/\*Example of Coding Technique Previously Written for Master's Thesis at GSU\*/

/\*Coded by Morgan Smith on SAS 9.4 and compiled on 9/21/17\*/

/\*Data taken from Publicly Available NHIS (National Health Interview Survey) 2015 Release\*/

Libname nhis "C:\NHIS2012";

options fmtsearch=(nhis);

libname thesis "C:\Users\mfsmi\Documents\SchoolFiles\Thesis";

**Proc** **contents** data=thesis.final\_merged varnum;

**run**;

/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/

/\*Descriptives for BMI\*/

**proc** **univariate** data=thesis.final\_merged plot normal;

class age\_d;

var new\_bmi;

**run**;

**proc** **means** data=thesis.final\_merged n median q1 q3 qrange nmiss;

var new\_bmi;

where age\_d=**1**;

**run**;

**proc** **surveymeans** data=thesis.final\_merged nobs median quartiles nmiss nomcar;

STRATA STRAT\_P;

CLUSTER PSU\_P;

WEIGHT WTFA\_SA;

var new\_bmi;

where age\_d=**1**;

**RUN**;

/\*BMI by Age\*/

**proc** **corr** data= thesis.final\_merged spearman;

var new\_bmi age\_p;

where age\_d=**1**;

**run**;

/\*BMI by Meditate\*/

**proc** **means** data=thesis.final\_merged n median qrange nmiss;

class meditate;

var new\_bmi;

where age\_d=**1** and new\_bmi ne miss;

**run**;

**proc** **surveymeans** data=thesis.final\_merged median quartiles missing nobs;

DOMAIN age\_d\*meditate;

STRATA STRAT\_P;

CLUSTER PSU\_P;

WEIGHT WTFA\_SA;

var new\_bmi;

where new\_bmi ne miss;

**RUN**;

/\*BMI on Region\*/

/\*Creating Dummy Variables for Region\*/

**proc** **freq** data=thesis.dummy;

table region;

**Run**;

**Data** thesis.dummy;

set thesis.dummy;

if region ne **.** then do;

if region=**1** then NE=**1**;

else NE=**0**;

if region =**2** then MW=**1**;

else MW=**0**;

if region=**3** then S=**1**;

else S=**0**;

end;

**run**;

**proc** **print** data=thesis.dummy (obs=**100**);

var region ne mw s;

**run**;

/\*unweighted linear regression\*/

ods csv;

**proc** **reg** data=thesis.dummy;

model log\_bmi=ne mw s/clb;

where age\_d=**1**;

**run**;

ods csv close;

/\*weighted linear regression\*/

ods csv;

**proc** **surveyreg** data=thesis.dummy nomcar;

DOMAIN age\_d;

STRATA STRAT\_P;

CLUSTER PSU\_P;

WEIGHT WTFA\_SA;

model log\_bmi=ne mw s/clparm;

where age\_d=**1**;

**RUN**;

ods csv close;

/\*unadjusted gamma regression\*/

ods csv;

**proc** **genmod** data=thesis.dummy;

model log\_bmi=ne mw s/dist=gamma link=log;

where age\_d=**1**;

**run**;

ods csv close;

/\*Adjusted Weighted Linear Regression\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/

ods csv;

title"adjusted weighted linear reg no age2";

**proc** **surveyreg** data=thesis.dummy nomcar;

DOMAIN age\_d;

STRATA STRAT\_P;

CLUSTER PSU\_P;

WEIGHT WTFA\_SA;

model log\_bmi=age\_p meditate dummy\_35 dummy\_75 dummy\_100 hsged college

advanced hispanic black asian other new\_sex excellent verygood good

fair married ne mw s/clparm;

where age\_d=**1**;

**run**;

ods csv close;

/\*Adjusted (GEE) Multilevel Model\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/

ods csv;

**proc** **mixed** data=thesis.dummy;

class region;

model log\_bmi=age\_p meditate dummy\_35 dummy\_75 dummy\_100 hsged college

advanced hispanic black asian other new\_sex excellent verygood good

fair married /solution cl;

where age\_d=**1**;

random intercept/subject=region;

**run**;

ods csv close;

/\*Adjusted Gamma Regression\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/

ods csv;

**proc** **genmod** data=thesis.dummy;

model log\_bmi=age\_p meditate dummy\_35 dummy\_75 dummy\_100 hsged college

advanced hispanic black asian other new\_sex excellent verygood good

fair married ne mw s/dist=gamma link=log;

where age\_d=**1**;

**run**;

ods csv close;

/\*Adjusted Gamma Regression\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/

ods csv;

**proc** **genmod** data=thesis.dummy;

model log\_bmi=age\_p meditate dummy\_35 dummy\_75 dummy\_100 hsged college

advanced hispanic black asian other new\_sex excellent verygood good

fair married ne mw s/dist=gamma link=log;

where age\_d=**1**;

**run**;

ods csv close;

/\*adjusted multilevel gamma regression\*/

ods csv;

**proc** **genmod** data=thesis.dummy;

class region;

model log\_bmi=age\_p meditate dummy\_35 dummy\_75 dummy\_100 hsged college

advanced hispanic black asian other new\_sex excellent verygood good

fair married/dist=gamma link=log;

where age\_d=**1**;

repeated subject=region;

**run**;

ods csv close;