

SAS Package and PharmaForest ハンズオンセミナー

PharmaForestについて

森岡 裕

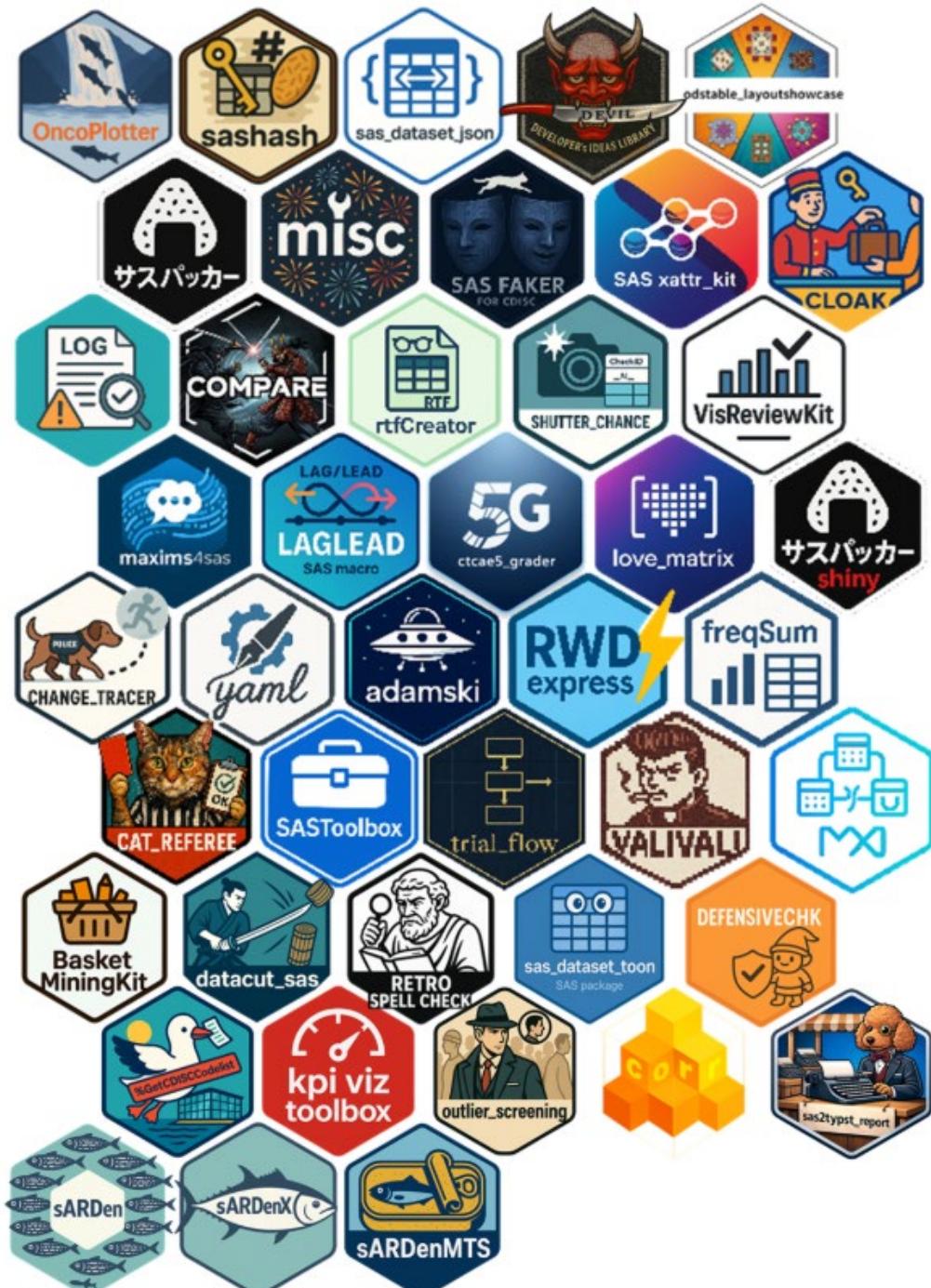


PharmaForestはSAS Package Framework(SPF)を使って製薬業界向けに構成されたエコシステム。PharmaverseのSAS版みたいなもので、実際Pharmaverseと同じ、現在 Phuse のグローバル公式のワーキングとなる予定で進行中。

<https://github.com/PharmaForest>

Packages

| # | Package | # | Package | # | Package |
|----|---|----|--|----|-----------------------------------|
| 1 | OncoPlotter (PharmaForest original package) | 16 | maxims4sas (PharmaForest original package) | 31 | basketMiningKit |
| 2 | sashash | 17 | laglead | 32 | datacut_sas |
| 3 | sas_dataset_json | 18 | ctcae5_grader | 33 | retro_spell_check |
| 4 | SASPACer | 19 | love_matrix | 34 | sas_dataset_toon |
| 5 | misc (PharmaForest original package) | 20 | SASPACerShiny (R Package) | 35 | defensivechk |
| 6 | SAS FAKER | 21 | change_tracer_dog | 36 | GetCDISCodelist |
| 7 | SASLogChecker | 22 | yaml_writer | 37 | kpi_viz_toolbox |
| 8 | sas_compare | 23 | Adamski (PharmaForest original package) | 38 | outlier_screening |
| 9 | rtfCreator | 24 | RWDExpress | 39 | sARDen |
| 10 | shutter_chance | 25 | freqsum | 40 | sARDenX |
| 11 | devil (PharmaForest original package) | 26 | qc_cat_referee | 41 | sARDenMTS |
| 12 | xattr_kit | 27 | SASToolbox | 42 | corr |
| 13 | cloak | 28 | trial_flow | 43 | sas2typst_report |
| 14 | vis_review_kit | 29 | valivali (PharmaForest original package) | 44 | |
| 15 | odstable_layoutshowcase | 30 | mergex | 45 | |

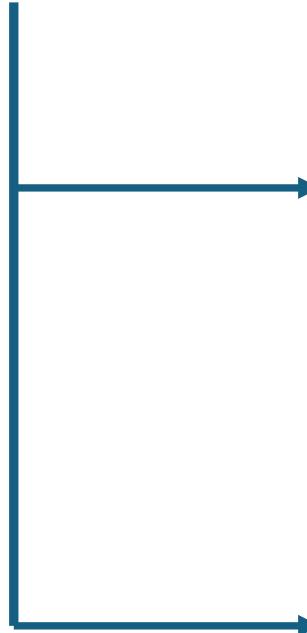


実際、OSS利用に慣れていないSASプログラマにとって、
オープンパッケージを利用して、研究や業務のプログラム開
発するというのがピンとこなくて、なんとなく忌避されてる
方も多いと思うので

とりあえず、動かしてみて、肌感だけでも 経験していって
もらえればっていうのが
本日のハンズオンの主旨です



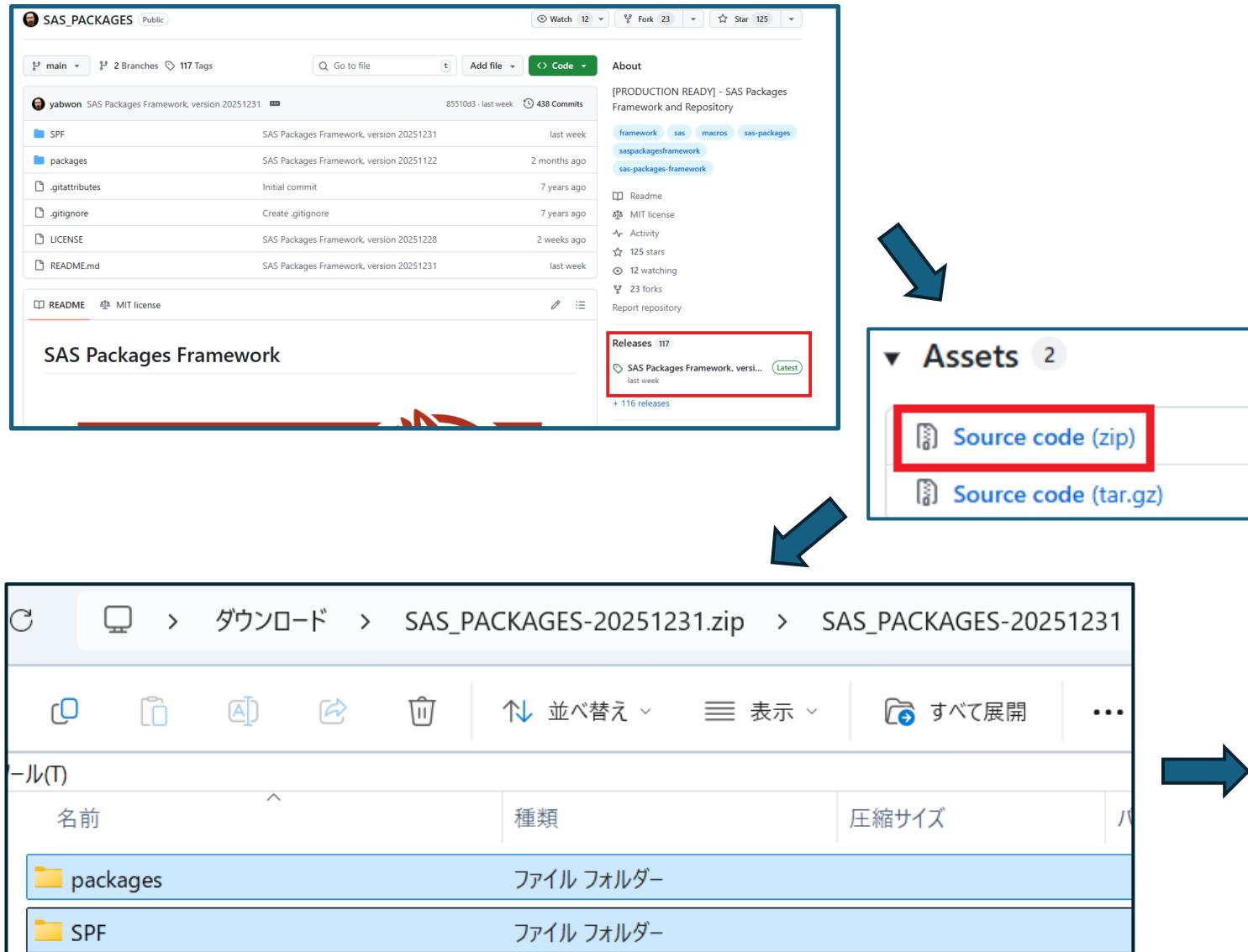
所属組織のSASサーバーのネット接続が制限されていていたりなど、
ウェブ経由でのパッケージのインストール、**%installPackage**が通らない場合でも
大丈夫



- ① あらかじめzipファイルをローカルにダウンロードしていただいて
そこに**%loadPackage** (パッケージ名)　かけていただく
- ② SAS ondemand (無料のSAS webサービス) でやっていただく
- ③ あらかじめ本ハンズオンで使用するもの全部集めたzipをつくれたので
とりあえずそれを丸ごと使ってもらう

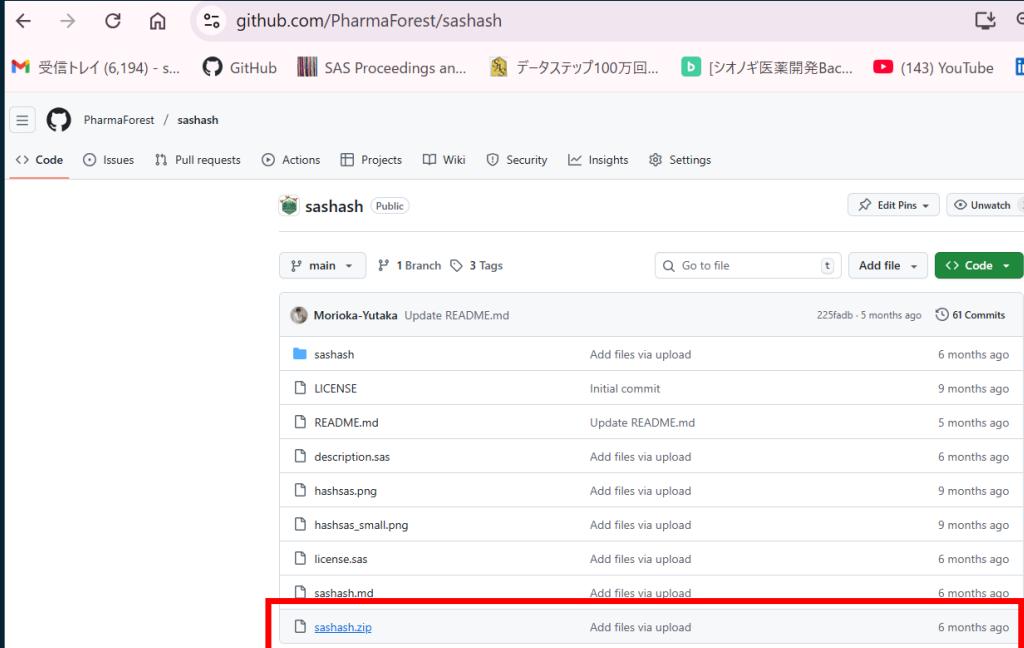
① 所属組織のSASサーバーのネット接続が制限されていて、あらかじめダウンロードして試したい方

https://github.com/yabwon/SAS_PACKAGES



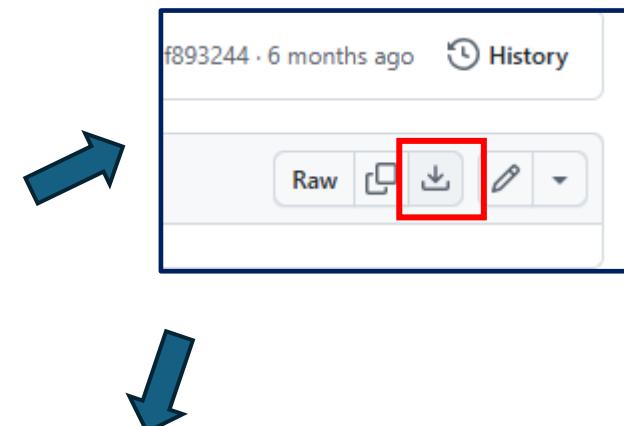
zipを展開して、[SPF]と[packages]を
SASから参照できるローカルのどこかに置く

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



A screenshot of a GitHub repository page. The repository name is 'sashash'. The file list shows several files: 'Morioka-Yutaka Update README.md', 'sashash', 'LICENSE', 'README.md', 'description.sas', 'hashsas.png', 'hashsas_small.png', 'license.sas', 'sashash.md', and 'sashash.zip'. The 'sashash.zip' file is highlighted with a red box.

使いたいパッケージのページ(github)の直下にそのパッケージ名でzipファイルがあるのでそれをクリックしてダウンロードして



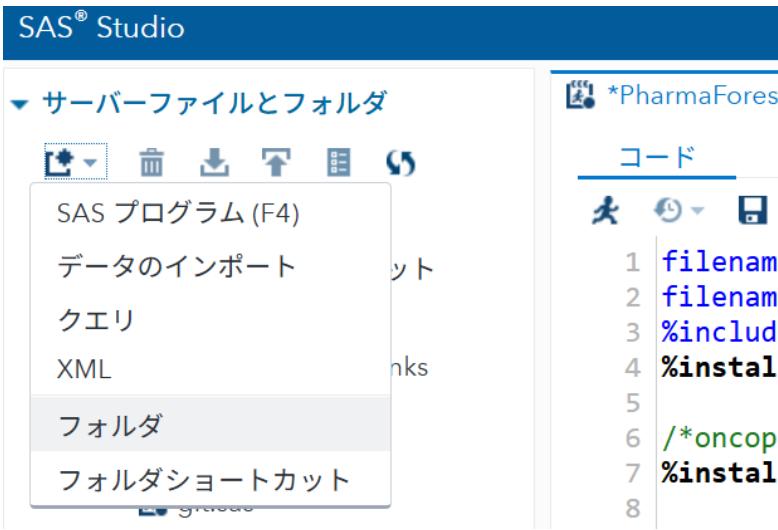
前ページで展開した「packages」 フォルダの中へ

| 名前 | 更新日時 | 種類 | サイズ |
|---------------------|------------------|--------------------|----------|
| datacut_sas.zip | 2025/11/09 22:51 | 圧縮 (zip 形式) フォル... | 16 KB |
| defensivechk.zip | 2025/11/21 22:57 | 圧縮 (zip 形式) フォル... | 12 KB |
| devil.zip | 2025/08/28 15:48 | 圧縮 (zip 形式) フォル... | 23 KB |
| dfa.zip | 2025/09/08 7:26 | 圧縮 (zip 形式) フォル... | 48 KB |
| getdiscodelist.zip | 2025/11/22 22:19 | 圧縮 (zip 形式) フォル... | 13 KB |
| gigs.zip | 2025/09/08 7:32 | 圧縮 (zip 形式) フォル... | 2,204 KB |
| gsm.zip | 2025/09/08 7:27 | 圧縮 (zip 形式) フォル... | 298 KB |
| kpi_viz_toolbox.zip | 2025/11/25 1:35 | 圧縮 (zip 形式) フォル... | 12 KB |
| laglead.zip | 2025/08/28 15:54 | 圧縮 (zip 形式) フォル... | 12 KB |
| love_matrix.zip | 2025/08/28 15:55 | 圧縮 (zip 形式) フォル... | 17 KB |
| macroarray.zip | 2025/09/08 7:25 | 圧縮 (zip 形式) フォル... | 53 KB |
| maxims4sas.zip | 2025/08/28 15:54 | 圧縮 (zip 形式) フォル... | 20 KB |

```
filename    spf "XXXX¥SPF" ;
%include    spf(SPFinit.sas) ;
filename    packages "XXXXXXXX¥packages" ;
```

```
%loadPackage (sashash)
```

② 所属組織のSASサーバーのネット接続が制限されていて、SAS on demandで試したい方



SAS® Studio

▼ サーバーファイルとフォルダ

SAS プログラム (F4)
データのインポート
クエリ
XML
フォルダ
フォルダショートカット

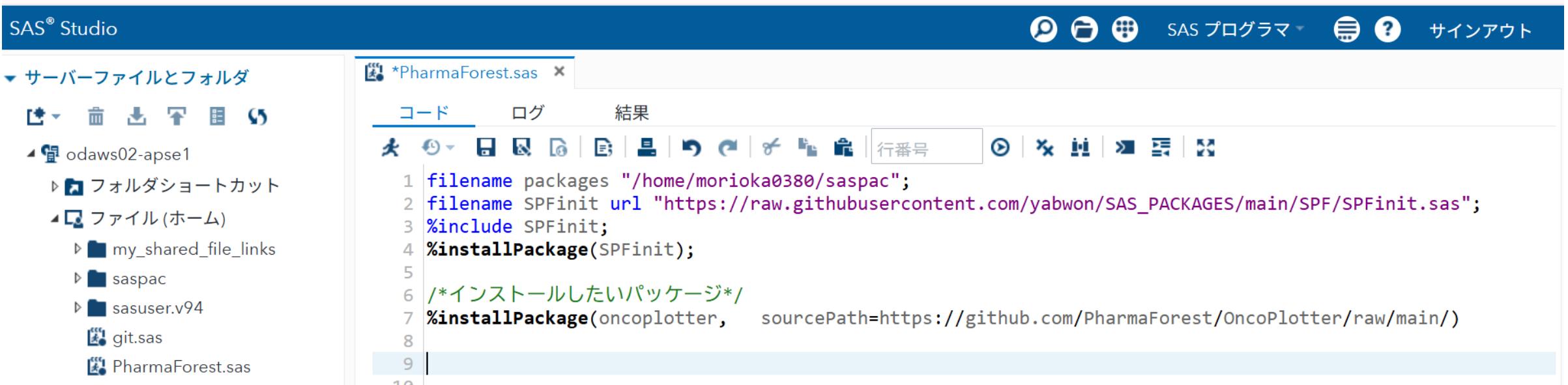
*PharmaForest.sas

コード

```
filename packages "/home/自身のアカウント/saspac";
filename SPFinit url "https://raw.githubusercontent.com/yabwon/SAS_PACKAGES/main/SPF/SPFinit.sas";
%include SPFinit;
%installPackage(SPFin...
/*oncoplotter*/
%installPackage(oncoplotter,
sourcePath=https://github.com/PharmaForest/OncoPlotter/raw/main/)
```

SAS on demandのアカウントを持っていない方はまずこちらから
[SAS ondemandガイド\(鈴木徳太さん\)](#)

```
filename packages "/home/自身のアカウント/saspac";
filename SPFinit url "https://raw.githubusercontent.com/yabwon/SAS_PACKAGES/main/SPF/SPFinit.sas";
%include SPFinit;
%installPackage(SPFin...
/*oncoplotter*/
%installPackage(oncoplotter,
sourcePath=https://github.com/PharmaForest/OncoPlotter/raw/main/)
```



SAS® Studio

▼ サーバーファイルとフォルダ

odaws02-apse1

- フォルダショートカット
- ファイル (ホーム)
- my_shared_file_links
- saspac
- sasuser.v94
- git.sas
- PharmaForest.sas

*PharmaForest.sas

コード ログ 結果

```
filename packages "/home/morioka0380/saspac";
filename SPFinit url "https://raw.githubusercontent.com/yabwon/SAS_PACKAGES/main/SPF/SPFinit.sas";
%include SPFinit;
%installPackage(SPFin...
/*インストールしたいパッケージ*/
%installPackage(oncoplotter, sourcePath=https://github.com/PharmaForest/OncoPlotter/raw/main/)
```

本日のハンズオンと一緒に動かしてみるパッケージ一覧

Rawdata

SDTM

ADaM

TLF





sas_faker (https://github.com/PharmaForest/sas_faker)

ダミーデータで、SDTM,ADaMのサンプルを作ってくれるパッケージ。群の数と群ごとの症例数を指定可能。作成される一連のデータセットは症例番号や投与日付・検査日付が一応整合している

/*インストール webアクセス可能の場合。無理な場合は先に説明した①の方法で直にインストール*/

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

/*パッケージのロード*/

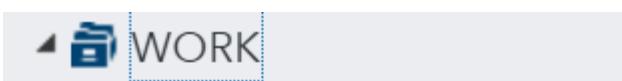
```
%loadPackage(sas_faker)
```

/*使用*/

```
%sas_faker(n_groups=2, n_per_group=50)
```

👉 これで2群で1群50例で、

ダミーのDM,SV,VS,AE,ADSL,ADAE,ADTTE,ADVSがWORKにできる



▶ ADAE

▶ ADSL

▶ ADTTE

▶ ADVS

▶ AE

▶ DM

▶ SV

▶ VS

| VIEWTABLE: Work.Ae | | | | | | | | | | |
|--------------------|------------|--------|------------|--------|----------------------|----------------------|-----------|----------------------|----------|--|
| | STUDYID | DOMAIN | USUBJID | AESSEQ | AETERM | F_AELLT | F_AELLTCD | AEDECODE | F_AEPTCD | |
| 1 | SEED123456 | AE | FAKE-00001 | 1 | Myomuscle Drift#fake | Myomuscle Drift#fake | 564 | Ear Buzz#fake | 57 | |
| 2 | SEED123456 | AE | FAKE-00001 | 2 | Endo Stutter#fake | Endo Stutter#fake | 325 | Renal Swell#fake | 34 | |
| 3 | SEED123456 | AE | FAKE-00001 | 3 | Myomuscle Slide#fake | Myomuscle Slide#fake | 328 | Renal Swell#fake | 34 | |
| 4 | SEED123456 | AE | FAKE-00001 | 4 | Ophtha Slip#fake | Ophtha Slip#fake | 18 | Cardiac Flutter#fake | 3 | |
| 5 | SEED123456 | AE | FAKE-00001 | 5 | Neuro Surge#fake | Neuro Surge#fake | 857 | Cardiac Flutter#fake | 87 | |
| 6 | SEED123456 | AE | FAKE-00001 | 6 | Derma Skip#fake | Derma Skip#fake | 655 | Retina Flicker#fake | 67 | |
| 7 | SEED123456 | AE | FAKE-00001 | 7 | Neuro Pulse#fake | Neuro Pulse#fake | 973 | Synaptic Drift#fake | 98 | |
| 8 | SEED123456 | AE | FAKE-00001 | 8 | Endo Spasm#fake | Endo Spasm#fake | 8 | Lung Haze#fake | 2 | |
| 9 | SEED123456 | AE | FAKE-00001 | 9 | Ophtha Blur#fake | Ophtha Blur#fake | 917 | Neural Twitch#fake | 93 | |
| 10 | SEED123456 | AE | FAKE-00001 | 10 | Gastro Ripple#fake | Gastro Ripple#fake | 688 | Gastro Slide#fake | 70 | |
| 11 | SEED123456 | AE | FAKE-00001 | 11 | Pulmo Stutter#fake | Pulmo Stutter#fake | 520 | Cerebral Flux#fake | 53 | |
| 12 | SEED123456 | AE | FAKE-00001 | 12 | Pulmo Flutter#fake | Pulmo Flutter#fake | 412 | Muscle Burst#fake | 42 | |
| 13 | SEED123456 | AE | FAKE-00001 | 13 | Audio Spasm#fake | Audio Spasm#fake | 659 | Retina Flicker#fake | 67 | |
| 14 | SEED123456 | AE | FAKE-00001 | 14 | Pulmo Stutter#fake | Pulmo Stutter#fake | 520 | Cerebral Flux#fake | 53 | |
| 15 | SEED123456 | AE | FAKE-00001 | 15 | Derma Snap#fake | Derma Snap#fake | 652 | Retina Flicker#fake | 66 | |
| 16 | SEED123456 | AE | FAKE-00001 | 16 | Ophtha Flutter#fake | Ophtha Flutter#fake | 939 | Retina Flicker#fake | 95 | |
| 17 | SEED123456 | AE | FAKE-00001 | 17 | Cardio Quiver#fake | Cardio Quiver#fake | 336 | Kidney Blink#fake | 35 | |
| 18 | SEED123456 | AE | FAKE-00001 | 18 | Neuro Quiver#fake | Neuro Quiver#fake | 904 | Tendon Jerk#fake | 91 | |
| 19 | SEED123456 | AE | FAKE-00002 | 1 | Renal Slip#fake | Renal Slip#fake | 606 | Retina Flicker#fake | 62 | |
| 20 | SEED123456 | AE | FAKE-00002 | 2 | Endo Pulse#fake | Endo Pulse#fake | 928 | Cerebral Flux#fake | 94 | |
| 21 | SEED123456 | AE | FAKE-00002 | 3 | Ophtha Flicker#fake | Ophtha Flicker#fake | 248 | Synaptic Drift#fake | 26 | |
| 22 | SEED123456 | AE | FAKE-00002 | 4 | Cardio Twitch#fake | Cardio Twitch#fake | 27 | Endo Flick#fake | 4 | |
| 23 | SEED123456 | AE | FAKE-00002 | 5 | Gastro Surge#fake | Gastro Surge#fake | 503 | Hormone Swing#fake | 52 | |
| 24 | SEED123456 | AE | FAKE-00002 | 6 | Cardio Spasm#fake | Cardio Spasm#fake | 814 | Gastro Slide#fake | 82 | |
| 25 | SEED123456 | AE | FAKE-00002 | 7 | Derma Dimple#fake | Derma Dimple#fake | 606 | Cardio Flicker#fake | 64 | |



sashash (<https://github.com/PharmaForest/sashash>)

事前のソートなしで、keyと参照先から結合したい変数をしているすると、データステップ中に何回でもいくつものデータセットでも自由に結合できる%kvlookupや、keyが存在するかをYNでフラグとして返せる%keycheckなどハッシュオブジェクトを利用したハンドリングパッケージ

```
/*インストール webアクセス可能の場合。無理な場合は先に説明した①の方法で直にインストール*/
```

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

```
/*パッケージのロード*/
```

```
%loadPackage(sashash)
```

```
/*USUBJIDをキーにして、VSにDMからAGEを結合*/
```

```
data wk1;
```

```
set vs (keep=USUBJID VSTESTCD VTEST VSORRES VSDTC);
```

```
%kvlookup(master = dm, key = USUBJID, var = AGE)
```

```
run;
```

```
/*SAEが発現しているかどうかをDMからAEをみてフラグづけ*/
```

```
data dm_sae;
```

```
set dm (keep=USUBJID ARM);
```

```
%keycheck(master = ae, key = USUBJID,
```

```
wh=%nrbquote(AESER="Y"), f1 = SAEFL)
```

```
run;
```

| VIEWTABLE: Work.Wk1 | | | | | | |
|---------------------|------------|----------|--------------------------|---------|------------|-----|
| | USUBJID | VSTESTCD | VTEST | VSORRES | VSDTC | AGE |
| 1 | FAKE-00001 | DIABP | Diastolic Blood Pressure | 109 | 2025-04-20 | 74 |
| 2 | FAKE-00001 | HEIGHT | Height | 172.8 | 2025-04-20 | 74 |
| 3 | FAKE-00001 | SYSBP | Systolic Blood Pressure | 84 | 2025-04-20 | 74 |
| 4 | FAKE-00001 | WEIGHT | Weight | 71.8 | 2025-04-20 | 74 |

| VIEWTABLE: Work.Dm_sae | | | |
|------------------------|------------|--------|-------|
| | USUBJID | ARM | SAEFL |
| 1 | FAKE-00001 | Group1 | Y |
| 2 | FAKE-00002 | Group1 | N |
| 3 | FAKE-00003 | Group1 | Y |
| 4 | FAKE-00004 | Group1 | Y |
| 5 | FAKE-00005 | Group1 | Y |
| 6 | FAKE-00006 | Group1 | Y |
| 7 | FAKE-00007 | Group1 | N |
| 8 | FAKE-00008 | Group1 | Y |
| 9 | FAKE-00009 | Group1 | N |



mergex (<https://github.com/PharmaForest/mergex>)

日付keyが完全一致しない場合、それに最も近い過去、または未来、あるいは過去未来の方向で一定期間内の最も近い日付をもつレコードを結合するRolling JoinなどSASに未実装の結合をサポート

```
/*インストール webアクセス可能の場合。無理な場合は先に説明した①の方法で直にインストール*/
```

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

```
/*パッケージのロード*/
```

```
%loadPackage(mergex)
```

```
/*SAE発現の2週間以内に測定されたもっとも新しい体重*/
```

```
data AE_WEIGHT;
```

```
set ADAE (keep=USUBJID AETERM ASTDT AESER);
```

```
where AESER="Y";
```

```
ADT=ASTDT;
```

```
%rolling_match(master=ADVS,
```

```
wh=%nrbquote(PARAMCD="WEIGHT")
```

```
, key=USUBJID,
```

```
rollvar=ADT, rolltype=BACK,
```

```
roll_back_limit=14, var=AVAL VSDTC);
```

```
drop ADT;
```

```
run;
```

Rolling Join

| | USUBJID | AETERM | ASTDT | AESER | VSDTC | AVAL |
|----|------------|---------------------|------------|-------|------------|------|
| 1 | FAKE-00001 | Neuro Surge#fake | 2025-06-07 | Y | 2025-06-03 | 70.8 |
| 2 | FAKE-00001 | Pulmo Stutter#fake | 2025-07-02 | Y | 2025-07-01 | 74.8 |
| 3 | FAKE-00001 | Neuro Quiver#fake | 2025-07-29 | Y | 2025-07-29 | 72.8 |
| 4 | FAKE-00003 | Renal Skip#fake | 2024-11-21 | Y | 2024-11-19 | 60.2 |
| 5 | FAKE-00004 | Gastro Skip#fake | 2025-05-13 | Y | 2025-05-10 | 92.6 |
| 6 | FAKE-00005 | Gastro Skip#fake | 2025-03-10 | Y | 2025-03-10 | 89.3 |
| 7 | FAKE-00005 | Neuro Slip#fake | 2025-04-25 | Y | 2025-04-24 | 92.3 |
| 8 | FAKE-00005 | Ophtho Stutter#fake | 2025-04-30 | Y | 2025-04-24 | 92.3 |
| 9 | FAKE-00006 | Myomuscle Snap#fake | 2025-08-26 | Y | 2025-08-26 | 61.2 |
| 10 | FAKE-00006 | Myomuscle Snap#fake | 2025-08-26 | Y | 2025-08-26 | 61.2 |



```
/*重複する変数を上書きせずに_データセット名で変数をわけるマージ*/
%varconf_merge(
  ds1=DM ,
  ds2=ADSL,
  byvars=USUBJID,
  output_ds=conf_merge_output (keep=USUBJID SUBJID: TRT01P: ARM:),
  in1=1,
  operator=AND,
  in2=1,
  auto_sort=N
);
```

| | USUBJID | SUBJID_DM | ARMCD | ARM_DM | SUBJID_ADSL | ARM_ADSL | TRT01P | TRT01PN |
|----|------------|-----------|-------|--------|-------------|----------|--------|---------|
| 1 | FAKE-00001 | 00001 | GR1 | Group1 | 00001 | Group1 | Group1 | 1 |
| 2 | FAKE-00002 | 00002 | GR1 | Group1 | 00002 | Group1 | Group1 | 1 |
| 3 | FAKE-00003 | 00003 | GR1 | Group1 | 00003 | Group1 | Group1 | 1 |
| 4 | FAKE-00004 | 00004 | GR1 | Group1 | 00004 | Group1 | Group1 | 1 |
| 5 | FAKE-00005 | 00005 | GR1 | Group1 | 00005 | Group1 | Group1 | 1 |
| 6 | FAKE-00006 | 00006 | GR1 | Group1 | 00006 | Group1 | Group1 | 1 |
| 7 | FAKE-00007 | 00007 | GR1 | Group1 | 00007 | Group1 | Group1 | 1 |
| 8 | FAKE-00008 | 00008 | GR1 | Group1 | 00008 | Group1 | Group1 | 1 |
| 9 | FAKE-00009 | 00009 | GR1 | Group1 | 00009 | Group1 | Group1 | 1 |
| 10 | FAKE-00010 | 00010 | GR1 | Group1 | 00010 | Group1 | Group1 | 1 |
| 11 | FAKE-00011 | 00011 | GR1 | Group1 | 00011 | Group1 | Group1 | 1 |
| 12 | FAKE-00012 | 00012 | GR1 | Group1 | 00012 | Group1 | Group1 | 1 |
| 13 | FAKE-00013 | 00013 | GR1 | Group1 | 00013 | Group1 | Group1 | 1 |



misc (<https://github.com/PharmaForest/misc>)

ちょっとした便利ツールの集合体パッケージ

/*インストール webアクセス可能の場合. 無理な場合は先に説明した①の方法で直にインストール*/

%installPackage(misc, mirror=PharmaForest)

/*パッケージのロード*/

%loadPackage(misc)

/*文字変数のLengthを必要最低限に変更する%minimize_charlen*/

%minimize_charlen(class, inlib=sashelp, outlib=work)

| VIEWTABLE: Sashelp.Class (Student Data) | | | | | |
|---|---------|-----|-----|--------|--------|
| | Name | Sex | Age | Height | Weight |
| 1 | Alfred | M | 18 | 74 | 70 |
| 2 | Alice | F | 21 | 62 | 65 |
| 3 | Barbara | F | 21 | 65 | 70 |
| 4 | Carol | F | 20 | 63 | 65 |
| 5 | Henry | M | 22 | 70 | 62 |
| 6 | James | M | 23 | 72 | 63 |
| 7 | Jane | F | 22 | 65 | 58 |
| 8 | Janet | F | 21 | 62 | 59 |
| 9 | Jeffrey | M | 20 | 65 | 57 |
| 10 | John | M | 24 | 73 | 66 |
| 11 | Joyce | F | 21 | 62 | 58 |
| 12 | Judy | F | 21 | 63 | 57 |
| 13 | Louise | F | 20 | 62 | 55 |
| 14 | Mary | F | 19 | 59 | 54 |
| 15 | Philip | M | 23 | 75 | 64 |
| 16 | Robert | M | 24 | 70 | 63 |
| 17 | Ronald | M | 24 | 70 | 63 |
| 18 | Thomas | M | 21 | 66 | 59 |
| 19 | William | M | 23 | 70 | 64 |



| VIEWTABLE: Work.Class (Student Data) | | | | | |
|--------------------------------------|---------|-----|-----|--------|--------|
| | Name | Sex | Age | Height | Weight |
| 1 | Alfred | M | 18 | 74 | 70 |
| 2 | Alice | F | 21 | 62 | 65 |
| 3 | Barbara | F | 21 | 65 | 70 |
| 4 | Carol | F | 20 | 63 | 65 |
| 5 | Henry | M | 22 | 70 | 62 |
| 6 | James | M | 23 | 72 | 63 |
| 7 | Jane | F | 22 | 65 | 58 |
| 8 | Janet | F | 21 | 62 | 59 |
| 9 | Jeffrey | M | 20 | 65 | 57 |
| 10 | John | M | 24 | 73 | 66 |
| 11 | Joyce | F | 21 | 62 | 58 |
| 12 | Judy | F | 21 | 63 | 57 |
| 13 | Louise | F | 20 | 62 | 55 |
| 14 | Mary | F | 19 | 59 | 54 |
| 15 | Philip | M | 23 | 75 | 64 |
| 16 | Robert | M | 24 | 70 | 63 |
| 17 | Ronald | M | 24 | 70 | 63 |
| 18 | Thomas | M | 21 | 66 | 59 |
| 19 | William | M | 23 | 70 | 64 |



laglead (<https://github.com/PharmaForest/laglead>)

あるレコードのnオブザベーション前の値やnオブザベーション後の値を取得できるパッケージ

```
/*インストール webアクセス可能の場合. 無理な場合は先に説明した①の方法で直にインストール*/
```

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

```
/*パッケージのロード*/
```

```
%loadPackage(laglead)
```

```
/*USUBJIDごとに1つ前と1つ後の体重を取得する*/
```

```
data weight;
set vs;
where VSTESTCD="WEIGHT";
keep USUBJID VSTESTCD VSDTC VSORRES;
run;
```

```
data weight_1;
```

```
set weight;
```

```
%laglead(dataset=weight, id=USUBJID, var=VSORRES,
offset=-1);
```

```
%laglead(dataset=weight, id=USUBJID, var=VSORRES,
offset=+1);
```

```
run;
```

| | USUBJID | VSTESTCD | VSORRES | VSDTC | VSORRES_prev_1 | VSORRES_next_1 |
|----|------------|----------|---------|------------|----------------|----------------|
| 1 | FAKE-00001 | WEIGHT | 71.8 | 2025-04-20 | | 72.8 |
| 2 | FAKE-00001 | WEIGHT | 72.8 | 2025-05-20 | 71.8 | 68.8 |
| 3 | FAKE-00001 | WEIGHT | 68.8 | 2025-05-21 | 72.8 | 67.8 |
| 4 | FAKE-00001 | WEIGHT | 67.8 | 2025-05-22 | 68.8 | 65.8 |
| 5 | FAKE-00001 | WEIGHT | 65.8 | 2025-05-23 | 67.8 | 73.8 |
| 6 | FAKE-00001 | WEIGHT | 73.8 | 2025-05-24 | 65.8 | 74.8 |
| 7 | FAKE-00001 | WEIGHT | 74.8 | 2025-05-27 | 73.8 | 70.8 |
| 8 | FAKE-00001 | WEIGHT | 70.8 | 2025-06-03 | 74.8 | 66.8 |
| 9 | FAKE-00001 | WEIGHT | 66.8 | 2025-06-10 | 70.8 | 65.8 |
| 10 | FAKE-00001 | WEIGHT | 65.8 | 2025-06-17 | 66.8 | 74.8 |
| 11 | FAKE-00001 | WEIGHT | 74.8 | 2025-06-24 | 65.8 | 74.8 |
| 12 | FAKE-00001 | WEIGHT | 74.8 | 2025-07-01 | 74.8 | 70.8 |
| 13 | FAKE-00001 | WEIGHT | 70.8 | 2025-07-08 | 74.8 | 74.8 |
| 14 | FAKE-00001 | WEIGHT | 74.8 | 2025-07-15 | 70.8 | 75.8 |
| 15 | FAKE-00001 | WEIGHT | 75.8 | 2025-07-22 | 74.8 | 72.8 |
| 16 | FAKE-00001 | WEIGHT | 72.8 | 2025-07-29 | 75.8 | |
| 17 | FAKE-00002 | WEIGHT | 83.2 | 2024-09-25 | | 90.2 |
| 18 | FAKE-00002 | WEIGHT | 90.2 | 2024-10-25 | 83.2 | 82.2 |
| 19 | FAKE-00002 | WEIGHT | 82.2 | 2024-10-26 | 90.2 | 87.2 |
| 20 | FAKE-00002 | WEIGHT | 87.2 | 2024-10-27 | 82.2 | 87.2 |
| 21 | FAKE-00002 | WEIGHT | 87.2 | 2024-10-28 | 87.2 | 84.2 |
| 22 | FAKE-00002 | WEIGHT | 84.2 | 2024-10-29 | 87.2 | 84.2 |
| 23 | FAKE-00002 | WEIGHT | 84.2 | 2024-11-01 | 84.2 | 83.2 |
| 24 | FAKE-00002 | WEIGHT | 83.2 | 2024-11-08 | 84.2 | 82.2 |
| 25 | FAKE-00002 | WEIGHT | 82.2 | 2024-11-15 | 83.2 | 87.2 |



ctcae5_grader (https://github.com/PharmaForest/ctcae5_grader)

CTCAE v5.0に基づいてGradingしてくれるパッケージ

```
/*インストール webアクセス可能の場合. 無理な場合は先に説明した①の方法で直にインストール*/
%installPackage(ctcae5_grader, mirror=PharmaForest)

/*パッケージのロード*/
%loadPackage(ctcae5_grader)

/*ヘモグロビン,ALT,好中球をGrading*/
data lab_testcases;
length PARAMCD $12 AVALU $16;
infile datalines dsd truncover;
input PARAMCD :$12. AVAL AVALU :$16. ANRLO ANRHI BASE
MFRHI;
datalines;
HGB, 14.5,g/dL, 12, 13.5, ., .
HGB, 15.4,g/dL, 12, 14.0, ., .
HGB, 17.0,g/dL, 12, 12.5, ., .
HGB, 7.5,g/dL, 12, 13.5, ., .
ALT, 70, U/L, ., 40, 30, .
ALT, 900, U/L, ., 40, 60, .
NEUT, 0.8, 10^9/L, 1.5, ., .
NEUT, 0.45,10^9/L, 1.5, ., .
;
run;
```

```
data lab_checked;
set lab_testcases;
%CTCAE5_HGB()
%CTCAE5_ALT()
%CTCAE5_NEUT()
run;
```

| | PARAMCD | AVALU | AVAL | ANRLO | ANRHI | BASE | MFRHI | ATOXGRH | ATOXGRL | ATOXGR | ATOXGRHN | ATOXGRLN | ATOXGRN | HGB_diff |
|---|---------|--------|------|-------|-------|------|-------|---------|---------|---------|----------|----------|---------|----------|
| 1 | HGB | g/dL | 14.5 | 12 | 13.5 | . | . | Grade 1 | Grade 0 | Grade 1 | 1 | 0 | 1 | 1 |
| 2 | HGB | g/dL | 15.4 | 12 | 14 | . | . | Grade 1 | Grade 0 | Grade 1 | 1 | 0 | 1 | 1.4 |
| 3 | HGB | g/dL | 17 | 12 | 12.5 | . | . | Grade 3 | Grade 0 | Grade 3 | 3 | 0 | 3 | 4.5 |
| 4 | HGB | g/dL | 7.5 | 12 | 13.5 | . | . | Grade 0 | Grade 3 | Grade 3 | 0 | 3 | 3 | -6 |
| 5 | ALT | U/L | 70 | . | 40 | 30 | . | Grade 1 | | Grade 1 | 1 | . | 1 | |
| 6 | ALT | U/L | 900 | . | 40 | 60 | . | Grade 3 | | Grade 3 | 3 | . | 3 | |
| 7 | NEUT | 10^9/L | 0.8 | 1.5 | . | . | . | | Grade 3 | Grade 3 | . | 3 | 3 | |
| 8 | NEUT | 10^9/L | 0.45 | 1.5 | . | . | . | | Grade 4 | Grade 4 | . | 4 | 4 | |



Adamski (<https://github.com/PharmaForest/adamski>)

ADaMを作成するためのユーティリティを提供するパッケージ。R, PharmaverseのadmiralをSASで真似たもの

/*インストール webアクセス可能の場合。無理な場合は先に説明した①の方法で直にインストール*/

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

/*パッケージのロード*/

```
%loadPackage(adamski)
```

/*DY変数の導出*/

```
data DY;  
set ADAE (keep=USUBJID ASTDT AENDT);  
%kvlookup(master=ADSL,  
key=USUBJID, var=TRTSDT)  
%derive_vars_dy(  
    reference_date = TRTSDT,  
    source_vars     = ASTDT AENDT  
);  
run;
```

| | USUBJID | ASTDT | AENDT | TRTSDT | ASTDY | AENDY |
|----|------------|------------|------------|------------|-------|-------|
| 1 | FAKE-00001 | 2025-05-27 | 2025-06-01 | 2025-05-22 | 6 | 11 |
| 2 | FAKE-00001 | 2025-05-29 | . | 2025-05-22 | 8 | . |
| 3 | FAKE-00001 | 2025-05-31 | 2025-05-31 | 2025-05-22 | 10 | 10 |
| 4 | FAKE-00001 | 2025-06-09 | 2025-06-09 | 2025-05-22 | 19 | 19 |
| 5 | FAKE-00001 | 2025-06-09 | 2025-06-12 | 2025-05-22 | 19 | 22 |
| 6 | FAKE-00001 | 2025-06-09 | 2025-06-13 | 2025-05-22 | 19 | 23 |
| 7 | FAKE-00001 | 2025-06-13 | 2025-07-03 | 2025-05-22 | 23 | 43 |
| 8 | FAKE-00001 | 2025-06-16 | 2025-06-17 | 2025-05-22 | 26 | 27 |
| 9 | FAKE-00001 | 2025-06-25 | . | 2025-05-22 | 35 | . |
| 10 | FAKE-00001 | 2025-06-28 | 2025-06-29 | 2025-05-22 | 38 | 39 |
| 11 | FAKE-00001 | 2025-07-04 | . | 2025-05-22 | 44 | . |
| 12 | FAKE-00001 | 2025-07-11 | 2025-07-14 | 2025-05-22 | 51 | 54 |
| 13 | FAKE-00001 | 2025-07-12 | . | 2025-05-22 | 52 | . |
| 14 | FAKE-00001 | 2025-07-13 | 2025-07-13 | 2025-05-22 | 53 | 53 |
| 15 | FAKE-00001 | 2025-07-14 | 2025-07-15 | 2025-05-22 | 54 | 55 |
| 16 | FAKE-00001 | 2025-07-17 | 2025-07-31 | 2025-05-22 | 57 | 71 |
| 17 | FAKE-00001 | 2025-07-19 | . | 2025-05-22 | 59 | . |
| 18 | FAKE-00001 | 2025-07-31 | 2025-07-31 | 2025-05-22 | 71 | 71 |
| 19 | FAKE-00002 | 2024-11-05 | 2024-11-06 | 2024-10-27 | 10 | 11 |
| 20 | FAKE-00002 | 2024-11-22 | 2024-11-22 | 2024-10-27 | 27 | 27 |



SASLogChecker (<https://github.com/PharmaForest/saslogchecker>)

対面実行時のログチェック(※SAS9.4/Windows環境のみ)

フォルダ指定でのログチェック(※SAS9.4/Windows環境のみ)

/*インストール webアクセス可能の場合. 無理な場合は先に説明した①の方法で直にインストール*/

%installPackage(SASLogChecker, mirror=PharmaForest)

/*パッケージのロード*/

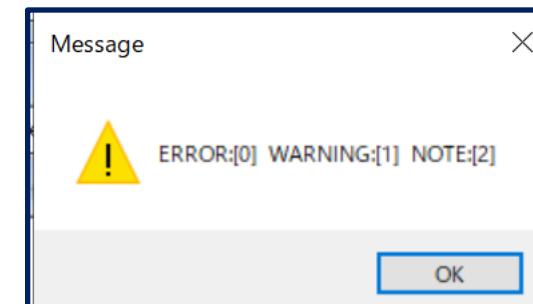
%loadPackage(SASLogChecker)

対面実行時のログチェック(※SAS9.4/Windows環境のみ)

```
data a;  
length x 8.;  
run;
```

```
data b;  
set a;  
c= 10/0;  
keep y;  
run;
```

%interact_logchk



| VIEWTABLE: _log | | | | |
|-----------------|---------|--|------------------|------|
| | date | record | target | line |
| 1 | NOTE | NOTE: Variable x is uninitialized. | is uninitialized | 6 |
| 2 | NOTE | NOTE: Division by zero detected during the compilation phase, detected at line 26250 column 6. | Division by zero | 17 |
| 3 | WARNING | WARNING: The variable y in the DROP, KEEP, or RENAME list has never been referenced. | | 21 |



フォルダ指定でのログチェック(※SAS9.4/Windows環境のみ)

```
%logchk2directory(folder=C:\logs, out_folder=C:\output);
```

| A | B | C | D |
|-------------|----------|---|--|
| FileName | Category | Hit keyword | Hit record |
| 2 aaaa.log | ERROR | ERROR | ERROR 73-322: Expecting an =. |
| 3 aaaa.log | ERROR | ERROR | ERROR 200-322: The symbol is not recognized and will be ignored. |
| 4 aaaa.log | WARNING | WARNING | WARNING: The data set WORKA may be incomplete. When this step was stopped there were 0 |
| 5 aaaa.log | NOTE | Division by zero | NOTE: Division by zero detected during the compilation phase, detected at line 6 column 5 |
| 6 aaaa.log | NOTE | Character values have been converted to | NOTE: Character values have been converted to numeric values at the places given by |
| 7 aaaa.log | ERROR | ERROR | ERROR: Errors printed on page 1 |
| 8 bbbb.log | NOTE | Division by zero | NOTE: Division by zero detected during the compilation phase, detected at line 2 column 5. |
| 9 bbbb.log | NOTE | Character values have been converted to | NOTE: Character values have been converted to numeric values at the places given by |
| 10 bbbb.log | NOTE | Invalid | NOTE: Invalid numeric data, 'A', at line 3 column 3. |
| 11 bbbb.log | | ERROR_=1 | x= _ERROR_=1 _N_=1 |
| 12 | | | |



sas_compare (https://github.com/PharmaForest/sas_compare)

フォルダ指定でのメイン・サブのコンペア(※SAS9.4/Windows環境のみ)

/*インストール webアクセス可能の場合. 無理な場合は先に説明した①の方法で直にインストール*/

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

/*パッケージのロード*/

```
%loadPackage(sas_compare)
```

```
%ads_compare(
```

```
    output_folder = D:/project/output,
```

```
    main_lib_path = D:/project/main,
```

```
    sub_lib_path = D:/project/sub,
```

```
    target_list = A
```

```
    B
```

```
    C
```

```
    D
```

```
    E
```

```
);
```

The screenshot shows the SAS Studio interface with two main panes. The left pane is a file browser titled '名前' (Name) showing files such as '_Compare_Status_Summary_20250709T0811.xlsx', '202507090811Compare.lst', and several PDF files named NG_A.pdf, NG_C.pdf, NG_D.pdf, NG_E.pdf, and OK_B.pdf. The right pane displays the results of a dataset comparison between MAIN_LIB.A and SUB_LIB.A using the EXACT method. It includes sections for Data Set Summary, Variables Summary, Observation Summary, and Values Comparison Summary. The Data Set Summary table shows two datasets: MAIN_LIB.A and SUB_LIB.A, both created and modified on 09JUL25 at 06:15:33, with 2 variables and 2 observations each. The Observation Summary table shows the count of observations for First Obs, First Unequal, Last Unequal, and Last Obs. The Values Comparison Summary table shows the number of variables compared with all observations equal (1) and some observations unequal (1).

| Dataset | Created | Modified | NVar | NObs |
|------------|------------------|------------------|------|------|
| MAIN_LIB.A | 09JUL25:06:15:33 | 09JUL25:06:15:33 | 2 | 2 |
| SUB_LIB.A | 09JUL25:06:15:33 | 09JUL25:06:15:33 | 2 | 2 |

| Observation | Base | Compare |
|---------------|------|---------|
| First Obs | 1 | 1 |
| First Unequal | 2 | 2 |
| Last Unequal | 2 | 2 |
| Last Obs | 2 | 2 |

| Number of Observations in Common: 2. | |
|---|--|
| Total Number of Observations Read from MAIN_LIB.A: 2. | |
| Total Number of Observations Read from SUB_LIB.A: 2. | |
| Number of Observations with Some Compared Variables Unequal: 1. | |
| Number of Observations with All Compared Variables Equal: 1. | |

| The COMPARE Procedure | | | | |
|---|------------------|------------------|------|------|
| Comparison of MAIN_LIB.A with SUB_LIB.A | | | | |
| (Method=EXACT) | | | | |
| Data Set Summary | | | | |
| Dataset | Created | Modified | NVar | NObs |
| MAIN_LIB.A | 09JUL25:06:15:33 | 09JUL25:06:15:33 | 2 | 2 |
| SUB_LIB.A | 09JUL25:06:15:33 | 09JUL25:06:15:33 | 2 | 2 |
| Variables Summary | | | | |
| Number of Variables in Common: 2. | | | | |
| The COMPARE Procedure | | | | |
| Comparison of MAIN_LIB.A with SUB_LIB.A | | | | |
| (Method=EXACT) | | | | |
| Observation Summary | | | | |
| Observation | Base | Compare | | |
| First Obs | 1 | 1 | | |
| First Unequal | 2 | 2 | | |
| Last Unequal | 2 | 2 | | |
| Last Obs | 2 | 2 | | |
| Number of Observations in Common: 2. | | | | |
| Total Number of Observations Read from MAIN_LIB.A: 2. | | | | |
| Total Number of Observations Read from SUB_LIB.A: 2. | | | | |
| Number of Observations with Some Compared Variables Unequal: 1. | | | | |
| Number of Observations with All Compared Variables Equal: 1. | | | | |
| The COMPARE Procedure | | | | |
| Comparison of MAIN_LIB.A with SUB_LIB.A | | | | |
| (Method=EXACT) | | | | |
| Values Comparison Summary | | | | |
| Number of Variables Compared with All Observations Equal: 1. | | | | |
| Number of Variables Compared with Some Observations Unequal: 1. | | | | |



sas_dataset_json (https://github.com/PharmaForest/sas_dataset_json)

Dataset-JSON v1.1に基づく Dataset-JSON と SAS データセットの相互読み書きができるパッケージ

/*インストール web アクセス可能の場合。無理な場合は先に説明した①の方法で直にインストール*/

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

/*パッケージのロード*/

```
%loadPackage(sas_dataset_json)
```

/*SAS データセットを Dataset-JSON へ */

```
%m_sas_to_json1_1(outpath  
=D:\Users\XXXXXX\Desktop\test,  
library = work,  
dataset = ads1,  
pretty = Y);
```

JSON の出力先は自環境にあわせて書き換えてください

```
ads1.json - メモ帳
ファイル(F) 編集(E) 書式(O) 表示(V) ヘルプ(H)
{
  "datasetJSONCreationDateTime": "2026-01-13T06:35:28",
  "datasetJSONVersion": "1.1.0",
  "fileOID": "www.cdisc.org/StudyMSGv2/1/Define-XML_2.1.0/2024-11-11//ads1",
  "dbLastModifiedDateTime": "2026-01-13T05:49:59",
  "originator": "DUMMY Corporation",
  "sourceSystem": [
    {
      "name": "SAS on X64_SRV19",
      "version": "9.04.01M8"
    }
  ],
  "studyOID": "DUMMY-111",
  "metaDataVersionOID": "MDV_MSGv2.0.SDTMIG.3.3.SDTM.1.7",
  "metaDataRef": "define.xml",
  "itemGroupOID": "IG.ADSL",
  "records": 100,
  "name": "ADSL",
  "label": "",
  "columns": [
    {
      "itemOID": "IT.ADSL.STUDYID",
      "name": "STUDYID",
      "label": "Study Identifier",
      "dataType": "string",
      "length": 10
    },
    {
      "itemOID": "IT.ADSL.USUBJID",
      "name": "USUBJID",
      "label": "Unique Subject Identifier",
      "dataType": "string",
      "length": 10
    }
  ]
}
```

Dataset-JSONを読み込みSASデータセットへ



```
%m_json1_1_to_sas(inpath=/data/definejson, ds=AE);
```

xptを読み込みSASデータセットへ



```
%xpt2sas(  
    indir=C:$place$for$xpt,          /* Directory with xpt files */  
    outdir=C:$place$for$sas7bdat    /* Directory for sas7bdat files */  
)
```



datacut_sas (https://github.com/PharmaForest/datacut_sas)

カットオフ解析用に、カットオフ日をさだめて、レコードの抽出、日付の補完を行い
トレセラビリティ用にカットオフ処理前後の履歴を出力する

/*インストール webアクセス可能の場合. 無理な場合は先に説明した①の方法で直にインストール*/

%installPackage(datacut_sas, mirror=PharmaForest)

/*パッケージのロード*/

%loadPackage(datacut_sas)

準備が少しうるるので、時間が余れば説明

Before cut-off

VIEWTABLE: C_init.Dim

| USUBJID | RFSTDTG | RFSTDTOTC | RFPENDTGC | DTHDTG | DTHFL |
|---------|------------|------------------|------------|------------|-------|
| A-001 | 2025-11-02 | 2025-11-02T10:00 | 2025-12-01 | | |
| A-002 | 2025-10-01 | 2025-10-01T10:00 | 2025-10-31 | | |
| A-003 | 2025-10-02 | 2025-11-02T10:00 | 2025-12-01 | | |
| A-004 | 2025-10-05 | 2025-10-13T10:00 | 2025-12-05 | 2025-12-05 | |
| A-005 | | | | | |
| A-006 | | | | | |

VIEWTABLE: C_init.Arc

| USUBJID | AESTDTG |
|---------|------------|
| A-003 | 2025-11-02 |
| A-004 | 2025-10-10 |

VIEWTABLE: C_init.Bas

| TSPARAMCD | ACTSUB |
|-----------|--------|
| | |

After cut-off

VIEWTABLE: C_out.Dim

| USUBJID | RFSTDTG | RFSTDTOTC | RFPENDTGC | DTHDTG | DTHFL |
|---------|------------|------------------|------------|--------|-------|
| A-002 | 2025-10-01 | 2025-10-01T10:00 | 2025-10-10 | | |
| A-003 | 2025-10-02 | 2025-11-01T10:00 | 2025-11-01 | | |
| A-004 | 2025-10-05 | 2025-10-12T10:00 | 2025-11-01 | | |
| A-005 | | | | | |

VIEWTABLE: C_out.Arc

| USUBJID | AESTDTG |
|---------|------------|
| A-004 | 2025-10-10 |

VIEWTABLE: C_out.Bas

| TSPARAMCD | ACTSUB |
|-----------|--------|
| | |

Cut-off report

| A | B | C | D | E | F | G | |
|----|-------------------|------------------|-----------|-------------|--------------------|------------------|---------------|
| 1 | Cutoff date: | 2025-11-01 | | | | | |
| 2 | Cutoff date time: | 2025-11-01T00:00 | | | | | |
| 3 | | | | | | | |
| 4 | USUBJID | Domain | Field | Observation | No Before | After | Delete Record |
| 5 | A-003 | AE | AESTDTG | | 1 | | 2025-11-02 |
| 6 | A-004 | DM | DTHFL | | 4 Y | | |
| 7 | A-004 | DM | DTHDTG | | 4 2025-12-05 | | |
| 8 | A-005 | DM | USUBJID | | 5 | | A-005 |
| 9 | A-006 | DM | USUBJID | | 6 | | A-006 |
| 10 | A-001 | DM | RFSTDTG | | 1 | | 2025-11-02 |
| 11 | A-003 | DM | RFPENDTGC | | 3 2025-12-01 | 2025-11-01 | |
| 12 | A-004 | DM | RFPENDTGC | | 4 2025-12-05 | 2025-11-01 | |
| 13 | A-003 | DM | RFXSTDTG | | 3 2025-11-02T10:00 | 2025-11-01T00:00 | |
| 14 | | | | | | | |
| 15 | | | | | | | |



sARDen (<https://github.com/PharmaForest/sARDen>)

CDISCのARS(Analysis Standard Result)にもとづくARD(Analysis Result Data)を作成する基礎
パッケージ

/*インストール webアクセス可能の場合. 無理な場合は先に説明した①の方法で直にインストール*/

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

/*パッケージのロード*/

```
%loadPackage(sARDen)
```

/*□□の年齢と体重の□□□□□*/

```
%sard_summary(
```

 data=ADSL,

 by=TRT01P,

 variable=AGE WEIGHTBL,

 statistic=N MEDIAN MIN MAX MEAN SD,

 out=sard_summary_mean

) ;

| | group1 | group1_level | variable | context | stat_name | stat_label | stat | fmt_fun |
|----|--------|--------------|----------|---------|-----------|------------|--------------|---------|
| 1 | TRT01P | Group1 | AGE | summary | n | N | 50 | 0 |
| 2 | TRT01P | Group1 | AGE | summary | median | Median | 56.5 | 1 |
| 3 | TRT01P | Group1 | AGE | summary | min | Min | 20 | 0 |
| 4 | TRT01P | Group1 | AGE | summary | max | Max | 80 | 0 |
| 5 | TRT01P | Group1 | AGE | summary | mean | Mean | 54.44 | 1 |
| 6 | TRT01P | Group1 | AGE | summary | sd | SD | 16.816124429 | 1 |
| 7 | TRT01P | Group1 | WEIGHTBL | summary | n | N | 50 | 0 |
| 8 | TRT01P | Group1 | WEIGHTBL | summary | median | Median | 65.35 | 2 |
| 9 | TRT01P | Group1 | WEIGHTBL | summary | min | Min | 37.7 | 1 |
| 10 | TRT01P | Group1 | WEIGHTBL | summary | max | Max | 113.3 | 1 |
| 11 | TRT01P | Group1 | WEIGHTBL | summary | mean | Mean | 68.62 | 2 |
| 12 | TRT01P | Group1 | WEIGHTBL | summary | sd | SD | 17.195395682 | 2 |
| 13 | TRT01P | Group2 | AGE | summary | n | N | 50 | 0 |
| 14 | TRT01P | Group2 | AGE | summary | median | Median | 38.5 | 1 |
| 15 | TRT01P | Group2 | AGE | summary | min | Min | 21 | 0 |
| 16 | TRT01P | Group2 | AGE | summary | max | Max | 80 | 0 |
| 17 | TRT01P | Group2 | AGE | summary | mean | Mean | 46.82 | 1 |
| 18 | TRT01P | Group2 | AGE | summary | sd | SD | 19.067484879 | 1 |
| 19 | TRT01P | Group2 | WEIGHTBL | summary | n | N | 50 | 0 |
| 20 | TRT01P | Group2 | WEIGHTBL | summary | median | Median | 67.85 | 2 |
| 21 | TRT01P | Group2 | WEIGHTBL | summary | min | Min | 40.6 | 1 |
| 22 | TRT01P | Group2 | WEIGHTBL | summary | max | Max | 107.9 | 1 |
| 23 | TRT01P | Group2 | WEIGHTBL | summary | mean | Mean | 69.212 | 2 |
| 24 | TRT01P | Group2 | WEIGHTBL | summary | sd | SD | 16.151459655 | 2 |



```
/*AEの群別SOC別PT別集計*/
%sard_stack_hierarchical(  
  data=ADAE,  
  variable=AEBODSYS AEDECOD,  
  variable_hieral_code=AEBDSYCD F_AEPTCD,  
  by=TRTA,  
  id=USUBJID,  
  denominator_dataset=ADSL(rename=(TRT01A=TRTA)),  
  out=sard_stack_hierarchical  
) ;
```

| | group1 | group1_level | variable | variable_level | context | stat_name | stat_label | stat | fmt_fun |
|----|--------|--------------|----------------------|-----------------------------|--------------|-----------|------------|----------|---------|
| 1 | | | TRTA | Group1 | tabulate | n | n | 50 0 | |
| 2 | | | TRTA | Group1 | tabulate | N | N | 100 0 | |
| 3 | | | TRTA | Group1 | tabulate | p | % | 0.5 xxx | |
| 4 | | | TRTA | Group2 | tabulate | n | n | 50 0 | |
| 5 | | | TRTA | Group2 | tabulate | N | N | 100 0 | |
| 6 | | | TRTA | Group2 | tabulate | p | % | 0.5 xxx | |
| 7 | TRTA | Group1 | hierarchical_overall | Y | hierarchical | n | n | 48 0 | |
| 8 | TRTA | Group1 | hierarchical_overall | Y | hierarchical | N | N | 50 0 | |
| 9 | TRTA | Group1 | hierarchical_overall | Y | hierarchical | p | % | 0.96 xxx | |
| 10 | TRTA | Group1 | AEBODSYS | Nervous System Events#fake | hierarchical | n | n | 32 0 | |
| 11 | TRTA | Group1 | AEBODSYS | Nervous System Events#fake | hierarchical | N | N | 50 0 | |
| 12 | TRTA | Group1 | AEBODSYS | Nervous System Events#fake | hierarchical | p | % | 0.64 xxx | |
| 13 | TRTA | Group1 | AEDECOD | Lung Haze#fake | hierarchical | n | n | 22 0 | |
| 14 | TRTA | Group1 | AEDECOD | Lung Haze#fake | hierarchical | N | N | 50 0 | |
| 15 | TRTA | Group1 | AEDECOD | Lung Haze#fake | hierarchical | p | % | 0.44 xxx | |
| 16 | TRTA | Group1 | AEDECOD | Cardiac Flutter#fake | hierarchical | n | n | 23 0 | |
| 17 | TRTA | Group1 | AEDECOD | Cardiac Flutter#fake | hierarchical | N | N | 50 0 | |
| 18 | TRTA | Group1 | AEDECOD | Cardiac Flutter#fake | hierarchical | p | % | 0.46 xxx | |
| 19 | TRTA | Group1 | AEDECOD | Endo Flick#fake | hierarchical | n | n | 15 0 | |
| 20 | TRTA | Group1 | AEDECOD | Endo Flick#fake | hierarchical | N | N | 50 0 | |
| 21 | TRTA | Group1 | AEDECOD | Endo Flick#fake | hierarchical | p | % | 0.3 xxx | |
| 22 | TRTA | Group1 | AEBODSYS | Cardiac Irregularities#fake | hierarchical | n | n | 32 0 | |
| 23 | TRTA | Group1 | AEBODSYS | Cardiac Irregularities#fake | hierarchical | N | N | 50 0 | |
| 24 | TRTA | Group1 | AEBODSYS | Cardiac Irregularities#fake | hierarchical | p | % | 0.64 xxx | |
| 25 | TRTA | Group1 | AEDECOD | Dermal Sway#fake | hierarchical | n | n | 19 0 | |
| 26 | TRTA | Group1 | AEDECOD | Dermal Sway#fake | hierarchical | N | N | 50 0 | |
| 27 | TRTA | Group1 | AEDECOD | Dermal Sway#fake | hierarchical | p | % | 0.38 xxx | |
| 28 | TRTA | Group1 | AEDECOD | Pulse Ripple#fake | hierarchical | n | n | 13 0 | |
| 29 | TRTA | Group1 | AEDECOD | Pulse Ripple#fake | hierarchical | N | N | 50 0 | |
| 30 | TRTA | Group1 | AEDECOD | Pulse Ripple#fake | hierarchical | p | % | 0.26 xxx | |
| 31 | TRTA | Group1 | AEBODSYS | Respiratory Complaints#fake | hierarchical | n | n | 25 0 | |
| 32 | TRTA | Group1 | AEBODSYS | Respiratory Complaints#fake | hierarchical | N | N | 50 0 | |



sARDenX (<https://github.com/PharmaForest/sARDenX>)

CDISCのARS(Analysis Standard Result)にもとづくARD(Analysis Result Data)を作成するパッケージ, sARDenXにない統計的処理をサポート

```
/*インストール webアクセス可能の場合. 無理な場合は先に説明した①の方法で直にインストール*/
```

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

```
/*パッケージのロード*/
```

```
%loadPackage(sARDenX)
```

```
/* ウエルチのt検定による二群の年齢の検定 */
```

```
%sard_stats_t_test(
```

```
  data=ADSL,
```

```
  out=sard_stats_t_test,
```

```
  class=TRT01PN,
```

```
  var=AGE,
```

```
  alpha=0.05,
```

```
  side=2,
```

```
  h0=0,
```

```
  Welch=Y
```

```
);
```

| | group1 | variable | context | stat_name | stat_label | stat | fmt_fun | Additional_Notes_in_SAS |
|----|---------|----------|--------------|-------------|---------------------|--------------|-----------------------------|-------------------------|
| 1 | TRT01PN | AGE | stats_t_test | estimate1 | Group 1 Mean | 54.44 | 1 | TRT01PN=1 |
| 2 | TRT01PN | AGE | stats_t_test | estimate2 | Group 2 Mean | 46.82 | 1 | TRT01PN=2 |
| 3 | TRT01PN | AGE | stats_t_test | estimate | Group Mean | 8.12 | 1 | Diff (1-2) |
| 4 | TRT01PN | AGE | stats_t_test | conf_low | CI Lower Bound | 0.9836193955 | 1 | |
| 5 | TRT01PN | AGE | stats_t_test | conf_high | CI Upper Bound | 15.256380605 | 1 | |
| 6 | TRT01PN | AGE | stats_t_test | statistic | t Statistic | 2.2584309249 | 1 | |
| 7 | TRT01PN | AGE | stats_t_test | parameter | Degrees of Freedom | 96.492562666 | 1 | |
| 8 | TRT01PN | AGE | stats_t_test | p_value | p-value | 0.0261708004 | 1 | |
| 9 | TRT01PN | AGE | stats_t_test | method | method | | 2 2:Welch Two Sample t-test | Satterthwaite |
| 10 | TRT01PN | AGE | stats_t_test | alternative | alternative | | 2 2:two.sided | |
| 11 | TRT01PN | AGE | stats_t_test | conf_level | CI Confidence Level | 0.95 | 1 | |
| 12 | TRT01PN | AGE | stats_t_test | mu | H0 Mean | 0 | 1 | |
| 13 | TRT01PN | AGE | stats_t_test | var_equal | Equal Variances | 0 | 0:N | |
| 14 | TRT01PN | AGE | stats_t_test | paired | Paired t-test | 0 | 0:N | |



freqsum (<https://github.com/PharmaForest/freqsum>)

要約統計やカウント集計について

Proc reportやproc odstableなどの帳票出力プロシージャで出しやすい OUT1, OUT2…の形で結果を
だすパッケージ

/*インストール webアクセス可能の場合. 無理な場合は先に説明した①の方法で直にインストール*/

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

/*パッケージのロード*/

```
%loadPackage(freqsum)
```

/*性別の群別集計*/

```
%FreqStat(inds=ADSL, sortNum=1, outds=sum01, grpNum=2, trtGrp=TRT01PN,  
label=%nrstr(Sex), trgtVar=SEX, trgtVarTyp=C, trgtValue=%str('M', 'F', 'U'),  
trgtLabel=%str('Male', 'Female', 'Unknown'));
```

| | num1 | num2 | out1 | out2 | out3 | out4 |
|---|------|------|-------|---------|-----------|-----------|
| 1 | | 1 | 1 Sex | Male | 20 (40.0) | 24 (48.0) |
| 2 | | 1 | 2 Sex | Female | 30 (60.0) | 26 (52.0) |
| 3 | | 1 | 3 Sex | Unknown | 0 | 0 |

/*年齢の群別要約統計*/

```
%SummaryStat(inds=ADSL, sortNum=2, outds=sum02, grpNum=2, trtGrp=TRT01PN, label=%str(Age), trgtVar=AGE);
```

| | NUM1 | NUM2 | out1 | out2 | out3 | out4 |
|---|------|------|------|------------|-------------|-------------|
| 1 | 2 | 1 | Age | n | 50 | 50 |
| 2 | 2 | 3 | Age | Mean (SD) | 54.4 (16.8) | 46.3 (19.1) |
| 3 | 2 | 4 | Age | Median | 56.5 | 38.5 |
| 4 | 2 | 6 | Age | [Min, Max] | [20, 80] | [21, 80] |



rtfCreator (<https://github.com/PharmaForest/rtfcreator>)

簡単な指定でRTFで帳票を作成

```
/*インストール webアクセス可能の場合. 無理な場合は先に説明した①の方法で直にインストール*/
%installPackage(rtfcreator, mirror=PharmaForest)

/*パッケージのロード*/
%loadPackage(rtfcreator)

/*前のfreqsumで出した解析結果を縦に積んでみる*/
data output;
set sum01 sum02;
out1_lag=lag(out1);
if out1=out1_lag then call missing(out1);
label out1="Item" out2="Category/Statics"
out3="Group1" out4="Group2";
run;

%rtfCreator(DS=output
,COLNUM =4
,VARLST =OUT1 OUT2 OUT3 OUT4
,JUSTLST =Left Left Center Center
,WIDTHLST=200 250 200 200
,TBLHEAD=%str(Table 14-1-2)
,TBLFOOT=%str(Table Foot xxxxx));
```

The SAS System

Table 14-1-2

| Item | Category/Statics | Group1 | Group2 |
|------|------------------|-------------|-------------|
| Sex | Male | 20 (40.0) | 24 (48.0) |
| | Female | 30 (60.0) | 26 (52.0) |
| | Unknown | 0 | 0 |
| Age | n | 50 | 50 |
| | Mean (SD) | 54.4 (16.8) | 46.3 (19.1) |
| | Median | 56.5 | 38.5 |
| | [Min, Max] | [20, 80] | [21, 80] |

Table Foot xxxxx



odstable_layoutshowcase (https://github.com/PharmaForest/odstable_layoutshowcase)

rtfcreatorで作れないRTF帳票を作成する際の見本を出力(※SAS9.4/Windows環境のみ)

/*インストール webアクセス可能の場合. 無理な場合は先に説明した①の方法で直にインストール*/

%installPackage(odstable_layoutshowcase, mirror=PharmaForest)

/*パッケージのロード*/

%loadPackage(odstable_layoutshowcase)

%odstable_layoutshowcase(sampleno=2);

Sample 2--Table 1
Proc ODSTABLE

| | | Treatment | | Placebo |
|------------------|------|----------------------------|----------------------------|-----------------|
| | | Group 1 N = xx n (%) | Group 2 N = xx n (%) | N = xx n (%) |
| AAAA | BBBB | CCCC | DDDD | EEEE |
| AAAA | BBBB | CCCC | DDDD | EEEE |
| AAAA | BBBB | CCCC | DDDD | EEEE |
| AAAA | BBBB | CCCC | DDDD | EEEE |
| AAAA | BBBB | CCCC | DDDD | EEEE |
| AAAA | BBBB | CCCC | DDDD | EEEE |
| AAAA | BBBB | CCCC | DDDD | EEEE |
| AAAA | BBBB | CCCC | DDDD | EEEE |
| Footer1 xxxxxxxx | | | | |
| Footer2 xxxxxxxx | | | | |

見本帳票とともに
その帳票を作成するProc templateの
スタイル設定と
Proc Odstableのコードがでてくるので
それをベースに自分の帳票を
作れる

template_style.txt - メモ帳

```

ファイル(F) 編集(E) 書式(O) 表示(V) ヘルプ(H)
ods path (prepend) work.rtfstyle(update);
proc template;
define style work.sample_style;
parent=styles.rtf;
style systemtitle/
  fontfamily = "Times New Roman"
  font_size = 9pt
  font_weight = medium
  font_style = roman
  foreground = black
  background = white
;
style systemfooter/
  font_face = "Times New Roman"
  font_size = 9pt
  font_weight = medium
  font_style = roman
  foreground = black
  background = white
;
style header/
  font_face = "Times New Roman"
  font_size = 9pt
  font_weight = medium
  font_style = roman
  foreground = black
  background = white
;
style footer/
  font_face = "Times New Roman"
  font_size = 9pt

```

sample2.txt - メモ帳

```

ファイル(F) 編集(E) 書式(O) 表示(V) ヘルプ(H)
options nocenter nodate nonumber orientation=landscape;
ods rtf file = "D:\Users\Y10089669\AppData\Local\Temp\79\SAS Temporary Files\TD231744_GAP-SAS64-001\sample_2_Table_1.rtf" style=work.sample_st
title "Sample 2--Table 1";
title2 "Proc ODSTABLE";
proc odstable data=dummy;
column out1 - out5;

define header header1: start=out1; end=out1; vjust=top; split="#" just=center;text "";end;
define header header2: start=out2; end=out2; vjust=top; split="#" just=center;text "";end;
define header header3: start=out3; end=out4; vjust=top; split="#" just=center;style=[borderbottomstyle=solid borderbottomwidth=1];text "Tre
define header header4: start=out4; end=out4; vjust=top; split="#" just=center;text "Group 1# N = xx## (%)" ;end;
define header header5: start=out5; end=out5; vjust=top; split="#" just=center;text "Placebo# N = xx## (%)" ;end;

define out1: print_headers=off; just=center; style=[cellwidth=220]; end;
define out2: print_headers=off; just=center; style=[cellwidth=200]; end;
define out3: print_headers=off; just=center; style=[cellwidth=150]; end;
define out4: print_headers=off; just=center; style=[cellwidth=150]; end;
define out5: print_headers=off; just=center; style=[cellwidth=150]; end;

define footer MYFOOT1: just=left; style=[borderbottomstyle=hidden]; text "Footer1 xxxxxxxx"; end;
define footer MYFOOT2: just=left; style=[borderbottomstyle=hidden]; text "Footer2 xxxxxxxx"; end;
run;
ods rtf close;
```



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

オンコロジー領域で頻出のグラフを出力

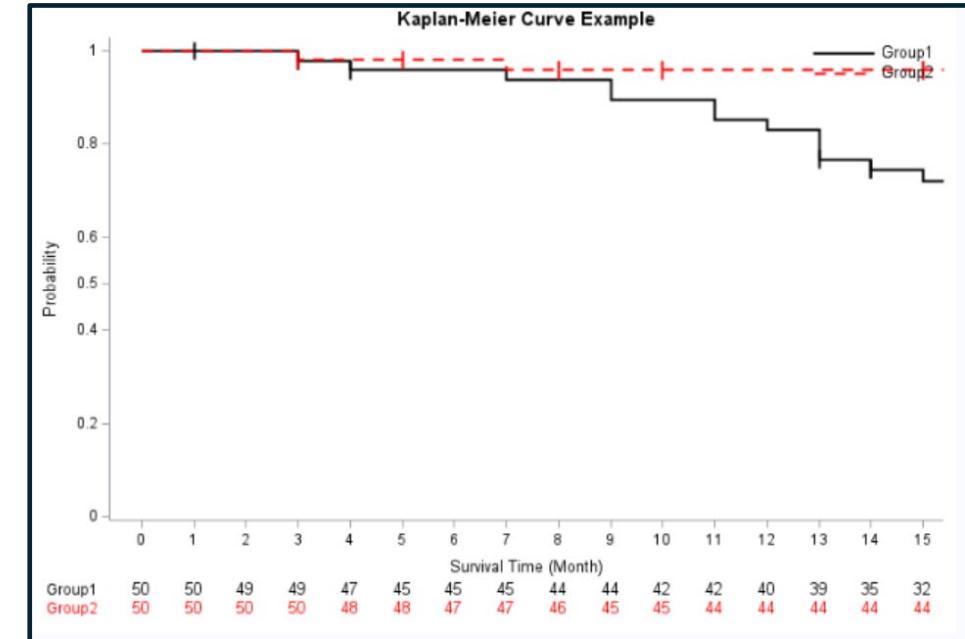
/*インストール webアクセス可能の場合。無理な場合は先に説明した①の方法で直にインストール*/

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

/*パッケージのロード*/

```
%loadPackage(oncoplotter)
```

```
%kaplan_meier_plot(  
  data = 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 = N  
) ;
```





trial_flow (https://github.com/PharmaForest/trial_flow)

症例フロー図を描くパッケージ

/*インストール webアクセス可能の場合. 無理な場合は先に説明した①の方法で直にインストール*/

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

/*パッケージのロード*/

```
%loadPackage(trial_flow)
```

```
%diagram_box(boxid=1,
  left_x=30,top_y=100
  ,right_x=70,bottom_y=90,
  text=Assessed for eligibility (n=100))

%diagram_line(lineid=1,
  start_x=50,
  start_y=90,
  end_x=50,
  end_y=55)

%diagram_line(lineid=2,
  start_x=50,
  start_y=73,
  end_x=65,
  end_y=73)

%diagram_box(boxid=2,
  left_x=65,top_y=87
  ,right_x=95,bottom_y=58
  ,text_just=left
  ,text=Excluded (n=10) # Not meeting inclusion criteria (n=4)
  #- Declined to Participate# (n=4)
  #- Other reasons# (n=2))

%diagram_box(boxid=3,
  left_x=37,top_y=55
  ,right_x=63,bottom_y=45,
  text=Randomized (n=90))

%diagram_line(lineid=3,
  start_x=37,
  start_y=50,
  midpoint_x=32,
  midpoint_y=50,
  end_x=32,
  end_y=30)

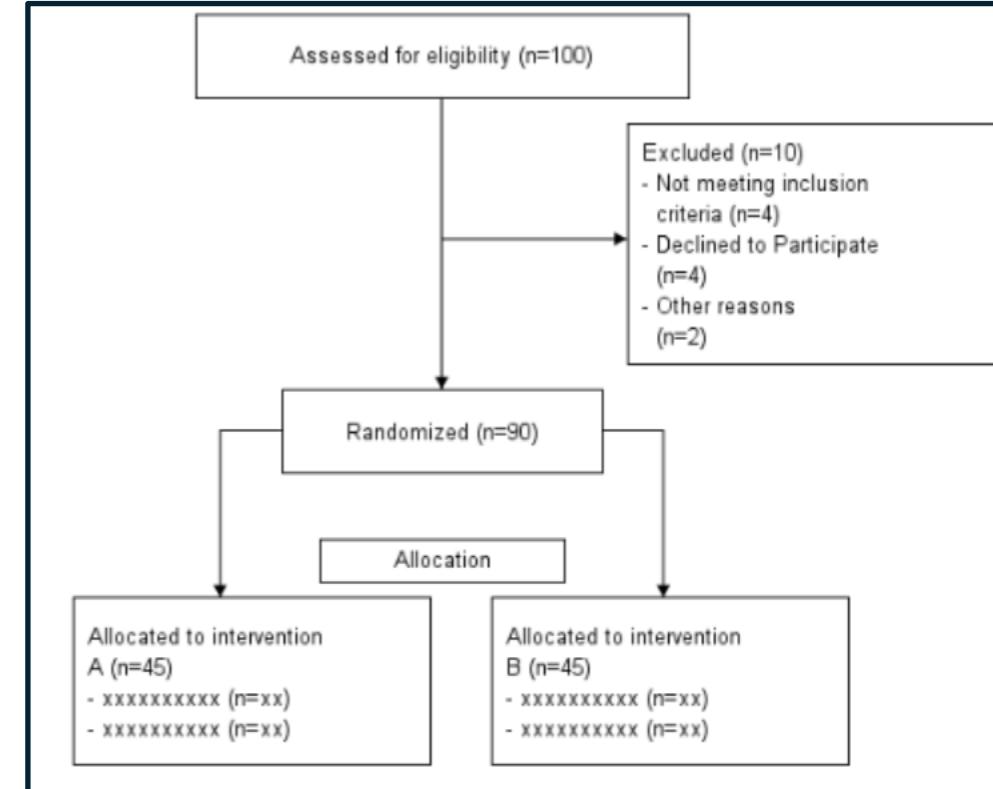
%diagram_line(lineid=4,
  start_x=63,
  start_y=50,
  midpoint_x=68,
  midpoint_y=50,
  end_x=68,
  end_y=30)

%diagram_box(boxid=5,
  left_x=40,top_y=37
  ,right_x=60,bottom_y=32
  ,text=Allocation)

%diagram_box(boxid=6,
  left_x=20,top_y=30
  ,right_x=45,bottom_y=10
  ,text_just=left
  ,text=Allocated to intervention A (n=45)
  #- XXXXXXXXXX (n=xx)
  #- XXXXXXXXXXXX (n=xx))

%diagram_box(boxid=7,
  left_x=54,top_y=30
  ,right_x=83,bottom_y=10
  ,text_just=left
  ,text=Allocated to intervention B (n=45)
  #- XXXXXXXXXX (n=xx)
  #- XXXXXXXXXXXX (n=xx))

/*plot*/
diagram_plot();
```



実務的なお話

- ・例えば、片側をPharmaForestのパッケージができるだけ利用するとかにしてもいいかもしれません
- ・例えば、片側をR/Pharmaverseをつかって片側SAS/PharmaForestを利用するなどでもいいかもしれません（統計解析の結果はパッケージとプロジェクトで差異があるので留意）
- ・承認申請やCROからメーカーへのプログラム納品に、PharmaForestのパッケージを含める場合はライセンスの記載や取り扱いにご注意ください。PharmaForestのパッケージはおおむねMITライセンスのため、それほど手間はかかりませんが。以下の資料の「使用にあたって注意すべき点-MITライセンス」を参考にしてください

<https://sas-user2025.ywstat.jp/download.html?n=107&key=zsngqfynpm>

- ・パッケージの利用はオープンですが、自己責任になるので、もしポリシー上、パッケージのテストを自組織でしないといけない場合などはSASパッケージをバリデーションするためのツールセットであるVALIVALIというパッケージがあり、レポートをだせるので、こちらを必要に応じてご利用ください

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



お疲れ様でした！

午後からのセッションもお楽しみください

