
SAS MELBOURNE USER GROUP

17 SEPTEMBER 2014



A journey into the world of SAS :: Statistics and the Pharmaceutical industry

VOTE FOR TODAY'S BEST PRESENTATION...

**DON'T FORGET TO CHECK YOUR EMAIL – TO COMPLETE
THE SMUG ONLINE SURVEY**

By completing the online survey you could win...



***2 x adult passes to
Hoyts La Premiere***

NOVOTECH

The Asia Pacific CRO

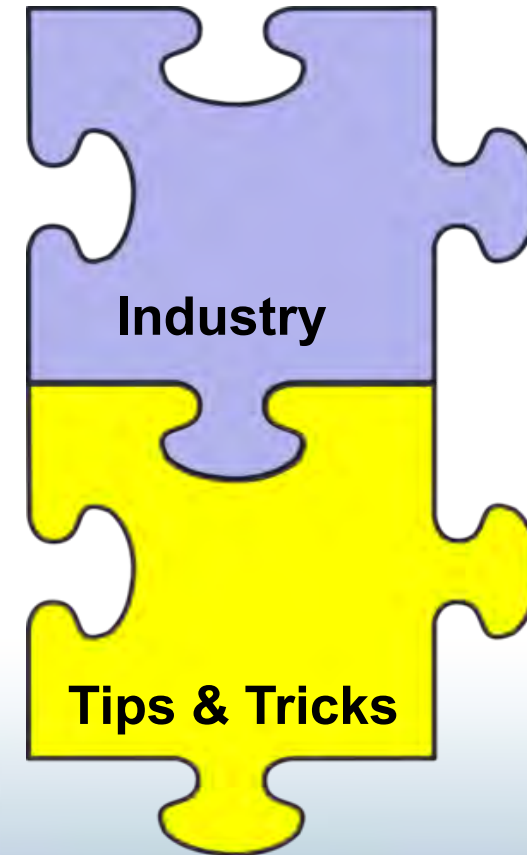
Entry into the world of SAS

Statistics in the Pharmaceutical Industry

SMUG Q3 2014

Dr Elisa Young

- **Statistics in the Pharmaceutical Industry**
 - Getting there...
 - The learning curve
 - Clinical trials
 - Statistical activities in clinical trials
- **Case Studies**
(Customising programs to meet client needs)
 - Case study 1: PROC REPORT
 - Case study 2: PROC SGPLOT
- **Lessons Learnt**
- **Help!**
- **Where to now?**



Statistics in the Pharmaceutical Industry

Getting there

How my journey began

BSc (Pharmacology); PhD (Pharmacology)



Clinical Biostatistician

MSc (Statistics)

Biostatistician/Statistical Programmer

We are looking for a Biostatistician to join our Biometrics Department. In this role you will design, develop and evaluate statistical analysis services and develop systems to determine the outcome of clinical trials. Some of the tasks you will be involved in include:-

- Design, analysis, review and interpretation of clinical trial data, Phase I-Phase IV
- Perform sample size estimations
- Ensure compliance with applicable regulatory requirements
- Participate in review and/or preparation of submissions of study protocols and study reports, presenting findings to internal/external stakeholders as required
- Review case report forms and data management plans to ensure efficient and accurate data collection
- Prepare and write statistical analysis plans
- Validate and execute statistical programs using SAS to generate tables, listings and figures
- Interact with project managers, data managers and statisticians during the data analysis phase, acting as client liaison for statistical matters
- Prepare randomisation specifications, generate schedules and verify randomisation components



Statistics in the Pharmaceutical Industry

Clinical Trials

‘any research study that prospectively assigns human participants or groups of humans to one or more health-related interventions to evaluate the effects on health outcomes’.

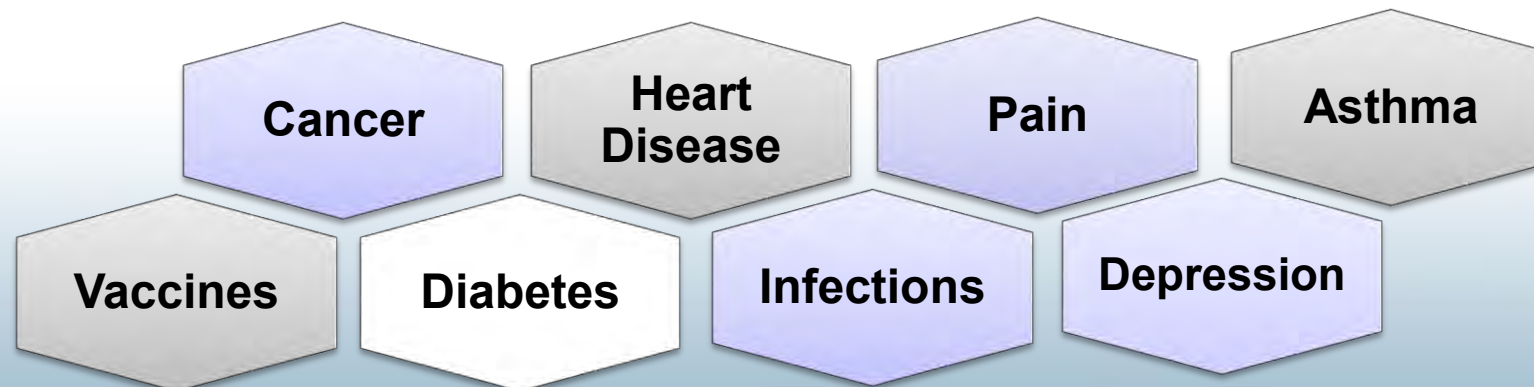
World Health Organisation (WHO)

- Examples:
 - New interventions: Does it work, is it safe, is it better than existing.
 - Compare existing interventions
 - New ways to use or combine existing interventions

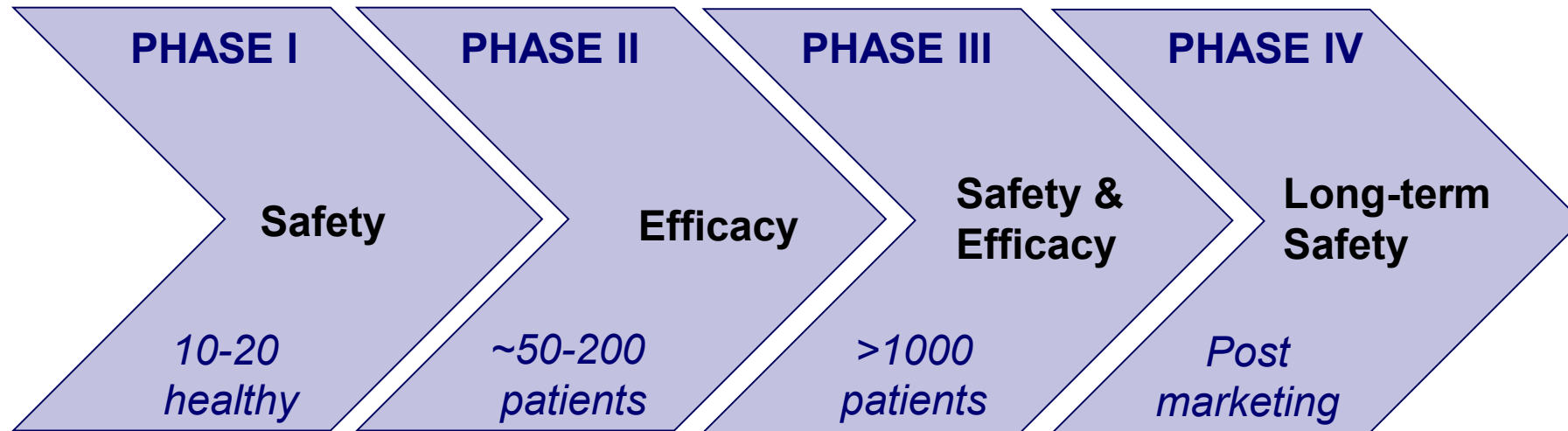
Why Conduct Clinical Trials?

Most modern medical interventions are a direct result of clinical research.

- Only way to properly determine whether new medicines are effective and safe.
- Ensures that any improvement as a result of the intervention occurs for many people and is not just a random effect for a one person.
- They help people to live longer and healthier lives, and help reduce pain and disability.
- Improve health care services by raising standards of treatment.



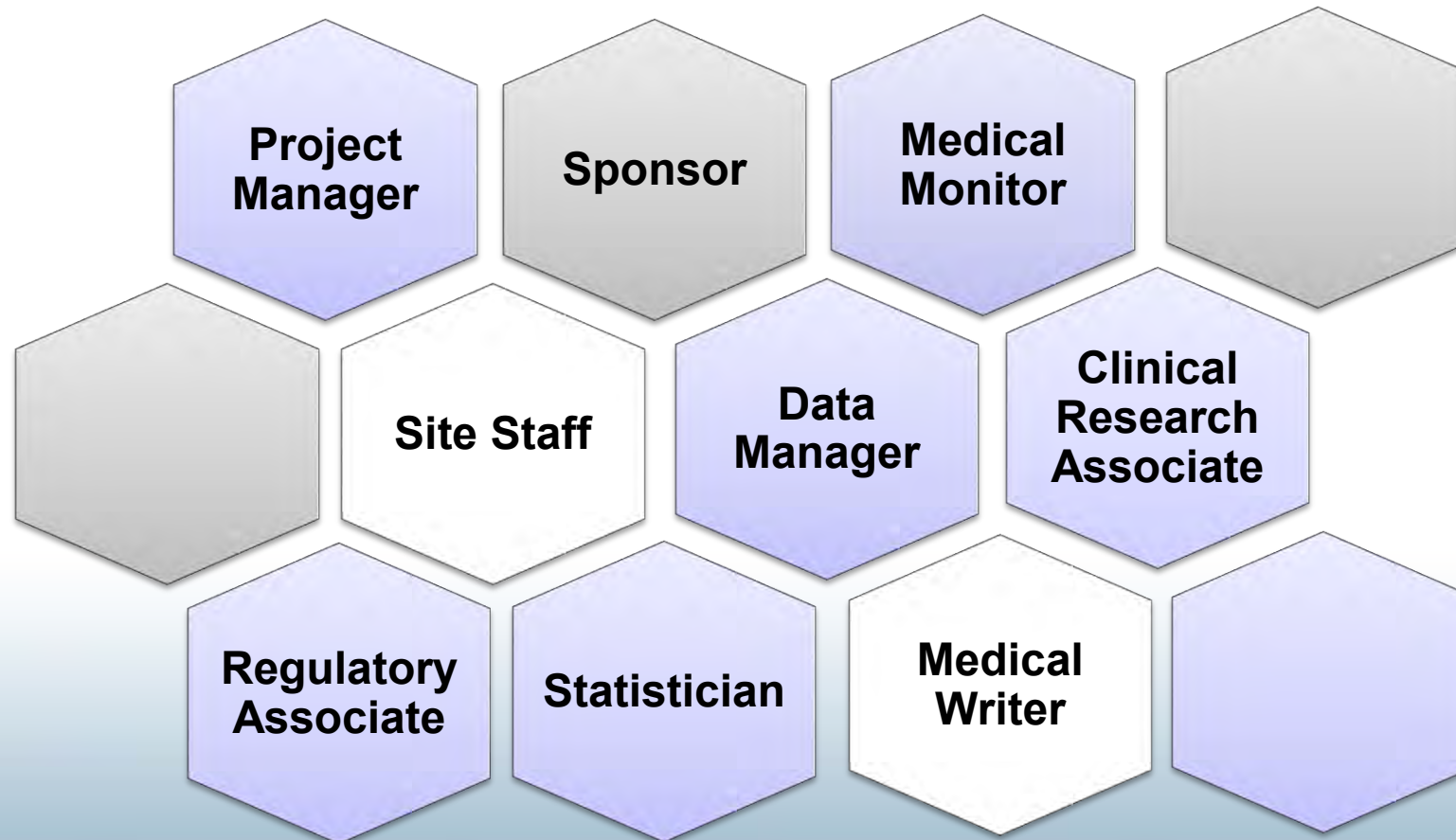
Clinical Trials - Phases



Service-based companies specialising in the high-quality conduct of clinical studies primarily on behalf of pharmaceutical, biotechnology and medical device companies.

- Independent (minimises bias)
- Quicker
- Cheaper
- Flexible
- Highly experienced







Clinical Trials – Study Team



Statistics in the Pharmaceutical Industry

The Role of the Statistician/SAS Programmer in Clinical Trials

Standard

- Study Design
- Sample Size Estimate 
- Randomization Schedule 
- Statistical Analysis Plan
- Mock Tables, Listings and Figures (Shells)
- Bring together datasets from various sources 
- Derived datasets 
- Programming of Tables, Listings and Figures 
- Quality Control 

Emerging

- *Risk Based Monitoring* 
- *Data Cleaning* 

➤ Federal Laws

- FDA: Title 21 of Code of Federal Regulations (CFR)
 - Part 11: Handling of electronic records
 - Part 50: Protection of Human Subjects
 - Part 820: Use of validated software

➤ Federal Guidelines

- ICH E9: Statistical Principles for Clinical Trials
- FDA Industry Guideline for E9: Statistical Principles for Clinical Trials

➤ Industry Statistical Standards

- CDISC

- SAS is globally recognized* as the de facto industry standard for clinical trial data analysis and reporting
- Validated, stable, FDA compliant, reproducible, scalable
- Powerful and flexible analytical and data management capabilities

* By Pharmaceutical Companies, Regulatory Bodies and Contract Research Organisations

Single desktop license:
SAS Base v9.4
SAS/STAT
SAS/GRAPH
Enterprise Guide

Case Studies

(Customising programs to meet client needs)

Tables, Listings and Figures

What do I mean by Tables, Listings & Figures?



Output that contains all the study data, to be submitted to regulatory bodies:

Listings: Raw data (per patient, per visit, etc.)

Tables: Summary data, i.e. descriptive statistics
Inferential statistics (ANCOVA, t-tests, etc.)

Figures: Graphical representations of critical parameters

Typical Listings and Figures:

Subject Disposition

Adverse Events

Demographics

Concomitant Medications

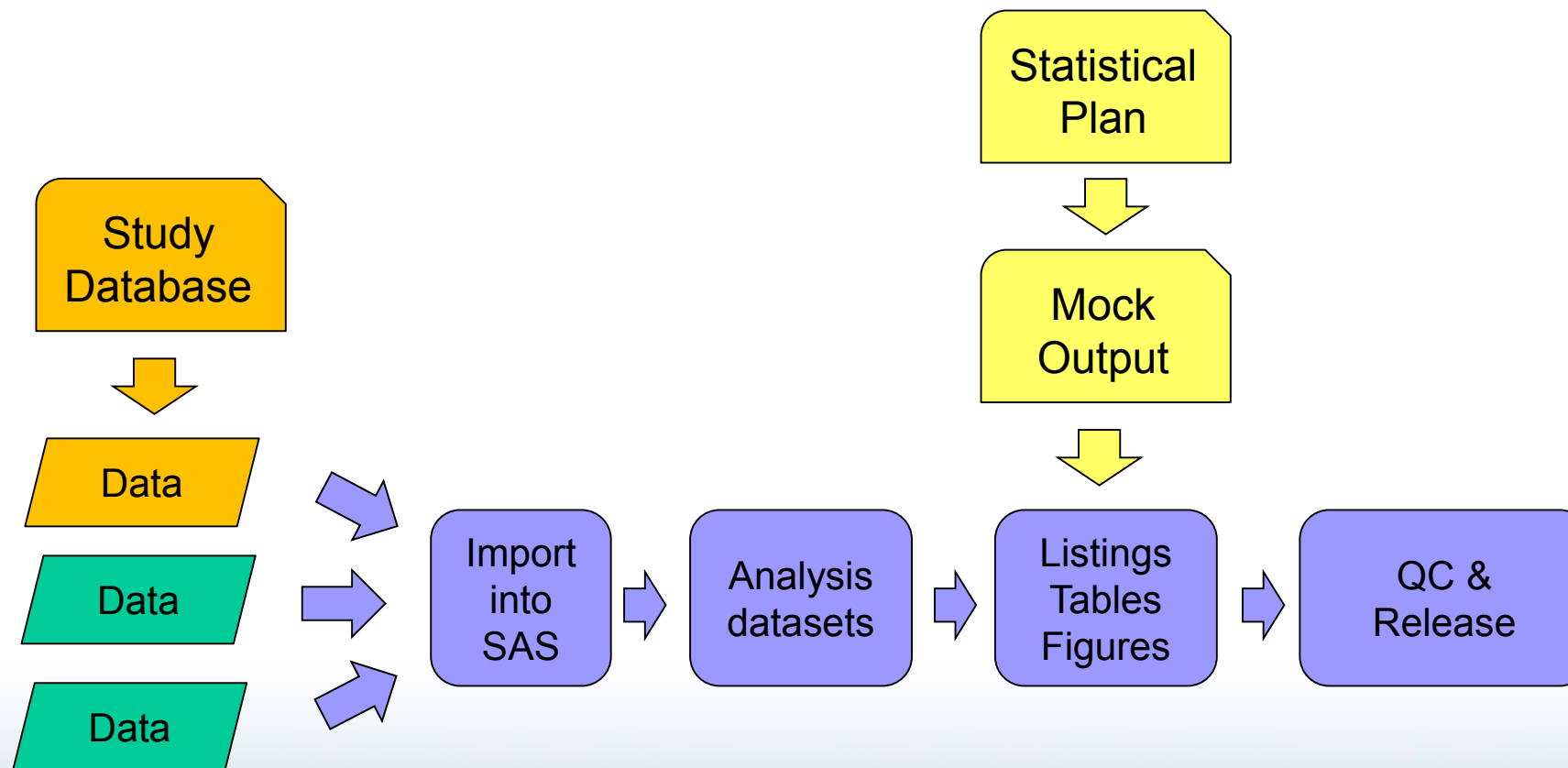
Medical History

Safety: Laboratory, ECG, vital signs

Efficacy (treatment & disease specific)

Questionnaires

Programming of Tables, Listings & Figures



Case Studies

(Customising programs to meet client needs)

PROC REPORT

The mock.....

Table 3a: Demographics and Baseline Information
 Protocol: ABC-111
 Population: Intent-to-Treat Population

	Cohort 1 (5mg/kg) (N=X)	Cohort 2 (2.5mg/kg) (N=X)	Cohort 3 (5mg/kg) (N=X)	Cohort 4 (5mg/kg) (N=X)	Cohort 5 (7.5mg/kg) (N=X)	Cohort 6 (10mg/kg) (N=X)	XXX (XXmg/kg) (N=X)	Total (N=X)
Age (years)								
n	X	X	X	X	X	X	X	X
Mean	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X
Median	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X
SD	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X
Min	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X
Max	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X
Gender n(%)								
Male	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)
Female	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)
Race n(%)								
White	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)
Asian	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)
Aboriginal	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)
Black or African American	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)
Native Hawaiian / Pacific Islander	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)
American Indian / Alaskan native	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)
Other	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)
Ethnicity n(%)								
Hispanic or Latino	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)
Not Hispanic or Not Latino	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)	X (XX.X%)
Height (cm)								
n	X	X	X	X	X	X	X	X
Mean	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X
Median	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X
SD	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X
Min	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X
Max	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X

SD: standard deviation
 Data cut-off date: DDMMYYYY

Program: filepath_name, Output: filepath_name

Date Created: DDMMYYYY Hr:Mn

Page x of y

- Data
- Style
- Page X of Y
- Row grouping
- Date/Time
- Column Headers

The data.....

VIEWTABLE: Abc.Table_final

	cohort	pod	pam	order	stat	result	_sortpage_	dummy
1	1	1	age	1	^^n	8	1	1
2	2	1	age	1	^^n	8	1	1
3	3	1	age	1	^^n	8	1	1
4	4	1	age	1	^^n	6	1	1
5	5	1	age	1	^^n	8	1	1
6	6	1	age	1	^^n	9	1	1
7	99	1	age	1	^^n	47	1	1
8	1	1	age	2	^^Mean	65.1	1	1
9	2	1	age	2	^^Mean	62.0	1	1
10	3	1	age	2	^^Mean	67.5	1	1
11	4	1	age	2	^^Mean	65.2	1	1
12	5	1	age	2	^^Mean	57.4	1	1
13	6	1	age	2	^^Mean	64.4	1	1
14	99	1	age	2	^^Mean	63.6	1	1
15	1	1	age	3	^^Median	63.5	1	1
16	2	1	age	3	^^Median	63.5	1	1
17	3	1	age	3	^^Median	69.0	1	1
18	4	1	age	3	^^Median	70.5	1	1
19	5	1	age	3	^^Median	59.0	1	1
20	6	1	age	3	^^Median	65.0	1	1
21	99	1	age	3	^^Median	65.0	1	1
22	1	1	age	4	^^SD	7.9	1	1
23	2	1	age	4	^^SD	9.0	1	1
24	3	1	age	4	^^SD	10.9	1	1
25	4	1	age	4	^^SD	11.7	1	1
26	5	1	age	4	^^SD	12.8	1	1

The Default - Program

```
ods listing close;  
ods rtf file = "&out\Table 3 - Demographics (1).rtf";  
  
options reset=footnote reset=title;  
options nonumber nodate orientation=landscape papersize="ISO A4";
```

```
proc report data = abc.table final nocenter;  
column (_sortpage_ pod parm order stat cohort,result dummy);
```

```
define _sortpage_ / group order=data noprint;  
define pod / group order=data noprint;  
define parm / group order=data " ";  
define order / group noprint;  
define stat / group " " style(column header)=[cellwidth=4.5cm just=l];  
define cohort / across " " style(column header)=[cellwidth=2.5cm just=c];  
define result / display " " style(column header)=[cellwidth=2.5cm just=c];  
define dummy /analysis noprint;
```

```
break after _sortpage_ / page;  
  
compute after _sortpage_ / style=[JUST=L];  
line "SD: Standard Deviation";  
endcomp;
```

```
Title1 j=1 "Table 3: Demographics";  
Title2 j=1 "Protocol: ABC";  
Title3 j=1 "Study Population: Intent-to-Treat (ITT) Population";
```

```
footnote1 "Data cut-off date: &cutdaterpt.";  
footnote2 "Program: Table 3 - Demographics.sas (version &version); Output: Table 3 - Demographics (1).rtf";
```

```
run;
```

```
ods rtf close;  
ods listing;
```

The Default - Output

Table 3: Demographics
 Protocol: ABC
 Study Population: Intent-to-Treat (ITT) Population

		1	2	3	4	5	6	99
age	n	8	8	8	6	8	9	47
	Mean	65.1	62.0	67.5	65.2	57.4	64.4	63.6
	Median	63.5	63.5	69.0	70.5	59.0	65.0	65.0
	SD	7.9	9.0	10.9	11.7	12.8	5.9	9.8
	Min	54	48	47	49	40	54	40
	Max	82	74	80	77	75	71	82
sex	Male	4 (50.0%)	6 (75.0%)	3 (37.5%)	3 (50.0%)	3 (37.5%)	2 (22.2%)	21 (44.7%)
	Female	4 (50.0%)	2 (25.0%)	5 (62.5%)	3 (50.0%)	5 (62.5%)	7 (77.8%)	26 (55.3%)
race	White	6 (75.0%)	7 (87.5%)	8 (100.0%)	6 (100.0%)	8 (100.0%)	8 (88.9%)	43 (91.5%)
	Asian	2 (25.0%)	0	0	0	0	1 (11.1%)	3 (6.4%)
	Aboriginal	0	0	0	0	0	0	0
	Black or African American	0	0	0	0	0	0	0
	Native Hawaiian / Pacific Islander	0	0	0	0	0	0	0
	American Indian / Alaskan native	0	0	0	0	0	0	0
	Other	0	1 (12.5%)	0	0	0	0	1 (2.1%)
ethnicity	Hispanic or Latino	0	0	0	0	0	0	0
	Not Hispanic or Not Latino	0	0	0	0	0	0	0
	Missing	8 (100.0%)	8 (100.0%)	8 (100.0%)	6 (100.0%)	8 (100.0%)	9 (100.0%)	47 (100.0%)

SD: Standard Deviation

- Data
- Style
- Page X of Y
- Row grouping
- Date/Time
- Column Headers

Data cut-off date: 11JUL2014
 Program: Table 3 - Demographics.sas (version 1.4); Output: Table 3 - Demographics (1).rtf

Table and Page Style – Program (1)

```
❏ proc template;
    define style Styles.Custom;
    parent = Styles.RTF;
    STYLE SystemTitle /
        FONT_FACE = "Arial, Times New Roman, Helvetica"
        FONT_SIZE = 1.8;
    STYLE SystemFooter /
        FONT_FACE = "Arial, Times New Roman, Helvetica"
        FONT_SIZE = 1.8;
    STYLE Header /
        FONT_FACE = "Arial, Times New Roman, Helvetica"
        FONT_SIZE = 1.8;
    STYLE Data /
        FONT_FACE = "Arial, Times New Roman, Helvetica"
        FONT_SIZE = 1.8;
    STYLE Table /
        FONT_FACE = "Arial, Times New Roman, Helvetica"
        FONT_SIZE = 1.8
        FONT_WEIGHT = medium
        FRAME = ABOVE
        RULES = GROUPS;
    replace Body from Document "Controls the Body file." /
        bottommargin = _undef_
        topmargin = _undef_
        rightmargin = _undef_
        leftmargin = undef ;
    CLASS text /
        'continued' = " ";
end;
run;
```

Table and Page Style – Program (2)



```
ods listing close;  
ods rtf style=custom file = "&out\Table 3 - Demographics (2).rtf";  
  
goptions reset=footnote reset=title;  
options nonumber nodate orientation=landscape papersize="ISO A4"  
topmargin="0.5 in" bottommargin="0.5 in"  
rightmargin="0.5 in" leftmargin="0.5 in";
```

Table and Page Style - Output



Table 3: Demographics
Protocol: ABC
Study Population: Intent-to-Treat (ITT) Population

	1	2	3	4	5	6	99
age							
n	8	8	8	6	8	9	47
Mean	65.1	62.0	67.5	65.2	57.4	64.4	63.6
Median	63.5	63.5	69.0	70.5	59.0	65.0	65.0
SD	7.9	9.0	10.9	11.7	12.8	5.9	9.8
Min	54	48	47	49	40	54	40
Max	82	74	80	77	75	71	82
sex							
Male	4 (50.0%)	6 (75.0%)	3 (37.5%)	3 (50.0%)	3 (37.5%)	2 (22.2%)	21 (44.7%)
Female	4 (50.0%)	2 (25.0%)	5 (62.5%)	3 (50.0%)	5 (62.5%)	7 (77.8%)	26 (55.3%)
race							
White	6 (75.0%)	7 (87.5%)	8 (100.0%)	6 (100.0%)	8 (100.0%)	8 (88.9%)	43 (91.5%)
Asian	2 (25.0%)	0	0	0	0	1 (11.1%)	3 (6.4%)
Aboriginal	0	0	0	0	0	0	0
Black or African American	0	0	0	0	0	0	0
Native Hawaiian / Pacific Islander	0	0	0	0	0	0	0
American Indian / Alaskan native	0	0	0	0	0	0	0
Other	0	1 (12.5%)	0	0	0	0	1 (2.1%)
ethnicity							
Hispanic or Latino	0	0	0	0	0	0	0
Not Hispanic or Not Latino	0	0	0	0	0	0	0
Missing	8 (100.0%)	8 (100.0%)	8 (100.0%)	6 (100.0%)	8 (100.0%)	9 (100.0%)	47 (100.0%)

SD: Standard Deviation

- Data
- Style
- Page X of Y
- Row grouping
- Date/Time
- Column Headers

```
ods listing close;
ods tagsets.rtf_sample style=custom file = "&out\Table 3 - Demographics (3).rtf";
ods escapechar = '^';
options reset=footnote reset=title;
options nonumber nodate orientation=landscape papersize="ISO A4"
        topmargin="0.5 in" bottommargin="0.5 in"
        rightmargin="0.5 in" leftmargin="0.5 in";

proc report data = abc.table_final nocenter;
  column (_sortpage_ pod parm order stat cohort,result dummy);

  define _sortpage_ / group order=data noprint;
  define pod / group order=data noprint;
  define parm / group order=data " ";
  define order / group noprint;
  define stat / group " " style(column header)=[cellwidth=4.5cm just=1];
  define cohort / across " " style(column header)=[cellwidth=2.5cm just=c];
  define result / display " " style(column header)=[cellwidth=2.5cm just=c];
  define dummy / analysis noprint;

  break after _sortpage_ / page;

  compute after _sortpage_ / style=[bordertopcolor=black bordertopwidth=2 just=1];
    line "SD: Standard Deviation";
  endcomp;

  Title1 j=1 "Table 3: Demographics";
  Title2 j=1 "Protocol: ABC";
  Title3 j=1 "Study Population: Intent-to-Treat (ITT) Population";

  footnote1 "Data cut-off date: &cutdaterpt." j=r "Page ^{pageof}";
  footnote2 "Program: Table 3 - Demographics.sas (version &version); Output: Table 3 - Demographics (3).rtf";
run;

ods tagsets.rtf_sample close;
ods listing;
```

Page X of Y - Output

Table 3: Demographics
Protocol: ABC
Study Population: Intent-to-Treat (ITT) Population

		1	2	
age	n	8	8	
	Mean	65.1	62.0	
	Median	63.5	63.5	
	SD	7.9	9.0	
	Min	54	48	
sex	Max	82	74	
	Male	4 (50.0%)	6 (75.0%)	
	Female	4 (50.0%)	2 (25.0%)	
race	White	6 (75.0%)	7 (87.5%)	
	Asian	2 (25.0%)	0	
	Aboriginal	0	0	
	Black or African American	0	0	
	Native Hawaiian / Pacific Islander	0	0	
	American Indian / Alaskan native	0	0	
	Other	0	1 (12.5%)	
	ethnicity	Hispanic or Latino	0	0
		Not Hispanic or Not Latino	0	0
		Missing	8 (100.0%)	8 (100.0%)

SD: Standard Deviation



```
Age (years)
n
Mean
Median
SD
Min
Max

Gender n(%)
Male
Female

Race n(%)
White
Asian
Aboriginal
Black or African American
Native Hawaiian / Pacific Islander
American Indian / Alaskan native
Other

Ethnicity n(%)
Hispanic or Latino
Not Hispanic or Not Latino

Height (cm)
n
Mean
Median
SD
Min
Max

SD: standard deviation
```

- Data
- Style
- Page X of Y
- Row Grouping
- Date/Time
- Column Headers

Row Grouping - Program

```
proc format;
  value podlabel
    1='Age (years)'
    2='Gender n(%)'
    3='Race n(%)'
    4='Ethnicity n(%)';
run;
```

VIEWTABLE: Abc.Table_final

	cohort	pod	parm	order	stat	result	_sortpage_	dummy
1	1	1	age	1	^^n	8	1	1
2	2	1	age	1	^^n	8	1	1
3	3	1	age	1	^^n	8	1	1
4	4	1	age	1	^^n	6	1	1
5	5	1	age	1	^^n	8	1	1
6	6	1	age	1	^^n	9	1	1
7	7	1	age	1	^^n	17	1	1

```
ods listing close;
ods tagsets.rtf_sample style=custom file = "&out\Table 3 - Demographics (4).rtf";
ods escapechar = '^';
goptions reset=footnote reset=title;
options nonumber nodate orientation=landscape papersize="ISO A4"
  topmargin="0.5 in" bottommargin="0.5 in"
  rightmargin="0.5 in" leftmargin="0.5 in";

proc report data = abc.table_final nocenter;
  column (_sortpage_ pod order stat cohort,result dummy);

  define _sortpage_ / group order=data noprint;
  define pod / group order=data noprint;
  define order / group noprint;
  define stat / group " " style(column header)=[cellwidth=6.0cm just=l];
  define cohort / across " " style(column header)=[cellwidth=2.5cm just=c];
  define result / display " " style(column header)=[cellwidth=2.5cm just=c];
  define dummy / analysis noprint;

  break after _sortpage_ / page;

  compute after _sortpage_ / style=[bordertopcolor=black bordertopwidth=2 just=l];
    line "SD: Standard Deviation";
  endcomp;

  compute before pod / style=[just=l];
    line " ";
    line @0 pod podlabel.;
  endcomp;

  title1 j=1 "Table 3: Demographics";
  title2 j=1 "Protocol: ABC";
  title3 j=1 "Study Population: Intent-to-Treat (ITT) Population";

  footnote1 "Data cut-off date: &cutdatertpt." j=r "Page ^(pageof)";
  footnote2 "Program: Table 3 - Demographics.sas (version &version); Output: Table 3 - Demographics (4).rtf";
run;

ods tagsets.rtf_sample close;
ods listing;
```


Row Grouping - Output

Table 3: Demographics
Protocol: ABC
Study Population: Intent-to-Treat(ITT) Population

	1	2	3	4	5	6	99
Age (years)							
n	8	8	8	6	8	9	47
Mean	65.1	62.0	67.5	65.2	57.4	64.4	63.6
Median	63.5	63.5	69.0	70.5	59.0	65.0	65.0
SD	7.9	9.0	10.9	11.7	12.8	5.9	9.8
Min	54	48	47	49	40	54	40
Max	82	74	80	77	75	71	82
Gender n(%)							
Male	4 (50.0%)	6 (75.0%)	3 (37.5%)	3 (50.0%)	3 (37.5%)	2 (22.2%)	21 (44.7%)
Female	4 (50.0%)	2 (25.0%)	5 (62.5%)	3 (50.0%)	5 (62.5%)	7 (77.8%)	26 (55.3%)
Race n(%)							
White	6 (75.0%)	7 (87.5%)	8 (100.0%)	6 (100.0%)	8 (100.0%)	8 (88.9%)	43 (91.5%)
Asian	2 (25.0%)	0	0	0	0	1 (11.1%)	3 (6.4%)
Aboriginal	0	0	0	0	0	0	0
Black or African American	0	0	0	0	0	0	0
Native Hawaiian / Pacific Islander	0	0	0	0	0	0	0
American Indian / Alaskan native	0	0	0	0	0	0	0
Other	0	1 (12.5%)	0	0	0	0	1 (2.1%)
Ethnicity n(%)							
Hispanic or Latino	0	0	0	0	0	0	0
Not Hispanic or Not Latino	0	0	0	0	0	0	0
Missing	8 (100.0%)	8 (100.0%)	8 (100.0%)	6 (100.0%)	8 (100.0%)	9 (100.0%)	47 (100.0%)

- Data
- Style
- Page X of Y
- Row grouping
- Date/Time
- Column Headers

Date and time - Program

```
data _null_;  
  call symput('exedate', put(today(),date9.));  
  call symput('exetime', put(time(),time5.));  
run;
```

```
ods listing close;  
ods tagsets.rtf_sample style=custom file = "&out\Table 3 - Demographics (5).rtf";  
ods escapechar = '^';  
options reset=footnote reset=title;  
options nonumber nodate orientation=landscape papersize="ISO A4"  
  topmargin="0.5 in" bottommargin="0.5 in"  
  rightmargin="0.5 in" leftmargin="0.5 in";
```

```
proc report data = abc.table_final nocenter;  
  column (_sortpage_ pod order stat cohort,result dummy);  
  
  define _sortpage_ / group order=data noprint;  
  define pod / group order=data noprint;  
  define order / group noprint;  
  define stat / group " " style(column header)=[cellwidth=6.0cm just=l];  
  define cohort / across " " style(column header)=[cellwidth=2.5cm just=c];  
  define result / display " " style(column header)=[cellwidth=2.5cm just=c];  
  define dummy / analysis noprint;  
  
  break after _sortpage_ / page;  
  
  compute after _sortpage_ / style=[bordertopcolor=black bordertopwidth=2 just=l];  
    line "SD: Standard Deviation";  
  endcomp;  
  
  compute before pod / style=[just=l];  
    line " ";  
    line @0 pod podlabel.;  
  endcomp;  
  
  Title1 j=1 "Table 3: Demographics";  
  Title2 j=1 "Protocol: ABC";  
  Title3 j=1 "Study Population: Intent-to-Treat (ITT) Population";  
  
  footnote1 "Data cut-off date: &cutdaterpt." j=r "Page ^{pageof}";  
  footnote2 "Program: Table 3 - Demographics.sas (version &version); Output: Table 3 - Demographics (5).rtf; Created on &exedate at &exetime.";  
run;  
  
ods tagsets.rtf_sample close;  
ods listing;
```

Date and time - Output

Table 3: Demographics
 Protocol: ABC
 Study Population: Intent-to-Treat (ITT) Population

1	2	3	4	5	6	99
---	---	---	---	---	---	----



Cohort 1 (5mg/kg) (N=X)	Cohort 2 (2.5mg/kg) (N=X)	Cohort 3 (5mg/kg) (N=X)	Cohort 4 (5mg/kg) (N=X)	Cohort 5 (7.5mg/kg) (N=X)	Cohort 6 (10mg/kg) (N=X)	XXX (XXXmg/kg) (N=X)	Total (N=X)
X	X	X	X	X	X	X	X
XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X
XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X
XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X	XX.X

Data
 Style
 Page X of Y
 Row grouping
 Date/Time
 Column Headers

Column Headings – Program (1)



```
data dd_demo;
  set dd_demo;
  if itt=1; /* Select itt population only */
run;
```

```
data dd_demo_all; /* Duplicate to create a TOTAL group */
  set dd_demo(in=a) dd_demo(in=b);
  if b then do;
    cohort=99;
    cohort_label='Total';
  end;
run;
```

dd_demo_all

	cohort	cohort_label	randno	sex	race	age	itt
1		Cohort 1(1.0mg/kg)	002-006-001	Male	White	82	1
2		Cohort 1(1.0mg/kg)	002-006-002	Male	Asian	62	1
3		Cohort 1(1.0mg/kg)	002-007-001	Male	White	63	1
4		Cohort 1(1.0mg/kg)	002-007-002	Female	White	67	1
5		Cohort 1(1.0mg/kg)	002-007-003	Female	White	63	1
6		Cohort 2(2.0mg/kg)	002-008-001	Male	White	66	1
7		Cohort 3(3.0mg/kg)	002-008-002	Male	White	47	1
8		Cohort 3(3.0mg/kg)	002-008-003	Female	White	66	1
9		Cohort 3(3.0mg/kg)	002-008-004	Female	White	79	1
10		Cohort 4(4.0mg/kg)	002-008-005	Male	White	49	1
11		Cohort 5(5.0mg/kg)	002-008-006	Male	White	68	1
12		Cohort 6(6.0mg/kg)	002-008-007	Female	White	63	1
13		Cohort 6(6.0mg/kg)	002-008-008	Female	White	69	1
14		Cohort 3(3.0mg/kg)	002-009-001	Female	White	59	1
15		Cohort 4(4.0mg/kg)	002-009-002	Male	White	69	1
16		Cohort 4(4.0mg/kg)	002-009-003	Female	White	72	1
17		Cohort 6(6.0mg/kg)	002-009-004	Male	White	71	1
18		Cohort 6(6.0mg/kg)	002-009-005	Male	White	68	1
19		Cohort 6(6.0mg/kg)	002-009-006	Female	White	60	1
20		Cohort 6(6.0mg/kg)	002-009-007	Female	Asian	65	1
21		Cohort 1(1.0mg/kg)	002-010-001	Female	White	66	1
22		Cohort 5(5.0mg/kg)	002-010-002	Female	White	66	1
23		Cohort 1(1.0mg/kg)	002-011-001	Female	Asian	64	1

Cohort 1 (5mg/kg) (N=X)	Cohort 2 (2.5mg/kg) (N=X)	Cohort 3 (5mg/kg) (N=X)	Cohort 4 (5mg/kg) (N=X)
-------------------------------	---------------------------------	-------------------------------	-------------------------------

X	X	X	X
XX.X	XX.X	XX.X	XX.X
XX.X	XX.X	XX.X	XX.X
XX.X	XX.X	XX.X	XX.X
XX.X	XX.X	XX.X	XX.X

Column Headings – Program (2)

	cohort	cohort_label	COUNT
1	1	Cohort 1(1.0mg/kg)	8
2	2	Cohort 2(2.0mg/kg)	8
3	3	Cohort 3(3.0mg/kg)	8
4	4	Cohort 4(4.0mg/kg)	6
5	5	Cohort 5(5.0mg/kg)	8
6	6	Cohort 6(6.0mg/kg)	9
7	99	Total	47

trtct

Cohort 1 (5mg/kg) (N=X)	Cohort 2 (2.5mg/kg) (N=X)	Cohort 3 (5mg/kg) (N=X)	Cohort 4 (5mg/kg) (N=X)
-------------------------------	---------------------------------	-------------------------------	-------------------------------

```
proc freq data=dd_demo_all noprint;      /* Generate count of subjects in each cohort */
  tables cohort*cohort_label/out=trtct (drop=percent);
run;
```

```
proc sql;
  create table fmts as
  select 'rndfmt' as fmtname,
         cohort as start,
         trim(cats(cohort_label, '|(N=', put(count, 3.), ')')) as label length=30
  from trtct
  order by cohort, cohort_label;
quit;
```

```
proc format cntlin=fmts;
run;
```

fmts

	fmtname	start	label
1	mdfmt	1	Cohort 1 (1.0mg/kg) (N=8)
2	mdfmt	2	Cohort 2 (2.0mg/kg) (N=8)
3	mdfmt	3	Cohort 3 (3.0mg/kg) (N=8)
4	mdfmt	4	Cohort 4 (4.0mg/kg) (N=6)
5	mdfmt	5	Cohort 5 (5.0mg/kg) (N=8)
6	mdfmt	6	Cohort 6 (6.0mg/kg) (N=9)
7	mdfmt	99	Total (N=47)

Column Headings – Program (3)



```
data _null_;
  call symput('exedate', put(today(),date9.));
  call symput('exetime', put(time(),time5.));
run;

ods listing close;
ods tagsets.rtf_sample style=custom file = "&out\Table 3 - Demographics (6).rtf";
ods escapechar = '^';
goptions reset=footnote reset=title;
options nonumber nodate orientation=landscape papersize="ISO A4"
  topmargin="0.5 in" bottommargin="0.5 in"
  rightmargin="0.5 in" leftmargin="0.5 in";

proc report data = abc.table_final nocenter split="|";
  column (_sortpage_ pod order stat cohort,result dummy);

  define _sortpage_ / group order=data noprint;
  define pod / group order=data noprint;
  define order / group noprint;
  define stat / group " " style(column header)=[cellwidth=6.0cm just=1];
  define cohort / across " " style(column header)=[cellwidth=2.5cm just=c] format=rndfmt.;
  define result / display " " style(column header)=[cellwidth=2.5cm just=c];
  define dummy / analysis noprint;

  break after _sortpage_ / page;

  compute after _sortpage_ / style=[bordertopcolor=black bordertopwidth=2 just=1];
    line "SD: Standard Deviation";
  endcomp;

  compute before pod / style=[just=1];
    line " ";
    line @0 pod podlabel.;
  endcomp;

  title1 j=1 "Table 3: Demographics";
  title2 j=1 "Protocol: ABC";
  title3 j=1 "Study Population: Intent-to-Treat (ITT) Population";

  footnote1 "Data cut-off date: &cutdaterpt." j=r "Page ^{pageof}";
  footnote2 "Program: Table 3 - Demographics.sas (version &version); Output: Table 3 - Demographics (6).rtf; Created on &exedate at &exetime.";
run;

ods tagsets.rtf_sample close;
ods listing;
```

Column Headings – Output



Table 3: Demographics
Protocol: ABC
Study Population: Intent-to-Treat (ITT) Population

	Cohort 1 (1.0mg/kg) (N=8)	Cohort 2 (2.0mg/kg) (N=8)	Cohort 3 (3.0mg/kg) (N=8)	Cohort 4 (4.0mg/kg) (N=6)	Cohort 5 (5.0mg/kg) (N=8)	Cohort 6 (6.0mg/kg) (N=9)	Total (N=47)
Age (years)							
n	8	8	8	6	8	9	47
Mean	65.1	62.0	67.5	65.2	57.4	64.4	63.6
Median	63.5	63.5	69.0	70.5	59.0	65.0	65.0
SD	7.9	9.0	10.9	11.7	12.8	5.9	9.8
Min	54	48	47	49	40	54	40
Max	82	74	80	77	75	71	82
Gender n(%)							
Male	4 (50.0%)	6 (75.0%)	3 (37.5%)	3 (50.0%)	3 (37.5%)	2 (22.2%)	21 (44.7%)
Female	4 (50.0%)	2 (25.0%)	5 (62.5%)	3 (50.0%)	5 (62.5%)	7 (77.8%)	26 (55.3%)
Race n(%)							
White	6 (75.0%)	7 (87.5%)	8 (100.0%)	6 (100.0%)	8 (100.0%)	8 (88.9%)	43 (91.5%)
Asian	2 (25.0%)	0	0	0	0	1 (11.1%)	3 (6.4%)
Aboriginal	0	0	0	0	0	0	0
Black or African American	0	0	0	0	0	0	0
Native Hawaiian / Pacific Islander	0	0	0	0	0	0	0
American Indian / Alaskan native	0	0	0	0	0	0	0
Other	0	1 (12.5%)	0	0	0	0	1 (2.1%)
Ethnicity n(%)							
Hispanic or Latino	0	0	0	0	0	0	0
Not Hispanic or Not Latino	0	0	0	0	0	0	0
Missing	8 (100.0%)	8 (100.0%)	8 (100.0%)	6 (100.0%)	8 (100.0%)	9 (100.0%)	47 (100.0%)

SD: Standard Deviation

- ☑ Data
- ☑ Style
- ☑ Page X of Y
- ☑ Row grouping
- ☑ Date/Time
- ☑ Column Headers

Data cut-off date: 11JUL2014

Program: Table 3 - Demographics.sas (version 1.4); Output: Table 3 - Demographics (6).rtf; Created on 12SEP2014 at 23:39

Page 1 of 1

Case Studies

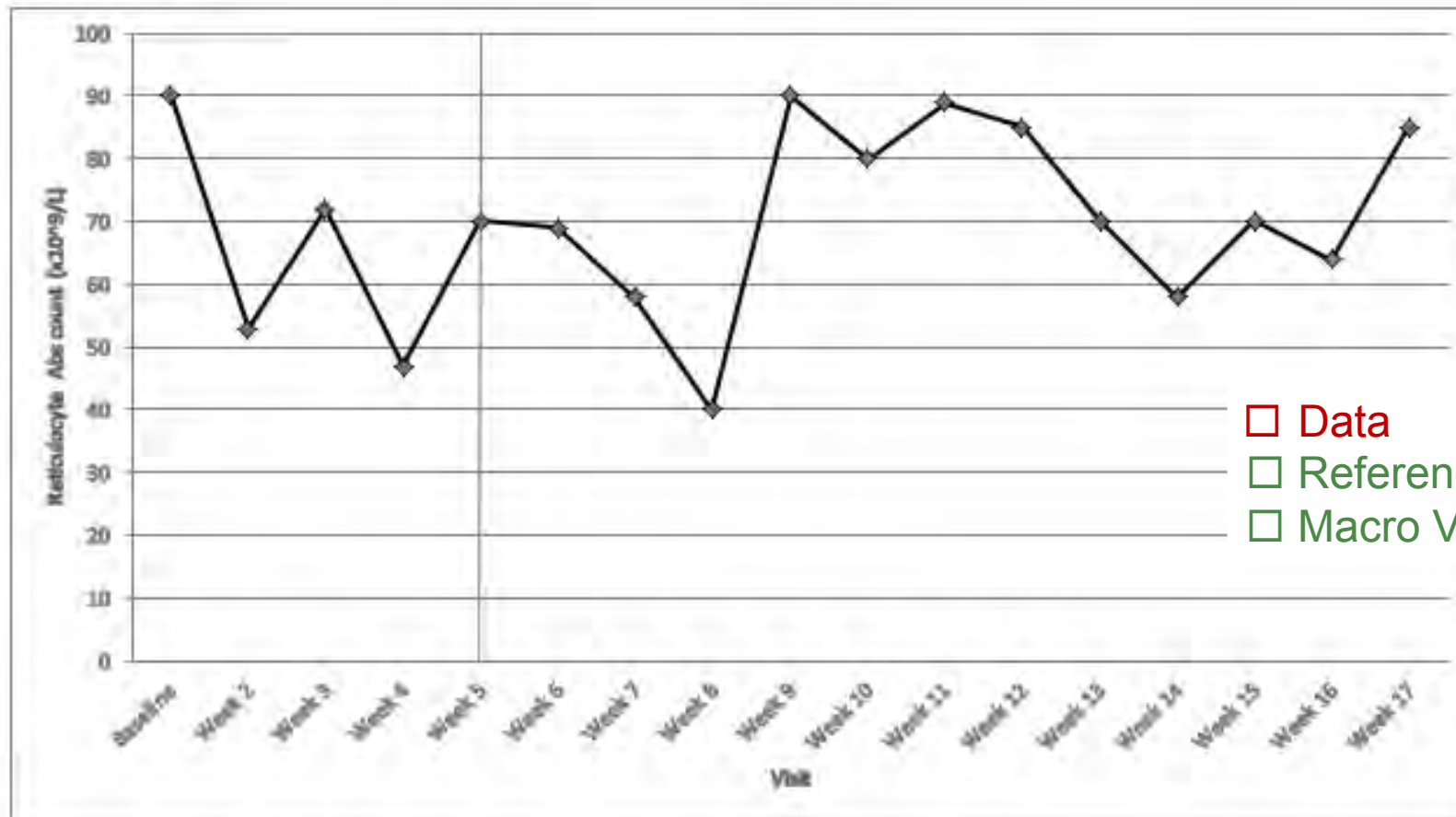
(Customising programs to meet client needs)

PROC SGPLOT

The mock.....

Figure 6.10.1 Individual Reticulocyte Abs count per visit – Subject SXX-XXX (Cohort X)

Protocol: BBC-123
Population: Safety



- Data
- Reference Line
- Macro Variables

Programming note: Date of switch to maintenance phase will be indicated by a vertical line

The data.....



VIEWTABLE: Bbc.Lbh6

	cohort	pid	visit2	visit_dt	result
1	Cohort 1	S04-003	Baseline	.	70.5
2	Cohort 1	S04-003	Week 2	2013-10-25	76
3	Cohort 1	S04-003	Week 3	2013-11-01	40
4	Cohort 1	S04-003	Week 4	2013-11-08	71
5	Cohort 1	S04-003	Week 5	2013-11-15	67
6	Cohort 1	S04-003	Week 6	2013-11-22	56
7	Cohort 1	S04-003	Week 7	2013-11-29	43
8	Cohort 1	S04-003	Week 8	2013-12-06	229
9	Cohort 1	S04-003	Week 9	2013-12-12	142
10	Cohort 1	S04-003	Week 10	2013-12-20	111
11	Cohort 1	S04-003	Week 11	2013-12-27	.
12	Cohort 1	S04-003	Week 12	2014-01-03	90
13	Cohort 1	S04-003	Week 13	2014-01-10	80
14	Cohort 1	S04-003	Week 14	2014-01-17	75
15	Cohort 1	S04-003	Week 15	2014-01-24	58
16	Cohort 1	S04-003	End of Study	2014-02-07	93
17	Cohort 1	S04-004	Baseline	.	18
18	Cohort 1	S04-004	Week 2	2013-11-04	22
19	Cohort 1	S04-004	Week 3	2013-11-11	17
20	Cohort 1	S04-004	Week 4	2013-11-18	25
21	Cohort 1	S04-004	Week 5	2013-11-25	17
22	Cohort 1	S04-004	Week 6	2013-12-02	16
23	Cohort 1	S04-004	Week 7	2013-12-09	16

Plotting the Data – Program (1)

```
data lbh7;          /* Restrict to one patient */
  set bbc.lbh6;
  if pid="S04-003";
run;
```

```
proc template;    /* Create custom template */
  define style styles.bbc;
    parent = styles.solutions;
    style GraphValueText from GraphValueText / font=('Arial', 10pt);
    style GraphLabelText from GraphLabelText / font=('Arial', 10pt, bold);
  end;
run;
```

```
ods escapechar = '~';
```

```
ods graphics / noborder width = 25cm height=12cm imagefmt=jpeg;      /* Set graphics size and format */
```

```
Title1 j=1 font = "Arial" height = 10pt color = black
  "Figure 6.10.1: Individual Reticulocyte Abs Count per visit - Subject S04-003 (Cohort 1)";
Title2 j=1 font = "Arial" height = 10pt color = black "Protocol: BBC-123";
Title3 j=1 font = "Arial" height = 10pt color = black "Study Population: Safety Population";

footnote1 j=1 font = "Arial" h = 10pt color = black " ";
footnote2 j=1 font = "Arial" h = 10pt color = black "Clinical cut-off date: &cutdaterpt" j=r "Page 1 of 1";
footnote3 j=1 font = "Arial" h = 10pt color = black
  "Program: Figure6.10-Reticuloctyes.sas (version &version);
  Output: Figure6.10.1-Reticuloctyes (S04-003).rtf;
  Date Created: &exedate &exetime";
```

Plotting the Data – Program (2)

```
ods listing close;
ods tagsets.rtf_sample style = bbc
  file = "%out\Figure6.10.1-Reticuloctyes (S04-003).rtf"
  nogfootnote nogtitle;
```

```
options nonumber nodate orientation=landscape papersize="ISO A4"
  topmargin="0.5 in" bottommargin="0.5 in" rightmargin="0.5 in" leftmargin="0.5 in";
```

```
proc sgplot data=lbh7;

  yaxis label = "Reticulocyte Abs Count (x109/L)"
    grid values = (0 to 250 by 50);

  xaxis label = "Visit"
    type=discrete
    fitpolicy=splitalways
    splitter="|"
    discreteorder=data;

  vline visit2 / response = result
    markers
    markerattrs = (color=black symbol=circle)
    lineattrs   = (color=black thickness=2);

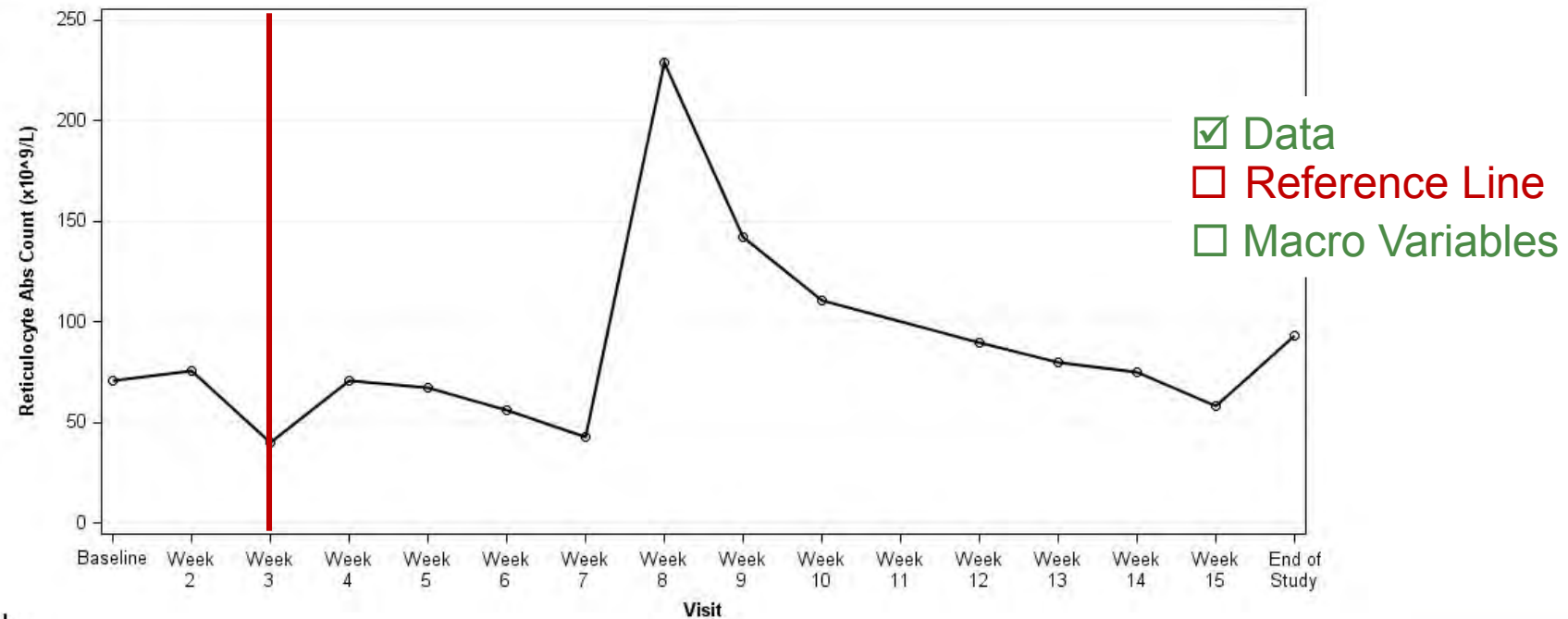
run;
```

Note: Couldn't use ^ as the escapechar due to the use of the symbol in the axis title. Hence set to "~"

```
ods tagsets.rtf_sample close;
ods listing;
```

Plotting the Data – Output

Figure 6.10.1: Individual Reticulocyte Abs Count per visit – Subject S04-003 (Cohort 1);
Protocol: BBC-123
Study Population: Safety Population



Clinical cut-off date: 11JUL2014

Program: Figure6.10-Reticuloctyes.sas (version 1.0);

Output: Figure6.10.1-Reticuloctyes (S04-003).rtf;

Date Created: 14SEP2014 21:29

Page 1 of 1

Reference line – Program (1)



*mp_visit = Name of visit
patient switched to
maintenance phase*

*mpyn = Did the patient switch to
maintenance phase (0 = no, 1 = yes)*

	cohort	pid	visit2	visit_dt	result	mpyn	mp_visit
1	Cohort 1	S04-003	Baseline	.	70.5	1	Week13
2	Cohort 1	S04-003	Week12	2013-10-25	76	1	Week13
3	Cohort 1	S04-003	Week13	2013-11-01	40	1	Week13
4	Cohort 1	S04-003	Week14	2013-11-08	7	1	Week13
5	Cohort 1	S04-003	Week15	2013-11-15	67	1	Week13
6	Cohort 1	S04-003	Week16	2013-11-22	56	1	Week13
7	Cohort 1	S04-003	Week17	2013-11-29	43	1	Week13
8	Cohort 1	S04-003	Week18	2013-12-06	229	1	Week13
9	Cohort 1	S04-003	Week19	2013-12-12	142	1	Week13
10	Cohort 1	S04-003	Week10	2013-12-20	11	1	Week13
11	Cohort 1	S04-003	Week11	2013-12-27		1	Week13
12	Cohort 1	S04-003	Week12	2014-01-03	9	1	Week13

Reference line – Program (2)

```
proc sgplot data=lbh7;

    yaxis label = "Reticulocyte Abs Count (x10^9/L)"
         grid values = (0 to 250 by 50);

    xaxis label = "Visit"
         type=discrete
         fitpolicy=splitalways
         splitchar="|"
         discreteorder=data;

    vline visit2 / response = result
         markers
         markerattrs = (color=black symbol=circle)
         lineattrs   = (color=black thickness=2);

    refline mp_visit / axis = X
         lineattrs = (pattern=solid color=grey)
         name='refline'
         legendlabel = 'Visit switched to Maintenance Phase';

    keylegend 'refline' / title=''
         valueattrs=(size=9)
         location=inside
         position=topleft
         across=1
         opaque;

run;

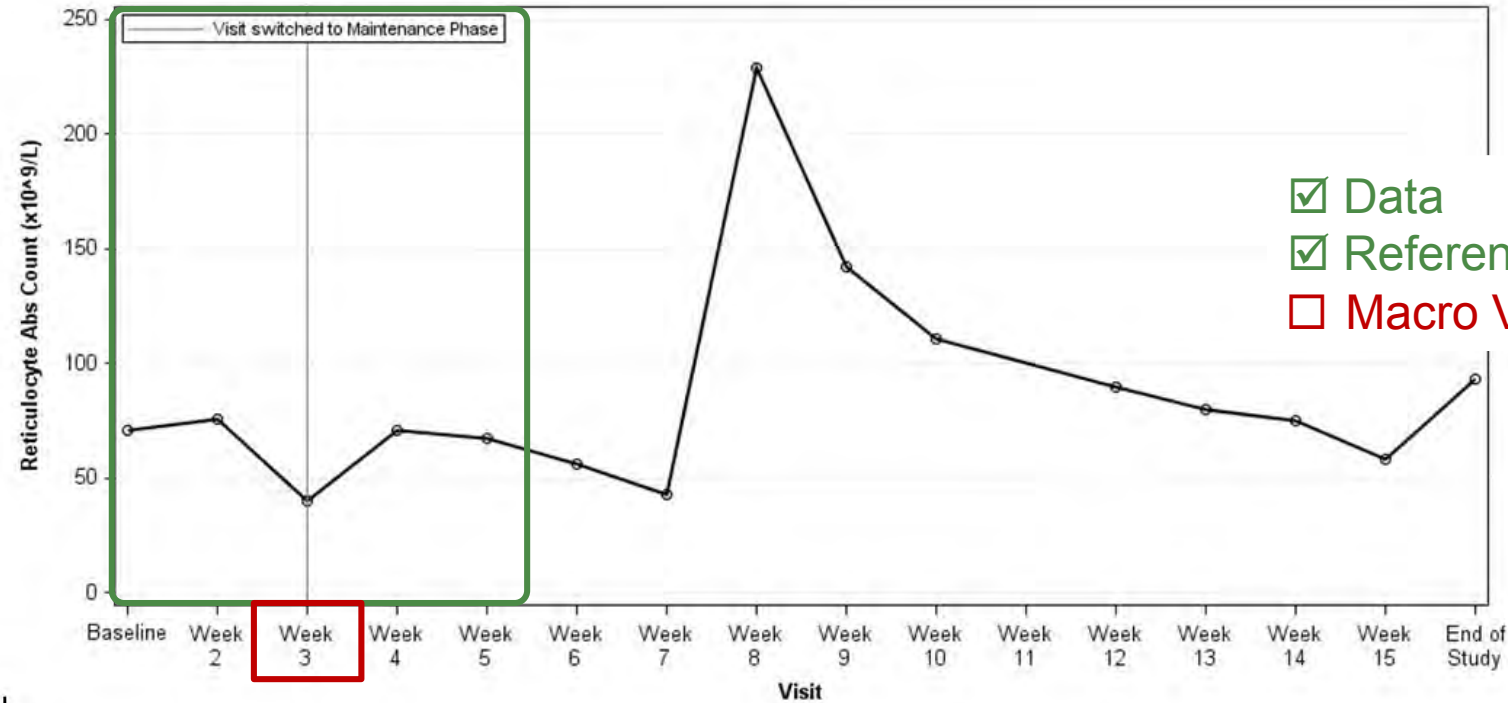
ods tagsets.rtf_sample close;
ods listing;
```

Reference line - Output

Figure 6.10.1: Individual Reticulocyte Abs Count per visit – Subject S04-003 (Cohort 1), &cohort
Protocol: BBC-123
Study Population: Safety Population

&alpha

&pid



- Data
- Reference Line
- Macro Variables

&mpref

&alpha

&pid

Clinical cut-off date: 11JUL2014

Program: Figure6.10-Reticulocytes.sas (version 1.0);

Output: Figure6.10.1-Reticulocytes S04-003.rtf;

Date Created: 14SEP2014 21:29

Page 1 of 1

Macro Variables – Program (1)

```
options symbolgen mprint mlogic;
```

```
%macro fig610;
```

```
proc sql noprint; /* Get distinct data */  
  create table _pid as  
  select distinct cohort, pid, mpyn, mp_visit  
  from bbc.lbh6;
```

```
data _pid; /* Put count into a macro variable */  
  set _pid;  
  n + 1;  
  call symput ('N', compress (put (n, best12.)));  
run;
```

```
%DO I=1 %TO &N; /* Use the count macro in a DO statement */  
  
  data _null_; /* Create remaining macro variables */  
    set _pid (where=(n=&I));  
    call symput ('pid', compress (pid));  
    call symput ('num', strip (put (&I, best.)));  
    call symput ('cohort', strip (put (cohort, F8F8.)));  
    call symput ('mpref', mp_visit);  
  run;
```

```
data lbh7; /* Select data for one subject only */  
  set bbc.lbh6;  
  if pid="&pid";  
run;
```

Macro Variables – Program (2)



```
ods escapechar = '~';

ods graphics / noborder width = 25cm height=12cm imagefmt=jpeg;

Title1 j=1 font = "Arial" height = 10pt color = black
      "Figure 6.10.&num: Individual Reticulocyte Abs Count per visit - Subject &pid (&cohort);";
Title2 j=1 font = "Arial" height = 10pt color = black "Protocol: BBC-123";
Title3 j=1 font = "Arial" height = 10pt color = black "Study Population: Safety Population";

footnote1 j=1 font = "Arial" h = 10pt color = black " ";
footnote2 j=1 font = "Arial" h = 10pt color = black "Clinical cut-off date: &cutdaterpt" j=r "Page 1 of 1";
footnote3 j=1 font = "Arial" h = 10pt color = black
      "Program: Figure6.10-Reticuloctyes.sas (version &version);
      Output: Figure6.10.&num-Reticuloctyes (S04-003).rtf;
      Date Created: &exedate &exetime";

ods listing close;
ods tagsets.rtf_sample style = bbc file = "&out\Figure6.10.&num-Reticuloctyes (&pid).rtf" nogfootnote nogtitle;

options nonumber nodate orientation=landscape papersize="ISO A4"
      topmargin="0.5 in" bottommargin="0.5 in" rightmargin="0.5 in" leftmargin="0.5 in";
```

Macro Variables – Program (3)



```
proc sgplot data=lbh7;

    yaxis label = "Reticulocyte Abs Count (x10^9/L)"
           grid values = (0 to 250 by 50);

    xaxis label = "Visit"
           type=discrete
           fitpolicy=splitalways
           splitchar="|"
           discreteorder=data;

    vline visit2 / response = result
                markers
                markerattrs = (color=black symbol=circle)
                lineattrs   = (color=black thickness=2);

    reflate mp_visit / axis = X
                 lineattrs = (pattern=solid color=grey)
                 name='refline'
                 legendlabel = 'Visit switched to Maintenance Phase';

    keylegend 'refline' / title=''
                valueattrs=(size=9)
                location=inside
                position=topleft
                across=1
                opaque;

run;

ods tagsets.rtf_sample close;
ods listing;

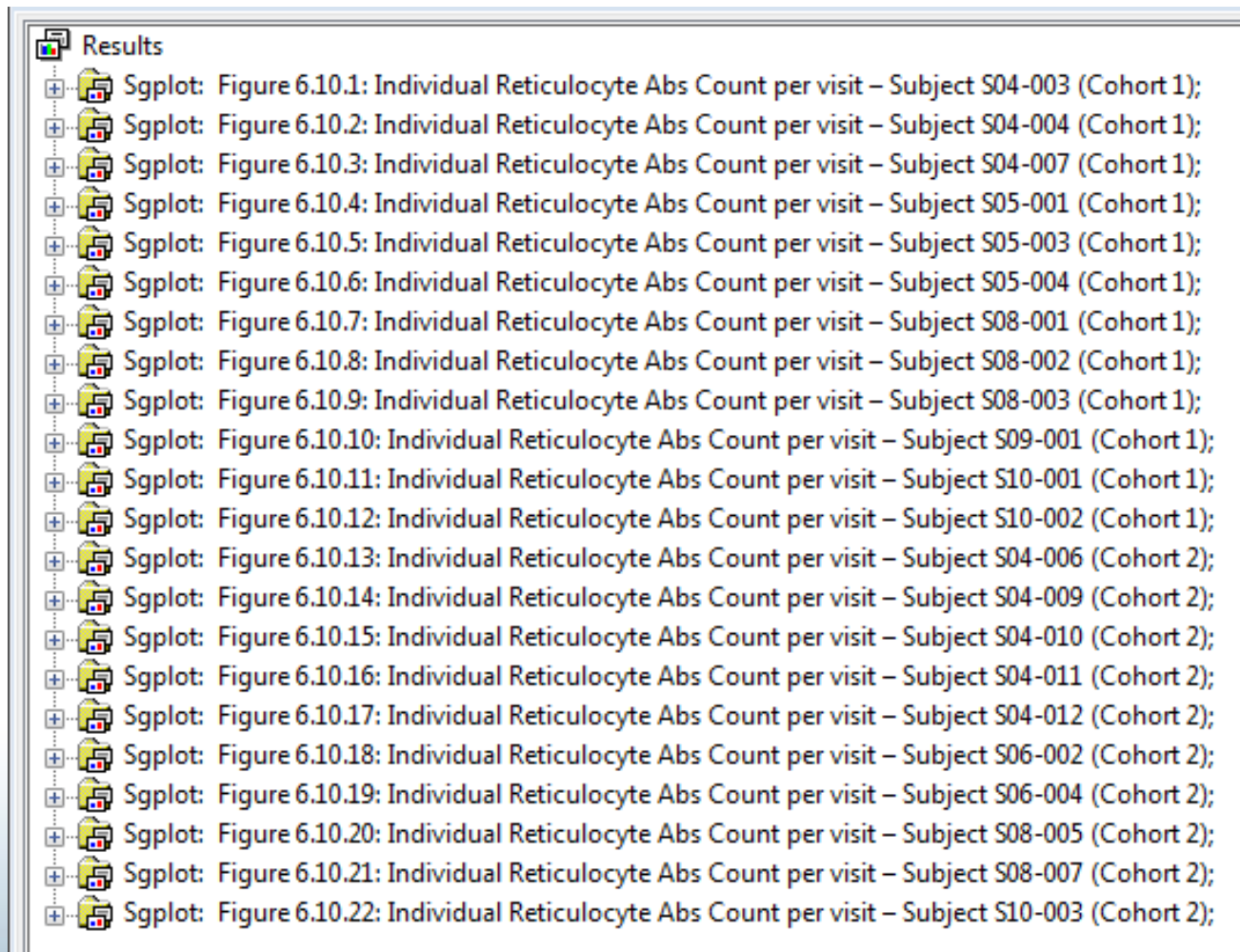
    %END;

%mend fig610;

%fig610;

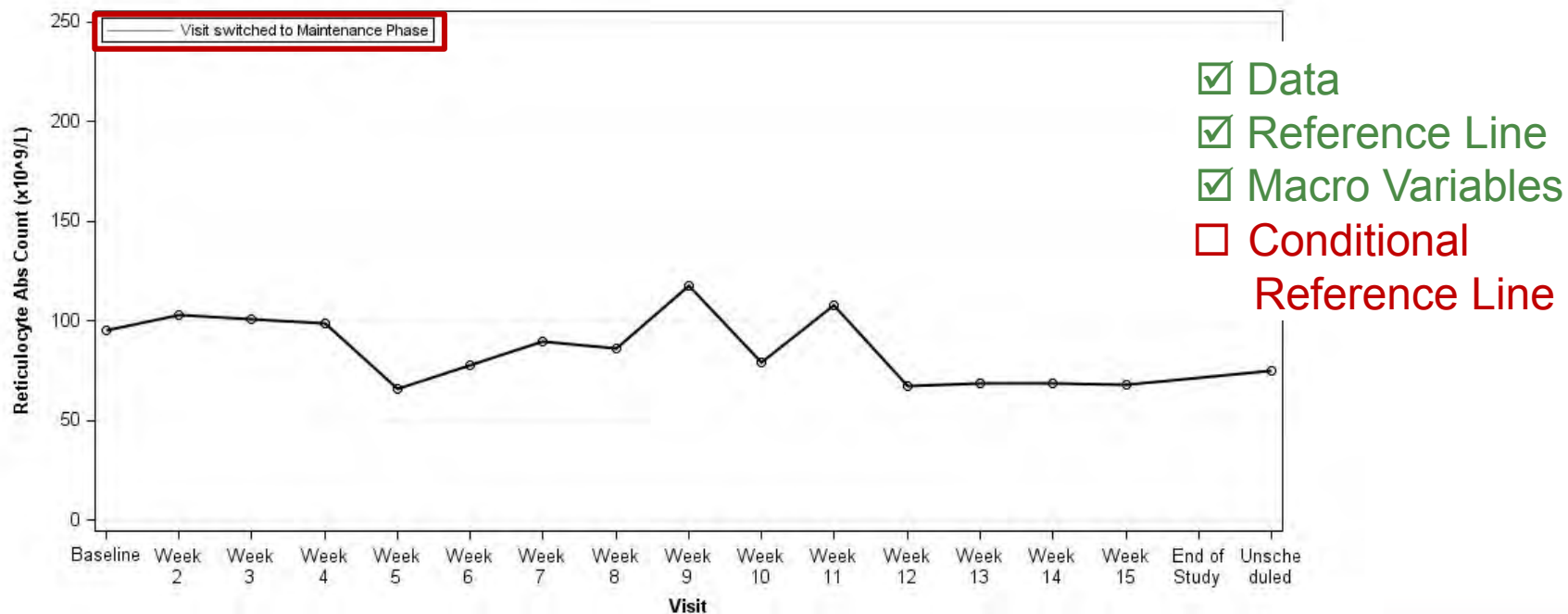
options nosymbolgen nomprint nomlogic;
```

Macro Variables – Output (1)



Macro Variables – Output (2)

Figure 6.10.4: Individual Reticulocyte Abs Count per visit – Subject S05-001 (Cohort 1);
Protocol: BBC-123
Study Population: Safety Population



Conditional Reference Line - Program



```
%DO I=1 %TO &N;      /* Use the count macro in a DO statement */

data _null_;        /* Create remaining macro variables */
  set _pid (where=(n=&I));
  call symput ('pid',compress(pid));
  call symput ('num',strip(put(&I,best.)));      proc sgplot data=bbc.lbh6 (where=(pid="&pid"));
  call symput ('cohort',strip(put(cohort,F8F8.)));
  call symput ('mpref',mp visit);              yaxis label = "Reticulocyte Abs Count (x10^9/L)"
  call symput ('mpynref',strip(mpyn));          grid values = (0 to 250 by 50);

run;                                                    xaxis label = "Visit"
                                                    type=discrete
                                                    fitpolicy=splitalways
                                                    splitchar="|"
                                                    discreteorder=data;

vline visit2 / response = result
              markers
              markerattrs = (color=black symbol=circle)
              lineattrs = (color=black thickness=2);

  %if "&mpynref"="1" %then %do;

  reflate mp_visit / axis = X
                    lineattrs = (pattern=solid color=grey)
                    name='refline'
                    legendlabel = 'Visit switched to Maintenance Phase';

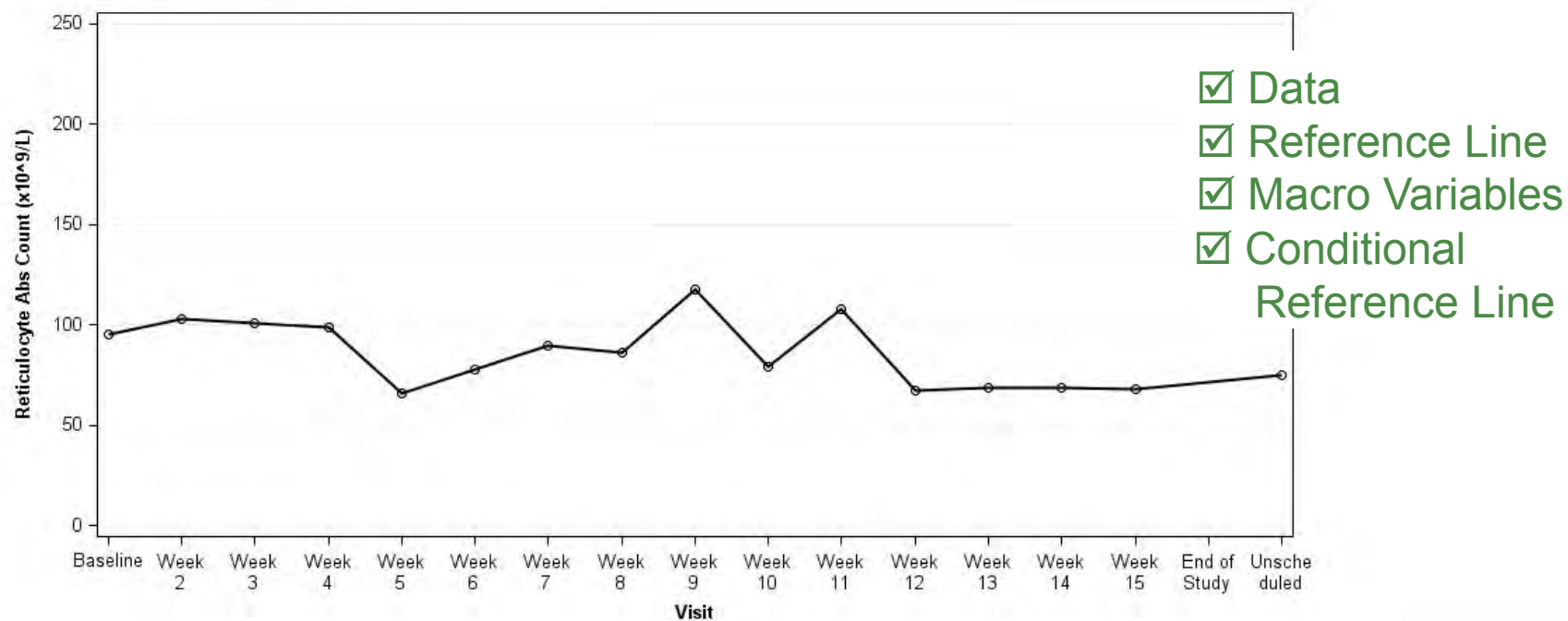
  keylegend 'refline' / title=''
              valueattrs=(size=9)
              location=inside
              position=topleft
              across=1
              opaque;

  %end;

run;
```

Conditional Reference Line - Output

Figure 6.10.4: Individual Reticulocyte Abs Count per visit – Subject S05-001 (Cohort 1)
Protocol: BBC-123
Study Population: Safety Population



Clinical cut-off date: 11JUL2014

Program: Figure6.10-Reticuloctyes.sas (version 1.0); Output: Figure6.10.4-Reticuloctyes (S05-001).rtf; Date Created: 14SEP2014 21:29

Page 1 of 1

Lessons Learnt

➤ Certification

- ✓ SAS Certified Base Programmer for SAS 9
- ✓ SAS Certified Advanced Programmer for SAS 9
- ✓ SAS Certified Clinical Trials Programmer Using SAS 9

➤ Experience

- ✓ Working on over 20 studies:
 - ✓ TLF packages
 - ✓ Sample size estimates
 - ✓ Randomisation schedules
 - ✓ Statistical Analysis Plans
 - ✓ Protocols
 - ✓ Statistical Reports
- ✓ Process improvement

Key points for new SAS (bio)statisticians



- Know the study (design, objectives, treatment, disease)
- Know the data
- Know the regulations
- Get the specifications right before programming
- SAS
 - Think “HOW” not “IF”
 - Try different programming approaches
 - Program using your logic (but don't assume others have the same logic)
 - Keep it readable – indentations, annotations
 - Use macros judiciously
 - Maintain a clean log*
 - Version control
 - Leave plenty of time for validation and QC
 - Be willing to admit “I don't know”
 - Ask for help

HELP!!



- SAS Online Support: <https://support.sas.com/>
- SAS User Group Whitepapers
 - <http://www.pharmasug.org/>
 - <http://www.lexjansen.com/> (various SAS proceedings)
- SAS Sample Programs and Data from SAS published books
 - <http://ftp.sas.com/samples/index>
- Specific to Statistical Analyses in SAS
 - <http://www.ats.ucla.edu/stat/sas/>

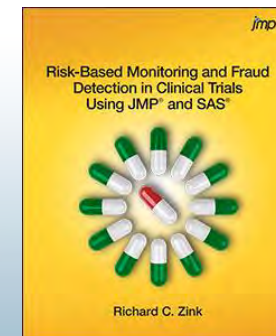
- SAS Community Forums
 - General
<https://communities.sas.com/community/support-communities>
 - Health Care, including pharmaceutical
https://communities.sas.com/community/support-communities/sas_in_health_care_related_fields
 - Australia and New Zealand
<https://communities.sas.com/groups/sanzoc>
 - Melbourne
[https://communities.sas.com/groups/sanzoc/content?filterID=content~category\[smug\]](https://communities.sas.com/groups/sanzoc/content?filterID=content~category[smug])
- http://www.sascommunity.org/wiki/Main_Page
- SAS-L RSS Feed (<https://listserv.uga.edu/cgi-bin/wa?A0=sas-l>)

HELP!! Offline



- SAS help 
- SAS Books / eBooks

My SAS Library



Wiki – Central repository for code snippets



Reports

ADMIN TALK PREFERENCES WATCHLIST CONTRIBUTIONS LOG OUT

Navigation page [discussion](#) [edit](#) [history](#) [delete](#) [move](#) [protect](#) [watch](#)

- Home Page
- Log in

TLFs

- General
- Graphs
- Headers & Footers
- Listings
- Macros
- Reports
- Tables

RANDOMISATION

- Randomisation

SAMPLE SIZE

- Sample Size

WIKIMEDIA

- Wikimedia Docs
- Recent changes
- Random page

Search

Search

Go Search

Tools

- What links here
- Related changes
- Special pages
- Printable version
- Permanent link
- Page information

Contents [\[hide\]](#)

- 1 REPORTS
 - 1.1 Superscript
 - 1.2 Page Numbering
 - 1.3 Calculating [_sortpage_](#)
 - 1.4 Auto Date and Time
 - 1.5 Span Headers (using variable)
 - 1.6 Span Headers (using free text)
 - 1.7 Styling in COLUMN statement
 - 1.8 Define statements
 - 1.9 Proc Template
 - 1.10 Adding breaks
 - 1.11 Compute

REPORTS [\[edit\]](#)

Superscript [\[edit\]](#)

```
~{super 2}      ^{super 2}
```

Page Numbering [\[edit\]](#)

```
"Page ~{pageof}"      "Page ^{pageof}"
```

Calculating [_sortpage_](#) [\[edit\]](#)

```
if first.cohort then lines=3;
else lines=1;
countlines+lines;
_sortpage_=ceil(countlines/30);

if first.cohort then lines=int(length(com)/16)+4;
else lines=int(length(com)/16)+1;
countlines+lines;
_sortpage_=ceil(countlines/30);

if first.cohort then lines=int(max((length(com)/16), (length(visit)/45)))+4;
else lines= int(max((length(com)/16), (length(visit)/45)))+1;
countlines+lines;
_sortpage_=ceil(countlines/27);
```


Where to now?

SAS

- Cleverer programming (work smarter, not harder)
- RRR (Reuse, Refine, Recycle) (*SAS Clinical Data Integration*)
- CDISC / XML (*SAS Clinical Standards Toolkit, PROC CDISC*)
- Risk-based monitoring (*JMP Clinical*)

Statistics

- Mixed modelling
- Multiple comparisons
- Time-to-event analyses
- Pharmacometrics



What should new SAS programmers focus on to become top SAS programmers?

Extra: Log Review



Search Terms*

Error
Warning
INFO: Character
INFO: The variable
NOTE: At least
NOTE: Character
NOTE: Division
NOTE: Mathematical
NOTE: Merge
NOTE: Missing
NOTE: NOSPOOL
NOTE: Numeric
NOTE: Variable
NOTE: A CASE

* "Validating Clinical Trial Data Reporting with SAS" by Carol Matthews & Brian Shiling

Tip: Use Notepad++ software to find all occurrences of a search term in 1 (or more) logs

```
209 (S04-007).xtf
210
211 NOTE: PROCEDURE SGPLOT used (Total process time):
212     real time          0.92 seconds
213     CPU time           0.39 seconds
214
215 NOTE: There were 16 observations read from the data set WORK.LBH7.
216
217
218 NOTE: Numeric values have been converted to character values at the places given by: (Line):(Column).
219     1:1
220 NOTE: There were 1 observations read from the data set WORK_PID.
221     WHERE n=4;
222 NOTE: DATA statement used (Total process time):
223     real time          0.01 seconds
224     CPU time           0.01 seconds
225
226
227
228 NOTE: There were 296 observations read from the data set WORK.LBH6.
```

Find result - 44 hits

Search "NOTE: Numeric" (44 hits in 1 file)

new 2 (44 hits)

Line 137:	NOTE: Numeric	values have been converted to character values at the places given by: (Line):(Column).
Line 164:	NOTE: Numeric	values have been converted to character values at the places given by: (Line):(Column).
Line 191:	NOTE: Numeric	values have been converted to character values at the places given by: (Line):(Column).
Line 218:	NOTE: Numeric	values have been converted to character values at the places given by: (Line):(Column).
Line 245:	NOTE: Numeric	values have been converted to character values at the places given by: (Line):(Column).
Line 272:	NOTE: Numeric	values have been converted to character values at the places given by: (Line):(Column).
Line 299:	NOTE: Numeric	values have been converted to character values at the places given by: (Line):(Column).
Line 326:	NOTE: Numeric	values have been converted to character values at the places given by: (Line):(Column).
Line 353:	NOTE: Numeric	values have been converted to character values at the places given by: (Line):(Column).
Line 380:	NOTE: Numeric	values have been converted to character values at the places given by: (Line):(Column).

Normal text file | length: 53201 | lines: 1463 | Ln: 218 | Col: 14 | Sel: 13 | 0 | Dos\Windows | ANSI as UTF-8 | INS



TIPS & TRICKS

Tips & tricks for the new and not so new to SAS

Brian Watts

TIPS AND TRICKS :: ABSTRACT

- Migrating old source code to EGuide
- Using code analyser to convert code to process flows
- Managing log capture interactively or in batch
- SAS Logs:
 - Post processing SAS logs and capturing more than just obvious errors
- ADsync:
 - Better practices to consider for synchronising Host Security (AD, LDAP etc) with SAS Metadata
- SAS VA:
 - A short drive through history on the way to Visual Analytics

TIPS & TRICKS



- EG note nodes, setting sasapp workspace default for file navigation
- EG Project Maintenance to change from sasapp to localhost
- Multiple flows in a project, moving code nodes from flow to flow
- Embedding code or leave it on disk and link it to EG flow?
- Using EG Analyse Program to convert code to a flow
- Filename to access many different non-SAS data types
- Filename to send basic email, set email system options
- Filename to allocate temporary log file in work library location
- Proc printto to redirect log to disk
- Use of data step to echo log back into EGuide
- Use of LogCheck macro to scan log
- Customising LogCheck macro to handle “known errors”

TIPS & TRICKS



- ADsync: What is a better practice for synchronising Host Security (AD, LDAP etc) with SAS Metadata
 - Decouple the riskier dependencies that break
 - Shift ownership to IT AD security team to push the data
 - maintaining people and process for AD extract is difficult to sustain
 - better if IT AD security are responsible to push the data
 - Once you have user and groups names landed pick them up with usual supplied user synchronisation
 - Optionally don't actually auto-delete groups/users from metadata
 - instead you could rename the users to indicate inactivation
 - easier to add in should they return to use
 - avoids 'deleterious' consequence of accidental auto-deletion !
 - Consider building the process as a custom DI transformation
 - another way to put more interactive control in your hands

- Narrative:
 - a quick journey through history to VA

ANALYTICS U & SANZOC UPDATE



Andrew Howell

USER COMMUNITY UPDATES



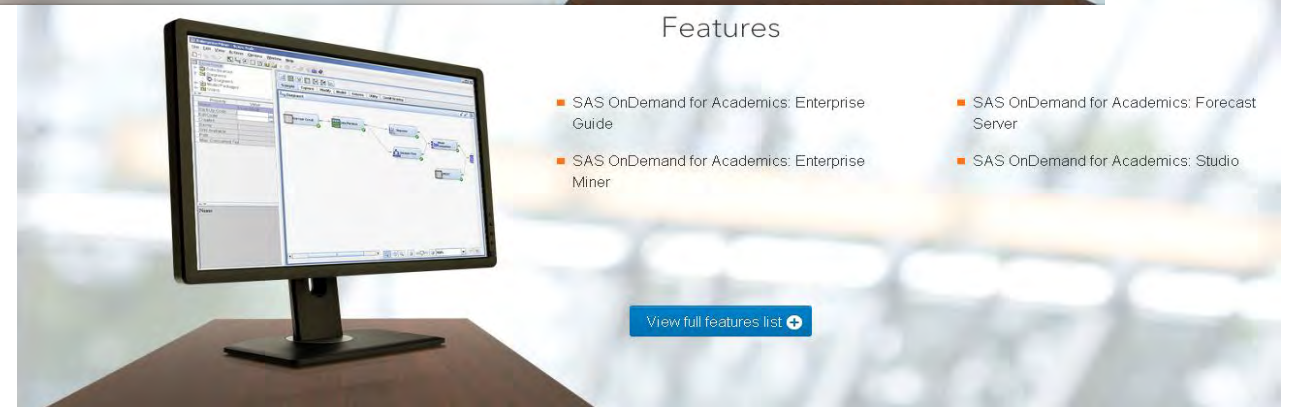
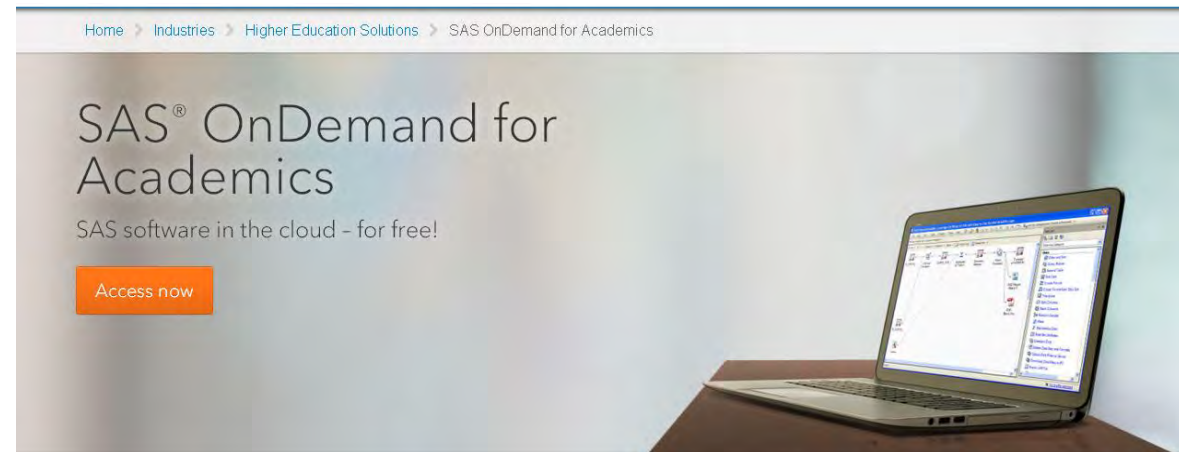
- SAS University Edition
 - Online solutions for Academics
 - Your own free copy of SAS
- SAS Global Forum 2015 (Dallas, TX)
 - Call for papers open
 - Win a trip to SAS Global Forum
- SANZOC Update

SAS ON-DEMAND FOR ACADEMICS



- Online solutions for Academics

- Enterprise Guide
- Enterprise Miner
- Forecast Server
- SAS Studio



- http://www.sas.com/en_us/industry/higher-education/on-demand-for-academics.html

SAS UNIVERSITY EDITION



- Your own free copy of SAS
 - Base/SAS
 - SAS/STAT
 - SAS/IML
 - SAS/Access
- Requirements
 - Windows 7+ (64-bit) / OS X 10.8+ / Linux
 - VMWare / VirtualBox
 - Web browser

The image shows a screenshot of the SAS University Edition website. The main heading is "SAS® University Edition" with the tagline "Free SAS software for tomorrow's analytics experts. Talk about smart." Below this is a "Download software now" button. The page also features a section titled "Free SAS® software. An interactive, online documentation. And the analytical skills to succeed." and a quote from McKinsey Global Institute: "By 2018, demand for workers skilled in analytics could outpace supply by 60 percent – or 1.5 million jobs – according to a McKinsey Global Institute study. Translation? Anyone with analytic prowess will be in high demand from employers around the world. What's more, a recent Monster.com article, 'Job Skills That Lead to Bigger Paychecks,' named SAS as the skill that nets the biggest paycheck. Bottom line, if you're a student, learning SAS is a..."

To the right of the screenshot is a diagram with a central circle labeled "SAS Studio". Four smaller circles are arranged around it, each connected to the central circle by a dashed arrow. The circles are labeled "SAS/ACCESS", "SAS/IML", "SAS/STAT", and "Base SAS".

- http://www.sas.com/en_us/software/university-edition.html

SAS UNIVERSITY EDITION



- Runs as a virtual SAS server
- Run via SAS Studio (HTML5 web interface) on the host PC

University - VMware Player (Non-commercial use only)

Welcome to your SAS University Edition Virtual Application
<http://www.sas.com>

You can connect to your SAS University software by entering this address in your browser:
<http://123.456.789.101>

It is safe to mind SAS® University Edition: Information Center

Welcome

sas
THE POWER TO KNOW.

Start SAS Studio >

NOTIFICATIONS

- ! SAS University Edition updates are available. [Update](#)

RESOURCES

- [Communities \(collaborate and share best practices\)](#)
- [Installation Documentation](#)
- [Frequently Asked Questions \(FAQ\)](#)

SAS® Studio

Search

Folders

- Folder Shortcuts
- My Folders

Program 1 x

CODE LOG RESULTS

1 Enter your code here

SAS® Studio

Program 1 x Distribution Analysis 1 x

Settings Code/Results Split

DATA OPTIONS INFORMATION

EXPLORING DATA

- Histogram
- Add normal curve
- Add kernel density estimate
- Add inset statistics
- Inset Statistics

CHECKING FOR NORMALITY

- Goodness-of-fit tests
- Histogram with normal curve
- Add inset statistics
- Normal probability plot
- Add inset statistics
- Normal quantile-quantile plot
- Add inset statistics

FITTING DISTRIBUTIONS

Inset Statistics

The SAS System

Distribution of Height

Curve: Normal(Mu=62.337 Sigma=5.1271)

The SAS System

Fitted Normal Distribution for Height

Parameter	Symbol	Estimate
Mean	Mu	62.33684

SAS GLOBAL FORUM 2015

26 – 29 APRIL, DALLAS TEXAS



- Call for papers now open
- Wide array of subject matter
 - Visual Analytics, Administration, Programming, Statistics
 - *And many more...*
- Benefits
 - International recognition, Peer review, Networking
 - *Looks great on a CV!*
- Speak to locals who have presented overseas:
 - Andrew Howell (SMUG & SANZOC) – SGF 2013, SGF 2014
 - Brian Watts (SMUG speaker) – SEUGI 2001, SEUGI 2002
 - Michelle Holmes (QUEST & SANZOC) – SGF 2014

A screenshot of a web browser displaying the SAS Global Forum 2015 website. The browser's address bar shows the URL: http://www.sas.com/en_us/events/2014Q1/sas-global-forum-2015/home.html. The website header features a colorful, circular mosaic logo on the left and the text 'SAS GLOBAL FORUM 2015' on the right. Below the title, it says 'The Journey Is Yours' and 'April 26-29 | Dallas, TX' at the 'Kay Bailey Hutchison Convention Center'. A navigation menu includes 'Home', 'Overview', 'Present', and 'Register'. A large image shows a group of people in a conference setting. Below the image, there is a section titled 'Call for Content Now Open' with a paragraph of text and an orange 'Submit Now' button.

- http://www.sas.com/en_us/events/2014Q1/sas-global-forum-2015/home.html

WIN A TRIP TO SAS GLOBAL FORUM 2015



- All presentations are judged by users
 - Last SMUG winner: **David Cross, BUPA Health Dialog**
- The Winner of each user group meeting, entered into the draw
 - From SMUG, SNUG, QUEST, SAUSAG, WASUP, etc



- One winner wins a free trip to SAS Global Forum 2015
 - Flights
 - Accommodation
 - Registration
- Last year's winner was **Bob Whitehead from Perth**

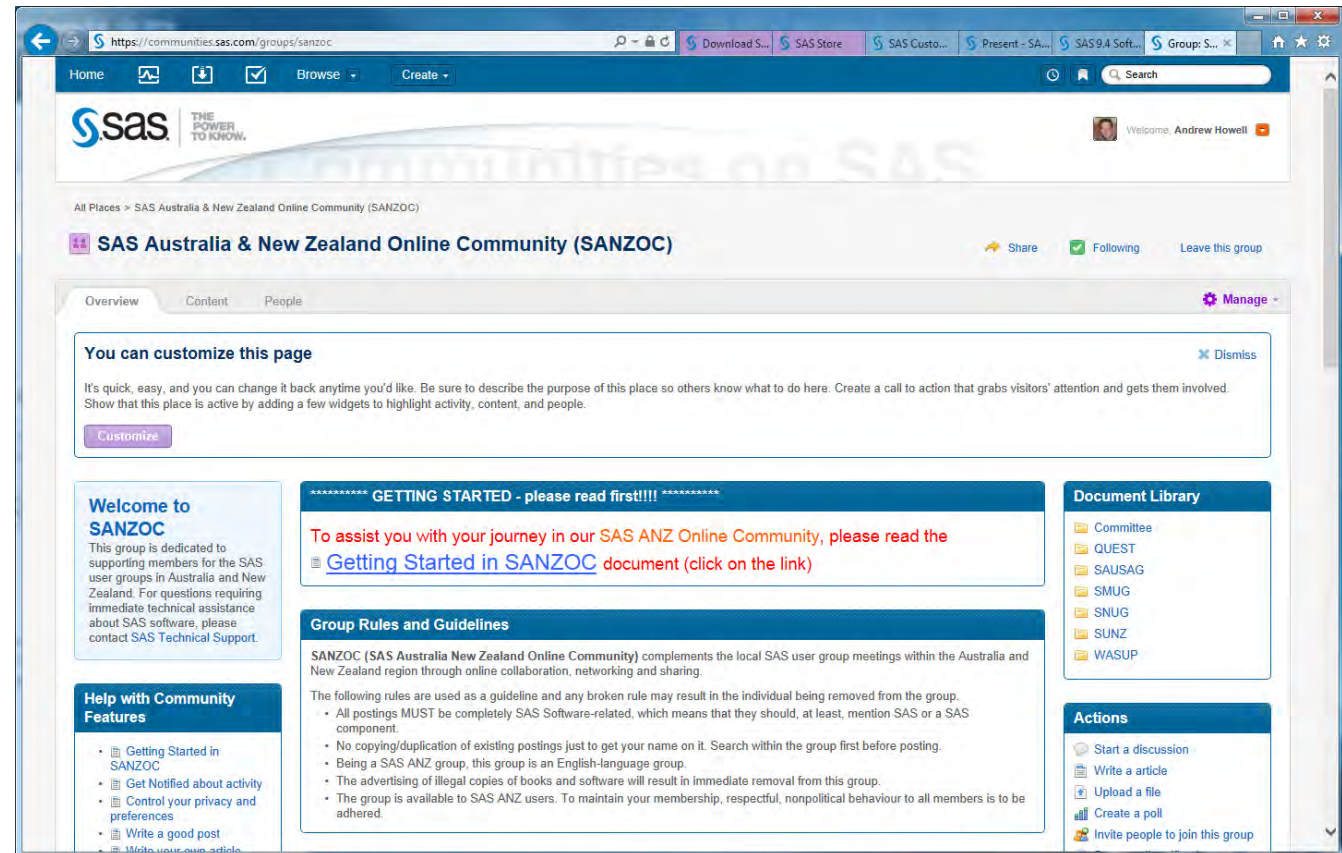


Speak to a **SMUG Committee member** about presenting at **SMUG**

SAS AUSTRALIA & NEW ZEALAND ONLINE COMMUNITY (SANZOC)



- SANZOC now an open group
 - Available to anyone, allows overseas experts to participate in local discussions
 - No waiting for approval
 - Still moderated, discussions may be relocated.
- Encourage you all to join
 - Discover online communities
 - Continue user discussions
 - Remember to follow the SMUG avatar & committee members

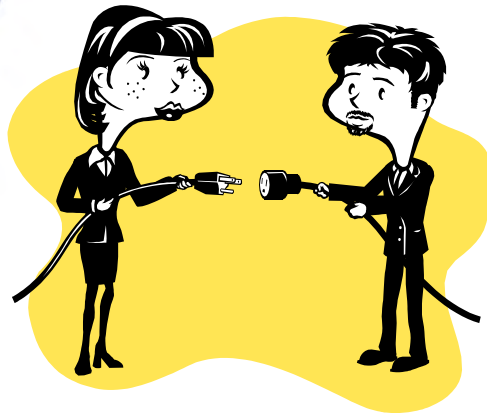


- <http://communities.sas.com/groups/sanzoc>

SAS EDUCATION TAKING YOU WHERE YOU WANT TO GO

SAS Education

*the skills to fully realise the power of the SAS software in
your hands*

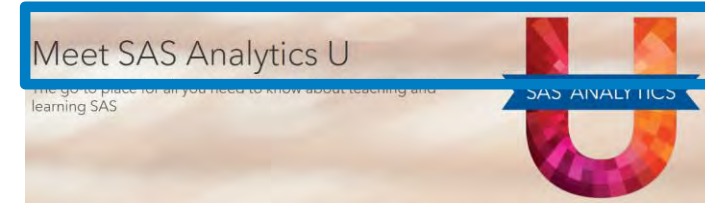


Get SAS certified

3 easy steps to help you....

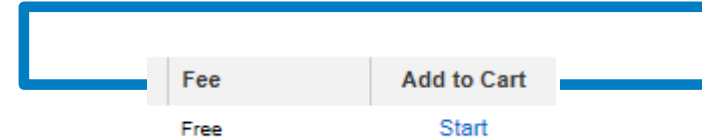
Validate your SAS software skills and earn the globally-recognised credential endorsed by SAS

1. Free Analytics U



2. Free e-Courses

- SAS Programming 1: Essentials
- SAS Statistics 1: Introduction to ANOVA, Regression, and Logistic Regression



3. Certification

- Set Yourself Apart
- Become More
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Base Programming "Finish Up" Certification Packages	
BEST VALUE! Save 30%	OR Save 10%
Classroom + e-Learning + Certification	e-Learning + Certification
Classroom training: SAS Programming 2 \$2,700	Classroom training: Not included
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Certification: e-Practice exam \$60 Certification exam voucher \$200	Certification: e-Practice exam \$60 Certification exam voucher \$200
Full retail price: -\$4,040	Full retail price: -\$1,340
Save 30% \$2,828	Save 10% \$1,206

Contact danny.cohen@sas.com for more information



QUESTIONS FOR THE PRESENTERS?

Q & A



THANK YOU FOR YOUR ATTENDANCE

DON'T FORGET TO COMPLETE THE EVALUATION SURVEY EMAIL

Please join us outside for Refreshments & Networking