/\*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";

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

/\*Descriptives for High Cholesterol\*/

**proc** **freq** data=thesis.final\_merged;

table highc;

where age\_d=**1**;

**run**;

**PROC** **SURVEYFREQ** Data=THESIS.final\_merged order=data;

STRATA STRAT\_P;

CLUSTER PSU\_P;

WEIGHT WTFA\_SA;

TABLES highc;

where age\_d=**1**;

**RUN**;

/\*highc by Meditate\*/

**Proc** **freq** data=thesis.final\_merged order=data;

table meditate\*highc/ nocol;

where age\_d=**1**;

**run**;

**PROC** **SURVEYFREQ** Data=THESIS.final\_merged order=data;

STRATA STRAT\_P;

CLUSTER PSU\_P;

WEIGHT WTFA\_SA;

TABLES age\_d\*highc\*meditate/col;

where age\_d=**1**;

**RUN**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

/\*Models\*/

/\*highc by Meditate\*/

/\*unadjusted unweighted\*/

**Proc** **Logistic** data=thesis.final\_merged order=data;

CLASS MEDITATE(ref='0')/param=ref;

Model highc(event='Ever told had high cholesterol')= MEDITATE;

where age\_d=**1**;

**run**;

/\*unadjusted weighted\*/

**proc** **surveylogistic** data=thesis.age\_centered order=data nomcar;

domain age\_d;

STRATA Strat\_p;

Cluster PSU\_P;

WEIGHT wtfa\_sa;

CLASS MEDITATE(ref='0')/param=ref;

Model highc(event='Ever told had high cholesterol')= MEDITATE;

where age\_d=**1**;

**run**;

/\* unadjusted unweighted gee\*/

**proc** **genmod** data=thesis.final\_merged;

class MEDITATE(ref='0') region/param=ref;

model highc(event='Ever told had high cholesterol')=Meditate/ dist=bin link=logit scale=pearson aggregate=(meditate highc);

where age\_d=**1** and highc ne miss;

repeated subject=region ;

estimate 'Meditation' meditate **1** -**1** / exp;

**run**;

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

/\*Weighted Adjusted Logistic\*/

ods csv;

**proc** **surveylogistic** data=thesis.age\_centered order=data nomcar;

domain age\_d;

STRATA Strat\_p;

Cluster PSU\_P;

WEIGHT wtfa\_sa;

class MEDITATE(ref='0') income\_fam(ref='$0-$34,999') school\_per(ref='Less than HS')

HISCODI3 (ref='2 Non-Hispanic White') NEW\_SEX(ref='Male') HEALTH\_STAT(ref='Poor') MARRIED(ref='Not Married') Region (ref='4 West')/param=ref;

model highc(event='Ever told had high cholesterol')=age\_p meditate income\_fam school\_per hiscodi3 new\_sex health\_stat married region;

where age\_d=**1**;

**run**;

ods csv close;

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

/\* Adjusted GEE \*/

ods csv;

**proc** **genmod** data=thesis.final\_merged;

class MEDITATE(ref='0') income\_fam(ref='$0-$34,999') school\_per(ref='Less than HS')

HISCODI3 (ref='2 Non-Hispanic White') NEW\_SEX(ref='Male') HEALTH\_STAT(ref='Poor') MARRIED(ref='Not Married') region/param=ref;

model highc(event='Ever told had high cholesterol')=age\_p meditate income\_fam school\_per hiscodi3 new\_sex health\_stat married / dist=bin link=logit;

where age\_d=**1** and highc ne miss;

repeated subject=region ;

**run**;

ods csv close;