Appendix 4.6: Awareness of cervical cancer and screening R script

# Benin

BJDHS$BJwt <- BJDHS$v005/1000000  
designBJ <- svydesign(ids = ~v021+v002, strata = ~v025, weights = ~BJwt, data = BJDHS)  
BJDHS2 = BJDHS[-which(is.na(BJDHS$s1423) & is.na(BJDHS$s1424)),] # includes only those responding to cervical cancer question in Benin  
BJDHS2$BJwt2 <- BJDHS2$v005/1000000  
designBJ2 <- svydesign(ids = ~v021+v002, strata = ~v025, weights = ~BJwt2, data = BJDHS2)  
# Mean Age  
BJttAge <- svyttest(v012~0, designBJ2)  
BJttAge  
svyby(~v012, ~s1423, designBJ2, svymean, vartype="ci") # mean age for awareness of cervical cancer   
svyby(~v012, ~s1424, designBJ2, svymean, vartype="ci") # mean age for awareness of cervical cancer screening  
svyttest(v012~s1423, designBJ2) # mean difference  
svyttest(v012~s1424, designBJ2)  
  
freq(BJDHS2$s1423, BJDHS2$BJwt2, plot = FALSE) #Heard of cervical cancer  
freq(BJDHS2$s1424, BJDHS2$BJwt2, plot = FALSE) # Heard of test for cervical cancer  
  
#Age  
freq(BJDHS2$v013, BJDHS2$BJwt2, plot = FALSE)   
crosstab(BJDHS2$s1423, BJDHS2$v013, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1423+v013, designBJ2, statistic="adjWald")  
crosstab(BJDHS2$s1424, BJDHS2$v013, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1424+v013, designBJ2, statistic="adjWald")  
# Age Regroup   
# Age regroup from other paper, Tiruneh et al. BMC Women's Health (2017)  
BJDHS2$BJAgeCat <- NA  
BJDHS2$BJAgeCat[BJDHS2$v012 >=15.0000 & BJDHS2$v012<=24.9999]<-"15-24"  
BJDHS2$BJAgeCat[BJDHS2$v012 >=25.0000 & BJDHS2$v012<=34.9999]<-"25-34"  
BJDHS2$BJAgeCat[BJDHS2$v012 >=35.0000 & BJDHS2$v012<=44.9999]<-"35-44"  
BJDHS2$BJAgeCat[BJDHS2$v012 >=45.0000]<-"45+"  
freq(BJDHS2$BJAgeCat, BJDHS2$BJwt2, plot = FALSE)   
class(BJDHS2$BJAgeCat) # Change to factor   
BJDHS2$BJAgeCat <- as.factor(BJDHS2$BJAgeCat)  
summary(BJDHS2$BJAgeCat)  
BJDHS2$BJwt2 <- BJDHS2$v005/1000000  
designBJ2 <- svydesign(ids = ~v021+v002, strata = ~v025, weights = ~BJwt2, data = BJDHS2)  
crosstab(BJDHS2$s1423, BJDHS2$BJAgeCat, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1423+BJAgeCat, designBJ2, statistic="adjWald")  
crosstab(BJDHS2$s1424, BJDHS2$BJAgeCat, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1424+BJAgeCat, designBJ2, statistic="adjWald")  
  
#Residential status  
freq(BJDHS2$v025, BJDHS2$BJwt2, plot = FALSE)   
crosstab(BJDHS2$s1423, BJDHS2$v025, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1423+v025, designBJ2, statistic="adjWald")  
crosstab(BJDHS2$s1424, BJDHS2$v025, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1424+v025, designBJ2, statistic="adjWald")  
# Marital status  
freq(BJDHS2$v502, BJDHS2$BJwt2, plot = FALSE)   
BJMS\_recoded <- c("never in union" = "never in union", "currently in union/living with a man" = "currently/formerly in union",   
 "formerly in union/living with a man" = "currently/formerly in union")  
  
BJDHS2$BJ\_MS <- BJMS\_recoded[BJDHS2$v502]  
freq(BJDHS2$BJ\_MS, BJDHS2$BJwt2, plot = FALSE)  
class(BJDHS2$BJ\_MS)   
BJDHS2$BJ\_MS <- as.factor(BJDHS2$BJ\_MS)  
summary(BJDHS2$BJ\_MS)  
BJDHS2$BJ\_MS <- factor(BJDHS2$BJ\_MS, levels = c("never in union",  
 "currently/formerly in union"))  
summary(BJDHS2$BJ\_MS)  
BJDHS2$BJwt2 <- BJDHS2$v005/1000000  
designBJ2 <- svydesign(ids = ~v021+v002, strata = ~v025, weights = ~BJwt2, data = BJDHS2)  
crosstab(BJDHS2$s1423, BJDHS2$BJ\_MS, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1423+BJ\_MS, designBJ2, statistic="adjWald")  
crosstab(BJDHS2$s1424, BJDHS2$BJ\_MS, BJDHS2$BJwt, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1424+BJ\_MS, designBJ2, statistic="adjWald")  
#Education  
freq(BJDHS2$v106, BJDHS2$BJwt2, plot = FALSE)   
crosstab(BJDHS2$s1423, BJDHS2$v106, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1423+v106, designBJ2, statistic="adjWald")  
crosstab(BJDHS2$s1424, BJDHS2$v106, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1424+v106, designBJ2, statistic="adjWald")  
#Wealth index  
freq(BJDHS2$v190, BJDHS2$BJwt2, plot = FALSE)   
crosstab(BJDHS2$s1423, BJDHS2$v190, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1423+v190, designBJ2, statistic="adjWald")  
crosstab(BJDHS2$s1424, BJDHS2$v190, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1424+v190, designBJ2, statistic="adjWald")  
#Religion\*  
freq(BJDHS2$v130, BJDHS2$BJwt2, plot = FALSE)   
BJRel\_recoded <- c("vodoun" = "Others", "other traditional"= "Others", "islam " = "Muslims", "catholic" = "Christians",   
 "protestant methodist" = "Christians", "other protestants" = "Christians", "celestes" = "Christians", "other christians" = "Christians",  
 "other religions" = "Others", "no religion"= "None", "other" = "Others")  
  
BJDHS2$BJ\_Religion <- BJRel\_recoded[BJDHS2$v130]  
freq(BJDHS2$BJ\_Religion, BJDHS2$BJwt2, plot = FALSE)  
class(BJDHS2$BJ\_Religion) # Change to factor   
BJDHS2$BJ\_Religion <- as.factor(BJDHS2$BJ\_Religion)  
summary(BJDHS2$BJ\_Religion)  
BJDHS2$BJwt2 <- BJDHS2$v005/1000000  
designBJ2 <- svydesign(ids = ~v021+v002, strata = ~v025, weights = ~BJwt2, data = BJDHS2)  
crosstab(BJDHS2$s1423, BJDHS2$BJ\_Religion, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1423+BJ\_Religion, designBJ2, statistic="adjWald")  
crosstab(BJDHS2$s1424, BJDHS2$BJ\_Religion, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1424+BJ\_Religion, designBJ2, statistic="adjWald")  
# Occupation  
freq(BJDHS2$v717, BJDHS2$BJwt2, plot = FALSE)  
BJOcc\_recoded <- c("not working" = "Not working", "professional/technical/managerial" = "Professional/Formal",   
 "clerical" = "Professional/Formal", "sales" = "NonProfessional/Informal", "agricultural - self employed" = "NonProfessional/Informal",   
 "agricultural - employee" = "NonProfessional/Informal", "household and domestic" = "NonProfessional/Informal",   
 "services" = "NonProfessional/Informal", "skilled manual" = "NonProfessional/Informal", "unskilled manual" = "NonProfessional/Informal",   
 "other unclassified" = "NonProfessional/Informal", "don't know" = "Not working")  
  
BJDHS2$BJ\_Occupation <- BJOcc\_recoded[BJDHS2$v717]  
freq(BJDHS2$BJ\_Occupation, BJDHS2$BJwt2, plot = FALSE)  
class(BJDHS2$BJ\_Occupation) # Change reference to "Not Working"  
BJDHS2$BJ\_Occupation <- as.factor(BJDHS2$BJ\_Occupation)  
summary(BJDHS2$BJ\_Occupation)  
BJDHS2$BJ\_Occupation <- factor(BJDHS2$BJ\_Occupation, levels = c("Not working",  
 "NonProfessional/Informal",  
 "Professional/Formal"))  
summary(BJDHS2$BJ\_Occupation)  
BJDHS2$BJwt2 <- BJDHS2$v005/1000000  
designBJ2 <- svydesign(ids = ~v021+v002, strata = ~v025, weights = ~BJwt2, data = BJDHS2)  
crosstab(BJDHS2$s1423, BJDHS2$BJ\_Occupation, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1423+BJ\_Occupation, designBJ2, statistic="adjWald")  
crosstab(BJDHS2$s1424, BJDHS2$BJ\_Occupation, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1424+BJ\_Occupation, designBJ2, statistic="adjWald")  
  
# Frequency of reading newspaper or magazine  
freq(BJDHS2$v157, BJDHS2$BJwt2, plot = FALSE)   
crosstab(BJDHS2$s1423, BJDHS2$v157, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1423+v157, designBJ2, statistic="adjWald")  
crosstab(BJDHS2$s1424, BJDHS2$v157, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1424+v157, designBJ2, statistic="adjWald")  
# Frequency of watching television  
freq(BJDHS2$v159, BJDHS2$BJwt2, plot = FALSE)   
crosstab(BJDHS2$s1423, BJDHS2$v159, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1423+v159, designBJ2, statistic="adjWald")  
crosstab(BJDHS2$s1424, BJDHS2$v159, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1424+v159, designBJ2, statistic="adjWald")  
# Frequency of listening to radio  
freq(BJDHS2$v158, BJDHS2$BJwt2, plot = FALSE)   
crosstab(BJDHS2$s1423, BJDHS2$v158, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1423+v158, designBJ2, statistic="adjWald")  
crosstab(BJDHS2$s1424, BJDHS2$v158, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1424+v158, designBJ2, statistic="adjWald")  
# Frequency of using Internet in last month  
freq(BJDHS2$v171b, BJDHS2$BJwt2, plot = FALSE)   
crosstab(BJDHS2$s1423, BJDHS2$v171b, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1423+v171b, designBJ2, statistic="adjWald")  
crosstab(BJDHS2$s1424, BJDHS2$v171b, BJDHS2$BJwt2, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1424+v171b, designBJ2, statistic="adjWald")

# CAMEROON

freq(CMAGE49$s1223, CMAGE49$CMwt, plot = FALSE) #Heard of cervical cancer  
freq(CMAGE49$s1224, CMAGE49$CMwt, plot = FALSE) # Heard of test for cervical cancer  
  
#So as to use awareness for cross tab  
freq(CMAGE49$s1224, CMAGE49$CMwt, plot = FALSE, na.rm = FALSE)   
CMAGE49$s1224[is.na(CMAGE49$s1224)] <- 0  
CMAware\_recoded <- c("no" = 0, "yes"= 1, "NA's" = 0)  
CMAGE49$CM\_Aware <- CMAware\_recoded[CMAGE49$s1224]  
freq(CMAGE49$CM\_Aware, CMAGE49$CMwt, plot = FALSE)   
is.numeric(CMAGE49$s1224)  
CMAGE49$s1224 <- as.numeric(CMAGE49$s1224)  
  
# CAMEROON  
CMAGE49$CMwt <- CMAGE49$v005/1000000  
designCM <- svydesign(ids = ~v021+v002, strata = ~v025, weights = ~CMwt, data = CMAGE49)  
# Mean Age  
CMttAge <- svyttest(v012~0, designCM)  
CMttAge  
svyby(~v012, ~s1223, designCM, svymean, vartype="ci") # mean age for awareness of cervical cancer   
svyby(~v012, ~s1224, designCM, svymean, vartype="ci") # mean age for awareness of cervical cancer screening  
svyttest(v012~s1223, designCM) # mean difference  
svyttest(v012~s1224, designCM)  
  
#Age  
freq(CMAGE49$v013, CMAGE49$CMwt, plot = FALSE)   
crosstab(CMAGE49$s1223, CMAGE49$v013, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1223+v013, designCM, statistic="adjWald")  
crosstab(CMAGE49$s1224, CMAGE49$v013, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1224+v013, designCM, statistic="adjWald")  
# Age Regroup   
# Age regroup from other paper, Tiruneh et al. BMC Women's Health (2017)  
CMAGE49$CMAgeCat <- NA  
CMAGE49$CMAgeCat[CMAGE49$v012 >=15.0000 & CMAGE49$v012<=24.9999]<-"15-24"  
CMAGE49$CMAgeCat[CMAGE49$v012 >=25.0000 & CMAGE49$v012<=34.9999]<-"25-34"  
CMAGE49$CMAgeCat[CMAGE49$v012 >=35.0000 & CMAGE49$v012<=49.9999]<-"35-44"  
CMAGE49$CMAgeCat[CMAGE49$v012 >=45.0000]<-"45+"  
freq(CMAGE49$CMAgeCat, CMAGE49$CMwt, plot = FALSE)   
class(CMAGE49$CMAgeCat)   
CMAGE49$CMAgeCat <- as.factor(CMAGE49$CMAgeCat)  
summary(CMAGE49$CMAgeCat)  
CMAGE49$CMwt <- CMAGE49$v005/1000000  
designCM <- svydesign(ids = ~v021+v002, strata = ~v025, weights = ~CMwt, data = CMAGE49)  
crosstab(CMAGE49$s1223, CMAGE49$CMAgeCat, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1223+CMAgeCat, designCM, statistic="adjWald")  
crosstab(CMAGE49$s1224, CMAGE49$CMAgeCat, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1224+CMAgeCat, designCM, statistic="adjWald")  
#Residential status  
freq(CMAGE49$v025, CMAGE49$CMwt, plot = FALSE)   
crosstab(CMAGE49$s1223, CMAGE49$v025, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1223+v025, designCM, statistic="adjWald")  
crosstab(CMAGE49$s1224, CMAGE49$v025, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1224+v025, designCM, statistic="adjWald")  
#Marital status  
freq(CMAGE49$v502, CMAGE49$CMwt, plot = FALSE)   
CMMS\_recoded <- c("never in union" = "never in union", "currently in union/living with a man" = "currently/formerly in union",   
 "formerly in union/living with a man" = "currently/formerly in union")  
  
CMAGE49$CM\_MS <- CMMS\_recoded[CMAGE49$v502]  
freq(CMAGE49$CM\_MS, CMAGE49$CMwt, plot = FALSE)  
class(CMAGE49$CM\_MS)   
CMAGE49$CM\_MS <- as.factor(CMAGE49$CM\_MS)  
summary(CMAGE49$CM\_MS)  
CMAGE49$CM\_MS <- factor(CMAGE49$CM\_MS, levels = c("never in union",  
 "currently/formerly in union"))  
summary(CMAGE49$CM\_MS)  
CMAGE49$CMwt <- CMAGE49$v005/1000000  
designCM <- svydesign(ids = ~v021+v002, strata = ~v025, weights = ~CMwt, data = CMAGE49)  
crosstab(CMAGE49$s1223, CMAGE49$CM\_MS, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1223+CM\_MS, designCM, statistic="adjWald")  
crosstab(CMAGE49$s1224, CMAGE49$CM\_MS, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1224+CM\_MS, designCM, statistic="adjWald")  
#Education  
freq(CMAGE49$v106, CMAGE49$CMwt, plot = FALSE)  
crosstab(CMAGE49$s1223, CMAGE49$v106, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1223+v106, designCM, statistic="adjWald")  
crosstab(CMAGE49$s1224, CMAGE49$v106, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1224+v106, designCM, statistic="adjWald")  
#Wealth index  
freq(CMAGE49$v190, CMAGE49$CMwt, plot = FALSE)   
crosstab(CMAGE49$s1223, CMAGE49$v190, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1223+v190, designCM, statistic="adjWald")  
crosstab(CMAGE49$s1224, CMAGE49$v190, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1224+v190, designCM, statistic="adjWald")  
#Religion\*  
freq(CMAGE49$v130, CMAGE49$CMwt, plot = FALSE)   
CMRel\_recoded <- c("catholic" = "Christians", "protestant" = "Christians", "other christians" = "Christians",  
 "muslim " = "Muslims", "animist" = "Others", "none"= "None", "other" ="Others" )  
CMAGE49$CM\_Religion <- CMRel\_recoded[CMAGE49$v130]  
freq(CMAGE49$CM\_Religion, CMAGE49$CMwt, plot = FALSE)  
class(CMAGE49$CM\_Religion)   
CMAGE49$CM\_Religion <- as.factor(CMAGE49$CM\_Religion)  
summary(CMAGE49$CM\_Religion)  
CMAGE49$CMwt <- CMAGE49$v005/1000000  
designCM <- svydesign(ids = ~v021+v002, strata = ~v025, weights = ~CMwt, data = CMAGE49)  
crosstab(CMAGE49$s1223, CMAGE49$CM\_Religion, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1223+CM\_Religion, designCM, statistic="adjWald")  
crosstab(CMAGE49$s1224, CMAGE49$CM\_Religion, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1224+CM\_Religion, designCM, statistic="adjWald")  
# Occupation  
freq(CMAGE49$v717, CMAGE49$CMwt, plot = FALSE)  
CMOcc\_recoded <- c("not working" = "Not working", "professional/technical/managerial"= "Professional/Formal", "clerical" = "Professional/Formal",   
 "sales"= "NonProfessional/Informal", "agricultural - self employed"= "NonProfessional/Informal",   
 "agricultural - employee"= "NonProfessional/Informal", "household and domestic" = "NonProfessional/Informal", "services" = "NonProfessional/Informal",  
 "skilled manual" = "NonProfessional/Informal", "unskilled manual" = "NonProfessional/Informal", "don't know"= "Not working")  
  
CMAGE49$CM\_Occupation <- CMOcc\_recoded[CMAGE49$v717]  
freq(CMAGE49$CM\_Occupation, CMAGE49$CMwt, plot = FALSE)  
class(CMAGE49$CM\_Occupation) # Change reference to "Not Working"  
CMAGE49$CM\_Occupation <- as.factor(CMAGE49$CM\_Occupation)  
summary(CMAGE49$CM\_Occupation)  
CMAGE49$CM\_Occupation <- factor(CMAGE49$CM\_Occupation, levels = c("Not working",  
 "NonProfessional/Informal",  
 "Professional/Formal"))  
summary(CMAGE49$CM\_Occupation)  
CMAGE49$CMwt <- CMAGE49$v005/1000000  
designCM <- svydesign(ids = ~v021+v002, strata = ~v025, weights = ~CMwt, data = CMAGE49)  
crosstab(CMAGE49$s1223, CMAGE49$CM\_Occupation, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1223+CM\_Occupation, designCM, statistic="adjWald")  
crosstab(CMAGE49$s1224, CMAGE49$CM\_Occupation, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1224+CM\_Occupation, designCM, statistic="adjWald")  
  
# Frequency of reading newspaper or magazine  
freq(CMAGE49$v157, CMAGE49$CMwt, plot = FALSE)   
crosstab(CMAGE49$s1223, CMAGE49$v157, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1223+v157, designCM, statistic="adjWald")  
crosstab(CMAGE49$s1224, CMAGE49$v157, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1224+v157, designCM, statistic="adjWald")  
# Frequency of watching television  
freq(CMAGE49$v159, CMAGE49$CMwt, plot = FALSE)   
crosstab(CMAGE49$s1223, CMAGE49$v159, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1223+v159, designCM, statistic="adjWald")  
crosstab(CMAGE49$s1224, CMAGE49$v159, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1224+v159, designCM, statistic="adjWald")  
# Frequency of listening to radio   
freq(CMAGE49$v158, CMAGE49$CMwt, plot = FALSE)   
crosstab(CMAGE49$s1223, CMAGE49$v158, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1223+v158, designCM, statistic="adjWald")  
crosstab(CMAGE49$s1224, CMAGE49$v158, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1224+v158, designCM, statistic="adjWald")  
# Frequency of using Internet in last month  
freq(CMAGE49$v171b, CMAGE49$CMwt, plot = FALSE)   
crosstab(CMAGE49$s1223, CMAGE49$v171b, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Cervical Cancer  
svychisq(~s1223+v171b, designCM, statistic="adjWald")  
crosstab(CMAGE49$s1224, CMAGE49$v171b, CMAGE49$CMwt, prop.c = TRUE, plot = FALSE) # Heard of Test for Cervical Cancer  
svychisq(~s1224+v171b, designCM, statistic="adjWald")

# Bar plot awareness of cervical cancer and screening

Prop\_Cerv <- c(9.5, 46.1, # Heard of cervical cancer  
 51.4, 59.7) # Heard of Cervical Screening  
  
PropCountry\_Cerv <- matrix(Prop\_Cerv, nrow = 2, byrow = T)  
colnames(PropCountry\_Cerv) <- c("Benin", "Cameroon")  
row.names(PropCountry\_Cerv) <- c("Aware of Cervical Cancer", "Aware of Cervical Screening")  
PropCountry\_Cerv  
color.names = c("red2", "green3")  
barplot(PropCountry\_Cerv, beside = T, xlab = "Country", ylab = "Percentage", col = color.names)  
legend(1, 2300, row.names(PropCountry\_Cerv), cex = 0.7, fill = color.names, bty = "n")  
  
# ggplot2 Grouped Bar Plot  
PropCountry\_Cervmelt <- melt(PropCountry\_Cerv)  
head(PropCountry\_Cervmelt)  
colnames(PropCountry\_Cervmelt) <- c( "Awareness", "Country", "Percentage")  
head(PropCountry\_Cervmelt)  
ggplot(PropCountry\_Cervmelt, aes(x= Country, y= Percentage, fill= Awareness))  
geom\_bar(stat = "identity", position = "dodge")  
scale\_fill\_brewer(palette = "Set1")  
labs(y= "Percentage")  
expand\_limits(y = c(0, 100))  
theme\_bw()  
theme(panel.grid.major.x = element\_blank())  
  
ggplot(PropCountry\_Cervmelt, aes(x= Country, y= Percentage, fill = Awareness)) +  
 geom\_bar(stat = "identity", position = "dodge") +  
 facet\_grid(.~Awareness) +  
 scale\_fill\_brewer(palette = "Set1") +  
 labs(y= "Percentage") +  
 expand\_limits(y = c(0, 100)) +  
 theme\_bw() +  
 theme(legend.position = "none")

# Mean age (95% confidence interval (CI) error bar) of female participants aged 15 -49 years on awareness of cervical cancer in Benin and Cameroon

#No  
my.dt1 <- data.frame(Country = c("Benin", "Cameroon"),  
 Mean = c(28.27, 26.56),  
 down = c(28.02, 26.25),  
 up = c(28.51, 26.86))  
  
  
my.dt1  
a <- ggplot(my.dt1, aes(x=Country, y=Mean, colour=Country)) +   
 geom\_point(size = 3) +  
 geom\_errorbar(aes(ymin = down, ymax = up)) +  
 theme\_classic() +  
 theme(legend.position="none")   
a  
# Yes   
my.dt2 <- data.frame(Country = c("Benin", "Cameroon"),  
 Mean = c(29.56, 29.36),  
 down = c(28.80, 29.05),  
 up = c(30.31, 29.67))  
  
  
my.dt2  
b <- ggplot(my.dt2, aes(x=Country, y=Mean, colour=Country)) +   
 geom\_point(size = 3) +  
 geom\_errorbar(aes(ymin = down, ymax = up)) +  
 theme\_classic() +  
 theme(legend.position="none")   
b  
ggarrange(a,b, labels = c("No", "Yes"))  
ggsave("ggpubrsave13.jpg", width = 10, height = 6, units = c("in"), dpi = 300)

# Mean age (95% confidence interval (CI) error bar) of female participants aged 15 -49 years on awareness of cervical cancer screening in Benin and Cameroon

# No  
  
my.dt3 <- data.frame(Country = c("Benin", "Cameroon"),  
 Mean = c(29.07 , 28.00),  
 down = c(28.00, 27.52),  
 up = c(30.14, 28.46))  
  
  
my.dt3  
c <- ggplot(my.dt3, aes(x=Country, y=Mean, colour=Country)) +   
 geom\_point(size = 3) +  
 geom\_errorbar(aes(ymin = down, ymax = up)) +  
 theme\_classic() +  
 theme(legend.position="none")   
c  
  
#Yes  
  
my.dt4 <- data.frame(Country = c("Benin", "Cameroon"),  
 Mean = c(30.02, 30.29),  
 down = c(29.06, 29.91),  
 up = c(30.98, 30.66))  
  
my.dt4  
d <- ggplot(my.dt4, aes(x=Country, y=Mean, colour=Country)) +   
 geom\_point(size = 3) +  
 geom\_errorbar(aes(ymin = down, ymax = up)) +  
 theme\_classic() +  
 theme(legend.position="none")   
d  
ggarrange(c,d, labels = c("No", "Yes"))  
ggsave("ggpubrsave14.jpg", width = 10, height = 6, units = c("in"), dpi = 300)

# Benin Logistic Regression -Heard of cervical cancer

BJDHS2$BJwt2 <- BJDHS2$v005/1000000  
designBJ2 <- svydesign(ids = ~v021+v002, strata = ~v025, weights = ~BJwt2, data = BJDHS2)  
# Unadjusted   
# Age  
BJlogitAge <- (svyglm(s1423~v013, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitAge)  
coef(BJlogitAge)  
exp(coef(BJlogitAge))  
round(exp(coef(BJlogitAge)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitAge)), exp(confint(BJlogitAge))), 2) # round to 2  
# Age Regroup  
BJlogitAge2 <- (svyglm(s1423~BJAgeCat, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitAge2)  
coef(BJlogitAge2)  
exp(coef(BJlogitAge2))  
round(exp(coef(BJlogitAge2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitAge2)), exp(confint(BJlogitAge2))), 2) # round to 2  
# Residential Status  
BJlogitRS <- (svyglm(s1423~v025, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitRS)  
coef(BJlogitRS)  
exp(coef(BJlogitRS))  
round(exp(coef(BJlogitRS)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitRS)), exp(confint(BJlogitRS))), 2) # round to 2  
# Marital Status  
BJlogitMS <- (svyglm(s1423~BJ\_MS, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitMS)  
coef(BJlogitMS)  
exp(coef(BJlogitMS))  
round(exp(coef(BJlogitMS)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitMS)), exp(confint(BJlogitMS))), 2) # round to 2  
# Education  
BJlogitEdu <- (svyglm(s1423~v106, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitEdu)  
coef(BJlogitEdu)  
exp(coef(BJlogitEdu))  
round(exp(coef(BJlogitEdu)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitEdu)), exp(confint(BJlogitEdu))), 2) # round to 2  
# Wealth Index  
BJlogitWI <- (svyglm(s1423~v190, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitWI)  
coef(BJlogitWI)  
exp(coef(BJlogitWI))  
round(exp(coef(BJlogitWI)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitWI)), exp(confint(BJlogitWI))), 2) # round to 2  
# Religion  
BJlogitRel <- (svyglm(s1423~BJ\_Religion, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitRel)  
coef(BJlogitRel)  
exp(coef(BJlogitRel))  
round(exp(coef(BJlogitRel)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitRel)), exp(confint(BJlogitRel))), 2) # round to 2  
# Occupation  
BJlogitOcc <- (svyglm(s1423~BJ\_Occupation, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitOcc)  
coef(BJlogitOcc)  
exp(coef(BJlogitOcc))  
round(exp(coef(BJlogitOcc)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitOcc)), exp(confint(BJlogitOcc))), 2) # round to 2  
# Frequency of reading newspaper or magazine  
BJlogitRnpm <- (svyglm(s1423~v157, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitRnpm)  
coef(BJlogitRnpm)  
exp(coef(BJlogitRnpm))  
round(exp(coef(BJlogitRnpm)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitRnpm)), exp(confint(BJlogitRnpm))), 2) # round to 2  
# Frequency of watching television  
BJlogitWt <- (svyglm(s1423~v159, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitWt)  
coef(BJlogitWt)  
exp(coef(BJlogitWt))  
round(exp(coef(BJlogitWt)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitWt)), exp(confint(BJlogitWt))), 2) # round to 2  
# Frequency of listening to radio   
BJlogitLr <- (svyglm(s1423~v158, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitLr)  
coef(BJlogitLr)  
exp(coef(BJlogitLr))  
round(exp(coef(BJlogitLr)), 2) # round to make BJDHS$BJ\_Occupation <- relevel(BJDHS$BJ\_Occupation, "Not working"it clearer  
round(cbind(OR = exp(coef(BJlogitLr)), exp(confint(BJlogitLr))), 2) # round to 2  
# Frequency of using Internet in last month  
BJlogitInt <- (svyglm(s1423~v171b, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitInt)  
coef(BJlogitInt)  
exp(coef(BJlogitInt))  
round(exp(coef(BJlogitInt)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitInt)), exp(confint(BJlogitInt))), 2) # round to 2  
# Adjusted  
BJlogit <- (svyglm(s1423~BJAgeCat+v025+BJ\_MS+v106+v190+BJ\_Religion+BJ\_Occupation+v157+v158+v159+v171b, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogit)  
coef(BJlogit)  
exp(coef(BJlogit))  
round(exp(coef(BJlogit)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogit)), exp(confint(BJlogit))), 2) # round to 2

# Benin Logistic Regression -Heard of cervical cancer Screening

# Unadjusted   
# Age  
BJlogitAge2 <- (svyglm(s1424~v013, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitAge2)  
coef(BJlogitAge2)  
exp(coef(BJlogitAge2))  
round(exp(coef(BJlogitAge2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitAge2)), exp(confint(BJlogitAge2))), 2) # round to 2  
# Age Regroup  
BJlogitAge2b <- (svyglm(s1424~BJAgeCat, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitAge2b)  
coef(BJlogitAge2b)  
exp(coef(BJlogitAge2b))  
round(exp(coef(BJlogitAge2b)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitAge2b)), exp(confint(BJlogitAge2b))), 2) # round to 2  
# Residential Status  
BJlogitRS2 <- (svyglm(s1424~v025, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitRS2)  
coef(BJlogitRS2)  
exp(coef(BJlogitRS2))  
round(exp(coef(BJlogitRS2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitRS2)), exp(confint(BJlogitRS2))), 2) # round to 2  
# Marital Status  
BJlogitMS2 <- (svyglm(s1424~BJ\_MS, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitMS2)  
coef(BJlogitMS2)  
exp(coef(BJlogitMS2))  
round(exp(coef(BJlogitMS2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitMS2)), exp(confint(BJlogitMS2))), 2) # round to 2  
# Education  
BJlogitEdu2 <- (svyglm(s1424~v106, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitEdu2)  
coef(BJlogitEdu2)  
exp(coef(BJlogitEdu2))  
round(exp(coef(BJlogitEdu2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitEdu2)), exp(confint(BJlogitEdu2))), 2) # round to 2  
# Wealth Index  
BJlogitWI2 <- (svyglm(s1424~v190, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitWI2)  
coef(BJlogitWI2)  
exp(coef(BJlogitWI2))  
round(exp(coef(BJlogitWI2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitWI2)), exp(confint(BJlogitWI2))), 2) # round to 2  
# Religion  
BJlogitRel2 <- (svyglm(s1424~BJ\_Religion, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitRel2)  
coef(BJlogitRel2)  
exp(coef(BJlogitRel2))  
round(exp(coef(BJlogitRel2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitRel2)), exp(confint(BJlogitRel2))), 2) # round to 2  
# Occupation  
BJlogitOcc2 <- (svyglm(s1424~BJ\_Occupation, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitOcc2)  
coef(BJlogitOcc2)  
exp(coef(BJlogitOcc2))  
round(exp(coef(BJlogitOcc2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitOcc2)), exp(confint(BJlogitOcc2))), 2) # round to 2  
# Frequency of reading newspaper or magazine  
BJlogitRnpm2 <- (svyglm(s1424~v157, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitRnpm2)  
coef(BJlogitRnpm2)  
exp(coef(BJlogitRnpm2))  
round(exp(coef(BJlogitRnpm2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitRnpm2)), exp(confint(BJlogitRnpm2))), 2) # round to 2  
# Frequency of watching television  
BJlogitWt2 <- (svyglm(s1424~v159, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitWt2)  
coef(BJlogitWt2)  
exp(coef(BJlogitWt2))  
round(exp(coef(BJlogitWt2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitWt2)), exp(confint(BJlogitWt2))), 2) # round to 2  
# Frequency of listening to radio   
BJlogitLr2 <- (svyglm(s1424~v158, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitLr2)  
coef(BJlogitLr2)  
exp(coef(BJlogitLr2))  
round(exp(coef(BJlogitLr2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitLr2)), exp(confint(BJlogitLr2))), 2) # round to 2  
# Frequency of using Internet in last month  
BJlogitInt2 <- (svyglm(s1424~v171b, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogitInt2)  
coef(BJlogitInt2)  
exp(coef(BJlogitInt2))  
round(exp(coef(BJlogitInt2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogitInt2)), exp(confint(BJlogitInt2))), 2) # round to 2  
# Adjusted, v025, v502, BJ\_Religion and v157 removed ços not significant in the Univariate analysis  
BJlogit2 <- (svyglm(s1424~BJAgeCat+v106+v190+BJ\_Occupation+v158+v159+v171b, family=quasibinomial, design=designBJ2, na.action = na.omit))   
summary(BJlogit2)  
coef(BJlogit2)  
exp(coef(BJlogit2))  
round(exp(coef(BJlogit2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogit2)), exp(confint(BJlogit2))), 2) # round to 2  
# Adding all the variables from the univariate analysis whether significant or not;.  
BJlogit2b <- (svyglm(s1424~BJAgeCat+v025+BJ\_MS+v106+v190+BJ\_Religion+BJ\_Occupation+v157+v158+v159+v171b, family=quasibinomial, design=designBJ2, na.action = na.omit))  
summary(BJlogit2b)  
coef(BJlogit2b)  
exp(coef(BJlogit2b))  
round(exp(coef(BJlogit2b)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(BJlogit2b)), exp(confint(BJlogit2b))), 2) # round to 2

# Cameroon Logistic Regression -Heard of cervical cancer

CMAGE49$CMwt <-CMAGE49$v005/1000000  
designCM <- svydesign(ids = ~v021+v002, strata = ~v025, weights = ~CMwt, data = CMAGE49)  
# Unadjusted   
# Age  
CMlogitAge <- (svyglm(s1223~v013, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitAge)  
coef(CMlogitAge)  
exp(coef(CMlogitAge))  
round(exp(coef(CMlogitAge)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitAge)), exp(confint(CMlogitAge))), 2) # round to 2  
# Age Regroup  
CMlogitAge2 <- (svyglm(s1223~CMAgeCat, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitAge2)  
coef(CMlogitAge2)  
exp(coef(CMlogitAge2))  
round(exp(coef(CMlogitAge2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitAge2)), exp(confint(CMlogitAge2))), 2) # round to 2  
# Residential Status  
CMlogitRS <- (svyglm(s1223~v025, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitRS)  
coef(CMlogitRS)  
exp(coef(CMlogitRS))  
round(exp(coef(CMlogitRS)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitRS)), exp(confint(CMlogitRS))), 2) # round to 2  
# Marital Status  
CMlogitMS <- (svyglm(s1223~CM\_MS, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitMS)  
coef(CMlogitMS)  
exp(coef(CMlogitMS))  
round(exp(coef(CMlogitMS)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitMS)), exp(confint(CMlogitMS))), 2) # round to 2  
# Education  
CMlogitEdu <- (svyglm(s1223~v106, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitEdu)  
coef(CMlogitEdu)  
exp(coef(CMlogitEdu))  
round(exp(coef(CMlogitEdu)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitEdu)), exp(confint(CMlogitEdu))), 2) # round to 2  
# Wealth Index  
CMlogitWI <- (svyglm(s1223~v190, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitWI)  
coef(CMlogitWI)  
exp(coef(CMlogitWI))  
round(exp(coef(CMlogitWI)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitWI)), exp(confint(CMlogitWI))), 2) # round to 2  
# Religion  
CMlogitRel <- (svyglm(s1223~CM\_Religion, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitRel)  
coef(CMlogitRel)  
exp(coef(CMlogitRel))  
round(exp(coef(CMlogitRel)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitRel)), exp(confint(CMlogitRel))), 2) # round to 2  
# Occupation  
CMlogitOcc <- (svyglm(s1223~CM\_Occupation, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitOcc)  
coef(CMlogitOcc)  
exp(coef(CMlogitOcc))  
round(exp(coef(CMlogitOcc)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitOcc)), exp(confint(CMlogitOcc))), 2) # round to 2  
# Frequency of reading newspaper or magazine  
CMlogitRnpm <- (svyglm(s1223~v157, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitRnpm)  
coef(CMlogitRnpm)  
exp(coef(CMlogitRnpm))  
round(exp(coef(CMlogitRnpm)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitRnpm)), exp(confint(CMlogitRnpm))), 2) # round to 2  
# Frequency of watching television  
CMlogitWt <- (svyglm(s1223~v159, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitWt)  
coef(CMlogitWt)  
exp(coef(CMlogitWt))  
round(exp(coef(CMlogitWt)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitWt)), exp(confint(CMlogitWt))), 2) # round to 2  
# Frequency of listening to radio   
CMlogitLr <- (svyglm(s1223~v158, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitLr)  
coef(CMlogitLr)  
exp(coef(CMlogitLr))  
round(exp(coef(CMlogitLr)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitLr)), exp(confint(CMlogitLr))), 2) # round to 2  
# Frequency of using Internet in last month  
CMlogitInt <- (svyglm(s1223~v171b, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitInt)  
coef(CMlogitInt)  
exp(coef(CMlogitInt))  
round(exp(coef(CMlogitInt)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitInt)), exp(confint(CMlogitInt))), 2) # round to 2  
# Adjusted  
CMlogit <- (svyglm(s1223~CMAgeCat+v025+CM\_MS+v106+v190+CM\_Religion+CM\_Occupation+v157+v158+v159+v171b, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogit)  
coef(CMlogit)  
exp(coef(CMlogit))  
round(exp(coef(CMlogit)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogit)), exp(confint(CMlogit))), 2) # round to 2

# Cameroon Logistic Regression -Heard of cervical cancer Screening

# Unadjusted   
# Age  
CMlogitAge2 <- (svyglm(s1224~v013, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitAge2)  
coef(CMlogitAge2)  
exp(coef(CMlogitAge2))  
round(exp(coef(CMlogitAge2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitAge2)), exp(confint(CMlogitAge2))), 2) # round to 2  
# Age Regroup  
CMlogitAge2b <- (svyglm(s1224~CMAgeCat, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitAge2b)  
coef(CMlogitAge2b)  
exp(coef(CMlogitAge2b))  
round(exp(coef(CMlogitAge2b)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitAge2b)), exp(confint(CMlogitAge2b))), 2) # round to 2  
# Residential Status  
CMlogitRS2 <- (svyglm(s1224~v025, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitRS2)  
coef(CMlogitRS2)  
exp(coef(CMlogitRS2))  
round(exp(coef(CMlogitRS2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitRS2)), exp(confint(CMlogitRS2))), 2) # round to 2  
# Marital Status  
CMlogitMS2 <- (svyglm(s1224~CM\_MS, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitMS2)  
coef(CMlogitMS2)  
exp(coef(CMlogitMS2))  
round(exp(coef(CMlogitMS2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitMS2)), exp(confint(CMlogitMS2))), 2) # round to 2  
# Education  
CMlogitEdu2 <- (svyglm(s1224~v106, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitEdu2)  
coef(CMlogitEdu2)  
exp(coef(CMlogitEdu2))  
round(exp(coef(CMlogitEdu2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitEdu2)), exp(confint(CMlogitEdu2))), 2) # round to 2  
# Wealth Index  
CMlogitWI2 <- (svyglm(s1224~v190, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitWI2)  
coef(CMlogitWI2)  
exp(coef(CMlogitWI2))  
round(exp(coef(CMlogitWI2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitWI2)), exp(confint(CMlogitWI2))), 2) # round to 2  
# Religion  
CMlogitRel2 <- (svyglm(s1224~CM\_Religion, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitRel2)  
coef(CMlogitRel2)  
exp(coef(CMlogitRel2))  
round(exp(coef(CMlogitRel2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitRel2)), exp(confint(CMlogitRel2))), 2) # round to 2  
# Occupation  
CMlogitOcc2 <- (svyglm(s1224~CM\_Occupation, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitOcc2)  
coef(CMlogitOcc2)  
exp(coef(CMlogitOcc2))  
round(exp(coef(CMlogitOcc2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitOcc2)), exp(confint(CMlogitOcc2))), 2) # round to 2  
# Frequency of reading newspaper or magazine  
CMlogitRnpm2 <- (svyglm(s1224~v157, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitRnpm2)  
coef(CMlogitRnpm2)  
exp(coef(CMlogitRnpm2))  
round(exp(coef(CMlogitRnpm2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitRnpm2)), exp(confint(CMlogitRnpm2))), 2) # round to 2  
# Frequency of watching television  
CMlogitWt2 <- (svyglm(s1224~v159, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitWt2)  
coef(CMlogitWt2)  
exp(coef(CMlogitWt2))  
round(exp(coef(CMlogitWt2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitWt2)), exp(confint(CMlogitWt2))), 2) # round to 2  
# Frequency of listening to radio   
CMlogitLr2 <- (svyglm(s1224~v158, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitLr2)  
coef(CMlogitLr2)  
exp(coef(CMlogitLr2))  
round(exp(coef(CMlogitLr2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitLr2)), exp(confint(CMlogitLr2))), 2) # round to 2  
# Frequency of using Internet in last month  
CMlogitInt2 <- (svyglm(s1224~v171b, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogitInt2)  
coef(CMlogitInt2)  
exp(coef(CMlogitInt2))  
round(exp(coef(CMlogitInt2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogitInt2)), exp(confint(CMlogitInt2))), 2) # round to 2  
# Adjusted  
CMlogit2 <- (svyglm(s1224~CMAgeCat+v025+CM\_MS+v106+v190+CM\_Religion+CM\_Occupation+v157+v159+v158+v171b, family=quasibinomial, design=designCM, na.action = na.omit))  
summary(CMlogit2)  
coef(CMlogit2)  
exp(coef(CMlogit2))  
round(exp(coef(CMlogit2)), 2) # round to make it clearer  
round(cbind(OR = exp(coef(CMlogit2)), exp(confint(CMlogit2))), 2) # round to 2

sessionInfo()

## R version 4.1.1 (2021-08-10)  
## Platform: x86\_64-w64-mingw32/x64 (64-bit)  
## Running under: Windows 10 x64 (build 19045)  
##   
## Matrix products: default  
##   
## locale:  
## [1] LC\_COLLATE=English\_Nigeria.1252 LC\_CTYPE=English\_Nigeria.1252   
## [3] LC\_MONETARY=English\_Nigeria.1252 LC\_NUMERIC=C   
## [5] LC\_TIME=English\_Nigeria.1252   
##   
## attached base packages:  
## [1] stats graphics grDevices utils datasets methods base   
##   
## loaded via a namespace (and not attached):  
## [1] compiler\_4.1.1 fastmap\_1.1.0 cli\_3.4.1 tools\_4.1.1   
## [5] htmltools\_0.5.2 rstudioapi\_0.15.0 yaml\_2.3.7 rmarkdown\_2.25   
## [9] knitr\_1.44 xfun\_0.40 digest\_0.6.28 rlang\_1.1.1   
## [13] evaluate\_0.22