

PharmaForestでのパッケージ紹介

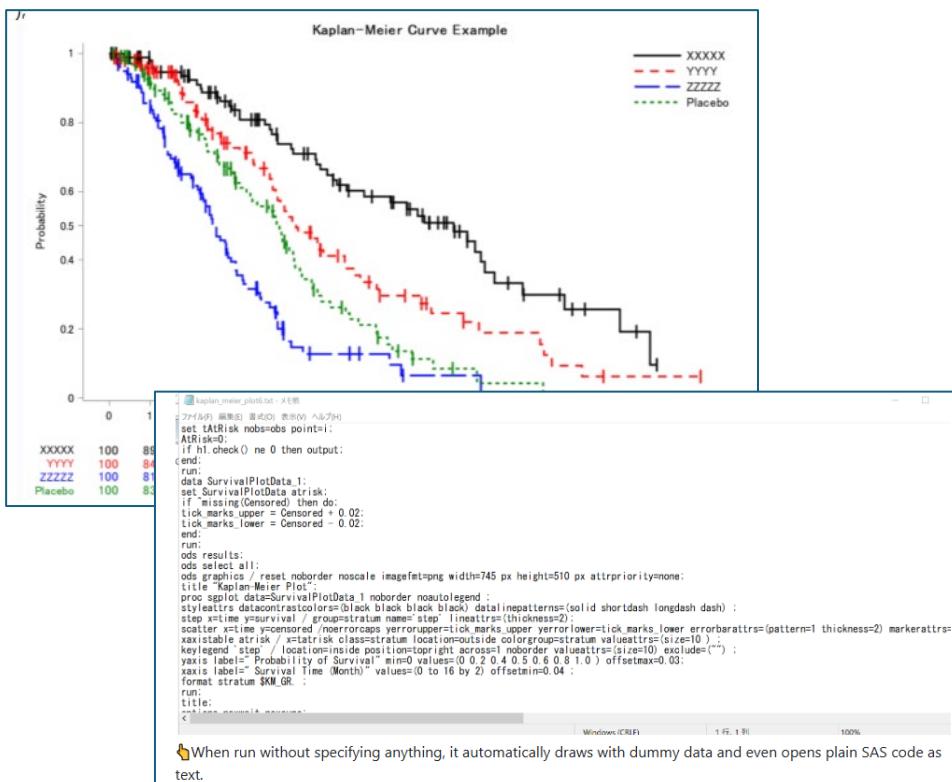
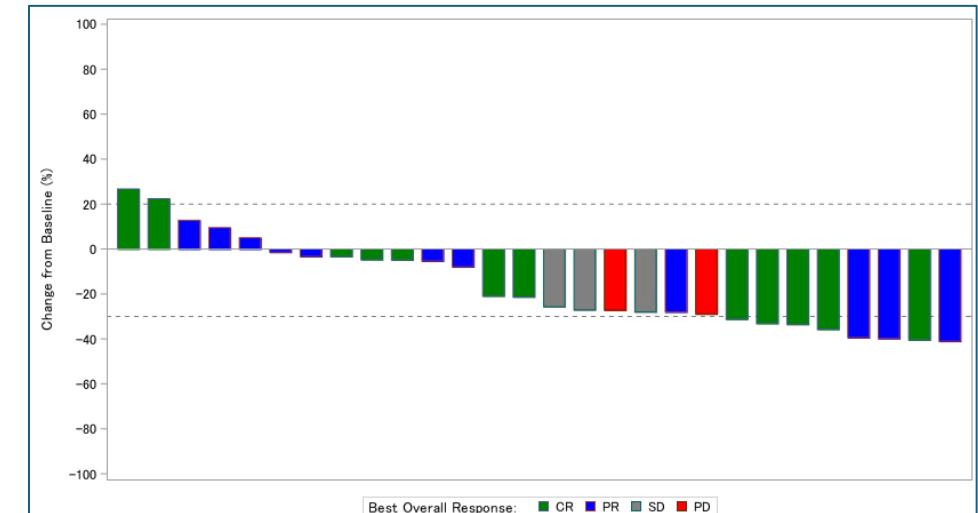
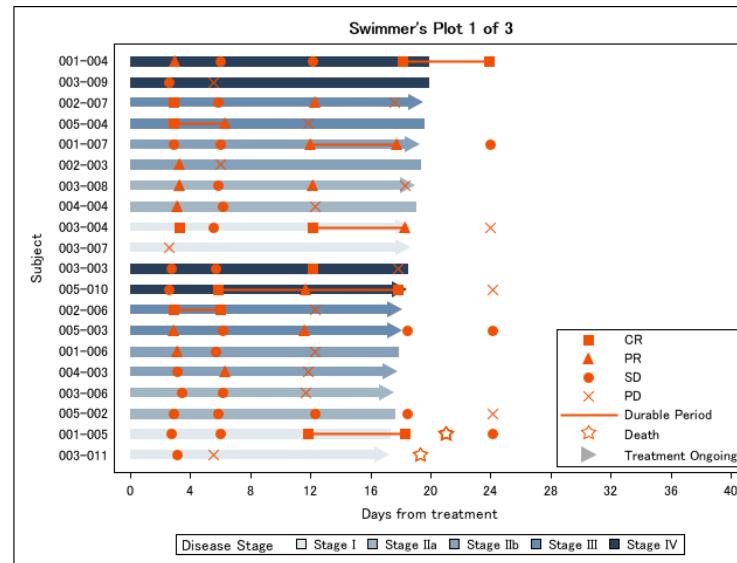
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<https://pharmaforest.github.io/>

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[No.1] OncoPlotter

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

Kaplan-Meier Plot, Swimmer Plot, Waterfall Plotなどオンコロジー領域で特によくつかわれるグラフについて、パラメーターを指定することでグラフを出力することができる。

あわせて、そのグラフを出力するためのSASプログラムコード 자체をテキストファイルとして提示してくれる



%kvlookup()

Enables efficient and dynamic retrieval of variables from a specified master dataset based on provided keys, directly within a single data step without separate sorting or merging.

PARAMETERS:

```
master : (Required) Name of the master dataset to lookup from.  
key   : (Required) Space-separated list of key variables for the lookup.  
var   : (Required) Space-separated list of variables to retrieve from the master dataset.  
wh    : (Optional) SQL WHERE clause condition to subset the master dataset before loading into has.  
warn  : (Optional) Y/N flag. If 'Y', issues a warning in the log when the lookup key is not found.  
dropviewflg: (Optional) Y/N flag. If 'Y', drops temporary SQL view created when the 'wh' parameter is u
```

Usage Example:

```
data a;  
set b;  
%kvlookup(master=sashelp.class,  
          key=Name,  
          var=Age Sex,  
          wh= %nrqquote(Age > 12),  
          warn=Y,  
          dropviewflg=Y);  
  
run;
```

%keycheck()

Dynamically validates the existence of keys within a master dataset directly within a single data step. Ideal for rapid data integrity checks and immediate flagging of key existence or non-existence.

PARAMETERS:

```
master : (Required) Name of the master dataset to check against.  
key   : (Required) Space-separated list of key variables to check.  
wh    : (Optional) SQL WHERE clause condition to subset the master dataset before loading into has.  
fl    : (Required) Name of the output variable indicating existence.  
cat   : (Optional) Controls output format of existence indicator:  
      - 'YN' (default): Returns 'Y' if key exists, 'N' otherwise.  
      - 'NUM': Returns 1 if key exists, 0 otherwise.  
dropviewflg: (Optional) Y/N flag. If 'Y', drops temporary SQL view created when the 'wh' parameter is u
```

Usage Example:

```
data a;  
set b;  
%keycheck(master=sashelp.class,  
          key=Name,  
          wh= %nrqquote(Age >= 15),  
          fl=exist_flag,  
          cat=YN,  
          dropviewflg=Y);
```

%kduppchk()

General-purpose duplicate key checker using SAS hash objects.

Parameters:

```
key : One or more key variables used to detect duplicates (space-delimited).
```

Usage Example:

```
data a;  
set sashelp.class;  
%kduppchk(AGE SEX);  
%kduppchk(NAME);  
run;
```

```
WARNING:Dupp Age=13 Sex=F  
WARNING:Dupp Age=14 Sex=M  
WARNING:Dupp Age=12 Sex=M  
WARNING:Dupp Age=14 Sex=F  
WARNING:Dupp Age=12 Sex=F  
WARNING:Dupp Age=15 Sex=F  
WARNING:Dupp Age=13 Sex=M  
WARNING:Dupp Age=15 Sex=M  
  
NOTE: There were 19 observations read from the data set SASHHELP.CLASS.  
NOTE: The data set WORK.A has 19 observations and 6 variables.  
NOTE: DATA statement used (Total process time):  
real time       0.01 seconds  
cpu time        0.01 seconds
```

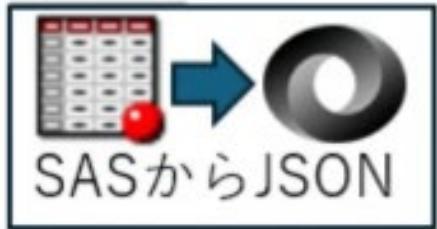
[No.2] sashash

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

Key – value のデータ処理をサポートするパッケージ
たとえばソートせずに、1ステップで、さまざまなSDTM
を参照してADSLを作成するといった離れ業が可能になる



%m_sas_to_json1_1
%m_sas_to_ndjson1_1



%m_json1_1_to_sas
%m_ndjson1_1_to_sas



```
class.json - メモ帳
ファイル(F) 編集(E) 書式(O) 表示(V) ヘルプ(H)
[{"datasetJSONCreationDateTime": "2025-05-22T05:36:33",
"datasetJSONVersion": "1.1.0",
"fileOID": "www.cdisc.org/Stu...Define-XML_2.1.0/2024-11-11//class",
"dbLastModifiedDateTime": "1989743495.2",
"originator": "DUMMY Corporation",
"sourceSystem": [
  {"name": "SAS on X64_SRV19",
  "version": "9.04.01M8"
],
"studyOID": "DUMMY-111",
"metaDataVersionOID": "MDV_MSGv2.0.SDTMIG.3.3.SDTM",
"metaDataRef": "define.xml",
"itemGroupData": "IG.CLASS",
"records": 19,
"name": "CLASS",
"label": "学生データ",
"columns": [
],
"rows": [
  {
    1: {
      "アルフレッド",
      "男子",
      14,
      69,
      112.5
    },
    2: {
      "アリス",
      "女子"
    }
  ]
}]
```

```
proc contents data=adae varnum;
run;
```

https://github.com/PharmaForest/sas_dataset_json

Dataset-JSON内のメタデータは拡張属性に自動的に格納されている

データセットの拡張属性のリスト(アルファベット順)			
拡張属性	数値	文字値	
datasetJSONCreationDateTime		2024-12-18T15:34:19	
datasetJSONVersion		1.1.0	
dbLastModifiedDateTime		2012-10-15T22:56:18	
fileOID		CDISCPILOT01.adae	
itemGroupID		ADAE	
metaDataRef		define.xml	
metaDataVersionOID		CDISC AdmM.2.1	
originator		CDISC Data Exchange Standards Team	
records		1191	
studyOID		CDISCPILOT01	

変数の拡張属性のリスト(アルファベット順)			
拡張属性	属性変数	数値	文字値
dataType	ADURN	.	integer
dataType	ADURU	.	string
dataType	AEACN	.	string
dataType	AEBODSYS	.	string
dataType	AEDECOD	.	string
dataType	AEHLGT	.	string
dataType	AEHLGTCOD	.	integer
dataType	AEHLT	.	string
dataType	AEHLTCOD	.	integer
dataType	AELLT	.	string
dataType	AELLTCOD	.	integer
dataType	AENDT	.	date
dataType	AENDY	.	integer

SASデータセットと、 Dataset-JSON v1.1規格の JSONおよびndjsonの相互変換を実施するパッケージ。

作成時にdefine.xmlを必要とせず、 SASの拡張属性を利用している。100%SASで基本的なライセンスで読み書きが可能である



%ex2pac() : excel to package

1. Put information of SAS package you want to create into an excel spreadsheet

(you can find template files in ./SASPACer/addcnt (simple_example.xlsx for simple example you can test as is, and template_package.xlsx for template contents for reference))

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

%pac2ex() : package to excel

It's very simple. You can convert package zip file into excel file with package information.

Sample code:

```
%pac2ex(  
  zip_path=C:\Temp\packagename.zip,      /* Path of package zip file */  
  xls_path=C:\Temp\package_info.xlsx,    /* Output excel path */  
  overwrite=N,                          /* Set N not to overwrite (default is Y) */  
  kill=Y)                                /* Set Y to delete all datasets in WORK (default is N) */
```

[No. 4] SASPACer

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

Excelのテンプレートに必要項目を記載して実行するだけで、誰でも簡単にSAS Packageを作れる魔法のパッケージ

PharmaForestの母といえるパッケージで、ほとんどすべてのパッケージがSASPACerによってパッケージ化されたものである。
逆にパッケージzipからExcelに展開する機能もあり



%minimize_charlen

Purpose: The macro analyzes all character variables in the dataset, determines the maximum length actually used, and alters the table to adjust each variable's length accordingly.

Sample code:

```
%minimize_charlen(dm)
```

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

%roundsig, %rounddec

Purpose: roundsig:This macro performs rounding based on the specified number of significant digits..
rounddec:Rounds a numeric variable to the specified number of decimal places and converts it to a character variable.

```
%roundSig(trgVal=RES,Sig=3);
```

/*Only integer values can be assigned to the "Sig" parameter.
For example, if set to "3",
"1.234" becomes "1.23",
"12.34" becomes "12.3",
"12.34" becomes "12.3",
"123.4" becomes "123",
"1234" becomes "1230".*/

%xpt2sas

Purpose: This macro converts xpt files in the folder into sas7bdat files.

Sample code:

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

%color_swatch()	
hex	dummy
hex: F0F8FF	
hex: FAEBD7	
hex: 00FFFF	
hex: 7FFF00	
hex: F0FFFF	
hex: F5F5DC	
hex: FF4A4C	
hex: 00:00:00	
hex: FFEB3B	
hex: 00:00:FF	
hex: 9A:2BE2	
hex: A5:2A:2A	
Brown	hex: A5:2A:2A
Burlywood	hex: DEBB87
CadetBlue	hex: 5F:9EA0
Chartreuse	hex: 7FFF00
Chocolate	hex: D2:69:1E
Coral	hex: FF:7F:50
CornFlowerBlue	hex: 64:95:ED

%color_swatch

Description: This macro retrieves SAS color definitions from the system registry (COLORNAMES section) and generates a visual color swatch table using PROC REPORT. Each row displays the color name, its hexadecimal code, and a cell shaded with the corresponding color.

Purpose: - Extract color name and hex values from SAS registry - Display each color with its background for visual reference - Useful for selecting and verifying colors for reports and graphics

Note: The color sample will not be displayed unless ODS HTML is turned on.

[No. 5] misc

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

様々な小道具的なマクロや関数を備えているパッケージ。
例えば、xptファイルの読み込みマクロ、
最大文字長にlengthを合わせるマクロ、四捨五入や有効
数字のマクロ、カラーパレットの指定を補助するマクロ
などの機能が現状含まれている



adsl dataset

It is created based on the information in the SDTM, mainly with VS domain information, which should basically be contained.

adsl

#	USUBJID	SUBJID	SITEID	AGE	AGEU
1	FAKE-00001	00001	FAKESITE001	74	YEAR
2	FAKE-00002	00002	FAKESITE001	72	YEAR
3	FAKE-00003	00003	FAKESITE001	46	YEAR
4	FAKE-00004	00004	FAKESITE001	66	YEAR
5	FAKE-00005	00005	FAKESITE001	42	YEAR
6	FAKE-00006	00006	FAKESITE001	53	YEAR
7	FAKE-00007	00007	FAKESITE001	31	YEAR
8	FAKE-00008	00008	FAKESITE001	50	YEAR
9	FAKE-00009	00009	FAKESITE001	71	YEAR
10	FAKE-00010	00010	FAKESITE001	63	YEAR
11	FAKE-00011	00011	FAKESITE001	48	YEAR
12	FAKE-00012	00012	FAKESITE001	59	YEAR
13	FAKE-00013	00013	FAKESITE001	21	YEAR
14	FAKE-00014	00014	FAKESITE001	20	YEAR

adae dataset

Created from AE domain information and ADSL

adae

#	TRT01AN	TRTP	TRTPN	TRTA	T	#	ADT	ADY	VISITNUM	VISIT	AVISIT	AVISIT
1	1	Group1	1	Group1	1	1	2024-10-10	-30	10	SCREENING	SCREENING	10
2	1	Group1	1	Group1	1	2	2024-10-10	-30	10	SCREENING	SCREENING	10
3	1	Group1	1	Group1	1	3	2024-10-10	-30	10	SCREENING	SCREENING	10
4	1	Group1	1	Group1	1	4	2024-10-10	-30	10	SCREENING	SCREENING	10
5	1	Group1	1	Group1	1	5	2024-11-09	1	110	Day 1	Day 1	110
6	1	Group1	1	Group1	1	6	2024-11-09	1	110	Day 1	Day 1	110
7	1	Group1	1	Group1	1	7	2024-11-09	1	110	Day 1	Day 1	110
8	1	Group1	1	Group1	1	8	2024-11-10	2	120	Day 2	Day 2	120
9	1	Group1	1	Group1	1	9	2024-11-10	2	120	Day 2	Day 2	120
10	1	Group1	1	Group1	1	10	2024-11-10	2	120	Day 2	Day 2	120
11	1	Group1	1	Group1	1	11	2024-11-11	3	130	Day 3	Day 3	130
12	1	Group1	1	Group1	1	12	2024-11-11	3	130	Day 3	Day 3	130
13	1	Group1	1	Group1	1	13	2024-11-11	3	130	Day 3	Day 3	130
14	1	Group1	1	Group1	1	14	2024-11-12	4	140	Day 4	Day 4	140

adv dataset

Created from VS domain information and ADSL

adv

#	ADT	ADY	VISITNUM	VISIT	AVISIT	AVISIT
1	2024-10-10	-30	10	SCREENING	SCREENING	10
2	2024-10-10	-30	10	SCREENING	SCREENING	10
3	2024-10-10	-30	10	SCREENING	SCREENING	10
4	2024-10-10	-30	10	SCREENING	SCREENING	10
5	2024-11-09	1	110	Day 1	Day 1	110
6	2024-11-09	1	110	Day 1	Day 1	110
7	2024-11-09	1	110	Day 1	Day 1	110
8	2024-11-10	2	120	Day 2	Day 2	120
9	2024-11-10	2	120	Day 2	Day 2	120
10	2024-11-10	2	120	Day 2	Day 2	120
11	2024-11-11	3	130	Day 3	Day 3	130
12	2024-11-11	3	130	Day 3	Day 3	130
13	2024-11-11	3	130	Day 3	Day 3	130
14	2024-11-12	4	140	Day 4	Day 4	140

adtte dataset

The event times are adjusted for differences in appearance in the Kaplan-Meier curves for each Treatment Group(TRTP). If there are many groups, the same distribution will appear.

adtte

#	TRTPN	TRTA	TRTAN	PARAM	PARAMCD	PARAMN	AVAL	AVALU	STARTDT	ADT	CNSR
1	1	Group1	1	Time to XXXX	TTE101	101	11	DAY	2024-11-09	2024-11-20	0
2	1	Group1	1	Time to XXXX	TTE101	101	56	DAY	2024-04-16	2024-06-11	0
3	1	Group1	1	Time to XXXX	TTE101	101	25	DAY	2024-03-23	2024-04-17	0
4	1	Group1	1	Time to XXXX	TTE101	101	71	DAY	2024-10-16	2024-12-26	1
5	1	Group1	1	Time to XXXX	TTE101	101	43	DAY	2024-08-26	2024-10-08	0
6	1	Group1	1	Time to XXXX	TTE101	101	29	DAY	2025-01-18	2025-02-16	1
7	1	Group1	1	Time to XXXX	TTE101	101	34	DAY	2025-01-14	2025-02-17	1
8	1	Group1	1	Time to XXXX	TTE101	101	43	DAY	2024-05-27	2024-07-09	0
9	1	Group1	1	Time to XXXX	TTE101	101	13	DAY	2024-06-08	2024-06-21	1
10	1	Group1	1	Time to XXXX	TTE101	101	36	DAY	2025-02-18	2025-03-18	0
11	1	Group1	1	Time to XXXX	TTE101	101	64	DAY	2024-04-25	2024-06-28	0
12	1	Group1	1	Time to XXXX	TTE101	101	4	DAY	2024-12-26	2024-12-30	1
13	1	Group1	1	Time to XXXX	TTE101	101	27	DAY	2024-03-24	2024-04-20	0
14	1	Group1	1	Time to XXXX	TTE101	101	67	DAY	2024-06-25	2024-08-31	1

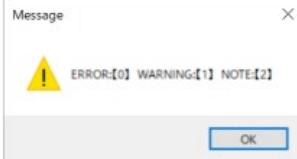
[No. 6] sas_faker

https://github.com/PharmaForest/sas_faker

群の数と、1群における参加者数を指定することでSDTM / ADaMのダミーデータを生成することができる
AEはMedDRAに似た構造の仮想の医療辞書でコーディングされている
SDTM～ADaMまでのデータは最低限、論理的に整合している
プログラムの仮組や、サンプルコードにつける適当なデータが欲しいときなどに利用



```
%interact_logchk;
```



	cate	record	target	line
1	NOTE	NOTE: Variable x is uninitialized.	is uninitialized	5
2	NOTE	NOTE: Division by zero detected during the compilation phase, detected at line 7 column 6.	Division by zero	16
3	WARNING	WARNING: The variable y in the DROP, KEEP, or RENAME list has never been referenced.		20

日本語環境でもそのまま動くのでご安心を。

	cate	record	target	line
1	NOTE	NOTE: 実数xは初期化されていません。	初期化されていません	5
2	NOTE	NOTE: コンパイルフェーズの途中の行 202 カラム 6で、0による除算が発生しました。	0による除算	16
3	WARNING	WARNING: DROP, KEEPまたはRENAMEリスト内の実数		20

Example Usage:

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

aaaa.log
bbbb.log

A	B	C	D
1	FileName	Category	Hit keyword
2	aaaa.log	ERROR	ERROR
3	aaaa.log	ERROR	ERROR
4	aaaa.log	WARNING	WARNING
5	aaaa.log	NOTE	Division by zero
6	aaaa.log	NOTE	Character values have been converted to
7	aaaa.log	ERROR	ERROR
8	bbbb.log	NOTE	Division by zero
9	bbbb.log	NOTE	Character values have been converted to
10	bbbb.log	NOTE	Invalid
11	bbbb.log		_ERROR_=1
12			

Hit record

ERROR 73-322: Expecting an =.
ERROR 200-322: The symbol is not recognized and will be ignored.
WARNING: The data set WORKA may be incomplete. When this step was stopped there were 0.
NOTE: Division by zero detected during the compilation phase, detected at line 8 column 5.
NOTE: Character values have been converted to numeric values at the places given by.
ERROR: Errors printed on page 1.
NOTE: Division by zero detected during the compilation phase, detected at line 2 column 5.
NOTE: Character values have been converted to numeric values at the places given by.
NOTE: Invalid numeric data, 'A', at line 3 column 3.
x=_ERROR_=1_N_=1

No	Issue Appearance Sample Codes	Message(Japanese)	Message(English)	Target keywords
1	data x;x= 1+;run;	欠損値を含んだ計算により、以下の箇所で欠損値が生成されました。	Missing values were generated as a result of performing an operation on missing values.	Missing values
2	data x:length x 8.;run;	変数xは初期化されていません	Variable x is uninitialized.	is uninitialized
3	data x;x= 1/0;run;	コンパイルフェーズの途中の行 8 カラム 5で、0による除算が発生しました。	Division by zero detected during the compilation phase, detected at line 11 column 5.	Division by zero
4	data x;set sashelp.class;x=age/0;run;	行 12 カラム 6で、0による除算が発生しました。	Division by zero detected at line 15 column 6	Division by zero

[No. 7] SASLogChecker

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

対面実行時のログウインドウにでている、 ERROR,WARNINGおよび、注目すべき（作成者独断）のNOTEを表示する マクロと

指定したフォルダに作成された複数のログファイルに対して一括で検索をかけるマクロの2つに分かれている



Usage Example :

```
%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
);
```

202507090811

名前
_Compare_Status_Summary_20250709T0811.xlsx
202507090811Compare.lst
NG_A.pdf
NG_C.pdf
NG_D.pdf
NG_E.pdf
OK_B.pdf

A	B	C
1 name	res	message
2 A	Unmatch	[A value comparison was unequal]
3 B	Perfect Match	
4 C	Unmatch	[Data set labels differ][Variable has different label][Sub data set has observation not in Main]
5 D	Unmatch	[Variable has different label][Sub data set has observation not in Main]
6 E	Unmatch	[Main does not exist][Sub does not exist]

[sas dataset] : MAIN.A vs Sub.A

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.

[No. 8] sas_compare

https://github.com/PharmaForest/sas_compare

メインとサブのライブラリを指定し、指定したデータセットをコンペアする
Compareプロシージャの出力結果ファイルにOKと接頭語がつき
なにか差異があればNGがつく、なにで差がでているかの詳細はExcelのステータスファイルに詳細が出力される。



Example A -- Simply Table;

```
%rtfcreator(DS=sashelp.class
,COLNUM =2
,VARLST =name sex
,JUSTLST =Left Center
,WIDTHLST=300 150
);
```

Name	Sex
Alfred	M
Alice	F
Barbara	F
Carol	F
Henry	M
James	M
Jane	F

Example B -- use your STYLE template. (e.g. Journal)

```
%rtfcreator(DS=sashelp.class
,COLNUM =2
,VARLST =name sex
,JUSTLST =Left Center
,WIDTHLST=300 150
,STYLENAME=Journal
);
```

Name	Sex
Alfred	M
Alice	F
Barbara	F
Carol	F
Henry	M
James	M
Jane	F

Example C -- Add text outside the table, bottom or top;

```
%rtfcreator(DS=sashelp.class
,COLNUM =2
,VARLST =name sex
,JUSTLST =Left Center
,WIDTHLST=300 150
,TBLHEAD=%str(Table Head)
,TBLFOOT=%str(Table Foot)
);
```

Table Head	
Name	Sex
Alfred	M
Alice	F
Barbara	F
Carol	F
Henry	M
James	M
Jane	F

Table Foot	
Name	Sex
Alfred	M
Alice	F
Barbara	F
Carol	F
Henry	M
James	M

Example D -- Page break (you need to create XXX = 1.);

```
data RTFDS1;
  set sashelp.class;
  if _n_ eq 7 then PAGEBRK=1;
run;
%rtfcreator(DS=RTFDS1
,COLNUM =2
,VARLST =name sex
,JUSTLST =Left Center
,WIDTHLST=300 150
,PAGEVAR=PAGEBRK
);
```

Table Head	
Name	Sex
Alfred	M
Alice	F
Barbara	F
Carol	F
Henry	M
James	M
Jane	F

Table Foot	
Name	Sex
Jane	F
Janet	F
Jeffrey	M
John	M
Joyce	F

Example E -- adding a bottom border (advance, e.g., XXX = 1.);

```
data RTFDS2;
  set sashelp.class;
  if _n_ eq 7 then BLINE=1;
run;
%rtfcreator(DS=RTFDS2
,COLNUM =2
,VARLST =name sex
,JUSTLST =Left Center
,WIDTHLST=300 150
,LINEVAR=BLINE
);
```

Table Head	
Name	Sex
Alfred	M
Alice	F
Barbara	F
Carol	F
Henry	M
James	M
Jane	F

Table Foot	
Name	Sex
Jane	F
Janet	F
Jeffrey	M
John	M
Joyce	F

[No. 9] rtfCreator

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

かなり少ない指定で、さまざまなRTF解析帳票を作れるパッケージ。
改行や罫線も設定可能で、ちょっとした一覧表表示から、多少のカスタマイズまで対応できる。



Usage example:

```
data wk1;
  set sashelp.class;
  %$shutter_chance(CheckID=A, n=1:3, varlist=Name Weight Height BMI);
  BMI = Weight / HEIGHT**2 * 703;
  %$shutter_chance(CheckID=B, n=1:3, varlist=Name Weight Height BMI);
run;
```

CheckID	_N_	Name	Weight	Height	BMI
A	1	Alfred	112.5	69	.

CheckID	_N_	Name	Weight	Height	BMI
B	1	Alfred	112.5	69	16.61153

CheckID	_N_	Name	Weight	Height	BMI
A	2	Alice	84	56.5	.

CheckID	_N_	Name	Weight	Height	BMI
B	2	Alice	84	56.5	18.49855

CheckID	_N_	Name	Weight	Height	BMI
A	3	Barbara	98	65.3	.

CheckID	_N_	Name	Weight	Height	BMI
B	3	Barbara	98	65.3	16.15679

The SAS System

Global Scope		Local Scope	
CheckID:A		CheckID:A	
Macro variable	Value	Macro	Macro variable
MVAR1	A		
SYSLOADEDPACKAGES	shutter_chance (0.2.0)		
MVAR2	B		

The SAS System

Global Scope		Local Scope	
CheckID:B		CheckID:B	
Macro variable	Value	Macro	Macro variable
MVAR1	D		
SYSLOADEDPACKAGES	shutter_chance (0.2.0)		
MVAR2	E		

The SAS System

Global Scope		Local Scope	
CheckID:B		CheckID:B	
Macro variable	Value	Macro	Macro variable
MVAR1	D		
SYSLOADEDPACKAGES	shutter_chance (0.2.0)		
MVAR2	E		

Results Viewer - sashml.htm

Global Scope		Local Scope		Automatic Global	
CheckID:ZZZ		CheckID:ZZZ		CheckID:ZZZ	
Macro variable	Value	Macro	Macro variable	Macro variable	Value
MVAR1	D			SYSINFO	0
SYSLOADEDPACKAGES	shutter_chance (0.2.0)			SYSSIZEOFLONG	4
MVAR2	E			SYSERRORTEXT	180-322: Statement is not valid or it is used out of proper order.
TEST	I	TEST	MVAR4	AFDSNAME	
				SYMSG	
				SYSENV	FORE
				SYSDESCAPECHAR	03
				SYSDMG	0
				SYSTEMENV	
				SYSCCHARWIDTH	1
				SYSSIZEOFUNICODE	2
				SYSDSN	WORK A
				SYSTIMEZONEOFFSET	32400
				SYSWARNINGTEXT	The data set WORK A may be incomplete. When this step was stopped there were 0 observations and 0 variables.

Usage example:

```
data wk1;
  set sashelp.class;
  %$shutter_chance(CheckID=A, n=1:3, varlist=Name Weight Height BMI);
  BMI = Weight / HEIGHT**2 * 703;
  %$shutter_chance(CheckID=B, n=1:3, varlist=Name Weight Height BMI);
run;
```

```
data wk2;
```

```
  set sashelp.class;
  %$shutter_chance(CheckID=C, if_condition=%nrbquote(SEX='F' and AGE=15), varlist=Name Sex Age);
run;
```

[No. 10] shutter_chance

データステップ中に差し込んで、PDVの中を可視化する%shutter_chanceと

差し込んだ位置でのマクロ変数のスコープと値を確認できる%macro_variable_shutter_chanceで構成される

プログラムのデバッグに利用できる

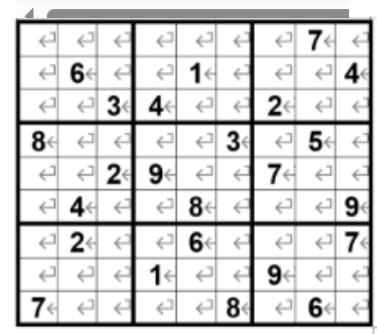


4. %sudoku_solver()

Sudoku solver is finally in SAS!

Parameters :

```
puzzle= : the Sudoku puzzle converted into a
outputpath= : the directory where the results are
rtfYU= : Default is N. If you change this pa
```



The number of Backtrack: 33968

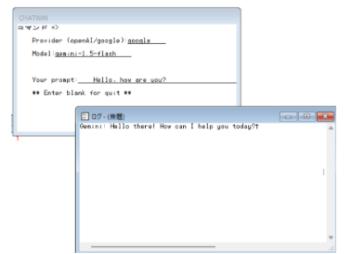


1. %chatDMS() :

Chat application in SAS DMS(Display Manager System) for those who cannot afford Viya Copilot 😊
This is available only for DMS. You need your API key for openAI or google to use the app.

Sample code:

```
%chatDMS(
  provider=google,           /* AI provider(openAI / Google / Anthropic available) */
  model=gemini-1.5-flash,    /* Model information */
  apikey=xxxxxxxxxxxxxx,     /* API key */
  max_tokens=512)            /* Max token */
```



5. %hanabi()

To celebrate someone or something with fireworks(hanabi).

The macro uses %color_swatch() in misc package, please install misc to use this.

Sample code:

```
%hanabi(
  giffile=C:\temp\hanabi.gif,  /*path for gif file*/
  ite=10)                      /*iteration(1-151)*/
```



2. text2morse() : Function

text2morse is a function that converts text to Morse code.



Sample code:

```
data test;
length x $200.;
x = "I M WITH YOU";output; /*Captain America: The First Avenger*/
x = "STAY";output; /*Interstellar*/
x = "SO HOPING";output; /*Parasite*/
run;
```

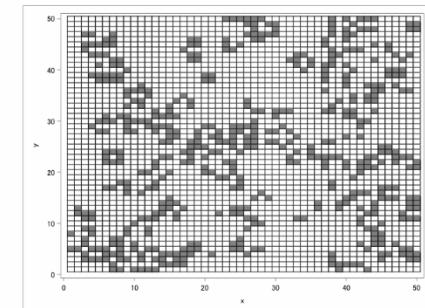
```
data a;
set test;
y = text2morse(x);
run;
```

	x	y
1	I M WITH YOU	.
2	STAY	-
3	SO HOPING	-----

3. %life_game() :



If you're tired of work, watch Life Game and reevaluate your life.



[No. 11] devil (Developer's Ideas Library)

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

試作段階のアイデアや試作品、インスピレーション、自慢話、POC提示による開発メンバー募集、あるいは冗談（楽しみのため）など、あらゆる段階の「悪魔」を共有してください。悪魔パッケージの説明ファイル(description.sas)には作者が「Any Developers」と記されています。このパッケージはPharmaForestの他パッケージとは一線を画し、有用性に関わらずあらゆるアイデアを歓迎する極めて協働的な性質を持っています（むしろ遊び心のあるものを歓迎します 😎）。さあ一息ついで、悪魔の扉を叩いてみましょう！



%xattr_set_var

Purpose: Assign an extended attribute to a variable.

Parameters:

lib - Library name where the dataset resides (default = WORK)
ds - Dataset name
var - Variable name to which the extended attribute will be assigned
xname - Name of the extended attribute
xvalue - Value of the extended attribute

Usage Example:

```
%xattr_set_var(ds=a, var=x, xname=xa1, xvalue="xxxx");
%xattr_set_var(ds=a, var=x, xname=xa2, xvalue=1111);
%xattr_set_var(ds=a, var=y, xname=ya1, xvalue="yyyy");
```

%xattr_set_ds

Purpose: Assign an extended attribute to a dataset.

Parameters:

lib - Library name where the dataset resides (default = WORK)
ds - Dataset name
xname - Name of the extended attribute
xvalue - Value of the extended attribute

Usage Example:

```
%xattr_set_ds(ds=a, xname=xds_a1, xvalue="ds attr 1");
```

%list_xattr

Purpose: List of attributes printed and/or logged; results stored in xatrs dataset.

Parameters:

lib	- (Optional) Library name to filter the results
ds	- (Optional) Dataset name to filter the results
cat	- (Optional) Category (VARIABLE or DATASET) to filter
xattr_name	- (Optional) Specific extended attribute name to filter
display_ods	- (Y/N) Whether to print the result table using PROC PRINT (default = Y)
put_log	- (Y/N) Whether to output results to log via PUT statement (default = Y)

Usage Example:

```
%list_xattr()
```

libname	ds	xattr_category	var	xattr	xtype	xvalue
WORK	A	DATASET		xd_a1	char	ds attr 1
WORK	A	VARIABLE	x	xa1	char	xxxx
WORK	A	VARIABLE	x	xa2	num	1111
WORK	A	VARIABLE	y	ya1	char	yyyy

VIEWTABLE: Work.Xatrs						
libname	ds	xattr_category	var	xattr	xtype	xvalue
1	WORK	A	DATASET	xd_a1	char	ds attr 1
2	WORK	A	VARIABLE	xa1	char	xxxx
3	WORK	A	VARIABLE	xa2	num	1111
4	WORK	A	VARIABLE	ya1	char	yyyy

%xattr2macrovar

Purpose: Convert extended attribute values into global macro variables.

Parameters:

lib - Library name (default = WORK)
ds - Dataset name
xattr_name - Specific attribute name to extract (optional)
macro_name_type - Naming convention for macro variables. Options:
"libname.ds.var.xattr", "ds.var.xattr", "var.xattr", "xattr"
Default = "ds.var.xattr"

Output: Creates macro variables in the global symbol table with corresponding values.
Usage Example:

```
%xattr2macrovar(lib=WORK)
```

```
NOTE: Global Macro variable[xds_a1] set with [ds attr 1]
NOTE: Global Macro variable[xa1] set with [xxxx]
NOTE: Global Macro variable[xa2] set with [1111]
NOTE: Global Macro variable[ya1] set with [yyyy]
```

[No. 12] xattr_kit

https://github.com/PharmaForest/xattr_kit

SASの拡張属性をマネジメントするためのパッケージ。拡張属性を設定したり、確認したりマクロ変数に変換したりを行う。

sas_dataste_jsonパッケージでは拡張属性が重要な役割を持つため、それを補助するために設計された



Usage:

```

data test;
do i = 1 to 10;
ID = char("ABCDEFGHIJ",i);
VAR1 =i ;
VAR2 =cats(ID,VAR1);
output;
end;
drop i;
run;

data test_output;
set test end=eof;
rc1 = cloak_num(ID,Var1);
rc2 = cloak_char(ID,Var2);

if _N_ in (5,6) then do;
out1 = cloak_num("B",.);
out2 = cloak_char("C","");
end;

if eof then do;
out1 = cloak_num("A",.);
out2 = cloak_char("A","");
end;

drop rc;;
run;

```

Usage:

```

data test;
do i = 1 to 10;
ID = char("ABCDEFGHIJ",i);
VAR1 =i ;
VAR2 =cats(ID,VAR1);
output;
end;
drop i;
run;

data test_output;
set test end=eof;
rc1 = cloak_num(ID,Var1);
rc2 = cloak_char(ID,Var2);

if _N_ in (5,6) then do;
out1 = cloak_num("B",.);
out2 = cloak_char("C","");
end;

if eof then do;
out1 = cloak_num("A",.);
out2 = cloak_char("A","");
end;

drop rc;;
run;

```

	ID	VAR1	VAR2	out1	out2
1	A	1	A1	.	
2	B	2	B2	.	
3	C	3	C3	.	
4	D	4	D4	.	
5	E	5	E5	2	C3
6	F	6	F6	.	
7	G	7	G7	.	
8	H	8	H8	.	
9	I	9	I9	.	
10	J	10	J10	1	A1

The value checked in with the A tag in the first line is checked out in the last line.

The value checked in with the B tag in the second line is checked out in the fifth line, so it is clear that it no longer exists in the sixth line.

	ID	VAR1	VAR2	out1	out2
1	A	1	A1	.	
2	B	2	B2	.	
3	C	3	C3	.	
4	D	4	D4	.	
5	E	5	E5	2	C3
6	F	6	F6	.	
7	G	7	G7	.	
8	H	8	H8	.	
9	I	9	I9	.	
10	J	10	J10	1	A1

The value checked in with the A tag in the first line is checked out in the last line.

The value checked in with the C tag in the third line is checked out in the fifth line, so it is clear that it no longer exists in the sixth line.

[No. 13] cloak

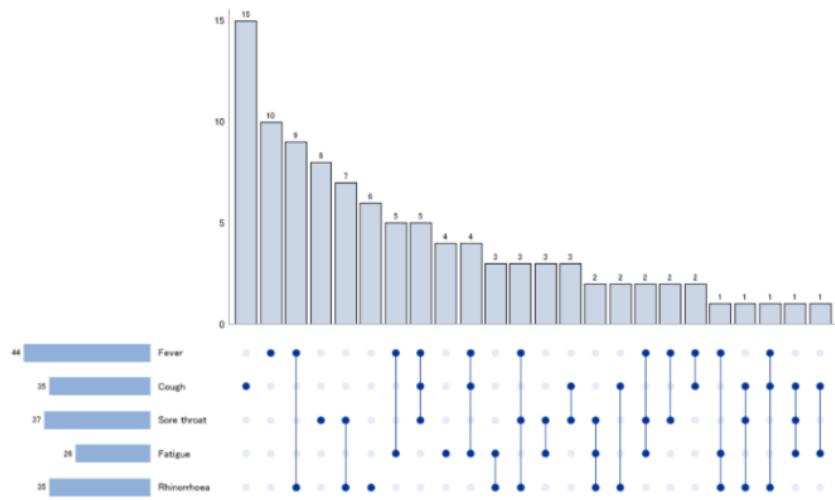
<https://github.com/PharmaForest/cloak>

FCMPプロシージャのdictionary空間を利用し、データステップ中に、keyをつけて、値の受け渡しを行う
チェックインとチェックアウトの機能を持つ



```
%event_gant_excel  
    outpath=F:\Project\output,  
    outfile=ae_gant.xlsx,  
    target_dataest=work.ae,  
    target_id=SUBJID,  
    target_event_name=AETERM,  
    target_st=AESTDY,  
    target_en=AEENDY  
);
```

```
%upset_plot(data=testdata_upset, personID=ID ,itemnum=itemnum, itemname=itemname);
```



[No. 14] vis_review_kit

https://github.com/PharmaForest/vis_review_kit

イベントの持続期間をガントチャートとしてExcel表示したり、
参加者ごとのイベント同時発現をupsetプロットでビジュアライゼーションすることができるパッケージ



odstable_layoutshowcase



Sample 1—Listing 1^{a3}
Proc ODSTABLE^{a3}

AAAA ^{a3}	BBBB ^{a3}	CCCC ^{a3}	DDDD ^{a3}	EEEE ^{a3}	FFFF ^{a3}	GGGG / ↓ HHHH ^{a3}	IIIIJJJJ ^{a3}
AAAA ^{a3}	BBBB ^{a3}	CCCC ^{a3}	DDDD ^{a3}	EEEE ^{a3}	FFFF ^{a3}	GGGG↓ HHHH ^{a3}	IIII ^{a3}
AAAA ^{a3}	BBBB ^{a3}	CCCC ^{a3}	DDDD ^{a3}	EEEE ^{a3}	FFFF ^{a3}	GGGG ^{a3}	III ^{a3}
AAAA ^{a3}	BBBB ^{a3}	CCCC ^{a3}	DDDD ^{a3}	EEEE ^{a3}	FFFF ^{a3}	GGGG ^{a3}	JJJJ ^{a3}
AAAA ^{a3}	BBBB ^{a3}	CCCC ^{a3}	DDDD ^{a3}	EEEE ^{a3}	FFFF ^{a3}	GGGG ^{a3}	III ^{a3}
AAAA ^{a3}	BBBB ^{a3}	CCCC ^{a3}	DDDD ^{a3}	EEEE ^{a3}	FFFF ^{a3}	GGGG ^{a3}	JJJJ ^{a3}
Footer1 XXXXXXXX ^{a3}							
Footer2 XXXXXXXX ^{a3}							

Sample 2—Table 1^{a3}
Proc ODSTABLE^{a3}

Treatment ^{a3}		Placeholder ^{a3}
Group 1 ^{a3}	Group 2 ^{a3}	N = xx ^{a3} n (%) ^{a3}
AAAA ^{a3}	BBBB ^{a3}	CCCC ^{a3}
AAAA ^{a3}	BBBB ^{a3}	CCCC ^{a3}
AAAA ^{a3}	BBBB ^{a3}	CCCC ^{a3}
AAAA ^{a3}	BBBB ^{a3}	CCCC ^{a3}

Sample 4—Table 3^{a3}
Proc ODSTABLE^{a3}

Treatment ^{a3}		Placeholder ^{a3}
Group 1 ^{a3}	Group 2 ^{a3}	N = xx ^{a3} n (%) ^{a3}
AAAA ^{a3}	BBBB ^{a3}	CCCC ^{a3}
AAAA ^{a3}	BBBB ^{a3}	CCCC ^{a3}
AAAA ^{a3}	BBBB ^{a3}	CCCC ^{a3}
AAAA ^{a3}	BBBB ^{a3}	CCCC ^{a3}

Footer1 XXXXXXXX^{a3}
Footer2 XXXXXXXX^{a3}

XXXX ^{a3}	YYYY ^{a3}
AAAA ^{a3}	BBBB ^{a3}
AAAA ^{a3}	BBBB ^{a3}

Footer1 XXXXXXXXXXXXXXXXXXXXXXXXX^{a3}
Footer2 XXXXXXXXXXXXXXXXXXXXXXXXX^{a3}

XXXX ^{a3}	YYYY ^{a3}
AAAA ^{a3}	BBBB ^{a3}
AAAA ^{a3}	BBBB ^{a3}

Footer1 XXXXXXXXXXXXXXXXXXXXXXXXX^{a3}
Footer2 XXXXXXXXXXXXXXXXXXXXXXXXX^{a3}

Sample 1—Listing 1 ^{a3} Proc ODSTABLE ^{a3}

```

title1 "Sample 1—Listing 1";
title2 "Proc ODSTABLE";
proc odstable data=dummy;
column out1 - out6 (out7-out8) out9 out10;
define header header1; start=out1; end=out1; vjust=top; split="#" just=left:text "AAAA"; end;
define header header2; start=out2; end=out2; vjust=top; split="#" just=left:text "BBBB#(bbbb)" ;end;
define header header3; start=out3; end=out3; vjust=top; split="#" just=left:text "CCCC"; end;
define header header4; start=out4; end=out4; vjust=top; split="#" just=left:text "DDDD"; end;
define header header5; start=out5; end=out5; vjust=top; split="#" just=left:text "EEEE#(eeee)" ; end;
define header header6; start=out6; end=out6; vjust=top; split="#" just=left;text "FFFF"; end;
define header header7; start=out7; end=out7; vjust=top; split="#" just=left;text "GGGG /#HHHH"; end;
define header header9_10; start=out9; end=out10; vjust=top; split="#" just=center; style=[borderbottomstyle=solid borderbottomwidth=1];text "III";
define header header9; start=out9; end=out9; vjust=top; split="#" just=center;text "IIII"; end;
define header header10; start=out10; end=out10; vjust=top; split="#" just=center;text "JJJJ"; end;
define out1; print_headers=off; just=left; style=[cellwidth=120]; end;
define out2; print_headers=off; just=left; style=[cellwidth=120]; end;
define out3; print_headers=off; just=left; style=[cellwidth=120]; end;
define out4; print_headers=off; just=left; style=[cellwidth=120]; end;
define out5; print_headers=off; just=left; style=[cellwidth=120]; end;
define out6; print_headers=off; just=left; style=[cellwidth=120]; end;
define out7; print_headers=off; just=left; style=[cellwidth=120]; end;
define out9; print_headers=off; just=center; style=[cellwidth=120]; end;
define out10; print_headers=off; just=center; style=[cellwidth=120]; 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;

```

[No. 15] odstable_layoutshowcase

https://github.com/PharmaForest/odstable_layoutshowcase

Proc Odstableの帳票サンプルとその、生成コードをサンプルギャラリーとして表示するマクロ。
Proc ReportからOdstableに帳票作成プロジェクトを切り替える際の参考用のパッケージ



Example 1. Print all maxims.

```
%sas_maxims()
```

Results Viewer - SAS Output
The SAS System

Maxims of Maximally Efficient SAS Programmers

Kurt Bremser, 2019

Maxim 1: Read the Documentation.

SAS provides extremely well done documentation for its products. Learning to read the documentation will enhance your problem-solving skills by orders of magnitude.

Maxim 2: Read the Log.

Everything you need to know about your program is in the log. Interpreting messages and NOTES is essential in finding errors.

Maxim 3: Know Your Data.

Having a clear picture of data structures - variable types, lengths, formats - and content will provide you with a fast-path to solving problems. Many simple problems can be cleared by taking a look at the 'Columns' section in dataset properties. Use proc contents frequently.

[No. 16] maxims4sas

<https://github.com/PharmaForest/maxims4sas>

SASプログラマにとって大切な52のmaxims(格言), SASコミュニティが生み出した至宝を未来につなぐため, 表示するためのパッケージ.

<https://communities.sas.com/t5/SAS-Communities-Library/Maxims-of-Maximally-Efficient-SAS-Programmers/ta-p/352068>

```
%sas_maxims(1:6, 42, 52)
```

Results Viewer - SAS Output
The SAS System

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Kurt Bremser, 2019

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Having a clear picture of data structures - variable types, lengths, formats - and content will provide you with a fast-path to solving problems. Many simple problems can be cleared by taking a look at the 'Columns' section in dataset properties. Use proc contents frequently.

Maxim 4: If in Doubt, Do a Test Run and Look at the Results. If Puzzled, Inquire Further.

SAS is in its core an interpreting language. Running one step is just a few mouse-clicks away. Use that to your advantage."Try it." (Grace Hopper, Admiral, US Navy)

Maxim 5: Ask, and You Will Be Answered.

SAS Technical Support and the SAS user community stand at the ready to help you. Provide a clear question, example data, your code (with or within the log, see Maxim 2), and where you seem to be stuck.

Maxim 6: Google Is Your Friend.

Just entering the text of an error message or problematic issue, preceded with "SAS", will often yield resources with at least a hint to solving your issue on the first result page; the same is true for Google.

Maxim 42: It's Not the Answer, It's the Question.

A well-formulated question may already lead you in the right direction before you speak it out loud or write it down. An ill-formulated question will get you the equivalent of "42".

Maxim 52: Take a Break.

Whenever you run into a seemingly unsolvable problem, turn away from it for a while. Play a game (or watch one), listen to music, have a conversation with your S.O., make up a good meal, or just have a night's sleep. Clearing your mind from all the (non-helping) thoughts you already had will open it up for the single new one you need to get over the obstacle. It may even be the case that a



```
data a;
set sashelp.class(keep=name);
%laglead(dataset=sashelp.class, var=name, offset=-1);
%laglead(dataset=sashelp.class, var=name, offset=+2);
run;
```

	Name	name_prev_1	name_next_2
1	Alfred	Barbara	
2	Alice	Alfred	Carol
3	Barbara	Alice	Henry
4	Carol	Barbara	James
5	Henry	Carol	Jane
6	James	Henry	Janet
7	Jane	James	Jeffrey
8	Janet	Jane	John
9	Jeffrey	Janet	Joyce
10	John	Jeffrey	Judy
11	Joyce	John	Louise
12	Judy	Joyce	Mary
13	Louise	Judy	Philip
14	Mary	Louise	Robert
15	Philip	Mary	Ronald
16	Robert	Philip	Thomas
17	Ronald	Robert	William
18	Thomas	Ronald	
19	William	Thomas	

```
data c;
set b;
%laglead(
dataset=b
,var=AVAL
,offset= -1
,id=SUBJID
);

%laglead(
dataset=b
,var=AVAL
,offset= +1
,id=SUBJID
);
run;
```

	SUBJID	VISITNUM	AVAL	AVAL_prev_1	AVAL_next_1
1	A	1	10	.	20
2	A	1	20	10	30
3	A	1	30	20	40
4	A	1	40	30	.
5	B	1	11	.	21
6	B	1	21	11	31
7	B	1	31	21	.

[No. 17] laglead

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

Nオブザベーション先の値や、前の値をいくらでも取得することができるパッケージ。

同症例内に限るといった縛りの中で前後を参照することも可能



```
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;
```

%ctcae5_alb()	%ctcae5_fev1()	%ctcae5_na()
%ctcae5_alp()	%ctcae5_fibrinog()	%ctcae5_neut()
%ctcae5_alt()	%ctcae5_ggt()	%ctcae5_plat()
%ctcae5_aptt()	%ctcae5_gluc()	%ctcae5_qtcf()
%ctcae5_ast()	%ctcae5_haptog()	%ctcae5_tni()
%ctcae5_bili()	%ctcae5_hco3()	%ctcae5_trig()
%ctcae5_ca()	%ctcae5_hgb()	%ctcae5_tropnt()
%ctcae5_cd4()	%ctcae5_k()	%ctcae5_wbc()
%ctcae5_chol()	%ctcae5_ldh()	
%ctcae5_ck()	%ctcae5_lvef()	
%ctcae5_creat()	%ctcae5_lym()	
%ctcae5_dlco()	%ctcae5_mg()	

VIEWTABLE: Work.Lab_checked												
	PARAMCD	AVALU	AVAL	ANRLO	ANRHI	BASE	ATOXGRH	ATOXGRL	ATOXGR	ATOXGRHN	ATOXGRLN	ATOXGRN
1	HGB	g/dL	14.5	12	13.5	.	Grade 1	Grade 0	Grade 1	1	0	1
2	HGB	g/dL	15.4	12	14	.	Grade 1	Grade 0	Grade 1	1	0	1
3	HGB	g/dL	17	12	12.5	.	Grade 3	Grade 0	Grade 3	3	0	3
4	HGB	g/dL	7.5	12	13.5	.	Grade 0	Grade 3	Grade 3	0	3	3
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

[No. 18] ctcae5_grader https://github.com/PharmaForest/ctcae5_grader

CTCAE v5.0 の基準に基づいて、数値のみでGradingを返すパッケージ



%matrix_mult() macro

VIEWTABLE: Work.Wk1			
	a	b	c
1	1	2	4
2	5	8	9

VIEWTABLE: Work.Wk2		
	d	e
1	3	6
2	2	1
3	0	10

VIEWTABLE: Work.Prod_matrix		
	outm1	outm2
1	7	48
2	31	128

%matrix_inverse() macro

VIEWTABLE: Work.Wk1			
	a	b	c
1	3	5	0
2	9	1	2
3	8	7	9

VIEWTABLE: Work.Inv_wk1			
	col1	col2	col3
1	0.0147058824	0.1323529412	-0.029411765
2	0.1911764706	-0.079411765	0.0176470588
3	-0.161764706	-0.055882353	0.1235294118

%matrix_identity()

Obs	col1	col2	col3
1	1	0	0
2	0	1	0
3	0	0	1

%matrix_determinant()

VIEWTABLE: Work.Wk1		
	a	b
1	2	1
2	3	4

Obs	col1
1	5

[No. 19] love_matrix

https://github.com/PharmaForest/love_matrix

IMLライセンスを使用せずにSAS Baseの機能で簡単な行列計算を可能にするパッケージ。
内部でFCMPの行列操作ルーチンを利用している
データセットを行列にみたてて、 基本的な操作を提供する



[No. 20] SASPACerShiny

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

R Shinyを利用して、SASパッケージを作成するという前衛的なパッケージ。RメインのユーザーでもSASの世界にJoinしやすいように。

Sample R code (to create SAS package folder/file structure):

```
remotes::install_github("Nakaya-Ryo/SASPACershiny")
SASPACerShiny::run_app()
```



Sample SAS code (to complete SAS package generation):

```
%generatePackage(
  filesLocation=\path\to\your\source\package\folder ,
  markdownDoc=1, easyArch=1)
```





%sniffer_compare() macro

Purpose: Compare the current dataset with one of its generations. The police dog "sniffs" both versions to detect differences.



```

data wk1;
  set test;
  if X > 6 then cat="A"; else cat="B";
run;
%sniffer_compare(target=wk1, scent_age=-1)

The COMPARE Procedure
Comparison of WORK.WK1 with WORK.WK1#001
(Method=EXACT)

Value Comparison Results for Variables

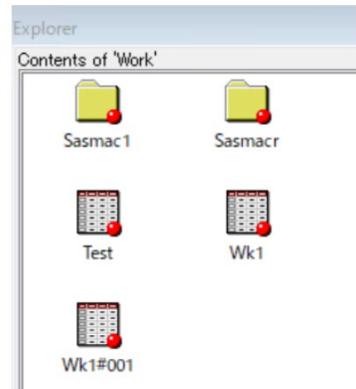
Obs || Base Value      Compare Value
    || cat              cat
    || -                -
6   || B                A

WARNING: [Police Dog] Bark! Bark! Differences detected in wk1
  
```

NOTE: [Police Dog] Woof! Patrol started. I am sniffing the target = wk1

```

data wk1;
  set test;
  if X > 6 then cat = "A";
  else cat="B";
run;
  
```



[No. 21] change_tracer_dog

SASの世代データセット機能を利用したパッケージ。指定したデータセットの匂いを犬に覚えさせることで、そのデータセットが同名で上書き更新された場合も、前の状態をn世代前まで自動保存できるようになる。1つ前の状態とどこが変わったかを調べることができる

コードを変更した時に、それによってデータセットの値がどう変わるかを精査しながら開発する際のパートナーとなるパッケージ。



```
%yaml_start()
sashelp.class: &nw.;
%dataset_export(ds=sashelp.class
    ,wh=%nrquote(AGE in (13:15))
    ,cat=mapping
    ,varlist=NAME AGE SEX
    ,indent=1)
%yaml_end();
```

```
sashelp.class:
Name: Alfred
Age: 14
Sex: M
Name: Alice
Age: 13
Sex: F
Name: Barbara
Age: 13
Sex: F
Name: Carol
Age: 14
Sex: F
Name: Henry
Age: 14
Sex: M
Name: Janet
```

```
%yaml_start(outpath=C:/tmp, file=sample);
#This YAML is a sample &nw.;
person: &nw.;
  name: Yutaka Morioka &nw.;
  age: 41 &nw.;
  height: 170 &nw.;
  weight: 63 &nw.;
%yaml_end();
```

```
#This YAML is a sample
person:
  name: Yutaka Morioka
  age: 41
  height: 170
  weight: 63
```

```
data class_inline;
  set sashelp.class;
  %inline_nest(key=HW_inline, varlist=HEIGHT WEIGHT, cat=mapping);
  %inline_nest(key=NAMEAGE_inline, varlist=NAME AGE, cat=sequence);
run;
%yaml_start()
class_inline: &nw.;
%dataset_export(ds=class_inline
    ,wh=%nrquote(AGE in (13:15))
    ,cat=mappingsequence
    ,varlist=name HW_inline NAMEAGE_inline
    ,indent=1)
%yaml_end();
```

```
class_inline:
  - Name: Alfred
    HW_inline: {Height: 69, Weight: 112.5}
    NAMEAGE_inline: [Alfred, 14]
  - Name: Alice
    HW_inline: {Height: 69, Weight: 112.5}
```

```
data class_1;
  set sashelp.class;
  %nest(key=HW, varlist=HEIGHT WEIGHT, cat=mapping, indent=3);
  %nest(key=AHHW, varlist=AGE HW, cat=mapping, indent=2);
run;
%yaml_start()
class_1: &nw.;
%dataset_export(ds=class_1
    ,wh=%nrquote(AGE in (13:15))
    ,cat=mappingsequence
    ,varlist=name HW AHHW
    ,indent=1)
%yaml_end();
```

```
class_1:
  - Name: Alfred
    HW:
      Height: 69
      Weight: 112.5
    AHHW:
      Age: 14
      HW:
        Height: 69
        Weight: 112.5
  - Name: Alice
    HW:
```

[No. 22] yaml_writer

https://github.com/PharmaForest/yaml_writer

SASからYAMLファイルを作成するパッケージ。
データセットの中身をYAML内に、指定の構造
にエクスポート可能



adamski package

The adamski package is currently under development to support ADaM creation. Let's build the spaceship [adamski] together! 🚀

Inspired by the admiral package in R, adamski aims to bring similar functionality — along with original functions and macros — to the SAS environment.

We are looking for collaborators and contributors to join us on this exciting journey. If you're passionate about ADaM programming or want to help shape tools for the clinical data community, we'd love to have you onboard! 🚀

[No.23] adamski

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

R言語での、Pharmaverseのadmiralパッケージにインスパイアされたパッケージプロジェクト
コラボレーション開発を前提にしている
Admiralで提供されているADaM作成のための機能をSASで実装することを目指している
ぜひ参加を！！



%index_single_key()

`%index_single_key` is a macro that creates an index for datasets in a library all at once. The index key should be a single variable, such as `patientid`, that exists in all target datasets.

Parameters

- `inlib` : Library reference containing the original datasets.
- `outlib` : Library reference where output datasets with index data to be stored
- `indexkey` : index key variable for all datasets.e.g: `patientid`
- `in_ds(optional)` : datasets to be extracted. e.g: AE CM DM
- `ex_ds(optional)` : datasets to be excluded. e.g: XX XY XS
- `ds_select_cond(optional)` : Condition to extract datasets. Note that condition to extract the datasets from output of proc contents. e.g: `index(memname,"D_")`

%small_world()

`%small_world` is a macro to extract data with subjects in `subject_level_ds` using WHERE expression. Optionally, the number of subjects can be specify to extract smaller number of subjects from large size datasets.

Parameters

- `inlib` : libname where original datasets are located. dataset with index is preferable
- `outlib` : libname output datasets extracted with specific subjects to be stored
- `subject_level_ds` : subject level dataset e.g: `work.DM, inds.ADSL`
- `subject_id_var` : variable with subject / patient id. e.g: `usubjid patientid`
- `no_sub` : Number of subjects you would like to extract. If this parameter is blank, all subjects in `subject_level_ds` is extracted
- `ds_select_cond(optional)` : Condition to extract datasets. Note that condition to extract the datasets from output of proc contents. e.g: `index(memname,"D_")`

%split_world()

`%split_world` is a macro which allow user to split the large dataset in to small pieces. so that user can process one by one.

Parameters

- `inlib` : libname where target dataset are located.
- `indata` : target dataset e.g: `act`
- `outlib(default to work)` : libname split datasets (e.g: `act001,act002...`) to be stored
- `nperBlock` : the number of records split dataset will have in one dataset
- `blockstart(default to 1)` : the start of block. It starts from the first block if not specified.
- `blockend` : the end of block, if not specified, it ends with the last block if not specified.

Sample code

create single index for variable patid on all datasets in rwd library and store them in rwdx

```
%index_single_key(inlib=rwd, outlib=rwdx, indexkey=patid);
```

```
%small_world(inlib=rwd, outlib=out,
             subject_level_ds=PATIENT,
             subject_id_var=patid);
```

```
%split_world(inlib=rwd, indata=disease, nperBlock=100000);
```

[No.24] RWD Express

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

RWDのようなビッグデータを扱うのに役立つSASパッケージ
SASインデックスを活用し、効率よくデータ抽出等を行うことができる



```
%SummaryStat(ind=ADSL_dummy, sortNum=2, outds=sum02, grpNum=3, trtGrp=TRT01PN, label=%str(Age), trgtVa
```

	NUM1	NUM2	out1	out2	out3	out4	out5
1		2	1 Age	n	17	17	16
2		2	3 Age	Mean (SD)	41.5 (13.2)	43.2 (13.1)	41.0 (13.0)
3		2	4 Age	Median	42.0	43.0	41.0
4		2	6 Age	[Min, Max]	[21, 63]	[22, 64]	[20, 62]

```
%FreqStat(ind=ADSL_dummy, sortNum=1, outds=sum01, grpNum=3, trtGrp=TRT01PN, label=%nrstr(Sex),  
%FreqStat(ind=ADSL_dummy, sortNum=3, outds=sum03, grpNum=3, trtGrp=TRT01PN, label=%nrstr(Age Category),  
%FreqStat(ind=ADSL_dummy, sortNum=4, outds=sum04, grpNum=3, trtGrp=TRT01PN, label=%nrstr(Stage),  
%FreqStat(ind=ADSL_dummy, sortNum=5, outds=sum05, grpNum=3, trtGrp=TRT01PN, label=%nrstr(Study Status),
```

	num1	num2	out1	out2	out3	out4	out5
1	1	1	1 Sex	Male	8 (47.1)	9 (52.9)	8 (50.0)
2	1	2	2 Sex	Female	9 (52.9)	8 (47.1)	8 (50.0)
3	1	3	3 Sex	Unknown	0	0	0

	num1	num2	out1	out2	out3	out4	out5
1	3	1	Age Category	<40	8 (47.1)	7 (41.2)	7 (43.8)
2	3	2	Age Category	>=40	9 (52.9)	8 (48.8)	9 (56.3)

	num1	num2	out1	out2	out3	out4	out5
1	4	1	Stage	Stage I	3 (17.6)	4 (23.5)	3 (18.8)
2	4	2	Stage	Stage IIa	4 (23.5)	3 (17.6)	3 (18.8)
3	4	3	Stage	Stage IIb	3 (17.6)	4 (23.5)	3 (18.8)
4	4	4	Stage	Stage III	3 (17.6)	3 (17.6)	4 (25.0)
5	4	5	Stage	Stage IV	4 (23.5)	3 (17.6)	3 (18.8)

	num1	num2	out1	out2	out3	out4	out5
1	5	1	Study Status	Study Ongoing	9 (52.9)	10 (58.8)	10 (62.5)
2	5	2	Study Status	Study Discontinued	8 (47.1)	7 (41.2)	6 (37.5)

[No. 25] freqsum

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

Demographicの帳票等で実施されがちな
頻度集計と、要約統計量の出力を簡易な指
定で行えるパッケージ。

ご清聴ありがとうございました！