**Example 1:**

ODS html close;

ODS html;

**data** hormone;

INFILE 'c:\users\---------\desktop\Hormone.DAT';

INPUT ID **1**-**8** Bisec\_pre **10**-**17** Biph\_pre **19**-**26** Pasec\_pre **28**-**35** Paph\_pre **37**-**44** Dose **46**-**53** Bisec\_post **55**-**62** Biph\_post **64**-**71** / Pasec\_post **1**-**8** Paph\_post **10**-**17** Hormone **19**-**26**;

\*Making the number of episodes of the exposure variable (1 Hormone, 0 no Hormone);

IF Bisec\_post GT **0** THEN Bisec\_post = **1**;

**run**;

\*Creating dummy variables for hormone;

**data** dummy;

SET Hormone;

IF Hormone = **2** then Hormone2 = **1**; ELSE Hormone2 = **0**;

IF Hormone = **3** then Hormone3 = **1**; ELSE Hormone3 = **0**;

IF Hormone = **4** then Hormone4 = **1**; ELSE Hormone4 = **0**;

IF Hormone = **5** then Hormone5 = **1**; ELSE Hormone5 = **0**;

\*Each of the variables Hormone2 Hormone3 Hormone4 Hormone5 is a 0-1 variable and can serve as Exposure;

**run**;

**proc** **logistic** data = dummy descending;

\*DESCENDING secures that the highest value of Bisec\_post;

MODEL Bisec\_post = ID Bisec\_pre Biph\_pre Pasec\_pre Paph\_pre Dose Biph\_post Pasec\_post Paph\_post Hormone2 Hormone3 Hormone4 Hormone5 / LINK =Logit;

\*Link=logit requests that SAS applies the logit function;

**run**;

**Example 2:**

**data** nhanes;

set 'C:\Users\-----------\Desktop\-------------.sas7bdat';

length bmi $10. bp $10.;

\*creating new variables;

if bmxbmi => **30** then bmi = 'obese'; else bmi = 'not obese';

if smq040 = **1** then smoke = 'current';

if smq040 = **2** then smoke = 'never';

if smq040 = **3** then smoke = 'former';

if bpxsy1 => **130** or bpxdi1 => **80** then bp = 'high'; else bp = 'not high';

\*dealing with missing values;

if dmdeduc2 = **9** then dmdeduc2 = **.**;

if dmdmartl = **77** then dmdmartl = **.**;

if dmdmartl = **99** then dmdmartl = **.**;

if smq020 = **7** then smq020 = **.**;

if smq020 = **9** then smq020 = **.**;

**run**;

**proc** **contents** data = nhanes;

**run**;

\*descriptive statistics for continuous variables;

**proc** **means** data = nhanes mean std median max min nmiss;

var ridageyr indfmpir bpxpls bpxsy1 bpxdi1 lbxgh lbxtc bmxwt bmxht bmxbmi;

**run**;

**proc** **univariate** data = nhanes normal plots;

var ridageyr indfmpir bpxpls bpxsy1 bpxdi1 lbxgh lbxtc bmxwt bmxht bmxbmi;

**run**;

\*descriptive statistics for discrete/categorical variables;

**proc** **freq** data = nhanes;

tables riagendr ridreth1 dmdeduc2 dmdmartl dmdhhsiz bpacsz smq020 smq040 bmi bp;

**run**;

\*Multiple Linear Regression;

**proc** **reg** data = nhanes;

model bpxsy1 = riagendr ridageyr ridreth1 dmdeduc2 dmdmartl dmdhhsiz indfmpir bpacsz

bpxpls bpxdi1 lbxgh lbxtc bmxbmi smq020 smq040 / clb;

**run**; **quit**;

\*Model Fitting;

**proc** **reg** data = nhanes;

model bpxsy1 = riagendr ridageyr ridreth1 dmdeduc2 dmdmartl dmdhhsiz indfmpir bpacsz

bpxpls bpxdi1 lbxgh lbxtc bmxbmi smq020 smq040 / selection = stepwise sls=**0.10** sle = **0.10** MSE CP;

**run**; **quit**;

\*Logistic Regression;

**proc** **logistic** data = nhanes;

class bmi (param = ref ref = 'not obese') riagendr (param = ref ref = '1');

model bp = bmi riagendr bmi\*riagendr / risklimits;

**run**;

**Example 3:**

**Data** example;

Infile "C:\Users\----------\desktop\---------------" dlm='09'x truncover ;

Input --------------------------------------;

**run**;

**proc** **format**;

value bmib low - **18.5** = underweight

**18.5** - **24.99** = normal

**25** - **29.99** = overweight

**30** - high = obese;

**run**;

\*Removing missing BMI participants from data set;

**data** harvest\_1;

set example;

if bmib = **.** then delete;

**run**;

\*ANOVA;

**PROC** **MEANS** DATA = harvest\_1 NWAY NoPRINT;

CLASS gender bmib;

VAR dbpab;

OUTPUT OUT = MEANS MEAN=MEAN\_BP;

**RUN**;

symbol1 interpol=join

value=dot;

**PROC** **GPLOT** DATA = MEANS;

PLOT MEAN\_BP\*bmib=gender;

FORMAT bmib bmib.;

**RUN**;

**PROC** **GLM** DATA = harvest\_1;

CLASS GENDER bmib;

MODEL dbpab = Gender|bmib/SS3;

LSMEANS GENDER\*bmib/SLICE=bmib;

LSMEANS GENDER\*bmib/SLICE=GENDER;

FORMAT bmib bmib.;

**RUN**;

**QUIT**;

**PROC** **GLM** DATA = harvest\_1;

CLASS bmib gender;

MODEL dbpab = bmib|gender/SS3;

CONTRAST "Normal Females vs. Males" BMIB **0** **0** **0** **0** Gender **1** -**1**

BMIB\*Gender **1** -**1** **0** **0** **0** **0** **0** **0** / E;

CONTRAST "Obese Females vs. Males" BMIB **0** **0** **0** **0** Gender **1** -**1**

BMIB\*Gender **0** **0** **1** -**1** **0** **0** **0** **0** / E;

CONTRAST "Overweight Females vs. Males" BMIB **0** **0** **0** **0** Gender **1** -**1**

BMIB\*Gender **0** **0** **0** **0** **1** -**1** **0** **0** / E;

CONTRAST "Underweight Females vs. Males" BMIB **0** **0** **0** **0** Gender **1** -**1**

BMIB\*Gender **0** **0** **0** **0** **0** **0** **1** -**1** / E;

FORMAT bmib bmib.;

**RUN**;

**QUIT**;

\*multivariate analysis;

**proc** **glm** data=assn\_2;

class gender;

model sbpab sbpa3 sbpa5 = gender/nouni;

repeated sbpa **3** contrast(**1**) / printe summary;

**run**;

**quit**;

\*differences in successive time points by gender;

**PROC** **GLM** DATA = assn\_2;

CLASS gender;

MODEL sbpab sbpa3 sbpa5 = gender/;

REPEATED sbpa profile/summary;

**RUN**;

**QUIT**;

**Proc** **Mixed** Data = assign\_2;

Class gender time;

Model sbpa = gender|Time;

Repeated Time/Type = CS Subject = ID(gender);

**Run**;

**Quit**;

**Proc** **GLM** Data= assign\_2;

Class ID gender Time;

MODEL sbpa = gender| Time Id(gender);

RANDOM ID(gender)/Test;

Contrast 'Month 3 vs Baseline for Females/Males' gender **0** **0** Time **1** -**1** **0** gender\*Time **1** -**1** **0** **0** **0** **0**/E;

Contrast 'Year 5 vs Baseline for Females/Males' gender **0** **0** Time **1** **0** -**1** gender\*Time **1** **0** -**1** **0** **0** **0**/E;

**RUN**;

**QUIT**;