

Unleashing Potential of Graphs for Oncology Trials

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ABSTRACT

Graphical representation of data is always instrumental in analysis and interpretation of complex clinical data. One of the multifaceted therapeutic area is oncology dealing with tumors. Usually in oncology trials, overall drug response is analyzed using the RECIST criteria. The graphical representation of the RECIST criteria elaborates the intricacies of the finer data points of the tumor responses. The different graphical representation brings out different pivotal points of the tumor response data.

This paper will discuss the different kinds of graphs like Kaplan-Meier plots, waterfall plots, swimmer plots, spider plots, bar and forest plots with the help of SAS Graph procedures.

INTRODUCTION

Graphical representation of data is always instrumental in analysis and interpretation of complex data. In oncology, survival plot is commonly used to demonstrate the progression-free survival (PFS), overall survival (OS) and other end points. Other types of graphs can also be used to visualize the RECIST criteria responses. Waterfall plot is used to depict the tumor growth or shrinkage. Other types of graphs can be used to show the individual patient tumor response change over time. Forest plot is used to show the effect of covariates on the primary outcome. Similarly, a simple bar graph can also be used to depict the change in lesion diameter over time.

In this paper, I have demonstrated the different types of graphs used in oncology trials and how these graphs can be generated by using SAS®. These graphs are generated with help of SAS® 9.4 ODS Statistical Graphics (SG) procedures and Graph Template Language (GTL).

BAR GRAPH

Bar graphs are simple graphs which visualize categorical data by using rectangular bars. The height or length of these bars are proportional to the values that they represent. These bars can be displayed vertically or horizontally. Bar graphs usually show the comparison between the different categories.

In the below example (Figure 1), a bar graph is used to display the change in sum of lesion diameter and lesion diameter results over time, for a single subject. For more than one subjects it can be generated by creating a macro. This can be easily generated by using GTL procedure. Below is the snippet of dataset used in GTL procedure. The graph also displays a secondary y axis that represents the Sum of Lesion diameter for the subject.

Table 1: Snippet of data set used for Bar Graph

Obs	PATIENTID	VISIT	TRSTRESN	SUMLD	TULOC
1	1001	Screening	28	107	Liver
2	1001	Screening	32	.	Liver2
3	1001	Screening	22	.	Lung
4	1001	Screening	11	.	Other
5	1001	Screening	14	.	Other2
6	1001	Week 6	21	82	Liver
7	1001	Week 6	21	.	Liver2
8	1001	Week 6	17	.	Lung
9	1001	Week 6	11	.	Other
10	1001	Week 6	12	.	Other2

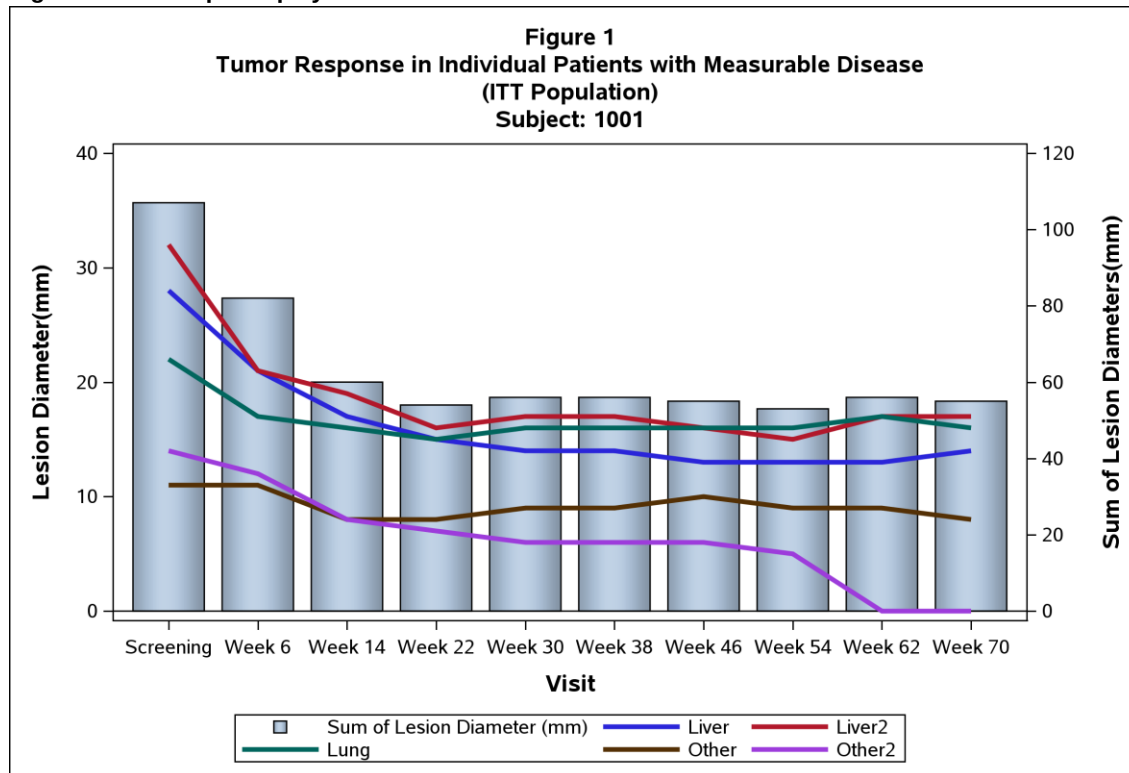
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Code for Figure 1

```
Proc Template;
  Define statgraph bar;
    dynamic xvar yvar _group patientid;
    Begingraph;
      Entrytitle "Figure 1";
      Entrytitle "Tumor Response in Individual Patients with Measurable Disease";
      Entrytitle "(ITT Population)";
      Entrytitle "Subject: " "1001";
      Layout overlay/ yaxisopts=(label="Lesion Diameter(mm) "
        labelattrs=(weight=bold size=11) linearopts=( viewmin=0.0
        thresholdmin=1 thresholdmax=1))
        y2axisopts=(label="Sum of Lesion Diameters(mm) "
        labelattrs=(weight=bold size=11) linearopts=( thresholdmin =1
        thresholdmax =1))
        xaxisopts=(label="Visit" labelattrs=(weight=bold size=11)) ;
      barchart x=visit y=SUMLD/yaxis = y2 skin=modern name="ser" barwidth=0.8;
      seriesplot x= visit y=trstresn/ group=tuloc name="series"
        lunettes=(pattern = solid thickness = 3 );
      discretelegend "ser" "series";
    Endlayout;
  Endgraph;
End;
Run;

Proc Sgrender data=bar template=bar;
Run;
```

Figure 1: Bar Graph displays Lesion Diameter for Measurable Disease



WATERFALL PLOT

Waterfall plot is a very common and widely used plot in Oncology trials. The idea of a waterfall plot is to show the individual patient's response to the therapy or drug. It shows the maximum percentage change in tumor measurement after therapy. A waterfall plot looks like an ordered bar, where each vertical bar represents an individual patient or subject's response and that can be further sub grouped by colors or symbols for easy visualization. Individual patient response is sorted in descending order from left to right for easy interpretation of the maximum percentage change in tumor measurement or response. Tumor response can be easily interpreted as shrinkage if it is below the baseline (negative) and tumor progression if it is above the baseline (positive). The length of these vertical bars is proportional to the percentage change in tumor response. In this plot (Figure 2), we could add the different colors for each response (e.g., complete response, stable disease, partial response, progressive disease etc.) to get more clarity about the responses. The general convention is to represent each subject on the horizontal axis.

The optimal percentage of change in the sum of target lesion dimensions is calculated and sorted by decreasing values of percent change. Below is the snippet of dataset, used for waterfall plot.

Table 2: Snippet of dataset used for Waterfall Plot

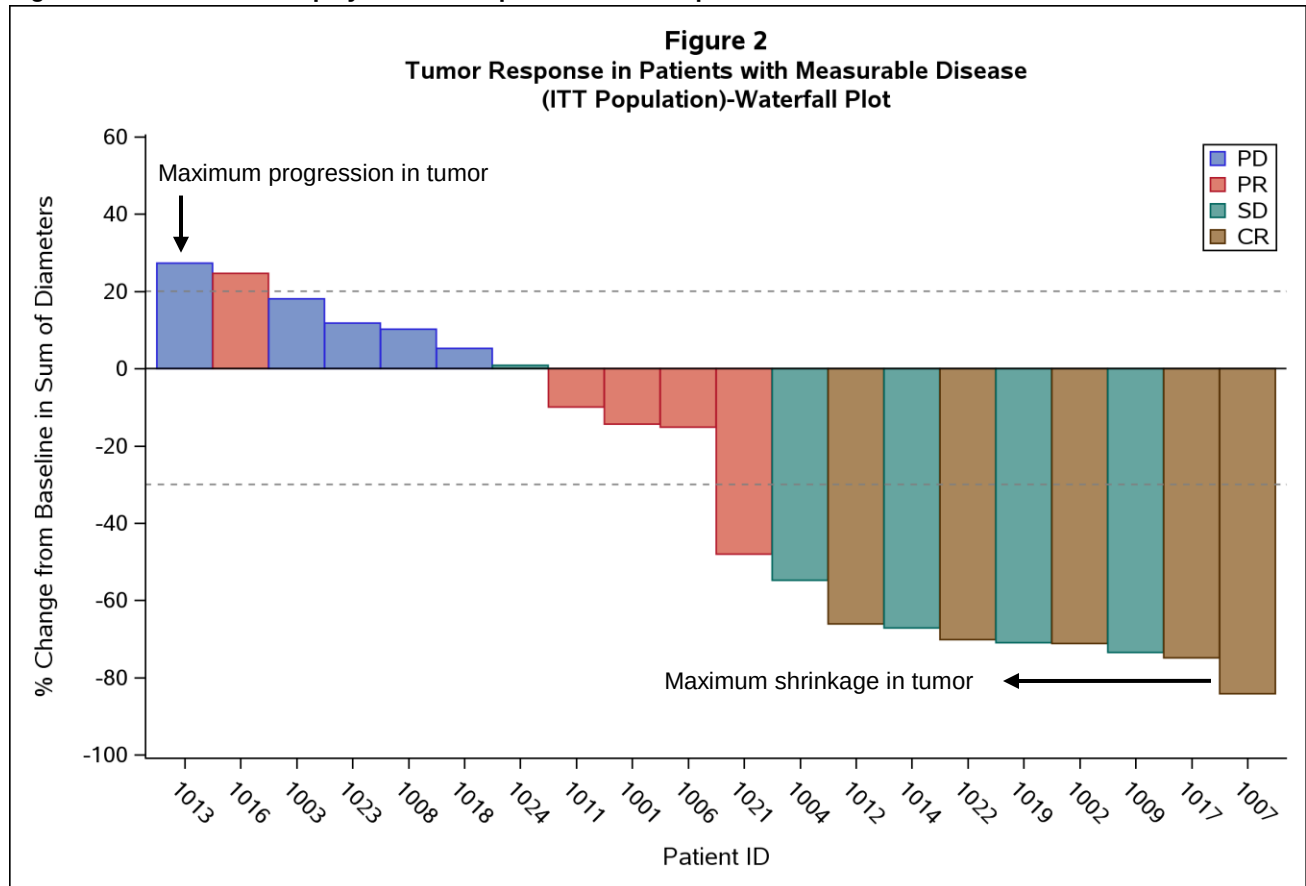
Obs	PATIENTID	CHANGE	LABEL
1	1013	27.2837	PD
2	1016	24.6283	PR
3	1003	18.0494	PD
4	1023	11.7591	PD
5	1008	10.1804	PD
6	1018	5.2145	PD
7	1024	0.8248	SD
8	1011	-9.9663	PR
9	1001	-14.3910	PR
10	1006	-15.1768	PR

Code for Figure 2

```
Title1 'Figure 2' ;
Title2 'Tumor Response in Patients with Measurable Disease';
Title3 '(ITT Population)-Waterfall Plot';

Proc Sgplot data=Tumor nowall noborder;
  Vbarparm category=patientid response=change / group=label
  Datalabelattrs=(size=5 weight=bold) groupdisplay=cluster clusterwidth=1;
  Refline 20 -30 / lineattrs=(pattern=shortdash);
  Xaxis label= "Patient ID";
  Yaxis values=(60 to -100 by -20) label= "% Change from Baseline in Sum of
  Diameters";
  Keylegend / title='' location=inside position=topright across=1 border;
Run;
```

Figure 2: Waterfall Plot displays Individual patient tumor response

**SWIMMER PLOT**

A swimmer plot is a very effective and powerful visual tool to display the multiple pieces of information of an individual patient in a single plot. In general, it tells **“a story”** of study drug effect(s) on tumor response for the individual patient.

In this example a swimmer plot shows different pieces of information about the individual patient's tumor response which are on X-axis, e.g., 1) duration of response (0 to 18 months), 2) when response started and ended, or responses are still ongoing, 3) whether these responses are complete or partial and 4) what is the disease stage at baseline. The Y-axis displays the individual subjects that received the study drug. Swimmer plot is sorted by the individual patient's response duration in ascending. A longer duration of treatment would suggest the better tolerability and treatment outcomes. Different type of symbols and colors are used to depict the individual patient's response to study drug. Swimmer plot is more effective to visualize small number of patient's tumor response with duration, but it becomes cluttered and uninformative if too many variables are included. It shows a clear graphical display of duration of individual response and shows which patient continues to benefit from the treatment.

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Table 3.1 Snippet of data set used for Swimmer Plot

Obs	PATIENTID	STAGE	LOW	HIGH	HIGHCAP	STATUS	START	END	DURABLE	STARTLINE	ENDLINE	YMIN
1	1001	Stage 1	0	16.5	FilledArrow	Complete response	6.5	13.5	-0.25	6.5	13.5	-1
2	1002	Stage 2	0	15.0		Complete response	10.5	14.0	-0.25	10.5	14.0	-1
3	1003	Stage 3	0	14.0	FilledArrow	Partial response	2.5	3.5	-0.25	2.5	3.5	-1
4	1003		0	14.0	FilledArrow	Partial response	6.0	.	.	6.0	13.7	-1
5	1004	Stage 4	0	13.5	FilledArrow	Partial response	7.0	11.0	.	7.0	11.0	-1
6	1004		0	13.5	FilledArrow	Partial response	11.5	.	.	11.5	13.2	-1
7	1005	Stage 1	0	12.5	FilledArrow	Complete response	3.5	4.5	-0.25	3.5	4.5	-1
8	1005		0	12.5	FilledArrow	Complete response	6.5	8.5	.	6.5	8.5	-1
9	1005		0	12.5	FilledArrow	Partial response	10.5	.	.	10.5	12.2	-1
10	1006	Stage 2	0	12.6	FilledArrow	Partial response	2.5	7.0	.	2.5	7.0	-1

Table 3.2. Snippet of annotation data set used in Swimmer Plot

Obs	ID	LINECOLOR	MARKERCOLOR	VALUE
1	status	green	green	Complete response
2	status	darkred	darkred	Partial response

Code for Figure 3

```

Title1 'Figure 3';
Title2 'Time to Response';

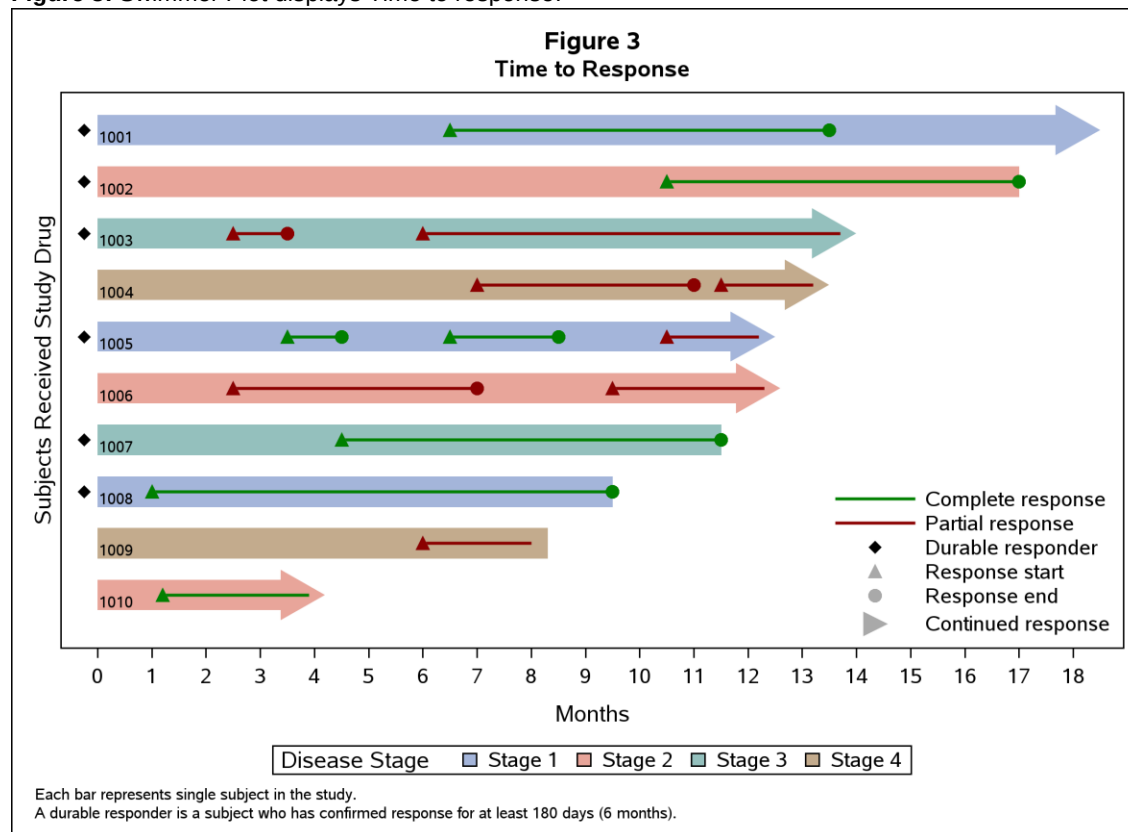
Footnote1 J=1 h=0.8 'Each bar represents single subject in the study.';
Footnote2 J=1 h=0.8 'A durable responder is a subject who has confirmed response for
                    at least 180 days (6 months).';

Proc Sgplot data= swimmer dattrmap=attrmap nocycleattrs;
  Highlow y=patientid low=low high=high / highcap=highcap type=bar group=stage fill
  nooutline
  Lineattrs=(color=black) name='stage' barwidth=1 nomissinggroup transparency=0.3;
  Highlow y=patientid low=startline high=endline / group=status
  lineattrs=(thickness=2 pattern=solid) name='status' nomissinggroup attrid=status;
  Scatter y=patientid x=start / markerattrs=(symbol=trianglefilled size=8
  color=darkgray) name='s' legendlabel='Response start';
  Scatter y=patientid x=end / markerattrs=(symbol=circlefilled size=8
  color=darkgray) name='e' legendlabel='Response end';
  Scatter y=ymin x=low / markerattrs=(symbol=trianglerightfilled size=14
  color=darkgray) name='x' legendlabel='Continued response ';
  Scatter y=patientid x=durable / markerattrs=(symbol=diamondfilled size=6
  color=black) name='d' legendlabel='Durable responder';
  Scatter y=patientid x=start / markerattrs=(symbol=trianglefilled size=8)
  group=status attrid=status;
  Scatter y=patientid x=end / markerattrs=(symbol=circlefilled size=8)
  group=status attrid=status;
  Scatter y=patientid x=low / DataLabel=patientid DataLabelattrs=(Color=black)
  markerattrs=(size=0);
  Xaxis label='Months' values=(0 to 20 by 1) valueshint;
  Yaxis reverse display=(noticks novalues noline)label='Subjects Received Study
  Drug' min=1;
  Keylegend 'stage' / title='Disease Stage';
  Keylegend 'status' 'd' 's' 'e' 'x' /noborderlocation=inside position=bottomright;
Run;

```

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Figure 3: Swimmer Plot displays Time to response.



SPIDER PLOT

A spider plot is yet another way to visualize the changes in tumor response of individual patients over time. Basically, the spider plot is a series plot but when the data represented generates a pattern of these series, it plots like legs of spider. In Figure 4, each leg of the spider represents a unique patient and horizontal reference line at 1 on Y axis shows the baseline relative value. In spider plot, pre-treatment (negative values on X axis) and post-treatment (positive values on X axis) tumor responses can be easily compared to baseline (0) for individual patient level, and thus the data plotted in percentage change from baseline over the period for the individual patient evaluation. We can add additional information by exploring the line color and line style. Though, there could be missing information in spider plot if a patient is dead early in the trial. Therefore, the spider plot is good to show the qualitative assessment of individual patient tumor response. These plots are less interpretable if larger number of patients are displayed because it will be difficult to follow the individual lines, especially when they overlapped and crossed with each other.

This plot will help to avoid the scenario of values getting missed out in the display. The usefulness of this graph stems from the fact that it tells a story of what happens to each of these tumors over time, while the waterfall plot focuses on the best response measure only.

Table 4: Snippet of dataset used for Spider Plot

Obs	PATIENTID	DUR	SIZE
1	1001	-40	1.2
2	1001	0	1
3	1001	30	0.8
4	1001	40	0.95
5	1001	65	0.99
6	1002	-50	0.8

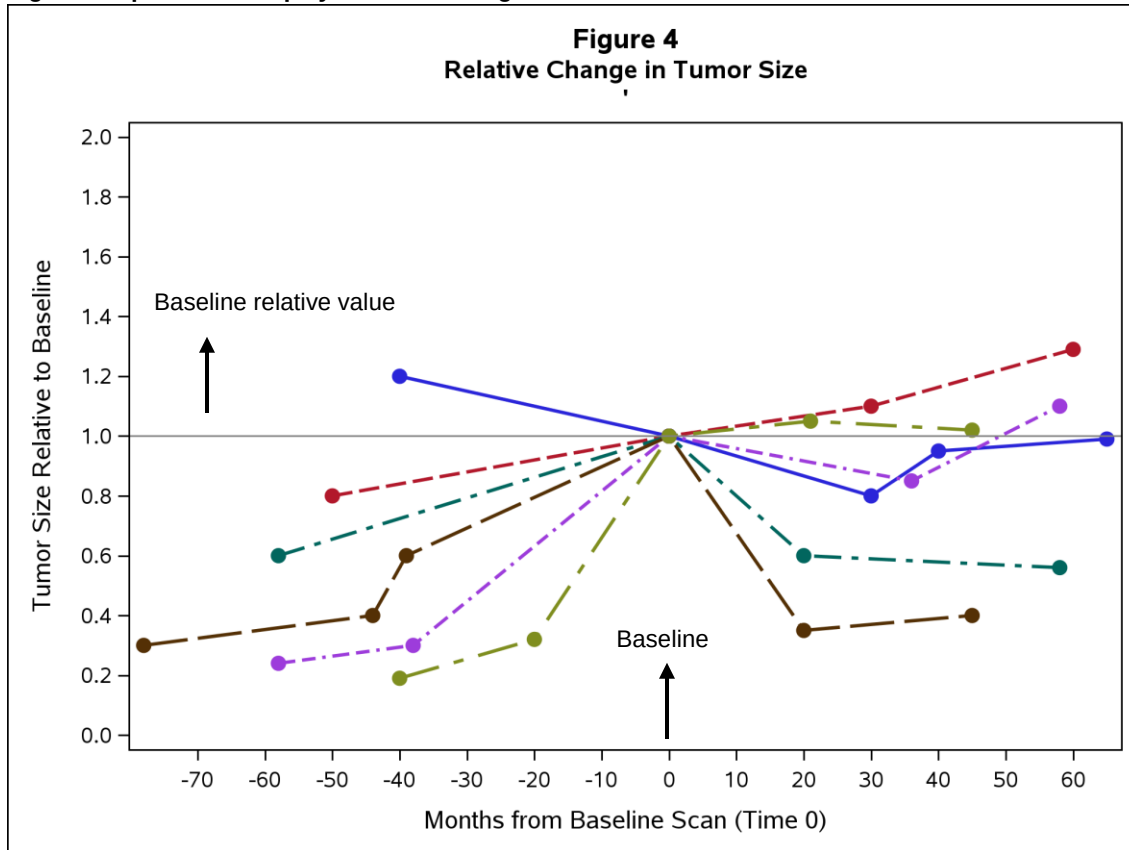
Code for Figure 4

```

Title1 "Figure 4";
Title2 "Relative Change in Tumor Size";

Proc Sgplot data=tumor noautolegend;
  Series x=dur y=size / lineattrs=(thickness=2)
  group=patientid markers markerattrs=(symbol=circlefilled size=8);
  Refline 1.0;
  Yaxis label="Tumor Size Relative to Baseline" values= (0 to 2 by .20);
  Xaxis label="Months from Baseline Scan (Time 0)" values=(-100 to 100 by 10)
  valueshint;
Run;

```

Figure 4: Spider Plot displays relative change in tumor size**KAPLAN-MEIER PLOT**

Mostly, phase III Oncology trials are often done to detect a progression-free survival or overall survival endpoint. Kaplan-Meier (KM) plot remains one of the best visualization tools for survival analysis data in oncology trials. This plot was introduced by Edward L. Kaplan and Paul Meier in 1958. In oncology trials, the effect of a study drug is often assessed by measuring the number of patients who survived or those free of progression/ disease after the therapy or treatment over a period. It allows the comparison of survival outcomes (eg; alive/dead, free of disease/relapsed) in different groups over time. To generate the KM plot, first step is to calculate the KM estimates with the help of Proc Lifetest procedure which needs the three key elements, namely, 1) serial time, 2) status of serial time (0=censored, 1=event) and 3) treatment group (1=group 1, 2=group2 etc.). Second step is graphing the outputted data with SAS GRAPH procedures and options.

In this example, the KM plot is generated by using ODS template with GTL graph template. This plot shows the survival rate by time in months for two treatment groups. The summary statistics can be displayed within the graph. Below is the snippet of survival dataset.

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Table 5: Snippet of data set used for Kaplan-Meier Plot

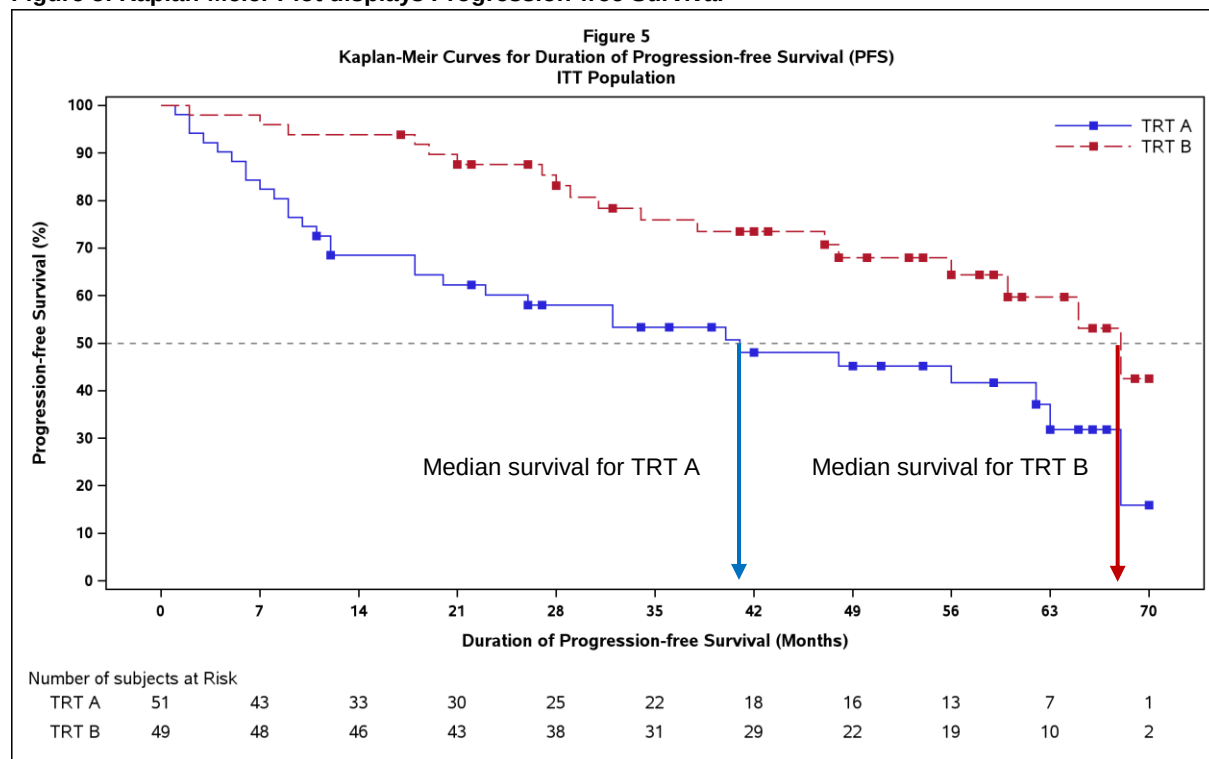
Obs	STRATUM	TIME	SURVIVAL	CENSORED	ATRISK	TATRISK
1	TRT A	0	100.000	.	51	.
2	TRT A	0	.	.	51	0
3	TRT A	1	98.039	.	51	.
4	TRT A	2	94.118	.	50	.
5	TRT A	2	94.118	.	50	.
6	TRT A	3	92.157	.	48	.
7	TRT A	4	90.196	.	47	.
8	TRT A	5	88.235	.	46	.
9	TRT A	6	84.314	.	45	.
10	TRT A	6	84.314	.	45	.

Code for Figure 5

```
Proc Template;
  Define statgraph SurvivalPlot;
    Begingraph / designwidth=8in designheight=5in;
      Entrytitle 'Figure 5' / textattrs=(size=8);
      Entrytitle 'Kaplan-Meier Curves for Duration of Progression-free Survival
        (PFS)' / textattrs=(size=8);
      Entrytitle 'ITT Population' / textattrs=(size=8);
      Layout lattice / rowweights=(0.75 .05 .08);
      Layout overlay /
        Xaxisopts=(Label="Duration of Progression-free Survival (Months)"
          type=linear offset min= .05 offsetmax= .05 labelattrs=(size=8pt
            weight=bold) tickvalueattrs=(size=7pt weight=bold)
            linearopts=(viewmin=0 viewmax=70 tickvaluelist=(0 7 14 21 28 35 42 49 56
              63 70)));
        yaxisopts=(Label="Progression-free Survival (%)" linearopts=(viewmin=0
          viewmax=100)
          labelattrs=(size=8pt weight=bold) tickvalueattrs=(size=7pt weight=bold)
          linearopts=(viewmin=0 viewmax=100 tickvaluelist=( 0 10 20 30 40 50 60
            70 80 90 100)));
        Stepplot x=time y=survival / group=stratum name='s';
        Scatterplot x=time y=censored / GROUP=stratum name='c'
          markerattrs=(symbol=squarefilled size=5); referenceline y=50/
          Lineattrs=(pattern=shortdash);
        Mergedlegend "c" "s" / location=inside halign=right valign=top
          order=columnmajor down=2 border=false valueattrs=(size=8pt)
          Pad=(top=5 bottom=5);
      Endlayout;
      Layout overlay;
        Entry halign=left 'Number of subjects at Risk' /pad=(left=0 )
          Valign=bottom textattrs=(size=8pt);
      Endlayout;
      Blockplot x=tatrisk block=atrisk / class=stratum display=(values label)
        Valuehalign=start valueattrs=(size=8) labelattrs=(size=8);
      Endlayout;
    Endgraph;
  End;
Run;

Proc Sgrender data=survival template=Survivalplot;
Run;
```


Figure 5: Kaplan-Meier Plot displays Progression-free Survival



FOREST PLOT

A forest plot is designed to illustrate the relative treatment effect of a study drug or therapy by providing a visual representation of the amount of variation between the groups. Traditionally, forest plots have been used in Meta-analysis to show the variability across studies. Forest plots are useful in considering the behaviors of subgroups in larger dataset. For example, the benefit of treatment may be small for in large sample but separating out and analyzing the effect of treatment in different subgroups may sometimes identify those who may benefit more.

In figure 6, for each subgroup are displayed on y axis and for each subgroup there is a square box which depicts the hazard ratio and horizontal line represents the 95% confidence interval of hazard ratio. A vertical line at 1, on x axis represents the null hypothesis. The direction of the effect of treatment depends on which side of central line the central point lies. Inserting the table of results in graph gives it more effective and quick interpretation of results. The overall summary of effect of treatment is represented by the diamond symbol.

Table 6: Snippet of data set used for Forest Plot

Obs	HEADING	SUBGROUP	TRTA	TRTB	MEAN	LOW	HIGH	CI	OBSID
1	All Patients		63 (42)	64 (48)	.	0.5	1.15	0.75 (0.50, 1.15)	1
2	Age				.	.	.		2
3		<= 65 Years	42 (26)	32 (27)	0.69	0.4	1.19	0.69 (0.40, 1.19)	3
4		> 65 Years	21 (16)	32 (21)	0.81	0.42	1.57	0.81 (0.42, 1.57)	4
5	Sex				.	.	.		5
6		Male	20 (13)	33 (27)	1.5	1.05	1.9	1.50 (1.05, 1.90)	6
7		Female	43 (10)	31 (21)	0.8	0.6	1.3	0.80 (0.60, 1.30)	7
8	Race or ethnic group				.	.	.		8
9		Non-white	37 (23)	36 (29)	0.61	0.35	1.07	0.61 (0.35, 1.07)	9
10		White	26 (19)	28 (19)	1.01	0.53	1.91	1.01 (0.53, 1.91)	10
11	Visceral Disease				.	.	.		11
12		Yes	36 (24)	32 (27)	0.5	0.29	0.88	0.50 (0.29, 0.88)	12
13		No	27 (18)	32 (21)	1.17	0.62	2.2	1.17 (0.62, 2.20)	13
14	Disease Free Interval (DFI)				.	.	.		14
15		DFI <= 12 months	19 (10)	17 (12)	0.67	0.29	1.55	0.67 (0.29, 1.55)	15
16		DFI > 12 months	44 (32)	47 (36)	0.8	0.49	1.3	0.80 (0.49, 1.30)	16

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Code for Figure 6

```
Proc Template;
  Define statgraph Forestplot;
    Dynamic _bandcolor _headercolor _subgroupcolor;
    Begingraph;
      Entrytitle 'Figure 5'/ textattrs=(size=8);
      Entrytitle 'Forest Plot for Duration of Radiographic Progression-free
        Survival (rPFS)-Subgroup Analysis'/ textattrs=(size=8);
      Entrytitle 'ITT Population'/ textattrs=(size=8);
      Entrytitle '';
      Layout lattice / columns=5 columnweights=(0.3 0.1 0.1 0.325 0.175);
      Sidebar / align=top;
      Layout lattice / rows=2 columns=4 columnweights=(0.23 0.1 0.35 0.15)
        Backgroundcolor=_headercolor opaque=true;
      Entry textattrs=(size=8 weight=bold) halign=left "Subgroup";
      Entry textattrs=(size=8 weight=bold) halign=left "Treatment A";
      Entry textattrs=(size=8 weight=bold) halign=left "Treatment B";
      Entry textattrs=(size=8 weight=bold) halign=left "Hazard Ratio 95% CI";
      Entry textattrs=(size=8 weight=bold) halign=left "";
      Entry textattrs=(size=8 weight=bold) halign=left "N (Events)";
      Entry textattrs=(size=8 weight=bold) halign=left "N (Events)";
      Endlayout;
    Endsidebar;

    Layout overlay / walldisplay=none
      Xxaxisopts=(display=none linearopts=(viewmin=0 viewmax=20))
      Yaxisopts=(reverse=true display=none tickvalueattrs=(weight=bold));
      Referenceline y=ref / lineattrs=(thickness=15 color=_bandcolor);
      Highlowplot y=obsid low=zero high=zero / highlabel=heading
        lineattrs=(thickness=0) labelattrs=(size=8 weight=bold);
      Highlowplot y=obsid low=zero high=one / highlabel=subgroup
        Lineattrs=(thickness=0) labelattrs=(size=8 );
      Endlayout;

    Layout overlay / xaxisopts=(display=none)
      Yaxisopts=(reverse=true display=none) walldisplay=none;
      Referenceline y=ref / lineattrs=(thickness=15 color=_bandcolor);
      Scatterplot y=obsid x=zero / markercharacter=trta
        Markercharacterattrs=graphvaluetext markercharacterattrs=(size=7.5);
      Endlayout;

    Layout overlay / xaxisopts=(display=none)
      Yaxisopts=(reverse=true display=none) walldisplay=none;
      Referenceline y=ref / lineattrs=(thickness=15 color=_bandcolor);
      Scatterplot y=obsid x=zero / markercharacter=trtb
        markercharacterattrs=graphvaluetext markercharacterattrs=(size=7.5);
      Endlayout;

    Layout overlay /xaxisopts=(labelattrs=(size=8pt) label='Treatment A Treatment B'
      linearopts=(tickvaluepriority=true tickvaluelist=(0.0 0.5 1.0 1.5 2.0 2.5)))
      Yaxisopts=(reverse=true display=none) walldisplay=none;
      Referenceline y=ref / lineattrs=(thickness=15 color=_bandcolor);
      Scatterplot y=obsid x=mean / xerrorlower=low xerrorupper=high
        Markerattrs=(symbol=squarefilled size=8);
      Scatterplot y=obsid x=dia / xerrorlower=low xerrorupper=high
        Markerattrs=(symbol=diamondfilled size=9);
      Referenceline x=1 ;
      Referenceline x=0.5 / lineattrs=(pattern=shortdash);
      Referenceline x=1.5 / lineattrs=(pattern=shortdash);
      Referenceline x=0.5 / lineattrs=(pattern=shortdash);
      Referenceline x=1.5 / lineattrs=(pattern=shortdash);
      Endlayout;
  End;
Run;
```

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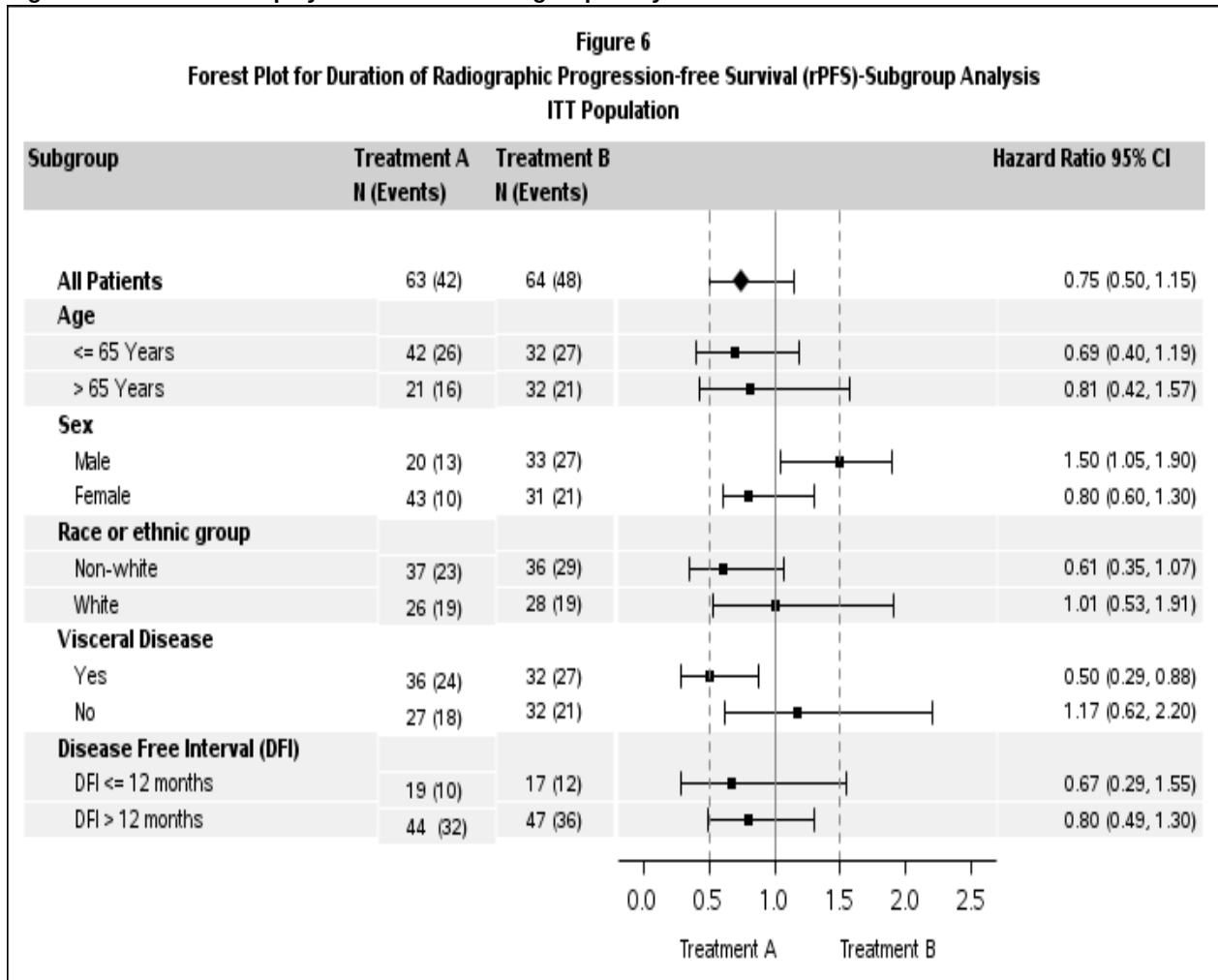
```

Layout overlay / x2axisopts=(display=(tickvalues) offsetmin=0.25 offsetmax=0.25)
                    Yaxisopts= (reverse=true display=none) walldisplay=none;
Referenceline y=ref / lineattrs= (thickness=15 color=_bandcolor);
InnerMargin / align=right;
AxisTable y=obsId value=ci / display=(values);
EndInnerMargin;
Endlayout;
Endlayout;
Endgraph;
End;
Run;

Proc Sgrender data=Forest template=Forestplot;
    dynamic _bandcolor='cxf0f0f0' _headercolor='cxd0d0d0';
Run;

```

Figure 6: Forest Plot displays the results of subgroup analysis



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Comparison between different types of graphs

Types of Graph	Pros	Cons
Bar graph	Easy to generate and interpret the results	Takes more space as compare to other plots
Waterfall plot	Summaries the best overall response in the individual patient	Only shows one response/measurement in time and tumor response which may not show the actual patient benefit in terms of overall survival or progression free survival
Swimmer plot	Shows tumor response and time duration of response	Become uninformative if the more subjects are included
Spider plot	Shows the tumor response across all time rather than specified time	Difficult to interpret if too many subjects are included and does not allow for formal statistical inference
Kaplan Meier plot	Shows the estimation of survival and comparison between groups	It's a univariate analysis, which does not include the other effects on drug
Forest plot	Determine the effects of groups/subgroups on drugs and also displays the efficacy results with inserted table	Could give the false interpretation if there are small number of datapoints with in sub groups

CONCLUSION

This paper has highlighted some of the plots that have emerged as useful tools to enhance the data visualization and interpretation of complex patients' outcome/results in oncology trials. Despite the complexity of oncology data, the conventional (eg; Kaplan-Meier plot) and novel (eg; spider and swimmer plot) representation of data visualization, along with some customization can tell a complete story of the oncology end points, such as overall survival (OS), progression free survival (PFS), objective response rate (ORR), percentage change in tumor size etc. SAS graphical procedures (SG Procedures/GTL) and SAS/GRAPH Annotate facility provide the flexibility to programmers to generate these customized graphs.

REFERENCES

- Past PharmaSUG Conference Proceedings. Available at <http://www.pharmasug.org/proceedings.html>.
- <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5017943/>
- <http://support.sas.com/resources/papers/proceedings16/7520-2016.pdf>
- Matange, Sanjay. "Clinical Graphs using ODS Graphics."

CONTACT INFORMATION

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