PharmaForest | Open-Source SAS Packages

OncoPlotter

A Next-Generation Open-Source SAS Package for Oncology

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Presenters: Yutaka Morioka, Hiroki Yamanobe, Sharad Chhetri , Ryou Nakaya

OncoPlotter is a SAS package designed to **easily create the major graphs typically required in oncology clinical trials**. It supports Kaplan-Meier, Swimmer, Waterfall, Forest, and Spider plots, producing graphs of a **quality usable for both clinical study reports and journal submissions**. The package also includes dummy datasets, so you can try each macro without preparing your own data. Because of this, it is especially useful for a wide range of users in the oncology data field, from beginners to advanced practitioners.

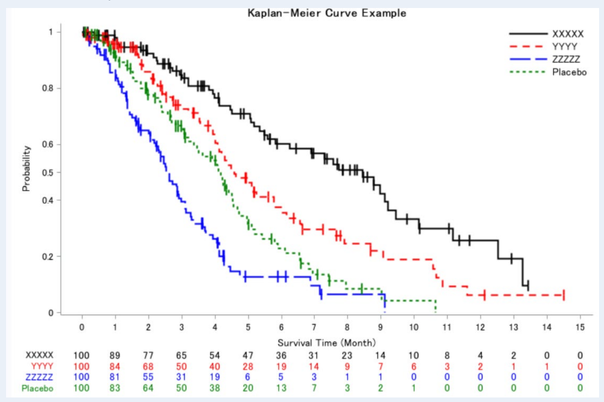
5	SPF	MIT	PharmaForest
Types of graphs available	Built on SAS Packages Framework	Open-source license	Public GitHub repository

PACKAGE FEATURES

Package Features: 5 graph-creation macros

%kaplan_meier_plot — Kaplan-Meier Survival Curve

PROC LIFETEST draws per-group survival curves, with censoring marks and the number at risk shown at each time point.




```
%kaplan_meier_plot(
 data = dummy_adtte,
 groupn = TRTPN,
 groupc = TRTP,
 Time_var = AVAL,
 Censore_var = CNSR,
 Censore_val = 1,
 Title = %nrquote(Kaplan-Meier Curve Example),
 Group_color_list = %nrquote(black red blue green),
 Group_linepattern_list =
          %nrquote(solid dash longdash shortdash),
 XLABEL = %nrquote(Survival Time (Month)),
 YLABEL = %nrquote(Probability),
 AxisValues = %nrquote(0 to 15 by 1),
 Generate_Code = Y
)
```

%swimmer_plot — Swimmer Plot

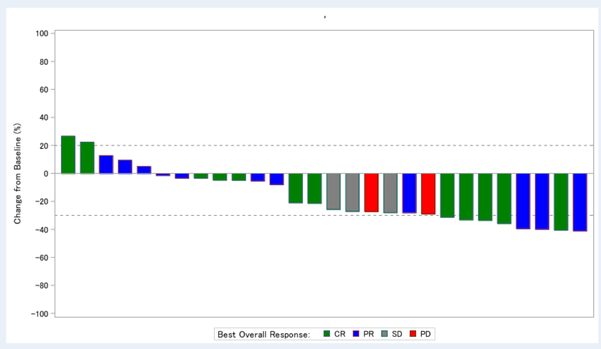
Visualizes each subject's treatment course as a horizontal bar. Suitable for CSRs as well as publication-quality figures, with five built-in color styles.




```
%Swimmer_Plot(
 adrs = adrs_dummy,
 adsl = adsl_dummy,
 whr_adrs = PARAM="Overall Response",
 whr_adsl = FASFL="Y",
 eotvar = EOTSTT,
 crprN = 1 2,
 durable = Y,
 groupvar = STAGEN,
 groupN = 1 2 3 4 5,
 groupC = Stage I | Stage IIa | Stage IIb | Stage III | Stage IV,
 responseN = 1 2 3 4,
 responseC = CR | PR | SD | PD,
 nperpage = 20,
 colorStyle = OncoPlotter,
 Generate_Code = Y
)
```

%waterfall_plot — Waterfall Plot

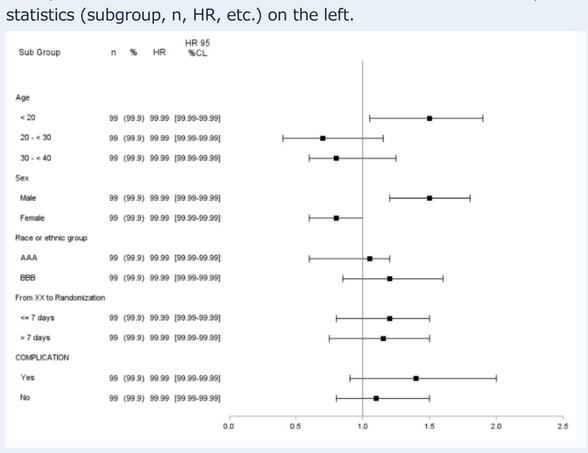
Displays the percent change in tumor diameter from baseline as descending bars by response category. Supports both CSR and publication formats.




```
%Waterfall_Plot(
 adrs     = adrs_dummy,
 adtr     = adtr_dummy,
 adsl     = adsl_dummy,
 whr_adrs   = PARAM="Best Overall Response",
 whr_adtr   = PARAM="Sum of Diameters",
 whr_adsl   = FASFL="Y",
 groupVar    = AVAL,
 groupN      = 1 2 3 4,
 groupC      = CR | PR | SD | PD,
 groupColor  = green | blue | gray | red,
 responseVar  = PCHG,
 VarWidth    = 0.7,
 y_refline=20 40,
 Generate_Code = Y
)
```

%forest_plot — Forest Plot

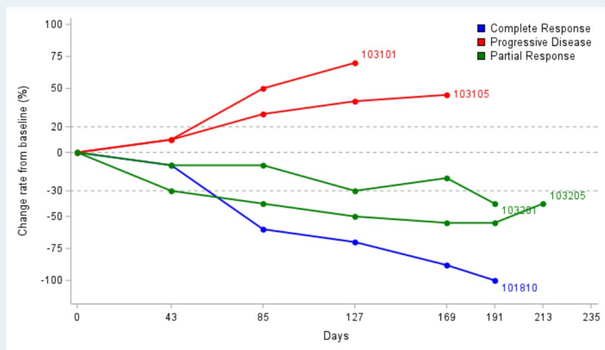
Plots point estimates and confidence intervals. YAXISTABLE adds up to six columns of descriptive statistics (subgroup, n, HR, etc.) on the left.




```
%forest_plot(
 data=dummy_forest_test,
 out1=col1,
 out2=col2,
 out3=col3,
 out4=col4,
 out5=col5,
 marker_point=estimate,
 bar_left=lower_limit,
 bar_right=upper_limit,
 out1_label=%nrbquote(Sub Group),
 out2_label=%nrbquote(n),
 out3_label=%nrbquote(%),
 out4_label=%nrbquote(HR),
 out5_label=%nrbquote(HR 95 %CL),
 refline_value=1,
 Generate_Code=Y
)
```

%spider_plot — Spider Plot

Overlays subject profiles. Plots days after dosing (X) against the rate of tumor-shrinkage change (Y) as per-subject series lines.




```
%spider_plot(
 data = dummy_spider,
 xvar = ADY,
 yvar = PCHG,
 subject_var = SUBJID,
 subject_category = BOR,
 xaxis_label = %nrbquote(Days),
 xaxis_values = %nrbquote(0 43 85 127 169 235),
 yaxis_label = %nrbquote(Change rate from baseline
(%)),
 yaxis_values = %nrbquote(-100 -50 -30 0 50 75 100),
 datacontrastcolors = %nrbquote(Blue Red Green
Yellow),
 refline_value = 0 20 -30,
 curvelabel = Y,
 Generate_Code = N
)
```

Version history

0.5.2(18June2026) : A bug fixed in swimmer plot and waterfall plot 0.5.1(03Apr2026) : Modified KM plot(removed reset in ods graphics)
0.5.0(09Feb2026) : Added spider plot. A bug fixed in forest plot's gerate code function.
0.4.0(05Feb2026) : Added forest plot. A bug fixed in kaplan-meier plot's gerate code function.
0.3.8(29Jan2026) : Default parameters have been changed in swimmer plot. Enhanced help information as well.
0.3.7(29Oct2025) : A bug fixed in swimmer plot.
0.3.6(8Oct2025) : A bug fixed and added parameter [imgPath] in waterfall plot.
0.3.5(2Oct2025) : A bug fixed for options of ods graphics in swimmer plot
0.3.4(18Sep2025) : A bug fixed for Generate_code parameter to be used in case of NOXCMD
0.3.3(16Sep2025) : A bug fixed for Generate_code parameter to be used in case of Linux
0.3.2(01Sep2025) : A bug fixed and made modification to &data parameter of Kaplan-Meier Plot
0.3.1(25Aug2025) : Added parameter [VARWIDTH], [DPI], [Y_REFLINE] in waterfall plot. And fixed adrs_dummy.
0.3.0(30July2025) : Added waterfall plot
0.2.2(23July2025) : A bug fixed and made modification to handle no groupvar in swimmer plot
0.2.1(14July2025) : Added functionality of output generated SAS codes to swimmer plot
0.2.0(5July2025) : added swimmer plot
0.1.0(24June2025) : Initial version

Tip: With Generate_Code=Y, each macro also outputs the generated SAS code as text, so you can use it as a basis to create graphs with your own customized code

HOW TO USE

How to use the package: 3 steps

1 Prepare SPF

```
filename packages "/path/to/packages";
filename SPFinit url
"https://raw.githubusercontent.com/yabwon/SAS_
PACKAGES/main/SPF/SPFinit.sas";
%include SPFinit;
%installPackage(SPFinit)
```

2 Install the package

```
%installPackage(OncoPlotter,
mirror=PharmaForest)
```

3 Load and plot

```
%loadPackage(OncoPlotter)
%Kaplan_meier_plot();
```

COMMUNITY

PharmaForest since 2025

Goal

Openly share SAS development know-how that tended to stay with individuals, aiming to build collective knowledge, improve productivity, ensure quality through standardization, and energize the community.

People

Admins: Hiroki Yamanobe, Yutaka Morioka, Sharad Chhetri, Ryou Nakaya
Members: More than 10 people from around the world (volunteers still welcome)

https://github.com/PharmaForest