A Brief History of ODS Graphics

ODS Graphics was first released with SAS 9.2

- The feature set focused on the needs for creating automatic graphs from SAS analytical procedures.
- The feature set was enhanced in SAS 9.3 and SAS 9.4 to make graphing easy for the general audience.
- Most clinical graphs are easy to create using SAS 9.4.
ODS Graphics Software

ODS Graphics includes the following components:

- Automatic graphs from SAS analytical procedures. No knowledge of graph syntax is required.
- SGRENDER procedure to create graphs using GTL templates. Audience – Advanced Graph Programmer
- SG procedures to create graphs with syntax. Audience – Graph Programmer

All of the above use the Graph Template Language (GTL) to create the graphs, so all graphs produced are consistent in appearance.
The Statistical Graphics (SG) Procedures

The SG Procedures provide an easy to use procedure type syntax for using the GTL features.

- SGPLOT procedure for single-cell graphs.
- SGPANEL procedure for Classification Panels.
- SGSCATTER procedure for comparative scatter plots.

In this presentation, We will primarily focus on the use of the SGPLOT procedure to create clinical graphs.
Structure of a Graph

A SGPILOT graph has the following features:

- Zero or more titles and or footnotes.
- One region in the middle that is used to display the data.
- One or more plots that are used to display the data.
- A set of axes that are shared by the plots in the cell.
- Zero or more legends and or Insets.

In this graph the axis labels are colored to match the data they represent.
SGPLOT Procedure Syntax

PROC SGPLOT <DATA=data-set> <SGANNO=data-set> <DATTRRMAP=data-set> <options>;
  plot-statement(s); /* One or more */
  <styleattrs-statement(s)>;
  <refline-statement(s)>;
  <dropline-statement(s)>;
  <inset-statement(s)>;
  <axis-statement(s)>;
  <keylegend-statement(s)>;
RUN;
SGPLOT Statement Groups

Plot statements can be grouped as follows:

- **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.
- **Other**: Reference line, Inset, Legend, etc.

Simple graphs can be created using just one plot statement. Complex graphs can be created by combining compatible plot statements in layers to create the final graph.
SGPLOT Statement Groups

Plot Combinations:

- **Basic and Fit plots** can be combined with each other and “Other” plots.
- **Distribution plots** can be combined with plots in same group and “Other” plots.
- **Categorical plots** can be combined with plots in same group and “Other” plots.

Now let us review how to create some popular clinical graphs using SAS 9.4 features.
Commonly Requested Clinical Graphs

Let us review how to build the following clinical graphs:

• Median of Lipid Profile by Visit and Treatment.
• Swimmer Plot for Tumor Response.
• Survival Plot.
• Forest Plot by Subgroups.
• Waterfall Chart of Change in Tumor Size.

**Note**: All these graphs will be built using plot statements only. Annotation is not used. This makes the graphs scalable to other data.
Median of Lipid Profile by Visit and Treatment

- This graph displays the median and CL of lipid data by visit and treatment.
- Note the visits are treated as categorical data, and equally spaced on the x-axis.
Median of Lipid Profile by Visit and Treatment

- The median values and CL by treatment for each visit are clustered around each x-axis tick value, so they can be seen clearly.
- The trend line joining the median values by treatment is also clustered so each trend line meets the appropriate value of the median.
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) <options>;
  keylegend 's' / title='Treatment' linelength=20;
  yaxis label='Median with 95% CL' grid;
  xaxis display=(nolabel);
run;
Median of Lipid Profile by Visit and Treatment

• When the visits are not at equal time intervals, it may be desirable to see the visits scaled by time.
• This graph uses a numeric “week” value for visit, and a numeric x-axis to view the data scaled by the visit interval.
Swimmer Plot of Tumor Response

Stacey Phillips: The Swimmer plot is a graphical way of showing multiple parts of a subject’s time to response “story” in one graph.

The graph includes:
• A bar for each subject showing the length of treatment classified by the disease stage.
• Indicators for the start and end of each response episode, classified by complete or partial response.
• Indicators showing “Durable responder”.

Swimmer Plot of Tumor Response

Data for plot

<table>
<thead>
<tr>
<th>Obs</th>
<th>Item</th>
<th>Stage</th>
<th>Low</th>
<th>High</th>
<th>Highcap</th>
<th>Status</th>
<th>Start</th>
<th>End</th>
<th>Durable</th>
<th>Startline</th>
<th>Endline</th>
<th>Xmin</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>Stage 1</td>
<td>0</td>
<td>18.5</td>
<td></td>
<td>Complete response</td>
<td>6.5</td>
<td>13.5</td>
<td>-0.25</td>
<td>6.5</td>
<td>13.5</td>
<td>.</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>Stage 2</td>
<td>0</td>
<td>17.0</td>
<td></td>
<td>Complete response</td>
<td>10.5</td>
<td>17.0</td>
<td>-0.25</td>
<td>10.5</td>
<td>17.0</td>
<td>.</td>
</tr>
<tr>
<td>3</td>
<td>3</td>
<td>Stage 3</td>
<td>0</td>
<td>14.0</td>
<td>FilledArrow</td>
<td>Partial response</td>
<td>2.5</td>
<td>3.5</td>
<td>-0.25</td>
<td>2.5</td>
<td>3.5</td>
<td>.</td>
</tr>
<tr>
<td>4</td>
<td>3</td>
<td></td>
<td>0</td>
<td>14.0</td>
<td>FilledArrow</td>
<td>Partial response</td>
<td>6.0</td>
<td></td>
<td></td>
<td>6.0</td>
<td>13.7</td>
<td>.</td>
</tr>
<tr>
<td>5</td>
<td>4</td>
<td>Stage 4</td>
<td>0</td>
<td>13.5</td>
<td>FilledArrow</td>
<td>Partial response</td>
<td>7.0</td>
<td>11.0</td>
<td></td>
<td>7.0</td>
<td>11.0</td>
<td>.</td>
</tr>
<tr>
<td>6</td>
<td>4</td>
<td></td>
<td>0</td>
<td>13.5</td>
<td>FilledArrow</td>
<td>Partial response</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>.</td>
</tr>
</tbody>
</table>

Tumor Response for Subjects in Study by Month

Subjects Received Study Drug

Each bar represents one subject in the study. Right arrow cap indicates continued response. A durable responder is a subject who has confirmed response for at least 183 days (6 months).

Let us see how we build this graph using SGPLLOT.
Swimmer Plot of Tumor Response

First we represent the duration for each subject by stage in the study using the HighLow plot.

- A Highcap is displayed to indicate continuing response.

```sas
footnote  J=1 h=0.8 'Each bar..";
footnote2 J=1 h=0.8 'A durable..';
title 'Tumor Response for ..';
proc sgplot data= swimmer
  dattrmap=attrmap;
  highlow y=item low=low high=high /
    group=stage highcap=highcap;
  xaxis display=(nolabel);
  yaxis reverse display=(<options>);
  keylegend 'stage';
run;
```
Then we layer the complete or partial response duration and other details.

```sas
proc sgplot data= swimmer dattrmap=attrmap;
  highlow y=item low=low high=high / group=stage highcap=highcap;
  highlow y=item low=startline high=endline / group=status;
  scatter y=item x=start / name='s' <options>;
  scatter y=item x=end / name='e' <options>;
  scatter y=item x=start / <options>;
  scatter y=item x=end / <options>;
  scatter y=item x=xmin / <options>;
  scatter y=item x=durable / <options>;
  xaxis display=(nolabel) label='Months';
  yaxis reverse display=(<options>);
  keylegend 'stage';
  keylegend 'status' 's' 'e' 'd' 'x';
run;
```

Swimmer Plot of Tumor Response
Swimmer Plot of Tumor Response

The graph features can be customize for a gray scale output.
- A YAxisTable is used to display “Stage” on the left of each bar.

Each bar represents one subject in the study. Right arrow cap indicates continued response. A durable responder is a subject who has confirmed response for at least 183 days (6 months).
Survival Plot

- The Product-Limit Survival Estimates plot displays the survival probabilities by stratum over time.
- This plot displays the subjects in the study by stratum over time along the bottom of the graph.
Survival Plot – Get the Data

The data for the graph is obtained from the LIFETEST procedure.

```sas
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=logrankadjust=sidak;
run;
```

<table>
<thead>
<tr>
<th>Obs</th>
<th>Time</th>
<th>Survival</th>
<th>AtRisk</th>
<th>Event</th>
<th>Censored</th>
<th>tAtRisk</th>
<th>Stratum</th>
<th>StratumNum</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0</td>
<td>1.00000</td>
<td>38</td>
<td>0</td>
<td>.</td>
<td>.</td>
<td>1: ALL</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>0</td>
<td>.</td>
<td>38</td>
<td>.</td>
<td>.</td>
<td>0</td>
<td>1: ALL</td>
<td>1</td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>0.97368</td>
<td>38</td>
<td>1</td>
<td>.</td>
<td>.</td>
<td>1: ALL</td>
<td>1</td>
</tr>
<tr>
<td>4</td>
<td>55</td>
<td>0.94737</td>
<td>37</td>
<td>1</td>
<td>.</td>
<td>.</td>
<td>1: ALL</td>
<td>1</td>
</tr>
<tr>
<td>5</td>
<td>74</td>
<td>0.92105</td>
<td>36</td>
<td>1</td>
<td>.</td>
<td>.</td>
<td>1: ALL</td>
<td>1</td>
</tr>
</tbody>
</table>

Note: The LIFETEST procedure creates a Survival Plot automatically. The goal here is to show how to create a customized version using data from the procedure.
Here is a traditional layout with “at-risk” table at the bottom.

- Note the use of solid line pattern for all curves.

```sas
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 / name='c';
  scatter x=time y=censored / group=stratum;
  xaxistable atrisk / x=tatrisk
    class=stratum colorgroup=stratum;
  keylegend 'c' / location=inside;
  keylegend 's';
run;
```
Survival Plot with Alternative Layout

The “At-Risk” table is traditionally displayed at the bottom of the graph.

- This normally places the text values far from the curves with a lot of intervening ink.
- An alternative is to place the table closer to the curves, reducing the distractions.
- This is easily done using the LOCATION=INSIDE option.

```proc lifetest;
xaxistable atrisk / x=tatrisk class=stratum
    colorgroup=stratum location=inside;
```
Survival Plot in Gray Scale

Survival plot for a gray scale medium has special needs.

- Line patterns can be used to distinguish the stratum levels.
- However, line patterns may not be optimal with a step plot.
- So, here I have used solid patterns with curve labels to identify the stratum levels.
### Forest Plot by Subgroups

- A forest plot is used for meta-analysis of the results of randomized controlled trials.
- This plot displays the Hazard Ratio Plot along with other statistics for the study in one plot.

<table>
<thead>
<tr>
<th>Subgroup</th>
<th>No. of Patients (%)</th>
<th>Hazard Ratio</th>
<th>PCI Group</th>
<th>Therapy Group</th>
<th>PValue</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Overall</strong></td>
<td></td>
<td></td>
<td>17.2</td>
<td>15.6</td>
<td>0.05</td>
</tr>
<tr>
<td>Age</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;= 65 Yr</td>
<td>1534 (71)</td>
<td></td>
<td>17</td>
<td>13.2</td>
<td></td>
</tr>
<tr>
<td>&gt; 65 Yr</td>
<td>632 (29)</td>
<td></td>
<td>17.8</td>
<td>21.3</td>
<td></td>
</tr>
<tr>
<td><strong>Sex</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>1690 (78)</td>
<td></td>
<td>16.8</td>
<td>13.5</td>
<td>0.13</td>
</tr>
<tr>
<td>Female</td>
<td>476 (22)</td>
<td></td>
<td>18.3</td>
<td>22.9</td>
<td></td>
</tr>
<tr>
<td><strong>Race or ethnic group</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nonwhite</td>
<td>428 (20)</td>
<td></td>
<td>18.8</td>
<td>17.8</td>
<td>0.52</td>
</tr>
<tr>
<td>White</td>
<td>1738 (80)</td>
<td></td>
<td>16.7</td>
<td>15.0</td>
<td></td>
</tr>
<tr>
<td><strong>From MI to Randomization</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;= 7 days</td>
<td>963 (44)</td>
<td></td>
<td>18.9</td>
<td>18.6</td>
<td>0.81</td>
</tr>
<tr>
<td>&gt; 7 days</td>
<td>1203 (56)</td>
<td></td>
<td>15.9</td>
<td>12.9</td>
<td></td>
</tr>
<tr>
<td><strong>Diabetes</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>446 (21)</td>
<td></td>
<td>29.3</td>
<td>23.3</td>
<td>0.41</td>
</tr>
<tr>
<td>No</td>
<td>720 (79)</td>
<td></td>
<td>14.4</td>
<td>13.5</td>
<td></td>
</tr>
</tbody>
</table>

---

**ssas Federal**

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Forest Plot by Subgroups - Data

- Data for the Forest Plot by Obsld.
- Id determines if the observation is a Group header or values.
- IndentWt determines the amount of indentation.
- Ref column values are missing where horizontal band is not shown.

<table>
<thead>
<tr>
<th>Obs</th>
<th>Obsld</th>
<th>Id</th>
<th>Subgroup</th>
<th>indentWt</th>
<th>Count</th>
<th>Percent</th>
<th>Mean</th>
<th>Low</th>
<th>High</th>
<th>PCIGroup</th>
<th>Group</th>
<th>PValue</th>
<th>ref</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>1</td>
<td>Overall</td>
<td>0</td>
<td>2166</td>
<td>100</td>
<td>1.3</td>
<td>0.90</td>
<td>1.50</td>
<td>17.2</td>
<td>15.6</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>1</td>
<td>Age</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0.05</td>
<td>2</td>
</tr>
<tr>
<td>3</td>
<td>3</td>
<td>2</td>
<td>&lt;= 65 Yr</td>
<td>1</td>
<td>1534</td>
<td>71</td>
<td>1.5</td>
<td>1.05</td>
<td>1.90</td>
<td>17.0</td>
<td>13.2</td>
<td></td>
<td>3</td>
</tr>
<tr>
<td>4</td>
<td>4</td>
<td>2</td>
<td>&gt; 65 Yr</td>
<td>1</td>
<td>632</td>
<td>29</td>
<td>0.8</td>
<td>0.60</td>
<td>1.25</td>
<td>17.8</td>
<td>21.3</td>
<td></td>
<td>4</td>
</tr>
<tr>
<td>5</td>
<td>5</td>
<td>1</td>
<td>Sex</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0.13</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>6</td>
<td>2</td>
<td>Male</td>
<td>1</td>
<td>1690</td>
<td>78</td>
<td>1.5</td>
<td>1.05</td>
<td>1.90</td>
<td>16.8</td>
<td>13.5</td>
<td></td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>7</td>
<td>2</td>
<td>Female</td>
<td>1</td>
<td>476</td>
<td>22</td>
<td>0.8</td>
<td>0.60</td>
<td>1.30</td>
<td>18.3</td>
<td>22.9</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Forest Plot by Subgroups – Hazard Ratio

First we display the graphical Hazard Ratio information by Study

title 'Impact on Treatment by Subgroups';
proc sgplot data=forest_subgroup_2;
    styleattrs axisextent=data;
    refline ref / <options>;
    highlow y=obsid low=low high=high;
    scatter y=obsid x=mean / <options>;
    refline 1 / axis=x;
    text x=xl y=obsid text=text / <options>;
    yaxis reverse display=none;
    xaxis display=(nolabel) <options>;
    x2axis label='Hazard Ratio' / <options>;
run;

Some options are trimmed to fit the space.
Add display of the columns on the left side

```javascript
title 'Impact on Treatment by Subgroups';
proc sgplot data=forest_subgroup_2;
  styleattrs axisextent=data;
  refline ref / <options>;
  highlow y=obsid low=low high=high;
  scatter y=obsid x=mean / <options>;
  refline 1 / axis=x;
  text x=xl y=obsid text=text / <options>;
  yaxistable subgroup / <options>;
  yaxistable countpct / <options>;
  yaxis reverse display=none;
  xaxis display=(nolabel) <options>;
  x2axis label='Hazard Ratio' / <options>;
run;
```

Some options are trimmed to fit the space.
Forest Plot by Subgroups – Left Columns

Add display of the columns on the right side

title 'Impact on Treatment by Subgroups';
proc sgplot data=forest_subgroup_2;
   styleattrs axisextent=data;
   refline ref / <options>;
   highlow y=obsid low=low high=high;
   scatter y=obsid x=mean / <options>;
   refline 1 / axis=x;
   text x=x1 y=obsid text=text / <options>;
   yaxistable subgroup / <options>;
   yaxistable countpct / <options>;
   yaxistable PCIGrp group pval / <options>;
   yaxis reverse display=none;
   xaxis display=(nolabel) <options>;
   x2axis label='Hazard Ratio' / <options>;
run;

Some options are trimmed to fit the space.

Impact on Treatment by Subgroups

<table>
<thead>
<tr>
<th>Subgroup</th>
<th>No. of Patients (%)</th>
<th>Hazard Ratio</th>
<th>PCI Group</th>
<th>Therapy Group</th>
<th>PValue</th>
</tr>
</thead>
<tbody>
<tr>
<td>Overall Age</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;= 65 Yr</td>
<td>2166 (100)</td>
<td>17.2</td>
<td>15.6</td>
<td></td>
<td>0.05</td>
</tr>
<tr>
<td>&gt; 65 Yr</td>
<td>1534 (71)</td>
<td>17.8</td>
<td>13.2</td>
<td></td>
<td>0.13</td>
</tr>
<tr>
<td>Sex</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>1690 (78)</td>
<td>16.8</td>
<td>13.5</td>
<td></td>
<td>0.52</td>
</tr>
<tr>
<td>Female</td>
<td>476 (22)</td>
<td>19.3</td>
<td>22.9</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Race or Ethnic Group</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nonwhite</td>
<td>428 (20)</td>
<td>18.8</td>
<td>17.8</td>
<td></td>
<td>0.81</td>
</tr>
<tr>
<td>White</td>
<td>1738 (80)</td>
<td>16.7</td>
<td>15</td>
<td></td>
<td></td>
</tr>
<tr>
<td>From MI to Randomization</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;= 7 days</td>
<td>983 (44)</td>
<td>18.9</td>
<td>16.6</td>
<td></td>
<td>0.41</td>
</tr>
<tr>
<td>&gt; 7 days</td>
<td>1203 (56)</td>
<td>15.9</td>
<td>12.9</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Diabetes</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>446 (21)</td>
<td>29.3</td>
<td>23.3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>720 (79)</td>
<td>14.4</td>
<td>13.6</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Each bar represents one subject in the study. Right arrow cap indicates continued response. A durable responder is a subject who has confirmed response for at least 183 days (6 months).
Waterfall Chart of 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.
- This plot displays the change in tumor size for each patient in the study as a bar classified by treatment, sorted by percent change.
Waterfall Chart of Change in Tumor Size

```sas
proc sgplot data=TumorSize noborder;
    styleattrs datacolors=(cxbf0000 cx4f4f4f);
    vbarparm category=cid response=change /
        group=group;
refline 20 -30;
xaxis display=none;
yaxis values=(60 to -100 by -20);
inset "C= Complete Response"
    "R= Partial Response " ...
    position=bottomleft border;
keylegend / location=inside
    across=1 border;
run;
```

Change in Tumor Size
ITT Population

- Treatment 1
- Treatment 2

- C= Complete Response
- P= Partial Response
- S= Stable Disease
- P= Progressive Disease
- E= Early Death

Change from Baseline (%)
Waterfall Chart of Change in Tumor Size

Here is an alternate view of the same graph with a band plot.
Conclusion

• The SAS 9.4 SGPLOT procedure provides new features that simplify creating clinical graphs.

• The XAxisTable and YAxisTable statement included in SAS 9.4 SGPLOT make it easy to add tabular data to graphs.

• The SAS 9.3 SGPLOT procedure can be used to create such graphs using the SGAnnotate feature. For more information on this, see:
  
References


- Graphically Speaking Blog by Sanjay Matange. Available at: http://blogs.sas.com/content/graphicallyspeaking/