**Supplemental File.** R codes to access, engineer, and analyze data from the NHANES.

library(nhanesA)

library(sqldf)

library(dplyr)

library(survey)

options(survey.lonely.psu="adjust")

library(gtools)

library(DescTools)

library(tableone)

library(mitools)

library(mice)

#Get Relevant Tables(2005-2016)

#Demographics

DEMO\_D<-nhanes("DEMO\_D")

DEMO\_E<-nhanes("DEMO\_E")

DEMO\_F<-nhanes("DEMO\_F")

DEMO\_G<-nhanes("DEMO\_G")

DEMO\_H<-nhanes("DEMO\_H")

DEMO\_I<-nhanes("DEMO\_I")

#questionaire data-depression

DPQ\_D<-nhanes("DPQ\_D")

DPQ\_E<-nhanes("DPQ\_E")

DPQ\_F<-nhanes("DPQ\_F")

DPQ\_G<-nhanes("DPQ\_G")

DPQ\_H<-nhanes("DPQ\_H")

DPQ\_I<-nhanes("DPQ\_I")

#questionaire data-reproductive data

RHQ\_D<-nhanes("RHQ\_D")

RHQ\_E<-nhanes("RHQ\_E")

RHQ\_F<-nhanes("RHQ\_F")

RHQ\_G<-nhanes("RHQ\_G")

RHQ\_H<-nhanes("RHQ\_H")

RHQ\_I<-nhanes("RHQ\_I")

#questionaire data-smoking-cigarette use

SMQ\_D<-nhanes("SMQ\_D")

SMQ\_E<-nhanes("SMQ\_E")

SMQ\_F<-nhanes("SMQ\_F")

SMQ\_G<-nhanes("SMQ\_G")

SMQ\_H<-nhanes("SMQ\_H")

SMQ\_I<-nhanes("SMQ\_I")

#examination data-body measures

BMX\_D<-nhanes("BMX\_D")

BMX\_E<-nhanes("BMX\_E")

BMX\_F<-nhanes("BMX\_F")

BMX\_G<-nhanes("BMX\_G")

BMX\_H<-nhanes("BMX\_H")

BMX\_I<-nhanes("BMX\_I")

#questionaire data-medical condition

MCQ\_D<-nhanes("MCQ\_D")

MCQ\_E<-nhanes("MCQ\_E")

MCQ\_F<-nhanes("MCQ\_F")

MCQ\_G<-nhanes("MCQ\_G")

MCQ\_H<-nhanes("MCQ\_H")

MCQ\_I<-nhanes("MCQ\_I")

#questioniaire-diabete

DIQ\_D<-nhanes("DIQ\_D")

DIQ\_E<-nhanes("DIQ\_E")

DIQ\_F<-nhanes("DIQ\_F")

DIQ\_G<-nhanes("DIQ\_G")

DIQ\_H<-nhanes("DIQ\_H")

DIQ\_I<-nhanes("DIQ\_I")

###############

#Data cleaning#

###############

#Demographics

DEMO\_D[]<- lapply(DEMO\_D, as.numeric)

q<-'SELECT SEQN,RIAGENDR,RIDAGEYR,RIDRETH1,DMDBORN AS DMDBORN4,DMDEDUC3,DMDEDUC2,DMDMARTL,INDFMPIR,WTMEC2YR,SDMVPSU,SDMVSTRA

FROM DEMO\_D

;'

DEMO\_D<-sqldf(q)

DEMO\_E[]<- lapply(DEMO\_E, as.numeric)

q<-'SELECT SEQN,RIAGENDR,RIDAGEYR,RIDRETH1,DMDBORN2 AS DMDBORN4,DMDEDUC3,DMDEDUC2,DMDMARTL,INDFMPIR,WTMEC2YR,SDMVPSU,SDMVSTRA

FROM DEMO\_E

;'

DEMO\_E<-sqldf(q)

DEMO\_F[]<- lapply(DEMO\_F, as.numeric)

q<-'SELECT SEQN,RIAGENDR,RIDAGEYR,RIDRETH1,DMDBORN2 AS DMDBORN4,DMDEDUC3,DMDEDUC2,DMDMARTL,INDFMPIR,WTMEC2YR,SDMVPSU,SDMVSTRA

FROM DEMO\_F

;'

DEMO\_F<-sqldf(q)

DEMO\_G[]<- lapply(DEMO\_G, as.numeric)

q<-'SELECT SEQN,RIAGENDR,RIDAGEYR,RIDRETH1,DMDBORN4,DMDEDUC3,DMDEDUC2,DMDMARTL,INDFMPIR,WTMEC2YR,SDMVPSU,SDMVSTRA

FROM DEMO\_G

;'

DEMO\_G<-sqldf(q)

DEMO\_H[]<- lapply(DEMO\_H, as.numeric)

q<-'SELECT SEQN,RIAGENDR,RIDAGEYR,RIDRETH1,DMDBORN4,DMDEDUC3,DMDEDUC2,DMDMARTL,INDFMPIR,WTMEC2YR,SDMVPSU,SDMVSTRA

FROM DEMO\_H

;'

DEMO\_H<-sqldf(q)

DEMO\_I[]<- lapply(DEMO\_I, as.numeric)

q<-'SELECT SEQN,RIAGENDR,RIDAGEYR,RIDRETH1,DMDBORN4,DMDEDUC3,DMDEDUC2,DMDMARTL,INDFMPIR,WTMEC2YR,SDMVPSU,SDMVSTRA

FROM DEMO\_I

;'

DEMO\_I<-sqldf(q)

demo<-rbind(DEMO\_D,DEMO\_E,DEMO\_F,DEMO\_G,DEMO\_H,DEMO\_I)

#depression-questionaire

DPQ\_D[]<- lapply(DPQ\_D, as.numeric)

q<-'SELECT SEQN,DPQ010,DPQ020,DPQ030,DPQ040,DPQ050,DPQ060,DPQ070,DPQ080,DPQ090,DPQ100

FROM DPQ\_D

;'

DPQ\_D<-sqldf(q)

DPQ\_E[]<- lapply(DPQ\_E, as.numeric)

q<-'SELECT SEQN,DPQ010,DPQ020,DPQ030,DPQ040,DPQ050,DPQ060,DPQ070,DPQ080,DPQ090,DPQ100

FROM DPQ\_E

;'

DPQ\_E<-sqldf(q)

DPQ\_F[]<- lapply(DPQ\_F, as.numeric)

q<-'SELECT SEQN,DPQ010,DPQ020,DPQ030,DPQ040,DPQ050,DPQ060,DPQ070,DPQ080,DPQ090,DPQ100

FROM DPQ\_F

;'

DPQ\_F<-sqldf(q)

DPQ\_G[]<- lapply(DPQ\_G, as.numeric)

q<-'SELECT SEQN,DPQ010,DPQ020,DPQ030,DPQ040,DPQ050,DPQ060,DPQ070,DPQ080,DPQ090,DPQ100

FROM DPQ\_G

;'

DPQ\_G<-sqldf(q)

DPQ\_H[]<- lapply(DPQ\_H, as.numeric)

q<-'SELECT SEQN,DPQ010,DPQ020,DPQ030,DPQ040,DPQ050,DPQ060,DPQ070,DPQ080,DPQ090,DPQ100

FROM DPQ\_H

;'

DPQ\_H<-sqldf(q)

DPQ\_I[]<- lapply(DPQ\_I, as.numeric)

q<-'SELECT SEQN,DPQ010,DPQ020,DPQ030,DPQ040,DPQ050,DPQ060,DPQ070,DPQ080,DPQ090,DPQ100

FROM DPQ\_I

;'

DPQ\_I<-sqldf(q)

dpq<-rbind(DPQ\_D,DPQ\_E,DPQ\_F,DPQ\_G,DPQ\_H,DPQ\_I)

dpq$dpqflag<-1 #dpq set up new var dpqflag

#questionaire data-reproductive data

RHQ\_D[]<- lapply(RHQ\_D, as.numeric)

q<-'SELECT SEQN,RHQ010, RHQ031

FROM RHQ\_D

;'

RHQ\_D<-sqldf(q)

RHQ\_E[]<- lapply(RHQ\_E, as.numeric)

q<-'SELECT SEQN,RHQ010, RHQ031

FROM RHQ\_E

;'

RHQ\_E<-sqldf(q)

RHQ\_F[]<- lapply(RHQ\_F, as.numeric)

q<-'SELECT SEQN,RHQ010, RHQ031

FROM RHQ\_F

;'

RHQ\_F<-sqldf(q)

RHQ\_G[]<- lapply(RHQ\_G, as.numeric)

q<-'SELECT SEQN,RHQ010, RHQ031

FROM RHQ\_G

;'

RHQ\_G<-sqldf(q)

RHQ\_H[]<- lapply(RHQ\_H, as.numeric)

q<-'SELECT SEQN,RHQ010, RHQ031

FROM RHQ\_H

;'

RHQ\_H<-sqldf(q)

RHQ\_I[]<- lapply(RHQ\_I, as.numeric)

q<-'SELECT SEQN,RHQ010, RHQ031

FROM RHQ\_I

;'

RHQ\_I<-sqldf(q)

rhq<-rbind(RHQ\_D,RHQ\_E,RHQ\_F,RHQ\_G,RHQ\_H,RHQ\_I)

rhq$rhqflag<-1 #rhq set up new var rhqflag

#questionaire data-smoking-cigarette use

SMQ\_D[]<- lapply(SMQ\_D, as.numeric)

q<-'SELECT SEQN,SMQ020,SMQ040

FROM SMQ\_D

;'

SMQ\_D<-sqldf(q)

SMQ\_E[]<- lapply(SMQ\_E, as.numeric)

q<-'SELECT SEQN,SMQ020,SMQ040

FROM SMQ\_E

;'

SMQ\_E<-sqldf(q)

SMQ\_F[]<- lapply(SMQ\_F, as.numeric)

q<-'SELECT SEQN,SMQ020,SMQ040

FROM SMQ\_F

;'

SMQ\_F<-sqldf(q)

SMQ\_G[]<- lapply(SMQ\_G, as.numeric)

q<-'SELECT SEQN,SMQ020,SMQ040

FROM SMQ\_G

;'

SMQ\_G<-sqldf(q)

SMQ\_H[]<- lapply(SMQ\_H, as.numeric)

q<-'SELECT SEQN,SMQ020,SMQ040

FROM SMQ\_H

;'

SMQ\_H<-sqldf(q)

SMQ\_I[]<- lapply(SMQ\_I, as.numeric)

q<-'SELECT SEQN,SMQ020,SMQ040

FROM SMQ\_I

;'

SMQ\_I<-sqldf(q)

smq<-rbind(SMQ\_D,SMQ\_E,SMQ\_F,SMQ\_G,SMQ\_H,SMQ\_I)

#examination data-body measures

BMX\_D[]<- lapply(BMX\_D, as.numeric)

q<-'SELECT SEQN,BMXBMI

FROM BMX\_D

;'

BMX\_D<-sqldf(q)

BMX\_E[]<- lapply(BMX\_E, as.numeric)

q<-'SELECT SEQN,BMXBMI

FROM BMX\_E

;'

BMX\_E<-sqldf(q)

BMX\_F[]<- lapply(BMX\_F, as.numeric)

q<-'SELECT SEQN,BMXBMI

FROM BMX\_F

;'

BMX\_F<-sqldf(q)

BMX\_G[]<- lapply(BMX\_G, as.numeric)

q<-'SELECT SEQN,BMXBMI

FROM BMX\_G

;'

BMX\_G<-sqldf(q)

BMX\_H[]<- lapply(BMX\_H, as.numeric)

q<-'SELECT SEQN,BMXBMI

FROM BMX\_H

;'

BMX\_H<-sqldf(q)

BMX\_I[]<- lapply(BMX\_I, as.numeric)

q<-'SELECT SEQN,BMXBMI

FROM BMX\_I

;'

BMX\_I<-sqldf(q)

bmx<-rbind(BMX\_D,BMX\_E,BMX\_F,BMX\_G,BMX\_H,BMX\_I)

bmx$bmxflag<-1 #bmx set up new var bmxflag

#questionaire data-medical condition

MCQ\_D[]<- lapply(MCQ\_D, as.numeric)

q<-'SELECT SEQN,MCQ160A,MCQ160B,MCQ160C,MCQ160D,MCQ160E,MCQ160F,MCQ160M,MCQ220,MCQ230A,MCQ230B,MCQ230C,MCQ230D

FROM MCQ\_D

;'

MCQ\_D<-sqldf(q)

MCQ\_E[]<- lapply(MCQ\_E, as.numeric)

q<-'SELECT SEQN,MCQ160a,MCQ160b,MCQ160c,MCQ160d,MCQ160e,MCQ160f,MCQ160m,MCQ220,MCQ230a,MCQ230b,MCQ230c,MCQ230d

FROM MCQ\_E

;'

MCQ\_E<-sqldf(q)

MCQ\_F[]<- lapply(MCQ\_F, as.numeric)

q<-'SELECT SEQN,MCQ160a,MCQ160b,MCQ160c,MCQ160d,MCQ160e,MCQ160f,MCQ160m,MCQ220,MCQ230a,MCQ230b,MCQ230c,MCQ230d

FROM MCQ\_F

;'

MCQ\_F<-sqldf(q)

MCQ\_G[]<- lapply(MCQ\_G, as.numeric)

q<-'SELECT SEQN,MCQ160a,MCQ160b,MCQ160c,MCQ160d,MCQ160e,MCQ160f,MCQ160m,MCQ220,MCQ230a,MCQ230b,MCQ230c,MCQ230d

FROM MCQ\_G

;'

MCQ\_G<-sqldf(q)

MCQ\_H[]<- lapply(MCQ\_H, as.numeric)

q<-'SELECT SEQN,MCQ160a,MCQ160b,MCQ160c,MCQ160d,MCQ160e,MCQ160f,MCQ160m,MCQ220,MCQ230a,MCQ230b,MCQ230c,MCQ230d

FROM MCQ\_H

;'

MCQ\_H<-sqldf(q)

MCQ\_I[]<- lapply(MCQ\_I, as.numeric)

q<-'SELECT SEQN,MCQ160a,MCQ160b,MCQ160c,MCQ160d,MCQ160e,MCQ160f,MCQ160m,MCQ220,MCQ230a,MCQ230b,MCQ230c,MCQ230d

FROM MCQ\_I

;'

MCQ\_I<-sqldf(q)

mcq<-rbind(MCQ\_D,MCQ\_E,MCQ\_F,MCQ\_G,MCQ\_H,MCQ\_I)

mcq$mcqflag<-1

#questioniaire-diabete

DIQ\_D[]<- lapply(DIQ\_D, as.numeric)

q<-'SELECT SEQN, DIQ010

FROM DIQ\_D

;'

DIQ\_D<-sqldf(q)

DIQ\_E[]<- lapply(DIQ\_E, as.numeric)

q<-'SELECT SEQN, DIQ010

FROM DIQ\_E

;'

DIQ\_E<-sqldf(q)

DIQ\_F[]<- lapply(DIQ\_F, as.numeric)

q<-'SELECT SEQN, DIQ010

FROM DIQ\_F

;'

DIQ\_F<-sqldf(q)

DIQ\_G[]<- lapply(DIQ\_G, as.numeric)

q<-'SELECT SEQN, DIQ010

FROM DIQ\_G

;'

DIQ\_G<-sqldf(q)

DIQ\_H[]<- lapply(DIQ\_H, as.numeric)

q<-'SELECT SEQN, DIQ010

FROM DIQ\_H

;'

DIQ\_H<-sqldf(q)

DIQ\_I[]<- lapply(DIQ\_I, as.numeric)

q<-'SELECT SEQN, DIQ010

FROM DIQ\_I

;'

DIQ\_I<-sqldf(q)

diq<-rbind(DIQ\_D,DIQ\_E,DIQ\_F,DIQ\_G,DIQ\_H,DIQ\_I)

#Merge together

q<-'SELECT \*

FROM demo

LEFT OUTER JOIN dpq ON demo.SEQN=dpq.SEQN

LEFT OUTER JOIN rhq ON demo.SEQN=rhq.SEQN

LEFT OUTER JOIN smq ON demo.SEQN=smq.SEQN

LEFT OUTER JOIN bmx ON demo.SEQN=bmx.SEQN

LEFT OUTER JOIN mcq ON demo.SEQN=mcq.SEQN

LEFT OUTER JOIN diq ON demo.SEQN=diq.SEQN

;'

dat<-sqldf(q)

#x-age of menarche early\_menarche=2;normal=1;late\_menarche=3

dat$menage[dat$RHQ010>=6 & dat$RHQ010<=11]<-2

dat$menage[dat$RHQ010>=12 & dat$RHQ010<=13]<-1

dat$menage[dat$RHQ010>=14 & dat$RHQ010<=25]<-3

#table(dat$menage[dat$rhqflag %in% c(1)],useNA = "ifany")

#table(dat$menage,useNA = "ifany")

#table(dat$RHQ010,useNA = "ifany")

#y-depression

#table(dat$dpq,useNA = "ifany")

dat$dpq1[dat$DPQ010 %in% c(0)]<-0

dat$dpq1[dat$DPQ010 %in% c(1)]<-1

dat$dpq1[dat$DPQ010 %in% c(2)]<-2

dat$dpq1[dat$DPQ010 %in% c(3)]<-3

dat$dpq1[dat$DPQ010 %in% c(7,9)]<-NA

dat$dpq2[dat$DPQ020 %in% c(0)]<-0

dat$dpq2[dat$DPQ020 %in% c(1)]<-1

dat$dpq2[dat$DPQ020 %in% c(2)]<-2

dat$dpq2[dat$DPQ020 %in% c(3)]<-3

dat$dpq2[dat$DPQ020 %in% c(7,9)]<-NA

dat$dpq3[dat$DPQ030 %in% c(0)]<-0

dat$dpq3[dat$DPQ030 %in% c(1)]<-1

dat$dpq3[dat$DPQ030 %in% c(2)]<-2

dat$dpq3[dat$DPQ030 %in% c(3)]<-3

dat$dpq3[dat$DPQ030 %in% c(7,9)]<-NA

dat$dpq4[dat$DPQ040 %in% c(0)]<-0

dat$dpq4[dat$DPQ040 %in% c(1)]<-1

dat$dpq4[dat$DPQ040 %in% c(2)]<-2

dat$dpq4[dat$DPQ040 %in% c(3)]<-3

dat$dpq4[dat$DPQ040 %in% c(7,9)]<-NA

dat$dpq5[dat$DPQ050 %in% c(0)]<-0

dat$dpq5[dat$DPQ050 %in% c(1)]<-1

dat$dpq5[dat$DPQ050 %in% c(2)]<-2

dat$dpq5[dat$DPQ050 %in% c(3)]<-3

dat$dpq5[dat$DPQ050 %in% c(7,9)]<-NA

dat$dpq6[dat$DPQ060 %in% c(0)]<-0

dat$dpq6[dat$DPQ060 %in% c(1)]<-1

dat$dpq6[dat$DPQ060 %in% c(2)]<-2

dat$dpq6[dat$DPQ060 %in% c(3)]<-3

dat$dpq6[dat$DPQ060 %in% c(7,9)]<-NA

dat$dpq7[dat$DPQ070 %in% c(0)]<-0

dat$dpq7[dat$DPQ070 %in% c(1)]<-1

dat$dpq7[dat$DPQ070 %in% c(2)]<-2

dat$dpq7[dat$DPQ070 %in% c(3)]<-3

dat$dpq7[dat$DPQ070 %in% c(7,9)]<-NA

dat$dpq8[dat$DPQ080 %in% c(0)]<-0

dat$dpq8[dat$DPQ080 %in% c(1)]<-1

dat$dpq8[dat$DPQ080 %in% c(2)]<-2

dat$dpq8[dat$DPQ080 %in% c(3)]<-3

dat$dpq8[dat$DPQ080 %in% c(7,9)]<-NA

dat$dpq9[dat$DPQ090 %in% c(0)]<-0

dat$dpq9[dat$DPQ090 %in% c(1)]<-1

dat$dpq9[dat$DPQ090 %in% c(2)]<-2

dat$dpq9[dat$DPQ090 %in% c(3)]<-3

dat$dpq9[dat$DPQ090 %in% c(7,9)]<-NA

dat$dpqtotal<-dat$dpq1+dat$dpq2+dat$dpq3+dat$dpq4+dat$dpq5+dat$dpq6+dat$dpq7+dat$dpq8+dat$dpq9

dat$dep[dat$dpqtotal<10]<-0

dat$dep[dat$dpqtotal>=10]<-1

dat$miss<-is.na(dat$dpq1)+is.na(dat$dpq2)+is.na(dat$dpq3)+is.na(dat$dpq4)+is.na(dat$dpq5)+is.na(dat$dpq6)+is.na(dat$dpq7)+is.na(dat$dpq8)+is.na(dat$dpq9)

dat$dep[dat$miss %in% c(0) & dat$dpqtotal<=9]<-0

dat$dep[dat$miss %in% c(0) & dat$dpqtotal>=10]<-1

dat$dep[dat$miss %in% c(1) & dat$dpqtotal<=6]<-0

dat$dep[dat$miss %in% c(1) & dat$dpqtotal>=10]<-1

dat$dep[dat$miss %in% c(2) & dat$dpqtotal<=3]<-0

dat$dep[dat$miss %in% c(2) & dat$dpqtotal>=10]<-1

dat$dep[dat$miss %in% c(3) & dat$dpqtotal %in% c(0)]<-0

dat$dep[dat$miss %in% c(3) & dat$dpqtotal>=10]<-1

dat$dep[dat$miss>=4 & dat$dpqtotal>=10]<-1

#table(dat$dep[dat$dpqflag %in% c(1)],useNA = "ifany")

#table(dat$dep,useNA = "ifany")

#AGE

dat$ageg<-7

dat$ageg[dat$RIDAGEYR>=18 & dat$RIDAGEYR<=29]<-1

dat$ageg[dat$RIDAGEYR>=30 & dat$RIDAGEYR<=39]<-2

dat$ageg[dat$RIDAGEYR>=40 & dat$RIDAGEYR<=49]<-3

dat$ageg[dat$RIDAGEYR>=50 & dat$RIDAGEYR<=59]<-4

dat$ageg[dat$RIDAGEYR>=60 & dat$RIDAGEYR<=69]<-5

dat$ageg[dat$RIDAGEYR>=70 & dat$RIDAGEYR<=85]<-6

#table(dat2$ageg,useNA = "ifany")

#RACE, 1=white, 2=black, 3=others

dat$race[dat$RIDRETH1 %in% c(3)]<-1

dat$race[dat$RIDRETH1 %in% c(4)]<-2

dat$race[dat$RIDRETH1 %in% c(1,2,5)]<-3

#table(dat$RIDRETH1,useNA = "ifany")

#EDUCATION, 1=<hs, 2=hs, 3=>hs

dat$edu<-4

dat$edu[dat$DMDEDUC3>=0 & dat$DMDEDUC3<=12]<-1

dat$edu[dat$DMDEDUC3 %in% c(55,66)]<-1

dat$edu[dat$DMDEDUC2 %in% c(1,2)]<-1

dat$edu[dat$DMDEDUC3 %in% c(13,14)]<-2

dat$edu[dat$DMDEDUC2 %in% c(3)]<-2

dat$edu[dat$DMDEDUC3 %in% c(15)]<-3

dat$edu[dat$DMDEDUC2 %in% c(4,5)]<-3

#table(dat$DMDEDUC2,useNA = "ifany")

#table(dat$DMDEDUC3,useNA = "ifany")

#MARITAL, 1=yes, 0=no

dat$marry<-3

dat$marry[dat$DMDMARTL %in% c(1)]<-1

dat$marry[dat$DMDMARTL %in% c(2,3,4,5,6)]<-2

dat$marry2[dat$DMDMARTL %in% c(1)]<-1

dat$marry2[dat$DMDMARTL %in% c(2,3,4,5,6)]<-0

#table(dat$DMDMARTL,useNA = "ifany")

#PIR, 1=<1, 2=1-2, 3=>=2

dat$pir<-4

dat$pir[dat$INDFMPIR>=0 & dat$INDFMPIR<1]<-1

dat$pir[dat$INDFMPIR>=1 & dat$INDFMPIR<2]<-2

dat$pir[dat$INDFMPIR>=2]<-3

#table(dat$INDFMPIR,useNA = "ifany")

#medical condition

#arthritis

dat$arth[dat$MCQ160A %in% c(1)]<-1

dat$arth[dat$MCQ160A %in% c(2)]<-0

#table(dat$arth, useNA = "ifany")

#congestive heart failure

dat$chf[dat$MCQ160B %in% c(1)]<-1

dat$chf[dat$MCQ160B %in% c(2)]<-0

#table(dat$chf, useNA = "ifany")

#coronary heart disease

dat$chd[dat$MCQ160C %in% c(1)]<-1

dat$chd[dat$MCQ160C %in% c(2)]<-0

#table(dat$chd, useNA = "ifany")

#angina

dat$angi[dat$MCQ160D %in% c(1)]<-1

dat$angi[dat$MCQ160D %in% c(2)]<-0

#table(dat$angi, useNA = "ifany")

#heart attack

dat$hat[dat$MCQ160E %in% c(1)]<-1

dat$hat[dat$MCQ160E %in% c(2)]<-0

#table(dat$hat, useNA = "ifany")

#stroke

dat$strok[dat$MCQ160F %in% c(1)]<-1

dat$strok[dat$MCQ160F %in% c(2)]<-0

#table(dat$strok, useNA = "ifany")

#cvd-all

dat$cvd[dat$MCQ160B %in% c(1) | dat$MCQ160C %in% c(1) | dat$MCQ160D %in% c(1) | dat$MCQ160E %in% c(1) | dat$MCQ160F %in% c(1)]<-1

dat$cvd[dat$MCQ160B %in% c(2) & dat$MCQ160C %in% c(2) & dat$MCQ160D %in% c(2) & dat$MCQ160E %in% c(2) & dat$MCQ160F %in% c(2)]<-0

#table(dat$cvd, useNA ="ifany")

#thyroid

dat$thyr[dat$MCQ160M %in% c(1)]<-1

dat$thyr[dat$MCQ160M %in% c(2)]<-0

#table(dat$thyr, useNA = "ifany")

#cancer

dat$cance[dat$MCQ220 %in% c(1)]<-1

dat$cance[dat$MCQ220 %in% c(2)]<-0

#table(dat$cance, useNA = "ifany")

#diabetes

dat$diabe[dat$DIQ010 %in% c(1,3)]<-1

dat$diabe[dat$DIQ010 %in% c(2)]<-0

#table(dat$diabe, useNA = "ifany")

#breast cancer

dat$brtcan[dat$MCQ220 %in% c(1,2)]<-0

dat$brtcan[(dat$MCQ220 %in% c(1)) & ((dat$MCQ230A %in% c(14))|(dat$MCQ230B %in% c(14))|(dat$MCQ230C %in% c(14))|(dat$MCQ230D %in% c(14)))]<-1

#table(dat$brtcan, useNA = "ifany")

#smoking-1=CURRENT SMOKER, 2=FORMER SMOKER, 3=NEVER SMOKER

dat$smoke<-4

dat$smoke[dat$SMQ020 %in% c(2)]<-3

dat$smoke[dat$SMQ020 %in% c(1) & dat$SMQ040 %in% c(3) ]<-2

dat$smoke[dat$SMQ020 %in% c(1) & dat$SMQ040 %in% c(1,2) ]<-1

#regular periods in the past 12 months

dat$rp<-2

dat$rp[dat$RHQ031 %in% c(1)]<-1

dat$rp[dat$RHQ031 %in% c(2)]<-0

#table(dat$SMQ040, useNA = "ifany")

#bmi(current) 1: <18.5 2: 18.5-25.0 3: 25-30 4: 30-35 5: 35+ 6: MISSING;

dat$bmig[dat$BMXBMI<18.5 & dat$BMXBMI>0]<-1

dat$bmig[dat$BMXBMI>=18.5 & dat$BMXBMI<25]<-2

dat$bmig[dat$BMXBMI>=25 & dat$BMXBMI<30]<-3

dat$bmig[dat$BMXBMI>=30 & dat$BMXBMI<35]<-4

dat$bmig[dat$BMXBMI>=35]<-5

dat$bmig[dat$BMXBMI %in% c(NA)]<-6

#table(dat$bmig,useNA = "ifany")

#table(dat$bmig[dat$bmxflag %in% c(1)], useNA = "ifany")

#Weight

dat$weight<-dat$WTMEC2YR/6

#Exclusion

dat2e<-dat[dat$rhqflag %in% c(1) & (is.na(dat$dep)|is.na(dat$menage)),]

dat2e$ageg[dat2e$ageg %in% c(7)]<-1

dat2ea<-dat[dat$rhqflag %in% c(1) & (is.na(dat$dep)|is.na(dat$menage)) & (dat$RIDAGEYR>=18),]

temp<-dat[(!is.na(dat$rhqflag))& (dat$RIAGENDR %in% c(2)) & (dat$RIDAGEYR>=18) ,]

temp<-dat[(!is.na(dat$rhqflag))& (dat$RIAGENDR %in% c(2)) & (dat$RIDAGEYR>=18) &(!is.na(dat$menage))&(!is.na(dat$dep)),]

dat2<-dat[(!is.na(dat$dep))&(!is.na(dat$menage)),]

#table1

CreateCatTable(vars = c("menage","ageg","race","edu","pir","marry","bmig","smoke","rp"),data = dat2,includeNA = T)

CreateCatTable(vars = c("menage","ageg","race","edu","pir","marry","bmig","smoke","rp"),strata = "dep",data = dat2,includeNA = T)

design <- svydesign(id = ~ SDMVPSU, strata = ~ SDMVSTRA, nest = TRUE, weight = ~ weight, data = dat2)

svyCreateCatTable(vars = c("menage","ageg","race","edu","pir","marry","bmig","smoke","rp"),data = design,includeNA = T)

svyCreateCatTable(vars = c("menage","ageg","race","edu","pir","marry","bmig","smoke","rp"),strata = "dep",data = design,includeNA = T)

#weighted CI

confint(svyciprop(~I(rp %in% c(0)), design, method="logit"))

#survey design for svyproportion-table1-weighted CI

#dep=1, calcualte covariates

dat3<-dat2[dat2$dep %in% c(1),]

design <- svydesign(id = ~ SDMVPSU, strata = ~ SDMVSTRA, nest = TRUE, weight = ~ weight, data = dat3)

(a<-svyciprop(~I(rp %in% c(NA)), design, method="logit"))

confint(a)

#dep=0, calculate covariates

dat3<-dat2[dat2$dep %in% c(0),]

design <- svydesign(id = ~ SDMVPSU, strata = ~ SDMVSTRA, nest = TRUE, weight = ~ weight, data = dat3)

(a<-svyciprop(~I(rp %in% c(NA)), design, method="logit"))

confint(a)

#logistic regression models

#survey design for logistic regression

#survey design

design <- svydesign(id = ~ SDMVPSU, strata = ~ SDMVSTRA, nest = TRUE, weight = ~ weight, data = dat2)

#original models

model1<-svyglm(dep ~ factor(menage), design = design, family=quasibinomial())

cbind(exp(coef(model1)),exp(confint(model1)))

model2<-svyglm(dep ~ factor(menage)+factor(ageg)+factor(race)+factor(edu)+factor(pir)+factor(marry), design = design, family=quasibinomial())

cbind(exp(coef(model2)),exp(confint(model2)))

model3<-svyglm(dep ~ factor(menage)+factor(ageg)+factor(race)+factor(edu)+factor(pir)+factor(marry)+factor(bmig)+factor(smoke)+factor(rp), design = design, family=quasibinomial())

round(cbind(exp(coef(model3)),exp(confint(model3))),2)

#continuous age at menarche

model1<-svyglm(dep ~ RHQ010, design = design, family=quasibinomial())

1/cbind(exp(coef(model1)),exp(confint(model1)))

model2<-svyglm(dep ~ RHQ010+factor(ageg)+factor(race)+factor(edu)+factor(pir)+factor(marry), design = design, family=quasibinomial())

1/cbind(exp(coef(model2)),exp(confint(model2)))

cbind(exp(coef(model2)),exp(confint(model2)))

model3<-svyglm(dep ~ RHQ010+factor(ageg)+factor(race)+factor(edu)+factor(pir)+factor(marry)+factor(bmig)+factor(smoke)+factor(rp), design = design, family=quasibinomial())

1/cbind(exp(coef(model3)),exp(confint(model3)))

round(cbind(exp(coef(model3)),exp(confint(model3))),2)

#interaction between age

model1<-svyglm(dep ~ factor(menage)\*factor(ageg), design = design, family=quasibinomial())

cbind(exp(coef(model1)),exp(confint(model1)))

model2<-svyglm(dep ~ factor(menage)\*factor(ageg)+factor(race)+factor(edu)+factor(pir)+factor(marry), design = design, family=quasibinomial())

summary(model2)

cbind(exp(coef(model2)),exp(confint(model2)))[2:3,]

model3<-svyglm(dep ~ factor(menage)\*factor(ageg)+factor(race)+factor(edu)+factor(pir)+factor(marry)+factor(bmig)+factor(smoke)+factor(rp), design = design, family=quasibinomial())

summary(model3)

cbind(exp(coef(model3)),exp(confint(model3)))[2:3,]

#multiple imputation

mdat<-dat[(!is.na(dat$rhqflag))&(!is.na(dat$dpqflag))&(dat$RIDAGEYR>=18)&(dat$RIAGENDR %in% c(2)),]

mdat$dep<-as.factor(mdat$dep)

mdat$menage<-as.factor(mdat$menage)

mdat$ageg<-as.factor(mdat$ageg)

mdat$race<-as.factor(mdat$race)

mdat$edu<-as.factor(mdat$edu)

mdat$pir<-as.factor(mdat$pir)

mdat$marry<-as.factor(mdat$marry)

mdat$bmig<-as.factor(mdat$bmig)

mdat$smoke<-as.factor(mdat$smoke)

mdat$rp<-as.factor(mdat$rp)

#categorical

mdat2<-mdat[,c("dep","menage","ageg","race","edu","pir","marry","bmig","smoke","rp")]

imp<-mice(data = mdat2,m = 50)

resm3<-data.frame(est1=numeric(),se1=numeric(),est2=numeric(),se2=numeric())

for (i in 1:50){

impdata<-complete(imp,i)

impdata<-cbind(impdata,mdat[,c("SDMVPSU","SDMVSTRA","weight")])

design <- svydesign(id = ~ SDMVPSU, strata = ~ SDMVSTRA, nest = TRUE, weight = ~ weight, data = impdata)

model3<-svyglm(dep ~ factor(menage)+factor(ageg)+factor(race)+factor(edu)+factor(pir)+factor(marry)+factor(bmig)+factor(smoke)+factor(rp), design = design, family=quasibinomial())

resm3[i,1]<-model3$coefficients[2]

resm3[i,2]<-SE(model3)[2]

resm3[i,3]<-model3$coefficients[3]

resm3[i,4]<-SE(model3)[3]

print(i)

}

c(exp(mean(resm3$est1)),exp(mean(resm3$est1)-1.96\*mean(resm3$se1)),exp(mean(resm3$est1)+1.96\*mean(resm3$se1)))

c(exp(mean(resm3$est2)),exp(mean(resm3$est2)-1.96\*mean(resm3$se2)),exp(mean(resm3$est2)+1.96\*mean(resm3$se2)))

#continuous

mdat2<-mdat[,c("dep","RHQ010","ageg","race","edu","pir","marry","bmig","smoke","rp")]

imp<-mice(data = mdat2,m = 50)

resm3<-data.frame(est1=numeric(),se1=numeric())

for (i in 1:50){

impdata<-complete(imp,i)

impdata<-cbind(impdata,mdat[,c("SDMVPSU","SDMVSTRA","weight")])

design <- svydesign(id = ~ SDMVPSU, strata = ~ SDMVSTRA, nest = TRUE, weight = ~ weight, data = impdata)

model3<-svyglm(dep ~ RHQ010+factor(ageg)+factor(race)+factor(edu)+factor(pir)+factor(marry)+factor(bmig)+factor(smoke)+factor(rp), design = design, family=quasibinomial())

resm3[i,1]<-model3$coefficients[2]

resm3[i,2]<-SE(model3)[2]

print(i)

}

c(1/exp(mean(resm3$est1)),1/exp(mean(resm3$est1)-1.96\*mean(resm3$se1)),1/exp(mean(resm3$est1)+1.96\*mean(resm3$se1)))

#alternatively

for (i in 1:50){

assign(paste0("imp",i),cbind(complete(imp,i),mdat[,c("SDMVPSU","SDMVSTRA","weight")]))

print(i)

}

il<-imputationList(datasets = list(imp1,imp2,imp3,imp4,imp5,imp6,imp7,imp8,imp9,imp10,imp11,imp12,imp13,imp14,imp15,imp16,imp17,imp18,imp19,imp20,imp21,imp22,imp23,imp24,imp25,imp26,imp27,imp28,imp29,imp30,imp31,imp32,imp33,imp34,imp35,imp36,imp37,imp38,imp39,imp40,imp41,imp42,imp43,imp44,imp45,imp46,imp47,imp48,imp49,imp50))

designs <- svydesign(id = ~ SDMVPSU, strata = ~ SDMVSTRA, nest = TRUE, weight = ~ weight, data = il)

results<-with(designs, svyglm(dep ~ RHQ010+factor(ageg)+factor(race)+factor(edu)+factor(pir)+factor(marry)+factor(bmig)+factor(smoke)+factor(rp), family=quasibinomial()))

1/exp(MIcombine(results)$coefficients[2])

1/exp(MIcombine(results)$coefficients[2]-1.96\*SE(MIcombine(results))[2])

1/exp(MIcombine(results)$coefficients[2]+1.96\*SE(MIcombine(results))[2])