Joe Brew – SAS and R code

PHC 6053 – Assignment 8

Question	SAS	R
Prep	*READ IN THE DATA FROM ASSIGNMENT 1; LIBNAME ass8 'C:\Users\BrewJR\Desktop\ass8'; DATA ass8.mydata; SET ass8.fghm122; RUN; *ASSIGN THE DATA TO &DAT; %let dat=ass8.mydata; RUN; /* TAKE A LOOK AT THE DATA */ proc print data=&dat (obs=7); run; *OPTIONAL: OUTPUT DIRECTLY AS A PDF FILE/; ods pdf file = "C:\Users\BrewJR\Desktop\ass8\ass8.pdf" notoc;	setwd("C:/Users/BrewJR/Desktop/ass8") library(sas7bdat) library(foreign) dat <- read.ssd("C:/Users/BrewJR/Desktop/ass8", "fghm122", sascmd="C:/Program Files/SASHome93/SASFoundation/9.3/sas.exe"))

1	/* 1(a) CREATE A BMIGROUP VARIABLE*/ data &dat; set &dat; BMIGROUP=.; if BMI<18.5 then BMIGROUP=1; if BMI >= 18.5 & BMI < 25 then BMIGROUP = 2; if BMI >= 25 & BMI < 30 then BMIGROUP = 3; if BMI >= 30 then BMIGROUP = 4; RUN; /* 1(b) CREATE HBP */ data &dat; set &dat; HBP=.; if SYSBP >=0 & SYSBP < 140 then HBP = 0; if SYSBP >= 140 then HBP = 1; RUN; /* 1(c) Remove all the individuals in the underweight BMI group AND all the individuals with a BMI which is 40 or larger*/ data dat2; set &dat; if BMIGROUP = 1 then delete; if BMI > 40 then delete; run;	# 1(a) CREATE A BMIGROUP VARIABLE*/ dat$BMIGROUP <- ifelse(dat$BMI<18.5, 1, ifelse(dat$BMI >= 18.5 & dat$BMI < 25, 2, ifelse(dat$BMI >= 25 & dat$BMI < 30, 3, ifelse(dat$BMI >= 30, 4, NA)))) # 1(b) CREATE HBP */ dat$HBP <- ifelse(dat$SYSBP >=0 & dat$SYSBP < 140, 0, ifelse(dat$SYSBP >= 140, 1, NA)) # 1(c) Remove all the individuals in the underweight BMI group AND #all the individuals with a BMI which is 40 or larger*/ dat2 <-dat[which(dat$BMIGROUP != 1 & dat$BMI <=40),]

2	``` /* AGE */ proc logistic data = dat2; model HBP(event="1") = AGE; run; /* BMI */ proc logistic data = dat2; model HBP(event="1") = BMI; run; /* BMIGROUP */ proc logistic data = dat2; class BMIGROUP (ref="2") / param=ref; model HBP(event="1") = BMIGROUP; run; /* SEX */ proc logistic data = dat2; model HBP(event="1") = SEX; run; /* BPMEDS */ proc logistic data = dat2; model HBP(event="1") = BPMEDS; run; /* PREVSTRK */ proc logistic data = dat2; model HBP(event="1") = PREVSTRK; run; ```	``` # AGE */ modelAGE <- glm(dat2$HBP ~ dat2$AGE, family="binomial") exp(cbind(OR = coef(modelAGE), confint(modelAGE))) # BMI */ modelBMI <- glm(dat2$HBP ~ dat2$BMI, family="binomial") exp(cbind(OR = coef(modelBMI), confint(modelBMI))) # BMIGROUP */ dat2$BMIGROUP <- factor(dat2$BMIGROUP, levels=c(2,3,4)) modelBMIGROUP <- glm(dat2$HBP ~ dat2$BMIGROUP, family="binomial") exp(cbind(OR = coef(modelBMIGROUP), confint(modelBMIGROUP))) # SEX */ modelSEX <- glm(dat2$HBP ~ dat2$SEX, family="binomial") exp(cbind(OR = coef(modelSEX), confint(modelSEX))) # BPMEDS */ modelBPMEDS <- glm(dat2$HBP ~ dat2$BPMEDS, family="binomial") exp(cbind(OR = coef(modelBPMEDS), confint(modelBPMEDS))) # PREVSTRK */ modelPREVSTRK <- glm(dat2$HBP ~ dat2$PREVSTRK, family="binomial") exp(cbind(OR = coef(modelPREVSTRK), confint(modelPREVSTRK))) ```

3	/* FIRST, CREATE AN INTERACTION TERM BETWEEN BMI AND BPMEDS */ **data** dat2; set dat2; intBMI_BPMEDS = BMI * BPMEDS; run; /*NOW RUN THE MODEL */ **proc logistic** data = dat2; class BPMEDS(ref="0") / param=ref; model HBP(event="1") = BMI BPMEDS intBMI_BPMEDS; **run**;	dat2$intBMI_BPMEDS <- dat2$BMI*dat2$BPMEDS #NOW RUN THE MODEL */ model3 <- glm(dat2$HBP ~ dat2$BMI + dat2$BPMEDS + dat2$intBMI_BPMEDS, family="binomial") exp(cbind(OR = coef(model3), confint(model3)))
4	**proc logistic** data = dat2; class BPMEDS(ref="0") / param=ref; class SEX(ref="1") / param=ref; class PREVSTRK(ref="0") / param=ref; model HBP(event="1") = AGE SEX PREVSTRK BMI BPMEDS intBMI_BPMEDS; **run**; ods pdf close;	model4 <- glm(dat2$HBP ~ dat2$AGE + dat2$SEX + dat2$PREVSTRK + dat2$BMI + dat2$BPMEDS + dat2$intBMI_BPMEDS, family="binomial") exp(cbind(OR = coef(model4), confint(model4)))

5		#Subset dat2 into bpmeds=yes and bpmeds=no dat2y <- dat2[which(dat2$BPMEDS == 1),] dat2n <- dat2[which(dat2$BPMEDS == 0),] #GET UNADJSUTED FOR BOTH #BPMEDS=Yes modelBMI_BPMEDSY <- glm(dat2y$HBP ~ dat2y$BMI, family="binomial") exp(cbind(OR = coef(modelBMI_BPMEDSY), confint(modelBMI_BPMEDSY))) #BPMEDS-No modelBMI_BPMEDSN <- glm(dat2n$HBP ~ dat2n$BMI, family="binomial") exp(cbind(OR = coef(modelBMI_BPMEDSN), confint(modelBMI_BPMEDSN))) #GET ADJUSTED FOR BOTH #BPMEDS=YES modelBMI_BPMEDSYadj <- glm(dat2y$HBP ~ dat2y$AGE + dat2y$SEX + dat2y$PREVSTRK + dat2y$BMI, family="binomial") exp(cbind(OR = coef(modelBMI_BPMEDSYadj), confint(modelBMI_BPMEDSYadj))) #BPMEDS=NO modelBMI_BPMEDSNadj <- glm(dat2n$HBP ~ dat2n$AGE + dat2n$SEX + dat2n$PREVSTRK + dat2n$BMI, family="binomial") exp(cbind(OR = coef(modelBMI_BPMEDSNadj), confint(modelBMI_BPMEDSNadj)))