



PharmaForest

Package Repository



Foresters

Contributors



OncoPlotter

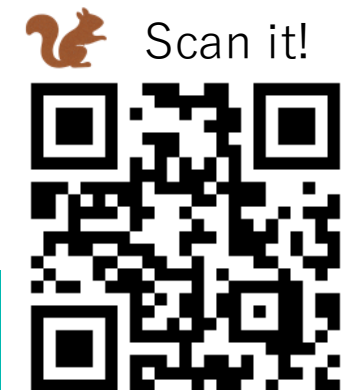
Plot Tools for Oncology
Area

Introduction of PharmaForest – Forest of SAS packages

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Phuse US Connect 2026 @ Austin
24March2026





Our team

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Objective

- Introduce and promote PharmaForest
- Find collaborators





Open-source in Pharma

- Recent trend in pharmaceutical industry to **leverage open-source software such as R and Python** is remarkable
- SAS is still in its position of center in the industry, but open-source mind is not yet flourished enough
- Potential of R and packages in statistical clinical reporting is increasingly explored and **Pharmaverse** was formed in 2020
- **AI/ML and automation** is often done by Python





Key factors of open-source

- License
- Standardized format to share





Definition of open-source

1. Free Redistribution
2. Source Code
3. Derived Works
4. Integrity of The Author's Source Code
5. No Discrimination Against Persons or Groups
6. No Discrimination Against Fields of Endeavor
7. Distribution of **License**
8. **License** Must Not Be Specific to a Product
9. **License** Must Not Restrict Other Software
10. **License** Must Be Technology-Neutral



<https://opensource.org/osd>

Having license matters!





Standardized structure (package)

```
yourpackage/  
├─ DESCRIPTION  
├─ NAMESPACE  
├─ R/  
│   ├── function1.R  
│   └─ function2.R  
├─ man/  
│   ├── function1.Rd  
│   └─ function2.Rd  
├─ tests/  
│   └─ testthat/  
├─ data/  
├─ vignettes/  
└─ README.md
```

Place to share (repository)



What about SAS??





**SAS Packages
Framework(SPF)**



**SAS Packages
Archive(SASPAC)**



Pharmaforest

Yes, we have.





SAS Packages Framework(SPF)

- SAS Package is based on **standardized structure** defined by SAS Packages Framework(SPF)
https://github.com/yabwon/SAS_PACKAGES
Started in 2019 by Bartosz Jablonski*



the way to share

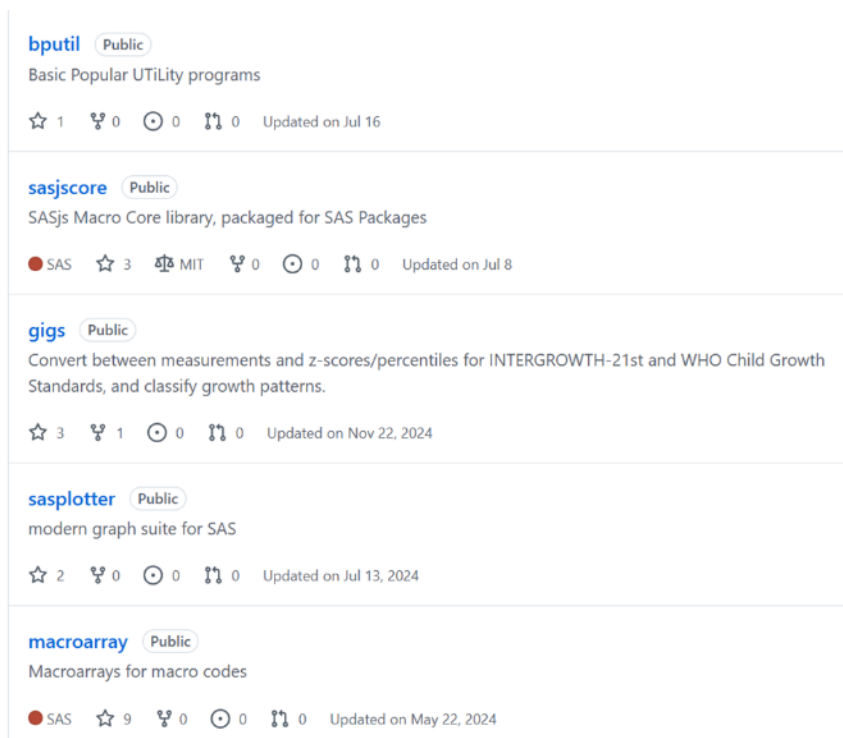
```
<packageName>/  
├─ description.sas  
├─ license.sas  
├─ 001_macro/  
│   └─ mymacro.sas  
├─ 002_function/  
│   └─ myfunc.sas  
├─ 003_format/  
│   └─ myformat.sas  
├─ 004_data/  
│   └─ mydata.sas  
├─ 005_exec/  
├─ 006_clean/  
└─ 999_test/
```





SAS Packages Archive(SASPAC)

- A repository of packages(12 packages as of December, 2025)
<https://github.com/SASPAC>
by Bartosz Jablonski





PharmaForest

- Collection of **SAS Packages** for pharmaceutical industry inspired by Pharmaverse project in R
- **Open-source**
- The repository has started in June, 2025
- Founded in Japan by authors of the presentation
- 43 packages
- Based on SAS Packages Framework(SPF)





Goal

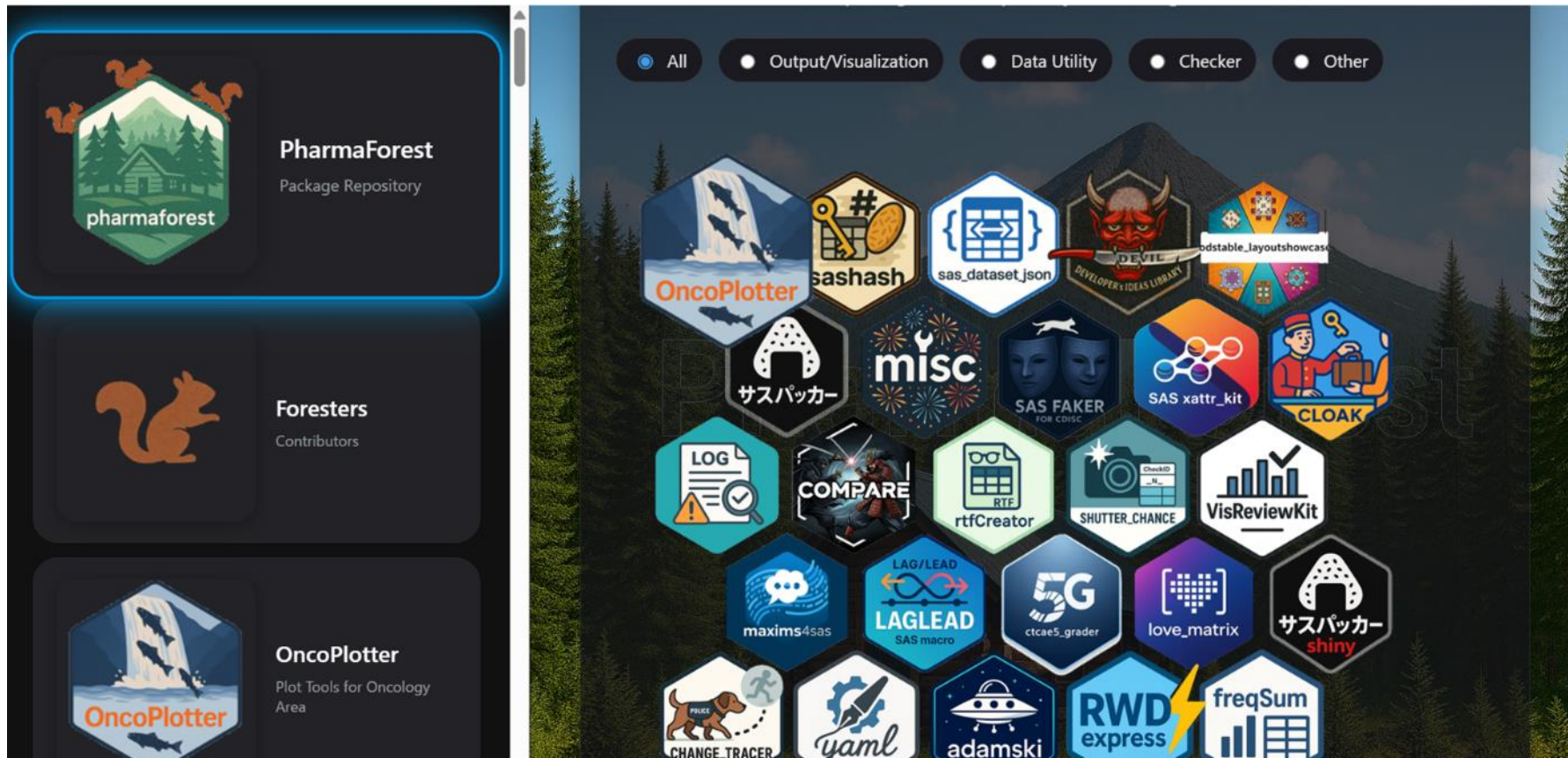
- *Through SAS Packages, we want to **actively encourage sharing** of SAS know-how that has often stayed within individuals. By doing this, we aim to build up collective knowledge, boost productivity, ensure quality through standardization, and energize our community.*
- <https://github.com/PharmaForest>





Gallery page of PharmaForest

- <https://pharmaforest.github.io/> or QR code





PharmaForest Ecosystem Map

Output / Visualization



Other



Checker



Data Utility



As of Nov2025

SASPACer package



- Support creating SAS Packages

<https://github.com/PharmaForest/SASPACer>

Type	Package
Package	testPackage
Title	My first SAS package
Version	0.0.1
Author	John Smith(john.smith@mail.com)
Maintainer	John Smith(john.smith@mail.com)
License	MIT
Encoding	UTF8
Required	"Base SAS Software"
ReqPackage	"Baseplus (2.1.0)"
Description	## The myPackage ## The 'myPackage' is my first SAS package. ### References ### 1. Bartosz Jablonski. "My First SAS Package - a How To". SGF

name	help	body	location
mcrone	This is mcrOne macro. (No need to write location column if content is written in body column.)	%macro mcrOne(); %put **Hi! This is macro &sysmacroname.**; data _null_; set myLib.smallDataset; p = f1(n); p + f2(n); put (n p) (= fmtNum.); run; %mend mcrOne;	
mcrtwo	This is mcrTwo macro. (No need to write body column if content is in a file written in location column, SASPACer reads the file.)		C:\temp\addcnt\mcrtwo.sas

```
%installPackage(SASPACer, mirror=pharmaforest)
%loadPackage(SASPACer)
```

```
%ex2pac(
    excel_file           = /path/to/excel/excelfile.xlsx,
    package_location     = /path/to/output,
    complete_generation = Y /* Y: Run %generatePackage() */
)
```

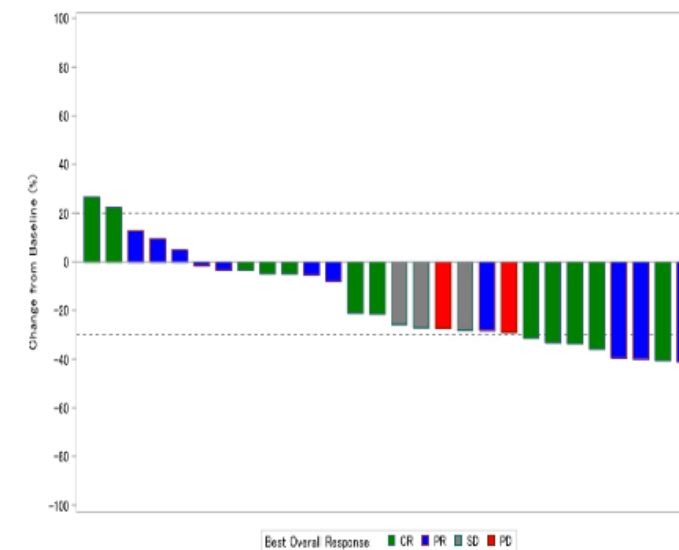
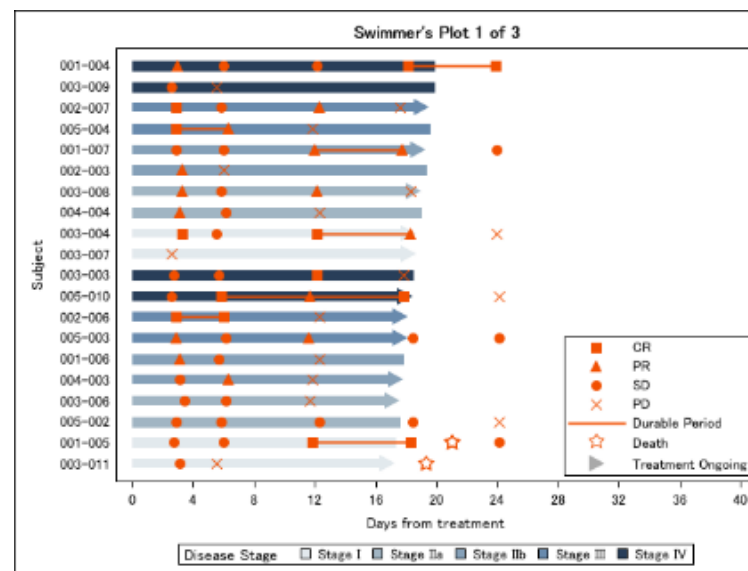
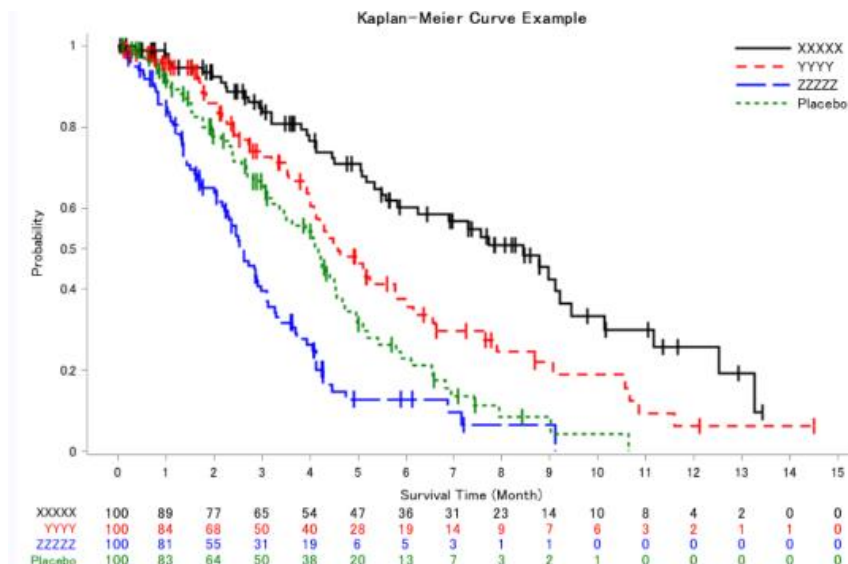


OncoPlotter package

- Plotter for Oncology figures



<https://github.com/PharmaForest/OncoPlotter>



```
%installPackage(OncoPlotter, mirror=pharmaforest)
%loadPackage(OncoPlotter)
```



Adamski package

- CDISC ADaM creation tool

```
%installPackage(adamski, mirror=pharmaforest)
%loadPackage(adamski)

data have;
  do SEX="F","M"; do AGE=12 to 17; output; end; end;
run;

data want;
  set have;

/* With condition */
%derive_var_merged_exist_flag(
  dataset_add = SASHELP.CLASS,
  by_vars      = AGE,
  condition    = %nrbquote( SEX = "F"),
  new_var      = AGE_IN_CLASS_F_ONLY,
  true_value   = Yes,
  false_value  = No
);
run;
```



<https://github.com/PharmaForest/adamski>



Aiming to create similar functionality to
admiral in R and add original macros



SAS_dataset_json package



- Dataset JSON

```
%installPackage(sas_dataset_json, mirror=pharmaforest)
%loadPackage(sas_dataset_json)
proc datasets nolist;
  modify adsl;
  xattr add ds originator="X corp."
    fileOID="www.cdisc.org/StudyMSGv2/1/Define-XML_2.1.0/2024-11-11/"
    studyOID="XX001-001"
    metaDataVersionOID="MDV.MSGv2.0.SDTMIG.3.4.SDTM.2.0"
    sourceSystem_name="SASxxxx"
    sourceSystem_version="9.4xxxx";
  xattr add var
    STUDYID (label="Study Identifier"
      dataType="string"
      length=8
      keySequence=1)
```

https://github.com/PharmaForest/sas_dataset_json

```
USUBJID (label="Unique Subject Identifier"
  dataType="string"
  length=7
  keySequence=2)
```

```
TRTSDT (label="Date of First Exposure to Treatment"
  dataType="date"
  targetDataType="integer"
  displayFormat="E8601DA.");
```

```
;
run;
quit;
```

```
%m_sas_to_json1_1(
  outpath = /project/json_out,
  library = WORK,
  dataset = adsl,
  pretty = Y
);
```



Yaml_writer package

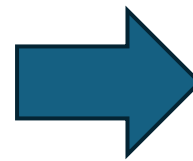


https://github.com/PharmaForest/yaml_writer

- Writing yaml in SAS

```
%installPackage(yaml_writer, mirror=pharmaforest)
%loadPackage(yaml_writer)
```

```
%yaml_start(outpath=C:/Temp, file=sample);
#This YAML is a sample &nw.;
all: &nw.;
- name: MHPRESP &nw.;
  operator: equal_to &nw.;
  value: "Y" &nw.;
- name: MHOCCUR &nw.;
  operator: equal_to &nw.;
  value: "N" &nw.;
%yaml_end();
```



```
! test.yaml x
C: > Temp > ! test.yaml
1  all:
2    - name: MHPRESP
3      operator: equal_to
4      value: "Y"
5    - name: MHOCCUR
6      operator: equal_to
7      value: "N"
8
```

Also have %dataset_export() for exporting data to yaml



Forest Navigators (GenAI-powered)



Dr. Forest
(Master Navigator,
General, #1-#15 packages)



Dr. Apple
(Support Navigator,
#16-#30 packages)



Rio
(Support Navigator,
#31- packages)



Oba-chan
(SAS package lady,
a SAS package cook)

<https://github.com/PharmaForest>





Conclusion

- PharmaForest was built to encourage SAS programmers to share their knowledge in a unified format of SAS Packages.
- We look forward to hearing from anyone from the world who are interested.

Let's create open-source community in SAS together!





References

- Bartosz Jabłonski, "SAS Packages: The Way to Share (a How To)", SAS Global Forum 2020 Proceedings, 4725-2020 <https://www.sas.com/content/dam/SAS/support/en/sas-global-forum-proceedings/2020/4725-2020.pdf>
- Pharmaverse. *Pharmaverse website*. Retrieved from <https://pharmaverse.org>
- SAS Institute Inc. *SAS Institute official website*. Retrieved from <https://www.sas.com>
- Bartosz Jabłonski (2019). *SAS Packages Framework (SPF)*. GitHub. Retrieved from https://github.com/yabwon/SAS_PACKAGES
- SAS Institute Inc. *SAS Support Communities*. Retrieved from <https://communities.sas.com>
- SAS Packages Archive. SASPAC GitHub repository. Retrieved from <https://github.com/SASPAC>
- CDISC. (2025). *COSA: CDISC Open-Source Alliance*. Retrieved from <https://www.cdisc.org/cosa>

