SESUG 2022 Paper 230

Using SAS Macro and ODS Output to efficiently examine the descriptive and analytic statistics in epidemiology studies Yue Pan, University of Miami Miller School of Medicine

ABSTRACT

The key feature of descriptive and analytic epidemiology is a comparison group, i.e. the exposure, and how it is associated with the study interest, i.e. the outcome. Researchers and investigators are required to present the descriptive and analytic statistics of both exposure and outcomes and test their relationship to describe their study sample. However, if there are many exposures and outcomes to examine, the syntax usually become repetitive and hard to navigate and identify useful results. This paper will present how to use SAS macro and ODS output to efficiently examine and generate descriptive and analytic statistics for epidemiology studies.

This presentation is aimed at beginner to intermediate SAS programmers and healthcare analysts who already have a basic understanding of SAS Macro and ODS Output and are looking to efficiently examine their data.

INTRODUCTION

There are three main types of Epidemiology studies (cohort studies, case-control studies, and cross-sectional studies). All required you to compare the relationship between at least two variables, i.e. primary outcomes, and primary exposures. Others also include multiple secondary outcomes and secondary exposures. In addition, it is commonly required to describe the study samples using descriptive statistics (i.e. mean or median, standard deviation, interquartile range, number, prevalence or proportion, etc) and basic statistical tests (Chi-square test, t-test, Wilcoxon-Mann-Whitney test, etc) for these variables.

I am using hypothetical data as an example to illustrate the steps to examine the descriptive and analytic statistics in epidemiology studies.

STEP 1. GENERATE TABLES FOR DESCRIPTIVE STATISTICS

We first generate the tables for descriptive statistics. We will use PROC Tabulate to generate the numbers and proportions for categorical variables while using mean or median, standard deviation, and interquartile range for continuous variables, depending on their normality test. This will set up the main structure of the descriptive table. In this example, we are interested in stratifying the sample statistics by the primary exposure: druguse_tri variable. We added MISSING to show the missingness. We also requested N and COLPCTN to show the numbers and proportions by druguse_tri. We added all after druguse_tri to also show the descriptive statistics for the overall sample.

The following code is for the descriptive statistics for categorical variables, overall, and stratified by druguse_tri:

PROC TABULATE DATA=PR_V2 MISSING ;
CLASS
DRUGUSE_TRI
CONTINOFCARE2

GENDER EDU INCOME INSURANCE EVERJAIL HOMELESS6M US1 ; TABLE (CONTINOFCARE2 GENDER EDU INCOME INSURANCE EVERJAIL HOMELESS6M US1), (DRUGUSE_TRI ALL)*(N COLPCTN);

RUN;

The following table is the output for descriptive statistics for categorical variables, overall, and stratified by druguse_tri from SAS:

| | | | dr | uguse_tri | | | All | |
|---|----|---------|-----|-----------|-----|---------|-----|---------|
| | | 0 | | 1 | | 2 | 1 | |
| | N | ColPctN | N | ColPctN | N | ColPctN | N | ColPctN |
| continofcare2 | | | | | | | | |
| 1 | 6 | 8.70 | 24 | 15.69 | 49 | 26.20 | 79 | 19.32 |
| 2 | 6 | 8.70 | 24 | 15.69 | 47 | 25.13 | 77 | 18.83 |
| 3 | 11 | 15.94 | 16 | 10.46 | 19 | 10.16 | 46 | 11.25 |
| 4 | 46 | 66.67 | 89 | 58.17 | 72 | 38.50 | 207 | 50.61 |
| sex assigned at birth | | | | | | | | |
| 1 | 40 | 57.97 | 112 | 73.20 | 163 | 87.17 | 315 | 77.02 |
| 2 | 29 | 42.03 | 41 | 26.80 | 24 | 12.83 | 94 | 22.98 |
| EDU | | | | | | | | |
| 0 | 23 | 33.33 | 64 | 41.83 | 59 | 31.55 | 146 | 35.70 |
| 1 | 46 | 66.67 | 89 | 58.17 | 128 | 68.45 | 263 | 64.30 |
| INCOME | | | | | | | | |
| 0 | 55 | 79.71 | 141 | 92.16 | 164 | 87.70 | 360 | 88.02 |
| 1 | 14 | 20.29 | 12 | 7.84 | 23 | 12.30 | 49 | 11.98 |
| Are you covered by health insurance or some other kind of health care plan? | | | | | | | | |
| 0 | 3 | 4.35 | 23 | 15.03 | 51 | 27.27 | 77 | 18.83 |
| 1 | 66 | 95.65 | 130 | 84.97 | 136 | 72.73 | 332 | 81.17 |
| ever jail or prison | | | | | | | | |
| 0 | 38 | 55.07 | 27 | 17.65 | 20 | 10.70 | 85 | 20.78 |
| 1 | 31 | 44.93 | 126 | 82.35 | 167 | 89.30 | 324 | 79.22 |
| Currently homeless | | | | | | | | |
| | | | 1 | 0.65 | | | 1 | 0.24 |
| 0 | 54 | 78.26 | 105 | 68.63 | 78 | 41.71 | 237 | 57.95 |
| 1 | 15 | 21.74 | 47 | 30.72 | 109 | 58.29 | 171 | 41.81 |
| Have you ever lived in the US? | | | | | | | | |
| | 4 | 5.80 | 1 | 0.65 | 2 | 1.07 | 7 | 1.71 |
| 0 | 36 | 52.17 | 67 | 43.79 | 88 | 47.06 | 191 | 46.70 |
| 1 | 29 | 42.03 | 85 | 55.56 | 97 | 51.87 | 211 | 51.59 |

We then use PROC Means to generate the results for the continuous variables, stratified by the same variable druguse_tri, and overall respectively. Particularly, we have requested N MEAN STD MIN MAX MEDIAN QRANGE Q1 Q3 as the results output.

The following code is for the descriptive statistics for continuous variables, overall and stratified by druguse_tri:

```
PROC MEANS DATA=PR_V2 N MEAN STD MIN MAX MEDIAN QRANGE Q1 Q3;
/*CLASS DRUGUSE_TRI;*/
VAR
AGE
VL
CD4
;
PROC MEANS DATA=PR_V2 N MEAN STD MIN MAX MEDIAN QRANGE Q1 Q3 ;
CLASS DRUGUSE_TRI;
VAR
AGE
VL
CD4
;
RUN;
```

The following table is the output for descriptive statistics for continuous variables, overall, and stratified by druguse_tri from SAS:

| druguse_tri | N Obs | Variable | Label | N | Mean | Std Dev | Minimum | Maximum | Median | Quartile Range | Lower Quartile | Upper Quartile |
|-------------|-------|------------------|--------------------------------|-------------------|---------------------------------------|---------------------------------------|--|-------------------------------------|---|---------------------------------------|---|---------------------------------------|
| 0 | 69 | AGE VL cd4 | age Viral Load CD4 count | 69 68 69 | 45.7391304 11555.79 636.0869565 | 10.0581430 27721.66 393.4920486 | 22.000000 2.6600000 9.0000000 | 72.0000000 158765.00 1629.00 | 47.0000000 20.0000000 587.0000000 | 13.0000000 4172.50 560.0000000 | 39.0000000 20.0000000 335.0000000 | 52.0000000 4192.50 895.0000000 |
| 1 | 153 | AGE VL cd4 | age Viral Load CD4 count | 153 153 153 | 47.9934641 20662.47 569.1176471 | 8.3599112 136027.55 357.8642410 | 24.000000 20.000000 6.000000 | 69.0000000 1667569.00 1707.00 | 49.000000 47.000000 533.000000 | 12.0000000 8359.00 449.0000000 | 42.0000000 20.0000000 321.0000000 | 54.0000000 8379.00 770.0000000 |
| 2 | 187 | AGE VL cd4 | age Viral Load CD4 count | 187 187 187 | 45.2085561 36743.32 478.4973262 | 8.6019710 140500.66 304.0018105 | 23.0000000 20.0000000 43.0000000 | 64.0000000 1266850.00 1972.00 | 48.000000 2346.00 422.000000 | 12.0000000 27767.00 366.0000000 | 39.0000000 20.0000000 253.0000000 | 51.0000000 27787.00 619.0000000 |

| Variable | Label | N | Mean | Std Dev | Minimum | Maximum | Median | Quartile Range | Lower Quartile | Upper Quartile |
|------------------|--------------------------------|-------------------|---------------------------------------|---------------------------------------|-----------|---------|---------------------------------------|---------------------------------------|--------------------------------------|-------------------------------------|
| AGE VL cd4 | age Viral Load CD4 count | 409 408 409 | 46.3398533 26515.08 538.9828851 | 8.8489171 127108.87 345.3411175 | 2.6600000 | | 47.000000 164.500000 472.000000 | 12.0000000 14638.00 449.0000000 | 40.000000 20.000000 276.000000 | 52.000000 14658.00 725.000000 |

STEP 2. ANALYTIC STATISTICS AND UNIVARIATE ANALYSIS

The second step is to test each of the variables' relationship with the primary exposure. In our example, it is druguse_tri. The normal approach is to run a separate model for each of the variables and then gather each of the results together. The syntax usually become repetitive and hard to navigate and identify the useful results. A better way is to use SAS macro and ODS output to efficiently run the analytic statistics and output the univariate analysis results into one single file.

Continued with our previous example. Our primary exposure druguse_tri was a categorical variable. We also have Continofcare2, Gender, Edu, Income, Insurance, Everjail, Homeless6m, Us1 as categorical variables. The Chi-square goodness of fit test allows us to test whether the observed proportions for a categorical variable differ from hypothesized proportions. We then used a Chi-square test to examine the association between druguse_tri and each of the categorical variables.

In this step, we first create an empty dataset CHISQ. The purpose is to use it later to save and hold the results output from the macro. We then created a macro. For the Chi-square test, only one macro variable &VAR. is needed to loop through all the categorical variables. Noticed that we added an "output out" statement to particularly export the Chi-square test results (i.e. PCHI) to a temporary dataset: STATS. Finally, we used a data step to append the result to the CHISQ dataset. Therefore, every time the macro change to a different &VAR, STATS dataset will be overwritten to reflect the new one. While after each macro, it is appended and saved to the CHISQ dataset.

The following code is for the analytic statistics for categorical variables and druguse_tri:

```
DATA CHISQ;
RUN;
%MACRO AA(VAR);
TITLE"CHISQ FOR &VAR.";
PROC FREQ DATA=PR V2 ;
TABLES (&VAR.) * DRUGUSE TRI / CHISQ CMH NOCOL NOPERCENT ;
OUTPUT OUT=STATS PCHI;
RUN;
DATA CHISQ;
SET CHISQ STATS;
RUN;
%MEND;
%AA( CONTINOFCARE2
                      );
%AA( GENDER
                );
%AA( EDU
         );
SAA ( INCOME
                 );
%AA( INSURANCE );
%AA( EVERJAIL
               );
%AA( HOMELESS6M );
%AA( US1
          );
```

The following table is the output for the PROC Freq statement, as an example, we showed the results of CONTINOFCARE2.

The FREQ Procedure

Frequency Row Pct

| Table of continofcare2 by druguse_tri | | | | | | |
|---------------------------------------|-------------|-------------|-------------|-------|--|--|
| | druguse_tri | | | | | |
| continofcare2 | 0 | 1 | 2 | Total | | |
| 1 | 6 7.59 | 24 30.38 | 49 62.03 | 79 | | |
| 2 | 6 7.79 | 24 31.17 | 47 61.04 | 77 | | |
| 3 | 11 23.91 | 16 34.78 | 19 41.30 | 46 | | |
| 4 | 48 22.22 | 89 43.00 | 72 34.78 | 207 | | |
| Total | 69 | 153 | 187 | 409 | | |

Statistics for Table of continofcare2 by druguse_tri

| Statistic | DF | Value | Prob |
|-----------------------------|----|---------|--------|
| Chi-Square | 6 | 30.4717 | <.0001 |
| Likelihood Ratio Chi-Square | 6 | 31.6894 | <.0001 |
| Mantel-Haenszel Chi-Square | 1 | 26.5379 | <.0001 |
| Phi Coefficient | | 0.2730 | |
| Contingency Coefficient | | 0.2633 | |
| Cramer's V | | 0.1930 | |

Sample Size = 409

Summary Statistics for continofcare2 by druguse_tri

| Cochran-Mantel-Haenszel Statistics (Based on Table Scores) | | | | | | |
|--|------------------------|-------|---------|--------|--|--|
| Statistic | Alternative Hypothesis | Value | Prob | | | |
| 1 | Nonzero Correlation | 1 | 26.5379 | <.0001 | | |
| 2 | Row Mean Scores Differ | 3 | 29.1341 | <.0001 | | |
| 3 | General Association | 6 | 30.3972 | <.0001 | | |

The following table is the output for the temporary STATS dataset, which includes _PCHI_ for Chi-square test value, DF_PCHI for degrees of freedom, and P_PCHI for p-value.

| _PCHI_ | DF_PCHI | P_PCHI |
|--------------|---------|--------------|
| 30.471679272 | 6 | 0.0000319685 |

The following table is the output for the temporary CHISQ dataset

| PCHI_ | DF_PCHI | P_PCHI |
|--------------|---------|--------------|
| | | |
| 30.471679272 | 6 | 0.0000319685 |
| 26.279307411 | 2 | 1.9657166E-6 |
| 4.0756058516 | 2 | 0.1303147077 |
| 7.0195198413 | 2 | 0.0299040929 |
| 19.63549085 | 2 | 0.0000544763 |
| 61.750881408 | 2 | 3.899119E-14 |
| 39.67585468 | 2 | 2.4238047E-9 |
| 2.3340151857 | 2 | 0.3112970765 |

Similarly, we can also change the code for the continuous variables. Depending on their normality test, we choose to use parametric or non-nonparametric tests for the continuous variables.

Here, I am using a non-parametric test as an example, based on the normality test (not included in the paper) for the variables. Particularly, I am interested in reporting the Kruskal Wallis test. The Kruskal Wallis test is used when you have one independent variable with two or more levels and an ordinal dependent variable. In other words, it is the nonparametric version of ANOVA. It is also a generalized form of the Mann-Whitney test method, as it permits two or more groups.

In this step, we first create an empty dataset WIL to store the results output later. We then created a macro, for the Kruskal Wallis test, with only one macro variable &VAR. to loop through all the continuous variables. Noticed that we added an "output out" statement to particularly export the Kruskal Wallis test (i.e. WILCOXON) to a temporary dataset: STATS. Finally, we used a data step to append the result to the WIL dataset. Therefore, every time the macro change to a different &VAR, STATS dataset will be overwritten to reflect the new one, but after each step, it is appended and saved to the WIL dataset.

The following code is for the analytic statistics for continuous variables and druguse tri:

DATA WIL; RUN; **%MACRO** BB(VAR); PROC NPAR1WAY DATA=PR V2; CLASS DRUGUSE TRI; VAR &VAR.; OUTPUT OUT=STATS WILCOXON; RUN; DATA WIL; SET WIL STATS; RUN; %MEND; %**BB**(AGE); %**BB(** VL); %**BB**(CD4

);

The following table is the output for the temporary STATS dataset (results for CD4), which includes _VAR_ for the variable name, _KW_for Kruskal Wallis test value, DF_KW for degrees of freedom, and P_KW for p-value.

| ▲ _VAR_ | ⊕ _KW_ | DF_KW | P_KW |
|---------|--------------|-------|--------------|
| cd4 | 11.093015012 | 2 | 0.0039010579 |

The following table is the output for the temporary WIL dataset

| ▲ _VAR_ | ۲ | _KW_ | DF_KW | ۲ | P_KW |
|---------|------|----------|-------|------|----------|
| | | | | | |
| AGE | 9.53 | 37193481 | 2 | 0.00 | 85070532 |
| VL | 21.3 | 92371635 | 2 | 0.00 | 00226311 |
| cd4 | 11.0 | 93015012 | 2 | 0.00 | 39010579 |

STEP 3. COMBINE RESULTS FROM STEP1 AND STEP2

The last step is to combine the results from STEP1 and STEP2, by adding the analytic results to the descriptive statistics. After editing the title and labels, this usually concludes the Table 1 results in an epidemiological paper.

CONCLUSION

This paper presents how to use SAS macro and ODS output to efficiently examine the descriptive and analytic statistics of epidemiology studies. The macro and the ods output is an efficient tool to help researchers and investigators to select the analytic statistical results and create the descriptive statistics table for an epidemiology study.

RECOMMENDED READING

- https://support.sas.com/resources/papers/proceedings/proceedings/sugi29/243-29.pdf
- https://documentation.sas.com/doc/en/pgmsascdc/9.4_3.5/procstat/procstat_freq_detai ls124.htm

ACKNOWLEDGMENTS

The author would like to thank all supporters and organizers of this conference. Special thanks to Barbara Okerson, SESUG 2022 Academic Chair for her support and advice.

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