

Building swimmer plots using SAS® 9.4

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Abstract

Swimmer plots provide the capability to quickly and intuitively understand the clinical progression of a subject during an oncology trial, as well as visually comparing individual subjects on various regimens. A variety of time to response variables can be plotted to give the viewer an easy-to-understand graphical overview of a subject's timeline, including tumor status milestones, duration of response, and prior/concomitant therapies. In addition, significant other occurrences such as adverse events of special interest can be identified and temporalized. Unlike other types of plots, a swimmer plot can also indicate the subject's eventual disposition or survival status.

New PROC SGPlot and SGRENDER options for SAS® 9.4 are available to further identify and highlight specified events. This poster will illustrate how these new options can be used for maximum visual effectiveness.

Introduction

What is a swimmer plot and why use it?

Swimmer plots are used to quickly get an overview of multiple subject data across the study timepoints in order to view the relationship between the treatments, different doses, disease stage at baseline and their time to events in the study.

The data is typically shown as a horizontal swim lane starting from randomization or treatment start date through the various study timepoints until study termination or subject death/disposition.

Different colors, symbols and graphical elements enhance the plot and provide additional detail surrounding the major milestones or events of interest for the given subject.

Advantages and Disadvantages

Advantages

- Provides a great visual of the individual subject's response to the therapy and gives an overall comparison to other subjects
- Many different time to event parameters can be displayed on a single graph
- Can be used to show the percent change tumor measurement after the treatment and patient survival/disposition

Disadvantages

- The number of subjects per graph is limited in order to keep details distinct
- Longer studies may have similar issues due to compression of x-axis.

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Methodology and Output

We started with a time-to-event dataset. Some of the relevant variables for the examples shown include: Total Duration of Exposure (months), Time to Special AE, Time to Disease Progression, Time to Partial Response, and Time to Complete Response among others. We also sorted the data in order of descending treatment duration.

Figure 1: The population is responders. With this graph, it's easy to identify the significant events such as when the subject achieved a partial response and whether treatment was ongoing.

```
proc sgplot data=final;
  title "Figure 1: Swimlane plot for Responders";
  styleattrs datacontrastcolors=(CxC0CCE4 cyan) datacolor=(CxC0CCE4 cyan);
  hbarparm category=subject response=trtdur / barwidth=0.6;

  scatter X=prresp Y=subject / markerattrs=(color=Green size=9 symbol=SquareFilled) name="PR" legendlabel="PR";
  scatter X=psa50 Y=subject / markerattrs=(color=Brown size=9 symbol=CircleFilled) name="PSA" legendlabel="PSA 50% Decline";
  scatter X=ctcresp Y=subject / markerattrs=(color=Red size=9 symbol=TriangleFilled) name="CTC" legendlabel="CTC Conversion";
  scatter X=aesi Y=subject / markerattrs=(color=yellow size=9 symbol=diamondFilled) name="AESI" legendlabel="AE's of special interest";
  scatter X=ttpd Y=subject / markerattrs=(color=Black size=9 symbol=Asterisk) name="TPD" legendlabel="Disease Progression";
  scatter X=eotdur Y=subject / markerattrs=(size=9 Symbol=TRIANGLERIGHTFILLED) name="EOTD" legendlabel="End of Treatment";

  axis type=discrete values=align=left label="Subjects" valueattrs=(size=7);
  axis type=linear label="Months" offsetmin=0 values=(0 to 15 by 1);
  keylegend "PR" "PSA" "CTC" "AESI" "TPD" "EOTD";
run;
```

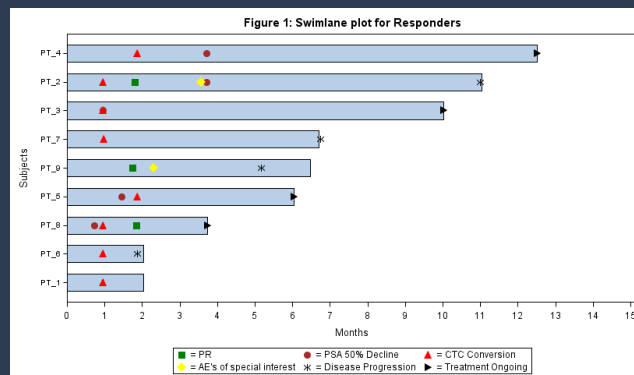


Figure 2: The focus for this graph is disposition status which is displayed in red for each subject. Significant events and their timepoints are also identified. Partial code below:

```
styleattrs datacontrastcolors=(CxC0CCE4 cyan) datacolor=(CxC0CCE4 cyan);
hbarparm category=subject response=trtdur / limitupper=ttmax barwidth=0.6;

scatter X=recistpd Y=subject / markerattrs=(symbol=squarefilled size=8 color=black) name="RPD" legendlabel="RECIST PD";
scatter X=bonopd Y=subject / markerattrs=(symbol=trianglefilled size=8 color=black) name="BPD" legendlabel="Bone PD";
scatter X=clindp Y=subject / markerattrs=(symbol=circlefilled size=8 color=black) name="CPD" legendlabel="Clinical Progression";
scatter X=death Y=subject / markerattrs=(symbol=diamondfilled size=8 color=black) name="DTH" legendlabel="Death";
scatter X=ttpd Y=subject / markerattrs=(color=green size=9) name="EOT" legendlabel="End of Treatment";
text X=ttpd Y=subject text=tttd / position=topright textattrs=(color=red size=9);
scatter X=eot Y=subject / markerattrs=(symbol=circlefilled size=8 color=red) name="EOTDATE" legendlabel="End of Treatment";
scatter X=ong Y=subject / markerchar=ongm markercharattrs=(color=blue size=9) name="EOTD" legendlabel="End of Treatment";

axis type=discrete values=align=left label="Subject" valueattrs=(size=7);
axis type=linear label="Months" offsetmin=0 values=(0 to 24 by 1);
keylegend "RPD" "BPD" "CPD" "DTH" "EOTDATE" "EOTD";
```

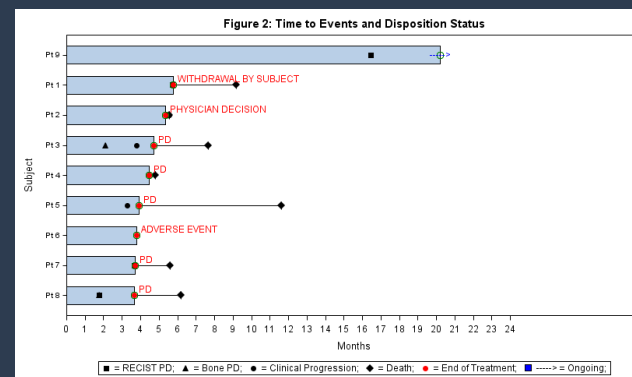


Figure 3: The prior graph is further modified to show just a few of the new color and display options available with SAS® 9.4. The inside and outline of each bar can be displayed with varying colors, the backcolor and wallcolor are identified and the treatment groups, prior therapy or other subset can be visually distinguished. Partial code below:

```
styleattrs datacontrastcolors=(purple red) datacolor=(CxC0CCE4 cyan) backcolor=paleturquoise wallcolor=lightblue;
hbarparm category=subject response=trtdur / group=priorth barwidth=0.5 name="Priortherapy" legendlabel="Therapy";

scatter X=recistpd Y=subject / markerattrs=(symbol=squarefilled size=8 color=black) name="RPD" legendlabel="RECIST PD";
scatter X=bonopd Y=subject / markerattrs=(symbol=trianglefilled size=8 color=black) name="BPD" legendlabel="Bone PD";
scatter X=clindp Y=subject / markerattrs=(symbol=circlefilled size=8 color=black) name="CPD" legendlabel="Clinical Progression";
scatter X=death Y=subject / markerattrs=(symbol=diamondfilled size=8 color=black) name="DTH" legendlabel="Death";
scatter X=ttpd Y=subject / markerattrs=(color=green size=9) name="EOT" legendlabel="End of Treatment";
text X=ttpd Y=subject text=tttd / position=topright textattrs=(color=red size=9);
scatter X=eot Y=subject / markerattrs=(symbol=circlefilled size=8 color=red) name="EOTDATE" legendlabel="End of Treatment";
scatter X=ong Y=subject / markerchar=ongm markercharattrs=(color=blue size=9) name="EOTD" legendlabel="End of Treatment";

keylegend "Priortherapy" / noborder location=inside position=bottomright across=1;
```

