Monday June 5, 2000

SLIDA (S-PLUS Life Data Analysis)

William Q. Meeker and Luis A. Escobar

Iowa State University and Louisiana State University

www.public.iastate.edu/~stat533/SLIDA.html

wqmeeker@iastate.edu, luis@lsu.stat

www.public.iastate.edu/~wqmeeker

1. Introduction

S-PLUS is a powerful, extendible, environment for data analysis and graphics. The “Standard Version” of S-PLUS provides access to the S-PLUS functionality through a point-and-click GUI. The “Professional Version” of S-PLUS includes, in addition, access to the S-PLUS command line and the capability to develop extensions to S-PLUS. These extensions may also include additions to the S-PLUS GUI.

SLIDA is a collection of S-PLUS extensions (both commands and GUI) for planning and analyzing the data from empirical reliability studies (e.g., laboratory life tests, accelerated life tests, warranty repair data, and other field data). Most SLIDA capabilities are available through the SLIDA extensions to the S-PLUS GUI. THUS, SLIDA can be used with either the Standard or the Professional versions of S-PLUS (although advanced users with the professional version have access to additional functionality and the ability to make further extensions to SLIDA/S-PLUS). The main part of this document describes and illustrates the SLIDA graphical user interface (GUI). The methods and analyses parallel closely the methods and examples used in Meeker and Escobar (1998). The items in the SLIDA menu correspond approximately to the chapters in the Meeker and Escobar (1998) textbook. *Italic text presents general concepts concerning SLIDA that pertain to most, if not all, of the available SLIDA functionality and dialogs.*

The Appendix contains an outline of the SLIDA menu structure.

There appears to be a non-serious bug in the S-PLUS 2000 GUI (both with and without the November 1999 Service Release) that causes the “white” part of a multi-select dialog box from a back page of a dialog to appear sporadically when a dialog box first appears. By paging across the different pages in the *dialog, this will fix itself without further difficulty. We have not noticed this problem with S-PLUS 4.5R2 (July 1998 service release).*

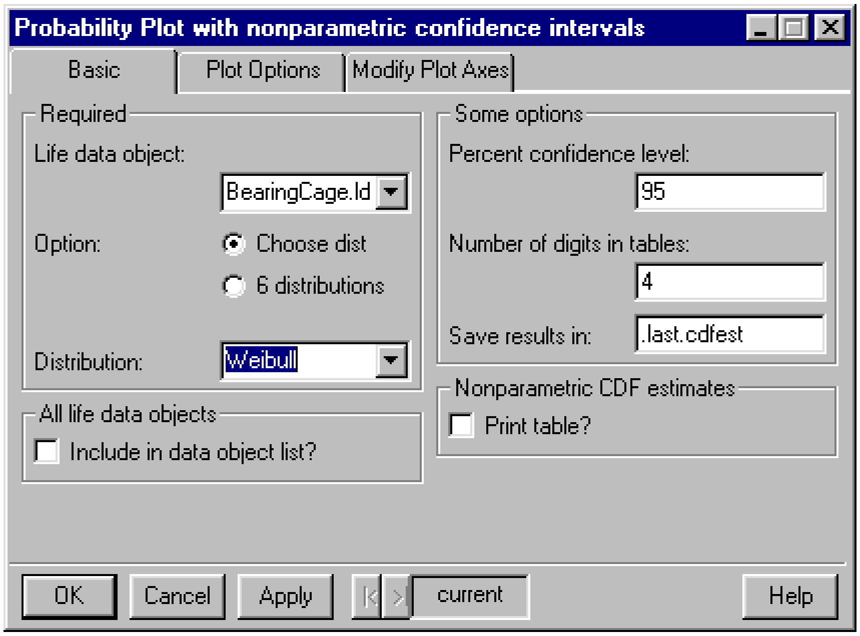
2. Getting Started with SLIDA

All SLIDA data analyses require a data object. Life data analyses use a SLIDA "life data object." A life data object contains, for a given data set, available information about failure times (e.g., failure times, running times, intervals in which failures are known to have occurred, etc.), time units (e.g., hours or days), explanatory variables (if any), and a data-set title. Having all of this information in a life data object makes it much easier to do various analyses on a particular data set. There are similar (but different) kinds of data objects for recurrence data analysis and for degradation data analysis, as described in subsequent sections of this document.

2.1 Example data sets and a simple example

For convenience of illustrating features of SLIDA and for purposes of teaching courses, SLIDA has a large number of built-in data objects. Data objects are included for most of the examples and many of the exercises in Meeker and Escobar (1998). The appendix contains an index of and references for the original sources for these data sets.

To see how easy it is to do an analysis with SLIDA Click SLIDA ➡ Single distribution analysis ➡ Probability plot with nonparametric confidence bands, to bring the dialog box in Figure 1. Choose from the list of life data objects (e.g., BearingCage.ld, for the Bearing Cage data from Abernathy et al. (1983), also analyzed in Example 8.16 of Meeker and Escobar , 1998). Now choose a distribution (e.g., Weibull), click "Apply" and a probability plot, like that in Figure 2, will appear in the graphics window.



Required

Life data object: BearingCage.ld

Option: ● Choose dist ○ 6 distributions

Distribution: Weibull

All life data objects

☐ Include in data object list?

Some options

Percent confidence level: 95

Number of digits in tables: 4

Save results in: .last.cdfest

Nonparametric CDF estimates

☐ Print table?

Figure 1 Dialog box to request a probability plot of the bearing cage data.

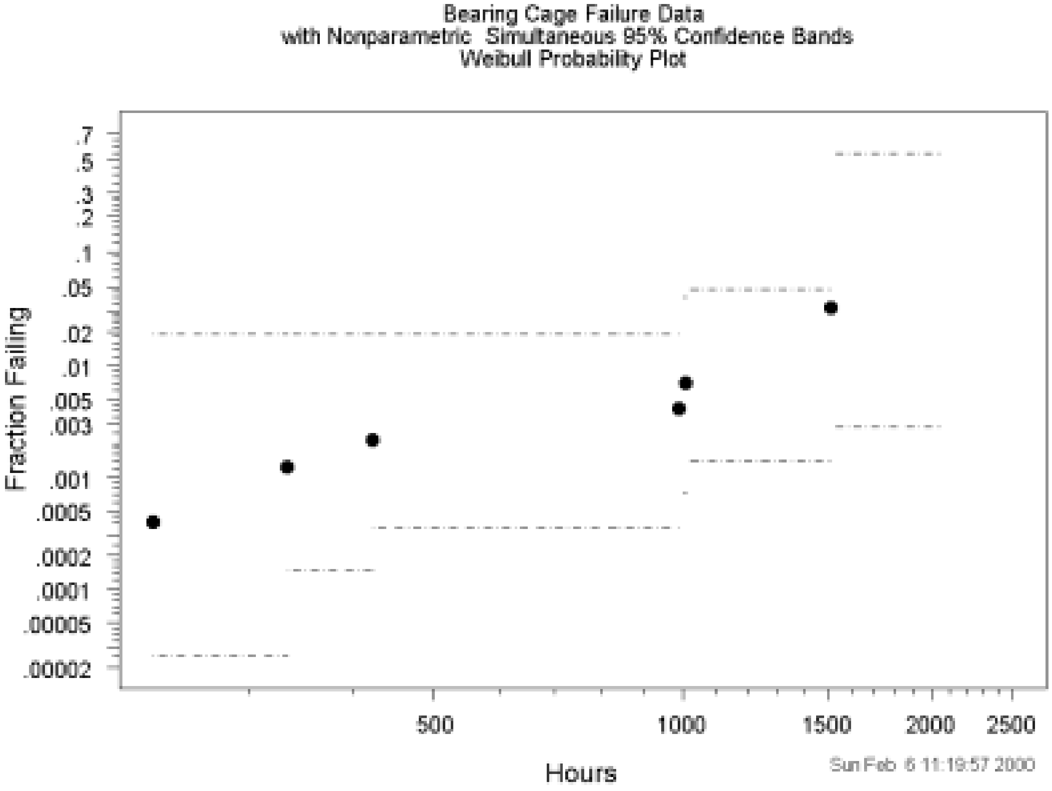


Figure 2 Weibull probability plot of the bearing cage data.

2.2 Inputting data directly into S-PLUS: Creating a data frame

In order to analyze your own data, you first have to enter the data into an S-PLUS data frame. This can be done by importing from an existing file, as described in Section 2.4. For a small data set, however, one can simply enter data directly to make a S-PLUS data frame and then create a SLIDA data object.

Here we use the titanium crack initiation times described in Problem 6.7 of Meeker and Escobar (1998). There were nine observed crack initiations (failures) out of 100 specimens that were tested until 100 thousand cycles. Choose Data ➡ Select Data. Then choose the "New Data" option in the dialog box, enter a name for the data frame (e.g. Prob6p7 for Problem 6.7), and click OK. A blank data frame will appear. Type the numbers 18, 32, 93 into the first column. In the second column, type the word Failure in each row. Then add a last row with time 100 and the word Censored. We also need a column of "Weights" to indicate observation multiplicity. Put "1" in all rows except the last, where you should put "91" for the 91 censored units. The default names on the columns are V1, V2, and V3. You can use these, but it is better to change them to something more meaningful. Right-click on a column, choose properties, change the name, and click "OK". Repeat for other columns. After doing this, your table (actually a data frame) should look something like Table 1.

Table 1 Data from Meeker and Escobar (1998) Exercise 6.7, as they would appear in an S-PLUS data frame

kcycles	Type	Count

18	**Failure**	**1**
32	**Failure**	**1**
39	**Failure**	**1**
53	**Failure**	**1**
59	**Failure**	**1**
68	**Failure**	**1**
77	**Failure**	**1**
78	**Failure**	**1**
93	**Failure**	**1**
100	**Censored**	**91**

Users can also easily import a data frame from an Excel worksheet or from a text file (as shown later).

2.3 Creating a life data object

To do life data analyses (e.g., when the response is time to failure from a set of independent units) with SLIDA, one needs to make a life data object (in effect, defining the purpose of the columns in the data frame and adding other important information like a data title and time units). Once constructed, the data in the life data object can be analyzed using different SLIDA methods. A data object is constructed by choosing an S-PLUS data frame containing the raw data, specifying which column is the response and, as needed or desired, making other choices. From the S-PLUS menu bar, choose SLIDA ➡ Make/summary/view/edit data object ➡ Make life data object to bring up the dialog box shown in Figure 3.

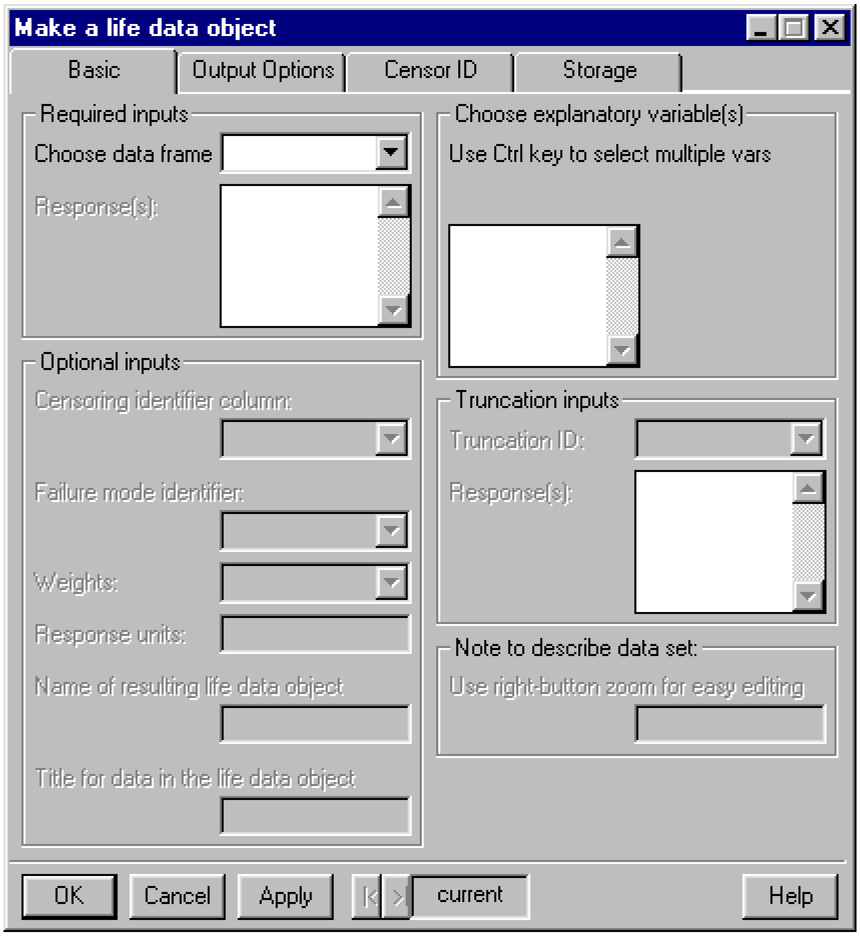
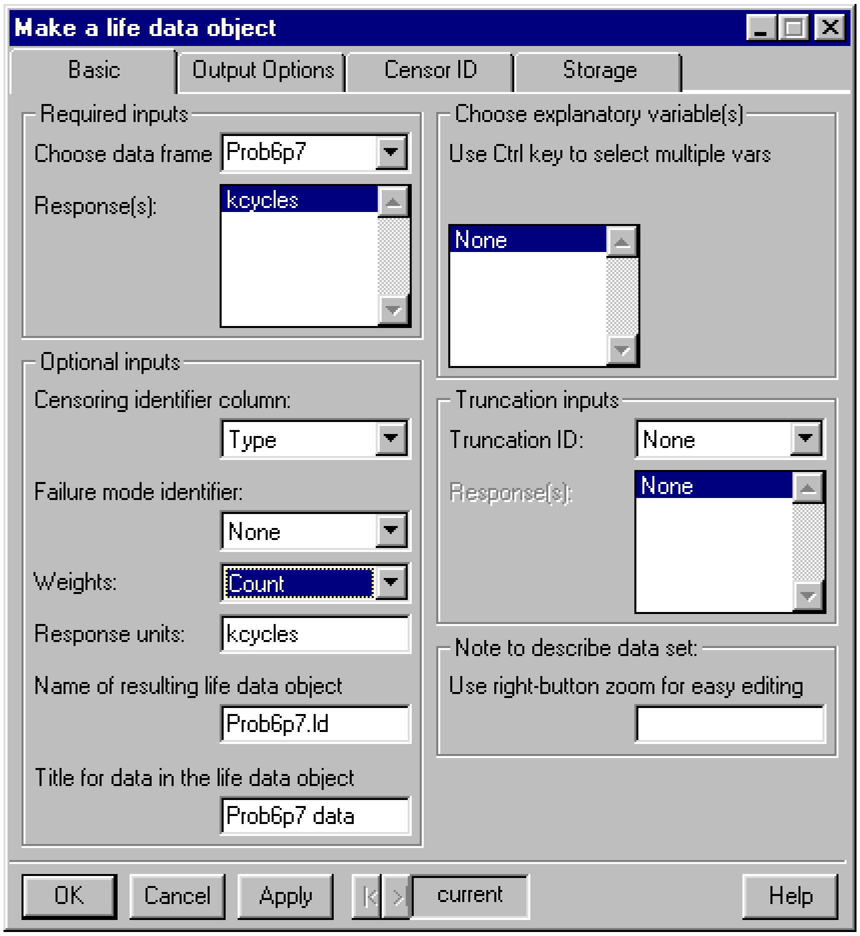


Figure 3 Blank (initial) dialog box for making a SLIDA life data object.

Clicking on the Choose data frame pull-down arrow will show data frames in the SLIDA database and in your working database. Data frames for most of the examples in Meeker and Escobar (1998) and many other examples from the reliability data analysis literature are included on the SLIDA database. ASCII text data sets are also given in one of the SLIDA folders (SLIDA_text_data).

Choose the data frame Prob6p7 from the list. Then choose the response (kcycles), the censoring indicator (Type), and weights (Count). Then click “Apply” (or OK). You will get a brief summary of the data.

After one chooses a data frame, SLIDA will use the column names in that frame to make lists of variables for other dialog box inputs. Choose the response column (named “kcycles” in the Prob6p7 titanium crack initiation data frame) and the fan censoring indicator (named “Status”). We will stay with the default name for the life data object (Prob6p7.ld). The Prob6p7 data frame also has a “Count” column indicating observation multiplicity. The Prob6p7 data has no failure mode column, explanatory variables, or truncation. A note can be added to the life data object. There is no limit to the length of this note, and it is printed when a summary of the data object is printed. In order to simplify use, SLIDA chooses, when possible, sensible defaults for inputs, but allows the user to easily change these if desired. The final dialog box for mapping the Prob6p7 data frame into a life data object Prob6p7.ld is shown in Figure 4.



Choose data frame: Prob6p7

Response(s): kcycles

Choose explanatory variable(s): None

Censoring identifier column: Type

Failure mode identifier: None

Weights: Count

Response units: kcycles

Name of resulting life data object: Prob6p7.ld

Title for data in the life data object: Prob6p7 data

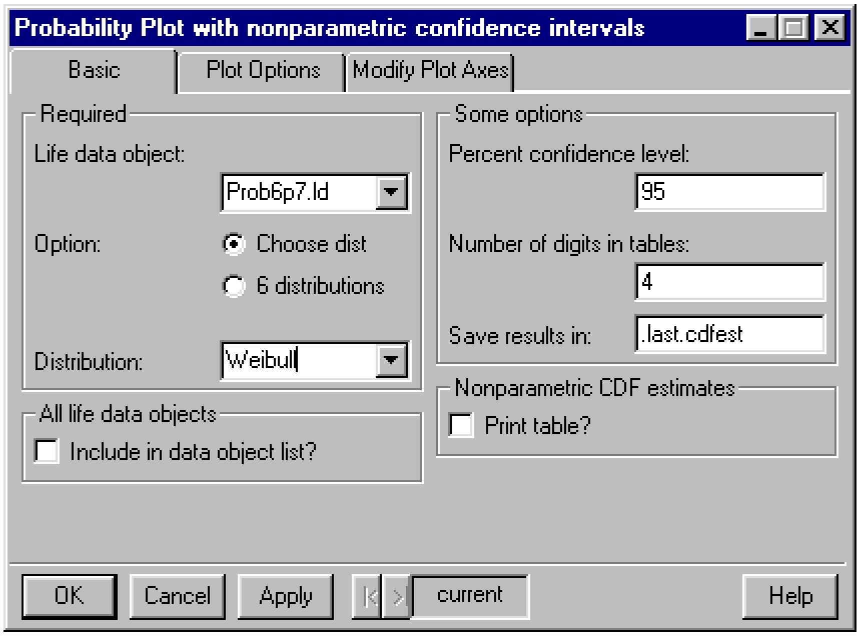
Truncation ID: None

Response(s): None

Figure 4 Dialog box to make a life data object.

Now when you launch the analysis dialog by using SLIDA ➡ Single distribution analysis ➡ Probability plot with nonparametric confidence bands (see Figure 5) Prob6p7.ld will appear in the list of life data objects (actually, if it was just created, SLIDA will have remembered it and chose it as the default in this list). Now choose a distribution (e.g., Weibull), click “Apply” and the probability plot shown in Figure 6 will come up in the graphics window.

In this and the other SLIDA dialog boxes, there are other options on the “back” pages of the dialog, but we do not need to use them at this time. Generally, the required and frequently-used options s are on the front page, with less frequently needed options on the back pages. In this documentation, the focus will be on the required and other most important inputs for SLIDA. Users are encouraged to experiment with the options on the back pages. These options are, for the most part, self explanatory and, as much as possible, their operation is consistent across different SLIDA dialogs.



Required

Life data object: Prob6p7.ld

Option: ● Choose dist ○ 6 distributions

Distribution: Weibull

All life data objects

☐ Include in data object list?

Some options

Percent confidence level: 95

Number of digits in tables: 4

Save results in: .last.cdfest

Nonparametric CDF estimates

☐ Print table?

Figure 5 Dialog to request a probability plot of the titanium crack initiation data.

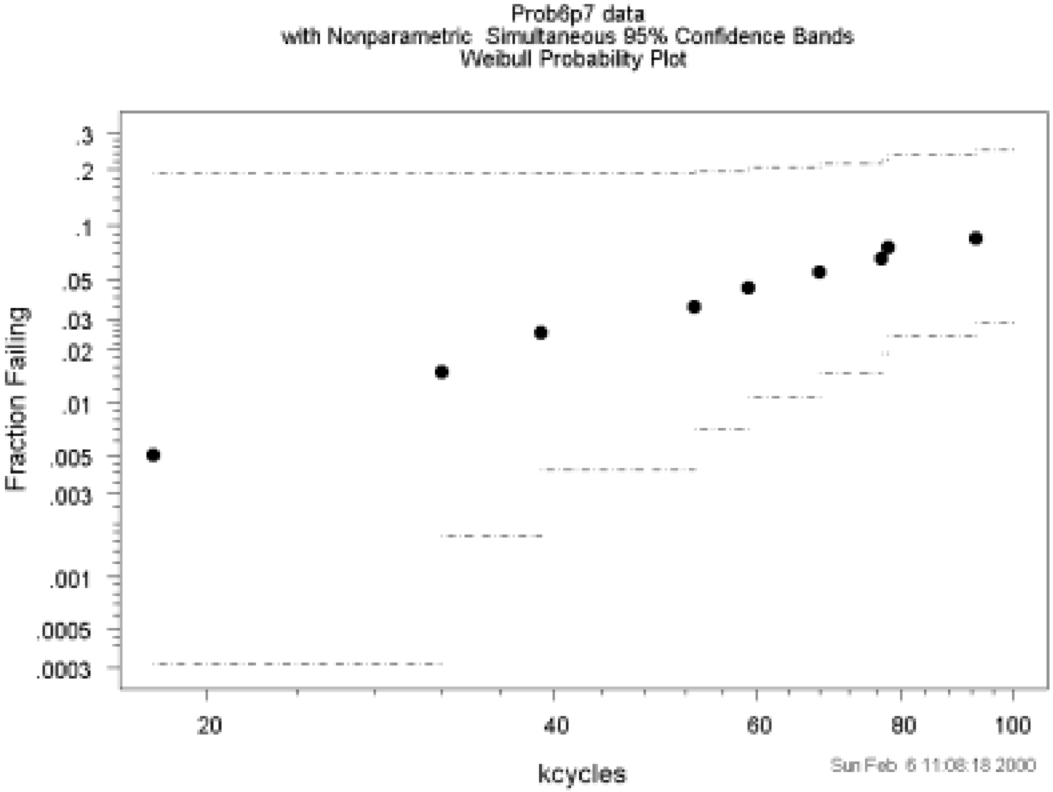


Figure 6 Weibull probability plot of the titanium crack initiation data.

2.4 Importing data from Excel and text files

S-PLUS has powerful tools for importing rectangular data sets (in which rows are cases and columns are variables) into a data frame. For example, to import from an Excel worksheet, into a data frame, use the following:

(a) From the S-PLUS File menu, choose Import Data ➡ From File... This will bring up the "Import Data" dialog box.

(b) On the "Files of type" line, select 'Microsoft Excel Files ("*.xls")'

(c) Find and left-click on the appropriate folder and then choose the desired Excel file (or optionally, type the path and file in the "File Name" box).

(d) In the “File name box”, type or select the name, and optionally the path, of the file you want to import.

(e) In the “Import to Data Frame”, box you can specify the target data frame name. Generally, the default name (aaaa if the Excel file is aaaa.xls) is a good choice, but you might choose aaaa.frame instead to remind you that the object is a frame.

(f) Click “Open” to import the file into the S-PLUS data frame object.

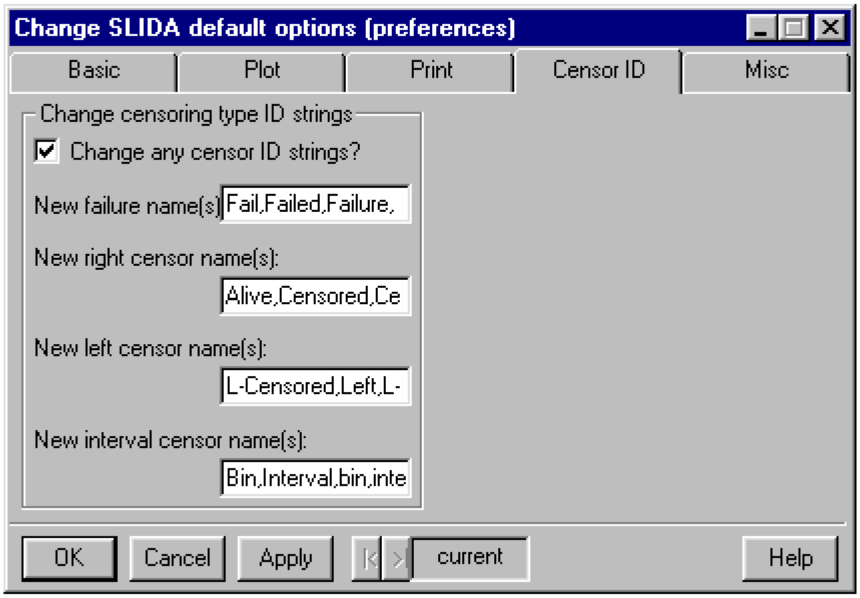
Importing from a text (or ASCII) file is similar, except that one needs to specify “.txt” files (or “All Files”), choose the appropriate column delimiters, and specify whether or not the first line in the file contains column names.

2.5 Changing SLIDA data-type aliases

SLIDA maintains internal lists of names or aliases that can be used to identify “exact failures” and three different kinds of censored observations: right censored, left censored, and interval censored. These lists are used in creating a data object when there is a “Status” or “Censoring” identifer column (e.g., used to differentiate between failures and censored observations). The default aliases for different kinds of observations are:

- Exact failures: Fail, Failed, Failure, Dead, Died, Exact, F, Report, fail, failed, failure, dead, died, exact, f, report, or the number 1.
- Right censored: Alive, Censored, Censor, C, Noreport, R-Censored, Removed, Right, S, Survived, Survive, Suspend, Suspended, alive, censored, censor, c, noreport, R-censored, removed, right, s, survived, survive, suspend, suspended, or the number 2.
- Left censored: L-Censored, Left, L-censored, left, or the number 3.
- Interval censored: Bin, Interval, bin, interval, or the number 4.

It is possible to add to or modify the default alias lists by using the Censor ID page of the Make life data object dialog box when creating a particular data object. Alternatively, it is possible to make a persistent change (either for the current session or across sessions) by using the SLIDA ➡ Change Slida default options menu item and going to the Censor ID page. In either case, the dialog page looks like Figure 7. To edit an entry, check the “Change any censor ID strings” box and then right-click on the list to be changed and choose zoom, to allow easy editing.



Change censoring type ID strings

☑ Change any censor ID strings?

New failure name(s) Fail,Failed,Failure,

New right censor name(s): Alive,Censored,Ce

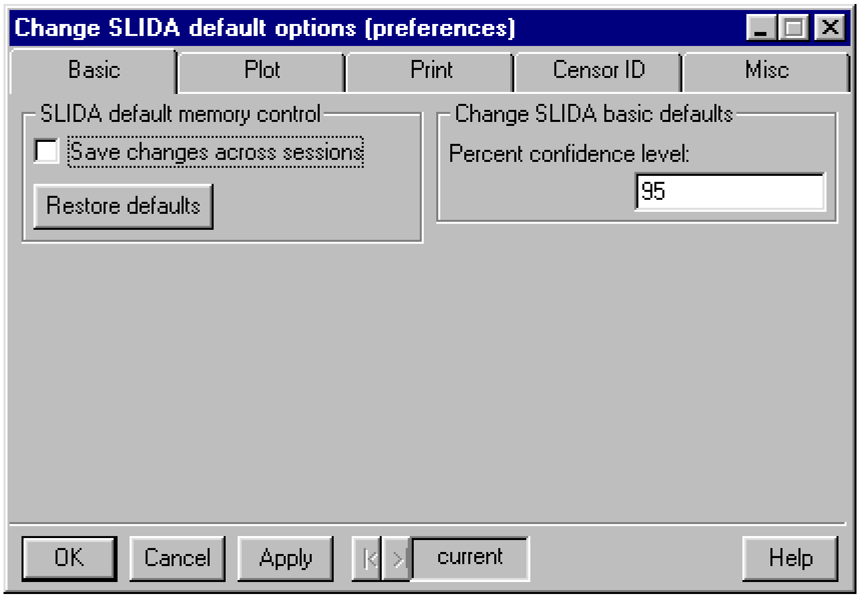
New left censor name(s): L-Censored,Left,L-

New interval censor name(s): Bin,Interval,bin,inte

Figure 7 Dialog page allowing changes in the default aliases for observation identification.

2.6 Other SLIDA default options (preferences)

Using the SLIDA ➡ Change Slida default options (preferences) brings up the dialog box shown in Figure 8, allowing changes in several of the SLIDA default options. There are dialog box pages for changing basic, plot, print, storage, and censor ID option defaults. Any options chosen while the “Save changes across sessions” box is checked will be saved and recalled in subsequent SLIDA sessions. Clicking the Restore defaults button will have all of the defaults revert to their original values. More details are given in Chapter 14.



SLIDA default memory control

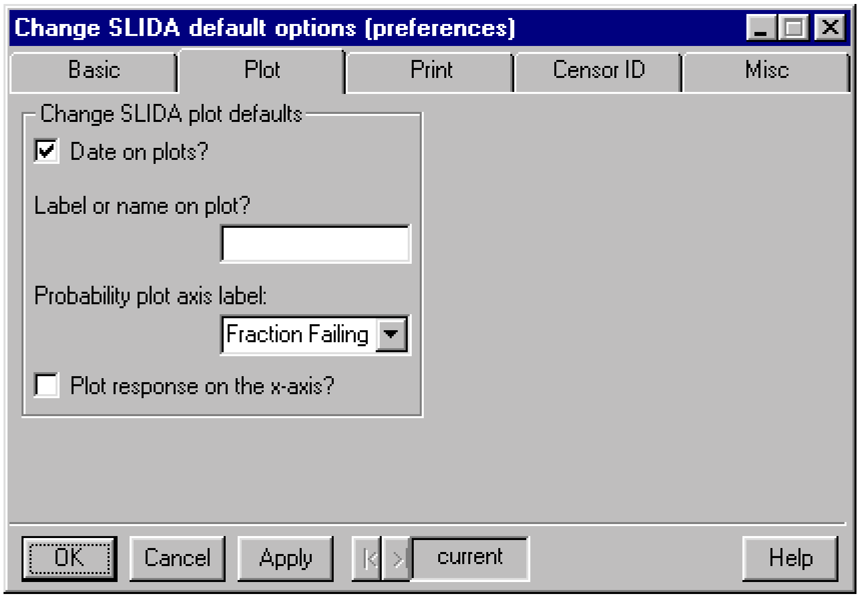
☐ Save changes across sessions

Change SLIDA basic defaults

Percent confidence level: 95

Figure 8 Basic page of the dialog box for changing SLIDA default options.

The plot page of the SLIDA ➡ Change Slida default options (preferences) dialog box, illustrated in Figure 9, allows the user to choose whether to date-stamp each plot (the default) or not. The “label or name on plot” option allows some personalization in which the user can insert a company or personal name on the plot.



Change SLIDA plot defaults

☑ Date on plots?

Label or name on plot?

Probability plot axis label: Fraction Failing

☐ Plot response on the x-axis?

Figure 9 Plot page of the dialog for changing SLIDA default options.

2.7 Graphics options and color schemes in SLIDA

S-PLUS allows the user to have control over various graphics options. Although it is not necessary for the beginner, frequent users of S-PLUS or SLIDA will want to become familiar with the available options. Some modifications of the default options have been implemented in the _prefs file that comes with SLIDA.

The default color scheme in SLIDA has been changed from “Standard” to “Cyan Magenta.” This option provides a much better (sharper and less washed-out looking) set of colors for SLIDA graphics. The standard or other build-in options can be chosen with Options ➡ Graph Style ➡ Color and changing the color option box.

Another useful option is to use Options ➡ Graph Options and change Graph Style to black and white. The SLIDA default for the black and white graph style (which differs from the S-PLUS default) uses just black on white, with no grey scales. Again, the S-PLUS standard black and white Graph option can be restored with Options ➡ Graph Styles ➡ Black and White.

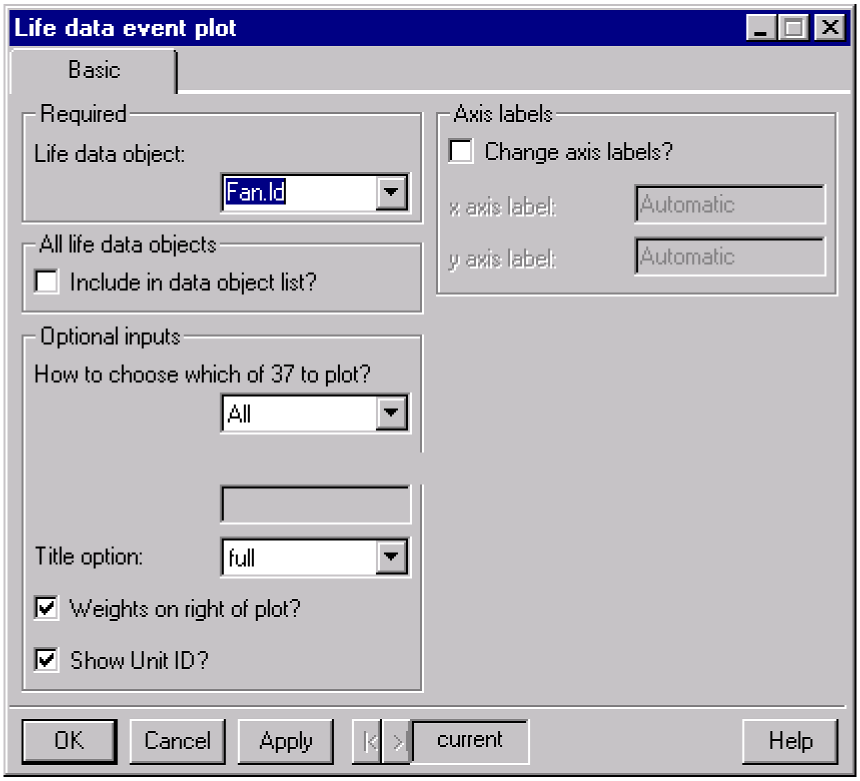
Under Options ➡ Graph Options, the SLIDA default for Auto Pages is “Every Page” so that new pages automatically are added to a graphsheet as new plots are created. This makes it easy to compare plots from different analyses. Beware, however, that saving a large number of graphs can tie up computer system resources and affect performance or even cause Windows to crash (saving a large number of previous dialog boxes also has the same effect). Delete unwanted pages by right-clicking on the page number to be deleted.

3. Single Distribution Life Data Analyses

Analysis of data for the purpose of estimating a *single* underlying failure-time distribution is the most common type of relaibility data analysis**.** This chapter describes methods for such analyses. Even when there are several different identifiable groups, it is often desired to focus on one group or another or (when appropriate) to pool data from different groups for analysis. Choosing **SLIDA ➡ Single distribution life data analyses** shows the SLIDA single distribution analysis options.

3.1 Event plot

For some data sets, an event plot provides a useful visualization of the nature of the data. Using **SLIDA ➡ Single distribution life data analyses ➡ Event Plot** brings up the dialog box shown in Figure 10.



Life data object: Fan.ld

☐ Include in data object list?

How to choose which of 37 to plot? All

Title option: full

☑ Weights on right of plot?

☑ Show Unit ID?

☐ Change axis labels?

x axis label: Automatic

y axis label: Automatic

Figure 10 Dialog box requesting a life data event plot for the fan data.

After choosing the Fan.ld life data object (based on the diesel generator fan failure data described on page 133 of Nelson 1982 and reanalyzed in Example 7.12 of Meeker and Escobar 1998) from the pull-down list, click “Apply” or “OK” to see the event plot shown in Figure 11. Lines in Figure 11 ending in an * indicate failures. Lines with a ⟶* at the end are units that had not failed at the time that the data were analyzed. The numbers indicate the observation multiplicity for those observations that have counts greater than one. In the case of the fan data, there is a complicated pattern of reported failure times and right-censored observations resulting from the different amounts of operating time for the systems in which the fans had been used.

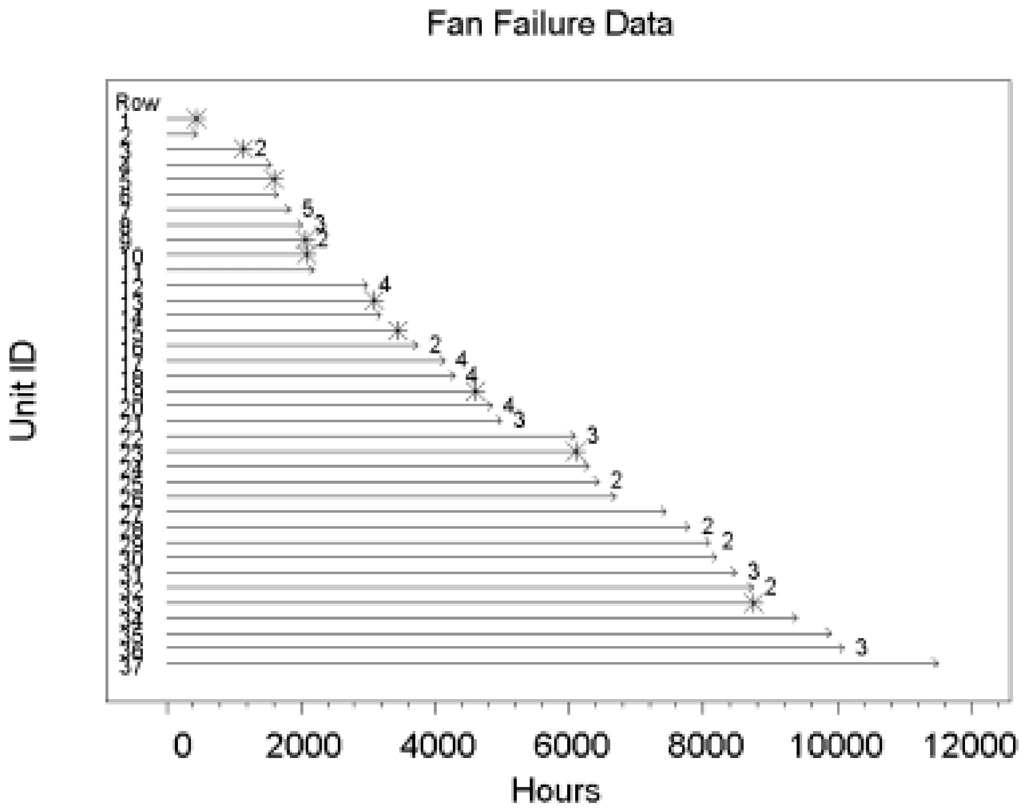
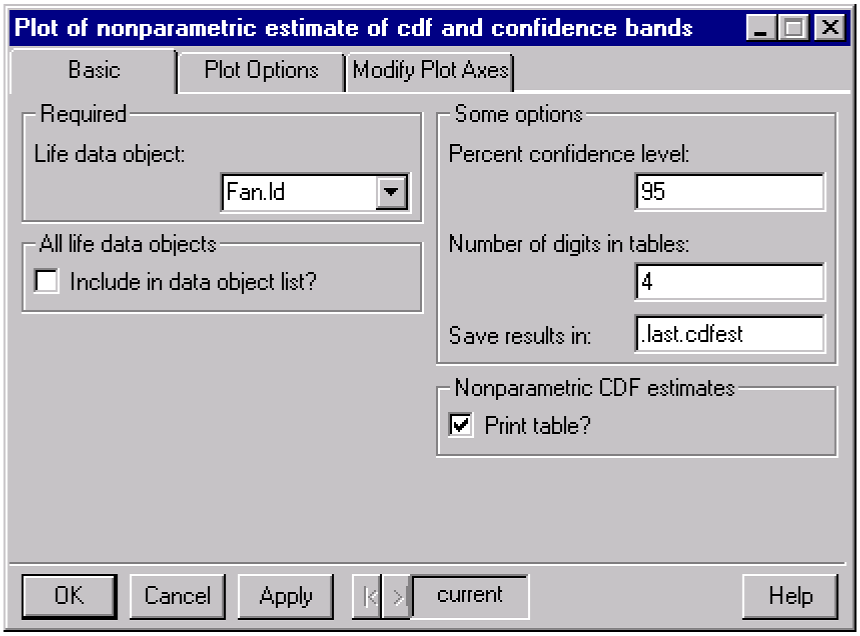


Figure 11 Life data event plot for the fan data.

3.2 Nonparametric estimation of the failure-time cdf

Using **SLIDA ➡ Single distribution life data analyses ➡ Plot nonparametric estimate of cdf and confidence bands** brings up the dialog box in Figure 12.



Required

Life data object: Fan.ld

All life data objects

☐ Include in data object list?

Some options

Percent confidence level: 95

Number of digits in tables: 4

Save results in: .last.cdfest

Nonparametric CDF estimates

☑ Print table?

Figure 12 Dialog box for requesting a plot and table of the estimated fraction failing as a function of time.

Then choose life data object `Fan.ld` (the only required input), put a check in “Print table” and click “Apply. This will produce a plot like that in Figure 13 and a table of the nonparametric estimate and confidence intervals for the fraction failing as a function of time. The estimates are computed using the Kaplan-Meier estimator. When data have complicated censoring pattterns such as interval-censored observations with overalpping intervals a generalized version of the Kaplan-Meier estimator, known as the Peto/Turnbull estimator is used instead, as described in Section 3.10 of Meeker and Escobar (1998). Chapter 3 of Meeker and Escobar (1998) describes the methods for computing nonparametric estimates and corresponding confidence intervals/bands from censored data (including complicated arbitrary censoring) and provides references and examples corresponding to these SLIDA capabilities.

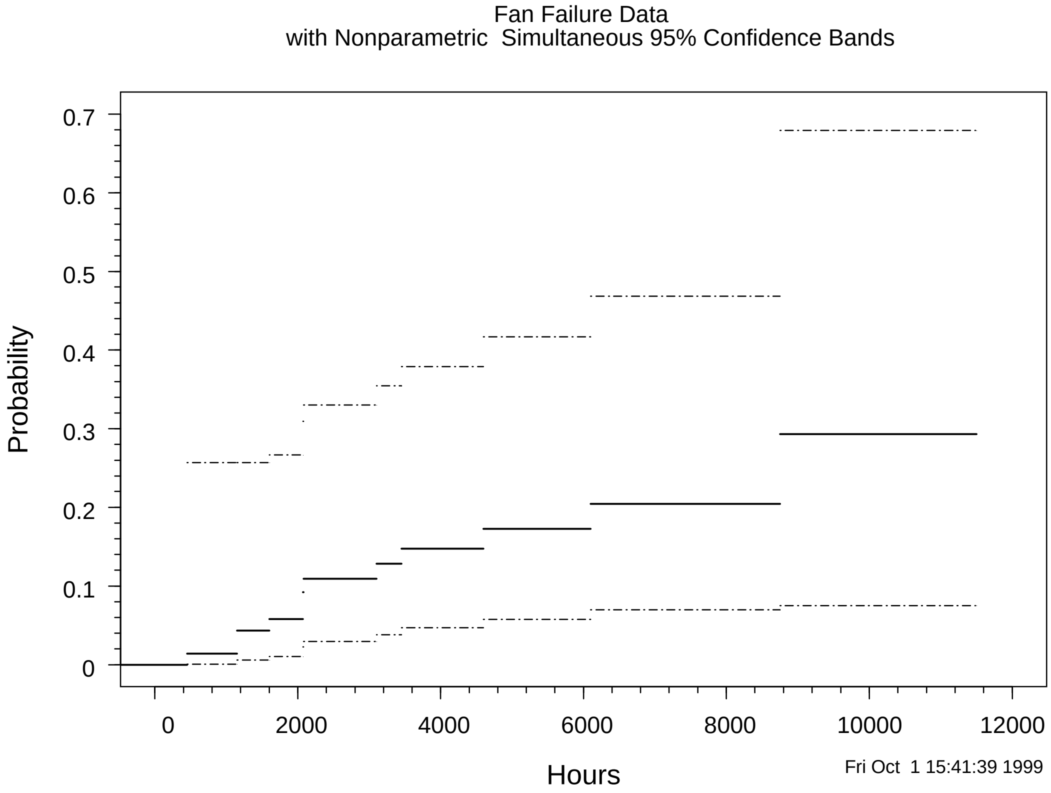


Figure 13 Plot of estimated fraction failing as a function of time for the turbine fans.

Table 2 provides a table of the nonparametric estimates from the turbine fan data, along with standard errors and approximate 95% pointwise confidence intervals.

Table 2 Kaplan-Meier nonparametric estimate of the fraction failing as a function of time for the turbine fans.

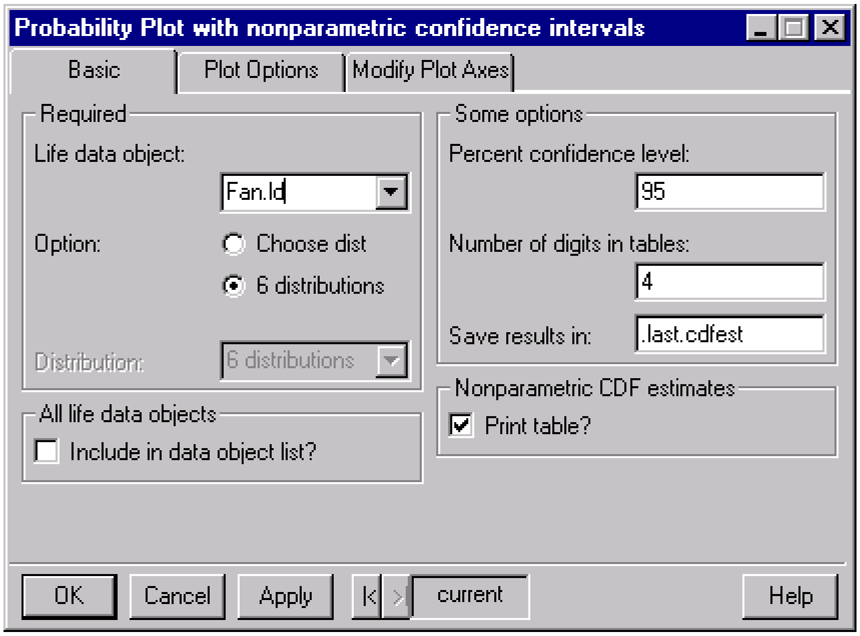
```
Nonparametric estimates from  Fan Failure Data
with approximate 95% pointwise confidence intervals

   Hours-lower Hours-upper    Fhat SE_Fhat 95% Lower 95% Upper
 1           0         450 0.00000 0.00000        NA        NA
 2         450        1150 0.01429 0.01418  0.002009   0.09449
 3        1150        1600 0.04328 0.02444  0.014024   0.12577
 4        1600        2070 0.05800 0.02815  0.021934   0.14459
 5        2070        2080 0.09225 0.03607  0.041857   0.19121
 6        2080        3100 0.10938 0.03925  0.052811   0.21291
 7        3100        3450 0.12833 0.04274  0.065085   0.23742
 8        3450        4600 0.14770 0.04597  0.078091   0.26173
 9        4600        6100 0.17277 0.05100  0.094016   0.29593
10        6100        8750 0.20458 0.05812  0.113253   0.34122
11        8750       11500 0.29296 0.09804  0.140791   0.51166
```

When using SLIDA, it is often better to click on “Apply” rather than on “OK” to request an analysis. Then minimize the dialog box to better see the results. Then to modify the analysis, restore the dialog box, make desired changes, click “Apply,” and minimize the dialog box again. When completely done with the dialog box, click “Cancel.” If one uses “OK” instead, it will be more difficult to modify previous analyses, as *certain steps in the analysis specification would need to be retraced. S-PLUS allows one to choose a previous dialog box state by clicking on the buttons at the bottom of the dialog box. When doing this, however, S-PLUS does not properly restore whether entries in the dialog box are active or inactive*

3.3 Probability plots and distribution assessment

Probability plots are one of the most important tools for reliability data analysis. The ideas and concepts underlying probability plots, along with a large number of examples, is given in Chapter 6 of Meeker and Escobar (1998). The basic idea is to plot a representation of a nonparametric estimate of the fraction failing as a function of time (traditionally, this estimate has been a set of points) on special distribution-dependent nonlinear plotting axes on which the specified theoretical distribution would plot as a straight line.

Use **SLIDA** ➡ **Single distribution life data analyses** ➡ **Probability plot with nonparametric confidence bands** to bring up the basic probability plot dialog, illustrated in Figure 14. Again, choose the life data object Fan.ld, choose “6 distributions,” click “Apply,” and iconify the dialog box. This will make a six-distributions probability plot like the one in Figure 15, from which one can visually compare several different distributions including the popular Weibull and lognormal distributions.



Required

Life data object: Fan.ld

Option: ○ Choose dist ● 6 distributions

Distribution: 6 distributions

All life data objects

☐ Include in data object list?

Some options

Percent confidence level: 95

Number of digits in tables: 4

Save results in: .last.cdfest

Nonparametric CDF estimates

☑ Print table?

Figure 14 Dialog box requesting the 6-distributions probability plots with (default) simultaneous confidence bands.

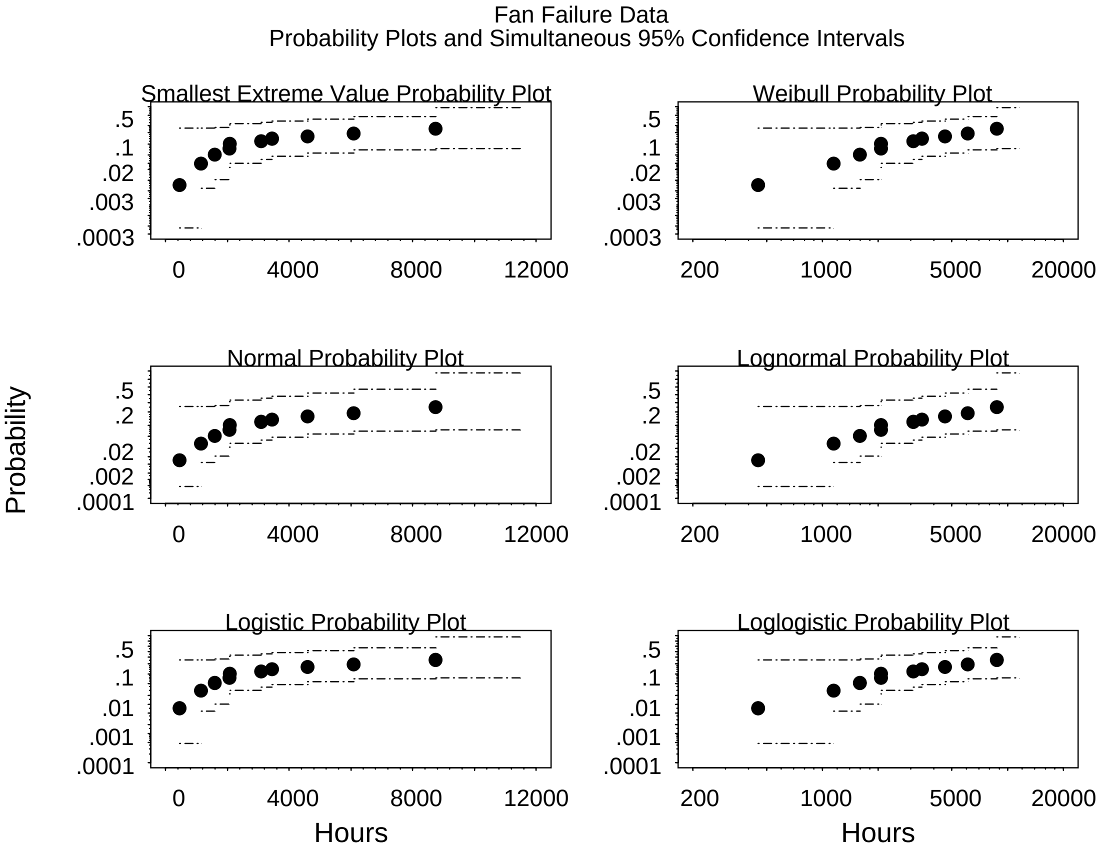


Figure 15 Six-distributions probability plots with simultaneous confidence bands.

Now, restore the dialog box in Figure 14, change to “Choose dist,” and choose a particular distribution (e.g., lognormal), and click “Apply.” This will create the probability plot, shown in Figure 16, that will allow one to focus the reasonableness of the specified distribution as a model for the data. By default, simultaneous confidence bands are also provided. See Sections 3.8 and 6.3 of Meeker and Escobar (1998) for technical details, references, and other examples of these simultaneous confidence bands.

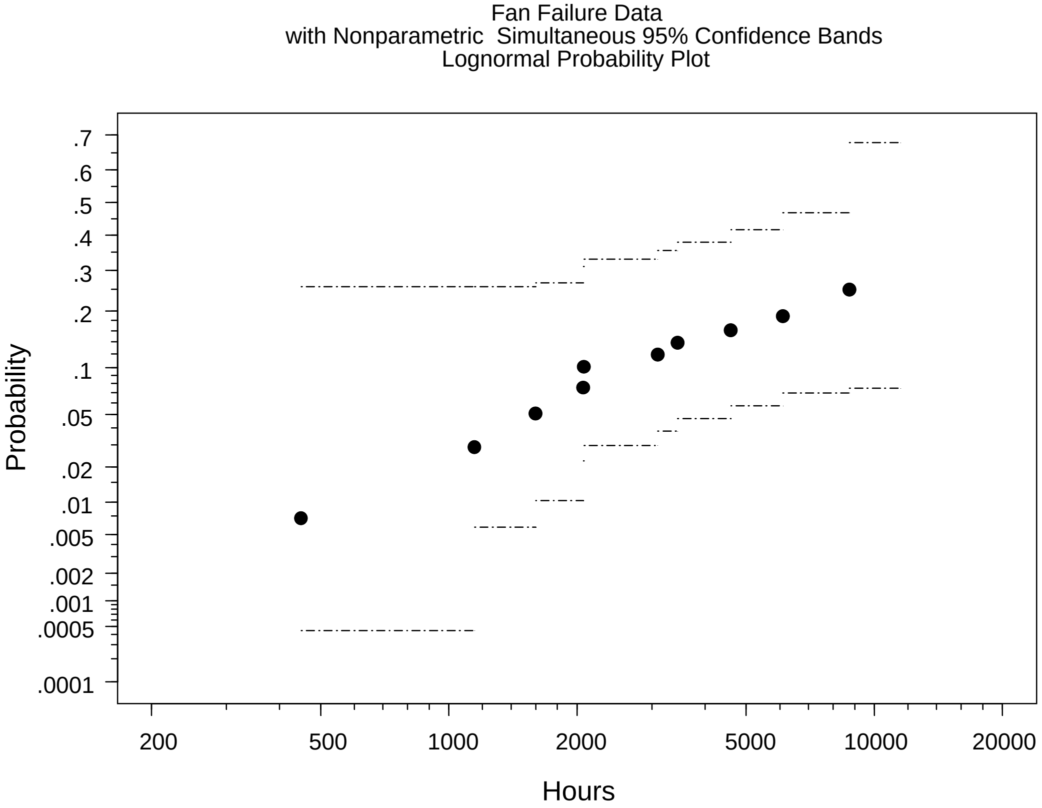


Figure 16 Lognormal probability plot with simultaneous confidence bands.

Chapter 6 of Meeker and Escobar (1998) provides theory and a detailed description of methods for interpreting these probability plots. If one can draw a straight line through the simultaneous confidence band, for the chosen distribution (lognormal in Figure 16), then there are lognormal distributions that are consistent with the data. Then it is not possible to rule out the possibility that the data were generated by a lognormal distribution. One should, of course, try other distributions and compare results.

Figure 17 is a snapshot of the **SLIDA ➡ Single distribution life data analyses** part of the SLIDA menu. *The SLIDA menu items (shown on the left) correspond to different tasks/analyses (e.g., plan a life test, analyze single-distribution life test data, compare two different populations, etc.). The SLIDA submenu items (shown on the right) are organized according to the order in which a complete analysis would be done, typically starting with simple graphical methods and then progressing to model fitting, graphical display of model-fitting results, and sensitivity analyses.*

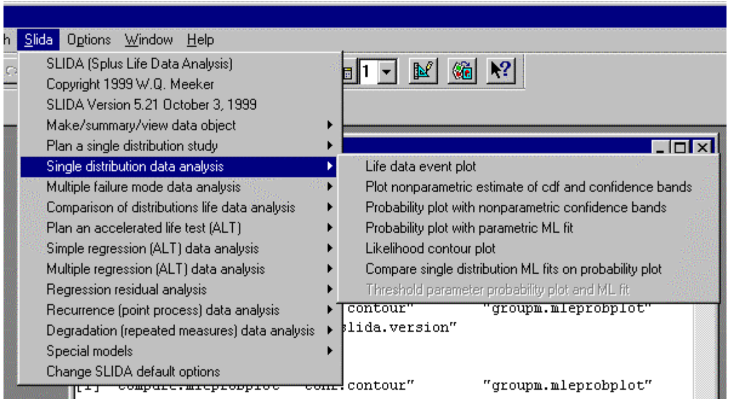
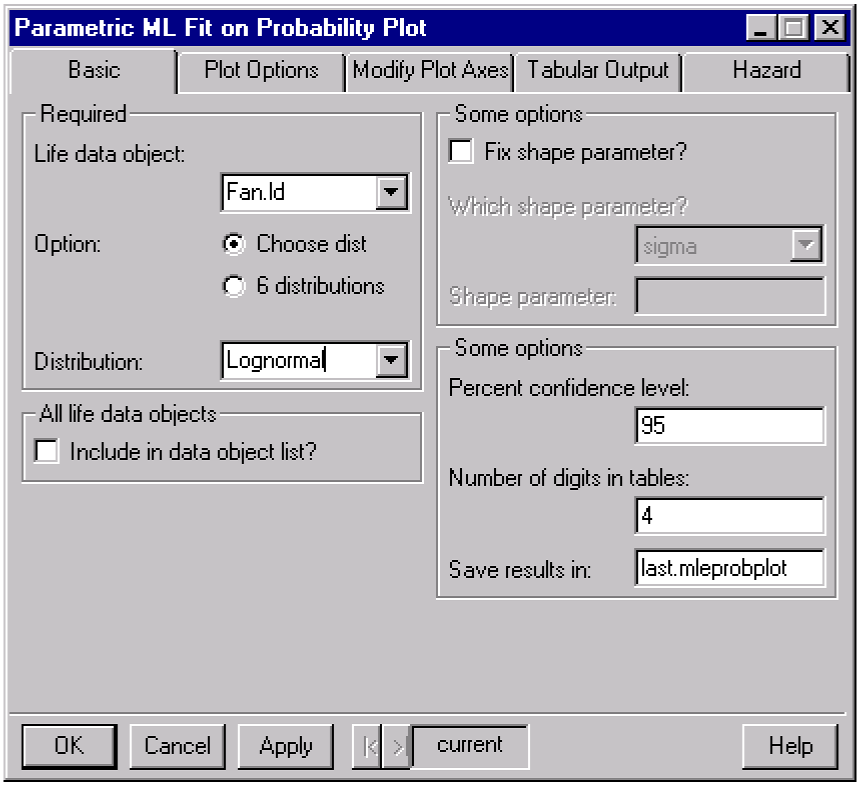


Figure 17 View of the SLIDA menu showing the options for single distribution analyses.

3.4 Maximum likelihood estimation of the failure-time cdf

Using **SLIDA ➡ Single distribution life data analyses ➡ Probability plot with parametric ML fit** produces the dialog in Figure 18. This dialog allows the user to request a probability plot showing the ML estimate for the chosen distribution (plotted as a straight line) along with the points usually plotted in the probability plot.



Required

Life data object: Fan.ld

Option: ● Choose dist ○ 6 distributions

Distribution: Lognormal

All life data objects

☐ Include in data object list?

Some options

☐ Fix shape parameter?

Which shape parameter? sigma

Shape parameter:

Some options

Percent confidence level: 95

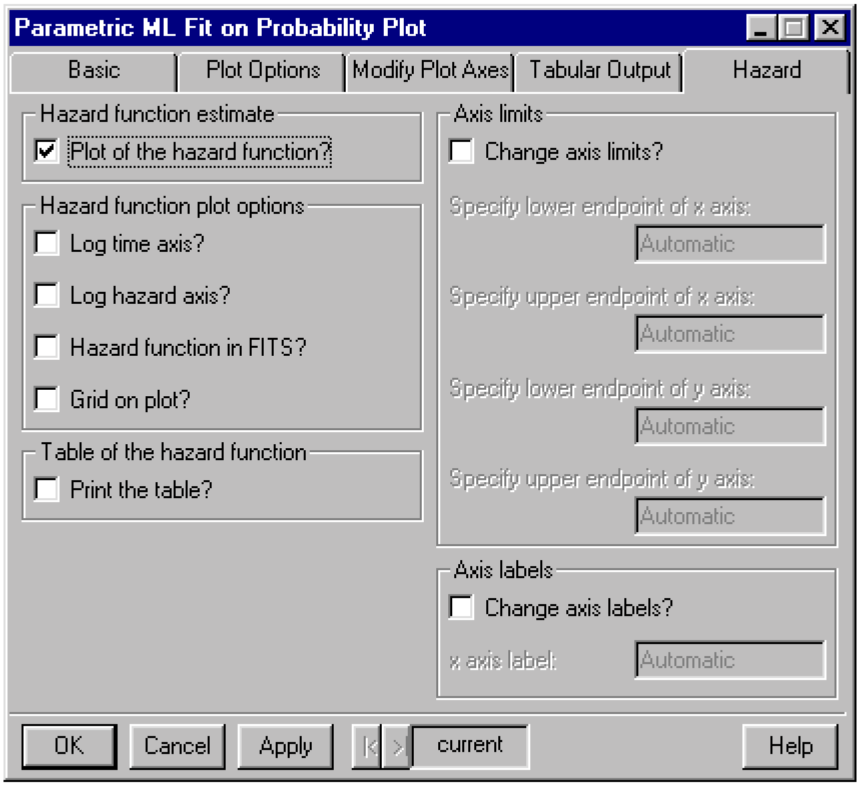
Number of digits in tables: 4

Save results in: last.mleprobplot

Figure 18 Dialog box for getting a probability plot with an ML fit.

By default, SLIDA also plots a set of normal-approximation 95% pointwise confidence intervals. These intervals allow one to obtain a visualization of estimates of both failure probabilities and distribution quantiles and the associated statistical uncertainty due to limited sample size. One of the back pages in the

Figure 18 dialog box, shown in Figure 19, allows the user also to obtain a plot of the corresponding parametric ML estimate of the hazard function versus time. A table of the hazard function estimates and corresponding confidence intervals is also available. The resulting probability plot with ML estimates is shown in Figure 20 and the plot of the hazard function is given in Figure 21. Chapters 2, 7 and 8 of Meeker and Escobar (1998) give the theory and methods for understanding functions and using the corresponding analyses.



Hazard function estimate
☑ Plot of the hazard function?

Hazard function plot options
☐ Log time axis?
☐ Log hazard axis?
☐ Hazard function in FITS?
☐ Grid on plot?

Table of the hazard function
☐ Print the table?

Axis limits
☐ Change axis limits?
Specify lower endpoint of x axis: Automatic
Specify upper endpoint of x axis: Automatic
Specify lower endpoint of y axis: Automatic
Specify upper endpoint of y axis: Automatic

Axis labels
☐ Change axis labels?
x axis label: Automatic

Figure 19 The Hazard page of the probability plot with ML fit dialog, allows the user to request and customize a plot of the hazard function ML estimate.

Table 3 gives tabular output from fitting the lognormal distribution to the fan data. The lines with the Greek letters mu (μ) and sigma (σ) are, respectively, ML estimates for the mean and standard deviation of the distribution of logarithm of fan life. Standard errors and 95% normal-approximation confidence intervals are also given.

Table 3 Lognormal ML estimation results for the turbine fan data.

```
Fan Failure Data
Maximum likelihood estimation results:
Response units: Hours
Lognormal Distribution
Log likelihood at maximum point: -134.5

  Parameter              Approx Conf. Interval

        MLE Std.Err. 95% lower 95% upper
   mu 10.14   0.5211     9.122    11.165
sigma  1.68   0.3893     1.066     2.645
```

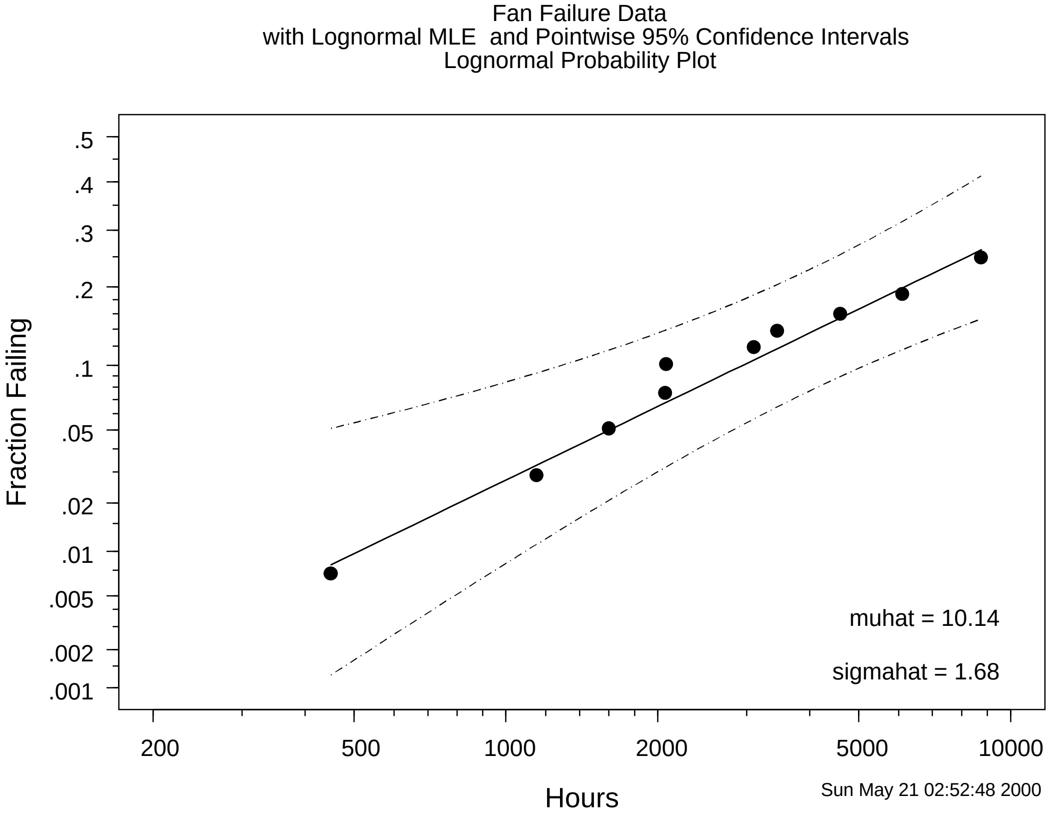


Figure 20 Lognormal probability plots of the fan data showing the ML estimate and parametric *pointwise* confidence intervals.

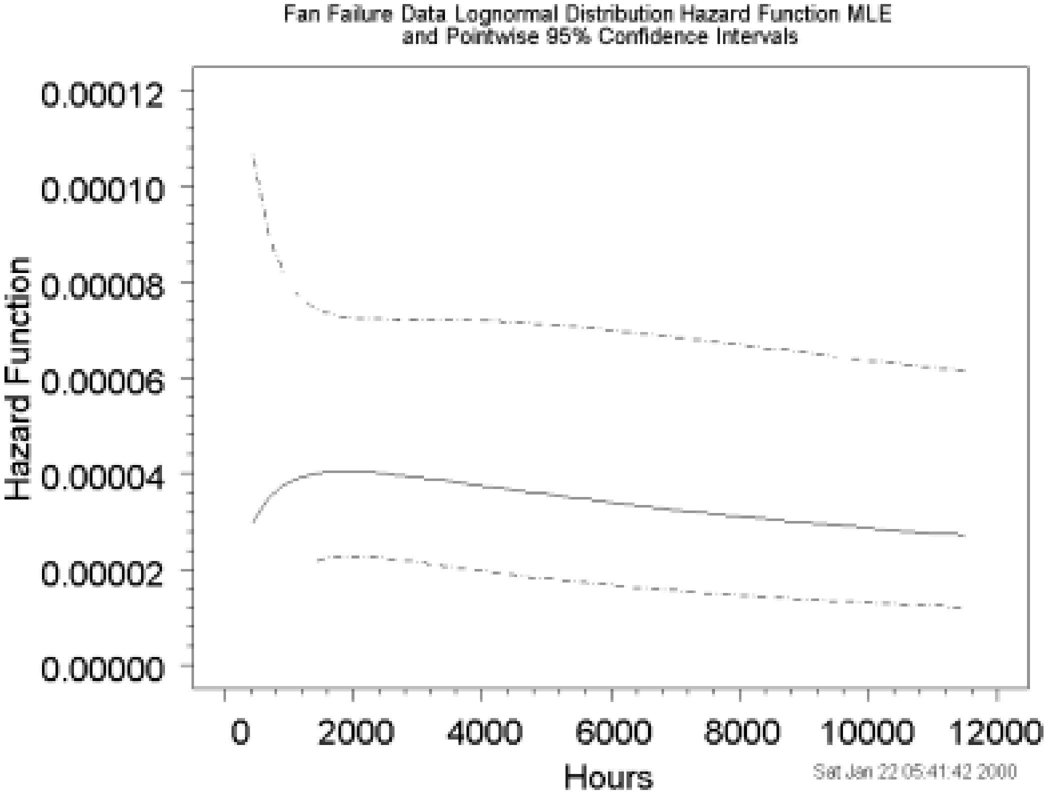
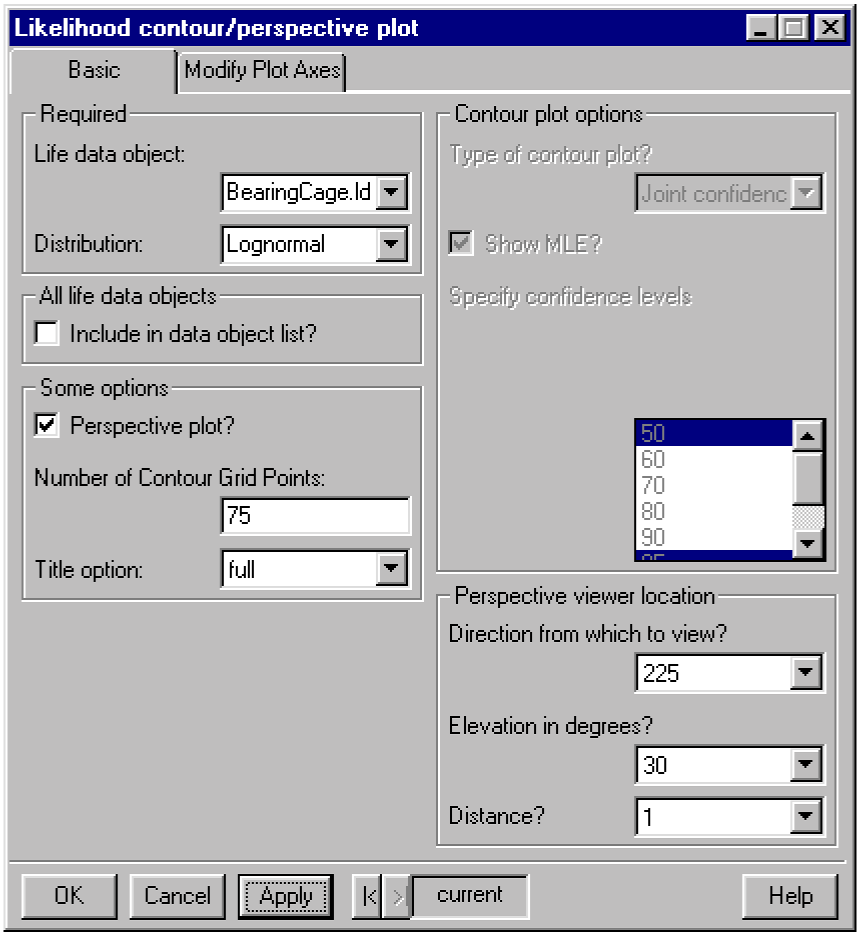


Figure 21 Lognormal hazard function estimate for the fan data.

3.5 Likelihood contour/perspective plot

Using **SLIDA ➡ Single distribution life data analyses ➡ Likelihood contour/perspective plot** produces the dialog box shown in Figure 22. This dialog box allows the user to request either a contour or a perspective plot of the relative likelihoood function or the corresponding joint confidence region (described and compared in Sections 8.2 and 8.3 of Meeker and Escobar,1998) for a given set of data. Alternatively, one can request a perspective (or wire-frame) plot of the relative likelihood function. The dialog has an option to indicate the position of the ML estimates as well as the usual options to control plot axes.

The dialog box shown in Figure 22 allows the user to request either a perspective plot or a contour plot showing the approximate joint confidence region for the paramters of a log-location-scale or location-scale distribution. We illustrate the use of this dialog box with the the bearing cage data (life data object BearingCage.ld) from Abernathy et al. (1983). Figure 23 shows the perspective plot of the relative likelihood, followed by the contour plot of the joint confidence region in Figure 24.



Life data object: BearingCage.ld

Distribution: Lognormal

☐ Include in data object list?

☑ Perspective plot?

Number of Contour Grid Points: 75

Title option: full

Direction from which to view? 225

Elevation in degrees? 30

Distance? 1

Figure 22 Dialog for requesting a contour or perspective plot of the bearing cage likelihood function.

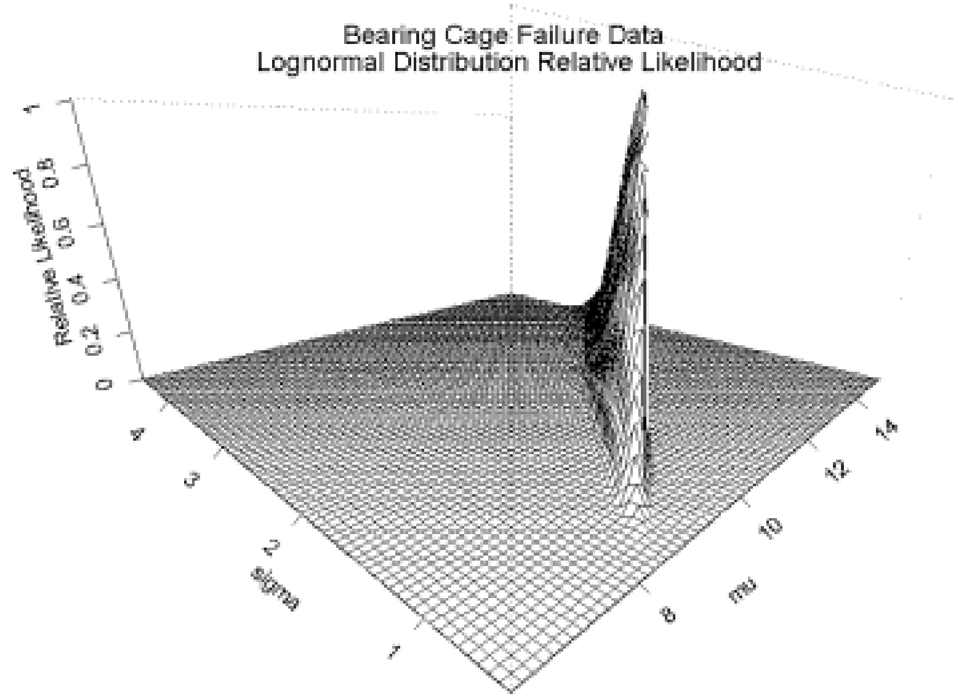


Figure 23 Perspective plot of the relative likelihood function for lognormal parameters based on the bearing cage data.

Notice the “shark-fin” shape of the relative likelihood in Figure 23. This reflects the strong positive correlation between the ML estimators of the lognormal parameters; this correlation is the result of the heavy right censoring in this data set. The contour plot of the joint confidence region for the lognormal parameters shown in Figure 24 is easier to interpret.

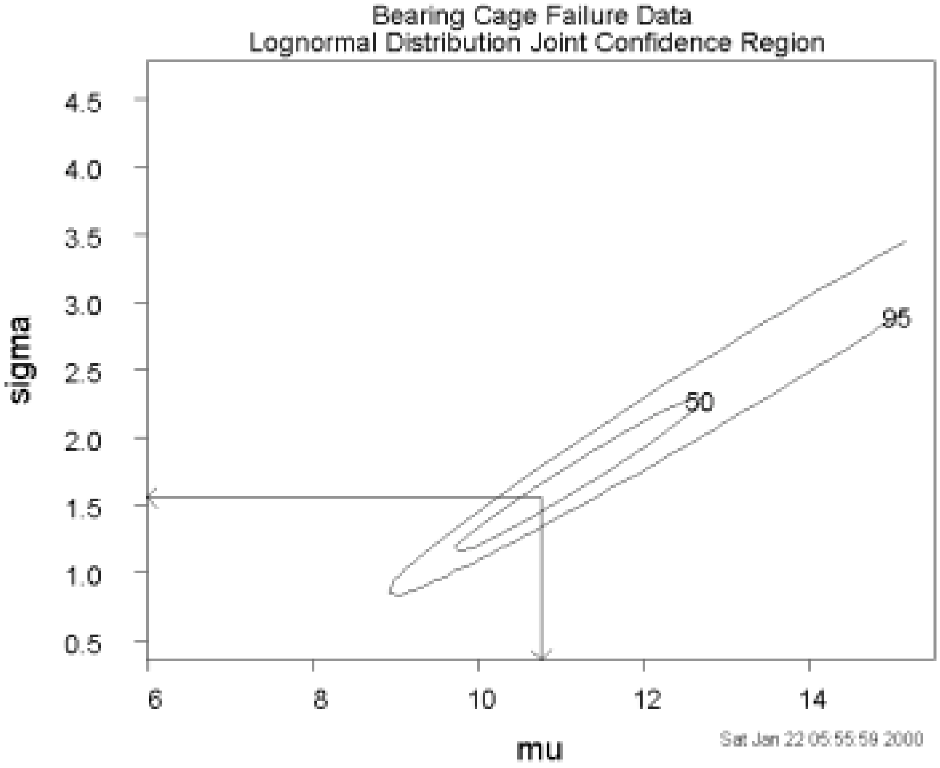
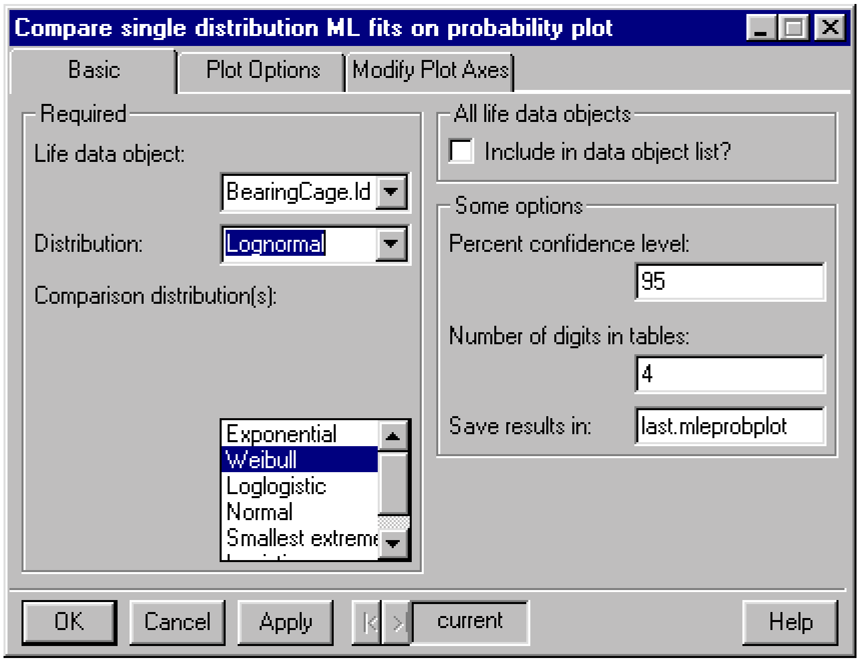


Figure 24 Joint confidence region for lognormal parameters based on the relative likelihood function for the bearing cage data.

3.6 Comparison of ML estimates from different distributions

The dialog box produced by **Single distribution life data analyses ➡ Compare distribution ML fits on probability plot,** shown in Figure 25, allows the comparison of ML estimates for a chosen baseline distribution with one or more other distributions. The required inputs are the life data object (for the following example we continue to use the BearingCage.ld life data object), the baseline distribution, and the comparison distribution.



Life data object: BearingCage.ld

Distribution: Lognormal

Comparison distribution(s): Exponential, Weibull, Loglogistic, Normal, Smallest extreme

☐ Include in data object list?

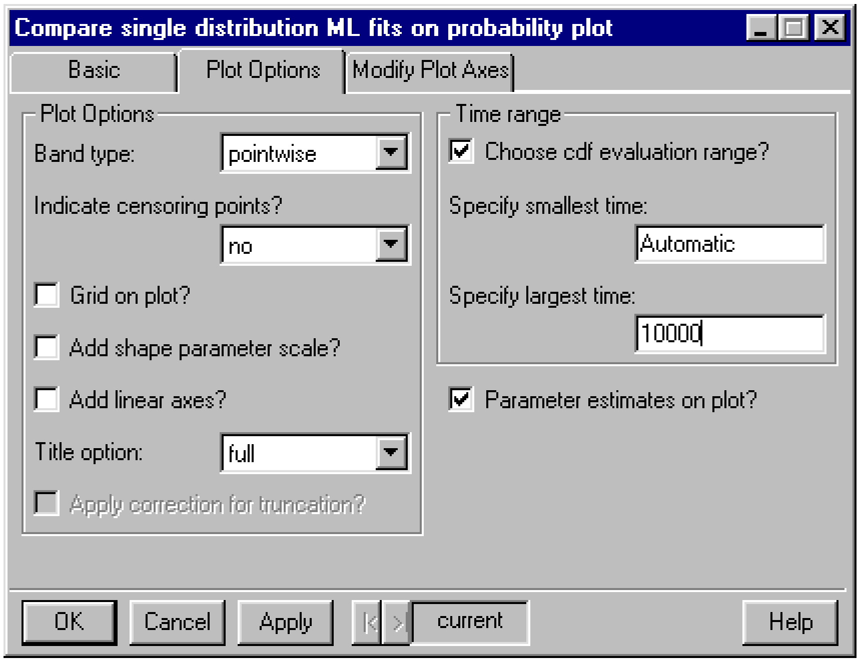
Percent confidence level: 95

Number of digits in tables: 4

Save results in: last.mleprobplot

Figure 25 Dialog box requesting a comparison of the lognormal and Weibull ML estimates on lognormal probability paper.

The objective of the analysis of the bearing cage data was to estimate life out to 10,000 hours. In order to do this, the Plot Options page of the Compare ML fit dialog box, shown in Figure 26, is used to request extrapolation outside of the range of the data, as shown in Figure 26. Clicking on “OK” or “Apply” will then produce the desired comparison probability plot shown in Figure 27 (changing the range using the options in the Modify Plot Axes page of the dialog box will change only the axis range and not the range of cdf evaluation).



Plot Options

Band type: pointwise

Indicate censoring points? no

☐ Grid on plot?

☐ Add shape parameter scale?

☐ Add linear axes?

Title option: full

☐ Apply correction for truncation?

Time range

☑ Choose cdf evaluation range?

Specify smallest time: Automatic

Specify largest time: 10000

☑ Parameter estimates on plot?

Figure 26 Plot Options page of the Compare ML fit dialog showing how to extend the range of cdf evaluation

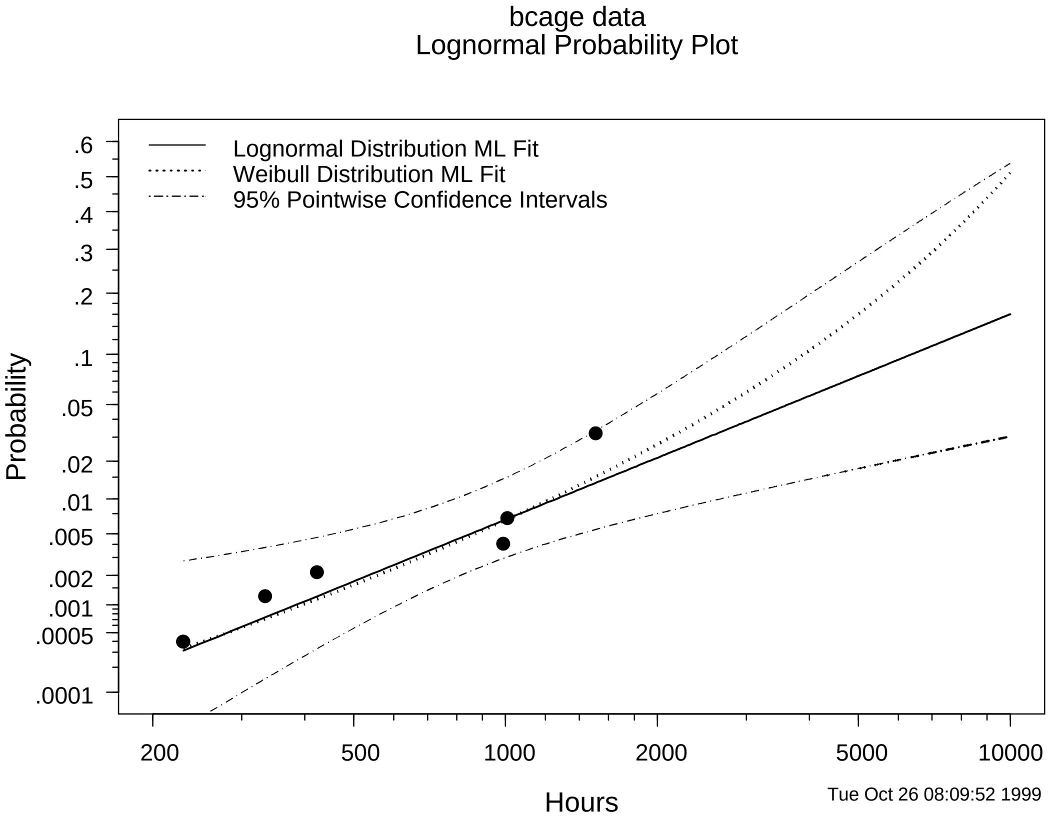


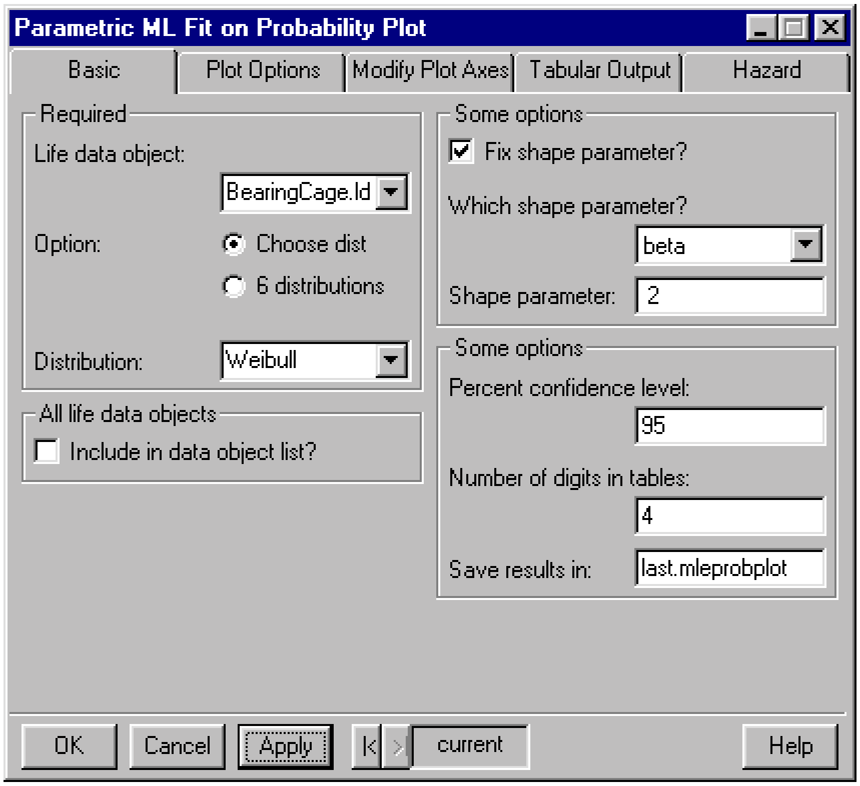
Figure 27 Lognormal probability plot comparing the lognormal and Weibull ML estimates for the bearing cage data.

There is little difference between the probability estimates up to 1000 hours. Note, however, the large difference between the lognormal and Weibull estimates of fraction failing outside the range of the data.

3.7 Fitting a log-location-scale (location-scale) distribution with a given shape (scale/slope) parameter

In some applications, especially when the amount of data is limited, it may be useful to fit a distribution with a given shape parameter. Although it is rare that one would know such a shape parameter exactly, such evaluations are useful if one repeats the analysis using different values of the given parameter within a given ranges, perhaps based on previous experience with a similar failure mode. More details are given in Section 8.5 of Meeker and Escobar (1998).

Fitting a location scale or log location scale distribution with a fixed shape (slope) parameter is easy in SLIDA. To illustrate this, we will continue with the bearing cage example. For the bearing cage data, the wide confidence intervals for $F(t)$ outside of the range of the data in Figure 27 are due, in large part, to the fact that the lognormal shape parameter is unknown and that there is only a small amount of data available. Important improvement in precision can be obtained by specifying a value for the shape parameter. Using **SLIDA ➡ Single distribution life data analyses ➡ Probability plot with parametric ML fit** produces the dialog in Figure 28.



Parametric ML Fit on Probability Plot

Required

Life data object: BearingCage.ld

Option: ● Choose dist ○ 6 distributions

Distribution: Weibull

All life data objects

☐ Include in data object list?

Some options

☑ Fix shape parameter?

Which shape parameter? beta

Shape parameter: 2

Some options

Percent confidence level: 95

Number of digits in tables: 4

Save results in: last.mleprobplot

Figure 28 Dialog box showing how to fit a Weibull distribution with a fixed shape (slope) parameter.

The resulting probability plot is given in Figure 29.

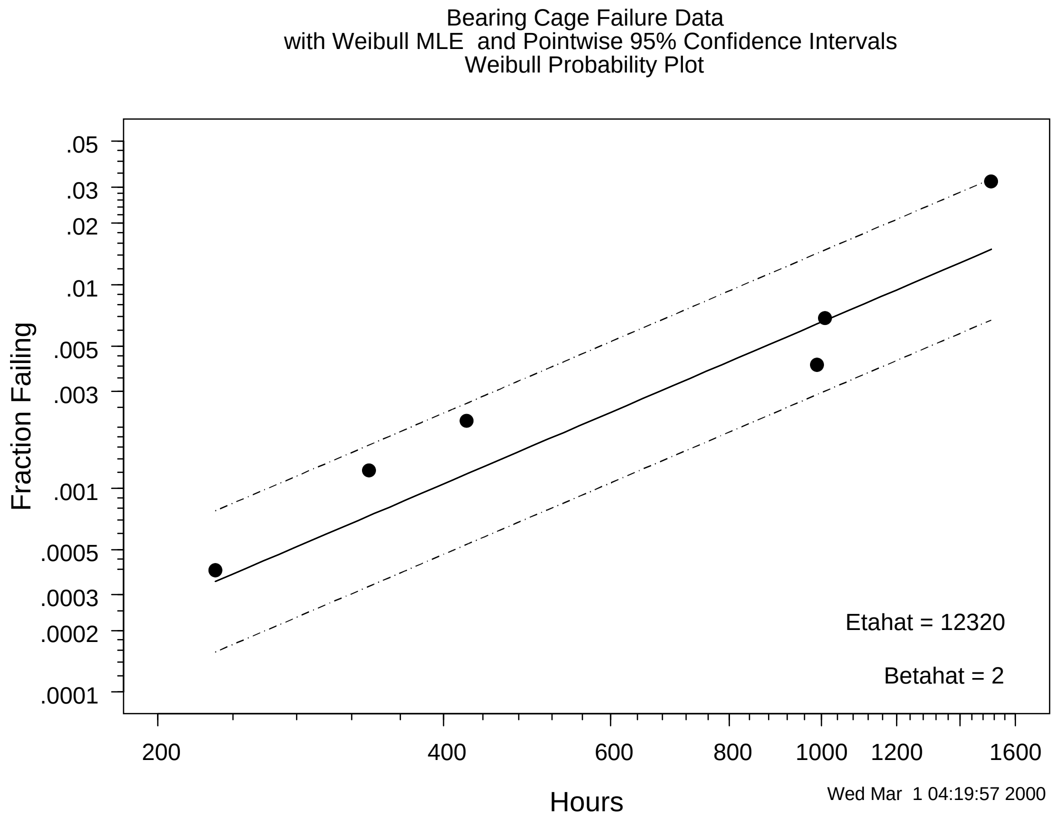


Figure 29 Bearing cage Weibull probability plot with the fixed β=2 ML estimate line.

Notice that the confidence interval lines in the Weibull probability plot are parallel. This implies that the intervals will be narrower outside of the range of the data. Of course, this would provide a false sense of precision if the Weibull shape parameter (not to mention the assumption of a Weibull distribution itself) does not provide an adequate approximation to the actual bearing cage distribution.

4. Planning a Single Distribution Study

This section describes tools for evaluating proposed lifetest plans. The tools presented here are based on theory and methods described in Chapter 10 of Meeker and Escobar (1998).

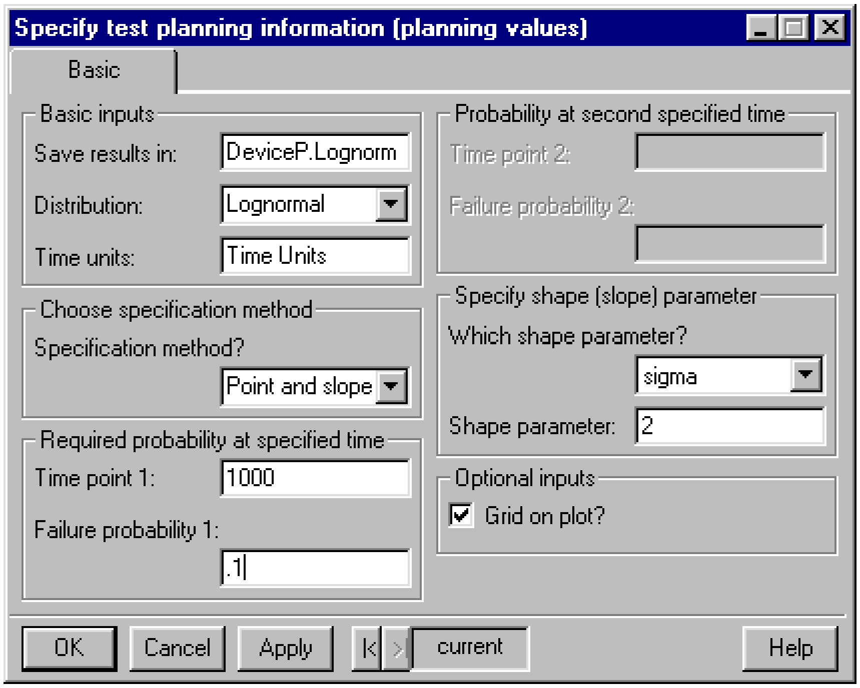
SLIDA single distribution life test evaluations are done in three stages.

- In the first stage the user specifies the testing situation by providing planning values (essentially, best guesses for the underlying model, including information on the life distribution, including the distribution's parameters values) in the form of a plan value object. Given such planning information, it is possible to evaluate any specified test plan or plans.
- In the second stage one can ask for a plot of approximate required sample size as a function of desired precision. This evaluation, based on large sample approximate variance computations, allows the test planner to see, at a glance, the effect of sample size for a given test length (as specified by time for Type I censoring number of test units for Type II censoring).
- In the last stage of evaluation, one can simulate a specified test plan a specified number of times. Plots of the samples from a few of the individual simulated experiments and a summary of ML estimates from all of the simulations (both presented on appropriate probability plots) provides a

visualization of the possible results from a life test experiment and the reasons why estimates of certain quantiles might or might not be estimated precisely.

4.1 Specifying test planning information (planning values)

Using **SLIDA ➡ Plan Single Distribution Analyis ➡ Specify test planning information (planning values)** brings up the dialog box in Figure 30, allowing the user to specify planning values needed to evaluate and compare different life test plans. The default name for the planning value object is last.xxx.pv where xxx is the chosen distribution. Generally it is a good idea to edit the suffix “last” to be something that describes the actual application (in the example below we use DeviceP). This “planning value object” will be used in the simulation/evaluation stage of planning. To specify the required distribution-parameter plannning values, start by choosing a method: a) point and slope or b) two points. Either method can be used to specify a line on a probability paper (with an underlying assumed distribution). For DeviceP, the engineers expect approximately 10% of the tested units to fail by 1000 hours and that the failure time distribution will be adequately described by a lognormal distribution with a shape parameter sigma (σ) in the neighborhood of 2. After specifing the needed information, click “Apply” and examine the resulting probability plot reflecting the inputted information, as illustrated in the Figure 31. Some tabular information is also provided in Table 4.


Specify test planning information (planning values)

Basic

Basic inputs

Save results in: DeviceP.Lognorm

Distribution: Lognormal

Time units: Time Units

Choose specification method

Specification method? Point and slope

Required probability at specified time

Time point 1: 1000

Failure probability 1: .1

Probability at second specified time

Time point 2:

Failure probability 2:

Specify shape (slope) parameter

Which shape parameter? sigma

Shape parameter: 2

Optional inputs

☑ Grid on plot?

Figure 30 Dialog box for specifying life test planning information.

Figure 31 Probability plot depicting life test planning information.

Table 4 Tabular output from the dialog used to specify planning values.

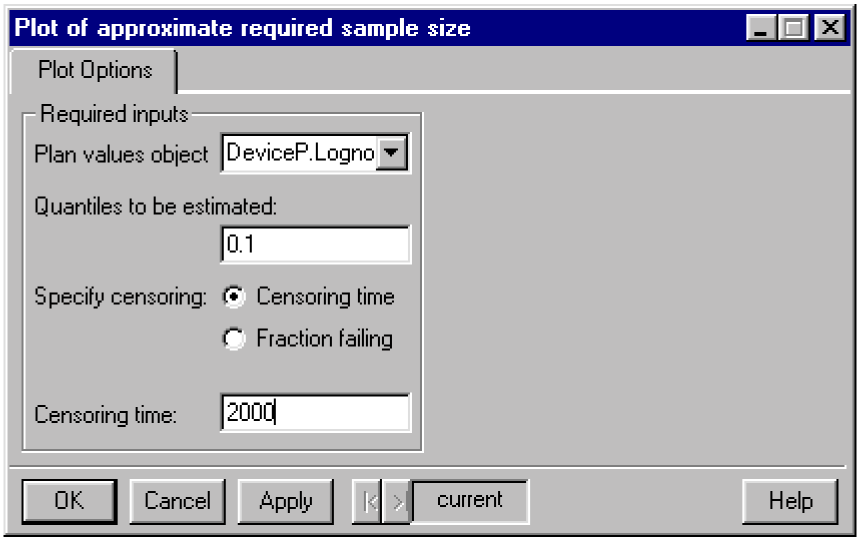
```
Distribution:  Lognormal
Time units are:  Hours

The  0.1 quantile is:  1000

Shape parameter beta is:  0.5
Characteristic life eta is:  12976   Hours

mu =  9.47
sigma =  2


Failure probabilities from the Lognormal distribution
   Hours fail.probs
  1e+001   0.000169
  1e+002   0.007490
  1e+003   0.100000
  1e+004   0.448181
  1e+005   0.846381
  1e+006   0.985084
  1e+007   0.999556
```

4.2 Plot test planning information (planning values)

Using **SLIDA** ➡ **Plan Single Distribution Analysis** ➡ **Plot test planning information (planning values)** allows the user obtain a plot and table, like those in Figure 31and Table 4, describing a previously created plan value object.

4.3 Plot of approximate required sample size

Using **SLIDA** ➡ **Plan Single Distribution Analyis** ➡ **Plot of required sample** will produce the dialog box in Figure 32.



Plan values object: DeviceP.Logno

Quantiles to be estimated: 0.1

Specify censoring: ● Censoring time ○ Fraction failing

Censoring time: 2000

Figure 32 Dialog box for requesting a required sample size plot.

Note that the most recently created plan value object (within the current session) is remembered and displayed as the default to be used. Alternatively, a different, previously created, plan values object can be chosen. Then one must choose a censoring type and either a censoring time or number of failures (for Type I and Type II censoring, respectively) and, if desired, a quantileof interest of other than the default of .1. Clicking on “OK” or “Apply” will produce a plot like the one in Figure 33. For log-location-scale distributions (Weibull, lognormal, loglogistic) confidence interval precision is described in terms of a factor R in that the normal-approximation confidence interval for a quantile has the form $[{}^\wedge t_p/R, {}^\wedge t_p \times R]$ where $R>1$ and the interval is more precise for small values of R (see Chapters 7 and 8 of Meeker and Escobar 1998). For location-scale distributions, precision is given in terms of the half-width of the two-sided confidence interval.

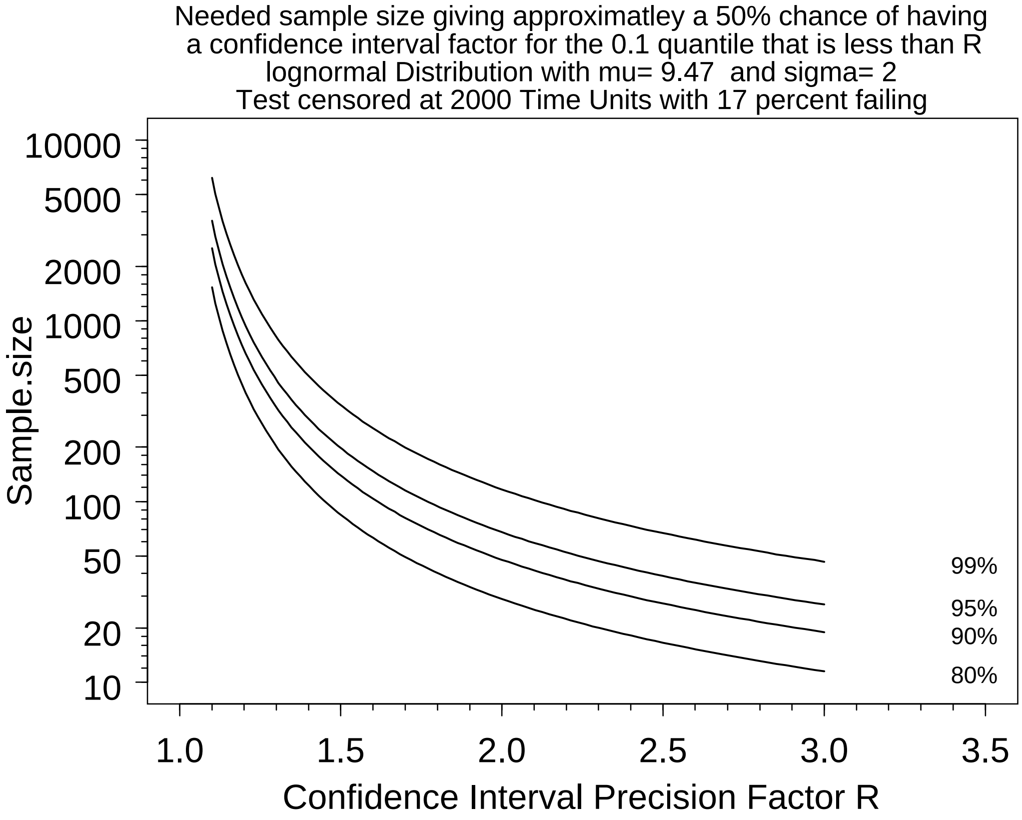
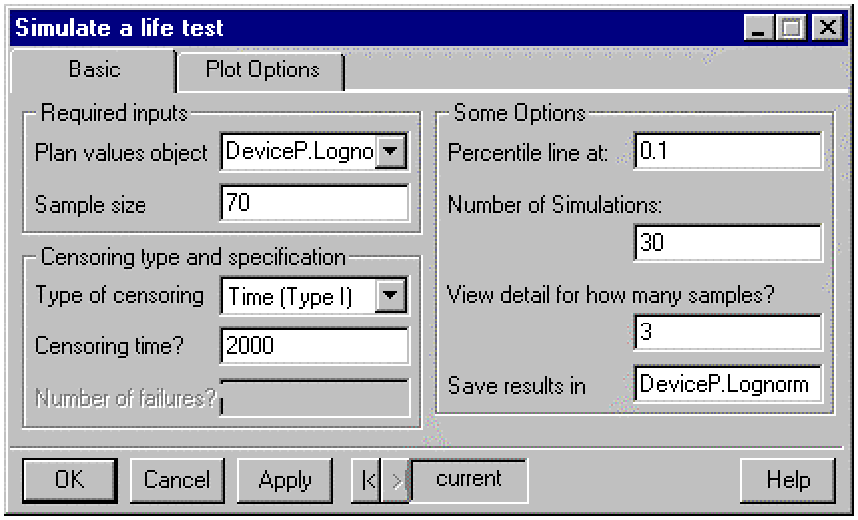


Figure 33 Plot giving sample size needed as a function of the target confidence interval precision factor.

For example, Figure 33 shows that a sample size of approximately 70 is required to have a 95% confidence interval target precision factor of 2. The actual precision factor R, because it depends on the data, is random for any given life test, but should be no more than the target value with probability of approximatley .5. To get a sense of how much R might vary from the target value, one can use the simulation tool described in Section 4.4.

4.4 Life test simulation

Although the plot of required sample size versus precision factor is useful for determining the approximate sample size needed for a life test, simulating the life test avoids large sample approximations, provides more insight into the results that might be obtained, and gives one a better sense of the trade-off between sample size and test length. Using **SLIDA ➡ Plan Single Distribution Analyis ➡ Simulate a life test** requests a dialog box like that shown in Figure 34. This dialog box allows one to specify the inputs needed to produce a simulation of a user-specified life test plan.



Required inputs

Plan values object: DeviceP.Logno

Sample size: 70

Censoring type and specification

Type of censoring: Time (Type I)

Censoring time? 2000

Number of failures?

Some Options

Percentile line at: 0.1

Number of Simulations: 30

View detail for how many samples? 3

Save results in: DeviceP.Lognorm

Figure 34 Dialog box to request a life test simulation.

The user specifies the number of units to be tested ("Sample size") and length of test ("Censoring time" for time or Type I censoring) or number of units to fail (for failure or Type II censoring) and, perhaps some other optional inputs (e.g., which quantile of the distribution is of primary interest). One can choose to look at the individual samples from some of the simulated samples by entering a small integer (usually 5 or 6 is sufficient) into the box marked "View detail for how many samples?" If an integer $k > 0$ is given in this cell, then after completion of the simulation, the graphsheet will contain k probability plots showing the planning value line (with a dark thick line) along with the observed failures and the ML estimate line (a thin line to contrast with the "true" planning value line) for each of the k samples. Figure 35 provides an example of such a plot. It is interesting to observe the variability in the failure times and corresponding ML estimate lines from sample to sample in a sequence of these plots. The final probability plot, illustrated in Figure 36, contains, in summary, the ML estimates from *all* of the simulated samples. When a quantile (number between 0 and 1) is given in the "Quantile line at" cell, a horizontal line is drawn at that level on the probability plot, allowing a visualization of the sampling variability in the estimates of that quantile, and the average precision factor for the confidence intervals for the corresponding confidence intervals is shown in the plot.

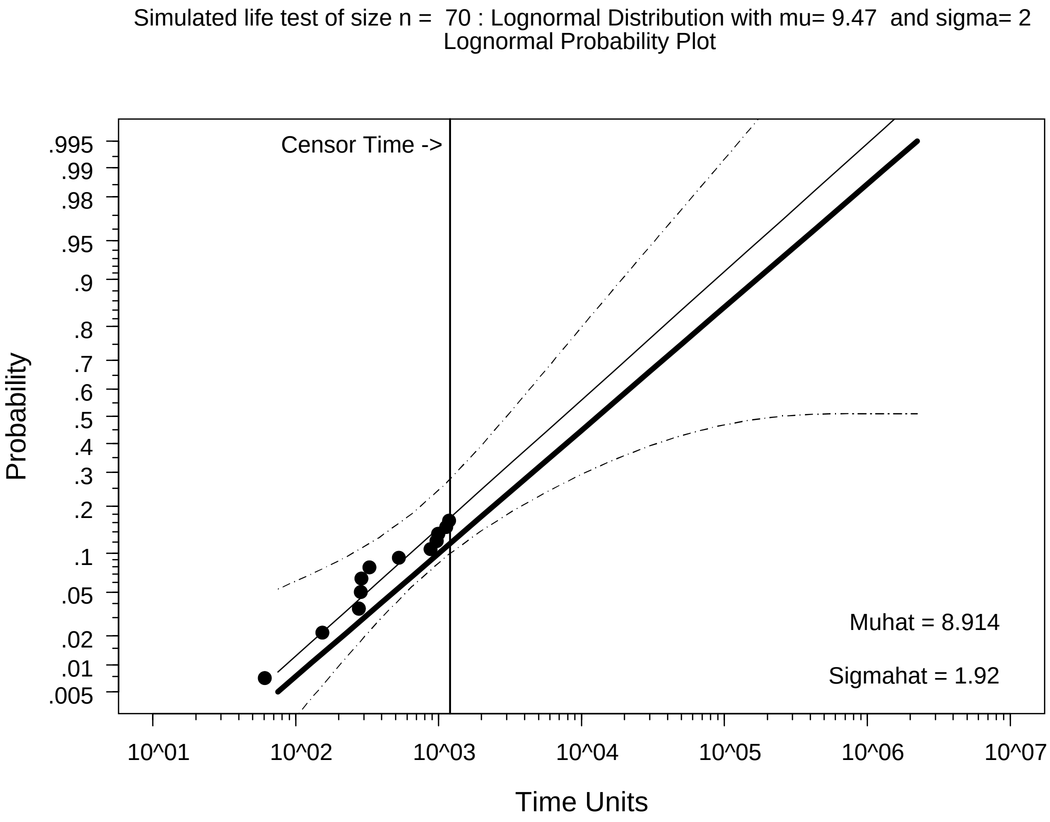


Figure 35 Probability plot and ML estimate for the first simulated life test.

Figure 35 shows the probability plot for the first simulated sample. Generally looking at three or four of these individual simulation results (we only show one here) is sufficient for getting a good idea how the samples in the proposed life test might behave (assuming that the inputted planning information is reasonably accurate).

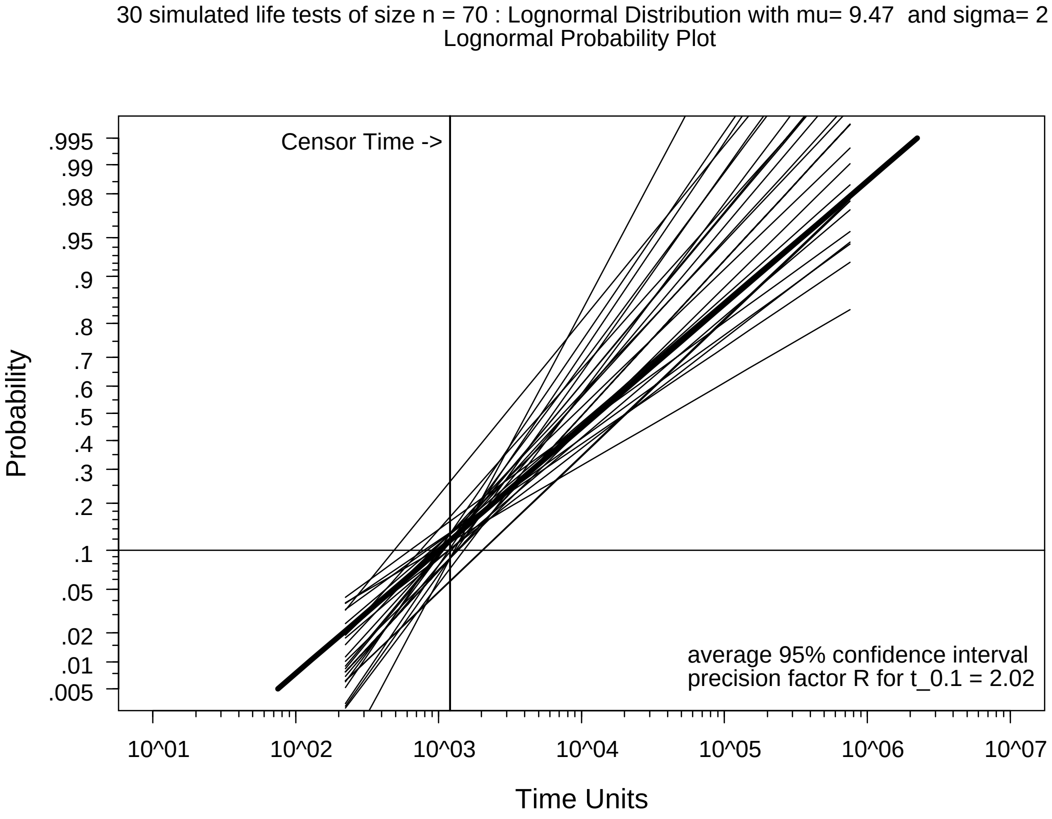


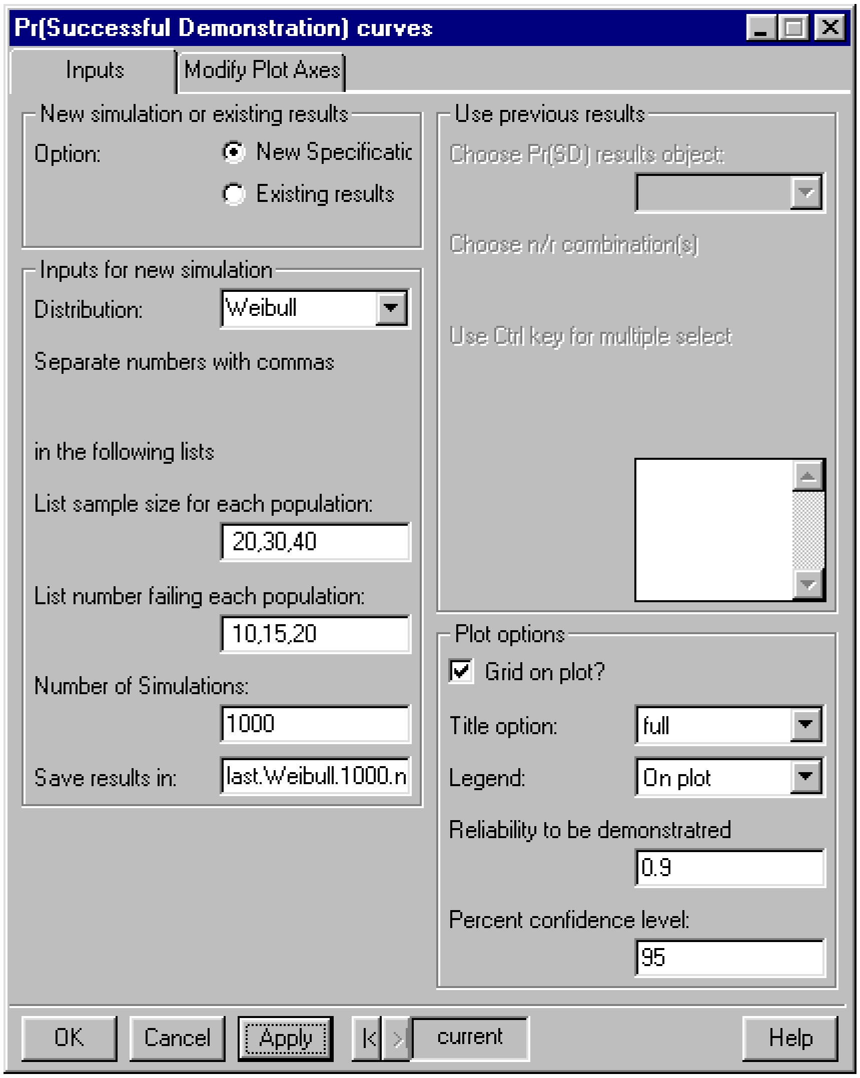
Figure 36 Summary showing ML estimates for all 30 life test simulations.

Figure 36 shows a summary of the ML estimates from 30 simulations. The average precision factor printed in this simulation-summary plot will vary somewhat from simlation to simulation unless the number of simulations is very large (e.g., 1000's of simulated life tests). Nevertheless, this numerical summary of the simulation provides a useful measure of sampling variability and the corresponding precision that one can expect to see in the results of one's life test.

4.5 Probability of successful demonstration

After conducting a life test, a successful demonstration of reliability has occurred if the lower confidence bound on reliability exceeds the given standard $q=1-F(t)$ [which is the same as the upper confidence bound on fraction failing being less than a standard $p=F(t)$]. Equivalently, the demonstration is successful if lower confidence bound on on the corresponding p quantile of the life distribution is larger than the corresponding standard (e.g., for demonstrating 95% reliability, the standard would be based on the .05 quantile of the life distribution). For a log-location-scale distribution, the probability of a successful demonstration for a type II censored life test (test run until a specified number of units fail) is a function of the level of reliability to be demonstrated, the number of units to be tested, the number needed to fail, and the underlying true reliability.

SLIDA has a tool to allow one to compute and make plots of the probability of successful demonstration. The dialog box in Figure 37 allows the user to specify the necessary inputs. In Figure 37, sample sizes n=20,30,40 with corresponding number failing r=10,15,20 (i.e., 50% failures) were chosen. In general, the number failing r must be at least 2 but no greater than n. The probabilities of successful demonstration are computed via simulation. The default number of simulations was increased from the default 300 (which allows quick but rough evaluations) to 1000, which is good enough for most practical purposes (although 3 or 4 thousand simulations might be used to make a publication-quality figure). The default reliability to be demonstrated was changed from the default 0.5 to 0.9.



Option: ● New Specificatic ○ Existing results

Distribution: Weibull

Separate numbers with commas

in the following lists

List sample size for each population: 20,30,40

List number failing each population: 10,15,20

Number of Simulations: 1000

Save results in: last.Weibull.1000.n

☑ Grid on plot?

Title option: full

Legend: On plot

Reliability to be demonstrated: 0.9

Percent confidence level: 95

Figure 37 Dialog box for requesting the computation of probability of successful demonstration curves from *q*=0.9.

Figure 38 is a plot of the probability of successful demonstration as a function of the actual (unknown) reliability. As expected, it is easier to make the demonstration (i.e., the probability of success is higher) if the actual reliability is much larger than the standard to be demonstrated.

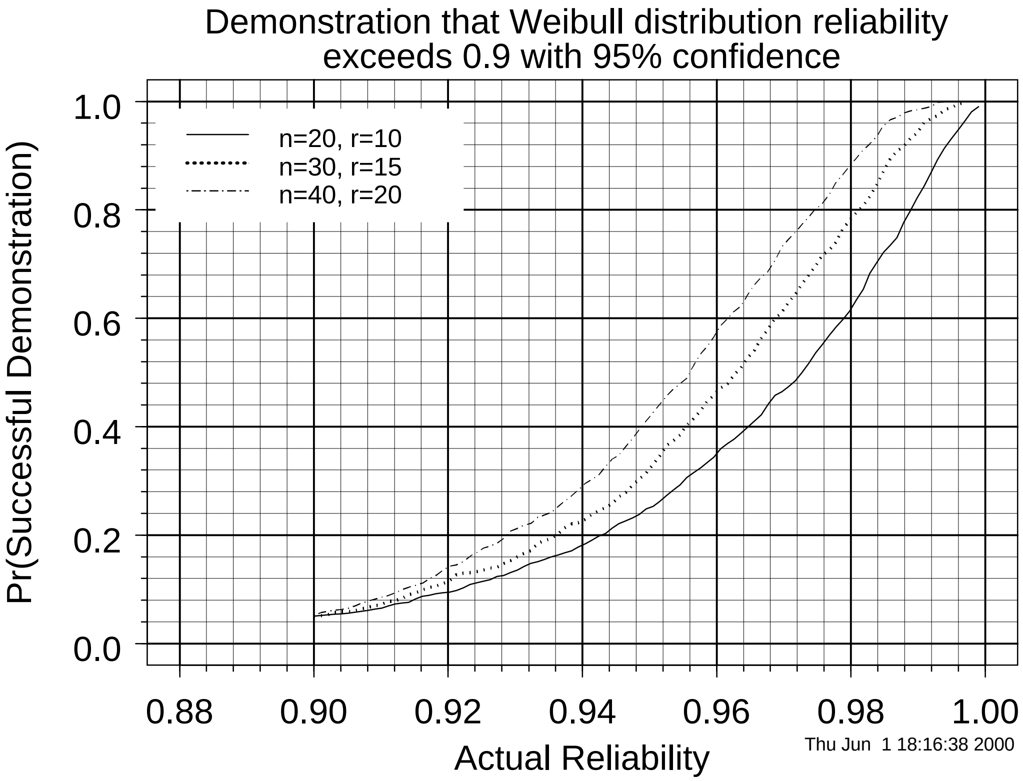
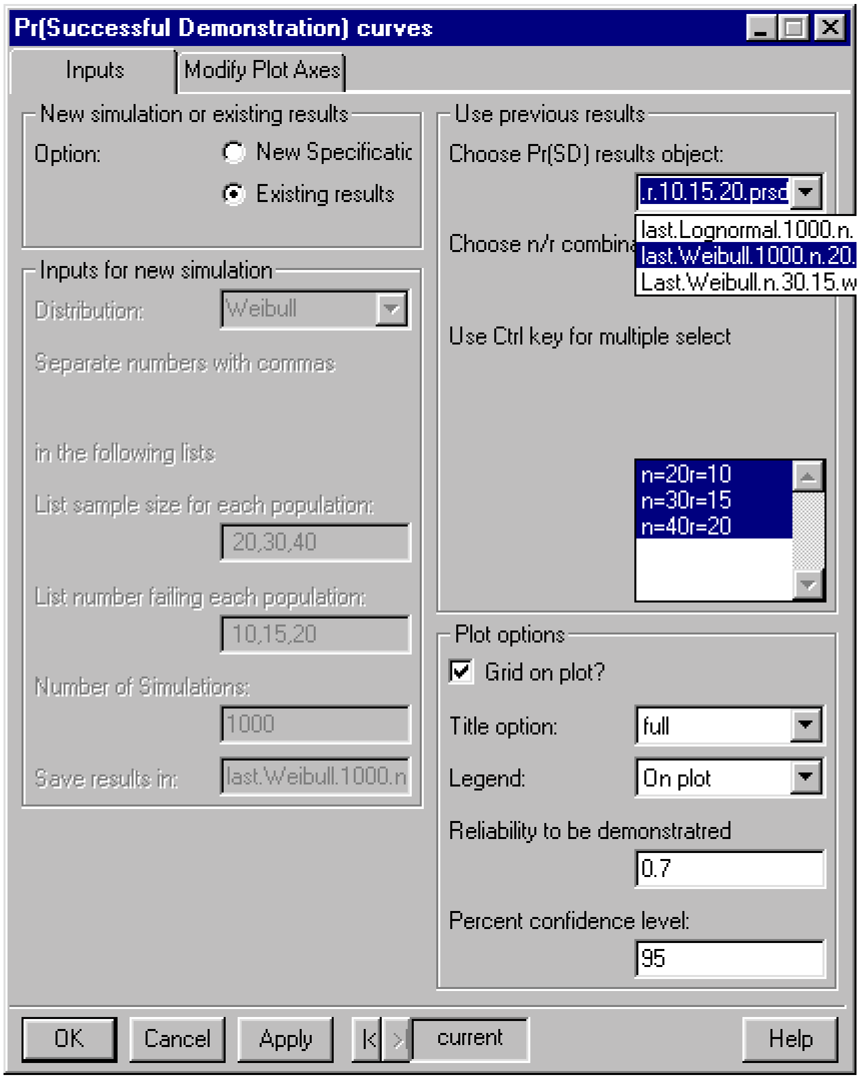


Figure 38 Weibull life test probability of successful demonstration curves for *q*=0.9.

After completing a simulation to compute the probability of successful demonstration, SLIDA will save the simulation results as an object, making it possible to reuse the results to make evaluations for other given values of reliability as the standard. Figure 39 shows a dialog box in which the results from the previous simulation will be used to compute another set of probability of successful demonstration curves with *q=0*.7. From this dialog box it is also possible to choose from among the *n,r* combinations used in the previous simulation to limit the number of curves to appear on the plot.



New simulation or existing results

Option: ○ New Specificatic ● Existing results

Inputs for new simulation

Distribution: Weibull

Separate numbers with commas

in the following lists

List sample size for each population: 20,30,40

List number failing each population: 10,15,20

Number of Simulations: 1000

Save results in: last.Weibull.1000.n

Use previous results

Choose Pr(SD) results object: .r.10.15.20.prsd

last.Lognormal.1000.n.
last.Weibull.1000.n.20.
Last.Weibull.n.30.15.w

Choose n/r combina

Use Ctrl key for multiple select

n=20r=10
n=30r=15
n=40r=20

Plot options

☑ Grid on plot?

Title option: full

Legend: On plot

Reliability to be demonstratred 0.7

Percent confidence level: 95

Figure 39 Dialog box using existing results (previously computed simulation) to compute probability of successful demonstration curves for *q*=0.7.

The resulting plot is shown in Figure 40. As expected, the required sample sizes in this plot are smaller because of the less demanding demonstration.

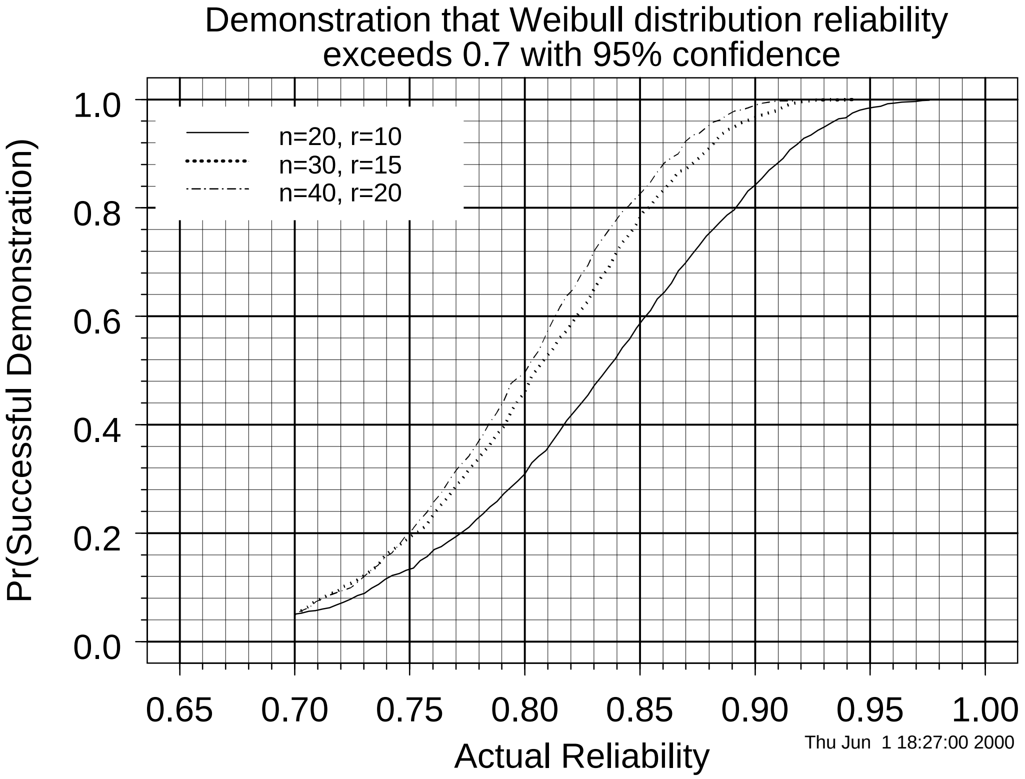


Figure 40 Weibull life test probability of successful demonstration curves for *q*=0.7.

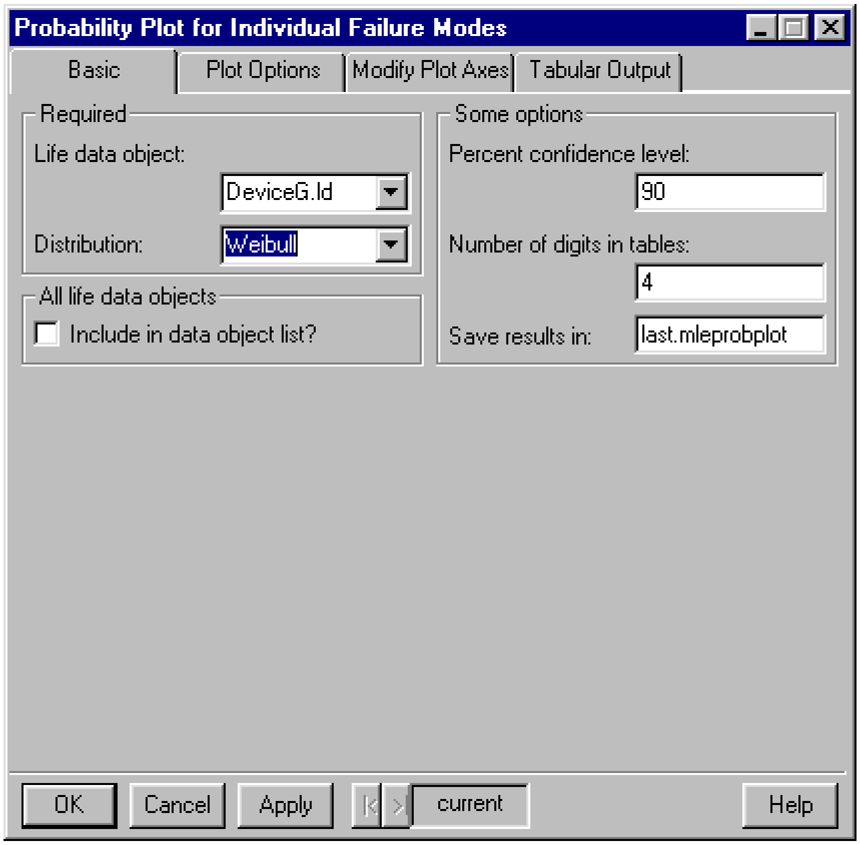
5. Analysis of Data with More Than One Cause of Failure

Both laboratory life tests and field-failure reporting systems (e.g., warranty repair processes) result in data with more than one failure mode. For example, a system may have several components and the failure of any one of these components could cause the system to fail. For many purposes, it is important to use failure mode information in the analysis and interpretation of one's data. This is especially true when the purpose of the analysis is to identify opportunities for improving product reliability.

One commonly used model for multiple failure modes supposes that each unit has a "potential" failure time for each of the possible "modes" of failure and that the distribution of these failure times can be described with a joint distribution. When it can be assumed that the different potential times to failure are approximately statistically independent, this modeling approach provides a simple method of modeling and analysis that allows estimation of the failure time distribution for any particular failure mode or for the entire system with any specified combination of failure modes active. See Chapter 15 of Meeker and Escobar (1998) for technical details and other information about the analysis of such data.

5.1 Summary analysis of individual failure modes

Consider the Device-G data described in Section 15.4 of Meeker and Escobar (1998). The devices that failed during the study failed from either a surge or a wear out failure mode. The underlying mechanisms causing these two failure modes were different and it would be reasonable to assume that the times to failure for these two different modes would be independent. In order to estimate the failure time distribution of the individual failure modes, under the assumption that the failure modes failure times are independent, use **SLIDA ➡ Multiple failure mode life data analysis ➡ Individual modes.** Then choose the life data object (DeviceG.ld in this case) and distribution (Weibull for this example) in the dialog box, as shown in Figure 41.



Life data object: DeviceG.ld

Distribution: Weibull

☐ Include in data object list?

Percent confidence level: 90

Number of digits in tables: 4

Save results in: last.mleprobplot

Figure 41 Dialog box requesting separate analyses of different failure modes for the Device-G data.

Other options for graphical and tabular output are available in the back pages of the dialog box. When done, click “OK” or “Apply,” producing the probability plot with estimated distributions for the two individual failure modes in Figure 42. Tabular output giving the Weibull parameter estimates is also provided, as shown in Table 5.

In this application, management was interested in answering a number of different questions with these data. Among the requested outputs was the failure-time distribution for the wear out failure mode alone, which would be the failure time distribution for the device if the surge failure mode could be eliminated. A table of these estimates (requested with the “Tabular Output” page of the dialog box) is also shown in Table 5.

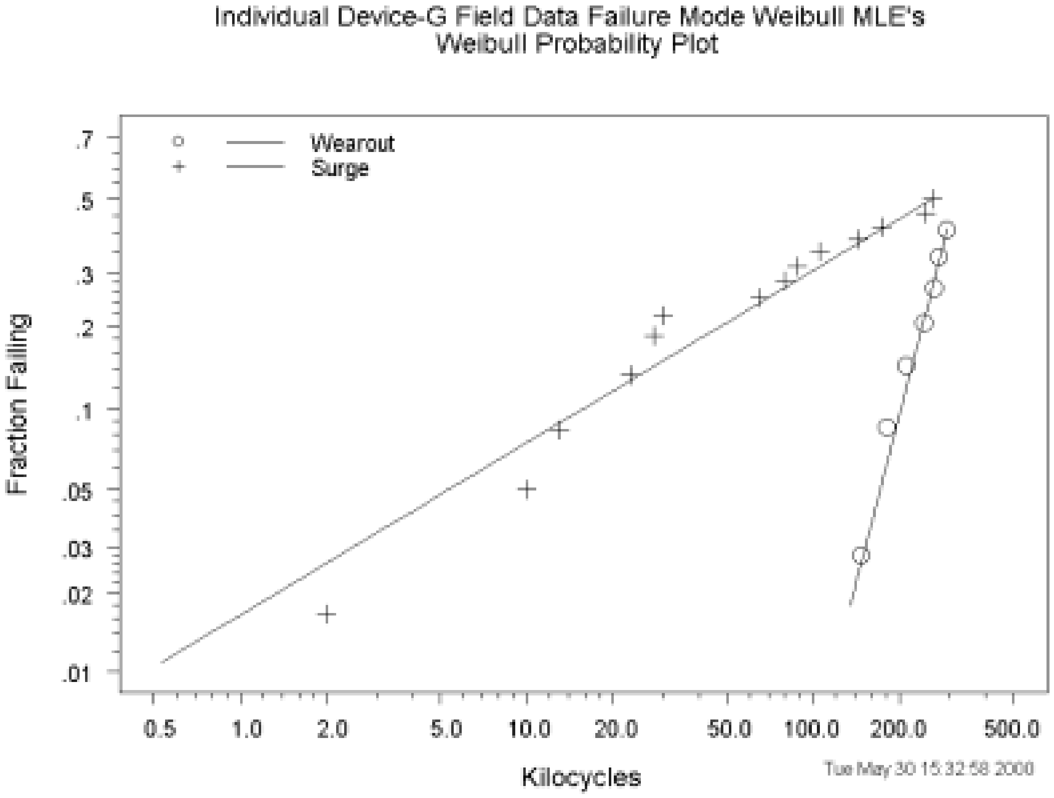


Figure 42 Analysis of the individual failure surge and wear out failure modes for the Device-G field data.

Figure 42 shows immediately that the surge failures tend to occur anytime during life, from early to late. No wearour failures were seen until after 100 thousand cycles. Table 5 provides a summary of separate ML estimations for both the Surge and the Wearout failure modes and some additional details for the Wearout failure mode

Table 5 Summary of ML estimation for Surge and Wearout failure modes and details for the Wearout failure mode

```
Response units: Kilocycles

Weibull Distribution
          Likelihood   eta  se_eta  beta se_beta
1 Wearout     -47.16 340.4  36.14 4.337  1.4506
2   Surge    -101.36 449.5 191.94 0.671  0.1578

Total likelihood= -148.5

Weibull Distribution Failure Probability Estimates

From DeviceG Wearout Failure Mode Group Wearout

with Weibull MLE and Pointwise 95% Confidence Intervals

Kilocycles    Fhat    Std.Err. 95% Lower 95% Upper
140           0.02098  0.02270  0.002453    0.1574
160           0.03714  0.03330  0.006179    0.1931
180           0.06113  0.04510  0.013764    0.2330
```

```
200           0.09482  0.05712  0.027638    0.2785
220           0.13983  0.06853  0.050521    0.3318
240           0.19722  0.07932  0.084269    0.3961
260           0.26718  0.09088  0.128000    0.4752
280           0.34864  0.10569  0.176941    0.5713
300           0.43911  0.12529  0.224124    0.6797
```

5.2 Combined modes (series system) analysis

SLIDA also computes estimates of the series-system failure-time distribution with all failure modes operating. To do this, use **SLIDA ➡ Multiple failure mode life data analysis ➡ Combined modes** and again choose the life data object and distribution and click "OK" or "Apply," producing the probability plot with estimated distribution for the system with both failure modes active, shown in Figure 43.

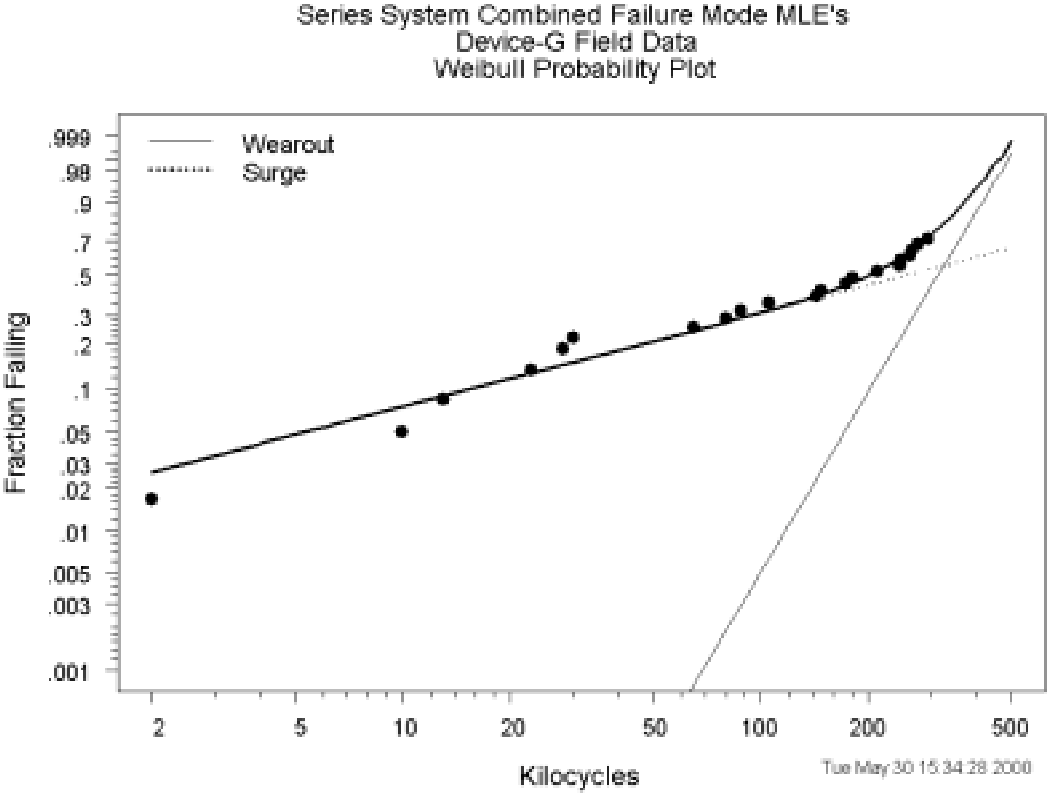
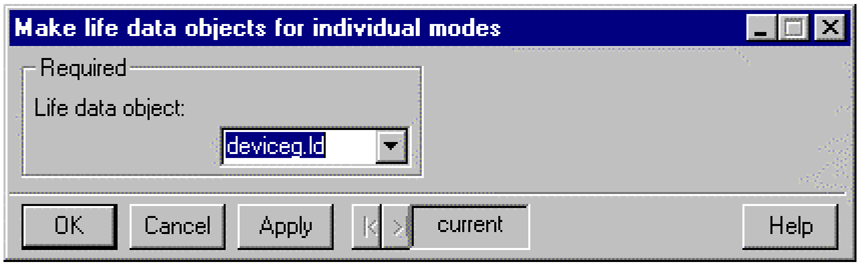


Figure 43 Series system competing risk analysis for the Device-G data.

5.3 Creating life data objects for individual failure modes

Using **SLIDA ➡ Multiple failure mode analysis ➡ Make life data objects for individual failure modes** will bring up the dialog box in Figure 44, allowing the user to create separate life data objects for each failure mode in the multiple failure mode life data object.



Life data object: deviceg.ld

Figure 44 Dialog box to ask that individual life data objects be made for individual failure modes.

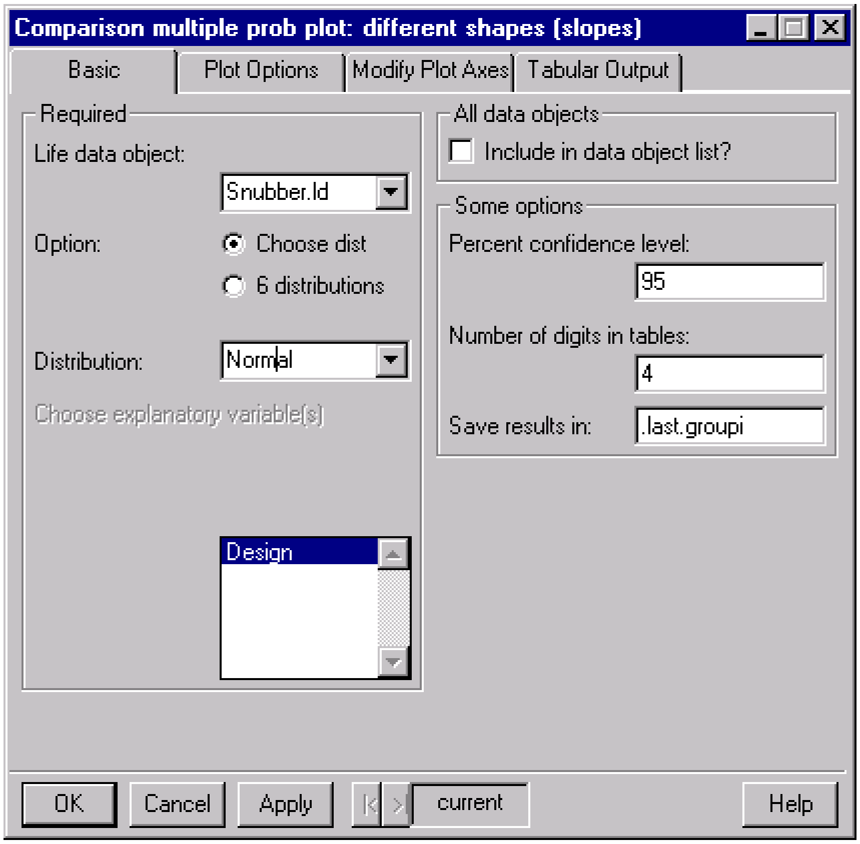
Names for the life data objects are chosen automatically by appending the failure mode name to the root of the failure mode life data object name (DeviceG.Surge.ld and DeviceG.Wearout.ld in the example). Once these individual life data objects have been created, all of the SLIDA methods for single-distribution analyses can be applied to the analysis of the individual failure modes, under the (important) assumption that the individual failure modes are acting independently.

6. Comparison of Distributions Life Data Analysis

Experiments are commonly conducted for the purpose of comparing the life distributions of different or competing materials, formulations, designs, manufacturers, and so on. Similar data arise from warranty data and field tracking studies. The analysis methods presented here for such data generalize methods in classical statistical methods commonly known as two-sample comparison and one-way analysis of variance. SLIDA generalizes these methods, allowing for censoring, non-normal distributions, and comparisons with non-constant shape (slope) in the distributions being compared.

6.1 Comparison with different shape (slope) parameters

Using **SLIDA** ➡ **Comparison of distributions life data analysis**➡ **Probability plot and ML fit: different shapes (slopes)** brings up a dialog box like that in Figure 45asking for input of a comparison life data object and a distribution, as shown below. A comparison life data object is a life data object that contains at least one categorical explanatory variable (in S-PLUS, an explanatory variable is assumed to be categorical (a “factor” in SPLUS jargon) if it contains any alphabetic characters). The Life data object list will contain all of the “comparison life data objects” found in the SLIDA data base or in the user’s local data base. As done for single distributions life data objects, comparison life data objects are created by using the **SLIDA** ➡ **Make data object** ➡ **Make life data object** part to the SLIDA menu. If there is more than one categorical explanatory variable in the comparison life data object, then one needs to choose which one to use in the comparison. The following example uses the Snubber data (life data object Snubber.ld) from Nelson (1984), page 529 and reanalyzed in Examples 17.13 to 17.15 in Meeker and Escobar (1998), comparing two different Snubber designs (a snubber is a toaster component). Following these previous analyses, the normal distribution is fit to the data.



Life data object: Snubber.ld

Option: ● Choose dist ○ 6 distributions

Distribution: Normal

Design

☐ Include in data object list?

Percent confidence level: 95

Number of digits in tables: 4

Save results in: .last.groupi

Figure 45 Dialog box requesting comparison of the Snubber data with separate normal distribution standard deviations.

Plot and output options, similar to those in the other dialogs boxes, are available on the back pages of dialog boxes like that shown in Figure 45. After the needed and desired optional inputs have been given in the dialog, click on “Apply” to do the analysis.

Figure 46 gives the resulting individual probability plots for each (in this case both) of the samples in the the data set. Table 6 gives a tabular summary of the results. Tests or confidence intervals to compare particular quantiles or other parameters are easy to construct, following the general approach given in Section 17.8 of Meeker and Escobar (1998).

Table 6 Normal distribution ML estimates for the Snubber data with separate normal distribution standard deviations.

```
Snubber Failure Data
Maximum likelihood estimation results:
Response units: Toaster Cycles
Normal Distribution
  Design Likelihood     mu   se_mu sigma se_sigma
1    Old     -146.8  908.1   76.19 362.4     63.4
2    New     -138.6 1126.6  123.21 546.0     99.5

Total likelihood= -285.4
```

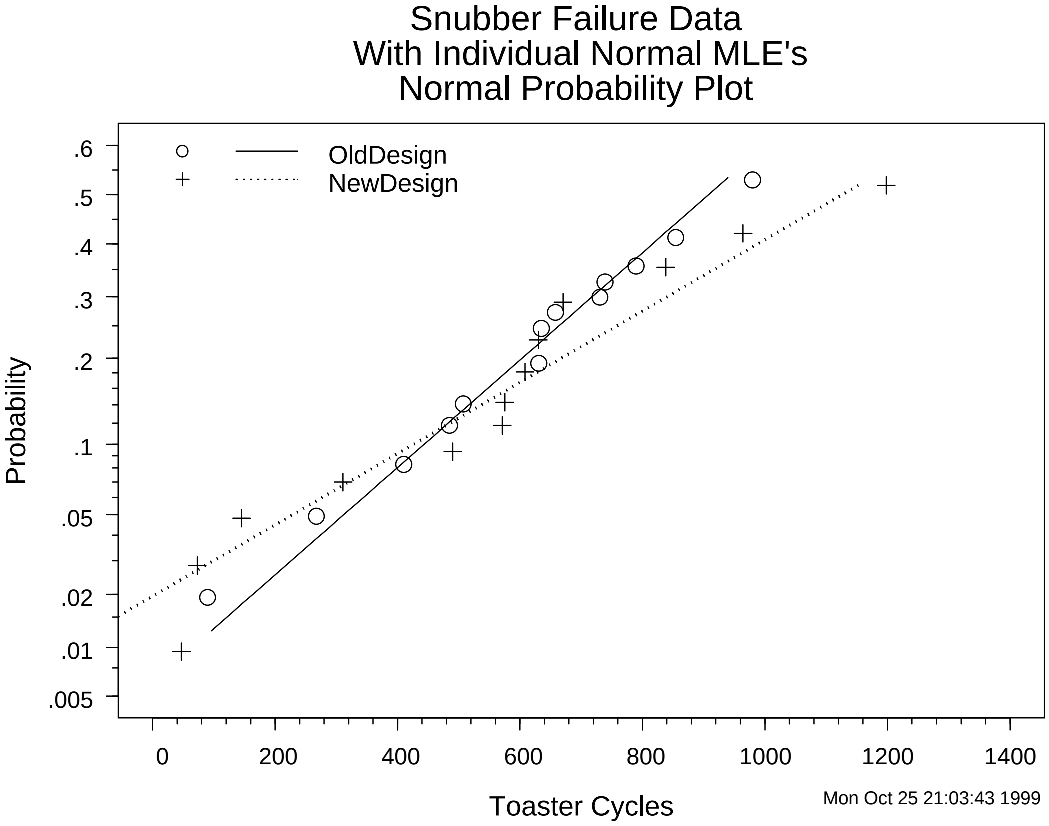
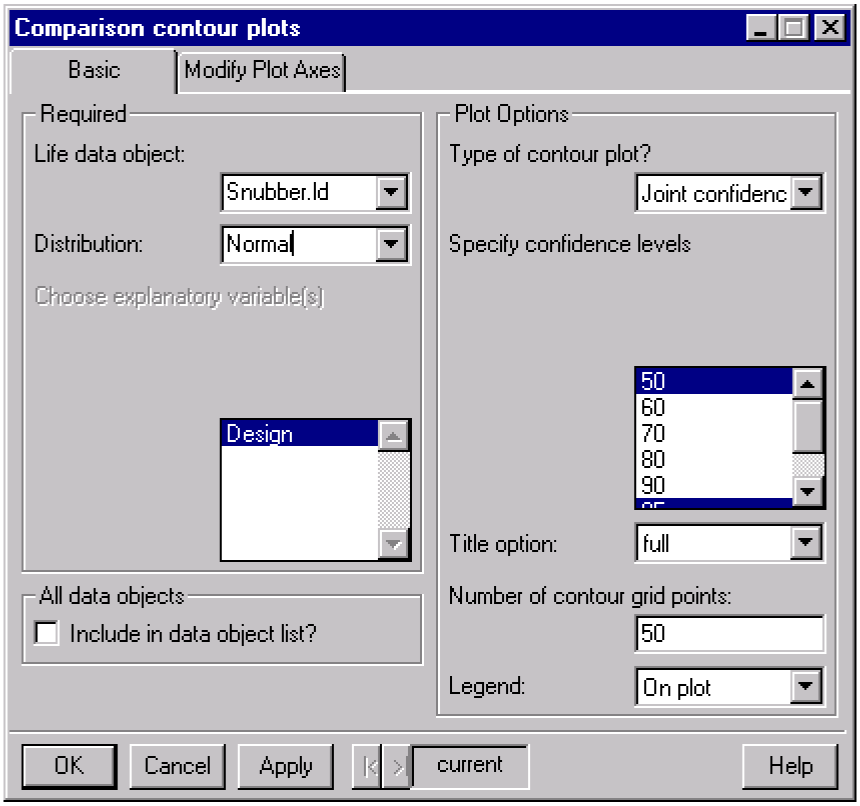


Figure 46 Normal probability plot comparing the new and old snubber designs with separate normal distribution standard deviations.

6.2 Comparison of likelihood contour plots

Using **SLIDA ➡ Comparison of distributions life data analysis➡ Comparison likelihood contour plot** brings up a dialog box like the one in Figure 47, allowing one to specify a comparison life data object and distribution in order to produce corresponding two-parameter contour plots for each of the groups being compared. Figure 48 shows a comparison contour plot of normal distribution joint confidence regions for μ and σ for the Snubber data.



Required

Life data object: Snubber.ld

Distribution: Normal

Choose explanatory variable(s): Design

All data objects

☐ Include in data object list?

Plot Options

Type of contour plot? Joint confidenc

Specify confidence levels: 50, 60, 70, 80, 90

Title option: full

Number of contour grid points: 50

Legend: On plot

Figure 47 Dialog box requesting contour plots comparing the new and old snubber designs assuming separate normal distribution standard deviations.

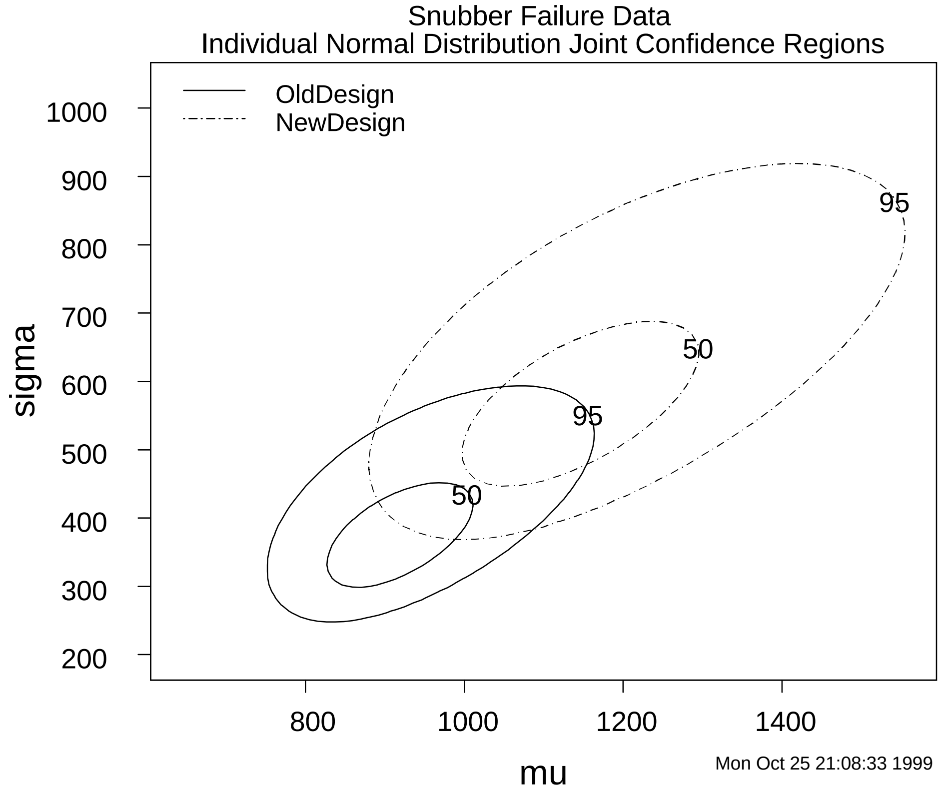


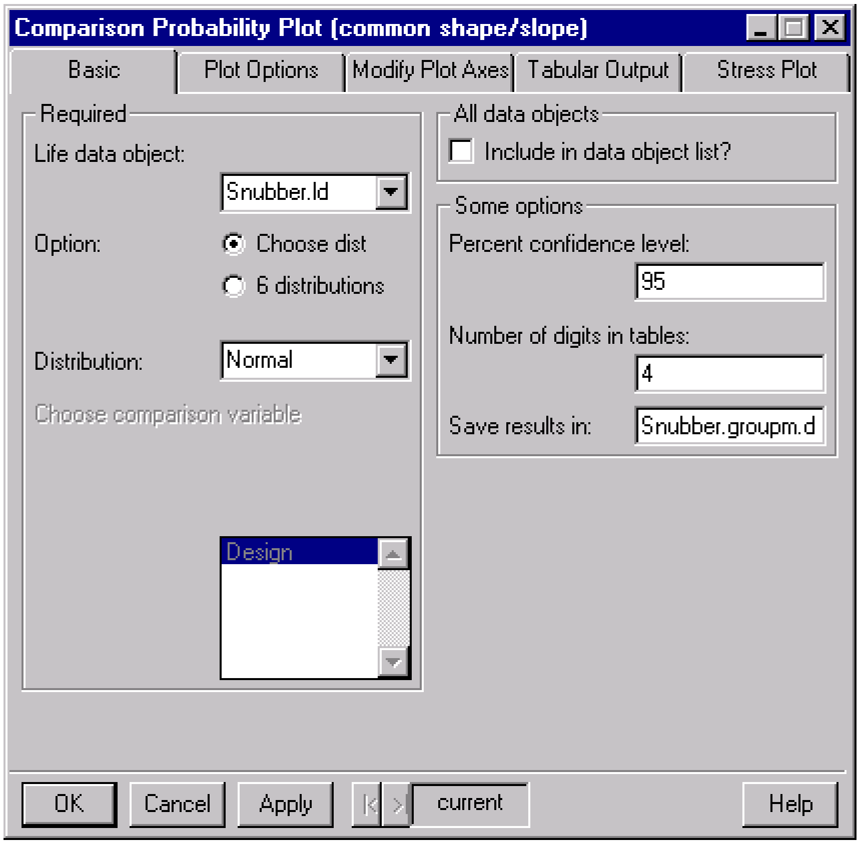
Figure 48 Contour plot showing joint confidence regions for the normal distribution parameters for the two different snubber designs.

The SW to NE orientation of the contours in Figure 48 is a result of the right censoring. The degree of overlap provides an alternative visualization of the statistical “closeness” of the parameters of the life-time distributions for the two different snubber designs.

6.3 Comparison with common shape (slope) parameters

For some applications, it is reasonable to model the different populations or processes being compared as having the same shape (or slope) parameters, differing only with respect to scale (for a log-location-scale distribution) or location (for a location-scale distribution). This tends to simplify the analysis because the equality of any particular distribution quantile would imply the equality of other distribution quantiles (this can be seen by noting that, with this assumption, cdfs plotted on probability paper are parallel).

Using **SLIDA ➡ Comparison of distributions life data analysis➡ Probability plot and ML fit: common shapes (slopes)** brings up a dialog box like that shown in Figure 49. This dialog box is similar to that used for the comparison with non-common shapes (slopes).



Life data object: Snubber.ld

Option: ● Choose dist ○ 6 distributions

Distribution: Normal

Design

☐ Include in data object list?

Percent confidence level: 95

Number of digits in tables: 4

Save results in: Snubber.groupm.d

Figure 49 Dialog box requesting a probability plot comparing the new and old snubber designs assuming a common normal distribution standard deviation.

As before, choose a “life data object” (by default SLIDA puts in the list only life data objects with a comparison or factor explanatory variable) and a “distribution.” An estimate of the model parameters is given in the S-PLUS report window. The right-most back page of the dialog box provides a dialog that allows one to obtain a plot of the estimated model (a “model plot”, sometimes also called a “stress plot” when the explanatory variable is a stress variable). Tables of estimates of distribution quantiles and failure probabilities are also available among the options in the back pages of the dialog box. These tabular and graphical outputs for the Snubber data common standard deviation analysis are given in Table 7 and Figure 50.

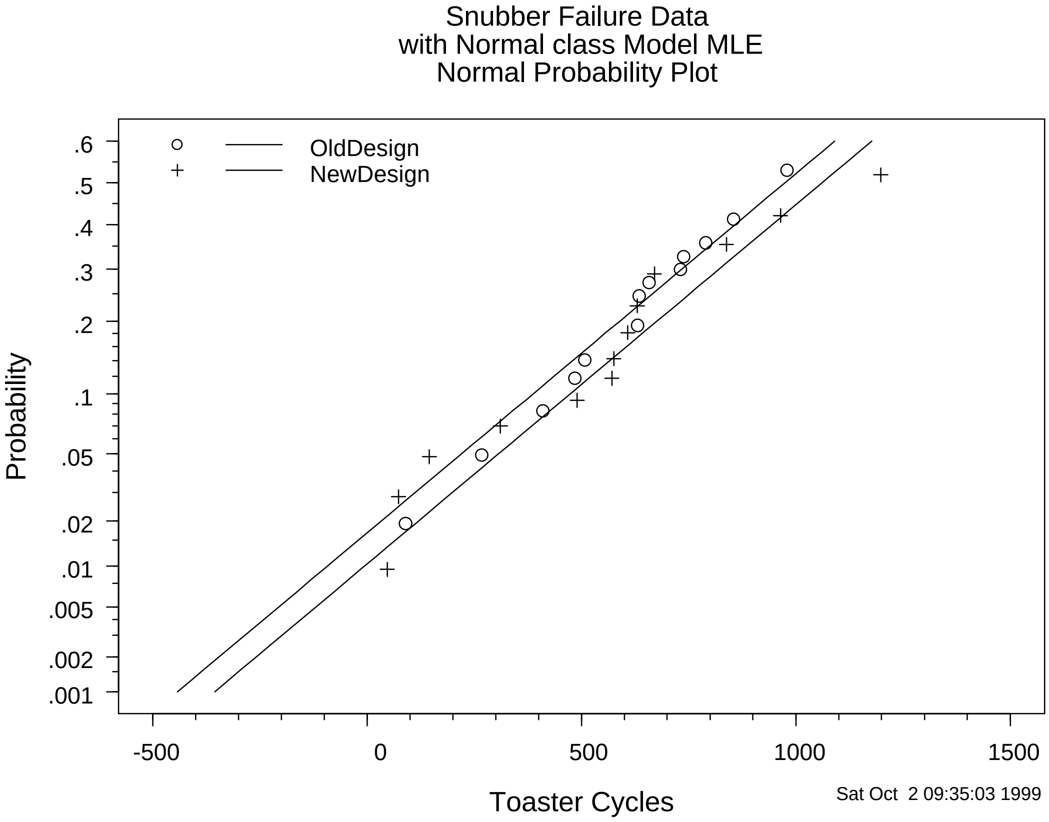


Figure 50 Normal probability plot comparing the data from the new and the old Snubber design assuming normal distributions with a common standard deviation.

The probability plot in Figure 50 shows nonparametric estimates of the life time distributions for both snubber designs along with ML estimates of the assumed normal distributions. The lines representing the ML estimates of the cdfs for the two designs are parallel because of assumption of common normal distribution standard deviations. For the normal distribution, the slope corresponds to the reciprocal of the standard deviation of life, which is also a scale parameter.

Table 7 Normal distribution ML estimates for the Snubber data with a common normal distribution standard deviation.

```
Snubber Failure Data

Maximum likelihood estimation results:

Response units: Toaster Cycles

Normal Distribution

 Relationship

1 : class

Log likelihood at maximum point: -286.7

  Parameter                  Approx Conf. Interval

             MLE Std.Err. 95% lower 95% upper
Intercept 974.63    89.11     800.0    1149.3
DesignNew  86.67   114.21    -137.2     310.5
```

```
     sigma 458.56     57.67      358.4      586.7
```

The table reproduced in Table 7 gives ML estimates and standard errors for an underlying dummy variable regression model used to distinguish between the two different designs (see Section 17.8 of Meeker and Escobar for a detailed description of this model). The Intercept row corresponds to the “baseline” category (old design in this case) giving the estimated parameter for the corresponding distribution (mean of the normal distribution in this case). The `DesignNew` row in the table gives the ML estimate of the difference in mean life between the baseline and the new design. The 95% approximate confidence interval for the `DesignNew` coefficient is `[-137.2310.5].` This interval is wide enough to contain 0, indicating that the observed difference between the two designs could well have been caused by the random variability in the snubber life distributions. The last row in the output gives the estimate of the normal distribution standard deviation, which is, in the model, assumed to be the same for both designs.

The model or “stress plot,” shown in Figure 51, plots estimates of the normal distribution density functions and distribution quantiles. This figure shows clearly that the observed difference in the designs is dominated by the variability in snubber life.

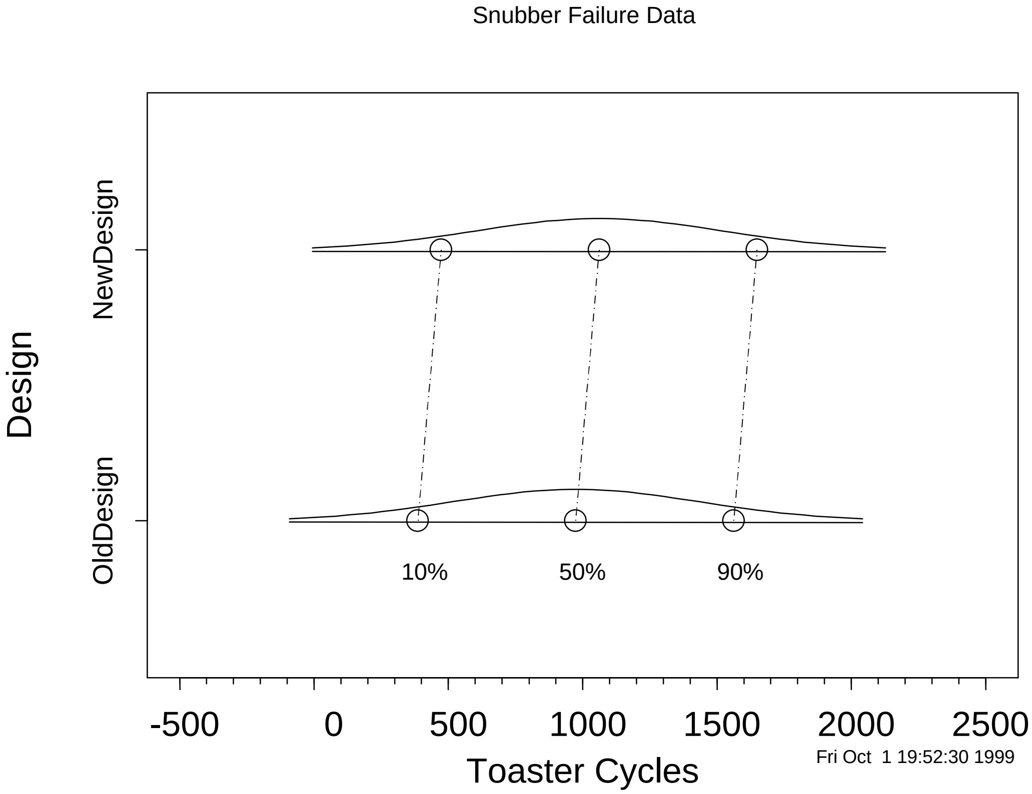
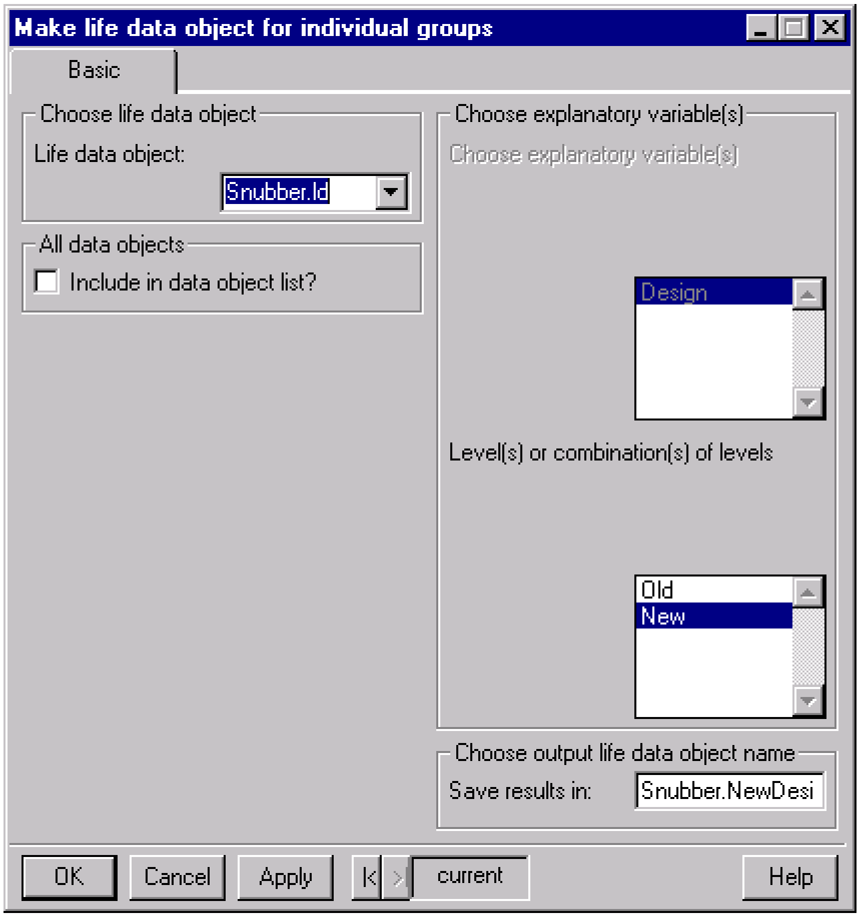


Figure 51 "Stress plot" showing the estimated normal distribution densities for the new and the old snubber designs assuming a common normal distribution standard deviation with response on the horizontal axis.

6.4 Make life data objects for individual groups

After comparing different groups, it is often desired to select one or more of the groups for more focused analysis. It is possible, for example to choose a particular group or groups and do single-distribution analyses for them. We will illustrate this by making a separate life data object for the New snubber design.

Using **SLIDA ➡ Comparison of distributions life data analysis➡ Make life data objects for individual groups** brings up the dialog box in Figure 52.



Life data object: Snubber.ld

☐ Include in data object list?

Choose explanatory variable(s): Design

Level(s) or combination(s) of levels: Old, New

Save results in: Snubber.NewDesi

Figure 52 Dialog box used to choose a data subset for a new life data object

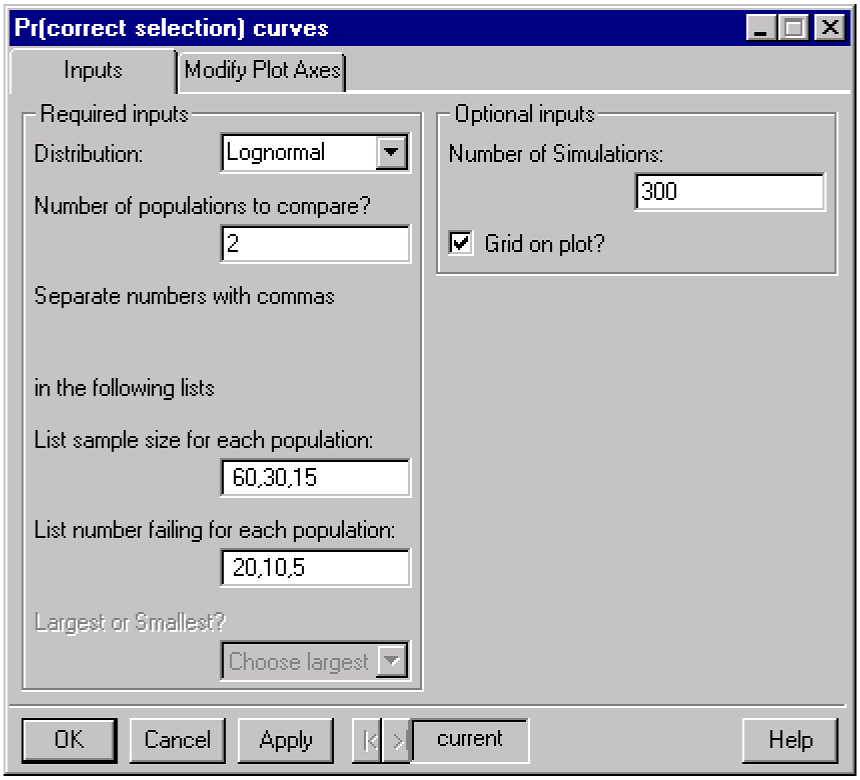
For the example, we choose the Snubber.ld comparison life data object. Design is the only explanatory in this life data objects, so it is automatically highlighted. Then choose "New" under the list of available levels (or in general combinations of levels). A name for the output data object is chosen automatically when the level(s) or combinations of levels are chosen, but it is possible to edit this name. Clicking on "OK" or "Apply" will execute the function to produce the new data object. For the example, the message "Saving subset data object Snubber.NewDesign.ld" is printed and this data object will appear subsequently in the lists of single-distribution life data objects.

6.5 Probability of correct selection

When planning a life test to compare two or more distributions, an important consideration is the sample size needed to make the comparison. For example, when comparing two different designs (as in the snubber example) if one only tested two units from each design, it is unlikely that the experiment would indicate a statistically significant difference, even if there were a difference of practical importance. Thus we would not have the information needed to choose one design over the other. Correspondingly, if the experiment had used 10,000 units of each design, it would be highly likely that any difference of practical importance (or indeed, small differences that would not be important!) would be detected with high probability. Additionally, when comparing life distributions, one also needs to decide how long to run the test. Generally it will not be possible to wait until all units have failed. An important part of planning the experiment is to determine how long to run the test or, alternatively, how many of the tested units need to fail before a decision should be made.

Typically, in comparative experiments, with all other things being equal, a decision would be made to choose the design that gives the best results in the experiment. Such a decision rule would have the largest probability of making the correct decision. When planning such an experiment it is important to have some idea about the actual probability of making a correct decision. An assessment of this probability can be obtained by using **SLIDA ➡ Comparison of Distributions ➡ Probability of correct selection for specified test plans.**

In the dialog box in Figure 53, one specifies the assumed distribution, the number of populations to be compared, as well as the sample sizes (separated by commas) and the corresponding number to fail within each sample size. Then, as with other SLIDA dialog boxes, click “Apply” and iconify dialog box.



Distribution: Lognormal

Number of populations to compare? 2

Separate numbers with commas in the following lists

List sample size for each population: 60,30,15

List number failing for each population: 20,10,5

Largest or Smallest? Choose largest

Number of Simulations: 300

☑ Grid on plot?

Figure 53 Dialog box requesting a probability of correct selection comparison of three different proposed comparison life tests.

Depending on how many simulations have been requested, the complete simulation may take a substantial amount of time to run. Periodic messages will be printed in the report window however, to give an indication of the simulation’s progress. Separate simulations are required for each sample size/number of failures pair and the computational time is approximately proportional to the number of failures. Figure 54 illustrates the output, giving a Probability of Correct Selection curve for each combination of sample size and number of failures, as a function of the standardized difference *d*. See Escobar, Pascual, and Meeker (2000) for more information on how to choose *d*.

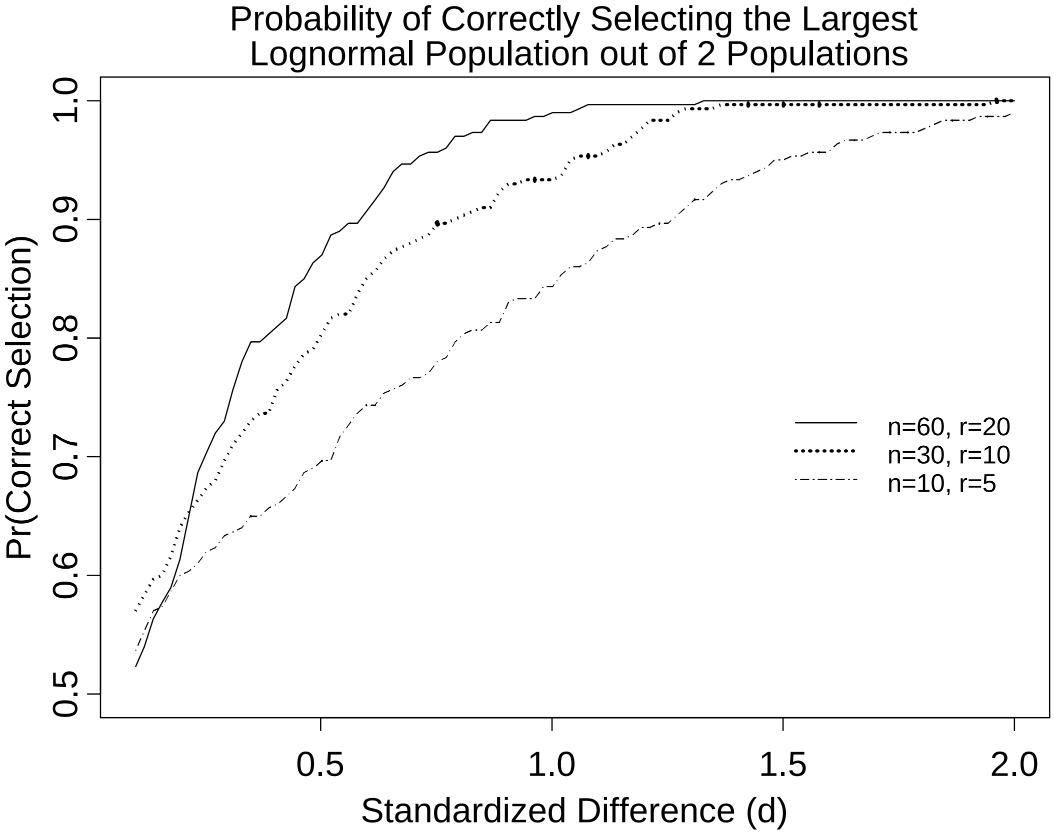


Figure 54 Plot showing the probability of correct selection as a function of the standardized difference between the populations being compared.

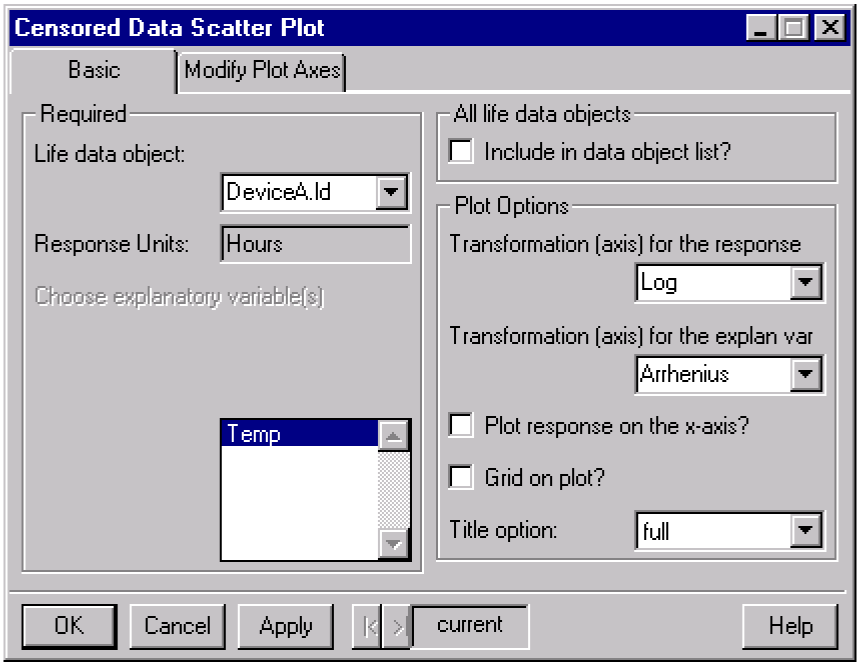
The jaggedness in the lines is due to the limited number of simulations that were done in this example, but such simulations are quick and adequate for most purposes. If smoother curves are desired, the simulation sample size can be increased to somethoong like 3000.

7. Simple Regression (ALT) Life Data Analysis

This Chapter describes methods for analyzing life data when there is a single explanatory variable. Technical background and further examples illustrating the statistical methods used here are given in Chapter 17 of Meeker and Escobar (1998). A common application of the methods in this chapter arises in accelerated testing where test units are, for example, tested at high temperature with the purpose of obtaining reliability information in a timely manner. Models and methods for accelerated testing are described in detail in Nelson (1990) and Chapters 18 and 19 of Meeker and Escobar (1998). Chapter 8 extends the methods of this chapter, allowing for more than one explanatory variable.

7.1 Scatter plot of censored data

One should always look first at available data through graphical displays. For single-variable accelerated test data, a scatter plot will provide useful information. To illustrate the tools in this section, we use the Device-A data from Hooper and Amster (1990), reanalyzed in Section 19.2 of Meeker and Escobar (1998). In order to make a scatter plot of the Device-A data, use **SLIDA ➡ Simple regression (ALT) data analysis ➡ Censored data scatter plot** to bring up the dialog box shown in Figure 55. Then choose the one of the life data objects from the list. We use the Device-A life data object in this example (only those life data objects with explanatory variables appear in the list). There is only one explanatory variable in the Device-A data object, so it is chosen automatically. Then choose the axis scales for the response and the explanatory variable. Linear response and linear explanatory variable axes are the defaults, but log and Arrhenius axes are chosen for this example, corresponding to the physically-suggested lognormal-Arrhenius accelerated lifetime model, described and illustrated in Chapters 18 and 19 of Meeker and Escobar (1998).



Life data object: DeviceA.ld

Response Units: Hours

Temp

☐ Include in data object list?

Transformation (axis) for the response: Log

Transformation (axis) for the explan var: Arrhenius

☐ Plot response on the x-axis?

☐ Grid on plot?

Title option: full

Figure 55 Dialog box requesting a censored-data scatter plot of the Device-A data.

Finally, click on “Apply” to produce the Arrhenius plot of the data shown in Figure 56.

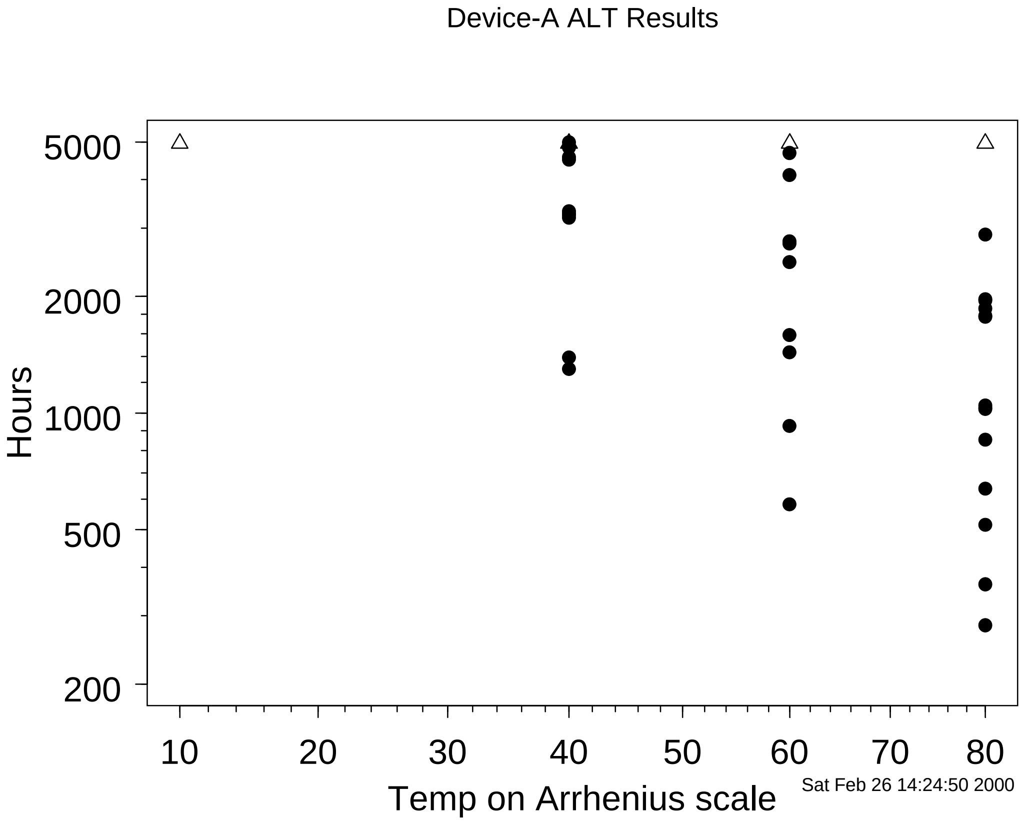
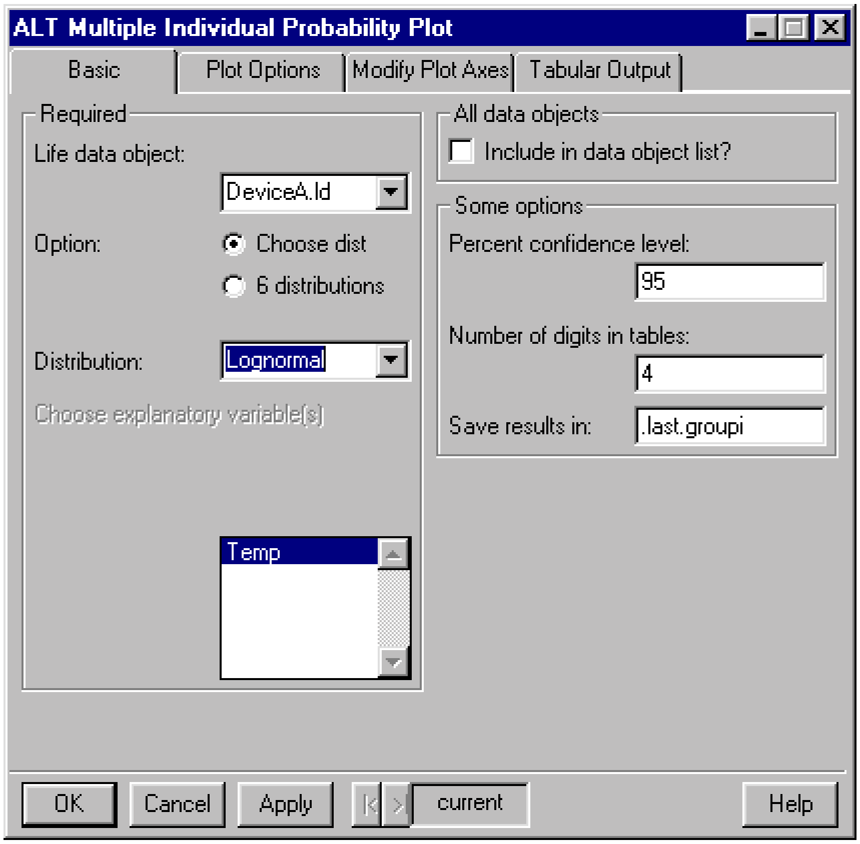


Figure 56 A censored-data scatter plot of the Device-A data.

Notice the nonlinear Arrhenius axis for temperature. The open upward-pointing triangles in the plot indicate right-censored observations. The number of censored observations at each level of temperature was added manually with S-PLUS GUI commands. For the Device-A data (as in most examples having heavy censoring), the censoring makes it difficult to assess the adequacy of the linear relationship between log time and transformed temperature. Still, however, there is nothing in the plot to suggest that the relationship does not provide a reasonable description of the relationship.

7.2 Group individual probability plots

After loooking at a scatter plot of data from a single-variable accelerated life tests, the next step in the analysis is usually to make an indivdual probability plot of the data at each level of the accelerating variable (e.g., at each temperature for the Device-A data). Such a plot can be made by using **SLIDA ➡ Simple regression (ALT) life data analysis➡ Probability plot and ML fit for individual conditions** to request the dialog box in Figure 57. Then one chooses the life data object and distribution (Lognormal was used in this example). Clicking “OK” or “Apply” produces Table 8 and the multiple probability plot in Figure 58.



Life data object: DeviceA.ld

Option: ● Choose dist ○ 6 distributions

Distribution: Lognormal

Temp

☐ Include in data object list?

Percent confidence level: 95

Number of digits in tables: 4

Save results in: .last.groupi

Figure 57 Dialog box requesting a lognormal probability plot for the individual temperature levels in the Device-A accelerated test.

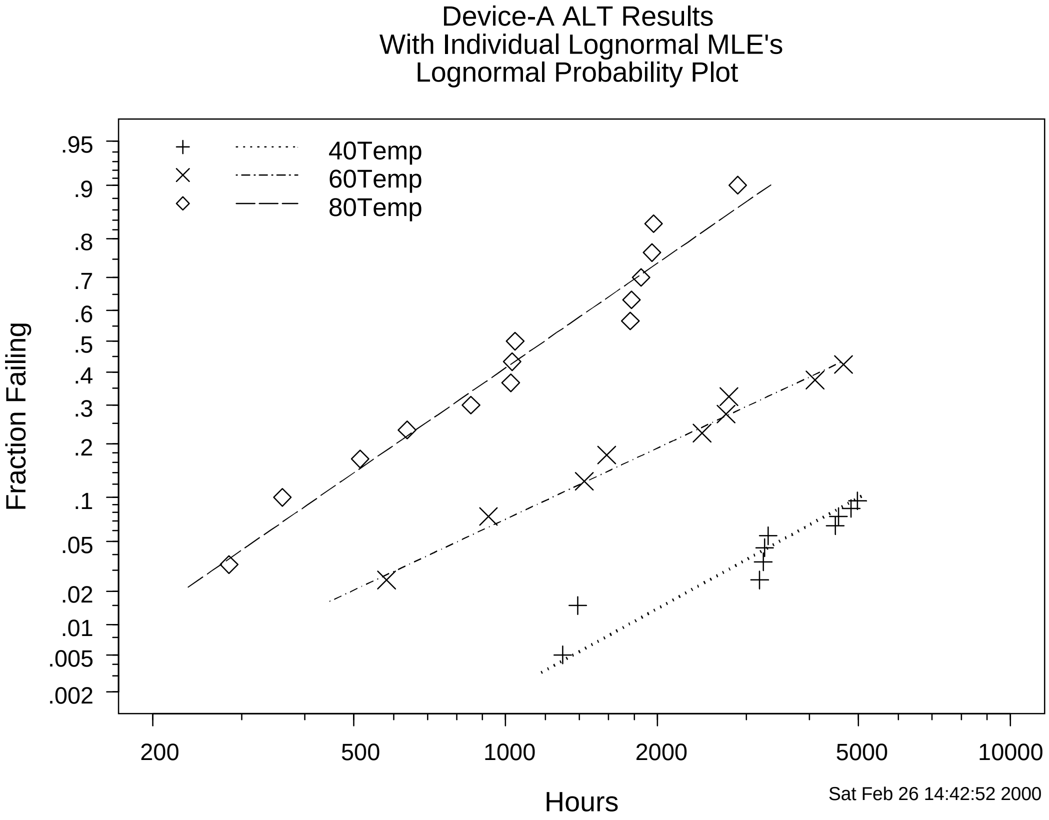


Figure 58 Lognormal probability plot showing the individual nonparametric and parametric estimates of life at the different temperatures in the Device-A accelerated life test.

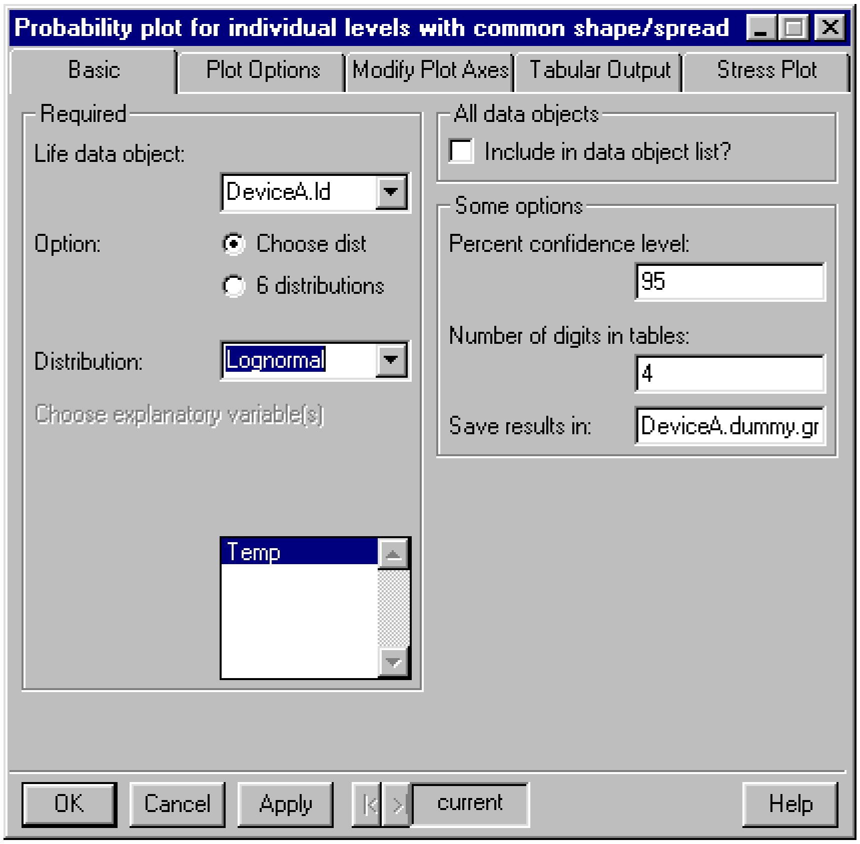
Figure 58 shows that the lognormal distribution fits the data at each level of temperature. The slopes of the lines (corresponding to the reciprocal of the lognormal shape parameters) vary somewhat (as expected from variability in the data), but not systematically. Table 8 summarizes the lognormal distribution ML estimation at each individual level of temperature for the Device-A accelerated life test. At 10 degrees C, there were no failures so no nonparametric or ML estimates could be computed.

Table 8 Tabular output summarizing lognormal distribution ML estimation at each individual level of temperature for the Device-A accelerated life test.

```
[1] "Skipping 10 because too few failures"

 Device A data

Maximum likelihood estimation results:

Response units: Hours

Lognormal Distribution
  Temp Likelihood    mu  se_mu  sigma se_sigma
1   10         NA    NA     NA     NA       NA
2   40    -115.46 9.815 0.4221 1.0083   0.2737
3   60     -89.72 8.644 0.3474 1.1876   0.3167
4   80    -115.58 7.084 0.2087 0.8046   0.1553

Total likelihood = -320.8
```

7.3 Group probability plot with common shape (slope) parameter

Many accelerated life test models relate the scale parameter of the life-time distribution (location parameter of the log life distribution) to the accelerating variable but have the shape of the life-time distribution (scale parameter of the log-life-time distribution) the same over all levels of the accelerating variable. Some physical-failure models, such as the Arrhenius relationship, suggest such a statistical model. In order to check the adequacy of such a model, it is useful to fit the candidate distribution to the data with a common shape (slope on a probability plot) assumption. This analysis is similar to that in the comparison-of-distributions example in Section 6.3, with Temperature being used as a class variable. This analysis can be done with **SLIDA ➡ Simple regression (ALT) life data analysis➡ Prob plot and ML fit for indiv cond: common shapes (slopes).** This dialog box, shown in Figure 59, is very similar to that in Figure 57.



Life data object: DeviceA.ld

Option: ● Choose dist ○ 6 distributions

Distribution: Lognormal

Choose explanatory variable(s): Temp

☐ Include in data object list?

Percent confidence level: 95

Number of digits in tables: 4

Save results in: DeviceA.dummy.gr

Figure 59 Dialog box requesting ML estimates at the different temperatures in the Device-A accelerated life test, with lognormal shape parameters constrained to be the same.

Specify the life data object and the distribution and click “OK” or “Apply” to obtain the multiple probability plot in Figure 60.

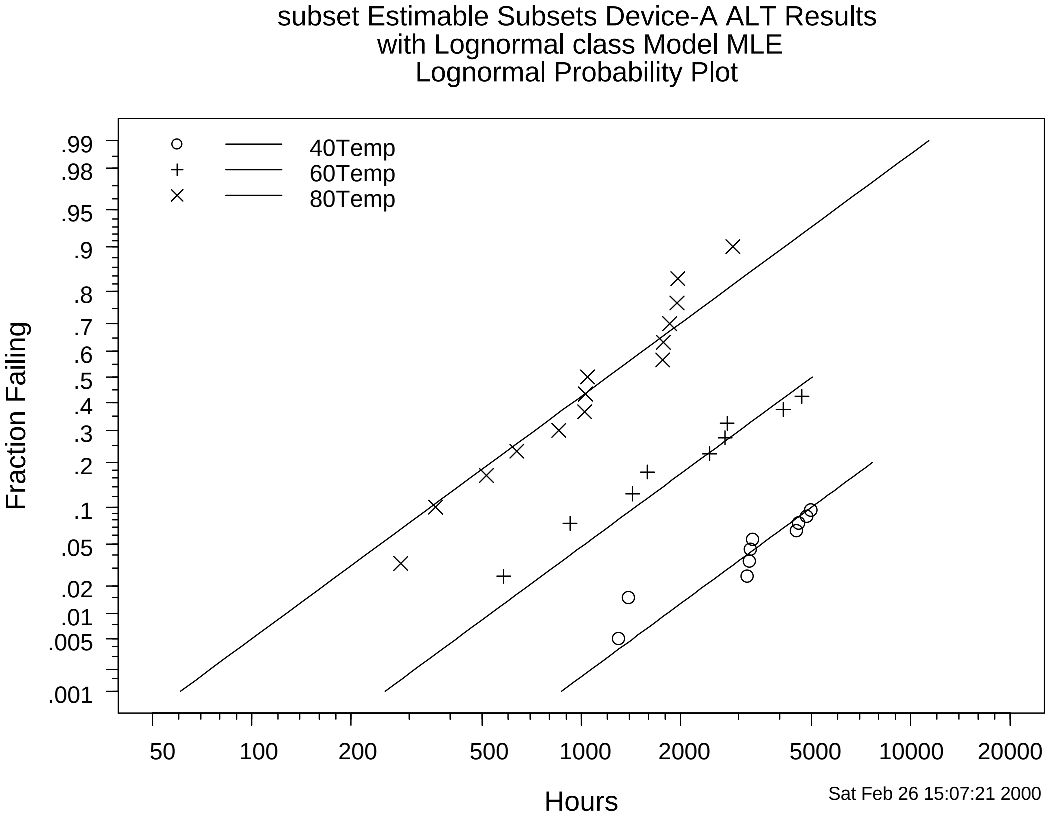


Figure 60 Lognormal probability plot showing ML estimates at the different temperatures in the Device-A accelerated life test, with lognormal shape parameters constrained to be the same.

Note the parallel lines in Figure 60, due to the common □ (standard deviation of log life) assumption in the fitted model.

The tabular output in Table 9 summarizes the lognormal distribution ML estimation for the Device-A accelerated life test. The estimate b0 is the estimate of □, the median of log life for the baseline of 40 degrees C (there were no failures at 10 degrees C, so these data are not used in the present analysis). The estimates corresponding to Temp60 and Temp80 give the estimated differences μ_{40}-μ_{60} and μ_{40}-μ_{80}. As expected, these latter two estimates are negative because of shorter life times at the higher temperatures. The tabular output in Table 9 can be used to compare this model fit with the unconstrained model fit to see if there is strong evidence for a departure from the constant-slope assumption. Figure 60 provides a visual assessment of this assumption.

Table 9 Tabular output summarizing lognormal distribution ML estimation for the Device-A accelerated life test.

```
Device A data

Maximum likelihood estimation results:
```

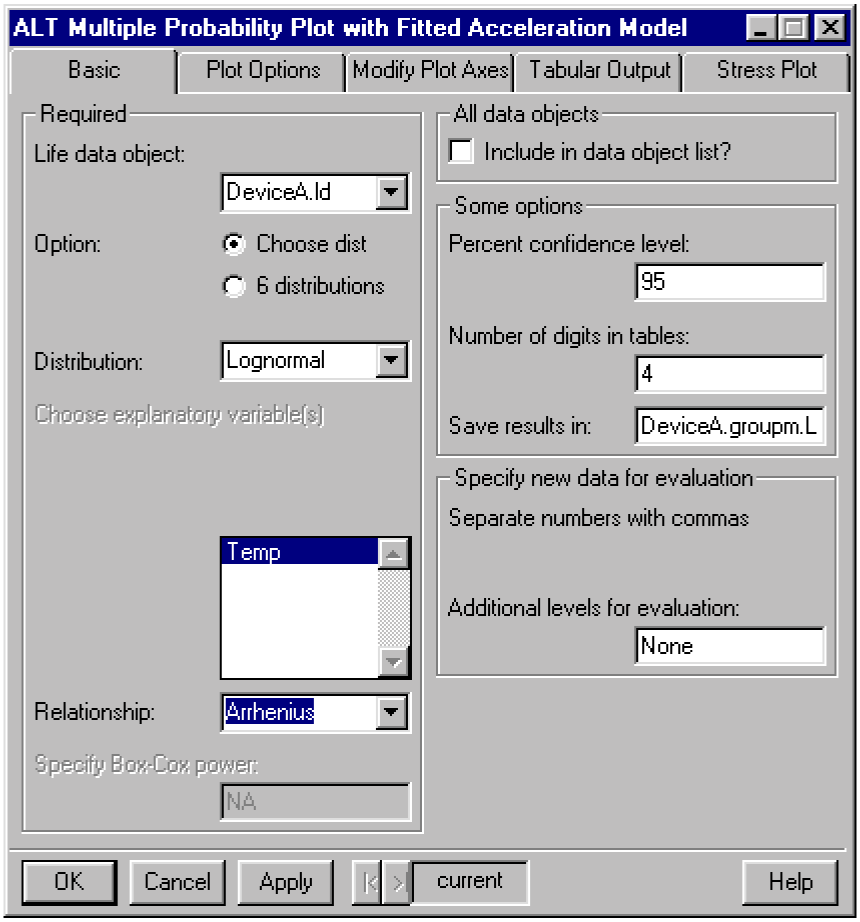
```
Response units: Hours

Lognormal Distribution

  Relationship
1 : class

Log likelihood at maximum point: -321.5

  Parameter            Approx Conf. Interval
         MLE Std.Err. 95% Lower 95% Upper
   b0  9.7543   0.2465    9.2711   10.2374
Temp60 -1.2330   0.3119   -1.8443   -0.6217
Temp80 -2.6634   0.3484   -3.3463   -1.9806
 sigma  0.9656   0.1320    0.7386    1.2623
```

One can compare the loglikelihoods from fitting the previous two models in order to see if the differences among the shape parameters at the three different temperature levels could be explained by random variability. In a formal maner we compute –2[(-320.8-321.5)] = 1.4, which is small relative to 5.99, the .95 quantile of a chi-square distribution with 2 degrees of freedom (the unconstrained model had six parameters while the constrained model had four and thus the difference in dimension is two). This numerical result suggests that there is not strong evidence of differing slopes.

In addition to the table of ML estimates of the distribution parameters, one can also request a table of failure probabilities or quantiles for any of the levels of the explanatory variable in the data by using the options on the Tabular Output of the dialog box in Figure 59.

7.4 Fitting simple regression and accelerated life test models

Accelerated life tests are often conducted for the purpose of using data at higher-than-usual levels of some explanatory variable to make predictions of life at lower typical or use levels of that variable. A model is used to describe the effect that the explanatory variable will have on life. For example, when temperatutre is used to accelerate a failure mechanism related to a chemical reaction, the Arrhenius relationship is often suggested as a model to describe the effect that temperature will have on life. The data can be used to estimate the parameters of this model, as described in Section 19.2 of Meeker and Escobar (1998). Use **SLIDA ➡ Simple regression (ALT) life data ➡ Probability plot and ML fit of a regression (acceleration) model** to bring up the dialog box in Figure 61.



Required

Life data object: DeviceA.ld

Option: ● Choose dist ○ 6 distributions

Distribution: Lognormal

Choose explanatory variable(s)

Temp

Relationship: Arrhenius

Specify Box-Cox power: NA

All data objects

☐ Include in data object list?

Some options

Percent confidence level: 95

Number of digits in tables: 4

Save results in: DeviceA.groupm.L

Specify new data for evaluation

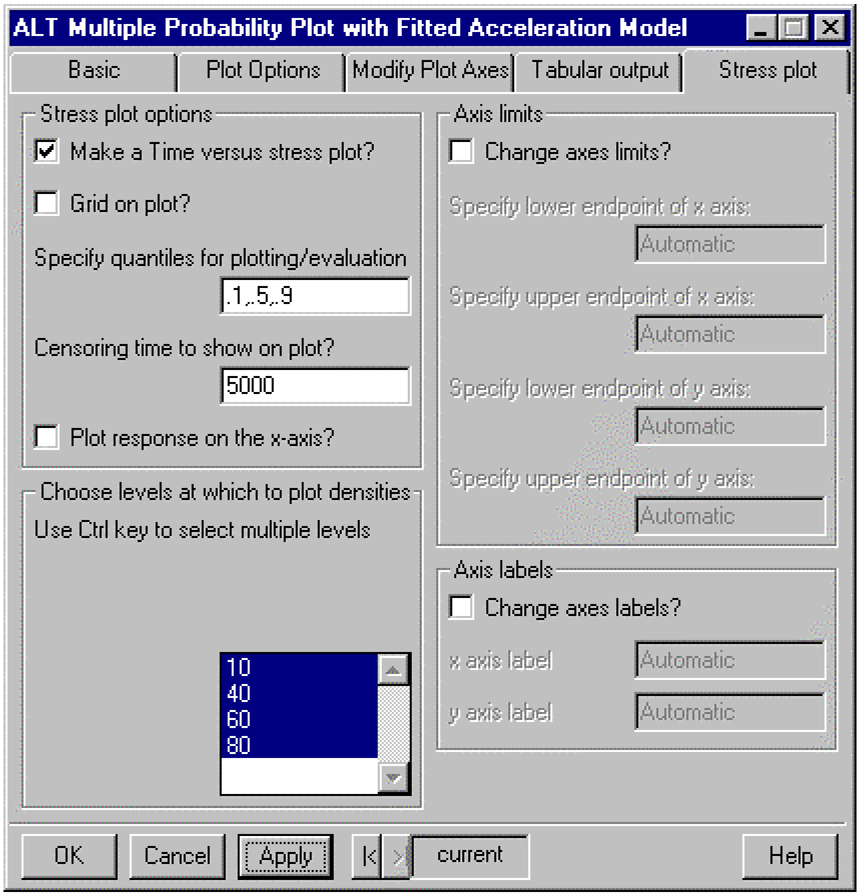
Separate numbers with commas

Additional levels for evaluation: None

Figure 61 Dialog box used to request a probability plot showing the ML fit of the lognormal/Arrhenius acceleration model to the Device-A data.

For many single-variable accelerated life tests, the model to be used is initially suggested by previous experience or physical theory. For the Device-A example, the well-known Arrhenius relationship will be used to describe the relationship between life and temperature, as shown on the dialog box. One can also specify additional levels of temperature at which to compute and plot estimates of life and associated confidence intervals. As with other dialog boxes, various options for customizing the plots and for requesting tabular output are available in the back pages of the dialog box.

Options on the “Stress Plot” page of the dialog box, shown in Figure 62, allows one to request and customize a plot of the life versus stress along with the other analyses (hours to failure as a function of temperature on log/Arrhenius scales for the Device-A example).



Stress plot options

☑ Make a Time versus stress plot?

☐ Grid on plot?

Specify quantiles for plotting/evaluation: .1,.5,.9

Censoring time to show on plot?: 5000

☐ Plot response on the x-axis?

Choose levels at which to plot densities

Use Ctrl key to select multiple levels

10
40
60
80

Axis limits

☐ Change axes limits?

Specify lower endpoint of x axis: Automatic

Specify upper endpoint of x axis: Automatic

Specify lower endpoint of y axis: Automatic

Specify upper endpoint of y axis: Automatic

Axis labels

☐ Change axes labels?

x axis label: Automatic

y axis label: Automatic

Figure 62 Dialog box showing the options on the "stress plot" dialog page.

When all of the requested options have been selected, click on “Apply.” This will produce the multiple probability plot in Figure 63, showing the lognormal/Arrhenius model estimates of fraction failing as a function of time at the diferent levels of temperature in the original (including 10 Degrees C, where there were no failures) and the Stress plot in Figure 64.

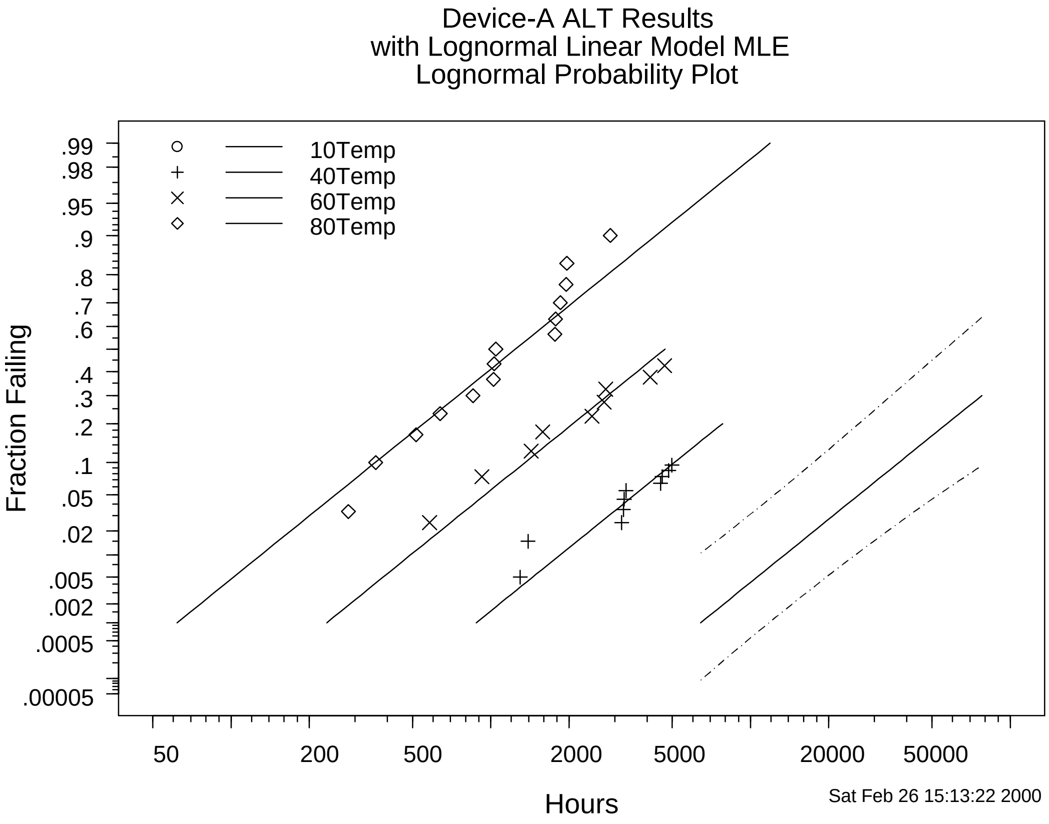


Figure 63 Lognormal probability plot showing the lognormal/Arrhenius model fit to the Device-A data with an extrapolation to the use conditions of 10 degrees C, including approximate pointwise 95% confidence intervals.

Table 10 gives a summary of the ML regression output, similar to what one would obtain from a standard least squares regression output.

Table 10 Maximum likelihood estimation results for the lognormal/Arrhenius model fit to the Device-A data

```
 Device-A ALT Results

Maximum likelihood estimation results:

Response units: Hours

Lognormal Distribution

  Relationship
1 : Arrhenius

Log likelihood at maximum point: -321.7

  Parameter                  Approx Conf. Interval
             MLE Std.Err. 95% Lower 95% Upper
Intercept -13.4686  2.88719  -19.1274   -7.8098
     Temp   0.6279  0.08284    0.4655    0.7902
    sigma   0.9778  0.13265    0.7495    1.2756
```

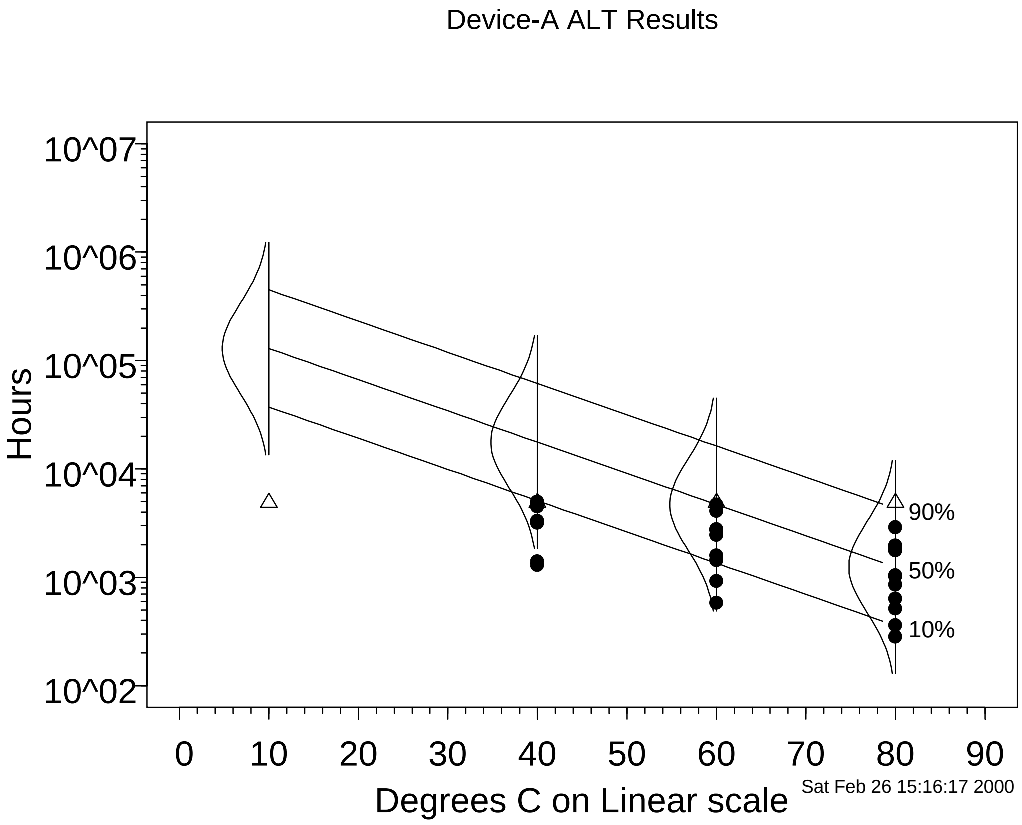
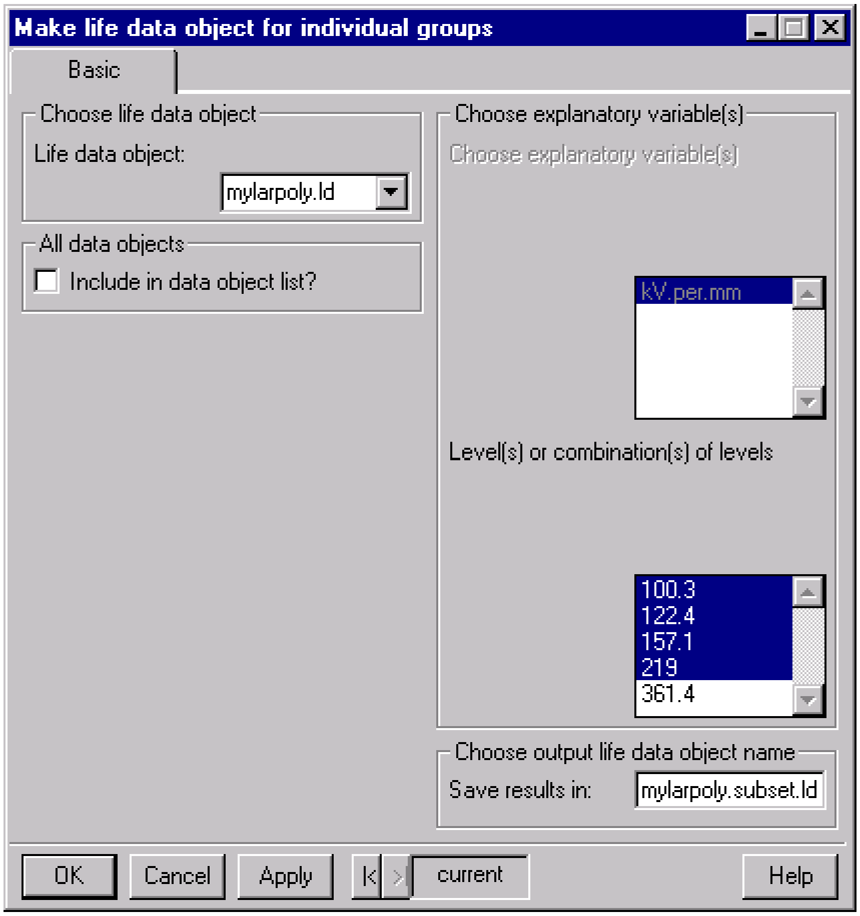


Figure 64 Stress plot on Arrhenius paper showing the estimated failure-time densities as a function of temperature.

There is nothing in either of these plots to indicate any serious departure form the fitted model. Of course it should be emphasized that just because the data fits the model well within the range of the data does not imply that one can safely extrapolate out side of the range of the data (10 degrees C for the Device-A example). The justification for the extrapolation comes from the Arrhenius rate-reaction model from physical chemistry. If this model does not adequately describe the effect of temperature on the underlying degradation mechanism, then seriously incorrect extrapolations could result.

7.5 Make life data objects for individual groups

In many applications, under certain circumstances, it will be desired to select one or more of the groups of regression data set for more focused analysis. It is possible, for example to choose a particular level of levels of an accelerating variable and do single-distribution analyses for them. Alternativley, one may want to delete one or more subsets for a data set either as a form of sensitivity analysis or because the data need to be deleted because they are incorrect. We will illustrate this by making a sunset life data object for Mylarpoly.ld life data object. As shown in Section 19.3.1 of Meeker and Escobar (1998), the specimens tested at 361.4 kV/mm failed from a failure mode different than those at other levels of voltage stress because voltage stress was too high. It is thus appropriate to drop these data from the analysis. Using **SLIDA ➡ Simple regression (ALT) life data ➡ Make life data objects for individual groups** brings up the dialog box like that shown in Figure 65.



Choose life data object

Life data object: mylarpoly.ld

All data objects

☐ Include in data object list?

Choose explanatory variable(s)

Choose explanatory variable(s)

kV.per.mm

Level(s) or combination(s) of levels

100.3
122.4
157.1
219
361.4

Choose output life data object name

Save results in: mylarpoly.subset.ld

Figure 65 Dialog box requesting the creation of a subset data object for the mylarploy data, omitting the 361.4 kV data.

For the example, we choose the mylarpolyld comparison life data object. The voltage stress variable kV.per.mm is the only explanatory in this life data objects, so it is automatically highlighted. Then choose the desired levels (all except 361.4 in this case) under the list of available levels (or in general combinations of levels). A name for the output data object is chosen automatically when the level(s) or combinations of levels are chosen, but it is possible to edit this name. In this example, because so many levels were chosen, the automatic name is a bit long, so it was edited to read mylarpoly.subset.ld. After clicking on "OK" or "Apply" the new life data object is created, we get the message "Saving subset data object mylarpoly.subset.ld," and this life data object will appear in subsequent lists of accelerated life test or regression life data objects.

8. Multiple regression (ALT) life data analysis

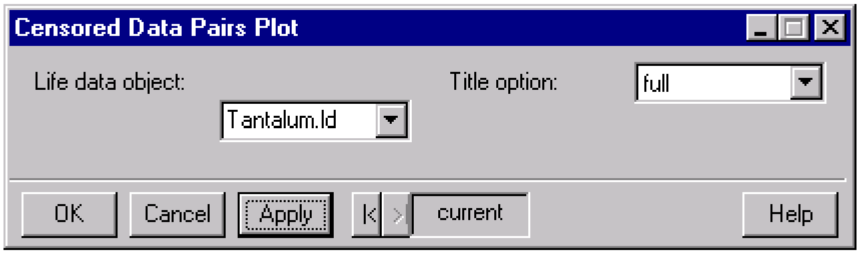
The methods illustrated in Section 7 are easily extended to allow one to fit failure time regression models with two or more explanatory variables. The methods presented here provide useful extensions to the multiple regression methods covered in a standard course in the subject of multiple regression analysis, allowing for non-normal distributions and censoring. To illustrate the methods for failure-time regression, we will use the tantalum capacitor life data (data object Tantalum.ld) from Singpurwalla, Castellino, and Goldschen (1975). These data were also analyzed in Section 19.3.3 of Meeker and Escobar (1998). The tabular summary of these data in Table 11 was obtained by using **SLIDA ➡Make/summary/view/edit data object ➡Summary/view data object.**

Table 11 Summary of the tantalum capacitor life data object

```
Summary of: Tantalum Capacitor Data

Number of rows in data matrix= 48
Response units:  Hours
Response minimum:  20
Response maximum:  37000
Number of cases in data set= 2204
Number of exact failures in data set= 40
Number of right censored observations in data set= 2164
No truncation information

Summary of numeric columns in X matrix:
         min  max  mean     sd     cv
   Volts  35 62.5 51.98  9.897 0.1904
DegreesC   5 85.0 42.50 36.349 0.8553

List of unique X values (or combinations)
  Volts DegreesC min-time max-time #exact #rcen
1  35.0       85       20    37000      4   996
2  40.6       85       20    27000      4   196
3  46.5       85      800     2800      2    48
4  51.5       85      500    10700      4    49
5  46.5       45      100    27300      6   496
6  46.5        5     1000     1000      1   174
7  62.5        5       25    12500     18   156
8  57.0       45     8900     8900      1    49
```

8.1 Censored data pairs plot

As described earlier, data analysis should begin with exploration using graphical tools. The dialog box in Figure 66, obtained from **SLIDA** ➡ **Multiple regression (ALT) life data** ➡ **Censored data pairs plot,** allows the user to plot all pairs of variables in one “matrix plot” (also known as a “pairs plot” in S-PLUS).



Life data object: Tantalum.ld

Title option: full

Figure 66 Dialog to request a censored data pairs plot.

Figure 67 shows a pairs plot for the tantalum capacitor data. As shown in the simple regression example with the Device-A data, the censoring makes it more difficult to interpret a scatter plot. The Volts versus Degrees C plot shows the complicated nature of the experimental design for this example.

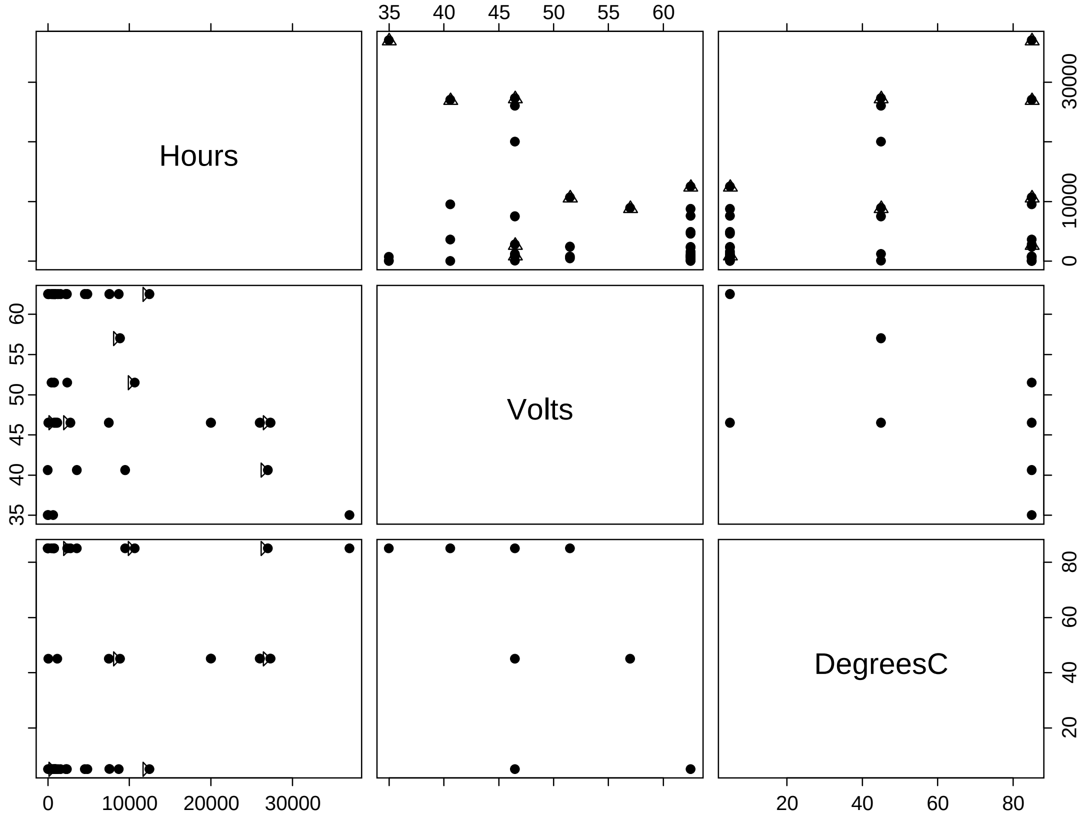


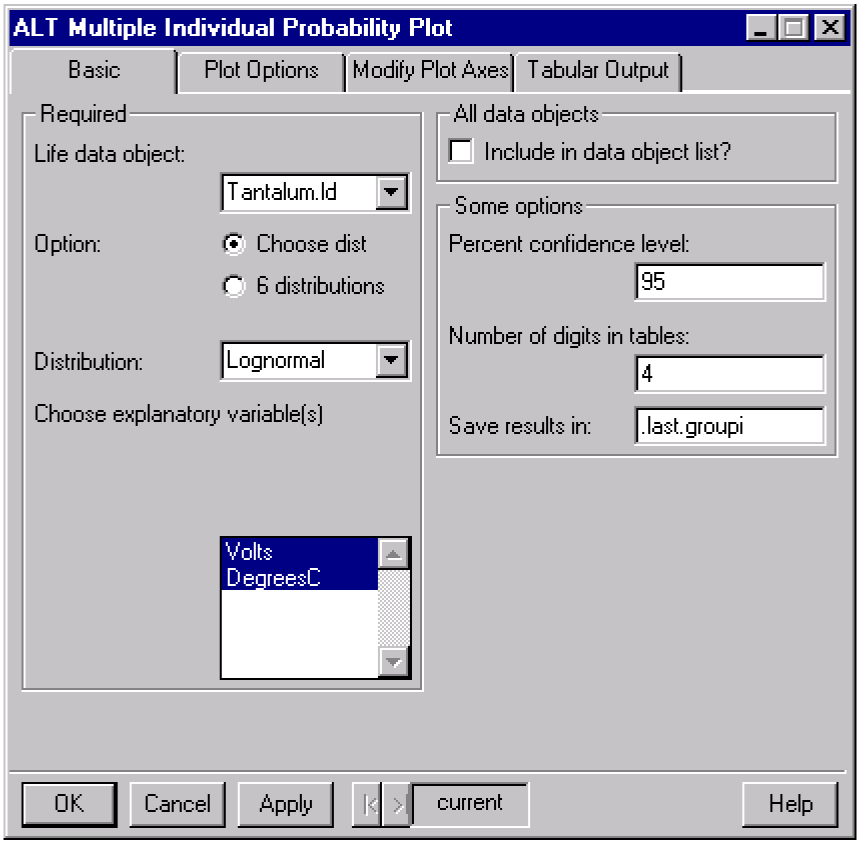
Figure 67 Censored data pairs plot show the tantalum capacitor life versus voltage and temperature.

8.2 Censored data scatter plot

The censored data scatter plot dialog box obtained with **SLIDA ➡ Multiple regression (ALT) life data ➡ Censored data scatter plot** is exactly the same as that shown in Figure 55, obtained with **SLIDA ➡ Simple regression (ALT) data analysis ➡ Censored data scatter plot**. As before the dialog allows one to request a single scatter plot of the response versus one explanatory variable, with an option to transform either or both of the data axes.

8.3 Probability plot and ML fit for individual conditions

The dialog obtained from **SLIDA ➡ Multiple regression (ALT) life data ➡ Probability plot and ML fit for individual conditions,** shown in Figure 68 allows one to request separate analyses for all combinations of experimental variable levels in one's data set, with all of the results plotted on one probability plot.



Required

Life data object: Tantalum.ld

Option: ● Choose dist ○ 6 distributions

Distribution: Lognormal

Choose explanatory variable(s): Volts, DegreesC

All data objects

☐ Include in data object list?

Some options

Percent confidence level: 95

Number of digits in tables: 4

Save results in: .last.groupi

Figure 68 Dialog box requesting a probability plot showing individual nonparametric estimates for each experimental factor level combination on lognormal paper.

After the dialog box appears, choose the life data object (only life data objects with explanatory variables appear in the list), a distribution, and all or some of the explanatory variables. Then click “Apply” or “OK,” producing a probability plot like that in Figure 69.

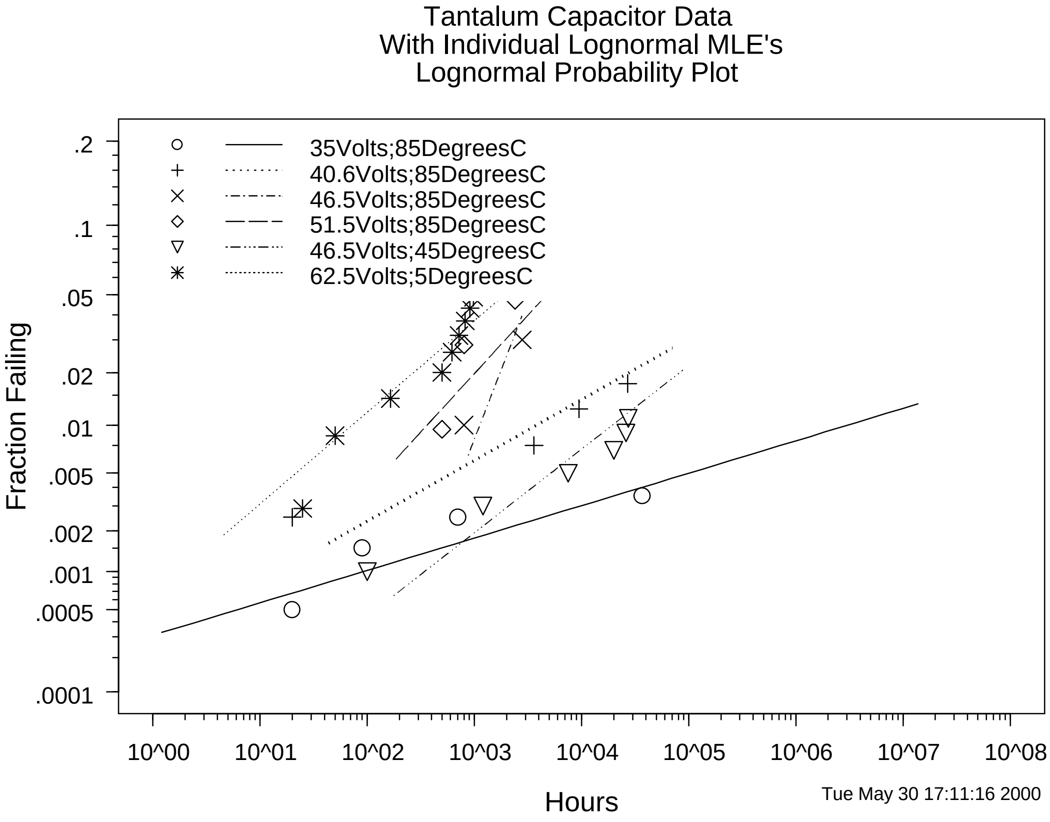


Figure 69 Probability plot showing individual nonparametric estimates for each experimental factor level combination on lognormal paper.

By using the Plot Options page of the dialog box in Figure 68, it is possible to suppress the printing of the legend or have it print on a separate page. There is a considerable amount of variation among the slopes of the ML estimate lines in Figure 69. This is due to the small number of failures at some combinations of voltage and temperature. Corresponding numerical results are given in Table 12. NAs are shown for test conditions for which there were not enough failures to compute ML estimates.

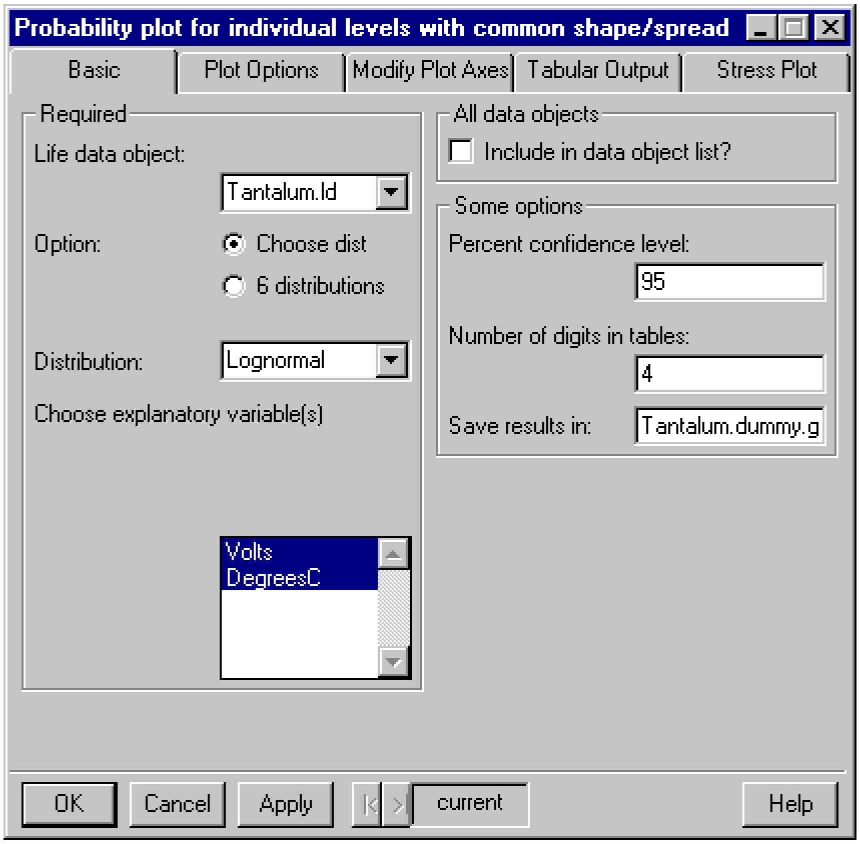
Table 12 Individual ML estimates for the different tantalum capacitor life test conditions

```
Tantalum Capacitor Data

Maximum likelihood estimation results:

Response units: Hours

 Distribution
label,        Log likelihood    mu  se_mu  sigma se_sigma
135  Volts;85 DegreesC        -60.45 46.57 17.297 13.599   6.3819
2 40.6 Volts; 85 DegreesC         -57.99 25.10  7.005  7.247   3.2394
3 46.5 Volts;85 DegreesC      -24.10 10.73  1.892  1.591 9949
4 51.5 Volts;  85 DegreesC         -50.28 14.67  2.759  3.772   1.6760
```

```
5 46.5 Volts;  45 DegreesC         -92.88 22.14  4.533  5.273   1.9315
6 46.5 Volts;  5 DegreesC              NA    NA     NA     NA       NA
7  62.5 Volts;  5 DegreesC        -217.19 15.47  1.513  4.809   0.9950
8   57  Volts; 45 DegreesC             NA    NA     NA     NA       NA

Total log likelihood= -502.9
```

8.4 Probability plot and ML fit for individual conditions: common shapes (slopes)

The methods described in this section are similar to those described in Sections 6.3 and 7.3, except that more than one explanatory variable can be specified for the analysis. Using **SLIDA ➡ Multiple regression (ALT) life data ➡ Prob plot and ML fit for indiv cond: common shapes (slopes)** brings up a dialog box like that in Figure 70. This dialog box is very much like that obtained with **SLIDA ➡ Simple regression (ALT) life data analysis➡ Prob plot and ML fit for indiv cond: common shapes (slopes),** except that one is allowed to choose more than one explanatory variable (including categorical variables, known as "factors" in S-PLUS). Using maximum likelihood, a model is fit that allows the scale parameter of log-location-scale distributions (location parameters of location-scale distributions) at the different combinations of experimental conditions to vary, but constrains the shape (slope) parameter of the log-location distributions (scale parameters of location-scale distributions) to be the same in the model.



Life data object: Tantalum.ld

Option: ● Choose dist ○ 6 distributions

Distribution: Lognormal

Choose explanatory variable(s): Volts DegreesC

☐ Include in data object list?

Percent confidence level: 95

Number of digits in tables: 4

Save results in: Tantalum.dummy.g

Figure 70 Dialog box to request, for the tantalum ALT data, a probability plot and maximum likelihood estimation for individual combinations of voltage and temperature, but with a common lognormal shape parameter.

As with previous similar dialog boxes, choose the life data object, a distribution, the explanatory variables to be used, and then click "Apply" or OK, giving the probability plot shown in Figure 71.

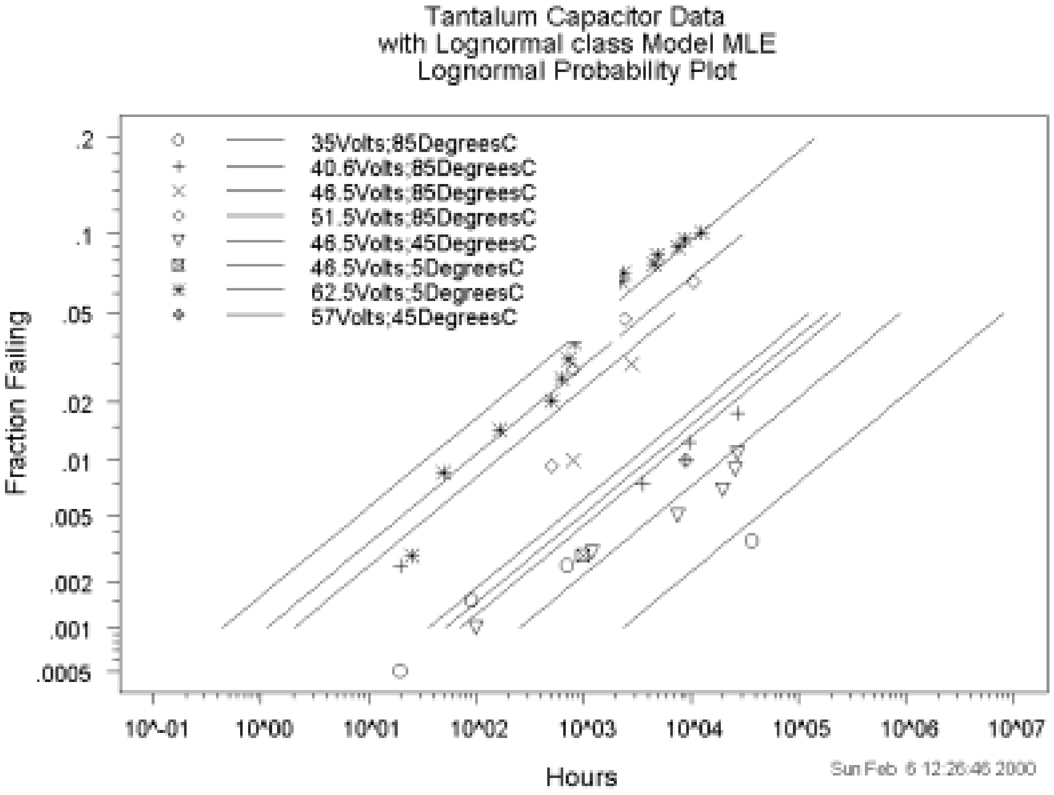


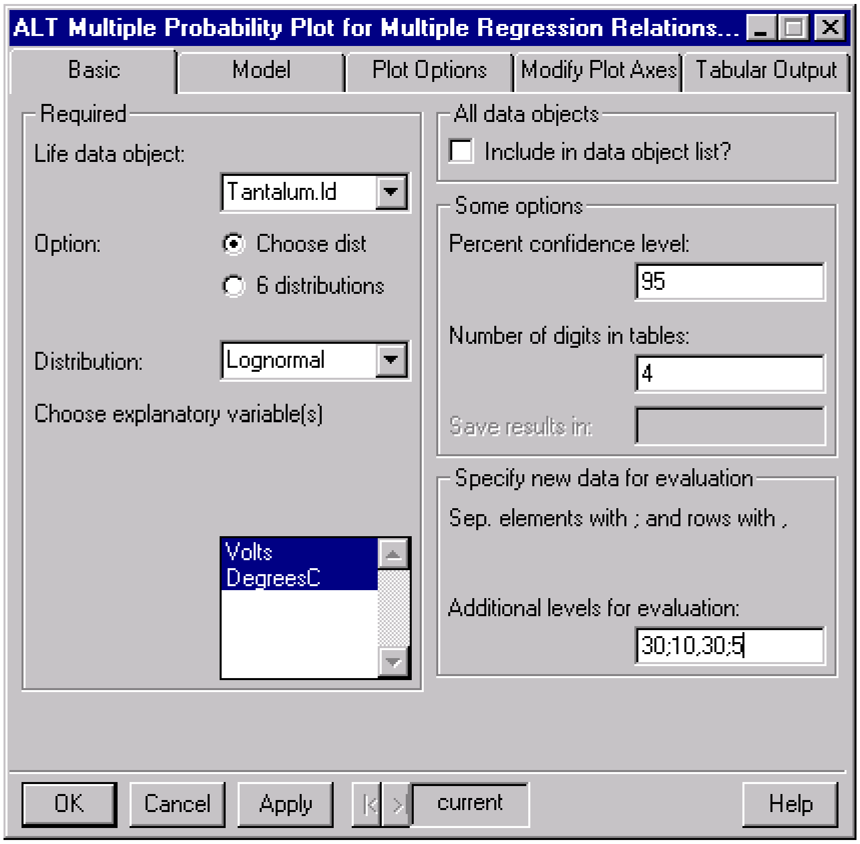
Figure 71 Tantalum ALT data probability plot and maximum likelihood estimation for individual combinations of voltage and temperature, but with a common lognormal shape parameter.

8.5 Probability plot and ML fit of a regression (acceleration) model

This section describes the fitting a multiple regression model. The dialog for doing this, while similar to the dialog for fitting a one-variable relationship, differs significantly. First, the model specification is more involved because more than one variable/relationship combination has to be specified. Relatedly, it is also more complicated to specify additional conditions ("new.data" in S-PLUS jargon) at which to do evaluations of distribution properties like failure probabilities and quantiles. Additionally, there is no option on the dialog for a "stress plot." Instead, after a model is fit, the user can make a "conditional stress plot," as described in the next Section 8.6.

Using **SLIDA ➡ Multiple regression (ALT) life data ➡ Probability plot and ML fit of a regression (acceleration) model** brings up a dialog box like the one in Figure 72. In this box, one chooses the life data object, a distribution (or the six-distribution option) and which explanatory variables to use. Then one moves to the model page of the dialog to specify the model (i.e., life-explanatory variable relationships). To illustrate these features, we continue with the tantalium capacitor example.

After the Tantalum.ld life data object has been chosen, one should choose the distribution and explanatory variables. The Plot Option and Tabular Output pages of the dialog box will show (when output options are actually selected) lists of explanatory variable combinations from which one can choose one or more combinations for particular focus. For example, as with simple regression analyses, one can ask for confidence intervals for ML estimates of the cdf (fraction failing as a function of time) on probability plots and for tables of distribution quantiles or failure probabilities at specified explanatory variable combinations. It is also possible to input user-specified combinations of levels of the explanatory variables ("new data" in S-PLUS jargon) other than those implied by the levels in the input data. This is illustrated in the dialog box shown in Figure 72 where the combinations 30 Volts is combined with 70 and 80 degrees C were specified. Note that each combination entered is separated by a comma, but that variables *within* a combination are separated by semicolons. When entering these numbers it is sometimes convenient to use the right-click Zoom option. The "Save results in:" box gets filled and becomes editable after a the life-explanatory variable relationships are chosen on the Model page.



Life data object: Tantalum.ld

Option: ● Choose dist ○ 6 distributions

Distribution: Lognormal

Choose explanatory variable(s): Volts, DegreesC

☐ Include in data object list?

Percent confidence level: 95

Number of digits in tables: 4

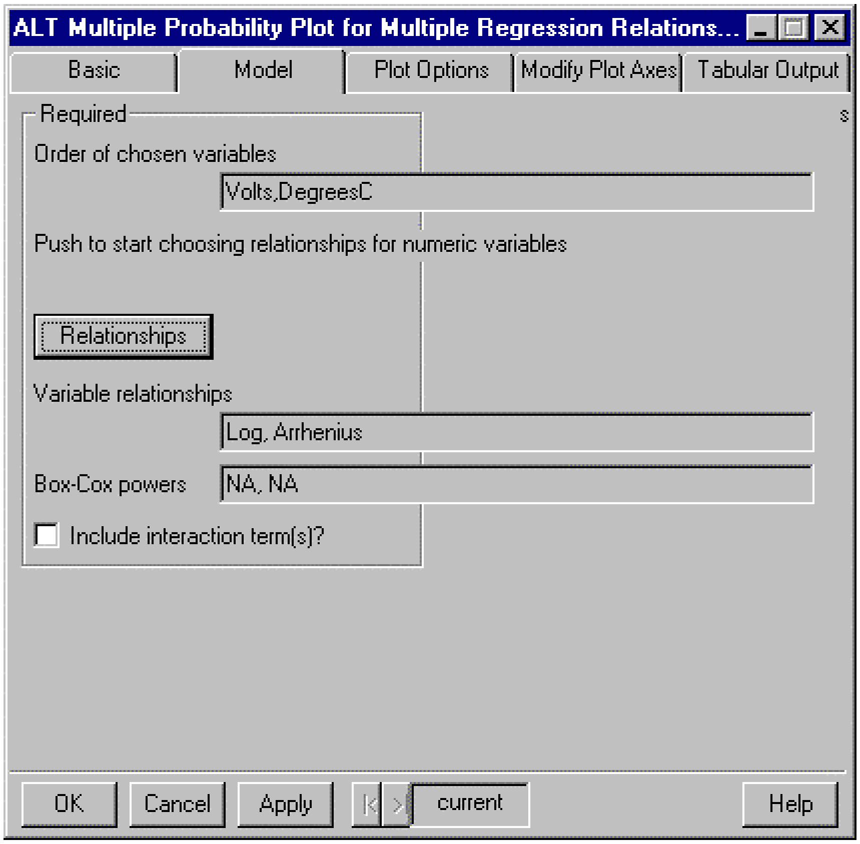
Save results in:

Additional levels for evaluation: 30;10,30;5

Figure 72 Basic page of the multiple regression dialog box requesting a probability plot showing a fitted lognormal/inverse power/Arrhenius regression model to the tantalum capacitor data.

On the Model page of the dialog box (shown in Figure 73), the user first chooses the relationships for each of the variables (except that categorical variables---factors in S-PLUS jargon---are automatically chosen to be class variables). This choosing process is initiated by clicking on the "relationships" button. For the example below, the standard log (equivalent to inverse power rule) and Arrhenius relationships were chosen for the voltage and temperature variables, respectively.

As with previous dialogs for requesting ML estimation, a Tabular Output page allows the user to request tables of distribution quantiles or failure probabilities for specified levels or combinations of levels of the explanatory variables.



Required

Order of chosen variables: Volts,DegreesC

Push to start choosing relationships for numeric variables

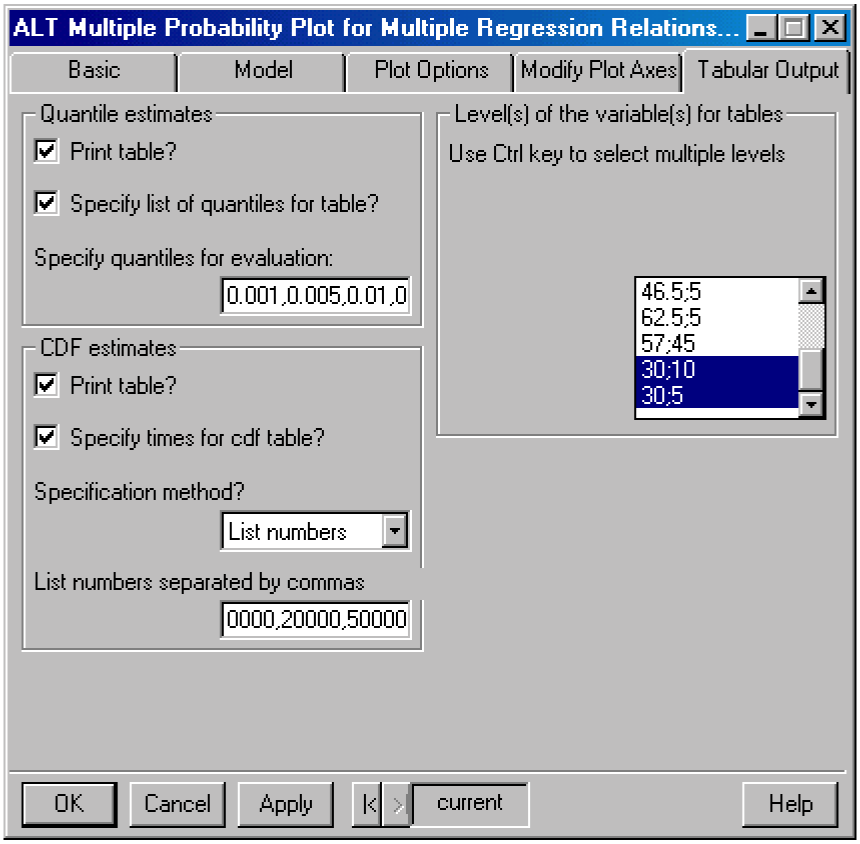
Variable relationships: Log, Arrhenius

Box-Cox powers: NA, NA

☐ Include interaction term(s)?

Figure 73 Model-specification page of the multiple regression dialog box requesting a probability plot showing a fitted Weibull/inverse power/Arrhenius regression model to the tantalum capacitor data.

The Tabular Output page of the dialog box in Figure 72, shown in Figure 74, lists the available levels of the explanatory variables (this list is full only if the explanatory variables have been chosen on the basic page and if one or the other of the tabular output options is checked). The user-inputted values appear at the bottom of the list. In this case, only the two user-inputted values have been chosen for generating the output tables.



Quantile estimates

☑ Print table?

☑ Specify list of quantiles for table?

Specify quantiles for evaluation: 0.001,0.005,0.01,0

CDF estimates

☑ Print table?

☑ Specify times for cdf table?

Specification method? List numbers

List numbers separated by commas 0000,20000,50000

Level(s) of the variable(s) for tables

Use Ctrl key to select multiple levels

46.5;5
62.5;5
57;45
30;10
30;5

Figure 74 Tabular Output page of the multiple regression dialog box requesting a probability plot showing a fitted Weibull/inverse power/Arrhenius regression model to the tantalum capacitor data.

Clicking on “OK” or “Apply” produces the probability plot in Figure 75 and the S-PLUS tabular output for this example shown in Table 13. Table 13 gives the usual regression output as well as the tabular output for 30 Volts and 5 Degrees C.

Table 13 ML estimates for the lognormal distribution acceleration model fit to the tantalum capacitor life test data

```
Maximum likelihood estimation results:

Response units: Hours

Lognormal Distribution

         Relationship
1 Volts: Log
2 DegreesC: Arrhenius

Log likelihood at maximum point: -541.3

  Parameter                  Approx Conf. Interval
               MLE Std.Err. 95% Lower 95% Upper
Intercept  87.5605  13.5007    61.100  114.0215
    Volts -19.8815   4.5457   -28.791  -10.9721
 DegreesC   0.3003   0.2103    -0.112    0.7125
    sigma   6.0175   0.8410     4.576    7.9137
```

```
Lognormal Distribution Failure Probability Estimates
From Tantalum Capacitor Data at  30Volts;5DegreesC
with Lognormal MLE and Pointwise Approximate 95% Confidence Intervals

  Hours       Fhat   Std.Err.  95% Lower 95% Upper
   5000 0.00003444 0.00006823 7.092e-007  0.001670
  10000 0.00005556 0.00010688 1.280e-006  0.002406
  20000 0.00008851 0.00016542 2.270e-006  0.003440
  50000 0.00016067 0.00028926 4.713e-006  0.005449


                 Quantile Estimates
From Tantalum Capacitor Data at  30Volts;5DegreesC
Lognormal MLE and Pointwise Approximate 95% Confidence Intervals

      p    Quanhat   Std.Err. 95% Lower  95% Upper
  0.001    1058114 3.021e+006      3930 2.849e+008
  0.005   23380061 6.909e+007     71378 7.658e+009
  0.010  104912433 3.173e+008    279421 3.939e+010
  0.050 6335885059 2.076e+010  10302254 3.897e+012
```

Figure 75 shows the probability plot for this example with lines also drawn for the user-specified combinations of 30 Volts and 5 Degrees C and 30 Volts and 10 Degrees C. The legend is covering some of the plotted information, so one might want to exercise the Plot Option to suppress or move the legend to a new page. Note that when the model is fit, the results are saved in a “results object” named Tantalum.groupm.Lognormal.VltsLog.DgrCArrh. Note that the name of the results object contains the life data object prefix, distribution name, and explanatory variable/relationship combinations, relieving the user from the chore of specifying such names and making it easier to distinguish among different results objects when requesting subsequent analyses (e.g., residual plots, conditional stress plots, and sensitivity analyses).

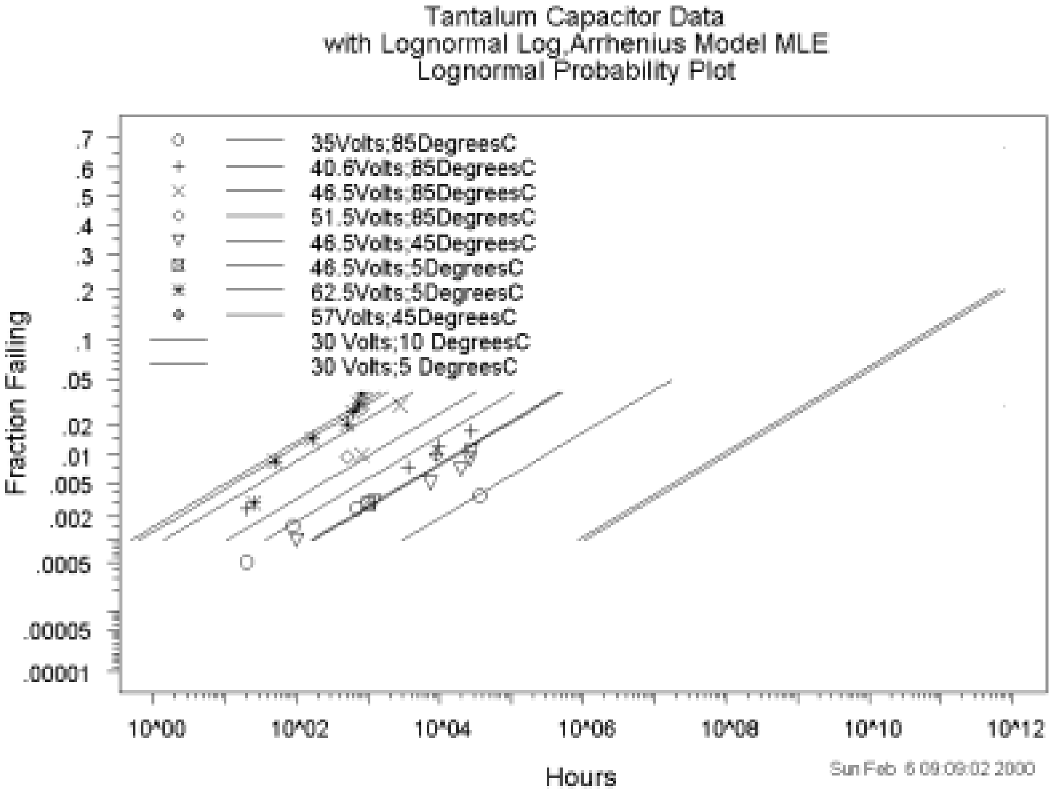


Figure 75 Probability plot showing a fitted lognormal/inverse power/Arrhenius regression model to the tantalum capacitor data.

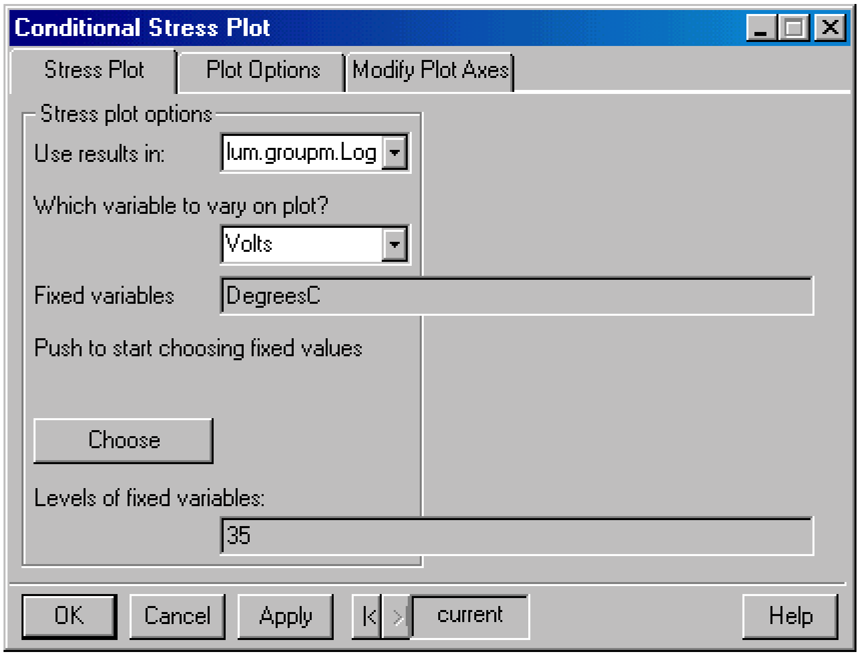
Table 14 shows ML estimates of lognormal distribution failure probabilities for tantalum capacitors at 30Volts and 10DegreesC. Note that the confidence intervals for failure probabilities are very wide.

Table 14 ML estimates of lognormal distribution failure probabilities for tantalum capacitors at 30Volts;10DegreesC

```
Lognormal Distribution Failure Probability Estimates
From Tantalum Capacitor Data at  30Volts;10DegreesC
with Lognormal MLE and Pointwise Approximate 95% Confidence Intervals

  Hours        Fhat   Std.Err.  95% Lower  95% Upper
     20 5.842e-007 1.414e-006 5.090e-009 0.00006704
     50 1.247e-006 2.884e-006 1.340e-008 0.00011604
    100 2.180e-006 4.875e-006 2.721e-008 0.00017458
    200 3.762e-006 8.140e-006 5.420e-008 0.00026114
    500 7.592e-006 1.573e-005 1.308e-007 0.00044060
   1000 1.272e-005 2.554e-005 2.490e-007 0.00064978
   2000 2.105e-005 4.095e-005 4.651e-007 0.00095205
   5000 4.018e-005 7.505e-005 1.032e-006 0.00156114
  10000 6.455e-005 1.170e-004 1.847e-006 0.00225073
  20000 1.024e-004 1.803e-004 3.247e-006 0.00322065
  50000 1.849e-004 3.136e-004 6.662e-006 0.00510952
```

8.6 Conditional stress plot

When a fitted regeression model has more than one explanatory variable, it is still possible to make a “stress plot” showing time as a function of stress (or other explanatory variable). In order to do this, however, it is necessary to specify fixed values of the other explanatory variables. Using **SLIDA ➡ Multiple regression (ALT) life data ➡ Conditional stress plot** brings up the dialog box in Figure 76. When the dialog box appears, it will remember the most recent results object (if the analysis was done in the current session). In this case the remembered name is Tantalum.groupm.Lognormal.VltsLog.DgrCArrh. Suppose now that design engineers want to estimate the life distribution of the capacitors when operating at 35 Degrees C for different levels of voltage. After specifying this information and clicking on “Apply” or “OK,” produces a plot like that in Figure 77.



Use results in: lum.groupm.Log

Which variable to vary on plot? Volts

Fixed variables DegreesC

Levels of fixed variables: 35

Figure 76 Dialog box for a conditional stress plot.

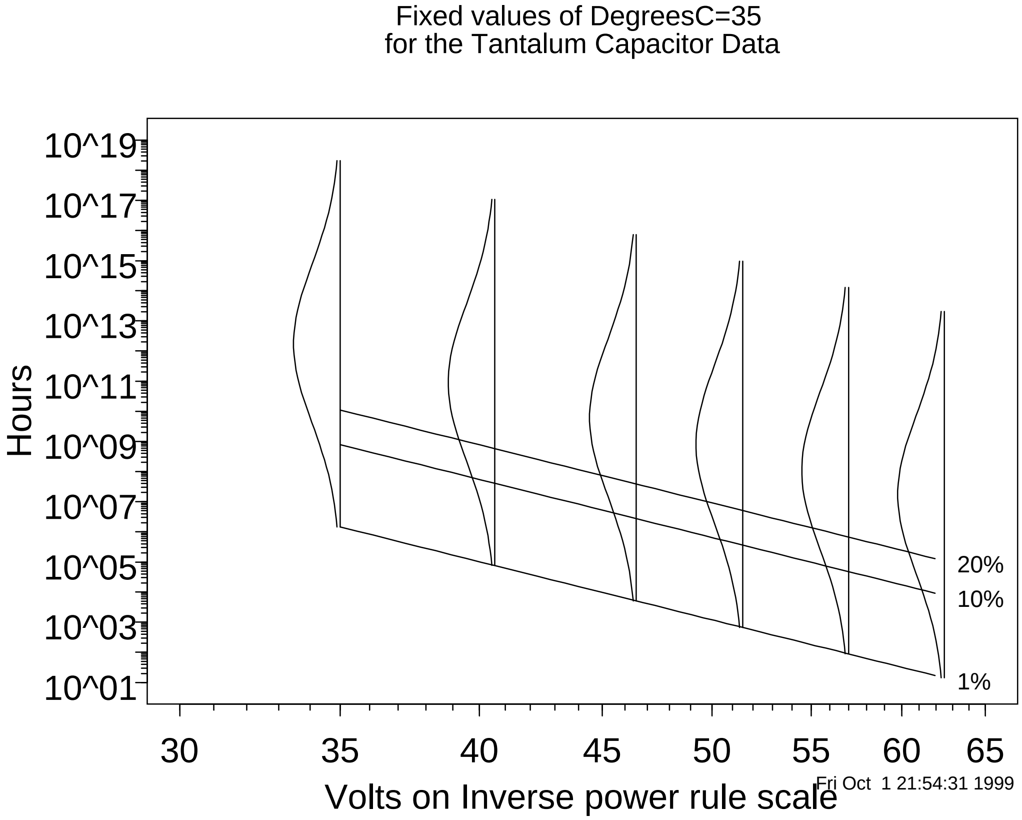
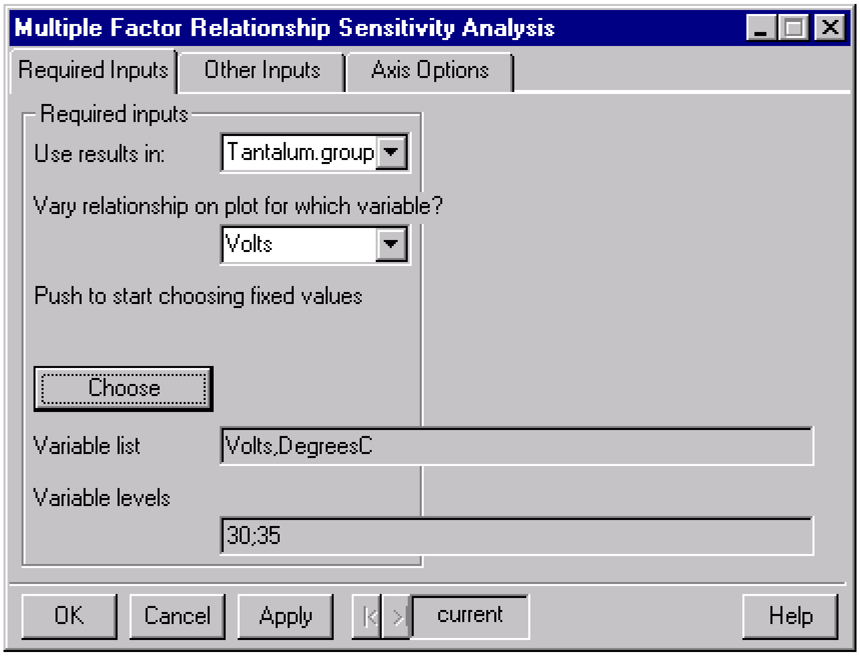


Figure 77 Conditional stress plot showing estimated tantalum capacitor life versus voltage for temperature fixed at 35 degrees C.

8.7 Sensitivity analysis plot

Generally when fitting several alternative models to data, among the models that fit the data well, there is usually relatively little difference in the results from the fitted model, as long as one is working within the range of one's data. SLIDA has a powerful tool that allows one to compare directly alternative analyses with different underlying model assumptions**.** Using **SLIDA ➡ Multiple regression (ALT) life data analysis ➡ Sensitivity analysis** plot brings up the dialog box in Figure 78. Similar to the Conditional stress plot dialog, the last results structure used in the current session is remembered, but any of the other existing results structures could be selected instead. The primary model purturbation used in the sensitivity analysis is the relationship assumption relating a continuous explanatory variable to life. This is done by fitting separate models using several different choices for the parameter in the Box-Cox family of transformations (the default values are –1 , –.5, 0, .5, 1, 1.5, and 2) on the chosen numerical explanatory variable. The output is a plot of the ML estimate of a selected quantile (or quantiles) as a function of the Box-Cox parameter (1 is the same as a linear transformation, .5 is the same as a square root relationship, 0 corresponds to a log relationship, and –1 corresponds to a reciprocal relationship).



Use results in: Tantalum.group

Vary relationship on plot for which variable? Volts

Push to start choosing fixed values

Variable list: Volts,DegreesC

Variable levels: 30;35

Figure 78 Dialog box requesting sensitivity analysis for the assumed relationship between tantalum capacitor life and voltage at 30 volts and 35 degrees C.

If only one quantile and one distribution are used in the comparison (the default), pointwise confidence intervals for the quantile are also plotted, as shown in Figure 79

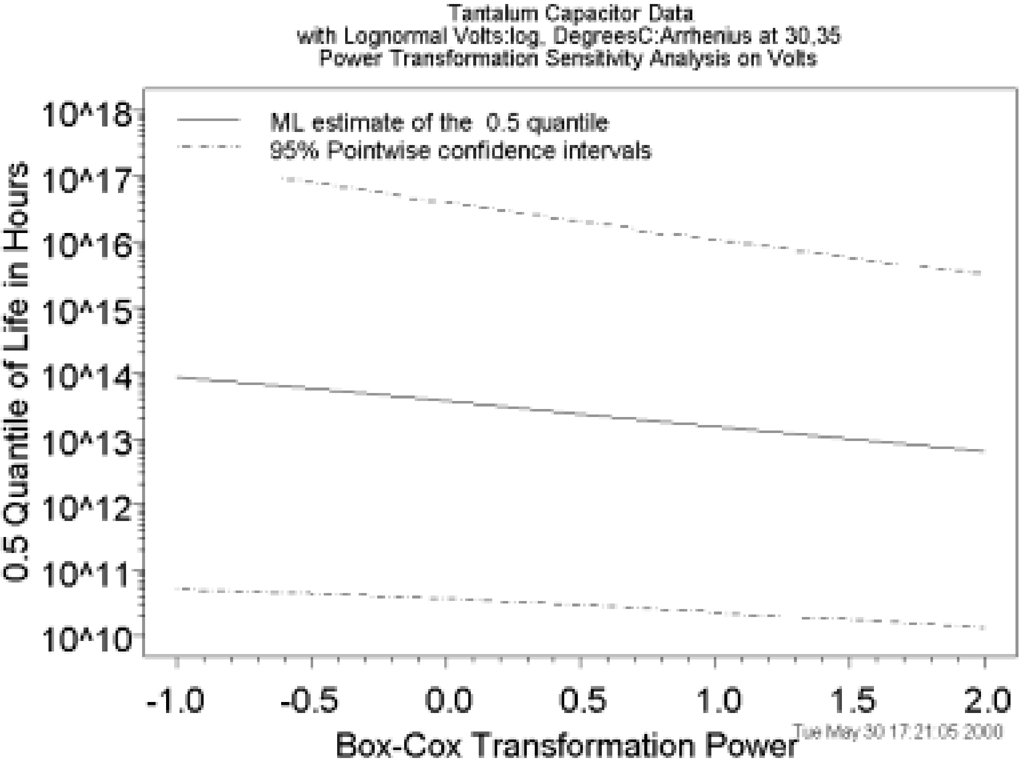


Figure 79 Sensitivity analysis plot showing the effect on tantalum capacitor life of the assumed relationship between life and voltage at 30 volts and 35 degrees C.

Also provided is a plot, like that shown in Figure 80, of the profile likelihood function for the Box-Cox parameter. This plot allows an assessment of the statistical power to discriminate among the different relationship parameters. Note that if there are only two levels of the transformed explanatory variable, the profile likelihood will be constant because there is no information in the data to discriminate among different transformations.

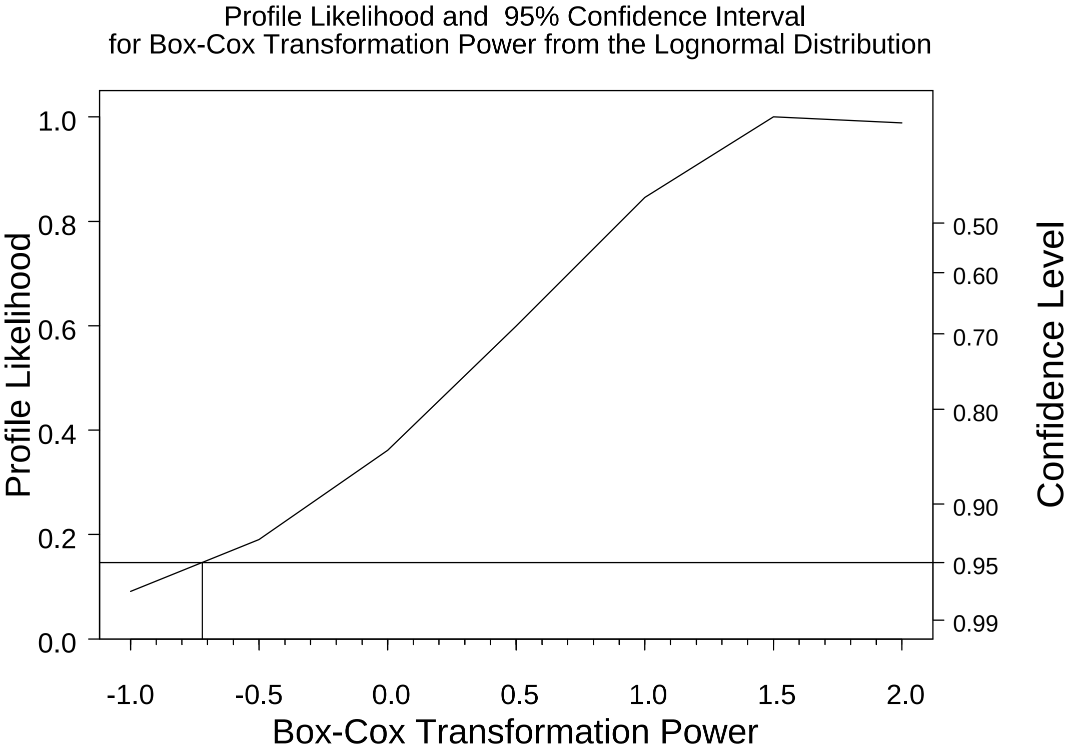
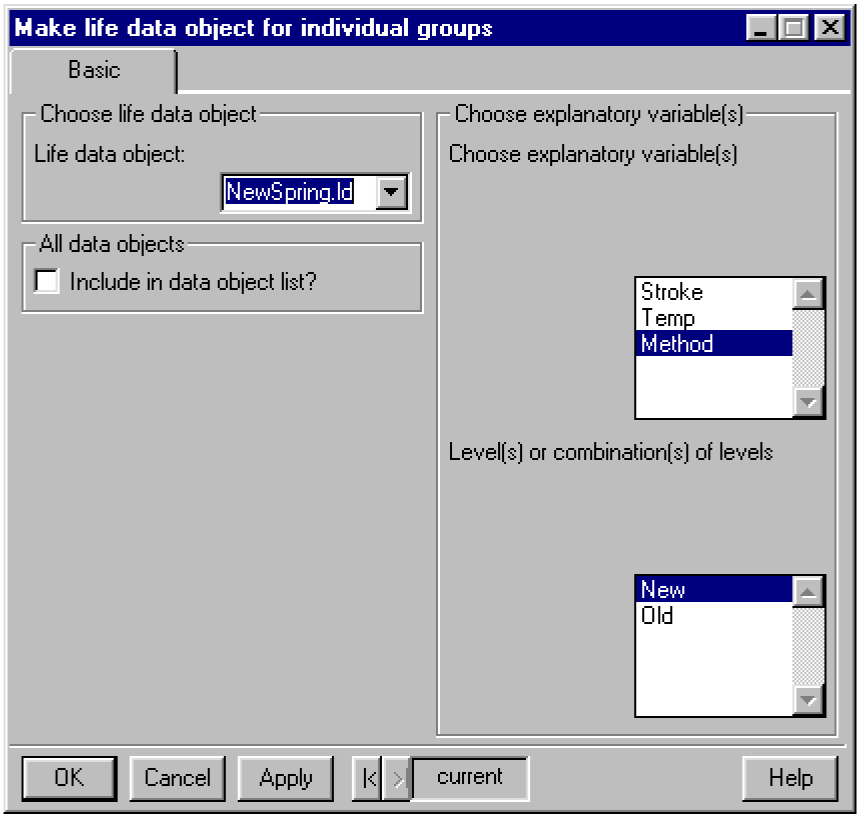


Figure 80 Profile plot showing the relative likelihood (probability) of the tantalum capacitor data as a function of the voltage relationship Box-Cox parameter.

In this case, the profile likelihood suggests that a transformation with the Box-Cox parameter less than $-.5$ is not consistent with the data. Values ranging from $-.5$ to larger than 2.0 do, however, seem to be consistent with the data. Based on previous, transformations used typically used for similar products have been 0 (corresponding to a log transformation). To be conservative, however, values between 1 and 1.5 might be used in reporting a plausible range of results.

8.8 Make life data objects for individual groups

It may, under certain circunstances be desired to select one or more of the groups of regression data for more focused analysis. It is possible, for example to choose a particular combination of levels of explanatory variables and do separate analyses for them. We will illustrate this by making a separate life data object for the new design within the NewSpring life data object. Using **SLIDA** ➡ **Simple regression (ALT) life data** ➡ **Make life data objects for individual groups** brings up the dialog box in Figure 81.


Make life data object for individual groups

Choose life data object

Life data object: NewSpring.ld

All data objects

☐ Include in data object list?

Choose explanatory variable(s)

Choose explanatory variable(s): Stroke, Temp, Method (Method selected)

Level(s) or combination(s) of levels: New (selected), Old

Figure 81 Dialog box requesting the creation of a single distribution life data object for the New Design data in the NewSpring data.

After clicking on “OK” or “Apply” the new life data object is created, we get the message “Saving subset data object NewSpring.NewMethod.ld,” and this life data object will appear in subsequent lists of single distribution life data object.

9. Regression Residual Plots

In any kind of statistical modeling, it is important to look for departures from models being fitted to data. This is especially true for regression models in which explanatory variables like temperature and humidity are used to describe the characteristics of a response variable like life time. Because it is possible to specify most model assumptions in terms of characteristics of model residuals (deviations between the response and some definition of expected or typical response), a useful method of diagnostic checking is to examine a model’s residuals, usually with various graphical displays. Examples illustrating the use of and some technical details concerning the definition of residuals for censored data are given in Section 17.6 of Meeker and Escobar (1998).

9.1 Residuals versus fitted values

It is common practice to plot residuals versus fitted values. Such a plot is useful for detecting departures from the structural model as well as model departures like nonconstant spread. Using **SLIDA** ➡ **Regression residual analysis** ➡ **Residuals versus fitted values** brings up a simple dialog box, shown in Figure 82.

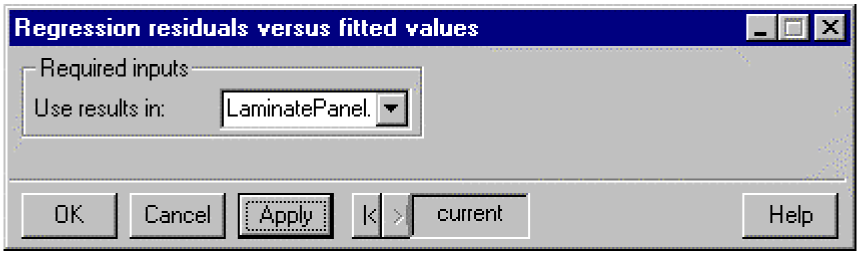


Figure 82 Dialog box requesting a plot of the regression residuals for the laminate panel data versus fitted values.

All one needs to do it to choose a results object (a list of all such objects in the user's data base is provided) and click on "Apply" or "OK" to request a plot of regression residuals versus fitted values like that shown in Figure 83 for the laminate panel data.

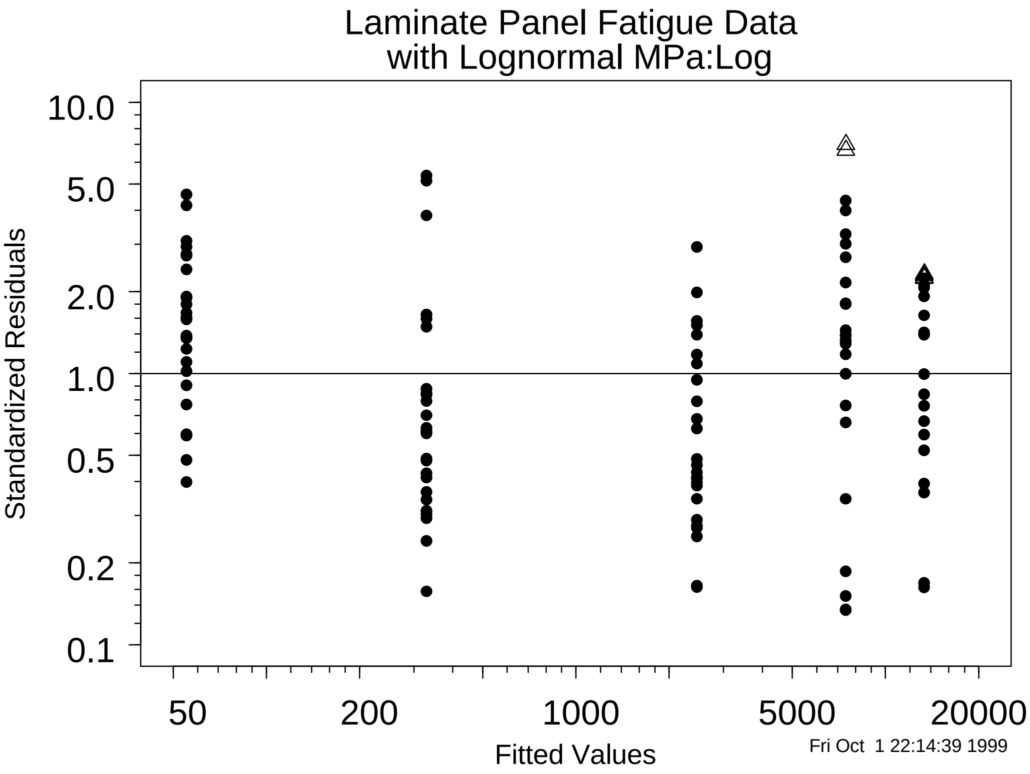
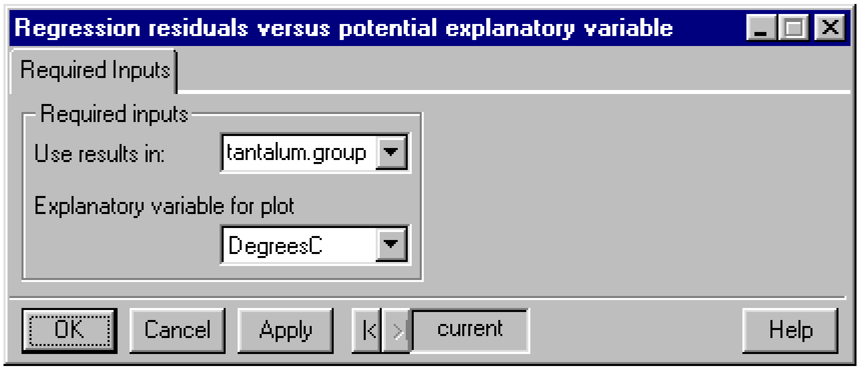


Figure 83 Plot of the regression residuals for the laminate panel data versus fitted values.

9.2 Residuals versus possible explanatory variables

The residual from a regression model should not have a strong relationship with any other external variable. If such a relationship is discovered, it suggests that the variable should have been included into the model. To illustrate this we return to the tantalum data used in Section 8.5, but using a model in which life is related to voltage only, omitting the temperature variable (this will be referred to as the reduced model). Using **SLIDA** ➡ **Regression residual analysis** ➡ **Residuals versus possible explanatory variables** brings up the dialog box shown in Figure 84.



Required inputs

Use results in: tantalum.group

Explanatory variable for plot: DegreesC

Figure 84 Dialog box requesting a plot of residuals versus an explanatory variable.

The results object for the reduced model is chosen (actually it is remembered as the default choice if the model was fit just before bringing up the dialog). Then DegreesC is chosen as the variable against which to plot. Clicking on “Apply” or “OK” gives the plot shown in Figure 85.

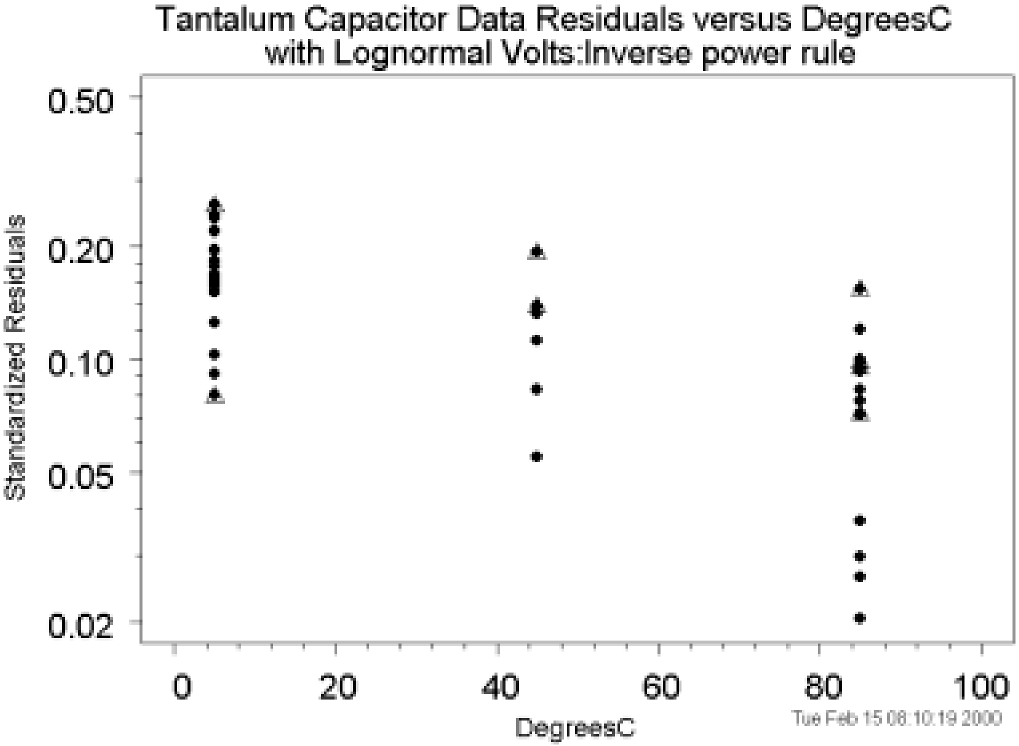


Figure 85 Residuals for the Lognormal/inverse power relationship model for the tantalum capacitor data plotted against the omitted variable Degrees C .

For the full model fitted in Section 8.5, the estimated Arrhenius coefficient (activation energy in eV) was .3, a value that is physically much larger than would be expected. This estimate, however, was not statistically different from zero. Nevertheless, physically we expect temperature to have an effect and would be inclined to keep temperature in the model. The residual plot in Figure 86, showing decreasing life for increasing temperature, reinforces this conclusion.

9.3 Residuals versus observation number

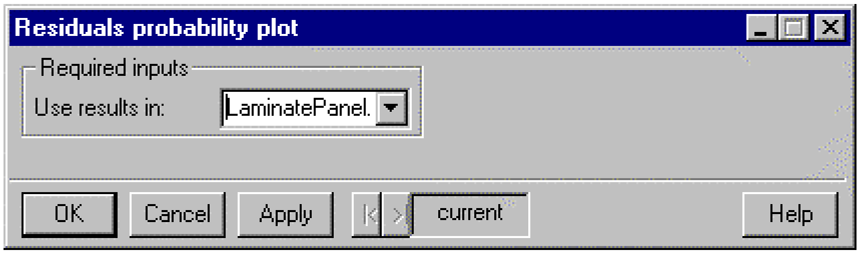
In some studies, data are obtained over time and the order of the cases in the resulting data set may have some importance. For example, if units are tested sequentially, one at a time, on a machine to do fatigue cycling, it is possible that some underlying “lurking factor” has an effect on the response. For example, there may be gradual drift of machine settings or an effect due to changes in ambient temperature or other environmental conditions**.** An analyst can check for such underlying time-dependent changes in a process by plotting residuals versus time order of the observations. Of course, in order for such a plot to be meaningful, it is necessary that the case ordering in the data set correspond to the actual time ordering that units were tested. If (as is often the case) available data are ordered according to observed failure time (which might be the natural ordering for commonly-used simultaneous testing) or according to explanatory variable levels, the potentially important time-sequence information is lost and plots made versus time order would probably have no meaning.

A plot of residuals versus observation number is easily obtained by using **SLIDA** ➡ **Regression residual analysis** ➡ **Residuals versus observation number** and choosing the desired regression results object from the list presented in the dialog.

9.4 Residual probability plot

As described in Section 17.6 of Meeker and Escobar (1998), residuals from a regression model, even with censoring, can be examined with the use of standard probability plotting methods. Residual probability plots are useful for assessing the reasonableness of particular distribution choice for a regression model. The multiple probability plots used in Sections 7 and 8 are useful for making this assessment at individual conditions. After fitting an overall model, however, plotting the residuals provides more information on the adequacy of the overall distribution**.**

SLIDA ➡ **Regression residual analysis** ➡ **Residual probability plot** brings up a dialog box like that shown in Figure 86, to request a residual probability plot of the residuals from a previously estimated model. Choose the desired regression results structure an click on “OK” or “Apply**.”**



Use results in: LaminatePanel.

Figure 86 Dialog requesting a probability plot of the regression residuals for the laminate panel data.

Figure 87 is a residual probability plot for the laminate panel data**.**

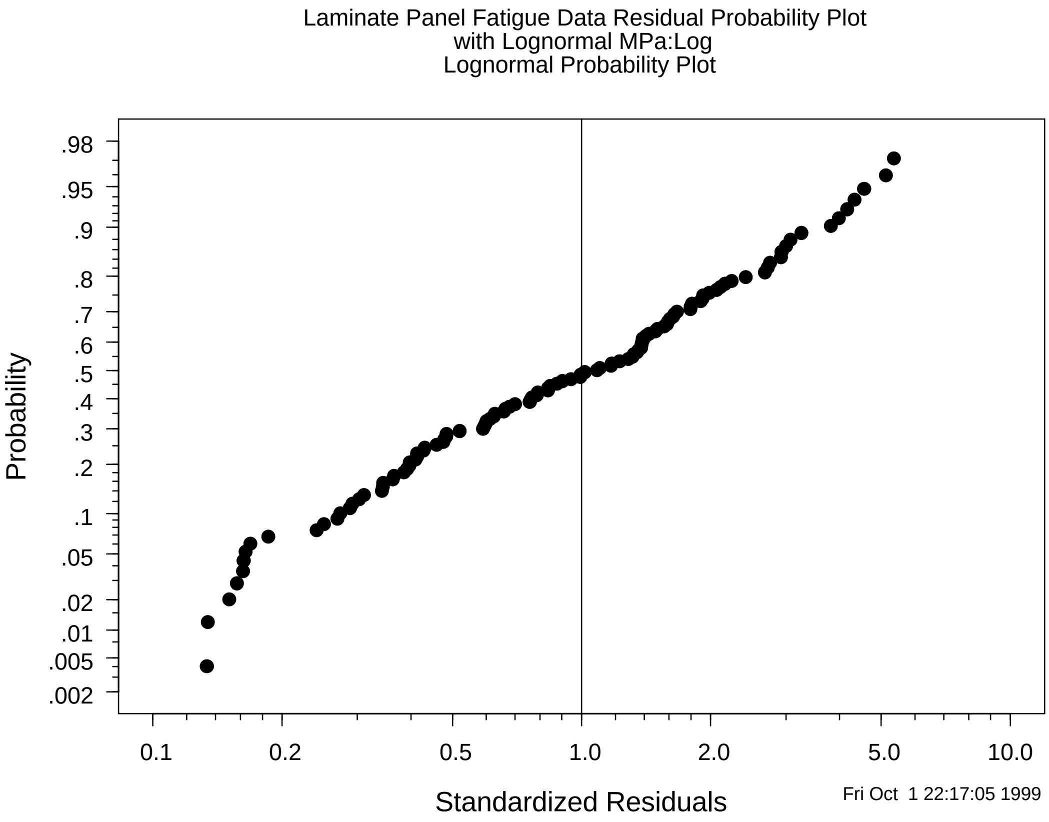


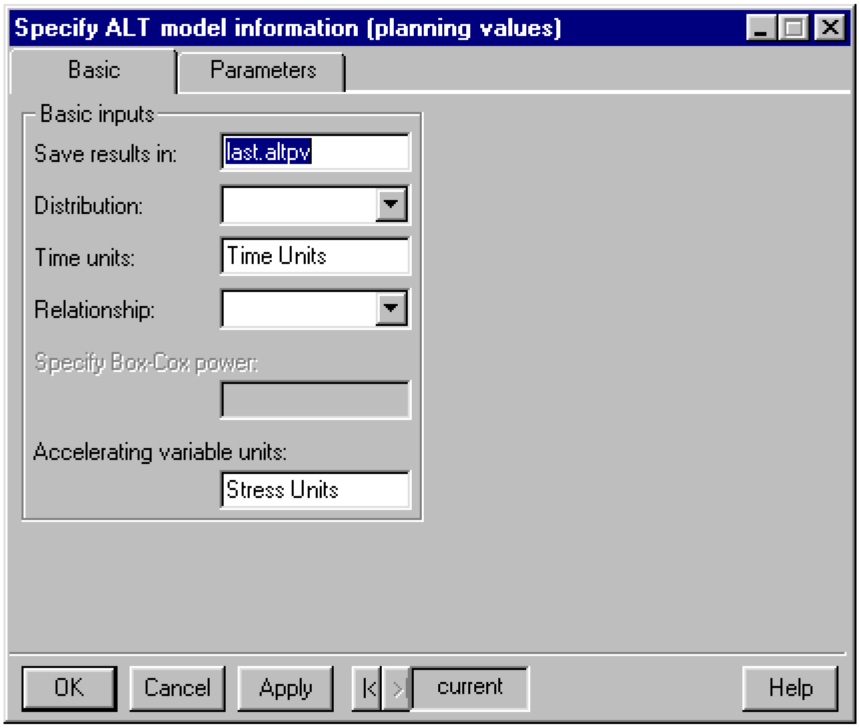
Figure 87 Probability plot of the regression residuals for the laminate panel data.

10. Planning an Acccelerated Life Test (ALT)

Accelerated life tests are complicated, expensive experiments. Careful planning of such experiments is important. SLIDA provides tools for the evaluation and comparison of proposed accelerated life test plans. To use these tools, on must specify model information (or planning information) and the proposed test plan(s).

10.1 Specification of ALT plan values

Using **SLIDA** ➡ **Plan an accelerated life test** ➡ **Specify ALT model information (planning values)** brings up a dialog box like the one shown in Figure 88.



Save results in: last.altpv

Distribution:

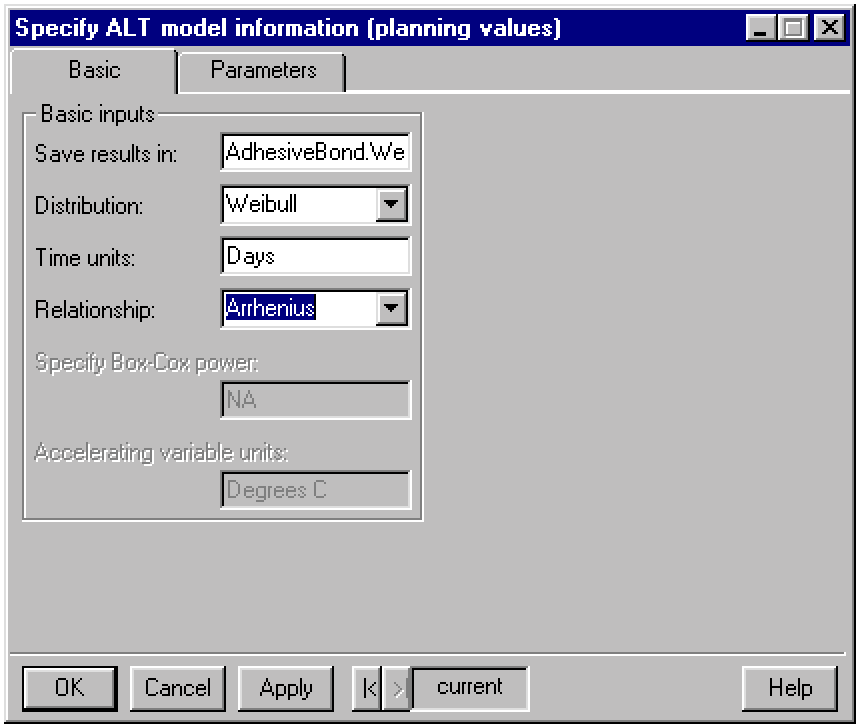
Time units: Time Units

Relationship:

Accelerating variable units: Stress Units

Figure 88 Beginning dialog box for specifying ALT-planning values.

As an example, we will specify the planning values corresponding to the adhesive bond used in Example 20.1 on page 535 of Meeker and Escobar (1998). On the first page of the dialog box, change “last.altpv” to the more descriptive AdhesiveBond.pv, choose a distribution (Weibull in this case), a relationship (Arrhenius) and edit the time units cell to the more descriptive “Hours,” as shown in Figure 88. Note that the distribution name was automatically inserted into the “Save results in” cell and the stress units cell was changed to Degrees C (*the object name is too large to see completely without using the right-click-Zoom option in the cell*).



Save results in: AdhesiveBond.We

Distribution: Weibull

Time units: Days

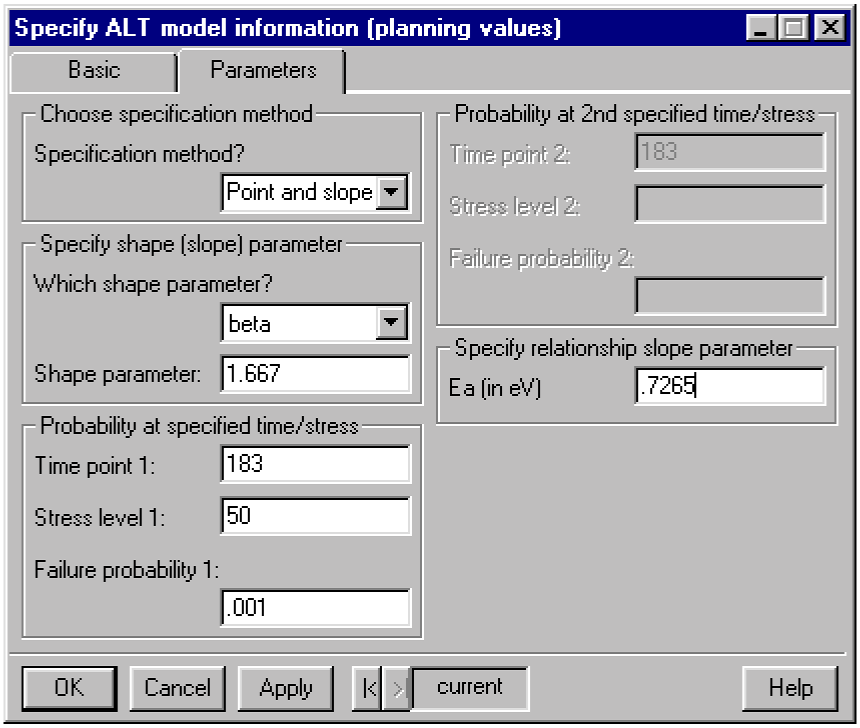
Relationship: Arrhenius

Specify Box-Cox power: NA

Accelerating variable units: Degrees C

Figure 89 Completed Basic page of the Get accelerated life test plan values dialog box.

After the Basic page of the dialog box has been completed, move to the Parameters page. There are two different options for specifying the ALT planning information corresponding to a quantile line or lines on the linearized life-stress relationship. One can specify two points or a point and a slope. For the adhesive bond example, the responsible engineers in the past had used a Weibull distribution to model the life of adhesives and the Weibull shape parameter was typically in the neighborhood of 1.667. In addition, for purposes of planning, the .001 quantile of the life distribution at 50 degrees C is specified as 183 days (or equivalently, the failure probability at 50 degrees and 183 days is specified to be .001). Additionally, the slope parameter in the life-temperature relationship is the effective activation energy (.7265 in eV). The completed dialog box is shown in Figure 90. Click on "OK" or "Apply" to create the ALT planning value object.



Specification method? Point and slope

Which shape parameter? beta

Shape parameter: 1.667

Time point 1: 183

Stress level 1: 50

Failure probability 1: .001

Time point 2: 183

Stress level 2:

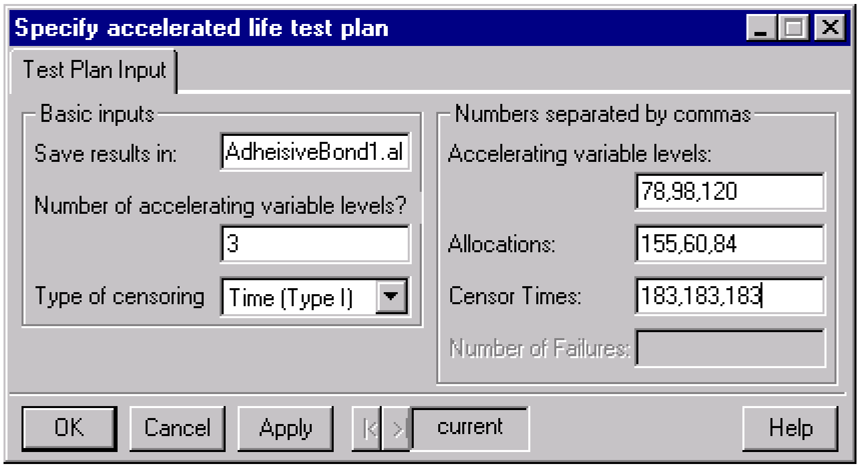
Failure probability 2:

Ea (in eV) .7265

Figure 90 Completed Parameter page of the Get accelerated life test planning values dialog box.

10.2 Specification of an ALT test plan

In order to specify an ALT plan, use **SLIDA ➡ Plan an accelerated life test ➡ Specify ALT test plan** to bring up a dialog box like that shown in Figure 91**.** Specify the number of accelerating variable levels, type of censoring, and the accelerating variable level at use conditions. You may also want to specify a particular root for the test plan object name (AdhesiveBond1 in the example). The suggested default suffix altpv is provided automatically. Then provide the actual plan information. Note that it is allowable to use an allocation of 0 for a level if desired.



Save results in: AdheisiveBond1.al

Number of accelerating variable levels? 3

Type of censoring Time (Type I)

Accelerating variable levels: 78,98,120

Allocations: 155,60,84

Censor Times: 183,183,183

Number of Failures:

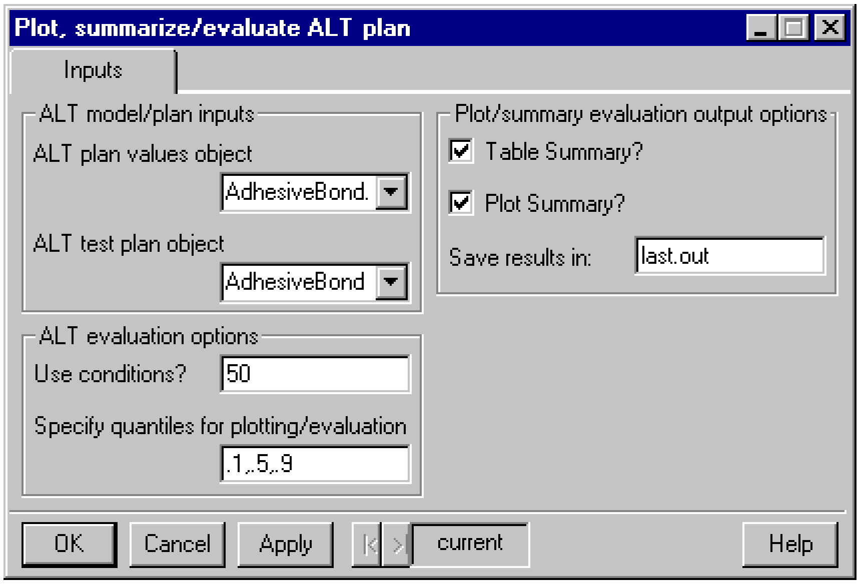
Figure 91 Completed dialog box specifying an ALT plan.

After the plan is specified, click on “OK” or “Apply” (in case that you want to make more than one related plan. To specify a second or third plan, edit the plan and the root of the plan object name (e.g., use

AhhesiveBond2 so that the previously specified plan(s) will not be overwritten) and again press “OK” or “Apply”.

10.3 Summarization and approximate evaluation of a specified ALT test plan

Using SLIDA ➡ **Plan an accelerated life test** ➡ **Plot, summarize, and evaluate ALT test plan** will bring up the dialog box shown in Figure 92. In this box, one specifies the ALT plan values object (AdhesiveBond.Weibull.altpv in this case), the ALT test plan object (AdhesiveBond1.altplan) to be evaluated, and the use conditions (50 Degrees C for the adhesive bond). By default, the output produced includes a tabular summary and a plot summary of the specified ALT test plan. Figure 93 shows an Arrhenius plot for the adhesive bond test plan specified in Figure 91, using the planning values that were specified in Figure 90.



ALT plan values object: AdhesiveBond.

ALT test plan object: AdhesiveBond

Use conditions? 50

Specify quantiles for plotting/evaluation: .1,.5,.9

☑ Table Summary?

☑ Plot Summary?

Save results in: last.out

Figure 92 Dialog box asking for a summary evaluation and plot of a proposed accelerated life test plan for the adhesive bond example.

Tabular output provides a printed summary of the planning values and the test plan, followed by a listing of the large-sample approximate standard deviation and confidence interval precision factor for confidence intervals corresponding to each of the quantiles listed in the “Plot, summarize/evaluate ALT Plan” dialog box shown in Figure 92.

Table 15 ALT planning information and test plan specification for the adhesive bond example.

```
Accelerated test planning values

Distribution:  Weibull
Relationship:  Arrhenius
Time units:  Days

For a censoring time of 183 Days
the failure probability at 50 Degrees C  is:  0.001

Intercept is:  -16.7
slope =  0.726

weibull.beta =  1.67
sigma =  0.6

Accelerated Test Plan
```

```
  level number censor.time     xi    pi    prfail Efail
1    78    155         183 0.4478 0.518 0.0315772  4.89
2    98     60         183 0.7264 0.201 0.242189  14.5
3   120     84         183 1      0.281 0.900543  75.6

Use condition is 50 Degrees C

Total number of test units= 299

The large sample approximate standard deviation
of the 0.1 log quantile at 50 Degrees C  = 0.4378
corresponding to a 95% confidence precision factor or R= 2.358

The large sample approximate standard deviation
of the 0.5 log quantile at 50 Degrees C  = 0.4911
corresponding to a 95% confidence precision factor or R= 2.619

The large sample approximate standard deviation
of the 0.9 log quantile at 50 Degrees C  = 0.532
corresponding to a 95% confidence precision factor or R= 2.837
```

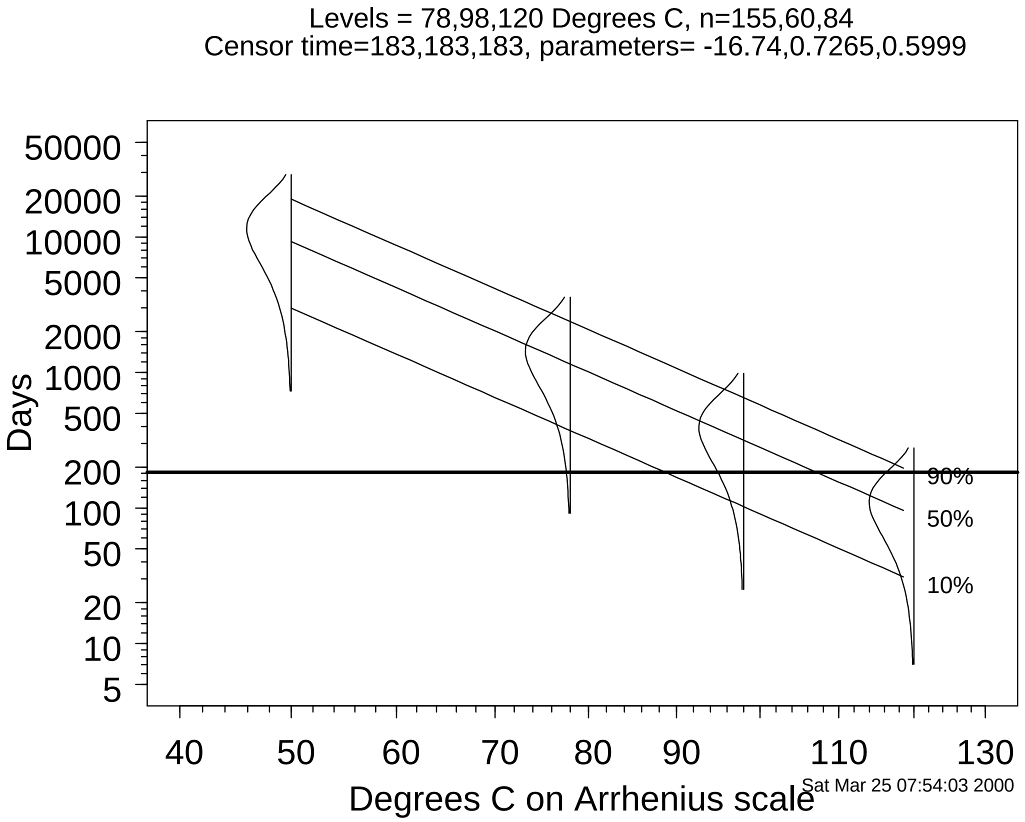
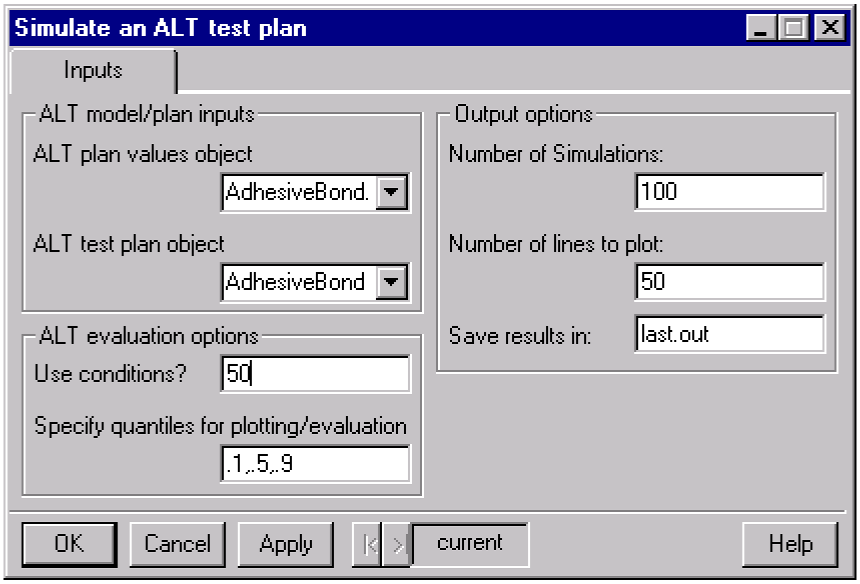


Figure 93 Arrhenius plot showing a proposed test plan for the Adhesive Bond example.

10.4 Simulation of an ALT test plan

Although the approximate evaluation given above is useful, doing a simulation of a proposed ALT test plan avoids the use of large-sample approximations (which will not be adequate when some of the test conditions have expected numbers of failures that are small) and will provide insight into the limitations of a proposed test plan. Using **SLIDA ➡ Plan an accelerated life test ➡ Simulate an ALT test plan** brings up the dialog box in Figure 94, allowing the user to request a simulation of a proposed ALT test plan.



ALT plan values object: AdhesiveBond.

ALT test plan object: AdhesiveBond

Use conditions? 50

Specify quantiles for plotting/evaluation: .1,.5,.9

Number of Simulations: 100

Number of lines to plot: 50

Save results in: last.out

Figure 94 Dialog box requesting a simulation to evaluate a proposed accelerated life test plan for the adhesive bond example.

Then specify the previously created ALT plan values (e.g., AdhesiveBond.Weibull.altpv), the ALT test plan object (e.g., AdhesiveBond1.Weibull.altplan), the Use conditions, and possibly change other optional inputs, and click on “OK” or “Apply.” The simulation will then begin to run, giving an indication of progress in the output window (completing the simulation will take from a few seconds to a few minutes depending on the number of simulations requested (100 is sufficient for most purposes). When completed, a summary of the results is depicted in a model plot (an Arrhenius plot for the example), as shown in Figure 95.

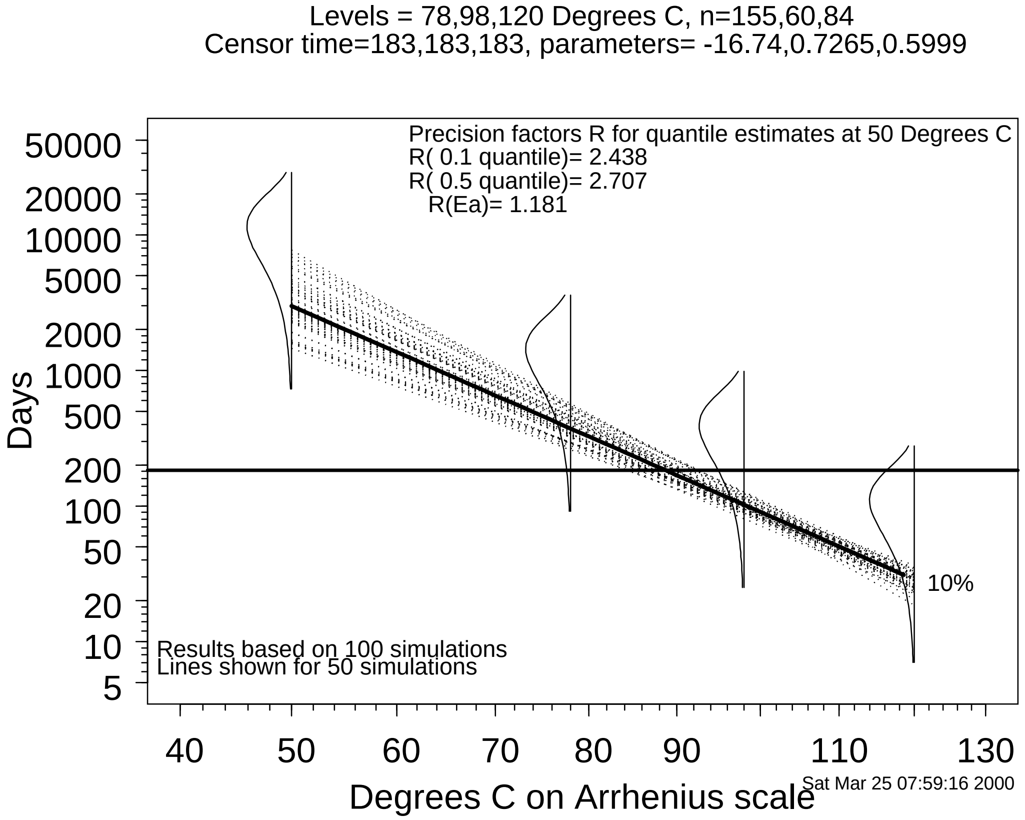


Figure 95 Arrhenius plot showing a summary of the simulation of the proposed accelerated life test for the Adhesive Bond.

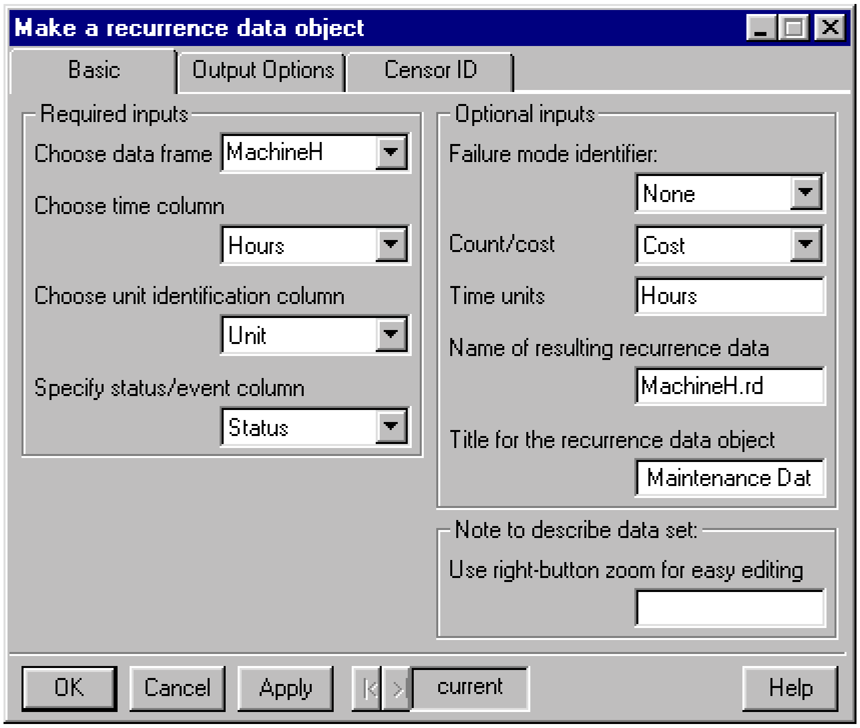
Accelerated life tests are complicated, expensive experiments. Careful planning of such experiments is important. SLIDA provides tools for the evaluation and comparison of proposed accelerated life test plans. To use these tools, on must specify model information (or planning information) and the proposed test plan(s).

11. Recurrence (point process) data analysis

Recurrence data (also known as point process data) arise when events are tracked on a collection (or sample) of units over time. Such data arise in many different applications. For example, in field tracking, a group of units is monitored over time and a record is kept of repairs for individual units, perhaps consisting of data, type of repair, and the cost of the repair. Interest, for example, may center on the recurrence rate or on the average cumulative cost of system maintenance as a function of time.

11.1 Creating a recurrence data object

As with life data, to do a SLIDA analysis of degradation data, one first has to construct a recurrence data object. Because the structure of recurrence data is different from that of life data, there is a different dialog box to making a recurrence data object. **SLIDA ➡ Make/edit/summary/view data object ➡ Make a recurrence (point process) data object** to bring up the dialog box in Figure 96.



Choose data frame: MachineH

Choose time column: Hours

Choose unit identification column: Unit

Specify status/event column: Status

Failure mode identifier: None

Count/cost: Cost

Time units: Hours

Name of resulting recurrence data: MachineH.rd

Title for the recurrence data object: Maintenance Dat

Use right-button zoom for easy editing

Figure 96 Dialog box used to make a recurrence data object.

Clicking on the Choose data frame arrow in the dialog box illustrated in Figure 96 will show all of the data frames in the SLIDA database and in the user's working database. Only some of these will be appropriate for making a repeated measures data object. SLIDA has no way to distinguish among different generic data frames (as it attempts to do with data objects when it decides which to put into a list available for use) , so all data frames appear in the list. When the needed inputs have been specified, click on "OK" or "Apply" to create the data object. In addition to creating the recurrence data object, a short summary of the data in the object is provided (as show in Table 16) and, if desired, a printout of the data can be requested by using the Output Options page of the dialog box.

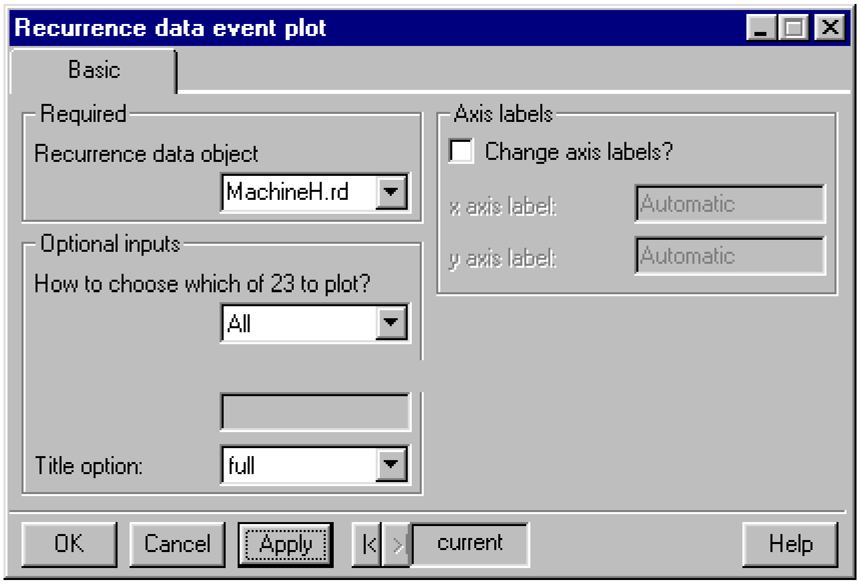
After choosing a data frame corresponding to a recurrence data set, one must choose the time, unit identifier, and the status/event columns from the frame (all are required for recurrence data). The dialog in Figure 96 uses the earth-moving machine maintenance data (MachineH is the frame name) from Chapter 16 of Meeker and Escobar (1998). For the earth-moving machine data there is also a cost variable giving the cost of each reported maintenance action. Because cost was of primary interest in this application, this variable is also specified in the dialog box. When the needed inputs have been specified, click on "OK" or "Apply" to create the data object. In addition to creating the recurrence data object, a short summary of the data in the object is provided (as shown in Table 16) and, if desired a printout of the data can be requested by using the Output Options page of the dialog box.

Table 16 Summary of: Earth-Moving Machine Maintenance Data

```
Number of rows in data matrix= 573
Number of units in the recurrence data object:  23
Number of event times = 550
Total cost/weight of events in the recurrence data set= 1958.7
Response units:  Hours
Response minimum:  52
Response maximum:  9249.5
```

11.2 Recurrence data event plot

As with the analysis of other types of data, one should start with simple graphical methods that provide insight into the nature of the data. Using **SLIDA** ➡ **Recurrence data analysis** ➡ **Recurrence event plot** will produce the dialog box in Figure 97. In this dialog box one specifies the name of a recurrence data. There are options to print the events for a subset of the data. This option is useful when there are a large number of units in a data set.



Recurrence data object: MachineH.rd

How to choose which of 23 to plot?: All

Title option: full

☐ Change axis labels?

x axis label: Automatic

y axis label: Automatic

Figure 97 Dialog box requesting an event plot for the earth-moving machine (Machine H) maintenance data.

Then, clicking “Apply” of “OK” produces the event plot in Figure 98, allowing one to visualize the events (maintenance actions in this example) as they unfolded in time (measured in hours of operation for this example).

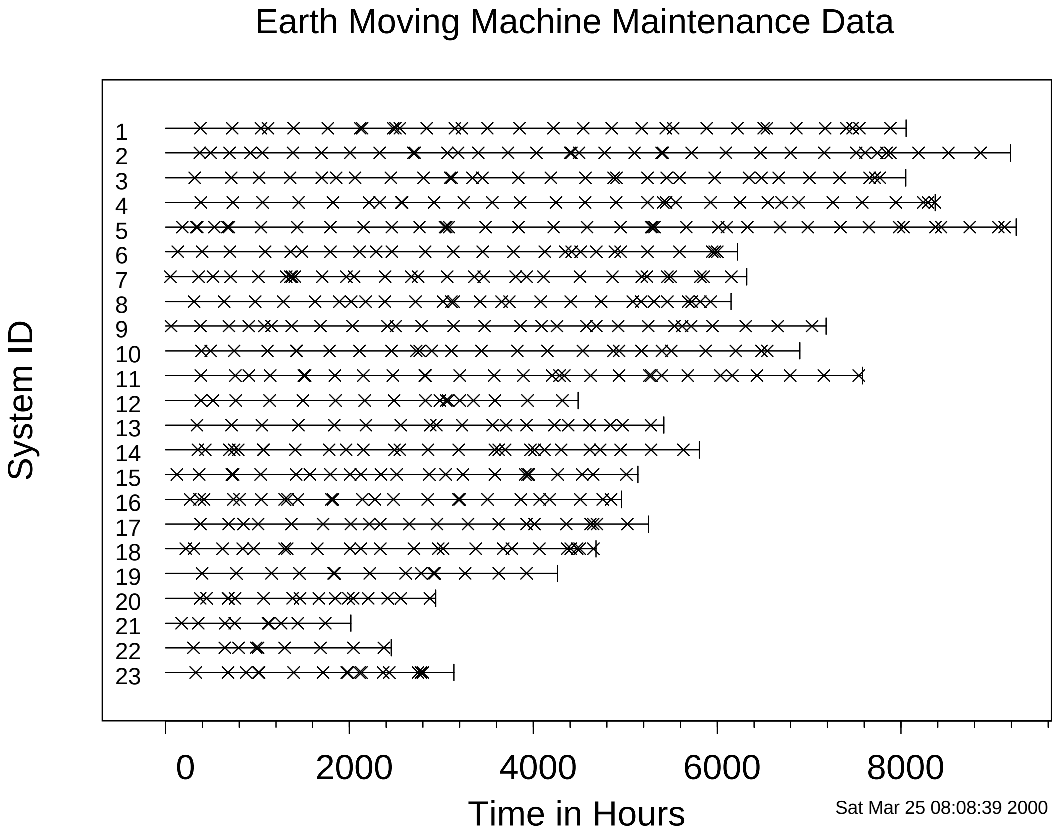
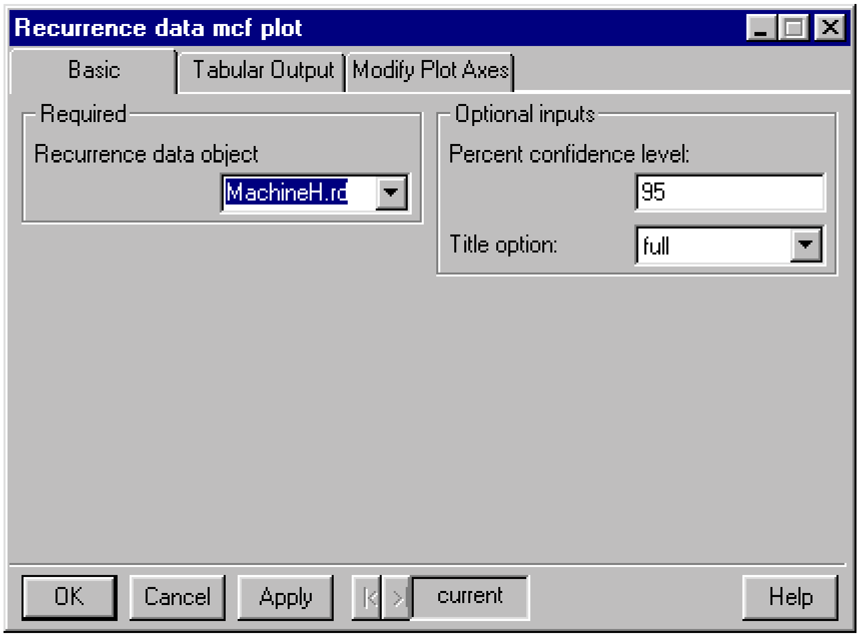


Figure 98 Event plot for the earth-moving machine (Machine H) maintenance data.

11.3 Recurrence data mean cumulative function

Using **SLIDA ➡ Recurrence data analysis➡ Mean cumulative function plot** will generate a dialog box from like that shown in Figure 99, from which one can request a plot of the mean cumulative function (MCF) and corresponding pointwise confidence intervals for a recurrence data set. There is an option to request a table giving the same information. Figure 100 shows the MCF for the earth-moving machine data. As described in Example 16.6 of Meeker and Escobar (1998), some of the irregular behavior in this function in the early part of life can be traced to the regularly scheduled maintenance of the machines in the fleet.



Recurrence data object: MachineH.rd

Percent confidence level: 95

Title option: full

Figure 99 Dialog box requesting a mean cumulative function (MCF) plot for the earth-moving machine (Machine H) maintenance data.

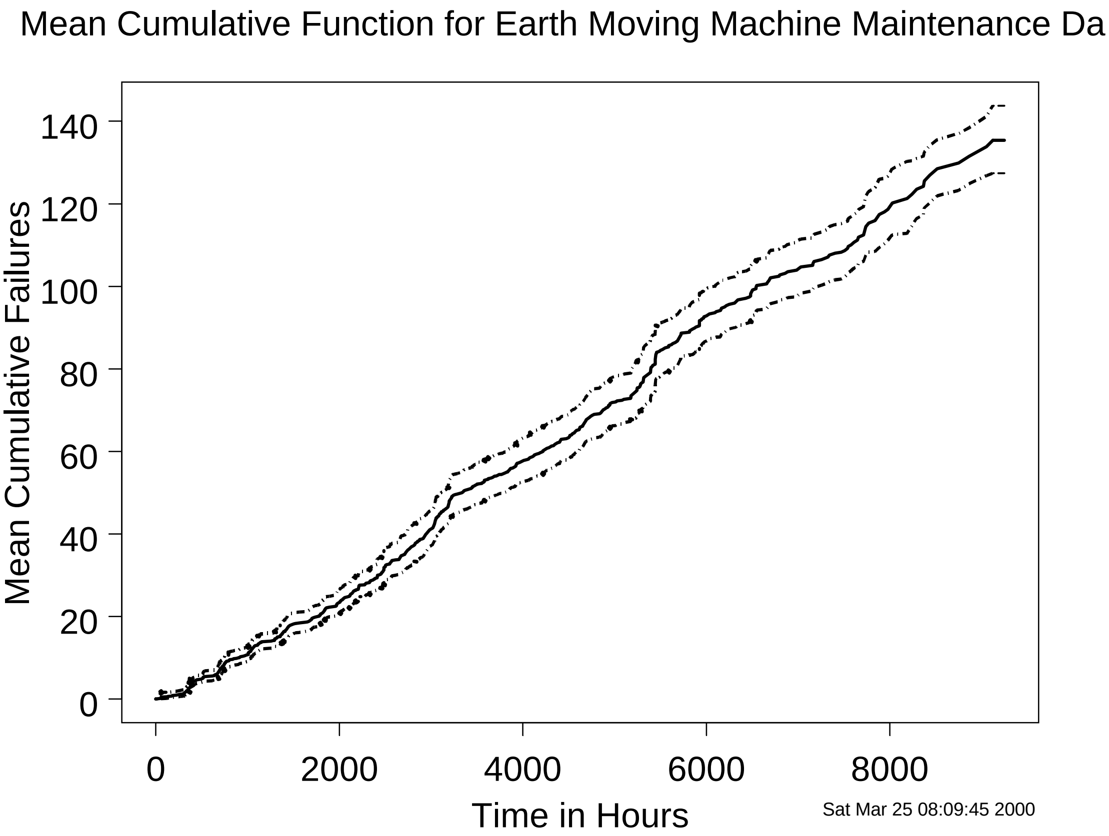
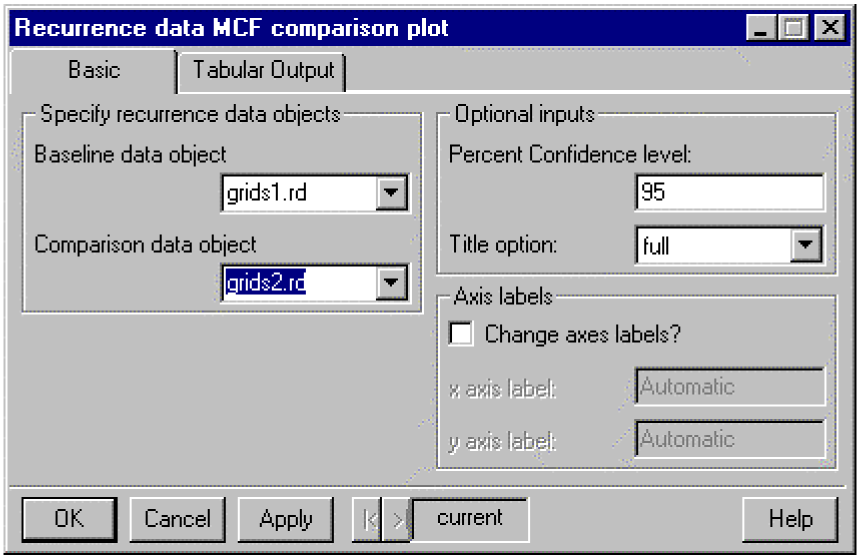


Figure 100 Mean cumulative function (MCF) plot for the earth-moving machine (Machine H) maintenance data.

11.4 Compare two mean cumulative functions

In some applications, there is a need to compare recurrence data from two fleets, manufacturers, methods, etc. The dialog obtained from **SLIDA** ➧ **Recurrence data analysis** ➧ **Compare two mean cumulative functions plot**, shown in Figure 101, allows one to request a plot making such a comparison. As an example, we use data from Doganaksoy and Nelson (1991) on the lifetime of breaking grids used in locomotives. This example was also used in Section 16.3 of Meeker and Escobar (1998). The plot in Figure 102 shows an estimate of the difference between the MCF functions for two different production batches of breaking grids along with corresponding pointwise confidence intervals. Because the zero line falls outside of the pointwise confidence interval, the plot suggests that there is a statistically important difference between the two batches.



Specify recurrence data objects

Baseline data object: grids1.rd

Comparison data object: grids2.rd

Optional inputs

Percent Confidence level: 95

Title option: full

Axis labels

☐ Change axes labels?

x axis label: Automatic

y axis label: Automatic

Figure 101 Dialog box requesting a plot comparing two mean cumulative function (MCF) plots.

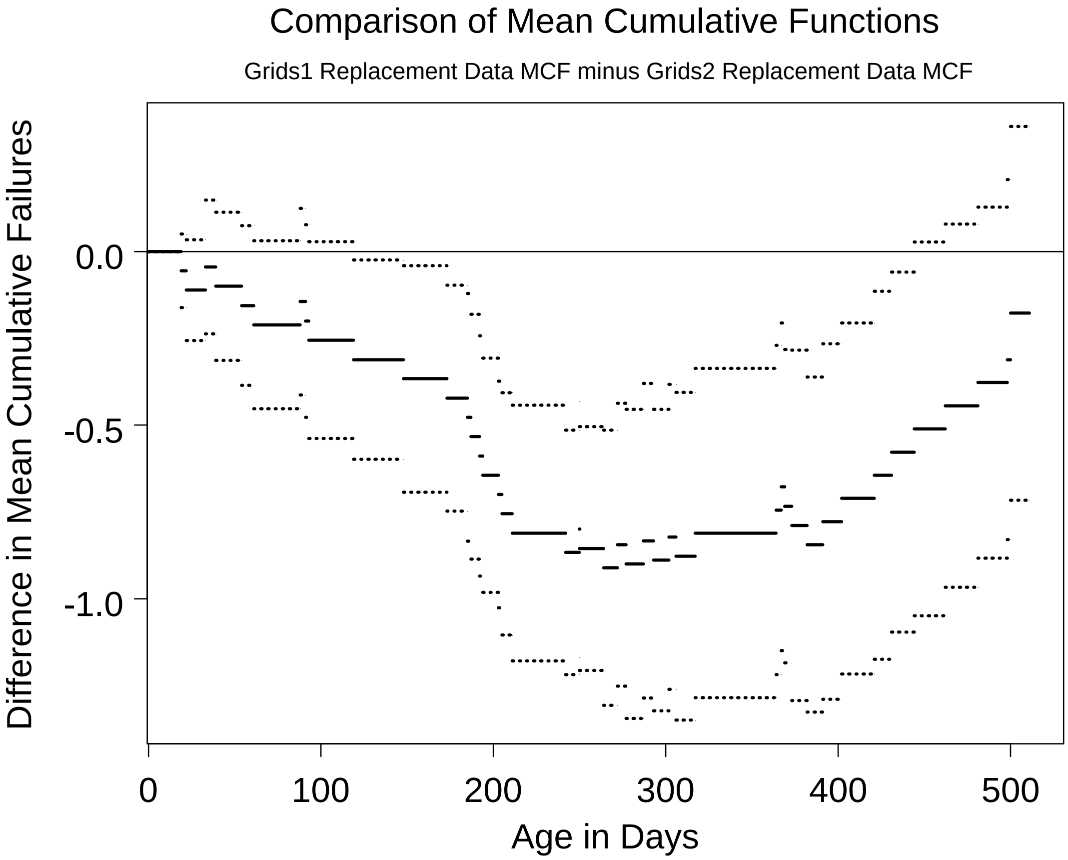


Figure 102 Plot comparing two mean cumulative function (MCF) plots.

11.5 Convert renewal recurrence data to life data (not yet available)

Using **SLIDA ➡ Recurrence data analysis➡ Convert renewal recurrence data to life data** will allow the user to convert certain kinds of recurrence data into life data. The underlying assumption that is needed for the output of the conversion to provide data that will not be misleading is that the randomness in times between events (perhaps conditioned on some explanatory variables) in the recurrence data process can be modeled adequately as a sequence of identically distributed independent observations.

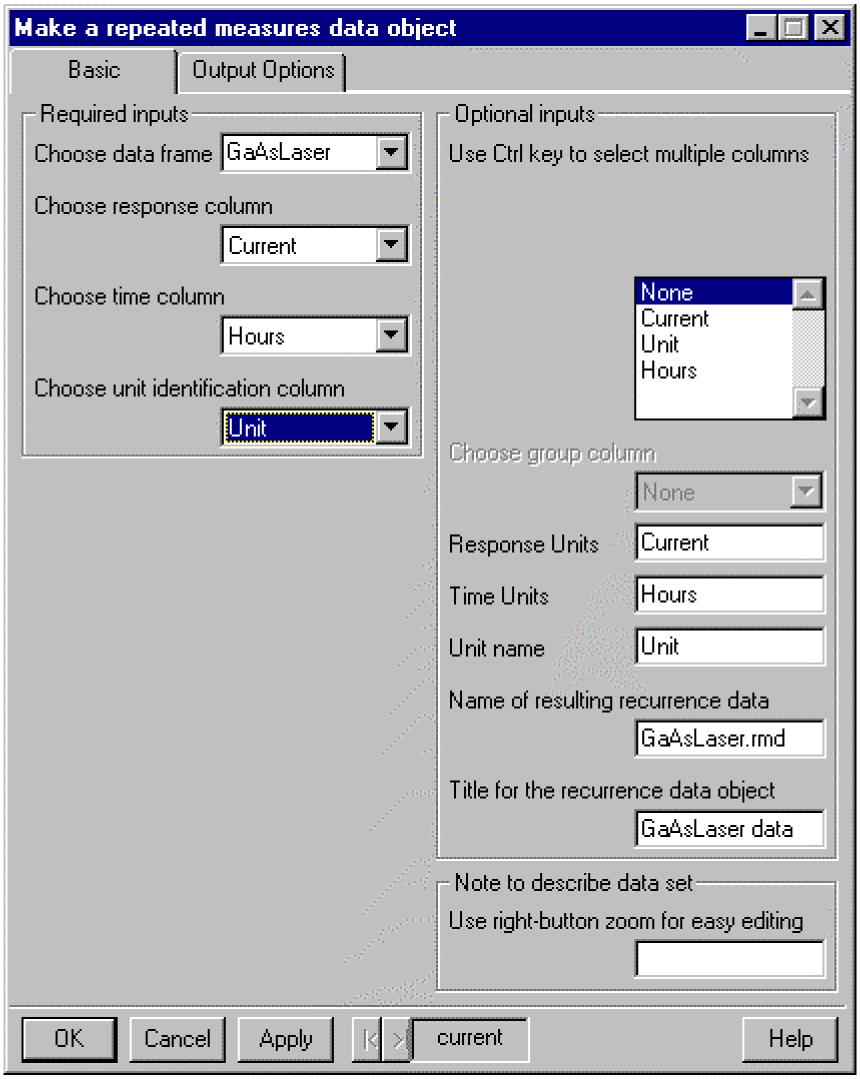
12. Degradation (Repeated Measures) Data Analysis

SLIDA provides convenient tools for doing the "simple degradation analysis" described in Chapters 13 and 21 of Meeker and Escobar (1998) and elsewhere (as indicated in their end-of-chapter bibliographic notes). In this simple method for degradation analysis, separate regression analyses are run on each individual degradation path to predict failure times (which we call pseudo failure times) for those units that have not failed. The idea is to squeeze a little more information out of one's data. This approach to degradation analysis (indeed any method of degradation analysis that will require any extrapolation) needs to have a solid basis for the underlying degradation path model. Ideally, this will be a model based on well-developed physical-chemical theory (e.g., some simple wear processes are known to be approximately linear after a break-in period). When such a physical model is not available, extrapolation may not be justified.

We do not recommend the use of model fitting and experimentation with different variable transformation in order to find, in a simple way, the relationship of "best fit" when there will ultimately be more than just a little extrapolation in time. In any case, when extrapolation is required, analyses should be accompanied by careful, systematic sensitivity analysis among a collection of models that are plausible. This sensitivity analysis is critical to obtaining an understanding of the magnitude of model uncertainty (which when extrapolating can dominate the statistical uncertainty quantified in our confidence intervals).

12.1 Make a degradation (repeated measures) data object

As with life data and recurrence data, one first has to construct a degradation data object. Because the structure of different data is different from that of life data, there is a different dialog box to making a recurrence data object. Using **SLIDA ➡ Make/summary/view data object ➡ Make a degradation (repeated measures) data object** will bring up a dialog box like that shown in Figure 103. Clicking on the Choose data frame arrow will show all of the data frames in the SLIDA database and in your working database. After choosing an appropriate repeated measures data frame, one must choose the response, time, and unit identifier (all are required for degradation data), and explanatory variables, if any. There are a number of other optional inputs or opportunities to change defaults. The example in Figure 103 uses the GaAs Laser (GaAsLaser is the data frame name) degradation data from Chapter 13 of Meeker and Escobar (1998). When the needed inputs have been specified, click on "OK" or "Apply" to create the data object. In addition to creating the degradation data object, a short summary of the data in the object is provided and, if desired a printout of the data can be requested by using the "Output Options" back page of the dialog box.



Required inputs

Choose data frame: GaAsLaser

Choose response column: Current

Choose time column: Hours

Choose unit identification column: Unit

Optional inputs

Use Ctrl key to select multiple columns

None
Current
Unit
Hours

Choose group column: None

Response Units: Current

Time Units: Hours

Unit name: Unit

Name of resulting recurrence data: GaAsLaser.rmd

Title for the recurrence data object: GaAsLaser data

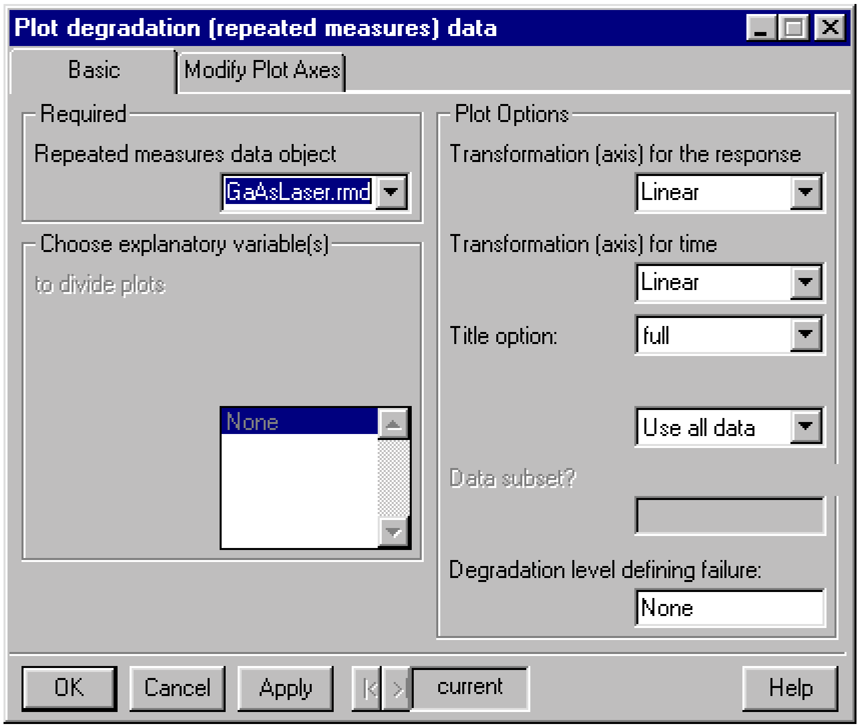
Note to describe data set

Use right-button zoom for easy editing

Figure 103 Dialog box used to make a repeated measures (degradation) data object.

12.2 Degradation data plot

Using **SLIDA ➡ Degradation data analysis➡ Degradation data plot** brings up a dialog box, like that shown in Figure 104, which can be used to request a plot of degradation paths. If there are explanatory variables, there is an option to group paths by explanatory variable levels, instead of plotting all paths on a single graph. It is possible to request special axes transforms (e.g., linear, log, or square root axes) to plot either time or the response. The Modify Plot Options page allows one to control the ranges of the plot axes.


Plot degradation (repeated measures) data

Required

Repeated measures data object: GaAsLaser.rmd

Choose explanatory variable(s) to divide plots: None

Plot Options

Transformation (axis) for the response: Linear

Transformation (axis) for time: Linear

Title option: full

Use all data

Data subset?

Degradation level defining failure: None

Figure 104 Dialog box to request a plot of degradation data for the GaAs Laser data.

Figure 105 shows a simple degradation plot for the GaAs laser data.

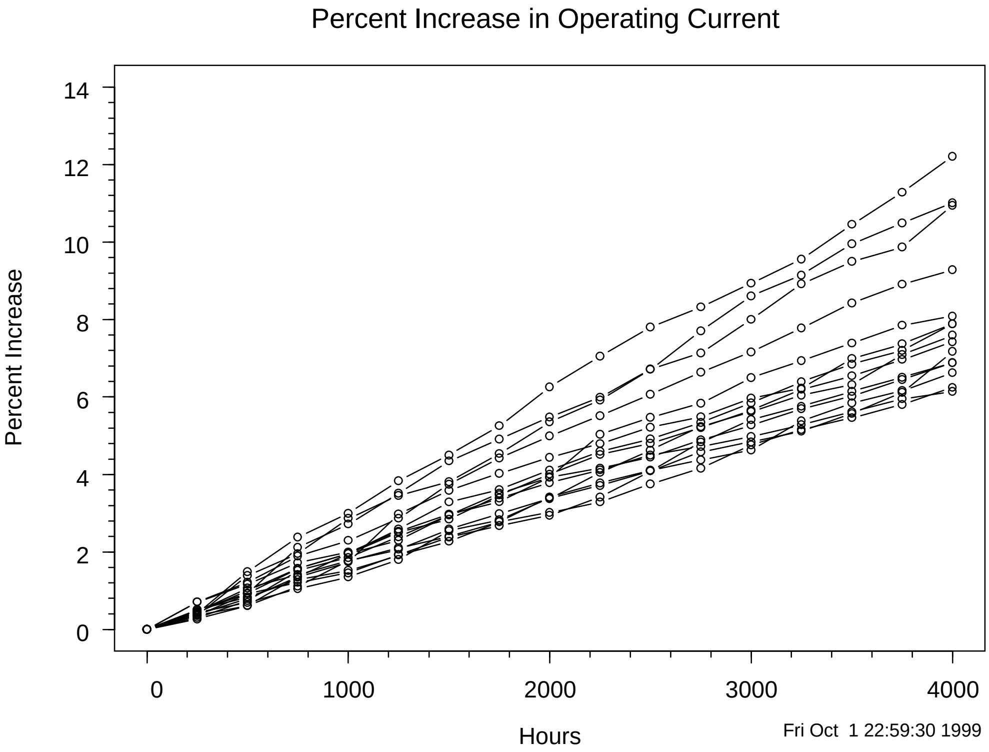
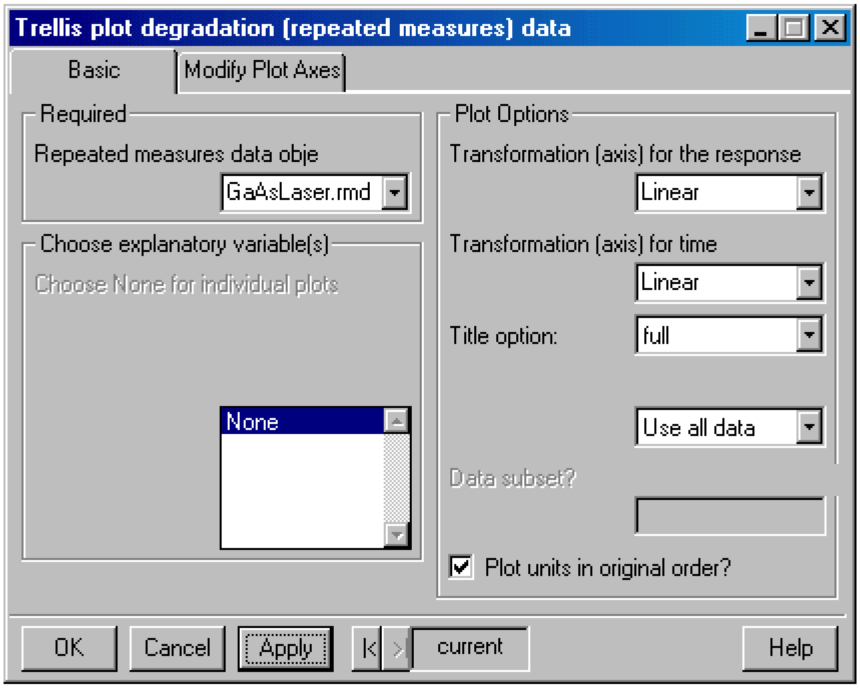


Figure 105 Plot of degradation data for the GaAs Laser data.

12.3 Degradation data trellis plot

Using **SLIDA** ➡ **Degradation data analysis**➡ **Degradation data trellis plot** brings up a dialog box like that shown in Figure 106. This dialog box is used to request a trellis plot of degradation paths. If there are explanatory variables, there is an option to group paths by explanatory variable levels, although the individual plots, as illustrated in Figure 107, are recommended because they can be importantly revealing.



Repeated measures data obje: GaAsLaser.rmd

Choose None for individual plots: None

Transformation (axis) for the response: Linear

Transformation (axis) for time: Linear

Title option: full

Use all data

Data subset?

☑ Plot units in original order?

Figure 106 Dialog box to request a trellis plot of the GaAs laser degradation paths.

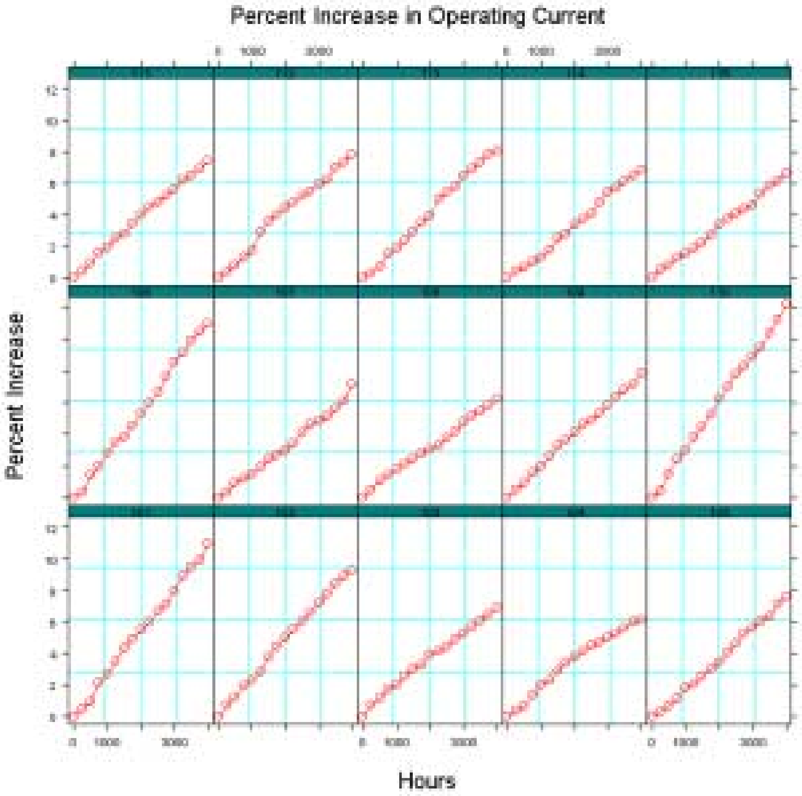
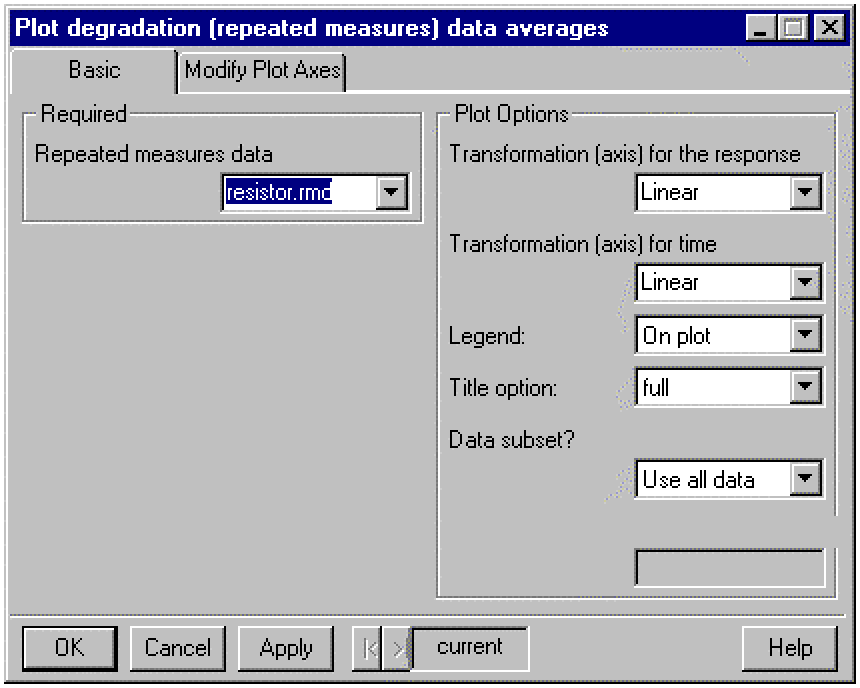


Figure 107 Trellis plot of the GaAs laser degradation paths.

12.4 Accelerated degradation cell-average plot

Many degradation experiments are run at accelerated conditions (e.g., high temperature) in order to accelerate the degradation process. A useful plot for such data is a cell-average plot giving the average degradation as a function of time for the different level(s) of an explanatory variable. Averages are computed across all units at combinations of the chosen explanatory variables The following example uses the resistor data (three levels of temperature) to make such a plot. The plot gives a good visual indication of the effect of temperature on degradation rate. Using **SLIDA** ➡ **Degradation data analysis**➡ **Accelerated degradation cell-average plot** brings up the dialog box in Figure 108.



Repeated measures data: resistor.rmd

Transformation (axis) for the response: Linear

Transformation (axis) for time: Linear

Legend: On plot

Title option: full

Data subset? Use all data

Figure 108 Dialog box requesting a plot of the average reading of all units at the different temperatures for the carbon-film resistor degradation data.

Figure 109 shows the resulting cell-average plot for the resistor degradation data.

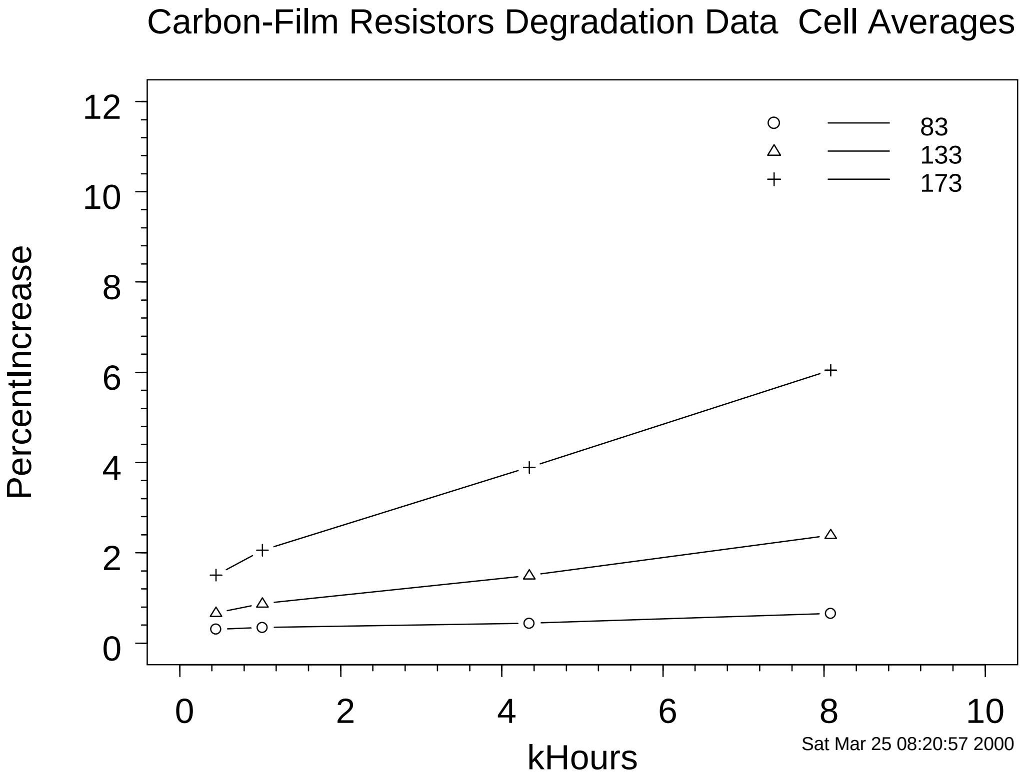
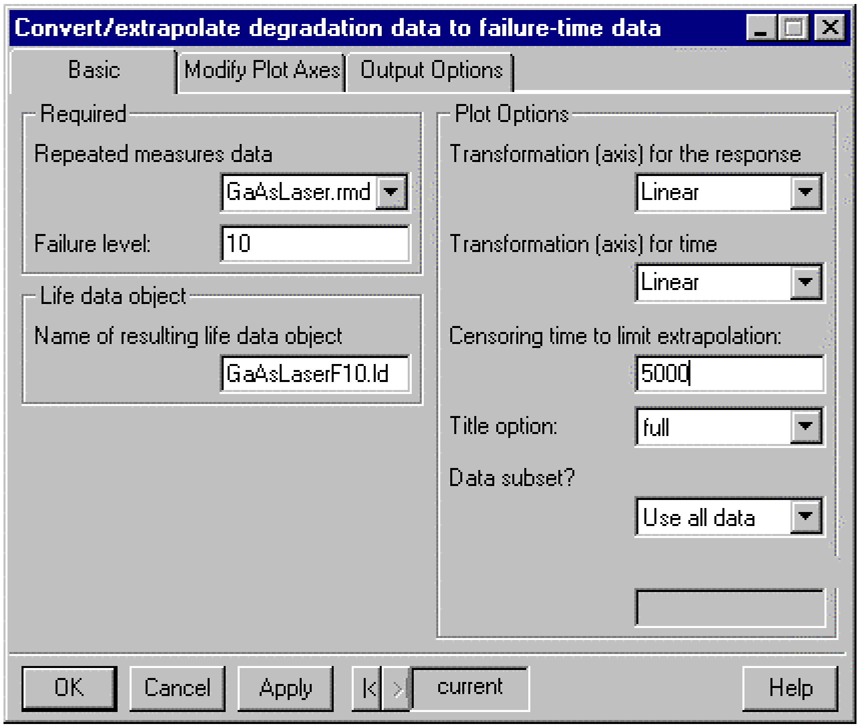


Figure 109 Plot of the average reading of all units at the different temperatures for the carbon-film resistor degradation data.

12.5 Convert/extrapolate data to failure-time data

The so-called “simple degradation analysis” method mentioned at the beginning of this section fits a specified model to each of the sample paths in an effort to “squeeze” a little more information out of such data by exptrapolating the paths (or some of the paths) to predict the time of failure. Then the “pseudo failure times” are analyzed using the standard methods for failure-time data. The conversion of degradation path data to failure-time data can be done easily with the **SLIDA ➡ Degradation data analysis ➡ Convert/extrapolate data to failure-time data** dialog. It is necessary to specify the repeated measures (degradation) data object and the degradation level defining failure. For the GaAs lasers, failure was defined as the time at which 10 mA of current was needed to provide a specified (constant) amount of light output. It is also possible to specify a maximum time (a pseudo censoring time), beyond which no failures are extrapolated. For the GaAs lasers, focus was on the lower quantiles of the failure-time distribution and thus the paths were extrapolated only to 5000 hours, where 6 out of 15 lasers had failed (i.e., had predicted current greater than 10 mA). As in the dialog box for plotting degradation paths, on has a choice of axis scales (e.g., linear, square root, or log). These same transformations are also used to determine the scale in which to fit the linear regression lines used to extrapolate the degradation paths to the compute the pseudo failure times. The effect of this choice can be quite pronounced (especially in the dangerous and discouraged practice where one is extrapolating far in time) and in the absence of strong physical motivation for one or the other, sensitivity analysis is strongly recommended.



Required

Repeated measures data: GaAsLaser.rmd

Failure level: 10

Life data object

Name of resulting life data object: GaAsLaserF10.ld

Plot Options

Transformation (axis) for the response: Linear

Transformation (axis) for time: Linear

Censoring time to limit extrapolation: 5000

Title option: full

Data subset? Use all data

Figure 110 Dialog box requesting that the GaAs laser degradation date be mapped into pseudo failure time data using 10 mA as the definition of failure and a censoring time of 5000 hours.

After clicking on “OK” or “Apply,” Slida procudes the plot in Figure 111 showing the degradation paths and extrapolations to the fiailure level of censoring time (which ever comes first) and the life data object GaAsLaserF10C5000.XLinear.YLinear.ld is available for doing failure-time analysis. Note that the default name (which could have been edited) reflects the failure definition level, pseudo censoring time, and the transformation/axes used in generating the pseudo faulure times. Such descriptive names are useful because analysts will often want to experiment with different choices for some or all of these and the automatic coding makes it easy to do such experiments and to compare the results of different analyses using all of the previously described tools for such data.

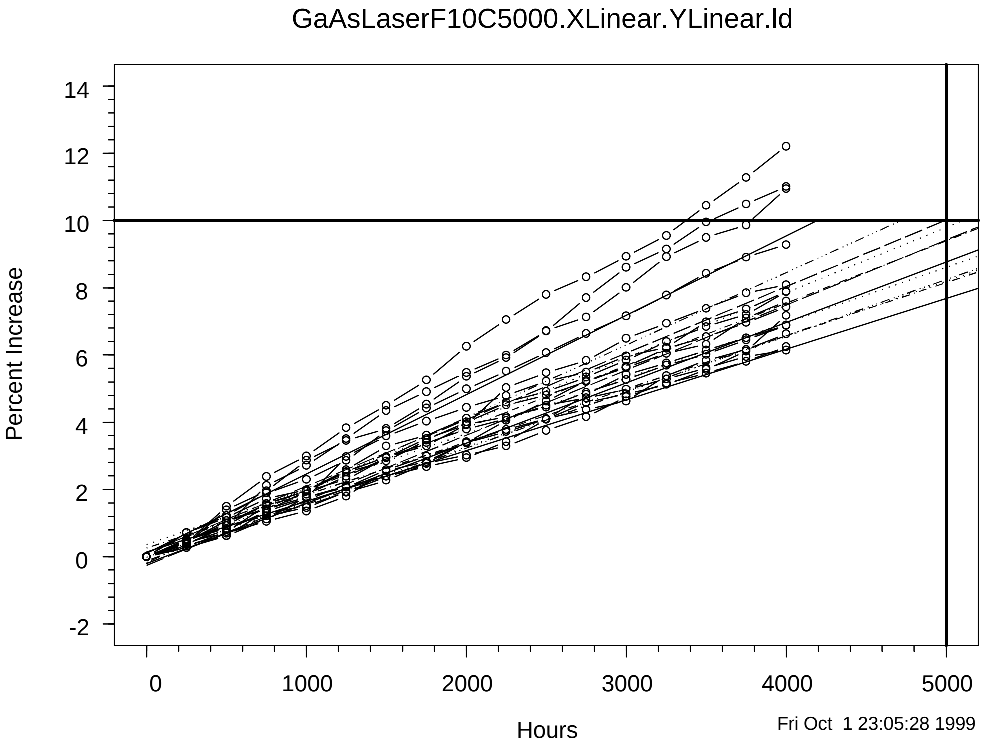


Figure 111 Plot showing the GaAs laser degradation data being mapped into pseudo failure time data using 10 percent as the definition of failure and a censoring time of 5000 hours.

Figure 112 is an event plot showing the six pseudo failure times and the nine observations censored at 5000 hours in `GaAsLaserF10C5000.XLinear.YLinear.ld`. In this example, the amount of extrapolation is small (especially because no extrapolation was done beyond 5000 hours) and the degradation paths are well behaved. Thus, the pseudo failure times should provide reasonably good predictions for the actual failure times.

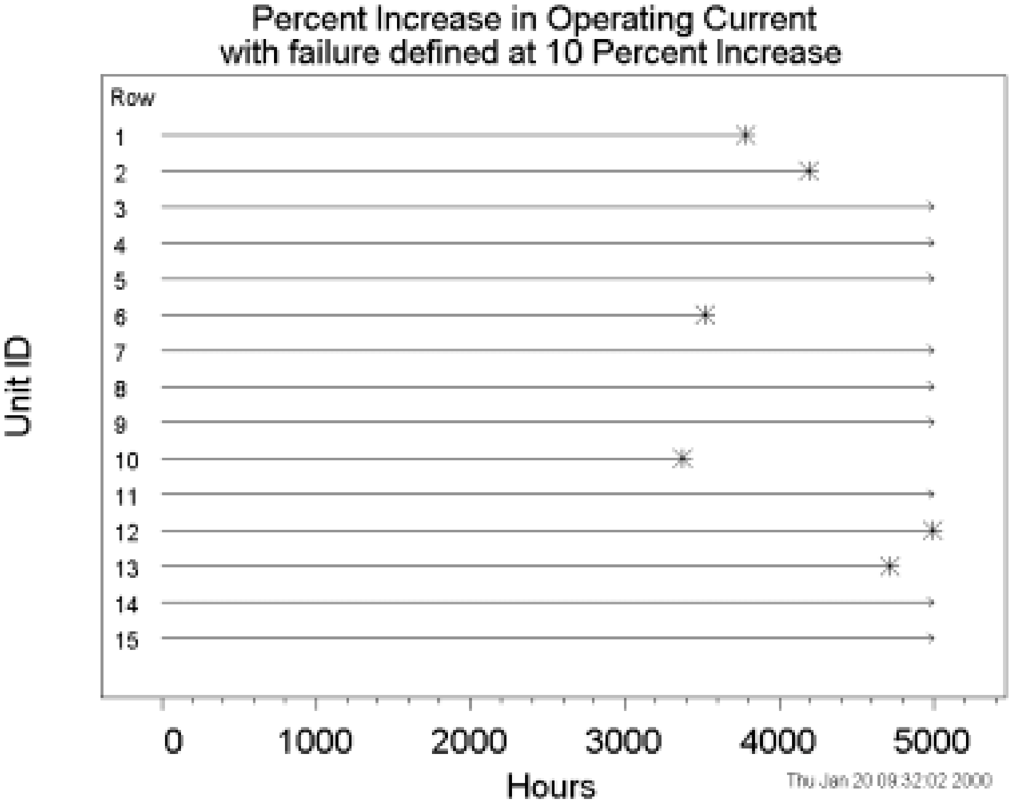
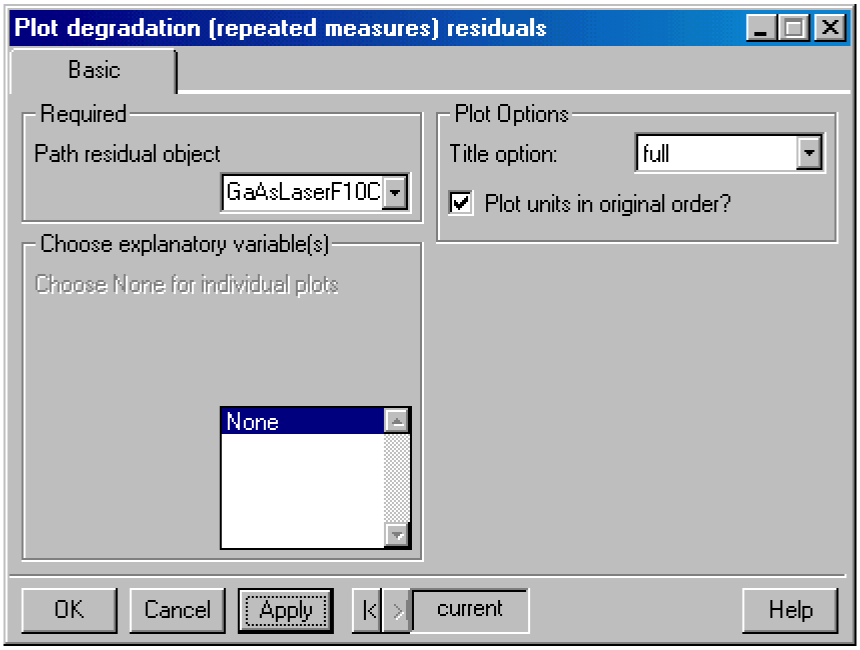


Figure 112 Event plot showing the predicted failure times for the GaAs laser degradation experiment.

12.6 Degradation residual trellis plot

We have emphasized the importance of having a solid basis for any model used in extrapolation of sample degradation paths. Whether or not such a model is available, it is important to assess the adequacy of the fitted models to the degradation paths. If the model does not even fit the data within the range of the data, careful consideration should be given to the usefulness of the data for purposes of predicting a failure-time distribution. Of course, one should always remember that just because the model provides a good fit to the data and may be adequate for making predictions within the range of the data, there is no guarantee that the degradation process will continue to follow the fitted model outside of the range of the available data.

The dialog box in Figure 113 allows the user to request a trellis plot of residuals for the straight lines fit to (possibly transformed) degradation data. Such plots help one to detect systematic departures from the fitted model. Figure 114 shows the residual trellis plot for the GaAs laser data. For this example, there appears not to be any systematic departures from the fitted straight-line model.



Plot degradation (repeated measures) residuals

Required

Path residual object: GaAsLaserF10C

Choose explanatory variable(s)

Choose None for individual plots

None

Plot Options

Title option: full

☑ Plot units in original order?

Figure 113 Dialog box to request a residual trellis plot for each of the GaAs laser data regression lines.

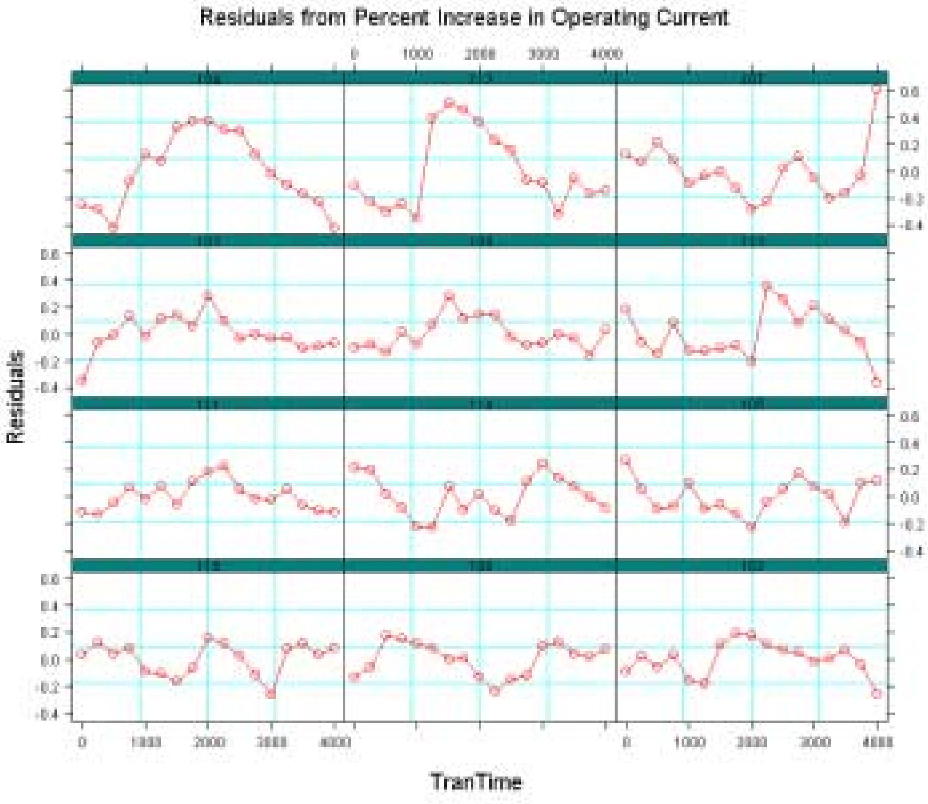


Figure 114 Trellis plot of residuals for each degradation path for the GaAs laser data.

13. Special Models

13.1 Generalized gamma distribution

SLIDA ➡ Special models ➡ Generalized gamma distribution

13.2 Limited failure population model

SLIDA ➡ Special models ➡ Limited failure population model

13.3 Generalized (two failure modes) limited failure population model

SLIDA ➡ Special models ➡ Generalized (two failure modes) limited failure population model

13.4 Random fatigue limit model

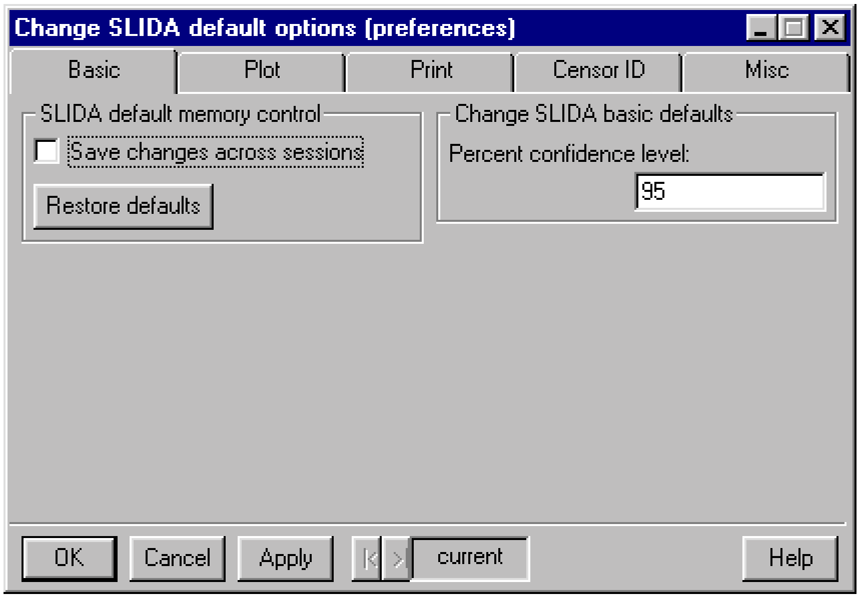
SLIDA ➡ Special models ➡ Random fatigue limit model

13.5 Two-dimensional warranty bivariate model

SLIDA ➡ Special models ➡Two-dimensional warranty bivariate model

14. Changing SLIDA Default Options

Using **SLIDA ➡ Change SLIDA default options** will bring up the dialog box shown in Figure 115, allowing one to make global changes to the several of the SLIDA defaults options. Some of these options were discussed in Sections 2.5 and 2.6. Changes are effected immediately after chosen on the dialog pages (no need to click on "OK" or "Apply"). Changes made when the "Save changes across sessions" box is checked are saved across sessions. To restore the original SLIDA defaults, click on the "Restore defaults" box. To erase across session changes, click on the Restore defaults" box when when the "Save changes across sessions" box is checked.

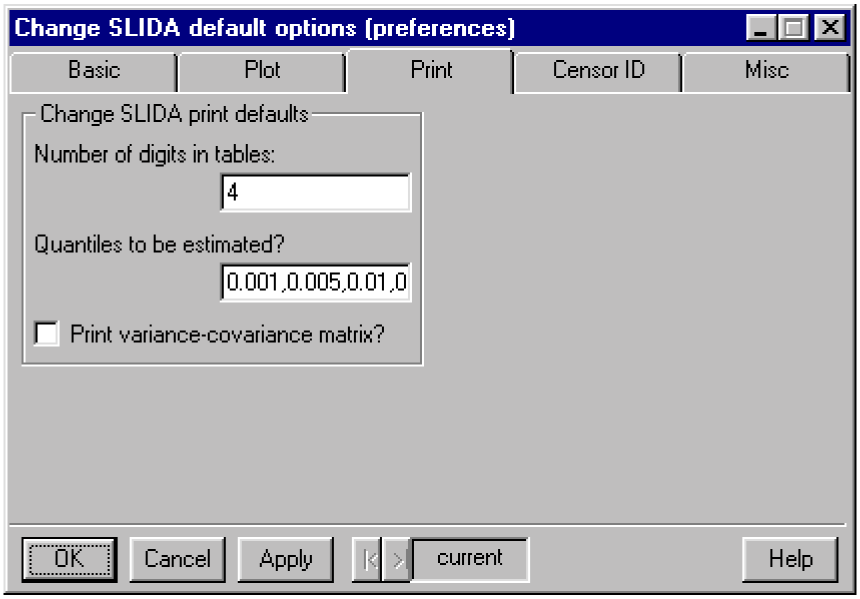


☐ Save changes across sessions

Percent confidence level: 95

Figure 115 Basic page of the dialog box for changing SLIDA operation defaults.

Figure 116 shows the “Print “option page of the dialog box, which allows changing the default number of digits used in SLIDA tabular output, the default list of quantiles to be estimated, and an option to print out the variance-covariance matrix of ML estimates when such estimation is performed.



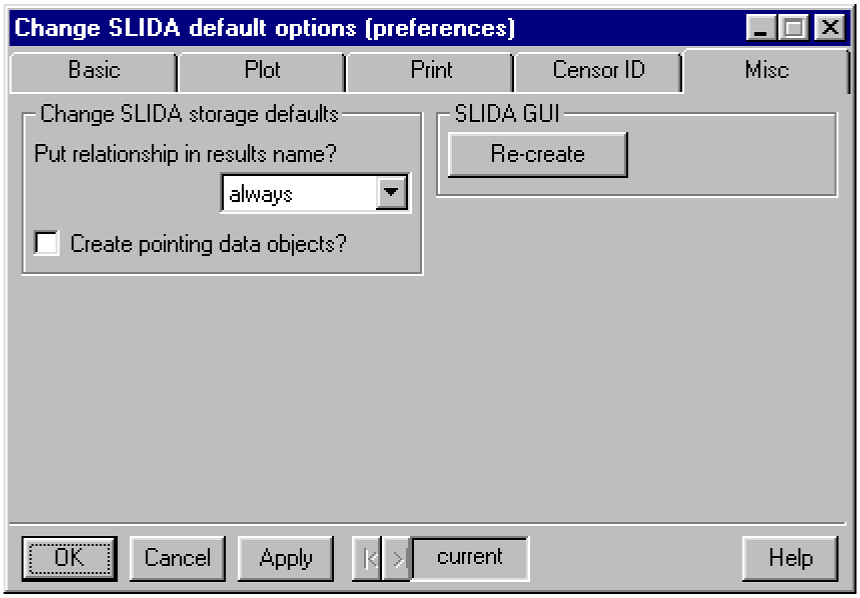
Number of digits in tables: 4

Quantiles to be estimated? 0.001,0.005,0.01,0

☐ Print variance-covariance matrix?

Figure 116 Print option page of the dialog box for changing SLIDA operation defaults.

The “Misc” page, shown in Figure 117, allows the user to choose whether to save the regression relationship in ML estimation results objects (the choices are: always, never, and multiple regression only). If the check box is checked, then when a life data object is created, the main part of the object is a character string giving the name of the data frame to use as part of the data object. Otherwise, the main part of the data object is the data frame itself. For most purposes, the difference between using these two different options is transparent to the user. For some kinds of analyses, the character string version may use less memory. The data frame objects are easier to use when it is desired to manually choose a subset of the data for analysis.



Put relationship in results name? always

☐ Create pointing data objects?

Figure 117 Misc page of the dialog box for changing SLIDA operation defaults.

The “Misc” page, in Figure 117, also allows one to recreate the SLIDA GUI. This is most useful when a new version of SLIDA has been installed on your system. Clicking the Recreate button will modify the S-PLUS _Prefs directory in the current working folder (most users have separate working folders for different projects and these would not otherwise be updated when a new version of SLIDA is installed elsewhere in the system).

15. SLIDA Setup and Operation

SLIDA is distributed as a self-extracting executable file Slida.exe. When Slida.exe is executed, it creates a folder (c:\Slida by default) that contains other folders and files. This is the "Slida folder." A snapshot of the inside of this folder is given in Figure 118.

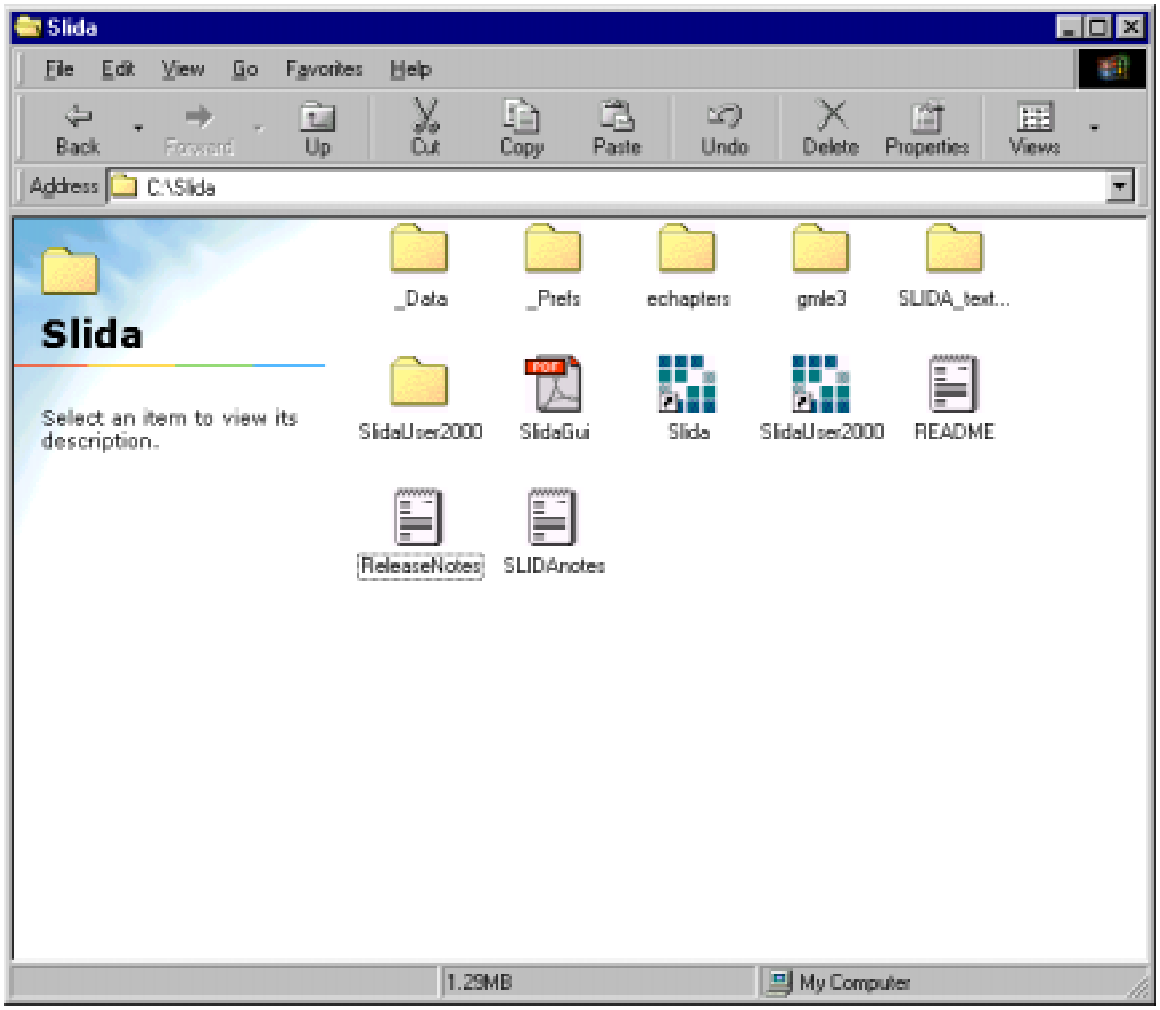


Figure 118 View inside the Slida folder

There are two different approaches for setting up SLIDA for operation. The first method, explained in Section 15.2, is a little simpler, but less flexible. It is appropriate only for a single user on a desktop computer and only allows the use of one project folder. The second method, described in Section 15.3, is more flexible and is preferred. It allows for multiple project folders (e.g., for different projects or different users sharing the same computer). It is possible to start with the first method and then subsequently create the alternative folders and shortcuts to use SLIDA in the more flexible mode.

15.1 Installing updated version of SLIDA

To install an updated version of SLIDA over an existing version, simply follow the same steps used in the initial install, outlined in step a) below, installing in the same location, using the default WinZip option to overwrite any old files.

15.2 New setup for Single-user/Single-project SLIDA operation

To install SLIDA:

a. Move theSlida.exe file to some location (like your Desktop) and double-click to execute the file. The WinZip self-extracting file will prompt you to ask if you can to change the default directory from C:\SLIDA. It is ok to change this, but the location of the Slida folder will then be different from that indicated in these instructions, requiring, for example, some minor changes in short cut properties.

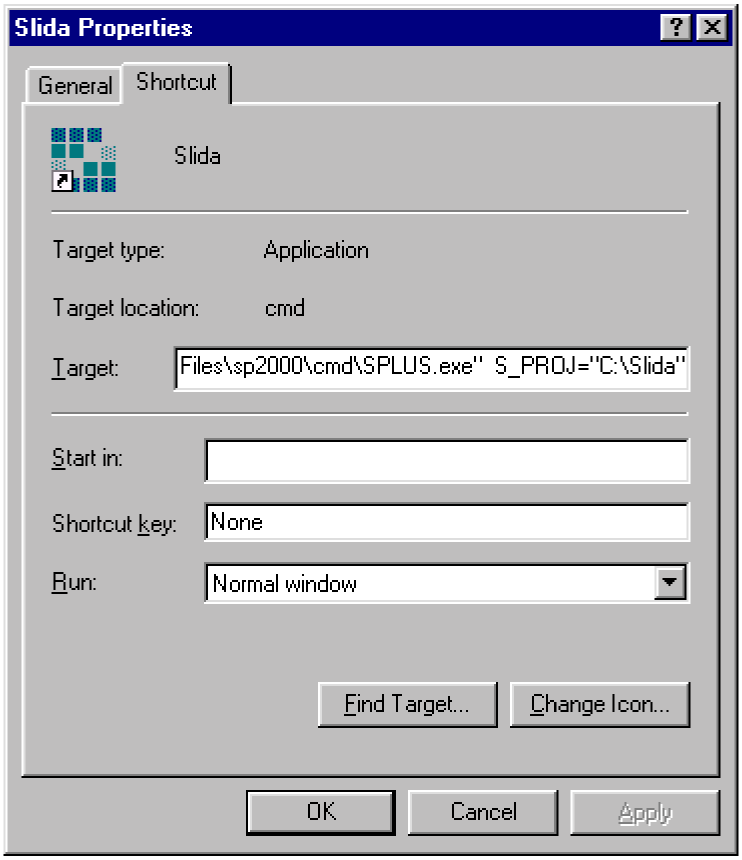
b. Create a copy of the S-PLUS startup icon shortcut (right-click on and drag the S-PLUS icon; release the right mouse button, and choose "copy"). Right click on the new icon and choose "properties" under "shortcut." This will bring up a dialog box like that shown in Figure 119. Set S_PROJ on the "Target" command line (note: do this on the "Target" and not on the "Start in" command line) of this shortcut to read:

   ```
   "c:\Program Files\sp2000\cmd\splus.exe" S_PROJ="c:\SLIDA"
   ```

   where "c:\Program Files\sp2000\cmd\splus.exe" is the existing path to S-PLUS and depends on the version of S-PLUS and the option used when S-PLUS was installed. Do not change the first part of this line. Only add the S_PROJ="c:\SLIDA" to the end of the line. ***Make sure there is a space between before the `S_PROJ="c:\SLIDA"`.*** After typing the S_PROJ="c:\SLIDA", click on "apply" and "Close." Then rename the new S-PLUS icon to S-PLUS_SLIDA or something similar (right-click on the icon to get choices including rename). A sample shortcut using the above default folder names is given in the Slida folder (c:\Slida). The shortcut tab page of the Slida shortcut Properties dialog box is shown in Figure 119.

c. Fire up S-PLUS using the S-PLUS_SLIDA icon.

To use SLIDA for analyzing data, you can use either the GUI or the command line (if you have the “Professional” version of S-PLUS).



Slida

Target type: Application

Target location: cmd

Target: Files\sp2000\cmd\SPLUS.exe" S_PROJ="C:\Slida"

Start in:

Shortcut key: None

Run: Normal window

Figure 119 Shortcut tab page of the Slida shortcut Properties dialog box

15.3 Creating multiple SLIDA project folders and using SLIDA on a shared computer

As described in the Section 15.2, after executing the Slida.exe install file and setting up a shortcut, SLIDA is ready to operate. In some situations, however, it may be desirable to set up an alternative folder or folders in which to run SLIDA. In particular, some S-PLUS users like to use separate startup folders for different projects, so that created objects do not get confused from one problem to another. Similarly, if different users work on the same computer usually they would want to operate using separate S-PLUS/SLIDA startup files. In addition, it may be desirable (on NT and Windows2000 computers) to install SLIDA in a write-protected folder to reduce any chance that files in the folder will become corrupted. The SLIDA folder (found atcC:\Slida by default) contains folders two example SlidaUser folders (SlidaUser2000 and SlidaUser45, respectively, for S-PLUS versions 2000 and 4.5) and corresponding shortcuts pointing to these folders.

Start by doing step a) in the Section 15.2 to install the SLIDA folder. If you copy a SlidaUser folder to C:\, and if SLIDA was installed in C:\, then the given SlidaUser shortcut can be copied to the desktop and used without change. Otherwise, some minor adjustments are needed. In particular, the SlidaUser shortcut properties must point to both the location of S-PLUS and the SlidaUser folder. The file path.txt in the SlidaUser folder must point to the place where SLIDA was installed.

In general, to set up a user- or project-specific folder to operate SLIDA, do the following (note the distinction between the SLIDA folder, the SlidaUser folders, and the SlidaUser shortcuts in the following instructions):

a. Make a ***copy*** of the appropriate SlidaUser ***folder*** (either SlidaUser2000 or SlidaUser45, depending on which version of S-PLUS you are running) in a convenient place (e.g., in C:\) and, if desired, give the folder a new name, say corresponding to a user's name or a project name.

b. If the Slida folder was installed in a place other than the default C:\Slida, the file Path.txt in the SlidaUser folder should be modified (e.g. using notepad) to point to the location of SLIDA (note that the \\ in this file is necessary when specifying a path name to S-PLUS). The SlidaUser folder can be copied and renamed as many times as necessary to create separate S-PLUS/SLIDA startup folders.

c. Make a ***copy*** of the appropriate SlidaUser shortcut (either SlidaUser2000 or SlidaUser45, depending on which version of S-PLUS you are running) in a convenient place (e.g., the desktop) and, if desired, give the shortcut a new name.

d. Right-click on the shortcut, choose properties, and go to the shortcut tab. E If necessary, edit the target line so that the first part points to S-PLUS (looking at an existing shortcut to S-Plus will show how to do this). Then, on the right-hand side of the target line, edit the S_PROJ="C:\SlidaUser2000" so that it points to the location of your particular SlidaUser folder (or what ever name the folder now has) and its location.

15.4 Making or remaking the SLIDA menu structure and startup folders

SLIDA is distributed with a Windows folder (in c:\Slida by default) containing a _Prefs folder that contains the definition of the SLIDA menu structure and a _Data folder containing a .First function that attaches the SLIDA object folders and loads the SLIDA life data analysis symbols. When you attempt to use S-PLUS in a target folder that does not contain either the _Prefs or the _Data folder, they are generally created automatically by S-PLUS (S-PLUS first asks if you want to do this), but when these folders are created by S-PLUS, they will not be set up to run SLIDA. The SlidaUser contains SLIDA-specific _Prefs and _Data folders, modified so that they can operate in locations other than inside the SLIDA folder.

If you are using the "professional" version of S-PLUS and, for some reason, you would like to regenerate the SLIDA/S-PLUS _Prefs folder from scratch, follow the following steps (you need the Professional version of S-PLUS to do this):

a. Delete the _Prefs folder in the SLIDA/S-PLUS target folder.
b. Fire up S-PLUS using a shortcut that points to the target folder (e.g., SlidaUser).
c. When S-PLUS warns you that _Prefs and/or _Data are missing, click OK.
d. Give the command **make.slida.gui( ).** Depending on the speed of your machine, it will take from 2 to 5 minutes to finish this setup. When done, S-PLUS will be operating with the default S-PLUS setup (which differs slightly from the SLIDA setup).

If you are usingthe standard version if S-PLUS, you can rebuild the SLIDA GUI with **SLIDA ➡ Change SLIDA default options**, selecting the Misc tab, and clicking on "Re-ceate SLIDA GUI."

15.5 Comments on using SLIDA (and S-PLUS) on Windows

a. If S-PLUS seems to be hanging or taking too long to execute, you can type <ESC> to break out of a command.
b. If graphics window becomes corrupted, try the S-PLUS command refresh( ). Alternatively, kill the graphics window (by clicking the x in the upper right-hand corner of the graphics window). A fresh graphics window will be started.
c. As you use S-PLUS over a period of time, memory usage can build up, and it may be necessary (especially if you are only working with 32 MB of memory) to restart S-PLUS. The command check.memory( ) will allow you to monitor this. If you can afford it, install more memory. I

noticed a big improvement when going from 32 MB to 64 MB, and now I use 128 MB or better. In extreme cases, S-PLUS may hang and it may be necessary to reboot your machine (. I do not know whether to blame this on S-PLUS or Windows, but it is clear to me that when taxing the resources of Windows, operation can get a bit flaky.

16. Outline of the SLIDA Menu Structure

The following table contains an outline of the SLIDA menu structure. The GUI dialog boxes for the items shown in regular-faced type **are still in development.**

- **SLIDA ➡**
  - **Make/summary/view data object ➡**
    - **Make a life data object**
    - **Make recurrence (point-process) data object**
    - **Make degradation (repeated measures) data object**
    - **Summary/view a data object**
    - **Edit a life data object**
  - **Plan single distribution study ➡**
    - **Specify life test planning information (planning values)**
    - **Plot life test planning information (planning values)**
    - **Plot of approximate required sample size**
    - **Simulate a life test**
    - **Probability of successful demonstration**
  - **Single distribution life data analyses ➡**
    - **Plot nonparametric estimate of cdf and confidence bands**
    - **Probability plot with nonparametric confidence bands**
    - **Probability plot with parametric ML fit**
    - **Likelihood contour plot**
    - **Compare distribution ML fits on probability plot**
    - **Threshold parameter probability plot with parametric ML fit**
  - **Multiple failure mode life data analysis ➡**
    - **Individual modes**
    - **Combined modes (with one or more omitted)**
    - **Make life data objects for individual modes**
  - **Comparison of distributions life data analysis ➡**
    - **Probability plot and ML fit: different shapes (slopes)**
    - **Comparison likelihood contour plot**
    - **Probability plot and ML fit: common shapes (slopes)**
    - **Make life data objects for individual groups**
    - **Probability of correct selection for specified test plans**
  - **Plan an accelerated life test (ALT) ➡**
    - **Specify an ALT model information (planning values)**
    - **Specify an ALT test plan**
    - **Plot, summarize, and evaluate an ALT test plan**
    - **Simulate an ALT test**
  - **Simple regression (ALT) data analysis ➡**
    - **Censored data scatter plot**
    - **Probability plot and ML fit for individual conditions**
    - **Prob plot and ML fit for indiv cond: common shapes (slopes)**
    - **Probability plot and ML fit of a regression (acceleration)**

  - **Make life data objects for individual groups**

- **Multiple regression (ALT) life data analysis ➡**
  - **Censored data pairs plot**
  - **Censored data scatter plot**
  - **Probability plot and ML fit for individual conditions**
  - **Prob plot and ML fit for indiv cond: common shapes (slopes)**
  - **Probability plot and ML fit of a regression (acceleration)**
  - **Conditional stress plot**
  - **Sensitivity analysis plot**
  - **Make life data objects for individual groups**

- **Regression residual analysis ➡**
  - **Residuals versus fitted values**
  - **Residuals versus possible explanatory variables**
  - **Residuals versus observation order**
  - **Residual probability plot**

- **Recurrence (point process) data analysis➡**
  - **Recurrence event plot**
  - **Mean cumulative function plot**
  - **Compare two mean cumulative functions plot**
  - **Convert renewal recurrence data to life data**

- **Degradation (repeated measures) data analysis➡**
  - **Degradation data plot**
  - **Degradation data trellis plot**
  - **Accelerated degradation cell-average plot**
  - **Convert/extrapolate degradation data to life data**
  - **Degradation residual plot**

- **Special models ➡**
  - **Extended generalized gamma (EGENG) distribution**
  - **Limited failure population (LFP) model**
  - **Dead on arrival (DOA) population model**
  - **Generalized (two failure modes) limited failure population model**
  - **Random fatigue limit (RFL) model**
  - **Two-dimensional warranty bivariate model**

- **Change SLIDA default options (preferences)**

17. Acknowledgements

Numerous individuals have provided valuable feedback to help with the development of SLIDA and the writing of this documentation. Many of our students made helpful suggestions when earlier versions of the software were used in short courses at Hewlett Packard and Ford Motor Company as well as in our university courses. We also would particularly like to thank Marci Conors, Danny Kluger, Victor Morin, Wayne Nelson, Chris Stanard, and Steve Zayac for their encouragement and helpful comments. Helpful comments and suggestions have also been received from Chuck Annis, José Ramirez, and David Olwell.

18. References

Abernethy, R. B., Breneman, J. E., Medlin, C. H., and Reinman, G. L. (1983), *Weibull Analysis Handbook*, Air Force Wright Aeronautical Laboratories Technical Report AFWAL-TR-83-2079. Available from the National Technical Information Service, Washington, DC.

Doganaksoy, N., and Nelson, W. (1991), A method and computer program MCFDIFF to compare two samples of repair data, TIS report 91CRD172, General Electric Company Research and Development, Schenectady, NY.

Doganaksoy, N., and Nelson, W. (1998), A method to compare two samples of recurrence data, Lifetime Data Analysis 4, 51-63.

Escobar, L. A., Pascual, F. G., and Meeker W. Q. (2000), Planning life tests to compare two or more products. In preparation.

Hooper, J. H., and Amster, S. J. (1990), Analysis and presentation of reliability data, in *Handbook of Statistical Methods for Engineers and Scientists*, Harrison M. Wadsworth, Editor. New York: McGraw Hill.

Meeker, W. Q., and Escobar, L. A. (1991), *Statistical Methods for Reliability Data*, New York: John Wiley & Sons.

Nelson, W. (1982), *Applied Life Data Analysis*, New York: John Wiley & Sons.

Nelson, W. (1990a), Accelerated Testing: *Statistical Models Test Plans, and Data Analyses*, New York: John Wiley & Sons.

Singpurwalla, N. D., Castellino, V. C., and Goldschen, D. Y. (1975), Inference from accelerated life tests using Eyring type re-parameterizations, *Naval Research Logistics Quarterly*, 22, 289--296.