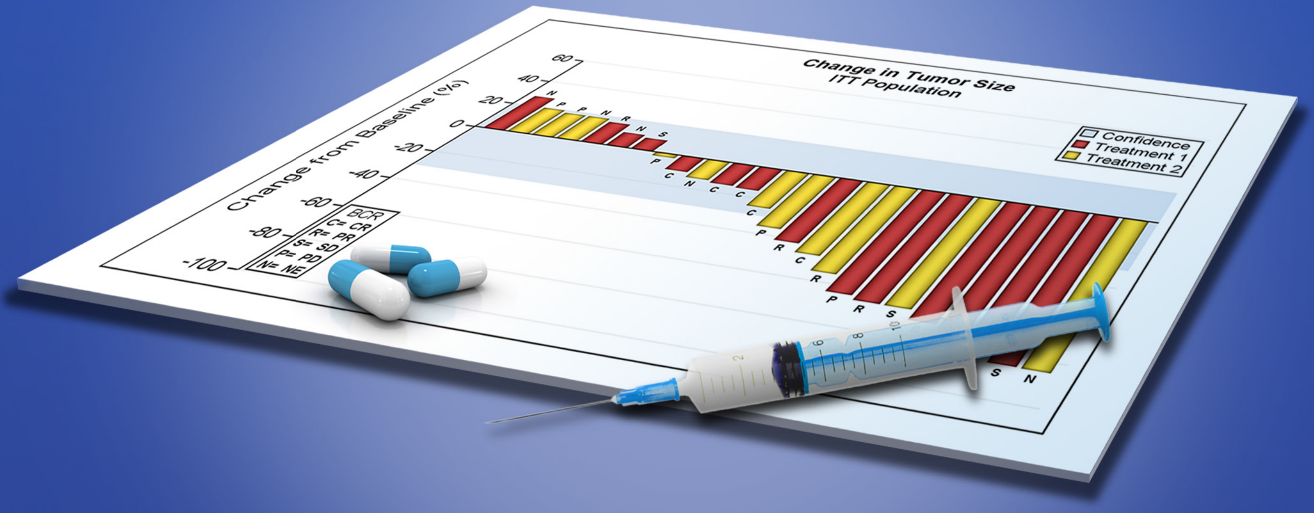
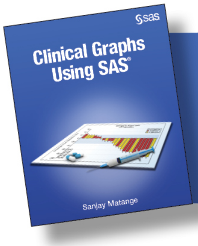
Clinical Graphs Using SAS®



Sanjay Matange



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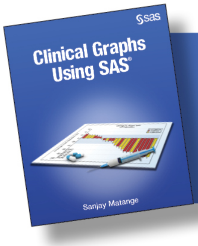

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Note: This short excerpt was taken from a chapter in the published book.

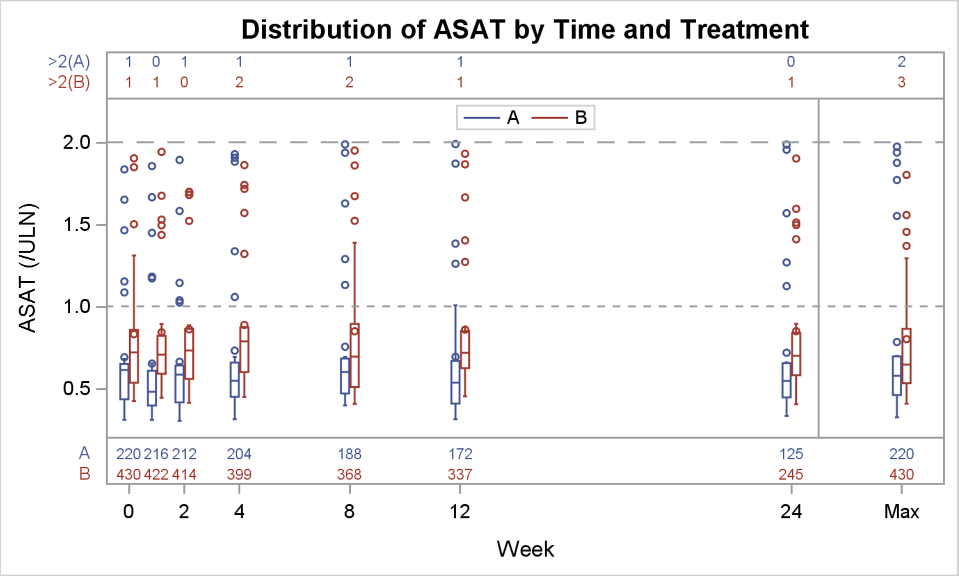
4.3 Distribution of ASAT by Time and Treatment

The graphs below consist of three sections. The main body of the graph contains the display of ASAT by Week and Treatment in the middle. A table of subjects in the study by treatment is at the bottom, and the number of subjects with value > 2 by treatment is at the top of the graph.

4.3.1 Distribution of ASAT by Time and Treatment

The values of ASAT by week and treatment are displayed using a box plot. The x-axis type is linear.

Figure 4.3.1 – Distribution of ASAT by Time and Treatment



This graph is likely one of the most complex displays that can be created using the SGPLOT procedure. This graph displays the distribution of ASAT by treatment over time using a grouped box plot on a linear x-axis. The visit values are scaled correctly on the time axis. The smallest interval between the visits determines the "effective" midpoint spacing used for adjacent placement of the treatment values.

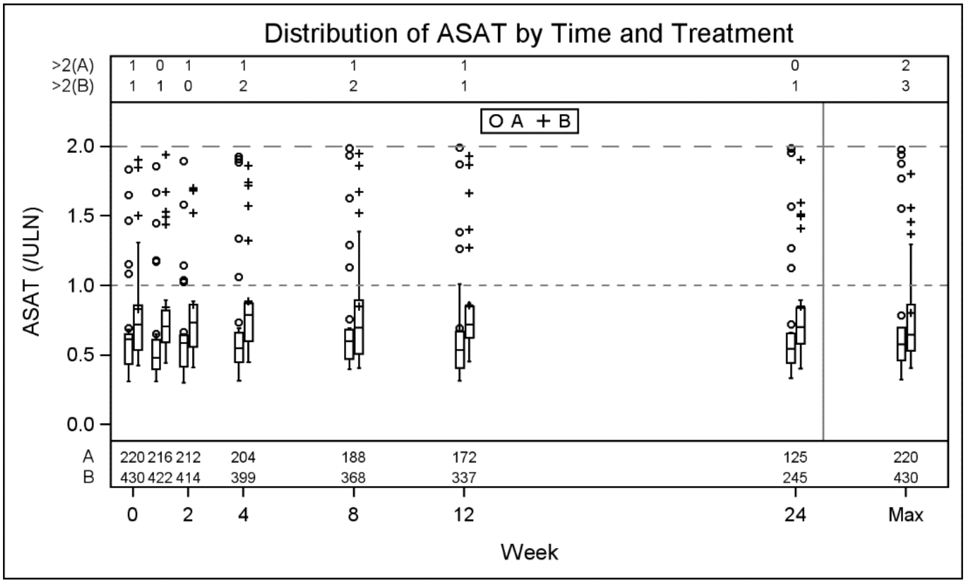
```
title 'Distribution of ASAT by Time and Treatment';
proc sgplot data=asat;
  vbox asat / category=week group=drug name='box' nofill;
  xaxistable gt2 / class=drugGT colorgroup=drugGT position=top
         location=inside separator valueattrs=(size=6)
         labelattrs=(size=7);
  xaxistable count / class=drug colorgroup=drug position=bottom
         location=inside separator valueattrs=(size=6)
         labelattrs=(size=7);
  refline 1 / lineattrs=(pattern=shortdash);
  refline 2 / lineattrs=(pattern=dash);
  refline 25 / axis=x;
  xaxis type=linear values=(0 2 4 8 12 24 28) offsetmax=0.05
       valueattrs=(size=7) labelattrs=(size=8);
  yaxis offsetmax=0.1 valueattrs=(size=7) labelattrs=(size=8);
  keylegend 'box' / location=inside position=top linelength=20;
run;
```

An XAXISTABLE statement is used to display the "Number of Subjects" values at the bottom of the graph. A second XAXISTABLE at the top is used to display the count of values above 2.0 by treatment.

4.3.2 Distribution of ASAT by Time and Treatment in Grayscale

The graph in Figure 4.3.2 is the same as above in grayscale. Markers are used in the legend for treatment.

Figure 4.3.2 – Distribution of ASAT by Time and Treatment in Grayscale



Drawing this graph using the Journal style poses a few challenges, mainly in the drawing of the boxes and their representation in the legend. Using the Journal style, the boxes for Drug "B" will get drawn using dashed lines. Because those look odd, I set the STYLEATTRS option to use only solid lines.

```
ods listing style=journal;
title 'Distribution of ASAT by Time and Treatment';
proc sgplot data=asat2;
  styleattrs datalinepatterns=(solid);
  vbox asat / category=week group=drug nofill;
  scatter x=week y=asat2 / group=drug name='s';
  xaxistable gt2 / class=drugGT colorgroup=drugGT position=top
       location=inside;
  xaxistable count / class=drug colorgroup=drug position=bottom
       location=inside;
  refline 1 / lineattrs=(pattern=shortdash);
  refline 2 / lineattrs=(pattern=dash);
  refline 25 / axis=x;
  xaxis type=linear values=(0 2 4 8 12 24 28) offsetmax=0.05;
  yaxis offsetmax=0.1 valueattrs=(size=8) labelattrs=(size=9);
  keylegend 's' / location=inside position=top linelength=20;
run;
```

Although this improves the rendering of the boxes, it will put two solid lines in the legend for "A" and "B". It would be better to show the mean markers in the legend instead. To do this, I have to add a scatter plot of asat2 by Week and Drug and include that in the legend. Because values in "asat2" are all missing, no markers are displayed in the graph itself, but the group markers are displayed in the legend. Relevant details are shown in the code snippet above. For full details, see Program 4_3.

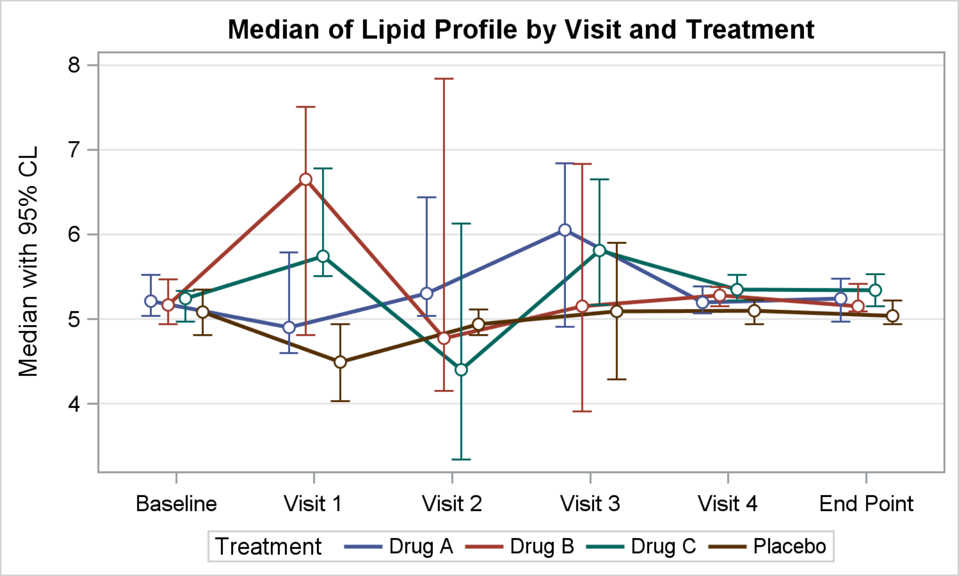
4.4 Median of Lipid Profile by Visit and Treatment

This graph displays the median of the lipid values by visit and treatment. The visits are at regular intervals and represented as discrete data.

4.4.1 Median of Lipid Profile by Visit and Treatment on Discrete Axis

The values for each treatment are displayed along with the 95% confidence limits as adjacent groups using GROUPDISPLAY option of "Cluster" and the option CLUSTERWIDTH=0.5. The HTMLBlue style is used.

Figure 4.4.1 – Median of Lipid Profile by Visit and Treatment



```
title 'Median of Lipid Profile by Visit and Treatment';
proc sgplot data=lipid_grp;
  series  x=day y=median / lineattrs=(pattern=solid) group=trt name='s'
          groupdisplay=cluster clusterwidth=0.5 lineattrs=(thickness=2);
  scatter x=day y=median / yerrorlower=lcl yerrorupper=ucl group=trt
          groupdisplay=cluster clusterwidth=0.5
          errorbarattrs=(thickness=1) filledoutlinedmarkers
          markerattrs=(symbol=circlefilled)
```

```
          markerfillattrs=(color=white);
  keylegend 's' / title='Treatment' linelength=20;
  yaxis label='Median with 95% CL' grid;
  xaxis display=(nolabel);
run;
```

This graph displays the median of the lipid data by visit and treatment. The visits are at regular intervals and represented as discrete data. However, they could also be on a time axis with unequal intervals. The values for each treatment are displayed along with the 95% confidence limits as adjacent groups using GROUPDISPLAY=Cluster and CLUSTERWIDTH=0.5.

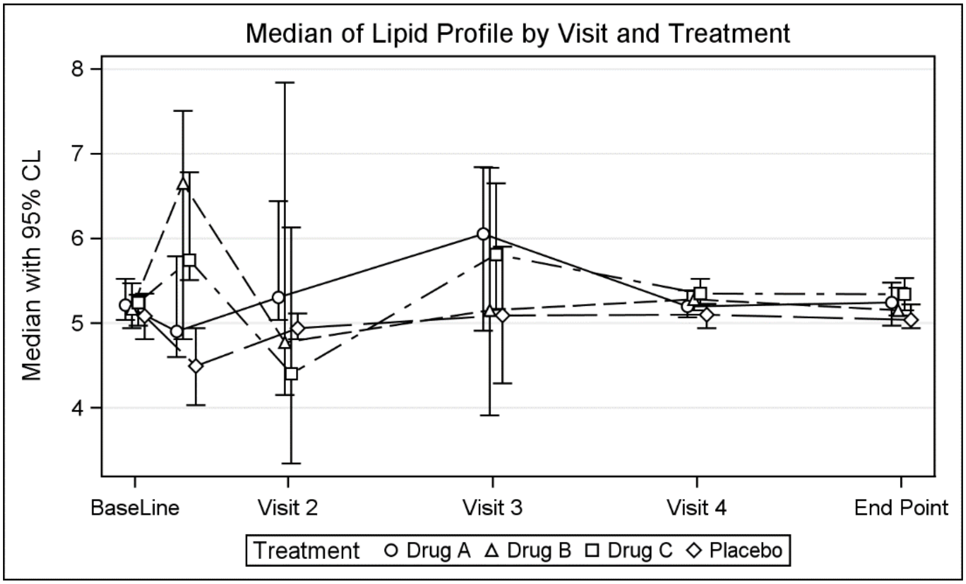
The values across visits are joined using a series plot. Note, the series plot also uses cluster groups with the same cluster width. The lengths of the line segments in the legends are reduced using the LINELENGTH option. Markers with fill and outlines are used with specific fill attributes.

Relevant details are shown in the code snippet above. For full details, see Program 4_4.

4.4.2 Median of Lipid Profile by Visit and Treatment on Linear Axis in Grayscale

This graph displays the median of the lipid data by treatment in grayscale on a linear x-axis.

Figure 4.4.2 – Median of Lipid Profile by Visit and Treatment on Linear Axis



```
title 'Median of Lipid Profile by Visit and Treatment';
proc sgplot data=lipid_Liner_grp;
  styleattrs datasymbols=(circlefilled trianglefilled
             squarefilled diamondfilled);
  series  x=n y=median /  group=trt groupdisplay=cluster
```

```
          clusterwidth=0.5;
  scatter x=n y=median / yerrorlower=lcl yerrorupper=ucl group=trt
          groupdisplay=cluster clusterwidth=0.5
          errorbarattrs=(thickness=1) filledoutlinedmarkers
          markerattrs=(size=7) name='s'
          markerfillattrs=(color=white);
  keylegend 's' / title='Treatment' linelength=20;
  yaxis label='Median with 95% CL' grid;
  xaxis display=(nolabel) values=(1 4 8 12 16);
run;
```

The visits are not at regular intervals and are displayed at the correct scaled location along the x-axis. The visits are at week 1, 2, 4, 8, 12, and 16. These values are formatted to the strings shown on the axis. "Visit 1" collides with "Baseline", causing alternate tick values to be dropped, so I removed "1" from the tick value list.

As you can see, the group values are displayed as clusters, and the "effective midpoint spacing" is the shortest distance between the values. The markers are reduced in size to show the clustering. This can be adjusted by setting marker SIZE=7. Four filled markers are assigned to the list of markers.

Relevant details are shown in the code snippet above. For full details, see Program 4_4.

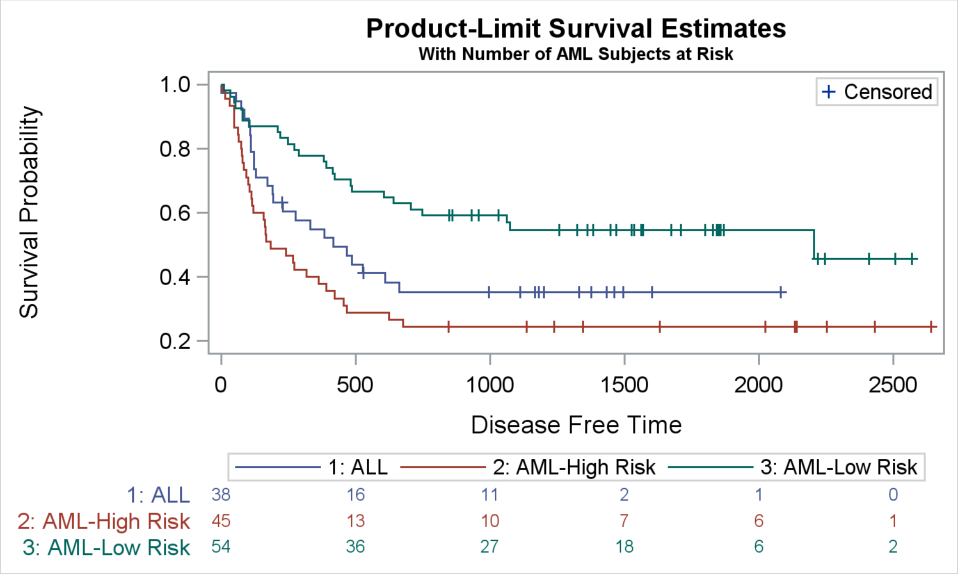
4.5 Survival Plot

The survival plot is one of the most popular graphs that users want to customize to their own needs. Here I have run the LIFETEST procedure to generate the data for this graph. The output is saved into the "SurvivalPlotData" data set. For more information about the LIFETEST procedure, see the SAS/STAT documentation.

4.5.1 Survival Plot with External "Subjects At-Risk" Table

The survival plot shown below in Figure 4.5.1 has the traditional arrangement where the table of Subjects At-Risk is displayed at the bottom of the graph, below the x-axis.

Figure 4.5.1 – Survival Plot with External "Subjects At-Risk" Table



```
ods output Survivalplot=SurvivalPlotData;
proc lifetest data=sashelp.BMT plots=survival(atrisk=0 to 2500 by 500);
   time T * Status(0);
   strata Group / test=logrank adjust=sidak;
   run;
```

A step plot of survival by time by strata displays the curves. A scatter overlay is used to draw the censored values, and an XAXISTABLE statement is used to display the at-risk values at the bottom of the graph. Relevant details are shown in the code snippet above. For full details, see Program 4_5.

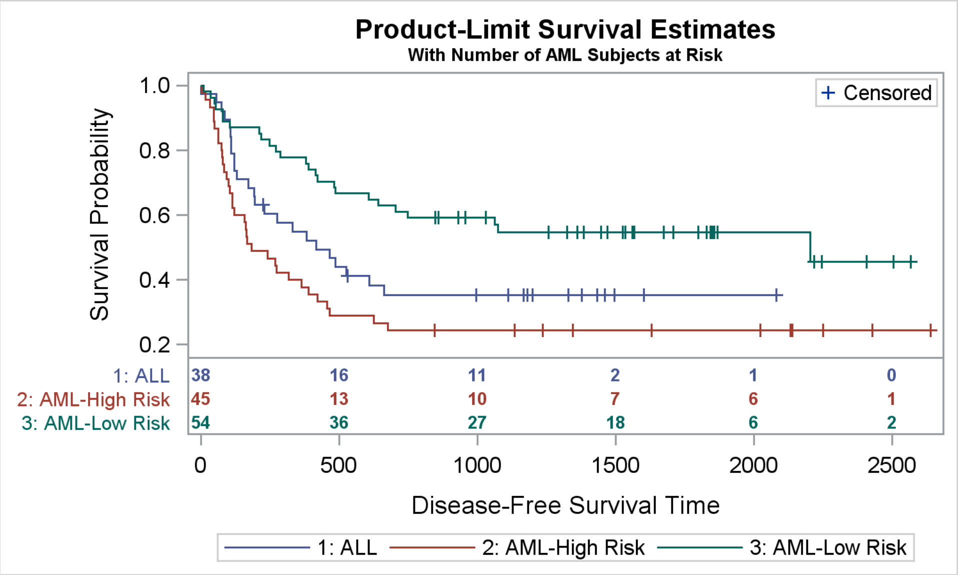
```
title 'Product-Limit Survival Estimates';
title2  h=0.8 'With Number of AML Subjects at Risk';
proc sgplot data=SurvivalPlotData;
  step x=time y=survival / group=stratum
```

```
      lineattrs=(pattern=solid) name='s';
  scatter x=time y=censored / markerattrs=(symbol=plus) name='c';
  scatter x=time y=censored / markerattrs=(symbol=plus) GROUP=stratum;
  xaxistable atrisk/x=tatrisk location=outside class=stratum
        colorgroup=stratum;
  keylegend 'c' / location=inside position=topright;
  keylegend 's';
run;
```

4.5.2 Survival Plot with Internal "Subjects At-Risk" Table

The graph shown here is mostly similar to the graph in Section 4.5.1, with the difference that the "Subjects At-Risk" table is moved above the x-axis, close to the rest of the data. Bringing all the data closer makes it easy to align the values with the data, and that improves the effectiveness of the graph.

Figure 4.5.2 – Survival Plot with Internal "Subjects At-Risk" Table



```
title 'Product-Limit Survival Estimates';
title2  h=0.8 'With Number of AML Subjects at Risk';
proc sgplot data=SurvivalPlotData;
  step x=time y=survival / group=stratum lineattrs=(pattern=solid)
      name='s';
  scatter x=time y=censored / markerattrs=(symbol=plus) name='c';
  scatter x=time y=censored / markerattrs=(symbol=plus) GROUP=stratum;
  xaxistable atrisk / x=tatrisk location=inside class=stratum
      colorgroup=stratum separator valueattrs=(size=7 weight=bold)
      labelattrs=(size=8);
```

```
    keylegend 'c' / location=inside position=topright;
    keylegend 's';
  run;
```

All this graph needs is to simply specify LOCATION=Inside for the XAXISTABLE statement. In addition to that, we have switched on the separator that draws the horizontal line between the table and the curves.

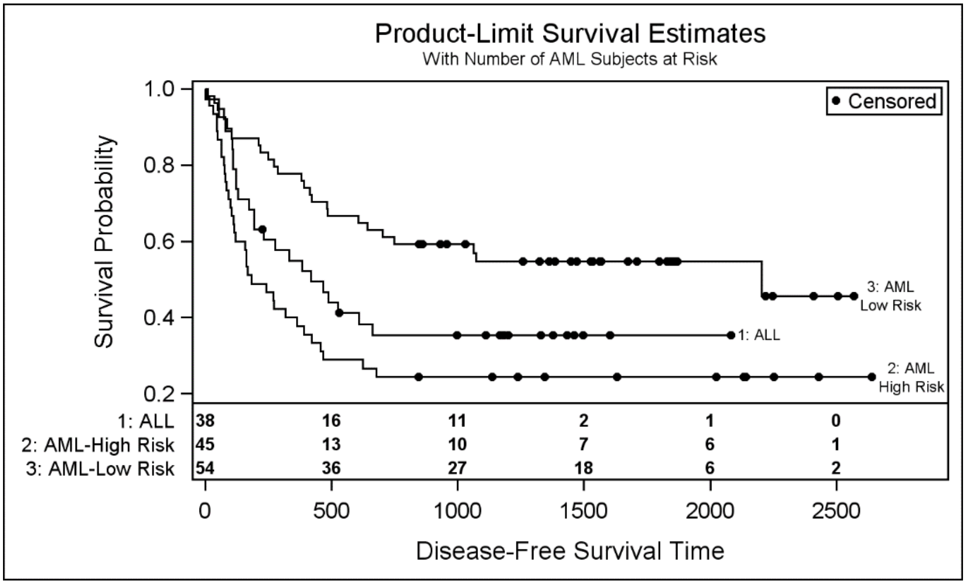
Relevant details are shown in the code snippet above. For full details, see Program 4_5.

4.5.3 Survival Plot with Internal "Subjects At-Risk" Table in Grayscale

Displaying the survival plot in a grayscale medium presents some challenges.

Here we cannot use colors to identify the strata. Normally, the Journal style uses line patterns to identify the groups. Although line patterns work well for curves, they are not so effective with step plots because of the frequent breaks. So, it is preferable to use solid lines for all the levels of the step plot and to use markers to identify the strata.

Figure 4.5.3 – Survival Plot with Internal "Subjects At-Risk" Table in Grayscale



```
    title 'Product-Limit Survival Estimates';
    title2  h=0.8 'With Number of AML Subjects at Risk';
    proc sgplot data=SurvivalPlotData;
      step x=time y=survival / group=stratum lineattrs=(pattern=solid)
           name='s' curvelabel curvelabelattrs=(size=6) splitchar='-';
      scatter x=time y=censored / name='c'
           markerattrs=(symbol=circlefilled size=4);
      xaxistable atrisk / x=tatrisk location=inside class=stratum
```

```
       colorgroup=stratum separator valueattrs=(size=7 weight=bold)
       labelattrs=(size=8);
  keylegend 'c' / location=inside position=topright;
run;
```

In this case, markers are also used to identify the censored observations. So, I have chosen to use the CURVELABEL option with the SPLITCHAR option to identify the curves. This results in a clean and effective graph, without the need for a legend for the strata.

Relevant details are shown in the code snippet above. For full details, see Program 4_5.

Note: This short excerpt was taken from a chapter in the published book.

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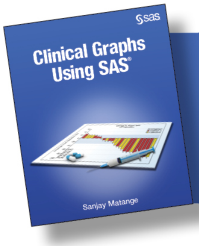

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About This Book

Purpose

SAS users in the Health and Life Sciences industry need to create complex graphs so that biostatisticians and clinicians can use them for analysis of the data. The graphs are also used for submissions to FDA for drug approvals. These graphs have specific requirements and must be designed to deliver the data accurately and clearly without distractions. Many users do not have the skills with SAS graphics tools such as Statistical Graphics (SG) procedures and the Graph Template Language (GTL) to create such graphs. This book provides the know-how and the code to create the graphs that are commonly used in this industry.

Is This Book for You?

This book is for the SAS graphics programmer who is responsible for creating sophisticated graphs for the analysis of clinical trials data. Most of these graphs are not automatically created by some analytical procedure, and must be custom built. However, many of these graphs are commonly used in the Health and Life Sciences industry, and there is an effort in the industry to standardize. This book describes how to create such graphs for intermediate and advanced graph programmers.

Prerequisites

Some knowledge of SAS DATA step programming may be required to get the data into the shape needed for the graphs. Knowledge of SG procedures and GTL will be helpful, but is not required.

Scope of This Book

This book includes detailed instructions about how to create some of the standard, commonly used graphs for analysis of data in the Health and Life Sciences industry. The book provides some introductory information on the use of SG procedures and GTL.

However, this book does not cover the features of SG procedures or of GTL in depth. Such comprehensive information is beyond the scope of this book.

About the Examples

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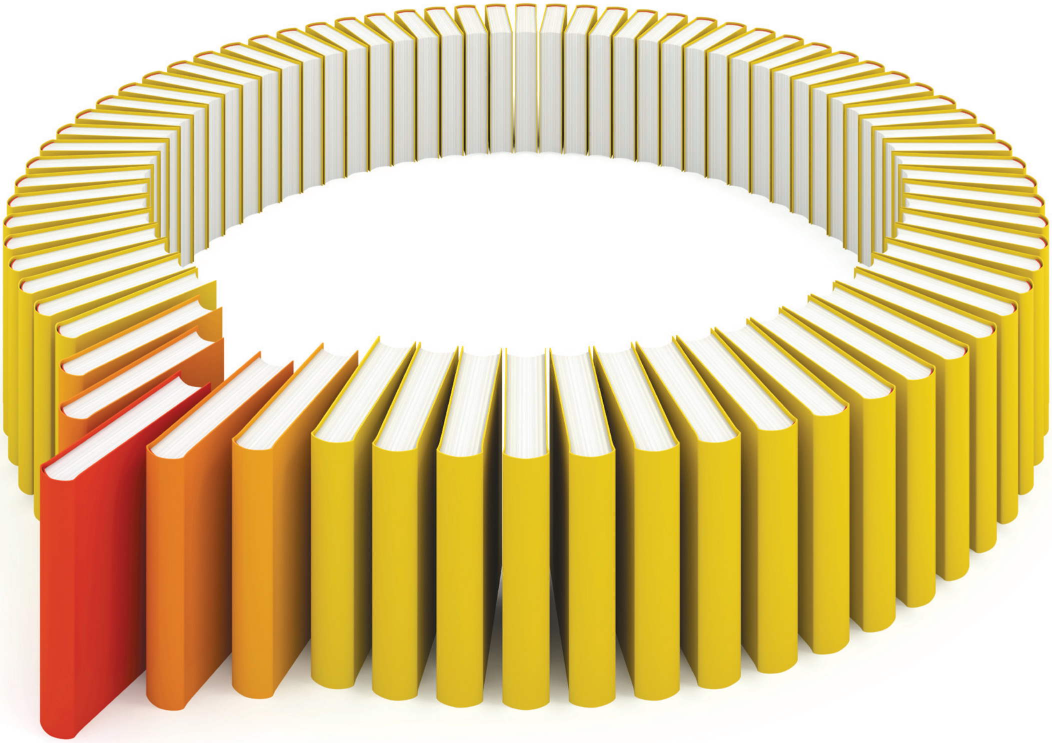
Learn more about this author by visiting his author page at http://support.sas.com/matange. There you can download free book excerpts, access example code and data, read the latest reviews, get updates, and more.



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