

Clinical Graphs using SAS

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ABSTRACT

Graphs are essential for analysis of Clinical Trials Safety Data or analysis of the efficacy of the treatment. Creating such graphs is easier with SAS® 9.4 SG Procedures. This paper will show how to create many industry standard graphs such as Lipid Profile, Swimmer Plot, Survival Plot, and Forest Plot with Subgroups, Waterfall Plot and Adverse Event Timelines with compact coding.

INTRODUCTION

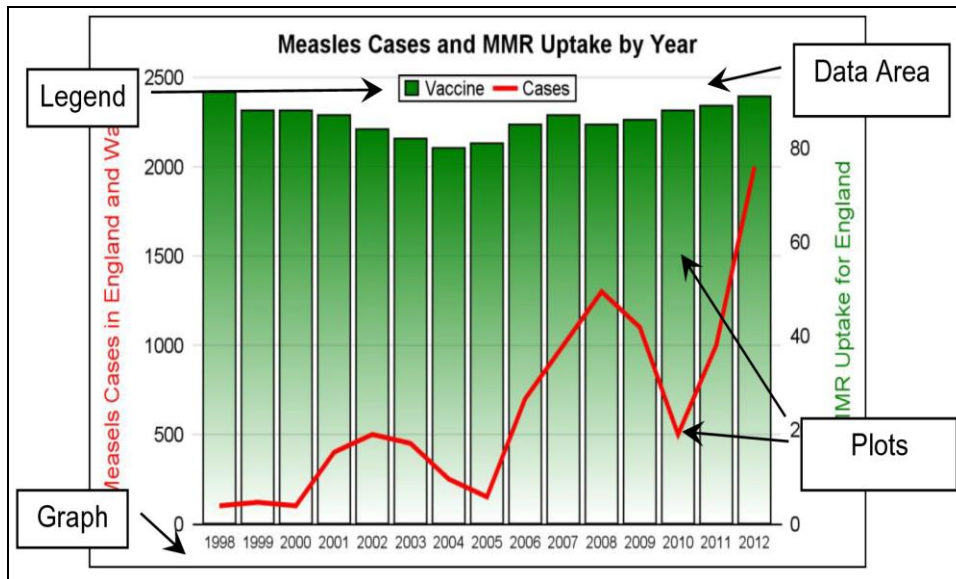
The SAS ODS Graphics system was first released in 2008 with SAS 9.2 and it included the Statistical Graphics (SG) procedures and the Graph Template Language (GTL). This opened up a new way to create graphs in SAS, and the feature set of these tools has been growing steadily, making it easier for you to create graphs with every release.

New features included with SAS 9.4, include the axis tables which simplifies the display of axis aligned statistics in a graph. The goal of this paper is to show you how to create some of the commonly requested graphs through step-by-step examples. These include the Lipid Profile graph, Swimmer Plot, Survival Plot, Forest Plot, Waterfall Plot, and Patient Profile graph using the SAS 9.4 SGPLOT procedure.

CREATING GRAPHS USING THE SGPLOT PROCEDURE

The SGPLOT procedure uses a process of layering multiple plot statements to create a composite graph with one data area. A typical single-cell graph is shown in Figure 1.

Figure 1. Single-cell graph using SGPLOT procedure.



We refer to contents of each output file from the graphical procedure as the "Graph". Statements responsible for drawing the data in the cell, whether it is a scatter plot or bar chart, is referred to as a "plot". Figure 1 shows a graph of the Measles and MMR Uptake by year created using the SGPLOT procedure. A typical single-cell graph has the following components:

- Zero or more titles and footnotes in the graph.
- One region in the middle often referred to as a "Cell" that displays the data.
- One or more plots used to display the data.
- A set of axes shared by the plots in the cell. A cell can have up to two horizontal and two vertical axes.
- Zero or more legends or insets.

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The SGPLOT code to create the graph in Figure 1 is shown below.

```
title 'Measles Cases and MMR Uptake by Year';
proc sgplot data=Measles noborder;
  vbar year / response=vaccine nostatlabel y2axis fillattrs=(color=green)
           filltype=gradient baselineattrs=(thickness=0) baseline=0;
  vline year / response=cases nostatlabel lineattrs=(color=red thickness=3);
  keylegend / location=inside position=top linelength=15;
  yaxis offsetmin=0 display=(noline noticks) thresholdmax=0 max=2500 grid
        label='Measels Cases in England and Wales' labelattrs=(color=red);
  y2axis offsetmin=0 min=0 max=95 display=(noline noticks) thresholdmax=0
        label='MMR Uptake for England' labelattrs=(color=green);
  xaxis display=(nolabel noticks) valueattrs=(size=7);
run;
```

A BRIEF REVIEW OF THE SGPLOT PROCEDURE

The structure of SGPLOT procedure syntax is as follows:

```
PROC SGPLOT <DATA=data-set> <SGANNO=data-set> <options>;
  plot-statement(s) required-parameters / <options>;
  <styleattrs-statement(s)>;
  <refline-statement(s)>;
  <dropline-statement(s)>;
  <inset-statement(s)>;
  <axis-statement(s)>;
  <keylegend-statement(s)>;
  <gradlegend-statement(s)>;
RUN;
```

The procedure statement supports multiple options. We will not attempt to describe each feature of the procedures. Instead, these features will become clear from the examples shown in this paper.

One or more plot statements can be used to represent the data. Each plot statement has its own set of required data-roles and options. These options will become evident as we create multiple clinical graphs. Many plot statements are supported, and can be grouped as shown below.

- Basic Plots: Such as scatter, series, and so on.
- Fit and Confidence Plots: Such as regression and loess plots.
- Distribution plots: Such as histograms and box plots.
- Categorical Plots: Such as bar charts and dot plots.

Supporting statements can be used to customize the graph.

- Style-attrs, symbol-char, and symbol-image statement.
- Reference lines and drop lines.
- Insets.
- Axes.
- Legends.

REQUIRED DATA ROLES

A role name allows the assigned variable to be used in a specific way for the plot. Some common role names are 'X', 'Y', 'GROUP', 'CATEGORY', 'RESPONSE' and so on. Each plot statement has required roles and options needed to render the plot. Data set variables must be assigned to the required roles to produce a graph. Some required roles can take scalar values and some do not require a role name. Here are some examples:

```
SCATTER X=var-name Y=var-name;
HISTOGRAM var-name ;
```

OPTIONAL DATA ROLES

Optional data roles can be provided for each statement that go after the "/". Data options are assigned variable names from the data set for rendering features that are data dependent, such as group classification, or color by response.

```
SCATTER X=var-name Y=var-name / GROUP=var-name;
VBAR var-name / RESPONSE=var-name COLORRESPONSE=num-var-name;
HIGHLOW X=var-name LOW=var-name HIGH=var-name / LOWLABEL=var-name;
```

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PLOT OPTIONS

Plot options can be used to change the behavior of the plot, or to assign attributes for different parts of the plot. These plot options are custom to each plot and may not be common with other plots.

```
VBAR var-name / RESPONSE=var-name BARWIDTH=0.6;  
SCATTER X=var-name Y=var-name / JITTER;
```

COMMON OPTIONS

Each plot also has many common options for setting axis association or visual attributes with consistent names across the plot statements. Options for visual attributes normally end with the suffix "ATTRS", such as FILLATTRS or LINEATTRS. Based on the type of the graph, the appropriate attribute option can be expected to be supported.

```
VBAR <var-name> / RESPONSE=<var-name> Y2AXIS;  
VBOX mileage / CATEGORY=Type MEANATTRS=(SYMBOL=circlefilled);
```

PLOT LAYERING

An important feature of the SGPLOT procedure is the ability to layer compatible plot statements to create more complex and intricate graphs. The SGPLOT procedure supports over thirty plot statements that are grouped in four groups as mentioned above. These are "Basic plots", "Fit and Confidence plots", "Distribution plots" and "Categorical plots". In general, plots can be layered as follows:

- "Basic Plots" can be combined with each other or with statements in the "Fit and Confidence plots".
- Plots in other groups can be combined with other plots in the same group.
- All plots can be combined with the "Supporting statements" like REFLINE and DROPLINE.
- Starting with SAS 9.4, box plots can be combined with Basic plots.

CREATING CLINICAL GRAPHS USING SAS 9.4

In this paper we will cover clinical graphs created using the SAS 9.4 SGPLOT procedure. These graphs are easy to create because some of the new statements and features have been specifically added to address the needs of such graphs. These include the XAXISTABLE and YAXISTABLE statements.

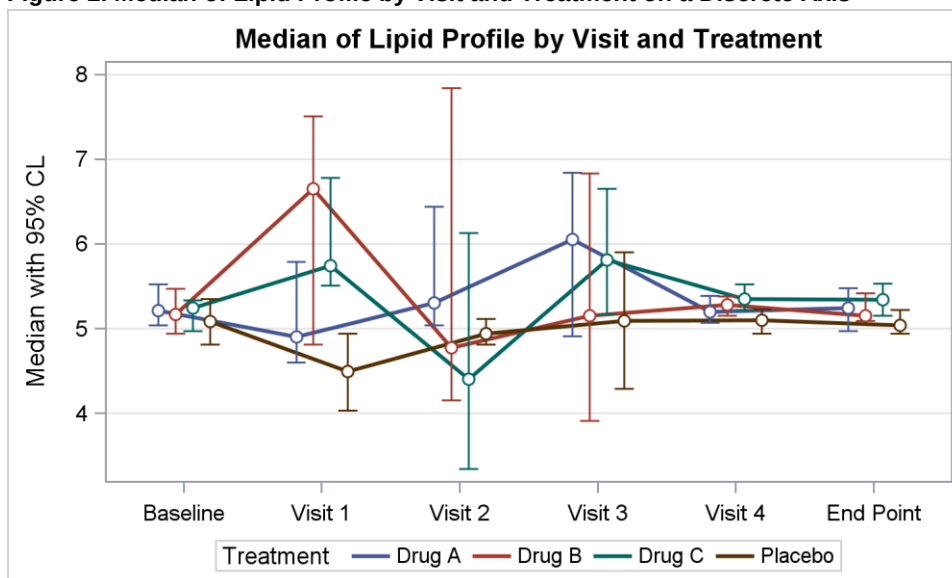
MEDIAN OF LIPID PROFILE BY VISIT AND TREATMENT

LIPID PROFILE ON A DISCRETE AXIS

This graph displays the median of the lipid values by visit and treatment on a discrete x-axis. In this graph, the visits are at regular intervals and represented as discrete data. The values for each treatment are displayed along with the 95% confidence limits as adjacent groups using GROUPDISPLAY of "Cluster" and CLUSTERWIDTH=0.5.

The style used for the graph is HTMLBlue, which is a "Color" priority style. This means for cycling of group attributes, first only the color is changed for each new group, holding the first marker symbol and the line style constant. After all 12 colors are used, the next marker symbol and line style are used.

Figure 2. Median of Lipid Profile by Visit and Treatment on a Discrete Axis



```
title 'Median of Lipid Profile by Visit and Treatment';  
proc sgplot data=lipid_grp;
```

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```

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. The median 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 which also uses cluster groups with the same cluster width. The individual group values are connected across visits, which is useful to guide the eye across the graph. The slope of the line is not significant since the x-axis is discrete.

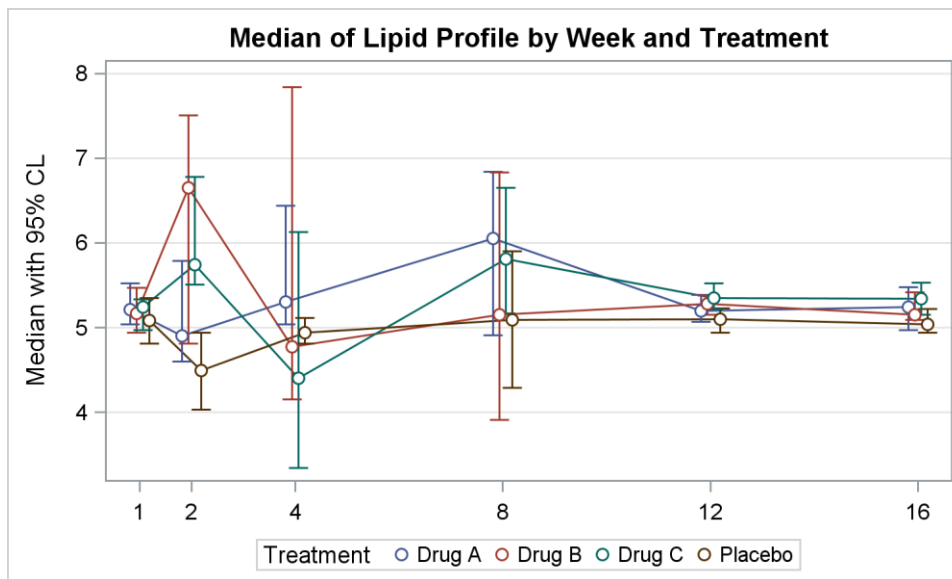
Two new SAS 9.4 options are worth noting.

- `FILLEDOUTLINEDMARKERS` option in the `SCATTER` statement: This option allows filled markers such as `CircleFilled` to be drawn using a fill color for the interior and the contrast color for the outline.
- `LINELENGTH` option in the `KEYLEGEND` statement is used to set the length of the line. When the patterns for the lines are all solid, as in this case, it is not necessary to have long line segments in the legend.

LIPID PROFILE ON A LINEAR AXIS

When the intervals along the x-axis are numeric, it is often useful to display the data using a scaled linear axis. In Figure 6, the visits are at unequal time intervals. The values for each treatment are displayed on a linear axis with the 95% confidence limits as adjacent groups using `GROUPDISPLAY` of "Cluster" and `CLUSTERWIDTH=0.5`.

Figure 3. Median of Lipid Profile by Week and Treatment on a Linear Axis



Now, each cluster of values is displayed at the time value starting with week 1. The first visit is at week 2, and the other visits are at week 4, 8, 12 and 16. The median data is shown at the correctly scaled linear distance from the origin. With a numeric x-axis, connecting the data along the x-axis provides more information about the rate of change represented by the slopes of the lines.

```

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

```

```

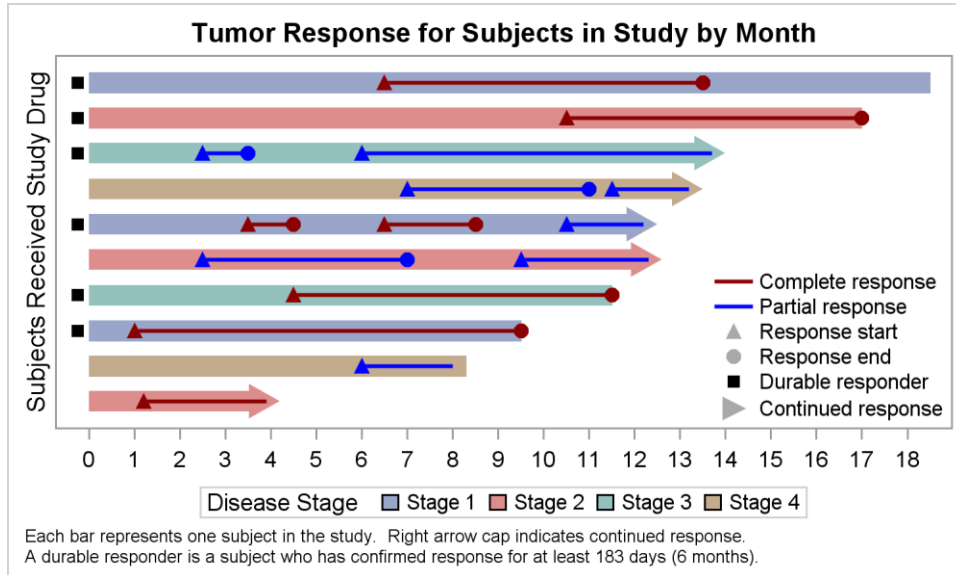
filledoutlinedmarkers markerattrs=(symbol=circlefilled)
markerfillattrs=(color=white) clusterwidth=0.5;
keylegend 's' / title='Treatment' linelength=20;
yaxis label='Median with 95% CL' grid;
xaxis display=(nolabel);
run;

```

SWIMMER PLOT

In her paper "Swimmer Plot: Tell a Graphical Story of Your Time to Response Data Using PROC SGPLOT", Stacey Phillips describes how investigators in oncology studies are frequently interested in the effects of a study drug on patients' tumor size and composition.

Figure 4. Swimmer Plot for Tumor Response



Investigators want to know whether an individual subject has a response, and the timing of the response in relation to the study drug. The Swimmer plot shown in Figure 4 is a graphical way of showing multiple pieces of a subject's response "story" in one graph. While Stacey uses annotation to build the graph, the code below shows how to build the same graph with use of HighLow plot with end caps without any annotations.

```

title 'Tumor Response for Subjects in Study by Month';
proc sgplot data= swimmer datrmap=attrmap nocycleattrs;
  highlow y=item low=low high=high / highcap=highcap type=bar group=stage
    lineattrs=(color=black) name='stage' barwidth=1 nomissinggroup
    transparency=0.3 fill nooutline;
  highlow y=item low=startline high=endline / group=status
    lineattrs=(thickness=2 pattern=solid)
    name='status' nomissinggroup attrid=statusC;
  scatter y=item x=start / name='s' legendlabel='Response start'
    markerattrs=(symbol=trianglefilled size=8 color=darkgray);
  scatter y=item x=end / name='e' legendlabel='Response end'
    markerattrs=(symbol=circlefilled size=8 color=darkgray);
  scatter y=item x=xmin / name='x' legendlabel='Continued response '
    markerattrs=(symbol=trianglerightfilled size=12 color=darkgray);
  scatter y=item x=durable / name='d' legendlabel='Durable responder'
    markerattrs=(symbol=squarefilled size=6 color=black);
  scatter y=item x=start / group=status attrid=statusC
    markerattrs=(symbol=trianglefilled size=8);
  scatter y=item x=end / group=status attrid=statusC
    markerattrs=(symbol=circlefilled size=8);
  xaxis display=(nolabel) label='Months' values=(0 to 20 by 1) valueshint;
  yaxis reverse display=(noticks novalues noline) label='Subjects Received ...';
  keylegend 'stage' / title='Disease Stage';
  keylegend 'status' 's' 'e' 'd' 'x' / noborder location=inside
    position=bottomright across=1 linelength=20;
run;

```

Figure 5. Data for the Swimmer Plot

Obs	Item	Stage	Low	High	Highcap	Status	Start	End	Durable	Startline	Endline	Xmin
1	1	Stage 1	0	18.5		Complete response	6.5	13.5	-0.25	6.5	13.5	.
2	2	Stage 2	0	17.0		Complete response	10.5	17.0	-0.25	10.5	17.0	.
3	3	Stage 3	0	14.0	FilledArrow	Partial response	2.5	3.5	-0.25	2.5	3.5	.

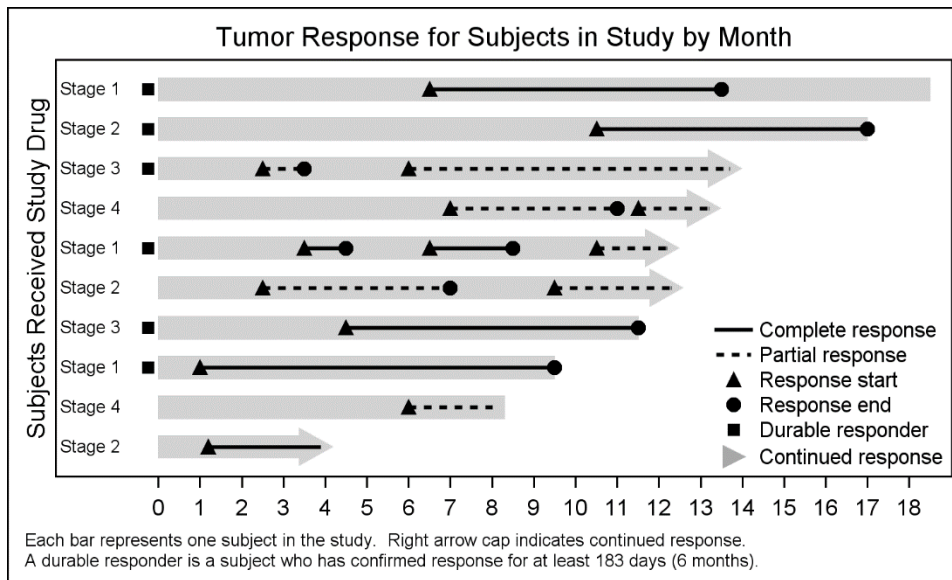
Note the following features of the program shown above.

- We use a HIGHLOW plot of TYPE=Bar of Low and High by Item and Stage to draw the main bars.
- Response duration is shown using a HIGHLOW plot of Start and End by Item and Status.
- We use overlaid SCATTER with TriangleFilled markers for Start by Item to populate the legend
- We use overlaid SCATTER with CircleFilled markers for the End by Item to populate the legend.
- We use overlaid SCATTER with TriangleRightFilled markers for the XMin by Item. This is used only to display a right triangle in the legend that represents the arrow head of the HIGHLOW plot.
- We use overlaid SCATTER with SquareFilled markers for Durable by Item.
- We use overlaid SCATTER with TriangleFilled markers for Start by Item by Status.
- We use overlaid SCATTER with CircleFilled markers for End by Item by Status.

SWIMMER PLOT IN GRAY SCALE

Often it is necessary to create a graph for inclusion in a report or journal where the graph needs to be rendered in gray-scale, as shown in Figure 6.

Figure 6. Swimmer Plot in Gray-scale.



In this case, the bar for each subject is displayed in gray, so it is not possible to use color to encode the Stage. In this graph, we have displayed the stage for each subject explicitly on the left side using the YAXISTABLE statement.

```
yaxistable stage / location=inside position=left nolabel;
```

A Discrete Attribute Map is used to set the attributes for the duration line and the start / end markers by Status using the "ATTRID" of StatusC for the color graph and StatusJ for the gray-scale graph. For the color graph in Figure 4, these are set to the red and blue colors. For the gray-scale graph in Figure 6, these use the solid or dashed line.

PRODUCT-LIMIT SURVIVAL ESTIMATES PLOT

The survival plot is one of the most popular graphs that is customized to individual needs. For this example, I have run the LIFETEST procedure to generate the data for this graph. The output is saved into the "SurvivalPlotData" data set. The procedure itself creates this graph automatically. However, here the intention is to show how you can get this data and customize the graph to your specifications.

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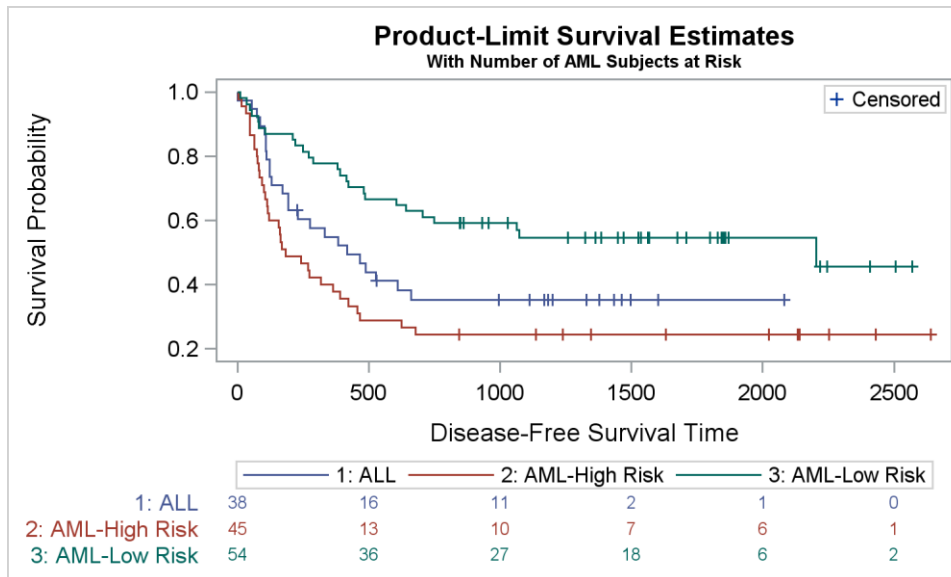
Here is the LIFETEST procedure code I have used that generates the data set needed to render the graph. The ODS OUTPUT statement is used to save the data in the "SurvivalPlotData" data set as shown in Figure 7 which is used to create the graph shown in Figure 8 using the SGLOT procedure.

```
ods graphics on;
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;
```

Figure 7. Data for the Survival Plot

Obs	Time	Survival	AtRisk	Event	Censored	tAtRisk	Stratum	StratumNum
1	0	1.00000	38	0	.	.	1: ALL	1
2	0	.	38	.	.	0	1: ALL	1
3	1	0.97368	38	1	.	.	1: ALL	1
4	55	0.94737	37	1	.	.	1: ALL	1
5	74	0.92105	36	1	.	.	1: ALL	1

Figure 8. Survival Plot



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

A few observations from the data set used for the graph are shown in Figure 8. The graph displays the survival probability using a STEP plot of Survival by Time and Stratum. The data has three distinct values for the Stratum column. Some key elements of the program are as follows:

- The survival curves are displayed using the STEP plot of Survival by Time and Stratum. The Stratum levels are displayed in the legend at the bottom of the graph.

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- The censored observations are first displayed using a SCATTER by Time where all markers are set to "Plus". This displays all markers in black, which are included in the inner legend.
- The censored markers are over-plotted using a SCATTER by Time and Stratum with all markers set to "Plus". This displays the markers colored by Stratum, hiding the black markers.
- A XAXISTABLE is used to display the AtRisk values by TAtRisk. TAtRisk values are non-missing only at increments of 500 on the x-axis. Hence, the table displays the risk values only at these locations.

SURVIVAL PLOT IN GRAY-SCALE

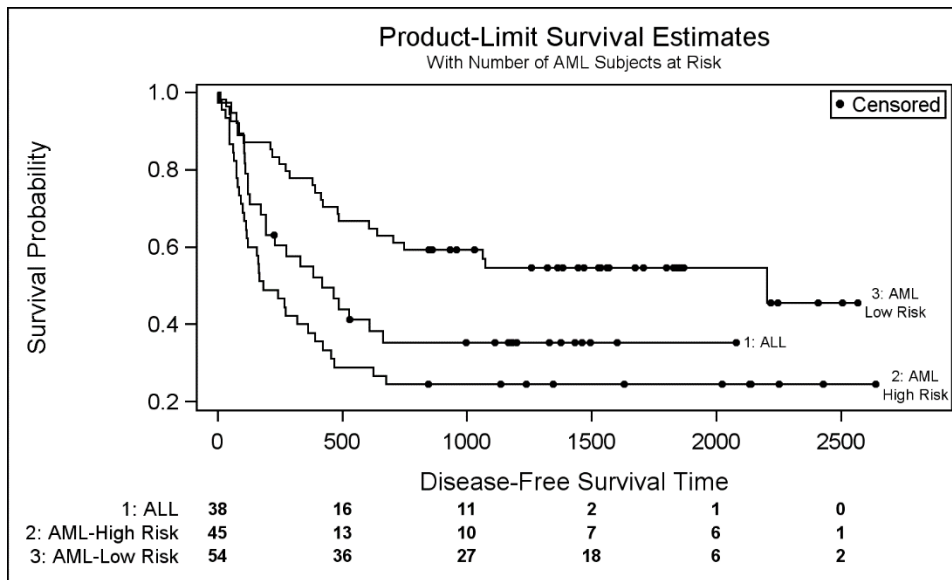
The graph shown in Figure 9 is the same Survival Plot rendered in gray-scale for inclusion in journals. We have used the JOURNAL style to render this graph.

Normally, the Journal style will use different line styles to represent the different group levels in the graph. In this case, the three values for "ALL", "AML Low-Risk" and "AML High-Risk" would be represented by three different line patterns, which can be identified in a legend. However, use of line patterns is not optimal for step plots. So, in this example, I have set all the curves to have a solid pattern, which works well for step plots.

To identify each group level for the Stratum variable, I have used the CURVELABEL option. This labels each curve with its group value at the end of the curve. This turns out to be a good solution in this case, especially as SAS 9.4 supports splitting curve label values on "white space".

The same Stratum values are also displayed as labels on the left for the risk table. A CircleFilled marker is used for the censored observations.

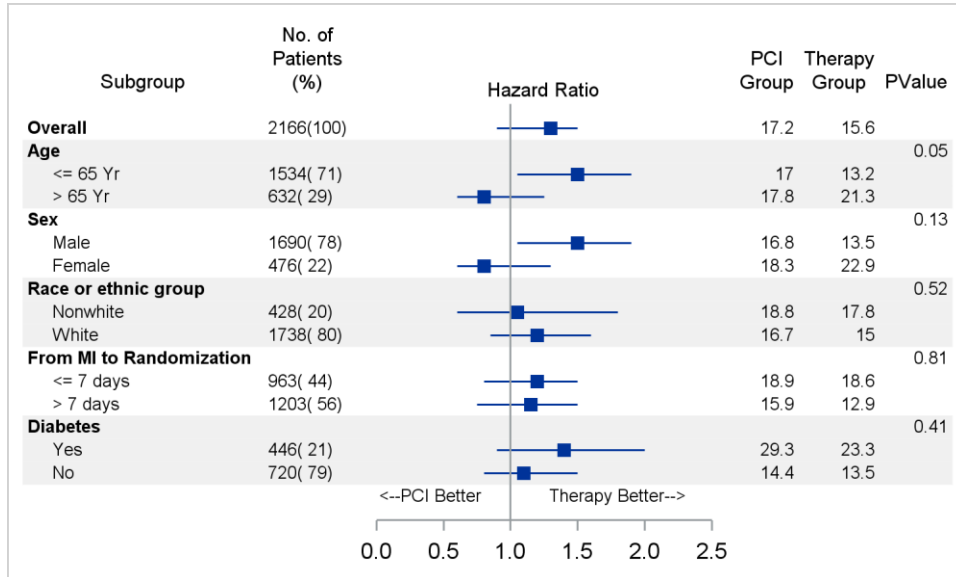
Figure 9. Survival Plot in Gray-scale



FOREST PLOT WITH SUBGROUPS

A forest plot is a graphical representation of a meta-analysis of the results of randomized controlled trials. Normally, the graph consists of the Odds Ratio of the outcome by study along with display of study names, and relevant statistics for each study. More recently, there has been an interest in such a graph where the information is displayed by sub groups, along with the relevant information as shown in Figure 10.

Figure 10. Forest Plot with subgroups



The SGPlot procedure code for this graph is shown below. The graph contains a hazard ratio plot in the middle created using high-low and scatter plots. The study values and statistics are displayed using axis tables. The data for this graph is shown in Figure 11 and the Discrete Attribute Map is shown in Figure 12.

```
proc sgplot data=forest_subgroup_2 nowall noborder nocycleattrs dattrmap=attrmap
noautolegend;
  styleattrs axisextent=data;
  reffline ref / lineattrs=(thickness=13 color=cxf0f0f0);
  highlow y=obsid low=low high=high;
  scatter y=obsid x=mean / markerattrs=(symbol=squarefilled);
  scatter y=obsid x=mean / markerattrs=(size=0) x2axis;
  reffline 1 / axis=x;
  text x=x1 y=obsid text=text / position=center contributeoffsets=none;
  yaxistable subgroup / location=inside position=left textgroup=id
    labelattrs=(size=8) textgroupid=text indentweight=indentWt;
  yaxistable countpct / location=inside position=left
    labelattrs=(size=8) valueattrs=(size=7);
  yaxistable PCIGroup group pvalue / location=inside position=right
    labelattrs=(size=8) valueattrs=(size=7);
  yaxis reverse display=none colorbands=odd
    colorbandsattrs=(transparency=1) offsetmin=0.0;
  xaxis display=(nolabel) values=(0.0 0.5 1.0 1.5 2.0 2.5);
  x2axis label='Hazard Ratio' labelattrs=(size=8)
    display=(noline noticks novalues);
run;
```

Figure 11. Data for Forest Plot with Subgroups

Obs	ObsId	Id	Subgroup	indentWt	Count	Percent	Mean	Low	High	PCIGroup	Group	PValue	ref
1	1	1	Overall	0	2166	100	1.3	0.90	1.50	17.2	15.6		
2	2	1	Age	0								0.05	2
3	3	2	<= 65 Yr	1	1534	71	1.5	1.05	1.90	17.0	13.2		3
4	4	2	> 65 Yr	1	632	29	0.8	0.60	1.25	17.8	21.3		4

Figure 12. Discrete Attribute Map for Column Attributes.

Obs	id	value	textcolor	textsize	textweight
1	text	1	Black	7	bold
2	text	2	Black	5	normal

Here is a step-by-step description of how we built this graph using the SGPLOT procedure. While this does not look like a one-cell graph, it still has only one region displaying the data in a graphical format. The SAS 9.4 SGPLOT has new features that allow us to build this graph as a one-cell graph, since the procedure takes care of creating the multiple cells for us behind the scenes.

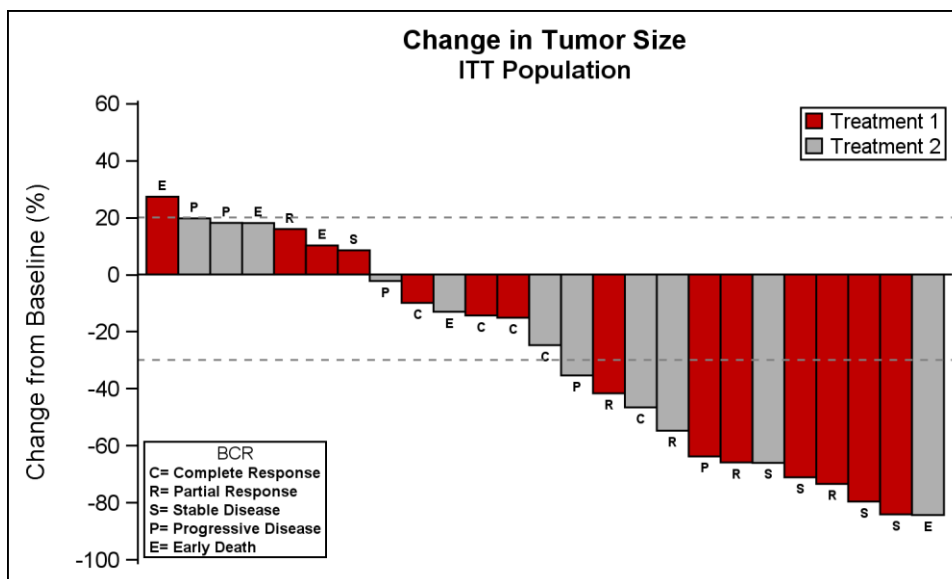
1. Note the graph has a clean table like appearance using the options NOBORDER and NOWALL.
2. The confidence range of the Hazard Ratio plot is displayed using a high-low plot of Low and High by ObsId.
3. The mean value of the Hazard Ratio plot is displayed using a scatter plot.
4. A reference line is drawn at $x=1$.
5. The annotation of "PCI Better" and "Therapy Better" are drawn using the text plot.
6. The subgroup and values are displayed on the left using a XAXISTABLE. Text attributes are controlled by the TEXTGROUP=ID option. The values for the text size and weight come from the Discrete Attribute Map shown in Figure 12. Regular values are displayed using 5 pt. normal font while the subgroups labels are displayed using 7 pt. bold font. The values are indented using the IndentWt column. The subgroup labels are not indented.
7. Count and percent values are displayed by another column on the left.
8. The statistics on the right are displayed by an XAXISTABLE of three columns. The labels are shown above each column.
9. The title "Hazard Ratio" is really the X2Axis label, which was enabled using the 2nd scatter plot with zero size markers.
10. Thick reference lines are used for every alternating 3 observations to help the eye across the graph.

The new XAXISTABLE statement provides many flexible options to display tabular data on the left and right side of the graph. The statement creates the appropriate multi-cell LATTICE structure in the generated GTL code to place the tables. The width of each table is computed automatically based on the text attributes.

WATERFALL CHART FOR CHANGE IN TUMOR SIZE

A waterfall chart is commonly used in the Oncology domain to track the change in tumor size for subjects in a study by treatment. The graph displays the change in tumor size for each subject in the study by descending percent change from baseline. A bar is displayed for each subject in decreasing order.

Figure 13. Waterfall Chart for Change in Tumor Size



Each bar is classified by the treatment. The response category is displayed at the end of the bar. Reference lines are drawn at RECIST threshold of -30% and at 20%. The data for the graph is shown in Figure 14, and the SGPLOT procedure code for this graph is shown below.

Figure 14. Data for Waterfall Chart

Obs	Cid	Change	Id	Group	Label
1	1	-14.3910	1	Treatment 1	C
2	2	-65.9578	2	Treatment 1	R
3	3	-71.1846	3	Treatment 1	S

The SGPLOT procedure code for this graph is shown below. The graph contains a hazard ratio plot in the middle created using high-low and scatter plots. The study values and statistics are displayed using axis tables.

```

title 'Change in Tumor Size';
title2 'ITT Population';
proc sgplot data=TumorSize nowall noborder;
  styleattrs datacolors=(cxbf0000 cx4f4f4f) datacontrastcolors=(black);
  vbar cid / response=change group=group categoryorder=respdesc
    datalabel=label datalabelattrs=(size=5 weight=bold)
    groupdisplay=cluster clusterwidth=1;
  refline 20 -30 / lineattrs=(pattern=shortdash);
  xaxis display=none;
  yaxis values=(60 to -100 by -20);
  inset "C= Complete Response" "R= Partial Response" "S= Stable Disease"
    "P= Progressive Disease" "E= Early Death" / title='BCR'
    position=bottomleft border textattrs=(size=6 weight=bold);
  keylegend / title='' location=inside position=topright across=1 border;
run;

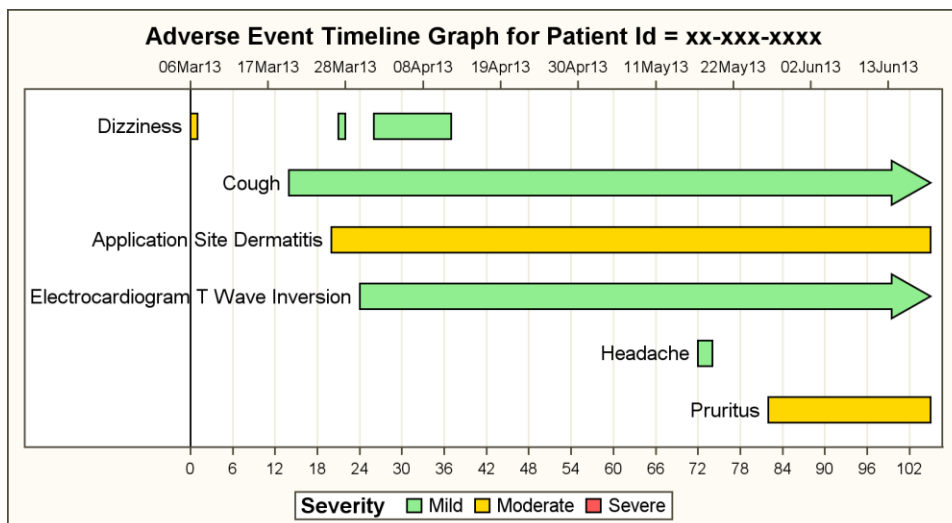
```

The program uses a VBAR statement to draw the bars with CATEGORYORDER=RESPDESC. The data is plotted in descending order of the response.

ADVERSE EVENT TIMELINE

The Adverse Event Timeline graph displays the adverse events for a specific subject by the adverse event and severity over time.

Figure 15. Adverse Event Timeline



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The data for the graph is shown in Figure 16. The columns aeecod, aeesev, stdate and enddate come from the SDTM AE domain. The data might need some cleaning. If the enddate is missing, the highest value from the data is substituted, and the high-cap value is set to "FilledArrow". If an aeecod is repeated, the multiple events are displayed in one row. The aeecod is displayed as the low-label only once.

Figure 16. Data for Adverse Event Timeline

Obs	aeseq	aeecod	aeesev	sev	stdate	enddate	stday	enday	highcap	lowlabel
1	1	Dizziness	Moderate	2	06MAR2013	06MAR2013	0	1		Dizziness
2	2	Cough	Mild	1	20MAR2013	18JUN2013	14	105	FilledArrow	Cough
3	6	Application Site Dermatitis	Moderate	2	26MAR2013	18JUN2013	20	105		Application Site Dermatitis

A discrete attribute map is used to ensure that the severity values are displayed using the colors defined in the map as shown in Figure 17. Green, Gold, and Red colors are used for severity of Mild, Moderate, and Severe. Also note the column "Show" with values of "Attrmap". This causes all values from the map to be displayed in the legend.

Figure 17. Discrete Attribute Map

Obs	Id	Show	Value	Fillcolor	Linecolor
1	Severity	Attrmap	Mild	lightgreen	darkgreen
2	Severity	Attrmap	Moderate	gold	cx9f7f00
3	Severity	Attrmap	Severe	lightred	darkred

CONCLUSION

This paper describes how you can create many commonly requested clinical graphs using the SAS 9.4 SGPLOT procedure. The SAS 9.4 version includes the XAXISTABLE and YAXISTABLE statements that are specifically designed to add axis aligned statistics to a graph.

The XAXISTABLE can be used to add one or more rows of textual data aligned with the x-axis as for a "Subjects At-Risk" table for a survival plot. The YAXISTABLE can be used to add one or more columns of textual data to a graph aligned with the y-axis, such as the statistics table for a forest plot.

REFERENCES

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Phillips, Stacey. 2014. "Swimmer Plot: Tell a Graphical Story of Your Time to Response Data Using PROC SGPLOT." PharmaSUG, San Diego. Available at <http://www.pharmasug.org/proceedings/2014/DG/PharmaSUG-2014-DG07.pdf>

RECOMMENDED READING

Base SAS® Procedures Guide

Statistical Graphics Procedures by Example: Effective Graphics using SAS®

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