.10319193	3.0980351787	0.0669793371	0.1658696184
15	0.063	3.11776689	3.0977974713	0.0671030156	0.1656536651
16	0.063	3.13233272	3.0975601698	0.0672265029	0.1654380873
17	0.063	3.1468894	3.0973232737	0.0673497993	0.165222885
18	0.063	3.16143692	3.0970867821	0.0674729049	0.1650080579
19	0.063	3.17597526	3.0968506943	0.06759582	0.1647936061
20	0.063	3.19050439	3.0966150098	0.0677185449	0.1645795293
21	0.063	3.2050243	3.0963797277	0.0678410799	0.1643658275
22	0.063	3.21953496	3.0961448474	0.0679634252	0.1641525006
23	0.063	3.23403635	3.0959103682	0.068085581	0.1639395483
24	0.063	3.24852845	3.0956762896	0.0682075476	0.1637269705
25	0.063	3.26301123	3.0954426107	0.0683293253	0.1635147672
26	0.063	3.27748468	3.095209331	0.0684509143	0.163302938
27	0.063	3.29194878	3.0949764498	0.0685723149	0.1630914829
28	0.063	3.3064035	3.0947439665	0.0686935273	0.1628804017
29	0.063	3.32084881	3.0945118805	0.0688145517	0.1626696942
30	0.063	3.3352847	3.0942801911	0.0689353885	0.1624593601
31	0.063	3.34971114	3.0940488977	0.0690560378	0.1622493994
32	0.063	3.36412812	3.0938179997	0.0691765	0.1620398118
33	0.063	3.3785356	3.0935874965	0.0692967752	0.1618305971
34	0.063	3.39293356	3.0933573875	0.0694168637	0.161621755
35	0.063	3.40732199	3.093127672	0.0695367658	0.1614132855
36	0.063	3.42170085	3.0928983495	0.0696564816	0.1612051882
37	0.063	3.43607013	3.0926694194	0.0697760116	0.1609974629
38	0.063	3.45042979	3.0924408811	0.0698953558	0.1607901095
39	0.063	3.46477983	3.092212734	0.0700145146	0.1605831276
40	0.063	3.4791202	3.0919849776	0.0701334882	0.160376517
41	0.063	3.4934509	3.0917576112	0.0702522768	0.1601702775
42	0.063	3.50777188	3.0915306343	0.0703708808	0.1599644088
43	0.063	3.52208314	3.0913040464	0.0704893002	0.1597589108
44	0.063	3.53638465	3.0910778468	0.0706075354	0.159553783
45	0.063	3.55067637	3.0908520349	0.0707255867	0.1593490254
46	0.063	3.5649583	3.0906266104	0.0708434542	0.1591446376
47	0.063	3.57923039	3.0904015725	0.0709611382	0.1589406193
48	0.063	3.59349263	3.0901769207	0.0710786389	0.1587369703
49	0.063	3.607745	3.0899526546	0.0711959567	0.1585336903
50	0.063	3.62198746	3.0897287734	0.0713130916	0.1583307791

The log-logistic distribution is more robust to large values of the response than the Weibull distribution, so one approach to improving the convergence performance is to fit a log-logistic distribution, and if this converges, use the resulting parameter estimates as initial values in a subsequent fit of a model with the Weibull distribution.

The following statements fit a log-logistic distribution to the data:

```
proc lifereg data=raw;
  model x*censor(1) = c1 / distribution = llogistic;
run;
```

The algorithm converges, and the maximum likelihood estimates for the log-logistic distribution are shown in [Output 48.3.3](#)

Output 48.3.3 Estimates from the Log-Logistic Distribution

OLS (default) initial values							
The LIFEREG Procedure							
Analysis of Maximum Likelihood Parameter Estimates							
Parameter	DF	Estimate	Standard Error	95% Confidence Limits		Chi-Square	Pr > ChiSq
Intercept	1	2.8983	0.0318	2.8360	2.9606	8309.43	<.0001
c1	1	0.1592	0.0133	0.1332	0.1852	143.85	<.0001
Scale	1	0.0498	0.0122	0.0308	0.0804		

The following statements refit the Weibull model by using the maximum likelihood estimates from the log-logistic fit as initial values:

```
proc lifereg data=raw outest=outest;
  model x*censor(1) = c1 / itprint distribution = weibull
    intercept=2.898 initial=0.16 scale=0.05;
  output out=out xbeta=xbeta;
run;
```

Examination of the resulting output in [Output 48.3.4](#) shows that the convergence problem has been solved by specifying different initial values.

Output 48.3.4 Final Estimates from the Weibull Distribution

OLS (default) initial values							
The LIFEREG Procedure							
Model Information							
Data Set	WORK.RAW						
Dependent Variable	Log(x)						
Censoring Variable	censor						
Censoring Value(s)	1						
Number of Observations	18						
Noncensored Values	12						
Right Censored Values	6						
Left Censored Values	0						
Interval Censored Values	0						
Number of Parameters	3						
Name of Distribution	Weibull						
Log Likelihood	11.232023272						
Algorithm converged.							
Analysis of Maximum Likelihood Parameter Estimates							
Parameter	DF	Estimate	Standard Error	95% Confidence Limits		Chi-Square	Pr > ChiSq
Intercept	1	2.9699	0.0326	2.9059	3.0338	8278.86	<.0001
c1	1	0.1435	0.0165	0.1111	0.1758	75.43	<.0001
Scale	1	0.0844	0.0189	0.0544	0.1308		
Weibull Shape	1	11.8526	2.6514	7.6455	18.3749		

As an example of an alternative way of specifying initial values, the following invocation of PROC LIFEREG, using the INEST= data set to provide starting values for the three parameters, is equivalent to the previous invocation:

```
data in;
  input intercept c1 scale;
  datalines;
2.898 0.16 0.05
;
proc lifereg data=raw inest=in outest=outest;
  model x*censor(1) = c1 / itprint distribution = weibull;
  output out=out xbeta=xbeta;
run;
```

Example 48.4: Analysis of Arbitrarily Censored Data with Interaction Effects

The artificial data in this example are from a study of the natural recovery time of mice after injection of a certain toxin. Twenty mice were grouped by sex (sex: 1 = Male, 2 = Female) with equal sizes. Their ages (in days) were recorded at the injection. Their recovery times (in minutes) were also recorded. Toxin density in blood was used to decide whether a mouse recovered. Mice were checked at two times for recovery. If a mouse had recovered at the first time, the observation is left censored, and no further measurement is made. The variable `time1` is set to missing and `time2` is set to the measurement time to indicate left censoring. If a mouse had not recovered at the first time, it was checked later at a second time. If it had recovered by the second measurement time, the observation is interval censored, and the variable `time1` is set to the first measurement time and `time2` is set to the second measurement time. If there was no recovery at the second measurement, the observation is right censored, and `time1` is set to the second measurement time and `time2` is set to missing to indicate right censoring.

The following statements create a SAS data set containing the data from the experiment:

```

title 'Natural Recovery Time';
data mice;
  input sex age time1 time2 ;
  datalines;
1 57 631 631
1 45 . 170
1 54 227 227
1 43 143 143
1 64 916 .
1 67 691 705
1 44 100 100
1 59 730 .
1 47 365 365
1 74 1916 1916
2 79 1326 .
2 75 837 837
2 84 1200 1235
2 54 . 365
2 74 1255 1255
2 71 1823 .
2 65 537 637
2 33 583 683
2 77 955 .
2 46 577 577
;

```

The following SAS statements create the SAS data sets `xrow1` and `xrow2`:

```

data xrow1;
  input sex age time1 time2 ;
  datalines;
1 50 . .
;

data xrow2;
  input sex age time1 time2 ;
  datalines;
2 60.6 . .
;

```

The following SAS statements fit a Weibull model with age, sex, and an age-by-sex interaction term as covariates, and create a plot of predicted probabilities against recovery time for the fixed values of age and sex specified in the SAS data set xrow1:

```

ods graphics on;
proc lifereg data=mice xdata=xrow1;
  class sex ;
  model (time1, time2) = age sex age*sex / dist=Weibull;

  probplot / nodata
    plower=.5
    vref(intersect) = 75
    vreflab = '75 Percent'
  ;
  inset;
run;

```

Standard output is shown in [Output 48.4.1](#). Tables containing general model information, Type III tests for the main effects and interaction terms, and parameter estimates are created.

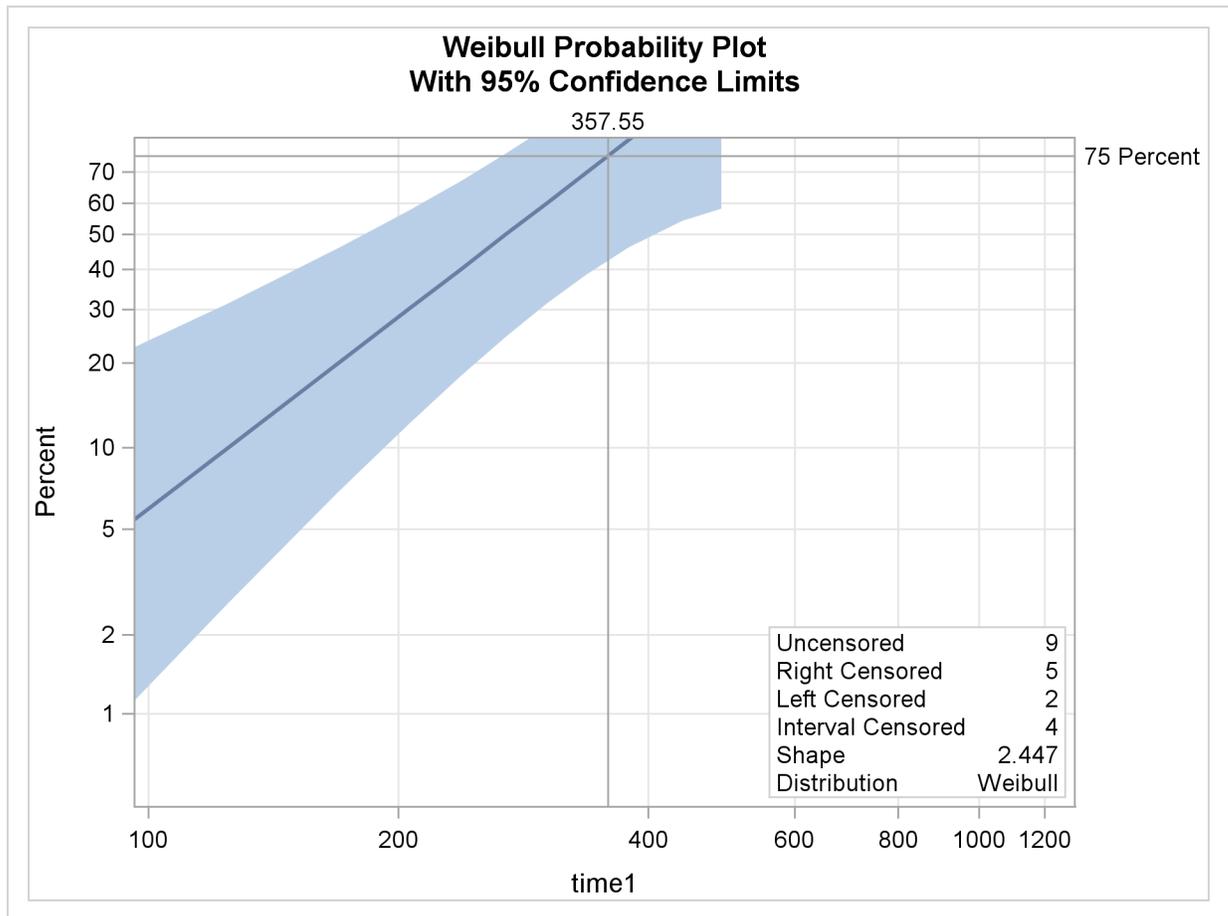
Output 48.4.1 Parameter Estimates for the Interaction Model

Natural Recovery Time	
The LIFEREG Procedure	
Model Information	
Data Set	WORK.MICE
Dependent Variable	Log(time1)
Dependent Variable	Log(time2)
Number of Observations	20
Noncensored Values	9
Right Censored Values	5
Left Censored Values	2
Interval Censored Values	4
Number of Parameters	5
Name of Distribution	Weibull
Log Likelihood	-25.91033295

Output 48.4.1 continued

Type III Analysis of Effects							
Effect	DF		Wald				
			Chi-Square			Pr >	ChiSq
age	1		33.8496			<.0001	
sex	1		14.0245			0.0002	
age*sex	1		10.7196			0.0011	
Analysis of Maximum Likelihood Parameter Estimates							
Parameter	DF	Estimate	Standard Error	95% Confidence Limits		Chi-Square	Pr > ChiSq
Intercept	1	5.4110	0.5549	4.3234	6.4986	95.08	<.0001
age	1	0.0250	0.0086	0.0081	0.0419	8.42	0.0037
sex	1	-3.9808	1.0630	-6.0643	-1.8974	14.02	0.0002
sex	2	0.0000
age*sex	1	0.0613	0.0187	0.0246	0.0980	10.72	0.0011
age*sex	2	0.0000
Scale	1	0.4087	0.0900	0.2654	0.6294		
Weibull Shape	1	2.4468	0.5391	1.5887	3.7682		

The following two plots display the predicted probability against the recovery time for two different populations. [Output 48.4.2](#) is created with the PROBLOT statement with the option XDATA=xrow1, which specifies the population with sex = 1, age = 50. [Output 48.4.3](#) is created with the PROBLOT statement with the option XDATA=xrow2, which specifies the population with sex = 2, age = 60.6. These are the default values that the LIFEREG procedure would use for the probability plot if the XDATA= option had not been specified. Reference lines are used to display specified predicted probability points and their relative locations in the plot.

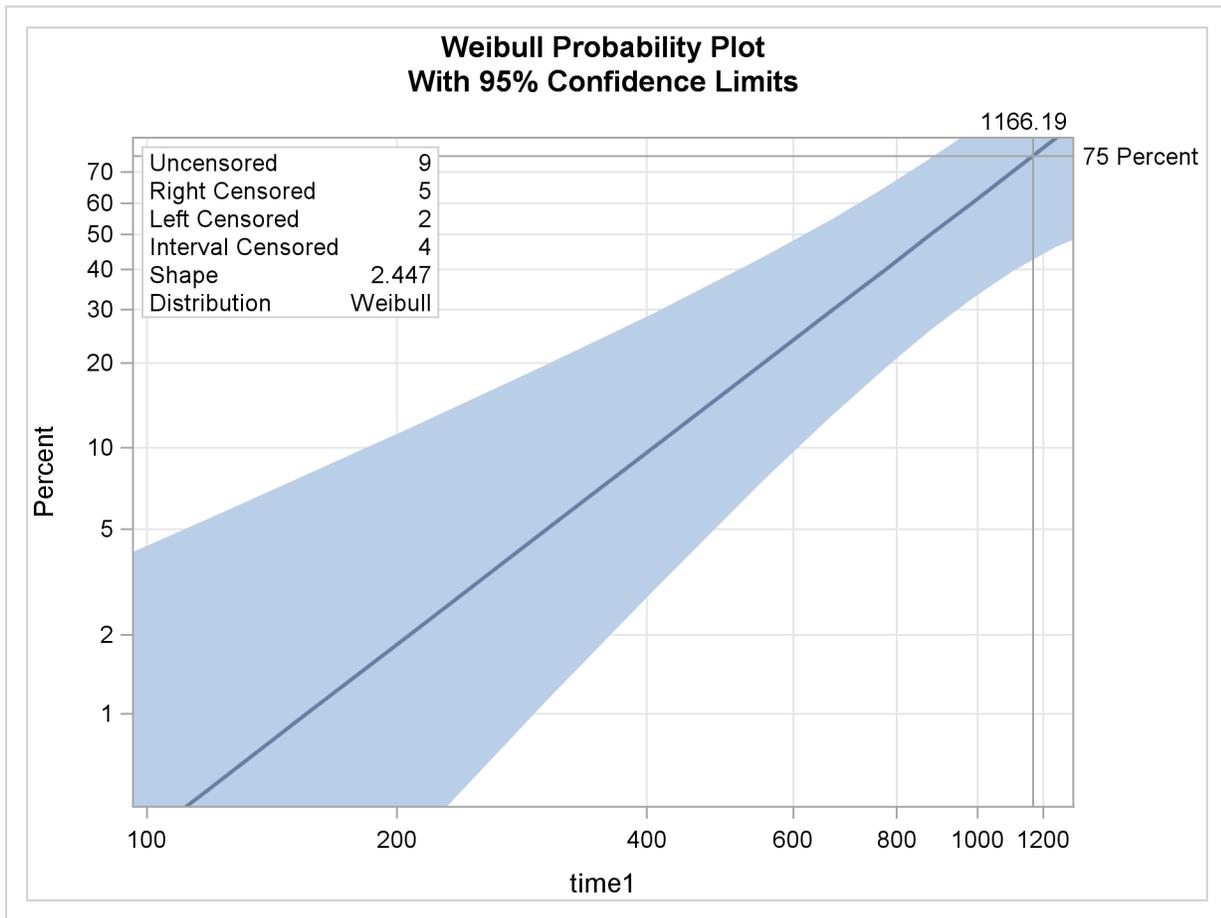
Output 48.4.2 Probability Plot for Recovery Time with sex = 1, age = 50

The following SAS statements fit a Weibull model with age, sex, and an age-by-sex interaction term as covariates, and create the plot of predicted probabilities against recovery time shown in [Output 48.4.3](#), for the fixed values of age and sex specified in the SAS data set xrow2:

```
proc lifereg data=mice xdata=xrow2;
  class sex ;
  model (time1, time2) = age sex age*sex / dist=Weibull;

  probplot / nodata
    plower=.5
    vref(intersect) = 75
    vreflab = '75 Percent'
  ;
  inset;
run;
title;
ods graphics off;
```

Output 48.4.3 Probability Plot for Recovery Time with sex = 2, age = 60.6



Example 48.5: Probability Plotting—Right Censoring

The following statements create a SAS data set containing observed and right-censored lifetimes of 70 diesel engine fans (Nelson 1982):

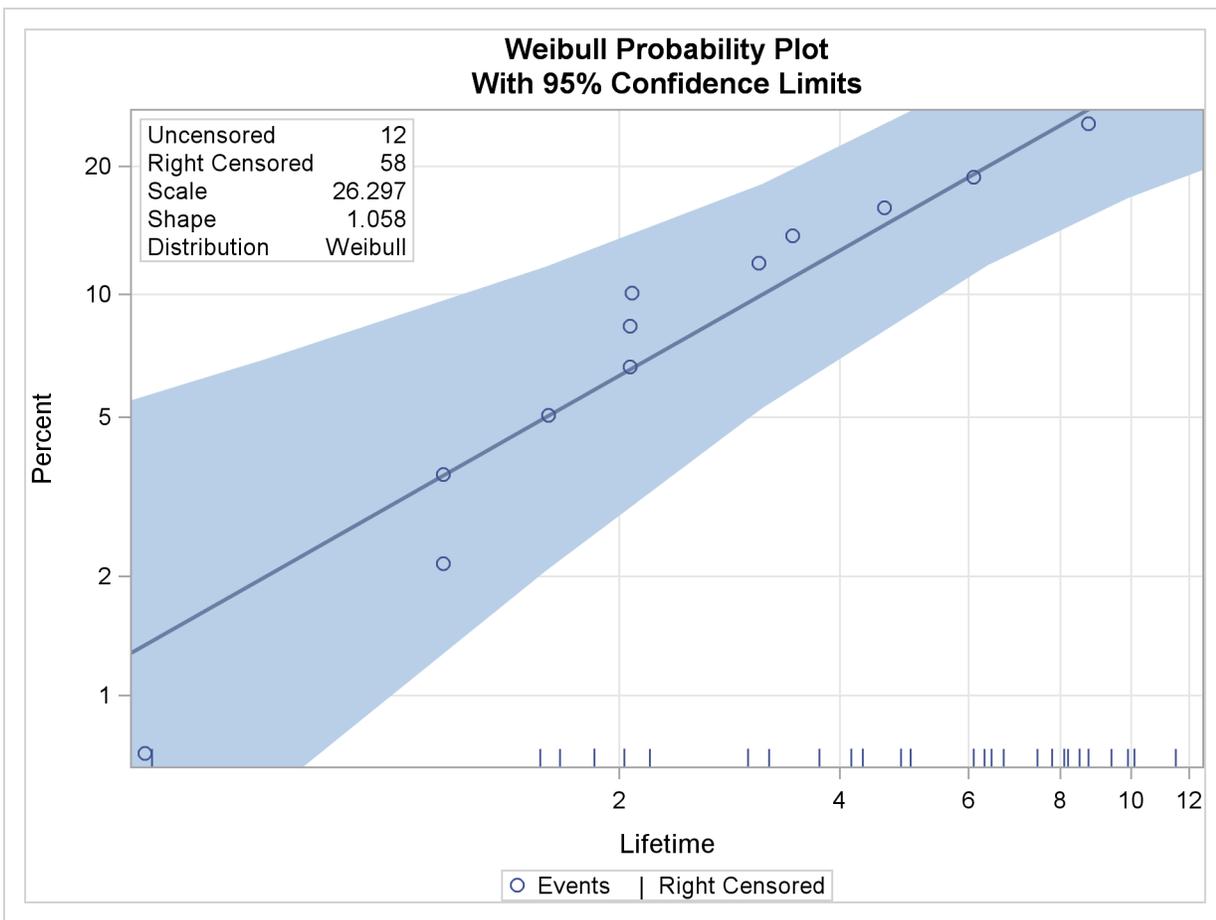
```
data Fan;
  input Lifetime Censor@@;
  Lifetime = Lifetime / 1000;
  datalines;
  450 0    460 1    1150 0    1150 0    1560 1
  1600 0    1660 1    1850 1    1850 1    1850 1
  1850 1    1850 1    2030 1    2030 1    2030 1
  2070 0    2070 0    2080 0    2200 1    3000 1
  3000 1    3000 1    3000 1    3100 0    3200 1
  3450 0    3750 1    3750 1    4150 1    4150 1
  4150 1    4150 1    4300 1    4300 1    4300 1
  4300 1    4600 0    4850 1    4850 1    4850 1
  4850 1    5000 1    5000 1    5000 1    6100 1
  6100 0    6100 1    6100 1    6300 1    6450 1
  6450 1    6700 1    7450 1    7800 1    7800 1
  8100 1    8100 1    8200 1    8500 1    8500 1
  8500 1    8750 1    8750 0    8750 1    9400 1
  9900 1    10100 1    10100 1    10100 1    11500 1
;
run;
```

Some of the fans had not failed at the time the data were collected, and the unfailed units have right-censored lifetimes. The variable LIFETIME represents either a failure time or a censoring time, in thousands of hours. The variable CENSOR is equal to 0 if the value of LIFETIME is a failure time, and it is equal to 1 if the value is a censoring time. The following statements use the LIFEREG procedure to produce the probability plot with an inset for the engine lifetimes:

```
ods graphics on;
proc lifereg data=Fan;
  model Lifetime*Censor( 1 ) = / d = Weibull;
  probplot
  ppout
  npintervals=simul
  ;
  inset;
run;
ods graphics off;
```

The resulting graphical output is shown in [Output 48.5.1](#). The estimated CDF, a line representing the maximum likelihood fit, and pointwise parametric confidence bands are plotted in the body of [Output 48.5.1](#). The values of right-censored observations are plotted along the bottom of the graph. The “Cumulative Probability Estimates” table is also created in [Output 48.5.2](#).

Output 48.5.1 Probability Plot for the Fan Data



Output 48.5.2 CDF Estimates

Lifetime	Cumulative Probability Estimates				Kaplan-Meier Estimate	Kaplan-Meier Standard Error
	Cumulative Probability	Simultaneous 95% Confidence Limits				
		Lower	Upper			
0.45	0.0071	0.0007	0.2114	0.0143	0.0142	
1.15	0.0215	0.0033	0.2114	0.0288	0.0201	
1.15	0.0360	0.0073	0.2168	0.0433	0.0244	
1.6	0.0506	0.0125	0.2304	0.0580	0.0282	
2.07	0.0666	0.0190	0.2539	0.0751	0.0324	
2.07	0.0837	0.0264	0.2760	0.0923	0.0361	
2.08	0.1008	0.0344	0.2972	0.1094	0.0392	
3.1	0.1189	0.0436	0.3223	0.1283	0.0427	
3.45	0.1380	0.0535	0.3471	0.1477	0.0460	
4.6	0.1602	0.0653	0.3844	0.1728	0.0510	
6.1	0.1887	0.0791	0.4349	0.2046	0.0581	
8.75	0.2488	0.0884	0.6391	0.2930	0.0980	

Example 48.6: Probability Plotting—Arbitrary Censoring

Table 48.7 contains microprocessor failure data (Nelson 1990). Units were inspected at predetermined time intervals. The data consist of inspection interval endpoints (in hours) and the number of units failing in each interval. A missing (.) lower endpoint indicates left censoring, and a missing upper endpoint indicates right censoring. These can be thought of as semi-infinite intervals with a lower (upper) endpoint of negative (positive) infinity for left (right) censoring.

Table 48.7 Interval-Censored Data

Lower Endpoint	Upper Endpoint	Number Failed
.	6	6
6	12	2
24	48	2
24	.	1
48	168	1
48	.	839
168	500	1
168	.	150
500	1000	2
500	.	149
1000	2000	1
1000	.	147
2000	.	122

The following SAS statements create the SAS data set Micro:

```

data Micro;
  input t1 t2 f ;
  datalines;
. 6 6
6 12 2
12 24 0
24 48 2
24 . 1
48 168 1
48 . 839
168 500 1
168 . 150
500 1000 2
500 . 149
1000 2000 1
1000 . 147
2000 . 122
;
run;

```

The following SAS statements compute the nonparametric Turnbull estimate of the cumulative distribution function and create a lognormal probability plot:

```
ods graphics on;
proc lifereg data=Micro;
  model ( t1 t2 ) = / d=lognormal intercept=25 scale=5;
  weight f;
  probplot
  pupper = 10
  itprintem
  printprobs
  maxitem = (1000,25)
  ppout;
  inset;
run;
ods graphics off;
```

The two initial values INTERCEPT=25 and SCALE=5 in the MODEL statement are used to aid convergence in the model-fitting algorithm.

The following tables are created by the PROBLOT statement in addition to the standard tabular output from the MODEL statement. [Output 48.6.1](#) shows the iteration history for the Turnbull estimate of the CDF for the microprocessor data. With both options ITPRINTEM and PRINTPROBS specified in the PROBLOT statement, this table contains the log likelihoods and interval probabilities for every 25th iteration and the last iteration. It would contain only the log likelihoods if the option PRINTPROBS were not specified.

Output 48.6.1 Iteration History for the Turnbull Estimate

The LIFEREG Procedure					
Iteration History for the Turnbull Estimate of the CDF					
Iteration	Loglikelihood	(., 6)	(6, 12)	(24, 48)	(48, 168)
		(168, 500)	(500, 1000)	(1000, 2000)	(2000, .)
0	-1133.4051	0.125	0.125	0.125	0.125
		0.125	0.125	0.125	0.125
25	-104.16622	0.00421644	0.00140548	0.00140648	0.00173338
		0.00237846	0.00846094	0.04565407	0.93474475
50	-101.15151	0.00421644	0.00140548	0.00140648	0.00173293
		0.00234891	0.00727679	0.01174486	0.96986811
75	-101.06641	0.00421644	0.00140548	0.00140648	0.00173293
		0.00234891	0.00727127	0.00835638	0.9732621
100	-101.06534	0.00421644	0.00140548	0.00140648	0.00173293
		0.00234891	0.00727125	0.00801814	0.97360037
125	-101.06533	0.00421644	0.00140548	0.00140648	0.00173293
		0.00234891	0.00727125	0.00798438	0.97363413
130	-101.06533	0.00421644	0.00140548	0.00140648	0.00173293
		0.00234891	0.00727125	0.007983	0.97363551

The table in [Output 48.6.2](#) summarizes the Turnbull estimates of the interval probabilities, the reduced gradients, and Lagrange multipliers as described in the section “Arbitrarily Censored Data” on page 3654.

Output 48.6.2 Summary for the Turnbull Algorithm

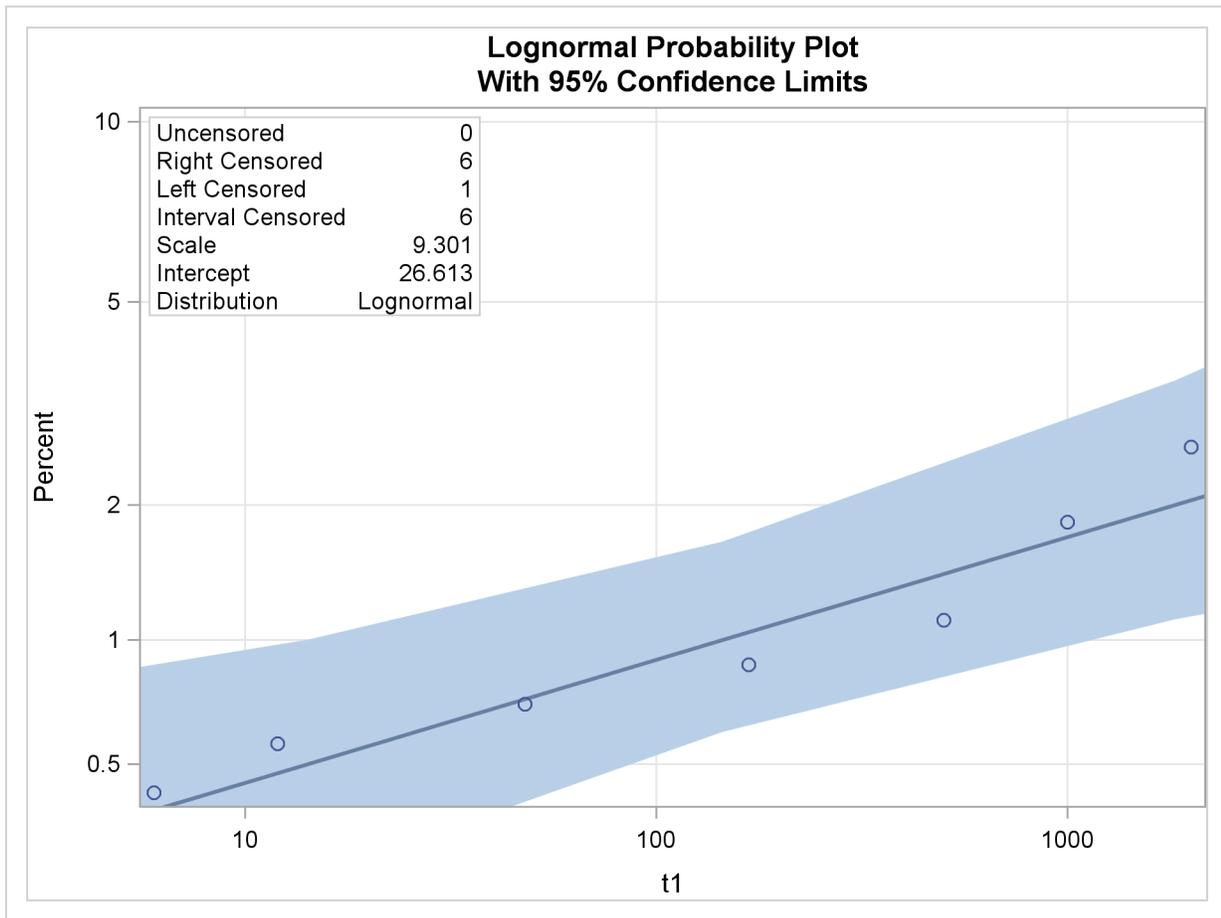
Lower Lifetime	Upper Lifetime	Probability	Reduced Gradient	Lagrange Multiplier
.	6	0.0042	0	0
6	12	0.0014	0	0
24	48	0.0014	0	0
48	168	0.0017	0	0
168	500	0.0023	0	0
500	1000	0.0073	-7.219342E-9	0
1000	2000	0.0080	-0.037063236	0
2000	.	0.9736	0.0003038877	0

Output 48.6.3 shows the final estimate of the CDF, along with standard errors and nonparametric confidence limits. Two kinds of nonparametric confidence limits, pointwise or simultaneous, are available. The default is the pointwise nonparametric confidence limits. You can specify the simultaneous nonparametric confidence limits by using the NPINTERVALS=SIMUL option.

Output 48.6.3 Final CDF Estimates for Turnbull Algorithm

Cumulative Probability Estimates					
Pointwise 95% Confidence Limits					
Lower Lifetime	Upper Lifetime	Cumulative Probability	Lower	Upper	Standard Error
6	6	0.0042	0.0019	0.0094	0.0017
12	24	0.0056	0.0028	0.0112	0.0020
48	48	0.0070	0.0038	0.0130	0.0022
168	168	0.0088	0.0047	0.0164	0.0028
500	500	0.0111	0.0058	0.0211	0.0037
1000	1000	0.0184	0.0094	0.0357	0.0063
2000	2000	0.0264	0.0124	0.0553	0.0101

Output 48.6.4 shows the CDF estimates, maximum likelihood fit, and pointwise parametric confidence limits plotted on a lognormal probability plot.

Output 48.6.4 Lognormal Probability Plot for the Microprocessor Data**Example 48.7: Bayesian Analysis of Clinical Trial Data**

Consider the data on melanoma patients from a clinical trial described in Ibrahim, Chen, and Sinha (2001). A partial listing of the data is shown in Output 48.7.1.

The survival time is modeled by a Weibull regression model with three covariates. An analysis of the right-censored survival data is performed with PROC LIFEREG to obtain Bayesian estimates of the regression coefficients by using the following SAS statements:

```
ods graphics on;
proc lifereg data=e1684;
  class Sex;
  model Survtime*Surv cens(1)=Age Sex Perform / dist=Weibull;
  bayes WeibullShapePrior=gamma seed=9999;
run;
ods graphics off;
```

Output 48.7.1 Clinical Trial Data

Obs	survtime	survcens	age	sex	perform
1	1.57808	2	35.9945	1	0
2	1.48219	2	41.9014	1	0
3	7.33425	1	70.2164	2	0
4	0.65479	2	58.1753	2	1
5	2.23288	2	33.7096	1	0
6	9.38356	1	47.9726	1	0
7	3.27671	2	31.8219	2	0
8	0.00000	1	72.3644	2	0
9	0.80274	2	40.7151	2	0
10	9.64384	1	32.9479	1	0
11	1.66575	2	35.9205	1	0
12	0.94247	2	40.5068	2	0
13	1.68767	2	57.0384	1	0
14	5.94247	2	63.1452	1	0
15	2.34247	2	62.0630	1	0
16	0.89863	2	56.5342	1	1
17	9.03288	1	22.9945	2	0
18	9.63014	1	18.4712	1	0
19	0.52603	2	41.2521	1	0
20	1.82192	2	29.5178	1	0

Maximum likelihood estimates of the model parameters shown in [Output 48.7.2](#) are displayed by default.

Output 48.7.2 Maximum Likelihood Parameter Estimates

The LIFEREG Procedure					
Bayesian Analysis					
Analysis of Maximum Likelihood Parameter Estimates					
Parameter	DF	Estimate	Standard Error	95% Confidence Limits	
Intercept	1	2.4402	0.3716	1.7119	3.1685
age	1	-0.0115	0.0070	-0.0253	0.0023
sex	1	-0.1170	0.1978	-0.5046	0.2707
sex	2	0.0000	.	.	.
perform	1	0.2905	0.3222	-0.3411	0.9220
Scale	1	1.2537	0.0824	1.1021	1.4260
Weibull Shape	1	0.7977	0.0524	0.7012	0.9073

Since no prior distributions for the regression coefficients were specified, the default uniform improper distributions shown in the “Uniform Prior for Regression Coefficients” table in [Output 48.7.3](#) are used. The specified gamma prior for the Weibull shape parameter is also shown in [Output 48.7.3](#).

Output 48.7.3 Model Parameter Priors

The LIFEREG Procedure					
Bayesian Analysis					
Uniform Prior for Regression Coefficients					
Parameter		Prior			
Intercept		Constant			
age		Constant			
sex1		Constant			
perform		Constant			
Independent Prior Distributions for Model Parameters					
Parameter	Prior Distribution	Hyperparameters			
Weibull Shape	Gamma	Shape	0.001	Inverse Scale	0.001

Fit statistics, descriptive statistics, interval statistics, and the sample parameter correlation matrix for the posterior sample are displayed in the tables in [Output 48.7.4](#). 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 48.7.4 Posterior Sample Statistics

Fit Statistics						
DIC (smaller is better)		875.251				
pD (effective number of parameters)		4.984				
The LIFEREG Procedure						
Bayesian Analysis						
Posterior Summaries						
Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
Intercept	10000	2.4668	0.3862	2.1989	2.4621	2.7256
age	10000	-0.0115	0.00733	-0.0163	-0.0115	-0.00652
sex1	10000	-0.1255	0.2004	-0.2584	-0.1247	0.00817
perform	10000	0.3304	0.3317	0.1071	0.3188	0.5470
WeibShape	10000	0.7834	0.0518	0.7481	0.7815	0.8178

Output 48.7.4 *continued*

Posterior Intervals					
Parameter	Alpha	Equal-Tail Interval		HPD Interval	
Intercept	0.050	1.7279	3.2368	1.7234	3.2264
age	0.050	-0.0260	0.00263	-0.0261	0.00244
sex1	0.050	-0.5197	0.2676	-0.5260	0.2583
perform	0.050	-0.2898	1.0072	-0.3200	0.9726
WeibShape	0.050	0.6846	0.8905	0.6805	0.8849

Posterior Correlation Matrix					
Parameter	Intercept	age	sex1	perform	Weib Shape
Intercept	1.0000	-.9018	-.3099	-.0888	-.1140
age	-.9018	1.0000	-.0259	-.0363	0.0493
sex1	-.3099	-.0259	1.0000	0.1248	0.0371
perform	-.0888	-.0363	0.1248	1.0000	-.0355
WeibShape	-.1140	0.0493	0.0371	-.0355	1.0000

The default diagnostic statistics are displayed in [Output 48.7.5](#). See the section “[Assessing Markov Chain Convergence](#)” on page 155 for more details on Bayesian convergence diagnostics.

Output 48.7.5 Convergence Diagnostics

The LIFEREG Procedure				
Bayesian Analysis				
Posterior Autocorrelations				
Parameter	Lag 1	Lag 5	Lag 10	Lag 50
Intercept	0.0564	0.0030	0.0082	0.0234
age	-0.0079	-0.0184	-0.0015	0.0239
sex1	0.6293	0.0700	0.0055	-0.0199
perform	0.6514	0.0773	0.0397	-0.0123
WeibShape	0.0719	-0.0083	-0.0062	0.0112

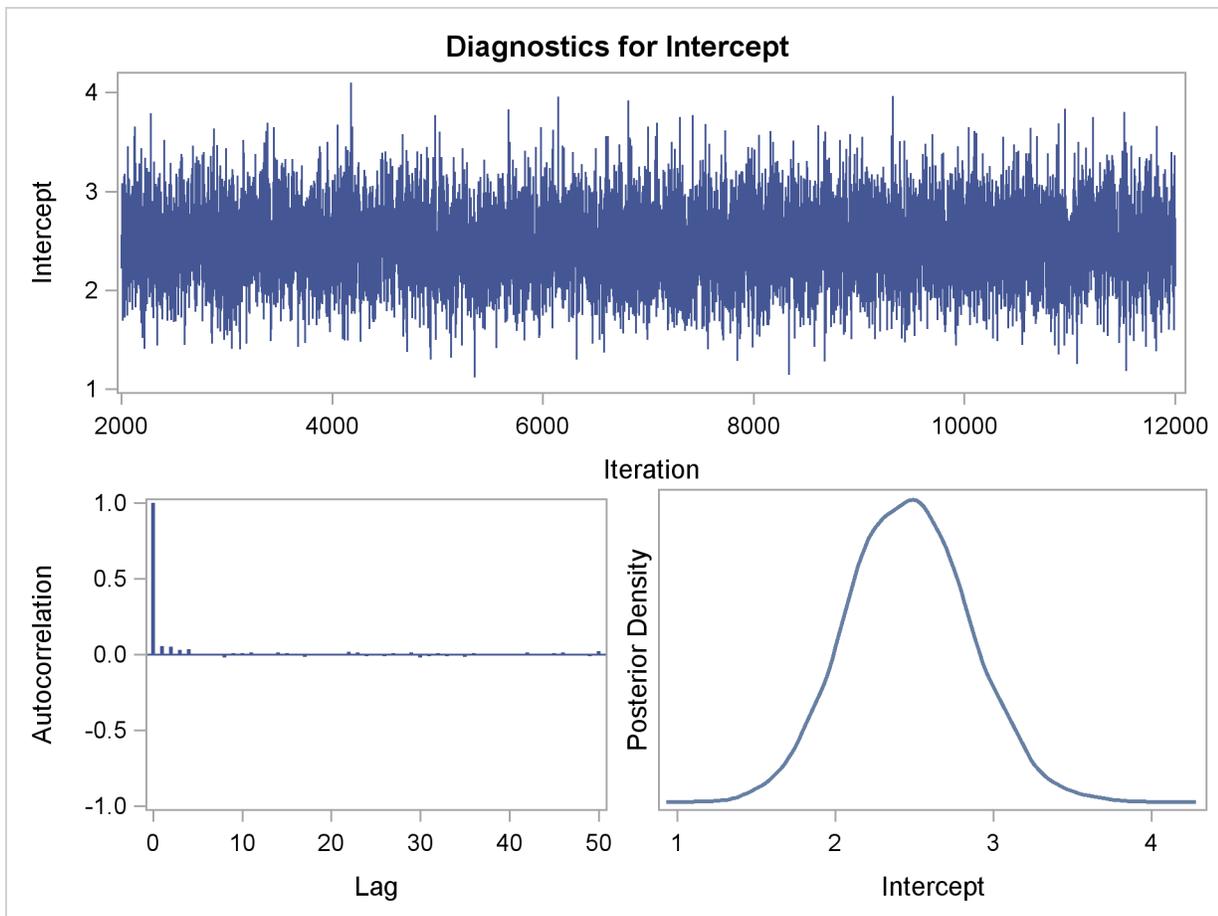
Geweke Diagnostics		
Parameter	z	Pr > z
Intercept	0.4962	0.6198
age	-0.4119	0.6804
sex1	-0.2519	0.8011
perform	-0.1049	0.9165
WeibShape	-0.6573	0.5110

Output 48.7.5 *continued*

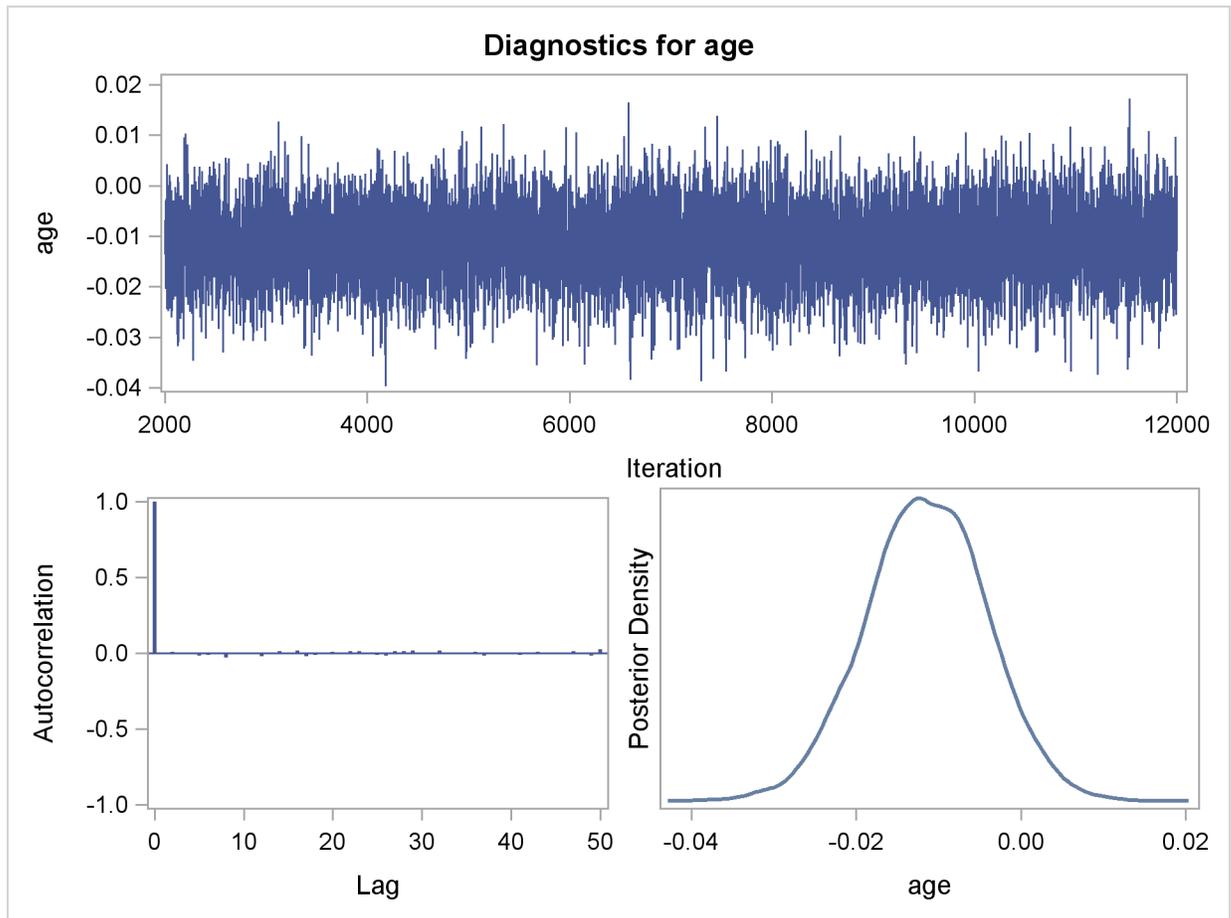
Effective Sample Sizes			
Parameter	ESS	Autocorrelation	
		Time	Efficiency
Intercept	7476.1	1.3376	0.7476
age	10000.0	1.0000	1.0000
sex1	2482.1	4.0288	0.2482
perform	2174.0	4.5998	0.2174
WeibShape	8538.8	1.1711	0.8539

Trace, autocorrelation, and density plots for the seven model parameters are shown in [Output 48.7.6](#) through [Output 48.7.10](#). These plots show no indication that the Markov chains have not converged. See the sections “[Assessing Markov Chain Convergence](#)” on page 155 and “[Visual Analysis via Trace Plots](#)” on page 155 for more information about assessing the convergence of the chain of posterior samples.

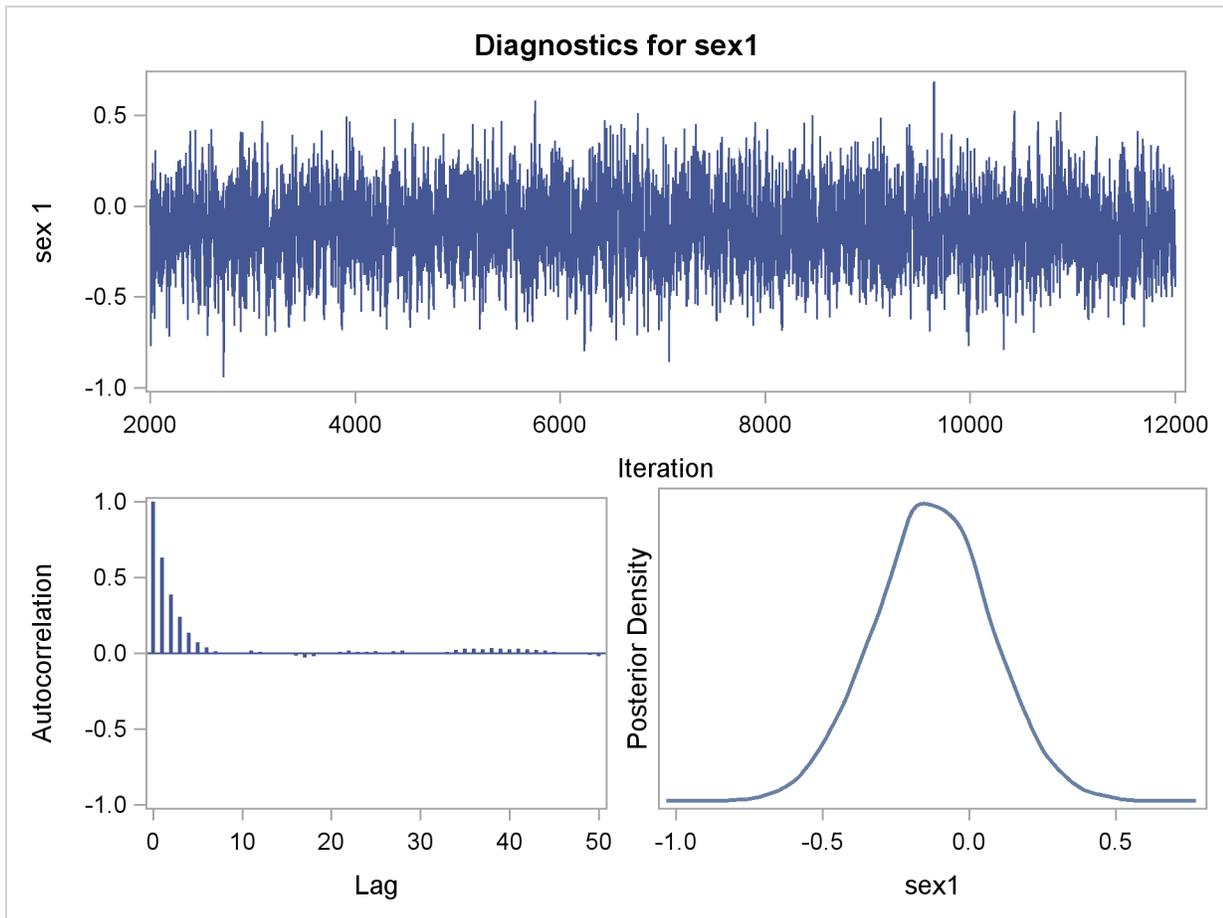
Output 48.7.6 Diagnostic Plots



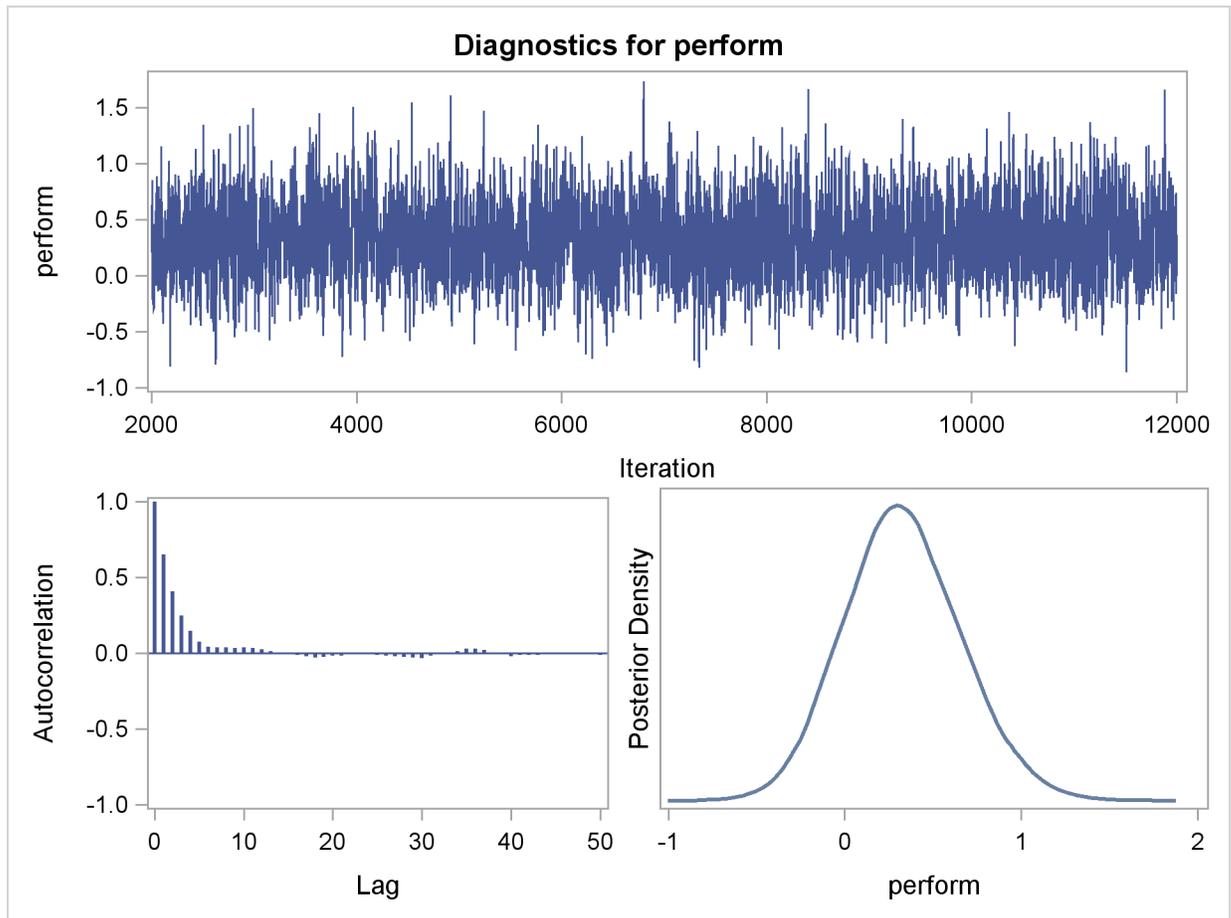
Output 48.7.7 Diagnostic Plots



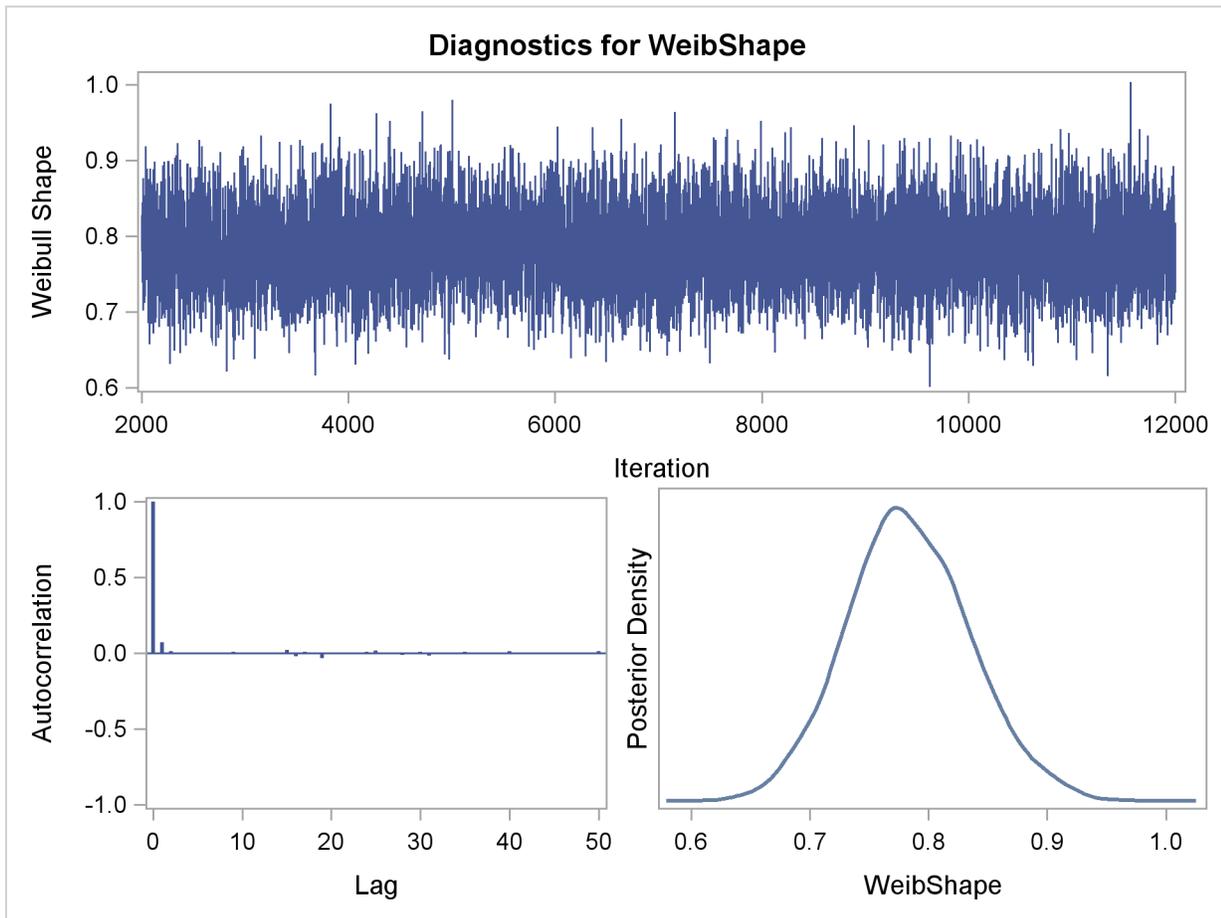
Output 48.7.8 Diagnostic Plots



Output 48.7.9 Diagnostic Plots



Output 48.7.10 Diagnostic Plots



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