

# RRG (Rapid Report Generator) Overview

<https://github.com/ipeszek/RRG>

- Imagine report programming that lets you glance at the program and immediately understand what the report shows and all relevant calculation logic...
- Imagine report programming that allows you to develop reports in a fraction of a time traditional programming takes...
- Imagine report programming that allows you to produce reports with layout tailored to each of your Clients...
- Imagine report programming that frees you from dependence on very experienced programmers...

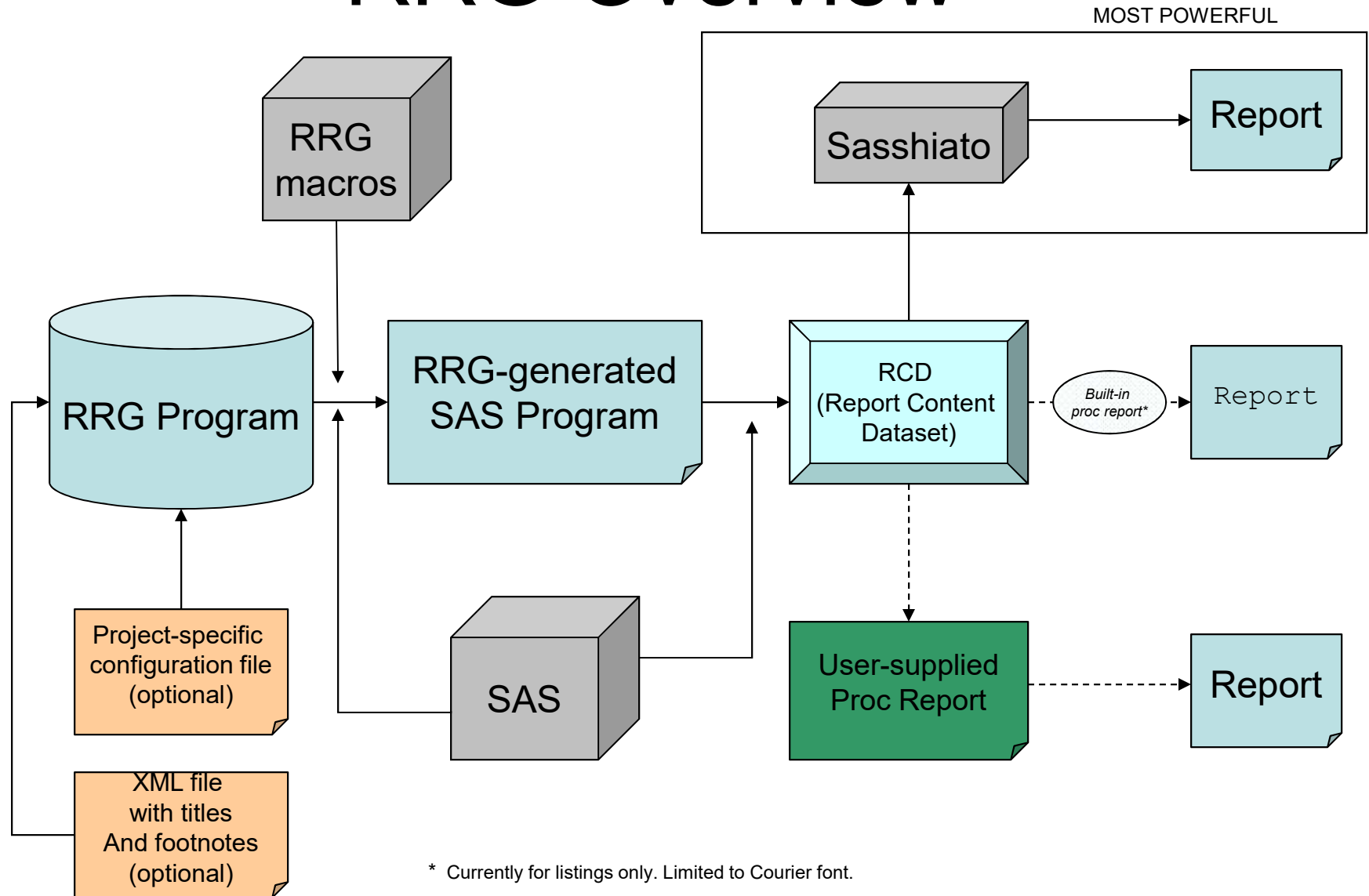
- Standardization of data sets (SDTM, ADaM) proved to be beneficial to pharma community.  
Why not reporting component?
- Some Big Pharma developed reporting systems at a cost upwards of several million dollars
- Too expensive for small companies
- Impossible for CROs

# Metrics from Recent Project

74 tables

Traditional programming for tables:	296 hrs
RRG:	32 hrs

# RRG Overview



# Example of RRG Table

Company Name  
Compound Number

Study Number  
FINAL  
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Table 143.1.5 Relationship of Treatment-Emergent Adverse Events to Study Drug by System Organ Class and Preferred Term  
Safety Analysis Set

System Organ Class Preferred Term	Relationship	Number of Subjects (%)		
		Treatment 1 (N=52)	Treatment 2 (N=49)	Total (N=101)
Total Subjects With Any TEAEs	Overall	44 (84.6)	35 (71.4)	79 (78.2)
	Not Related	41 (78.8)	34 (69.4)	75 (74.3)
	Related	3 (5.8)	1 (2.0)	4 (4.0)
BLOOD AND LYMPHATIC SYSTEM DISORDERS	Overall	3 (5.8)	0	3 (3.0)
	Not Related	2 (3.8)	0	2 (2.0)
	Related	1 (1.9)	0	1 (1.0)
ANAEMIA	Overall	3 (5.8)	0	3 (3.0)
	Not Related	2 (3.8)	0	2 (2.0)
	Related	1 (1.9)	0	1 (1.0)
CARDIAC DISORDERS	Overall	6 (11.5)	3 (6.1)	9 (8.9)
	Not Related	6 (11.5)	3 (6.1)	9 (8.9)
	Related	0	0	0
CARDIAC FAILURE CONGESTIVE	Overall	1 (1.9)	2 (4.1)	3 (3.0)
	Not Related	1 (1.9)	2 (4.1)	3 (3.0)
	Related	0	0	0

Note 1: A treatment-emergent adverse event (TEAE) is defined as an AE whose date of onset occurs after the first dose of study drug.

Note 2: A subject who reported two or more AEs with the same preferred term was counted only once for that term using the related incident. A subject who reported two or more AEs with different preferred terms that are in the same system organ class was counted only once in the system organ class using the most related event.

Note 3: System Organ Class terms are sorted using alphabetical order and Preferred Terms are sorted in decreasing frequency based on the total number of AE reports.

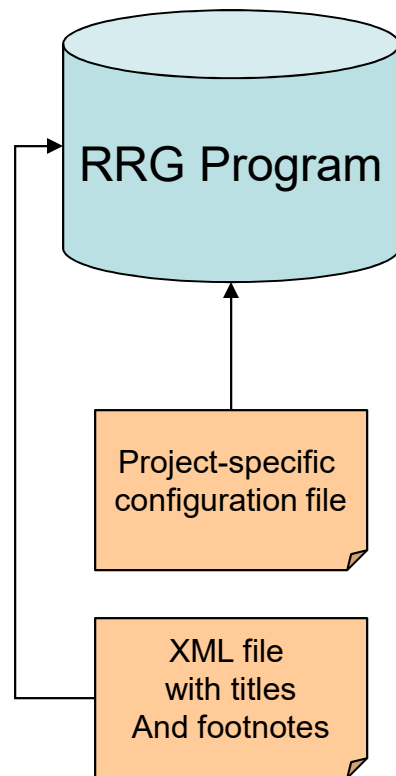
Note 4: MedDRA Dictionary Version 12.1 was used for coding adverse events.

Source: username/pubstudies/...primary/progress/t\_ae\_rls.sas

13:02 13 APR 2010



# RRG Program



```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);

%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  reptype=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta, autospan=N,
  label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max,
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  indent=-1, pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```

# RRG-Generated Program

```
*****
*****
** PROGRAM NAME: V_T_AEREL.SAS
**
** DESCRIPTION: TO GENERATE TABLE T14_3_G1_05
**
**
**
** CODED BY:   possaki ON 13FEB2010
** MODIFIED
**
** INPUT:
**   SASDATA=  ADAE.SAS7BDAT
**
**
**
** OUTPUT:
** TABLES=    V_T_AEREL.TXT
**
** MACROS:
** TOOLS=
**
** NOTE:
**
**
*****
* %inc "macros you may need";
%inc "/pub/studies/.../primary/formats/analfmt_1.sas";
%inc "/pub/studies/.../primary/tools/binom.sas";
%inc "/pub/studies/.../primary/tools/ttest_cim.sas";
%inc "/pub/studies/.../primary/tools/validate.sas";
libname sasdata "/pub/studies/.../primary/sasdata";

* -----
* BEGIN CUSTOM CODE;
* -----

data adae;
set sasdata.adae;
anyae="Total Subjects With Any TEARs";
run;

* -----
* END CUSTOM CODE;
* -----
```



Full generated  
program



# RCD Dataset

Obs	__col_0	__col_1	__col_2	__col_3
1				
2			Number of Subjects (%)	Number of Subj
3	System Organ Class/t1 Preferred Term	Relationship	Treatment A //(N=42)	Treatment B
4	Total Subjects With Any TEAEs			
5		Overall	4 (9.5)	14 (33.3)
6		Not Related	5 (11.9)	12 (24.0)
7		Related	1 (2.4)	0
8	CARDIAC DISORDERS			
9		Overall	1 (2.4)	1 (2.0)
10		Not Related	1 (2.4)	1 (2.0)
11		Related	0	0
12	CARDIAC FAILURE CONGESTIVE			
13		Overall	1 (2.4)	1 (2.0)
14		Not Related	1 (2.4)	1 (2.0)
15		Related	0	0
16	ATRIAL FIBRILLATION			
17		Overall	1 (2.4)	0
18		Not Related	1 (2.4)	0
19		Related	0	0
20	EYE DISORDERS			
21		Overall	1 (2.4)	0
22		Not Related	1 (2.4)	0
23		Related	0	0
24	CONJUNCTIVITIS			
25		Overall	1 (2.4)	0
26		Not Related	1 (2.4)	0
27		Related	0	0
28	GASTROINTESTINAL DISORDERS			
29		Overall	4 (9.5)	6 (12.0)
30		Not Related	5 (11.9)	5 (10.0)
31		Related	1 (2.4)	1 (2.0)

## Example 2 of RRG Table

Company Name  
Compound Number

Study Number  
FINAL  
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Table 14.2.6.4 Summary of Subjects with RBC Transfusion during the Titration and Evaluation Periods  
Full Analysis Set

Transfusion Rate (%)	Treatment A (N=52)	Treatment B (N=49)	Total (N=101)
No. of Subjects Who Received $\geq 1$ Transfusion During the Titration and Evaluation Period	3/52 (5.8%)	0/49	3/101 (3.0%)
95% CI (a)	0.0%, 13.1%	0.0%, 1.0%	0.0%, 6.8%
No. of Subjects Who Received $\geq 1$ Transfusion During the Titration Period	3/52 (5.8%)	0/49	3/101 (3.0%)
95% CI (a)	0.0%, 13.1%	0.0%, 1.0%	0.0%, 6.8%
No. of Subjects Who Received $\geq 1$ Transfusion During the Evaluation Period	0/52	0/49	0/101
95% CI (a)	0.0%, 1.0%	0.0%, 1.0%	0.0%, 0.5%

(a) 2-sided 95% CI of the estimate is calculated from the normal approximation with continuity correction.

Source: [456789/pub/studies/.../primary/progress/tit\\_ebc\\_sas](#)

15:33 13APR2010

# Example 2 (cont.)

```
%rrg_init(uri=T15_2_6_4);

%rrg_defreport(
Dataset=sasdata.adpr,
popwhere=fullset='Y',
tabwhere=,
Colhead1=Transfusion Rate (%));

%rrg_defmodelparms(modelname=binom, macroname=binom, parms=%str(pctci_label=CI (a)));

%rrg_addtrt(name=trtan, decode=trta, autospan=N);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addcond(
where=numevenp>0 and prtrt='PRBC' and aperiodn>0,
label=%str(No. of Subjects Who Received >=1 Transfusion During the Titration and Evaluation Period),
stats=nnpct binom.pctci);

%rrg_addcond(
where=numevenp>0 and prtrt='PRBC' and aperiodn=1,
label=%str(No. of Subjects Who Received >=1 Transfusion During the Titration Period),
stats=nnpct binom.pctci);

%rrg_addcond(
where=numevenp>0 and prtrt='PRBC' and aperiodn=2,
label=%str(No. of Subjects Who Received >=1 Transfusion During the Evaluation Period),
stats=nnpct binom.pctci);

%rrg_generate;
%rrg_finalize;
```

# RRG Programming blocks

- RRG\_init:
  - Prepares RRG for program generation; links report to TFLs entry in external file with tiles/footnotes/output TLG names
- RRG\_defReport
  - Define general report properties (input dataset, population, additional sub-setting, column headings, placement of statistics etc)
- RRG\_codeBefore
  - Lets programmer prepare input dataset (if needed)
- RRG\_defModelParms
  - Specifies parameters for statistical plugins

# RRG Programming blocks

- RRG\_addTrt
  - Define “attributes” of treatment variable
- RRG\_maketrt
  - Define pooled treatment groups
- RRG\_addGroup
  - Define attributes of grouping variable

# RRG Programming blocks (cont.)

- RRG\_addVar
  - Define attributes of continuous variable
- RRG\_addCatvar
  - Define attributes of categorical variable
- RRG\_addLabel
  - Define extra text lines inside report
- RRG\_addCond
  - Define attributes of “condition” (binary variable)

# RRG Programming blocks (cont.)

- RRG\_generate
  - Fires-up report generating step
- RRG\_codeAfter
  - Lets programmers do some massaging of RCD (if needed)
- RRG\_finalize
  - Submits generated program for execution

# RRG Capabilities

- Basic summary statistics for continuous variables
  - whatever PROC MEANS offers, plus common combinations (“Mean (SD)”, “Min, Max”, geometric mean)
- Basic summary statistics for categorical variables
  - counts and percents, and combination of the two
  - control over denominator
  - control on calculation of “total”
  - pre-specified list of values
- Built-in most common statistical models
  - ANOVA, Chi-square, CMH, Fisher Exact, Odds Ratio, CI for binomial proportion and difference between binomial proportions
- User can write their own plugin macros to calculate additional statistics



# RRG Capabilities (cont)

- Flexibility of report layout
  - via RRG parameters
- Flexibility of report content
  - via RRG parameters and custom plugins
- Flexibility of report format
  - via configuration file



Configuration File

# Programming with RRG

- Clarity of what program is doing
- Programming syntax maps directly to Report Requirements
- Ease of modifications
- Relief from tedious tasks
- Less error prone programming
- Generated code: consistent, self-documented
- Generated RCD: standard for validation
- Allows for data independent programming

# RRG Usage

- Full advantage: RRG + SASSHIATO to generate format-rich report
- Partial advantage: RRG without SASSHIATO
  - Use RCD for validation
  - Use built-in proc report to generate simple report (currently for listings only, subject to some limitations)
  - Write your own proc-report using RCD

# SASSHIATO

- Fully automates output-generating step
- Auto-calculation of column widths
- Auto-calculation of page breaks
- Relevant information (e.g. SOC) repeated on top of every page
- Words do not break in the middle
- Indentation maintained when text wraps to next line
- Support for standard fonts (Times New Roman, Helvetica, Courier)
- Flexibility in placement of headers/footers
- Support for special symbols and watermarks
- Choice of RTF or PDF output format (or both)
- Define your own margins and title/footnote “schema”

# Additional Functionality

Automatically (if requested) generates \*.txt file for validation purpose;  
defines standard structure of validation txt file for validators to follow

```
1 -4
2 Albumin g/L
3 n 1 1 0
4 Mean (SD) 47.0 (.) 46.0 (.)
5 Median 47.0 46.0
6 Min : Max 47 : 47 46 : 46
7 AlkalinePhosphatase IU/L
8 n 1 1 0
9 Mean (SD) 64.0 (.) 68.0 (.)
0 Median 64.0 68.0
1 Min : Max 64 : 64 68 : 68
2 ALT(SGPT);ALAT IU/L
3 n 2 1 0
4 Mean (SD) 35.5 (3.54) 21.0 (.)
5 Median 35.5 21.0
6 Min : Max 33 : 38 21 : 21
7 -2
8 Albumin g/L
9 n 58 51 43
0 Mean (SD) 43.2 (2.60) 43.5 (2.63) 43.1 (2.63)
1 Median 43.0 44.0 43.0
2 Min : Max 39 : 49 38 : 48 37 : 49
3 AlkalinePhosphatase IU/L
4 n 58 51 43
5 Mean (SD) 76.1 (15.81) 75.8 (18.21) 73.6 (21.09)
```

# Additional Functionality

Automatically (if requested) creates meta-data dataset to facilitate creation of DEFINE file for TLGs

metadata					
rrgun	datasets	variables	popwhere	tabwhere	
train_ex1_01	TESTDATA.ADSL; testdata.testlb	ADSL.SEXN; ADSL.SUBJID; ADSL.TRTP; ADSL.TRTPN; ADSL.USUBJID; TESTLB.ADY; TESTLB.AVAL; T...	(saffl=Y)		

tabwhere	invarwhere	title1	title2	title3	title4	title5	title6
		Continuous Data...	Safety Population				

title5	title6	o_where	fname	macrosused
			train_ex1_01	

# Additional Functionality

## Color – Coded Comparison of Outputs

Table 14.1.6.1 Demographic and Baseline Characteristics Full Analysis Set	
	Number of Subjects (N=59)
Age (Years)	
N	59
Mean (SD)	54.3 (15.86)
	54.0 (15.99)
Median	52.8
	52.0
Minimum, Maximum	22, 81
	21, 81
Age Categories [N(%)] (a)	
< 65	42 (71.2)
>=65 - <75	10 (16.9)
>=75	7 (11.9)
Gender [N(%)]	
Male	27 (45.8)
Female	32 (54.2)
Ethnicity [N(%)]	
Hispanic or Latino	11 (18.6)
Non-Hispanic and Latino	26 (44.1)
Not Collected	22 (37.3)
<p>(a) Age=integer (enrollment date - date of birth + 1)/365.25</p> <p>(b) Baseline data is from central laboratory data.</p> <p>Note: For race, a subject may choose more than one category for race. Subjects who indicated more than one race category are included in each category indicated.</p> <p>Note 1: For race, a subject may choose more than one category for race. Subjects who indicated more than one race category are included in each category indicated.</p> <p>Note 2: Ethnicity is not collected for sites outside the US.</p>	

# RRG for Listings



# RRG Blocks for Listings

- Rrg\_initList
  - link report to TFLs entry
- Rrg\_defList
  - Define general report properties (input dataset, sort order)
- Rrg\_defCol
  - Defines column attributes

# Listing Example

RRG Sample Reports

www.btcisp.com/rrg

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## Example 25 Adverse Events

Investigator: Name 1  
Treatment group: Miracle Drug

Subject No./ Age,Gender,Race	System Organ Class Preferred Term	Start/Stop Date (Study Days)	Severity Relation to Study Drug	Action Taken Outcome Serious
1002/80, M, W	BLOOD AND LYMPHATIC SYSTEM DISORDERS EOSINOPHILIA	2008-07-15(50)/ (.)	Moderate Not Related	No Action Taken Unknown/Lost to Follow-Up No
1004/82, F, B	NERVOUS SYSTEM DISORDERS SOMNOLENCE	2008-07-31(44)/ 2008-08-26(70)	Mild Possibly Related	No Action Taken Resolved No
	GENERAL DISORDERS AND ADMINISTRATION SITE CONDITIONS OEDEMA PERIPHERAL	2008-08-10(54)/ 2008-10-07(112)	Moderate Not Related	No Action Taken Resolved No
1006/80, F, W	VASCULAR DISORDERS HOT FLUSH	2008-08-11(20)/ 2008-08-13(22)	Mild Not Related	No Action Taken Resolved No
	NERVOUS SYSTEM DISORDERS SOMNOLENCE	2008-08-24(33)/ (.)	Moderate Possibly Related	No Action Taken Not Resolved No

An example of Listings

F:\RRGPrivate\regression\_test\generated\progs\rrg\_gen\ex25.sas (iza SAS Win 9.1.3)

# RRG Listing Program

```
proc sort data=testdata.adae (where=(aedecone "")) out=adae;
by usubjid;
run;

data adae;
set adae;
by usubjid ;
length aeser_ sid $ 200 socpt dates fir raud $ 2000;

if aeacn='No Action Taken' then aeacn = 'No Action Taken';
sid = cats(subjid," ", asr);
socpt = cats(aebodsys,"/t1 ",aedecone);
dates = cats(aestdtc,"(", aestdy,")","/",aeendtc,"(", aeendy,")");
fir = cats(aesev,"/t1 ",aerel);
aeser_ =put(aeser, yn.);
raud = cats(aeacn,"/t1",aeout,"/t1 ", aeser_);
run;
```

```
%rrg_initlist(uri=ex25);

%rrg_deflist(
Dataset=adae,
orderby=invnam trta usubjid sid aestdy aebodsys aedecone socpt);

%rrg_defcol(name=invnam,decode=namedec, label="Investigator: ",page=Y);

%rrg_defcol(name=trta, label="Treatment group: ", page=Y);

%rrg_defcol(name=sid, label="Subject No.//Age,Gender,Race", group=Y, id=Y);
%rrg_defcol(name=socpt, label="System Organ Class/t1 Preferred Term", skipline=Y);
%rrg_defcol(name=dates, label="Start/Stop Date// (Study Days)");
%rrg_defcol(name=fir, label="Severity/t1 Relation to Study Drug");
%rrg_defcol(name=raud, label="Action Taken/t1 Outcome/t1 Serious");

%rrg_genlist;
```

# RRG Program Dissected

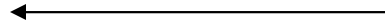
```
%rrg_init(uri=T15_3_1_5);  
  
%rrg_codebefore(  
data adae;  
set sasdata.adae;  
anyaec='Total Subjects With Any TEAEs';  
run;  
);  
  
%rrg_defreport(  
  Dataset=adae,  
  popwhere=safety='Y',  
  tabwhere=anyae='Y' and AETEFLL='Y' ,  
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,  
  reptype=events,  
  statsincolumn=y  
);  
  
%rrg_addtrt(name=trtan, decode=trta, autospan=N,  
  label=%str(Number of Subjects (%)), sortcolumn=3);  
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);  
  
%rrg_addgroup(name=anyaec );  
%rrg_addgroup(name=aebodsys );  
%rrg_addgroup(name=aedecod, freqsort=y );  
  
%rrg_addcatvar(name=aerelan, countwhat=max,  
  codelist=%str(0='Not Related', .='Missing', 1='Related'),  
  pctfmt=pctfb., totaltext=Overall, totalpos=first,  
  sortcolumn=_TOTAL_);  
  
%rrg_generate;  
%rrg_finalize;
```

Link to entry in optional TFLs file : determine titles/footnotes and output file name. If TFL file does not exist, just determines the output file name (titles/footnotes can be specified in rrg\_defreport)

# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);
```

```
%rrg_codebefore(  
data adae;  
set sasdata.adae;  
anyaec='Total Subjects With Any TEAEs';  
run;  
);
```



Prepare input data set

```
%rrg_defreport(  
  Dataset=adae,  
  popwhere=safety='Y',  
  tabwhere=anyae='Y' and AETEFLL='Y' ,  
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,  
  reptype=events,  
  statsincolumn=y  
);  
  
%rrg_addtrt(name=trtan, decode=trta, autospan=N,  
  label=%str(Number of Subjects (%)), sortcolumn=3);  
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);  
  
%rrg_addgroup(name=anyaec );  
%rrg_addgroup(name=aebodsys );  
%rrg_addgroup(name=aedecod, freqsort=y );  
  
%rrg_addcatvar(name=aerelan, countwhat=max,  
  codelist=%str(0='Not Related', .='Missing', 1='Related'),  
  pctfmt=pctfb., totaltext=Overall, totalpos=first,  
  sortcolumn=_TOTAL_);  
  
%rrg_generate;  
%rrg_finalize;
```

# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);
```

```
%rrg_codebefore(  
data adae;  
set sasdata.adae;  
anyaec='Total Subjects With Any TEAEs';  
run;  
);
```

```
%rrg_defreport(  
  Dataset=adae,  
  popwhere=safety='Y',  
  tabwhere=anyae='Y' and AETEFL='Y' ,  
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,  
  reptype=events,  
  statsincolumn=y  
);  
  
%rrg_addtrt(name=trtan, decode=trta, autospan=N,  
  label=%str(Number of Subjects (%)), sortcolumn=3);  
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);  
  
%rrg_addgroup(name=anyaec );  
%rrg_addgroup(name=aebodsys );  
%rrg_addgroup(name=aedecod, freqsort=y );  
  
%rrg_addcatvar(name=aerelan, countwhat=max,  
  codelist=%str(0='Not Related', .='Missing', 1='Related'),  
  pctfmt=pctfb., totaltext=Overall, totalpos=first,  
  sortcolumn=_TOTAL_);  
  
%rrg_generate;  
%rrg_finalize;
```



Specify Input data set

# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);

%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  reptime=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta, autospan=N,
  label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max,
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```



Specify population

# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);

%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  reptype=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta, autospan=N,
  label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max,
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```

Specify additional  
sub-setting of data



# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);

%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  reptime=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta, autospan=N,
  label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max,
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```



Column header

# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);

%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  reptime=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta, autospan=N,
  label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max,
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```

Event-type report

# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);

%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  retype=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta, autospan=N,
  label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max,
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```

here Events to Study Drug by System Organ Class and Preferred Term  
Adverse Event Analysis Set

Relationship	Number of Subjects (%)	
	Treatment 1 (N=52)	Treatment 2 (N=49)
Overall	44 (84.6)	35 (71.4)
Not Related	41 (78.8)	34 (69.4)
Related	3 (5.8)	1 (2.0)
Overall	3 (5.8)	0

Values of analysis variables  
placed in separate column

# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);


%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  reptype=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta,
label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max,
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```



Treatment variable  
(numeric, for sorting)  
and its display variable

# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);

%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFLL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  reptype=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta, autospan=N,
  label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max,
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```

Text to show above  
treatment columns

# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);

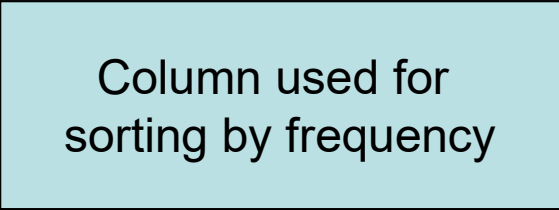
%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  reptype=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta, autospan=N,
  label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max,
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```



Column used for  
sorting by frequency

# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);

%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  reptype=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta, autospan=N,
  label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max,
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```

Create “Total”  
treatment column

# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);

%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  reptype=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta, autospan=N,
  label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max,
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```



Grouping variables



# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);

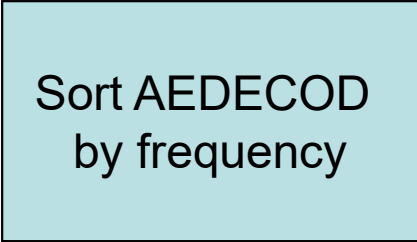
%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  reptype=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta, autospan=N,
  label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max,
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```



Sort AEDECOD  
by frequency

# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);

%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  reptype=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta, autospan=N,
  label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max,
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```

“analysis” variable

# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);

%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  reptype=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta, autospan=N,
  label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max, ←
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```

For each subject,  
count only maximum  
value of AERELAN

# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);

%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  reptype=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta, autospan=N,
  label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max,
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```

Show this list even  
if there is no data  
for some values.\*  
Also defines order  
to determine “maximum”

\* Missing is shown only if there is data

# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);

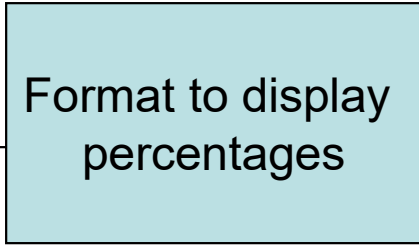
%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  reptype=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta, autospan=N,
  label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max,
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```



Format to display  
percentages

# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);

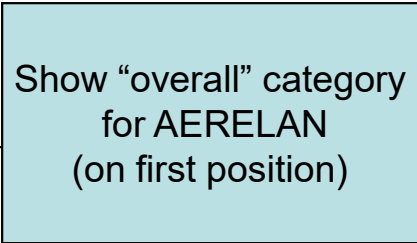
%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  reptype=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta, autospan=N,
  label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max,
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```



Show “overall” category  
for AERELAN  
(on first position)

# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);

%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  reptype=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta, autospan=N,
  label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max,
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```

Sort AEDECOD  
by frequency  
in “Total” treatment  
and “Overall”  
relationship

# RRG Program Dissected

```
%rrg_init(uri=T15_3_1_5);

%rrg_codebefore(
data adae;
set sasdata.adae;
anyaec='Total Subjects With Any TEAEs';
run;
);

%rrg_defreport(
  Dataset=adae,
  popwhere=safety='Y',
  tabwhere=anyae='Y' and AETEFLL='Y' ,
  Colhead1=System Organ Class/t1 Preferred Term!Relationship,
  reptype=events,
  statsincolumn=y
);

%rrg_addtrt(name=trtan, decode=trta, autospan=N,
  label=%str(Number of Subjects (%)), sortcolumn=3);
%rrg_maketrt(name=trtan, newdecode='Total', values=1 2, newvalue=3);

%rrg_addgroup(name=anyaec );
%rrg_addgroup(name=aebodsys );
%rrg_addgroup(name=aedecod, freqsort=y );

%rrg_addcatvar(name=aerelan, countwhat=max,
  codelist=%str(0='Not Related', .='Missing', 1='Related'),
  pctfmt=pctfb., totaltext=Overall, totalpos=first,
  sortcolumn=_TOTAL_);

%rrg_generate;
%rrg_finalize;
```

Generate program  
and  
submit it for execution



# Ockham's Razor Principle

RRG does not try to do “everything”

Small display adjustments are done via %RRG\_codeAfter

Desired Layout

System Organ Class Preferred Term	Relationship
Total Subjects With Any TEAEs	Overall Not Related Related
CARDIAC DISORDERS	Overall Not Related Related
CARDIAC FAILURE CONGESTIVE	Overall Not Related Related
ATRIAL FIBRILLATION	Overall Not Related Related

RRG Table

System Organ Class Preferred Term	Relationship
Total Subjects With Any TEAEs	Overall Not Related Related
CARDIAC DISORDERS	Overall Not Related Related
CARDIAC FAILURE CONGESTIVE	Overall Not Related Related
ATRIAL FIBRILLATION	Overall Not Related Related

# RRG\_codeafter

```
%rrg_generate;

%rrg_codeafter(
data t_aerel; set t_aerel;
if __datatype='TBODY' then do;
  if __col_1='Overall' and __col_0 = '' then do;
    if aedecod ne '' then do;
      __col_0 = aedecod;
      __indentlev=1;
    end;
  else if aebodsys ne '' then do;
    __col_0 = aebodsys;
    __indentlev=0;
  end;
  else do;
    __col_0 = 'Total Subjects With Any TEAEs';
    __indentlev=0;
  end;
end;
if __col_1 ='' then delete;
end;
);

%rrg_finalize;
```

# Table after RRG\_codeAfter

System Organ Class Preferred Term	Relationship	Number of Subjects (%)		
		Treatment 1 (N=52)	Treatment 2 (N=49)	Total (N=101)
Total Subjects With Any TEAEs	Overall	44 (84.6)	35 (71.4)	79 (78.2)
	Not Related	41 (78.8)	34 (69.4)	75 (74.3)
	Related	3 (5.8)	1 (2.0)	4 (4.0)
BLOOD AND LYMPHATIC SYSTEM DISORDERS	Overall	3 (5.8)	0	3 (3.0)
	Not Related	2 (3.8)	0	2 (2.0)
	Related	1 (1.9)	0	1 (1.0)

# Examples of Fancy Output

Example 06  
Summary of Response to Treatment  
Per-Protocol Population

Response Category	Placebo (N=50)	Comparator (N=51)	Miracle Drug (N=51)	Overall P-value <sup>a</sup>
Responder, n (%)	38 (76.0%)	32 (64.0%)	35 (68.6%)	0.4236
Non-Responder, n (%)	12 (24.0%)	18 (36.0%)	16 (31.4%)	
Total non-missing, n (%)	50 (100%)	50 (100%)	51 (100%)	
Parwise Comparisons <sup>b</sup>				
Odds Ratio vs Placebo		0.56	0.69	
95% CI for Odds Ratio vs Placebo		(0.24, 1.34)	(0.29, 1.66)	
P-value <sup>b</sup> vs Placebo		0.1904	0.4079	

<sup>a</sup> from CMH Test for General Association

<sup>b</sup> from Chi-Square Test

Illustrates adding statistics for binomial proportion

F:/RRGPrivate/regression\_test/generated/progs/rrg\_gen/ex06.sas (iza SAS Win 9.1.3)

Example 07  
Descriptive Summary of Laboratory Parameters  
Safety Population

Laboratory test Visit Treatment	Observed			Change from Baseline					
	n	Mean	SD	n	Mean	SD	Median	Min	Max
Albumin g/L									
Visit 1									
Placebo	103	42.87	2.845	58	-0.69	1.739	-0.50	-4.0	2.0
Comparator	92	43.10	2.746	51	-0.76	1.914	-1.00	-5.0	3.0
Miracle Drug	79	42.70	2.638	43	-1.05	1.939	-1.00	-5.0	3.0
Visit 2									
Placebo	284	41.57	2.742	284	-1.67	2.411	-2.00	-8.0	5.0
Comparator	279	42.16	2.884	279	-1.42	2.468	-1.00	-8.0	6.0
Miracle Drug	221	41.41	3.419	221	-1.67	2.631	-2.00	-8.0	6.0
Visit 99									
Placebo	3	42.67	1.528	3	-0.33	1.155	-1.00	-1.0	1.0
Comparator	1	45.00		0					
Miracle Drug	3	43.67	2.082	3	-1.00	2.646	-2.00	-3.0	2.0
AlkalinePhosphatase IU/L									
Visit 1									
Placebo	110	75.836	15.2228	58	-0.914	6.2640	0.000	-16.00	17.00
Comparator	99	74.343	17.1489	51	-1.157	6.6524	-1.000	-16.00	12.00
Miracle Drug	81	73.457	20.6471	43	-1.442	7.6448	0.000	-22.00	14.00
Visit 2									
Placebo	507	80.288	17.4757	507	3.750	10.4053	3.000	-21.00	75.00
Comparator	438	79.518	17.5921	438	3.114	9.2130	3.000	-24.00	40.00
Miracle Drug	344	76.578	20.1744	344	2.064	10.1451	2.000	-31.00	59.00

Illustrates placing two variables - observed and change from baseline - side by side with statistics in columns and treatment in rows.

Also illustrates that different decimal precision can be requested for different grouping variables (labs)

F:\RRGPrivate/regression\_test/generated/progs/rrg\_gen/ex07.sas (iza SAS Win 9.1.3)