P8123 Final

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```
library(tidyverse)
library(survey)
library(ggsurvey)
library(tableone)
library(gtsummary)
library(sjPlot)

knitr::opts_chunk$set(
  message = FALSE,
  warning = FALSE
)

theme_set(theme_minimal() + theme(legend.position = "bottom"))


load("./data/nhanes_data.rda") #put files into data folder so everyone can run this
load("./data/nhanes_key.rda")
load("./data/key_guide.rda")
```

Problem statement: Controlling blood pressure (BP) reduces the risk for cardiovascular disease. However, the prevalence of BP control (i.e., systolic BP < 140 and diastolic BP < 90) among US adults with hypertension has decreased since 2013. We invite teams to analyze publicly available data from US adults to help identify potential causes or correlates of worsening BP control among US adults with hypertension over the past decade, as this may allow for development of effective interventions to help control BP and prevent cardiovascular disease.

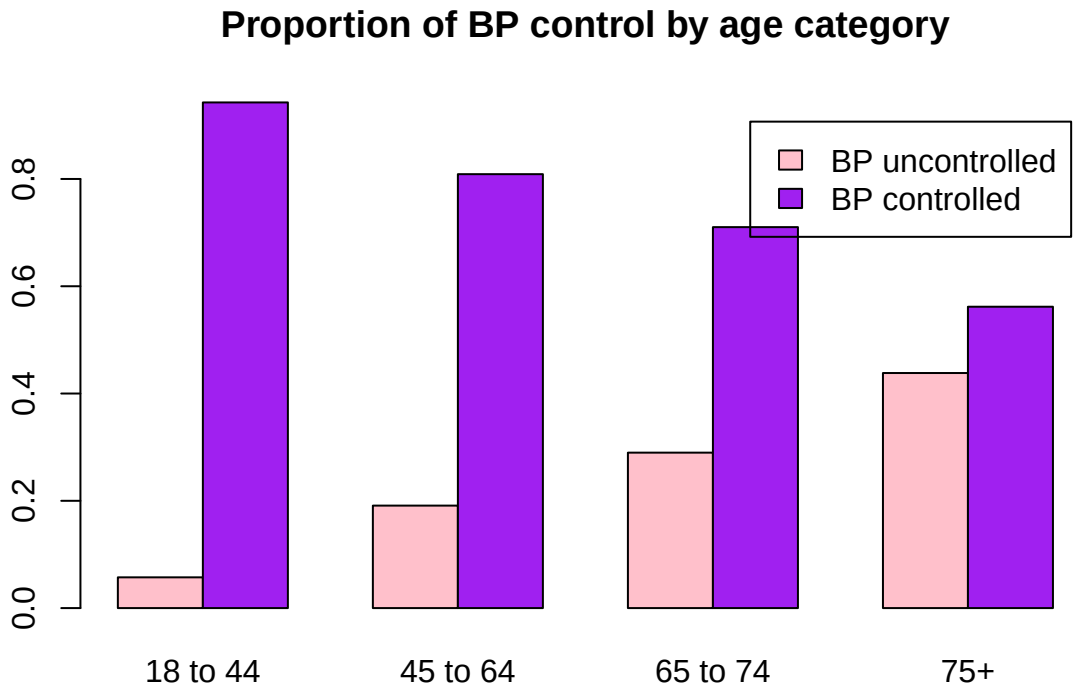
Svydesign and subset for hypertension patients 2013 onwards

```
dstrat <- svydesign(ids=~svy_psu, strata=~svy_strata, weights=~svy_weight_mec, data=nhanes_data, nest=T

htsub <- subset(dstrat, svy_subpop_htn==1) #limited to hypertension patients

htsub2 <- subset(htsub, svy_year=="2013-2014" | svy_year=="2015-2016" | svy_year=="2017-2020") #limited
```

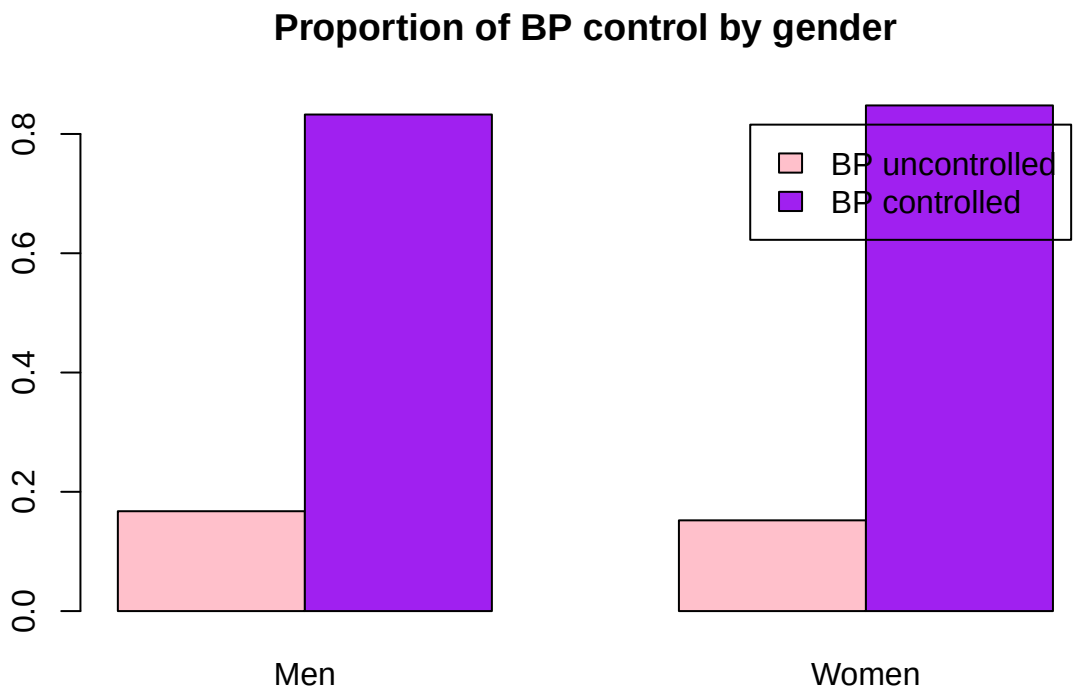
Some EDA

The **outcome** of interest -> **bp_control_140_90** OR **bp_uncontrolled_140_90**

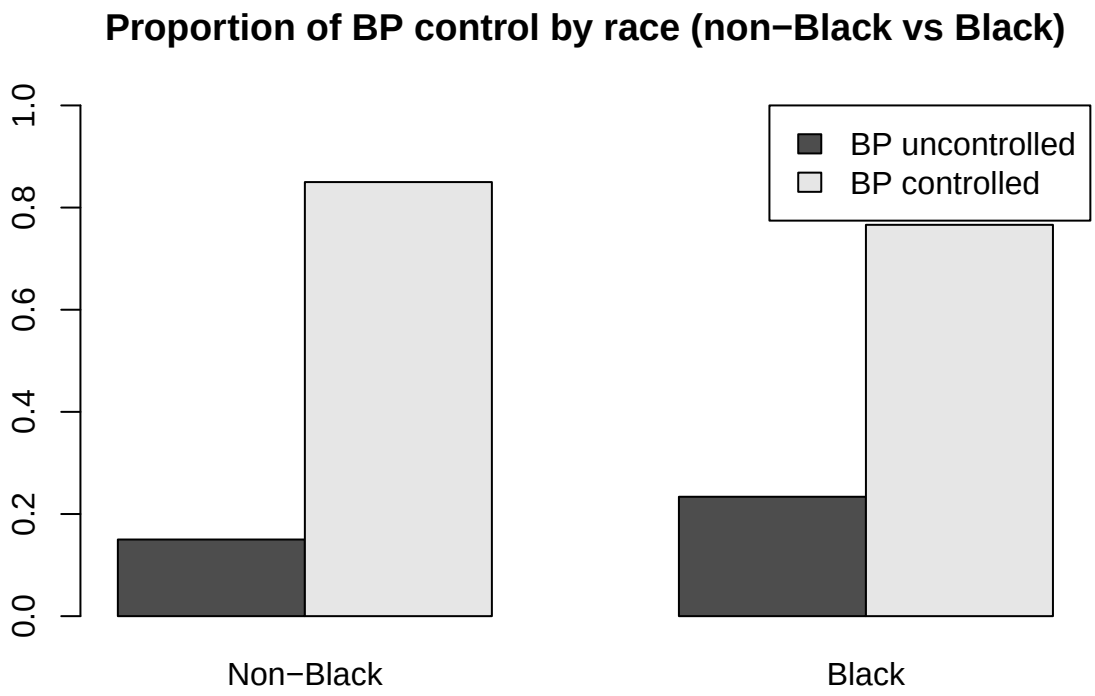
```r
#age -> so for older people, BP control is definitely lower
age <- svyby(~factor(bp_control_140_90), ~factor(demo_age_cat), design=htsub2, svymean, na.rm=TRUE)
barplot(age, legend.text=c("BP uncontrolled", "BP controlled"), col=c("pink", "purple"), main="Proporti
```



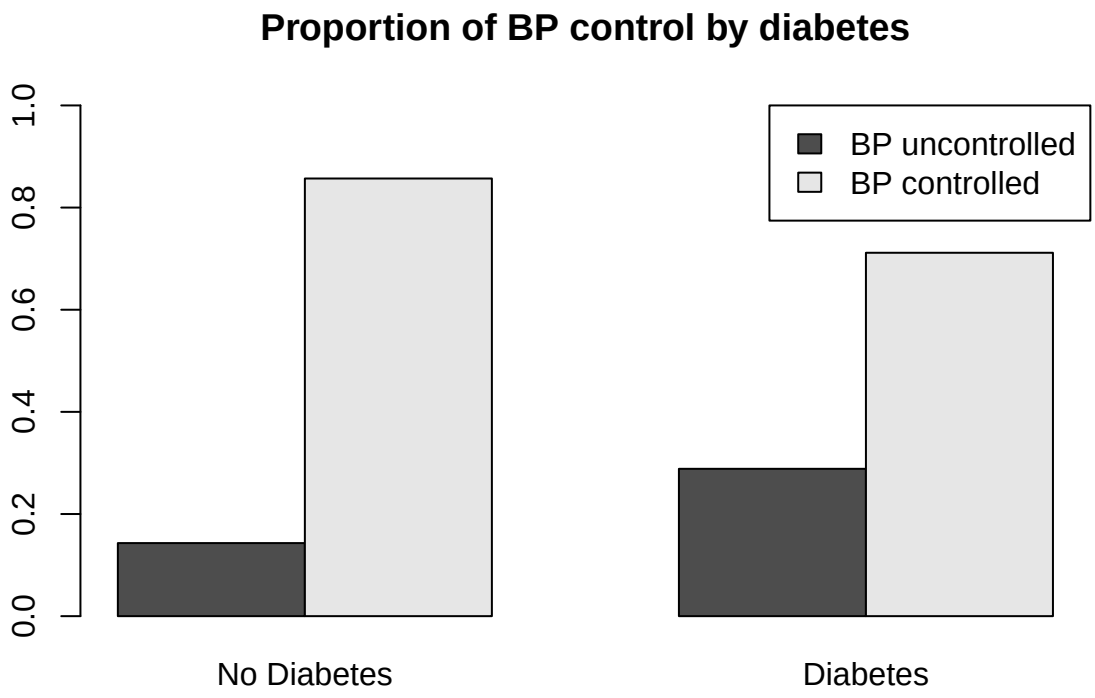

```r
#gender -> not really any difference
gender <- svyby(~factor(bp_control_140_90), ~factor(demo_gender), design=htsub2, svymean, na.rm=TRUE)
barplot(gender, legend.text=c("BP uncontrolled", "BP controlled"), col=c("pink", "purple"), main="Propo
```



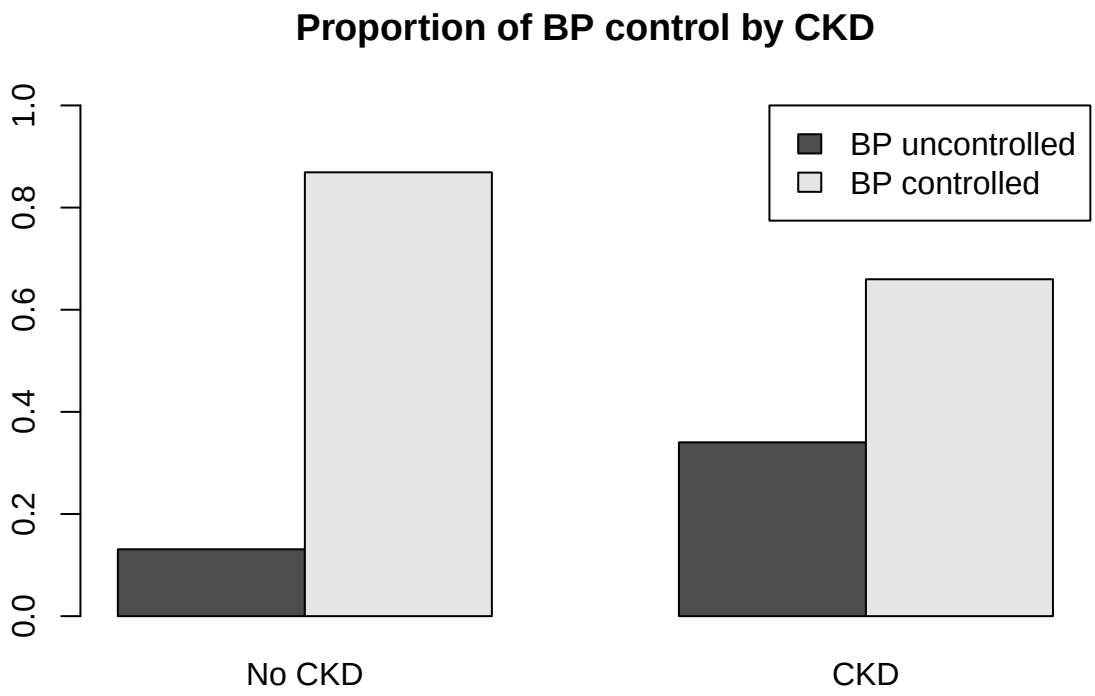

```r
#race -> for Black people vs non-Black people, BP control is lower
race <- svyby(~factor(bp_control_140_90), ~factor(demo_race_black), design=htsub2, svymean, na.rm=TRUE)
barplot(race,
        legend.text=c("BP uncontrolled", "BP controlled"),
        names.arg=c("Non-Black", "Black"),
        ylim=c(0, 1.0),
        args.legend = list(x = "topright"),
        main="Proportion of BP control by race (non-Black vs Black)")
```



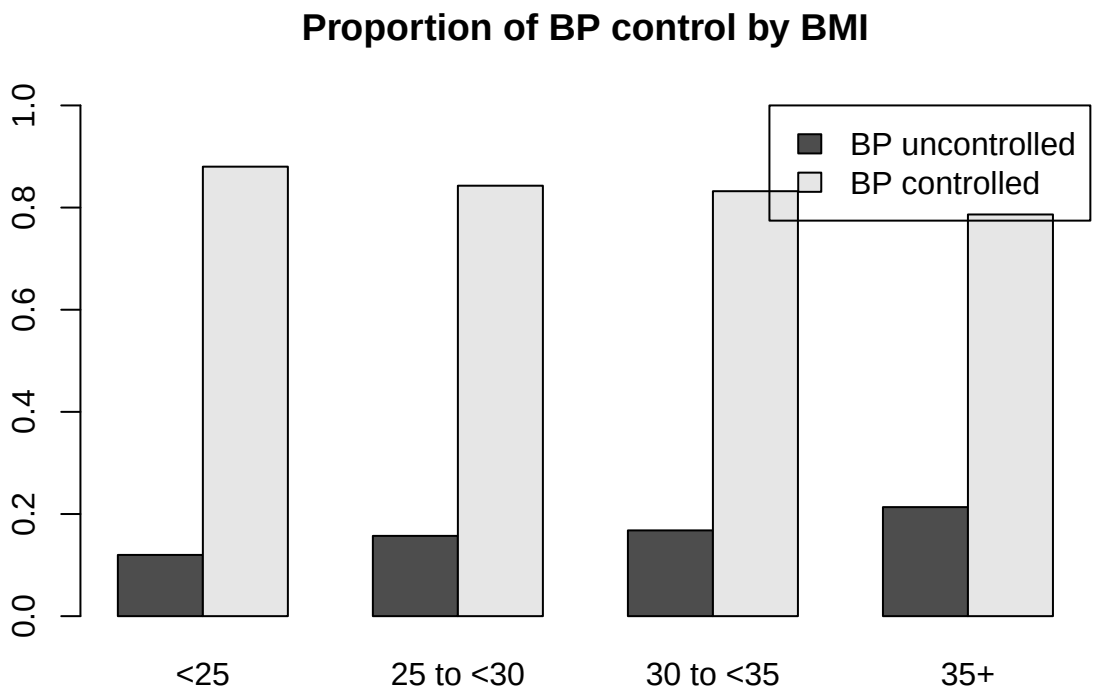

```
#diabetes
diabetes <- svyby(~factor(bp_control_140_90), ~factor(cc_diabetes), design=htsub2, svymean, na.rm=TRUE)
barplot(diabetes,
        legend.text=c("BP uncontrolled", "BP controlled"),
        names.arg=c("No Diabetes", "Diabetes"),
        ylim=c(0, 1.0),
        args.legend = list(x = "topright"),
        main="Proportion of BP control by diabetes")
```




```
#ckd
ckd <- svyby(~factor(bp_control_140_90), ~factor(cc_ckd), design=htsub2, svymean, na.rm=TRUE)
barplot(ckd,
        legend.text=c("BP uncontrolled", "BP controlled"),
        names.arg=c("No CKD", "CKD"),
        ylim=c(0, 1.0),
        args.legend = list(x = "topright"),
        main="Proportion of BP control by CKD")
```




```r
#bmi
bmi <- svyby(~factor(bp_control_140_90), ~factor(cc_bmi), design=htsub2, svymean, na.rm=TRUE)
barplot(bmi,
        legend.text=c("BP uncontrolled", "BP controlled"),
        ylim=c(0, 1.0),
        args.legend = list(x = "topright"),
        main="Proportion of BP control by BMI")
```




```
#meds recommended -> 100% for those with uncontrolled BP
# look at med recommended and meds taken ratio by different subgroups?

table(nhanes_data$bp_med_recommended_jnc7, nhanes_data$bp_med_use) #48% of people recommended medicatio
```

```
##
##          No   Yes
##   No  37755     0
##   Yes  7062 14690
```

```
svyCreateCatTable(vars= c("bp_med_recommended_jnc7" ,"bp_med_use"),
                  strata="demo_race",
                  data=htsub2) #across all races, the % of med use is lower than % recommended -? this
```

```
##                                    Stratified by demo_race
##                                     Non-Hispanic White  Non-Hispanic Black
##   n                                  443841370.8         78256419.3
##   bp_med_recommended_jnc7 = Yes (%) 156173388.2 (35.2)  33534720.2 (42.9)
##   bp_med_use = Yes (%)              111473163.2 (25.1)  23255215.8 (29.7)
##                                    Stratified by demo_race
##                                     Non-Hispanic Asian Hispanic
##   n                                  37820092.9         105372525.4
##   bp_med_recommended_jnc7 = Yes (%) 11080831.4 (29.3)  26424308.7 (25.1)
##   bp_med_use = Yes (%)               6822774.8 (18.0)  15828214.5 (15.0)
```

```
##                                     Stratified by demo_race
##                                      Other             p      test
##   n                                  24220134.3
##   bp_med_recommended_jnc7 = Yes (%) 8029041.0 (33.2)  <0.001
##   bp_med_use = Yes (%)              5443707.4 (22.5)  <0.001
```

```
## table 1

reset_gtsummary_theme()
theme_gtsummary_compact()
tab1 <- tbl_svysummary(data = htsub2, by = "bp_control_140_90", include = c("demo_age_cat", "demo_gende
                       label = list(demo_age_cat ~ "Age",
                                    demo_gender ~ "Gender",
                                    demo_race ~ "Race",
                                    cc_bmi ~ "BMI",
                                    cc_ckd ~ "Chronic Kidney Disease",
                                    cc_diabetes ~ "Diabetes",
                                    cc_cvd_any ~ "Cardiovascular Disease",
                                    bp_med_use ~ "BP Medication Use",
                                    chol_total ~ "Total Cholesterol",
                                    chol_hdl ~ "HDL",
                                    chol_ldl ~ "LDL",
                                    chol_trig ~ "Triglycerides",
                                    chol_med_use ~ "Cholesterol Medication Use")) %>%  add_stat_label()
  italicize_levels()

tab1
```

Table 1: **Subject Characteristics (Survey Weighted)**

Characteristic	**No**, N = 110,019,543	**Yes**, N = 579,490,999
Age, n (%)		
18 to 44	18,218,707 (17%)	299,580,713 (52%)
45 to 64	45,525,230 (41%)	192,746,908 (33%)
65 to 74	23,816,079 (22%)	58,369,736 (10%)
75+	22,459,527 (20%)	28,793,643 (5.0%)
Gender, n (%)		
Men	55,991,881 (51%)	278,426,528 (48%)
Women	54,027,662 (49%)	301,064,472 (52%)
Race, n (%)		
Non-Hispanic White	68,928,072 (63%)	374,913,299 (65%)
Non-Hispanic Black	18,291,583 (17%)	59,964,836 (10%)
Non-Hispanic Asian	5,715,421 (5.2%)	32,104,671 (5.5%)
Hispanic	13,404,152 (12%)	91,968,373 (16%)
Other	3,680,315 (3.3%)	20,539,820 (3.5%)
BMI, n (%)		
<25	23,597,988 (22%)	173,248,879 (30%)
25 to <30	33,526,572 (31%)	179,795,985 (32%)
30 to <35	23,810,864 (22%)	117,994,322 (21%)
35+	26,600,214 (25%)	97,987,747 (17%)
Unknown	2,483,906	10,464,066
Chronic Kidney Disease, n (%)	32,045,575 (29%)	62,111,324 (11%)
Diabetes, n (%)	22,552,554 (20%)	55,629,143 (9.6%)

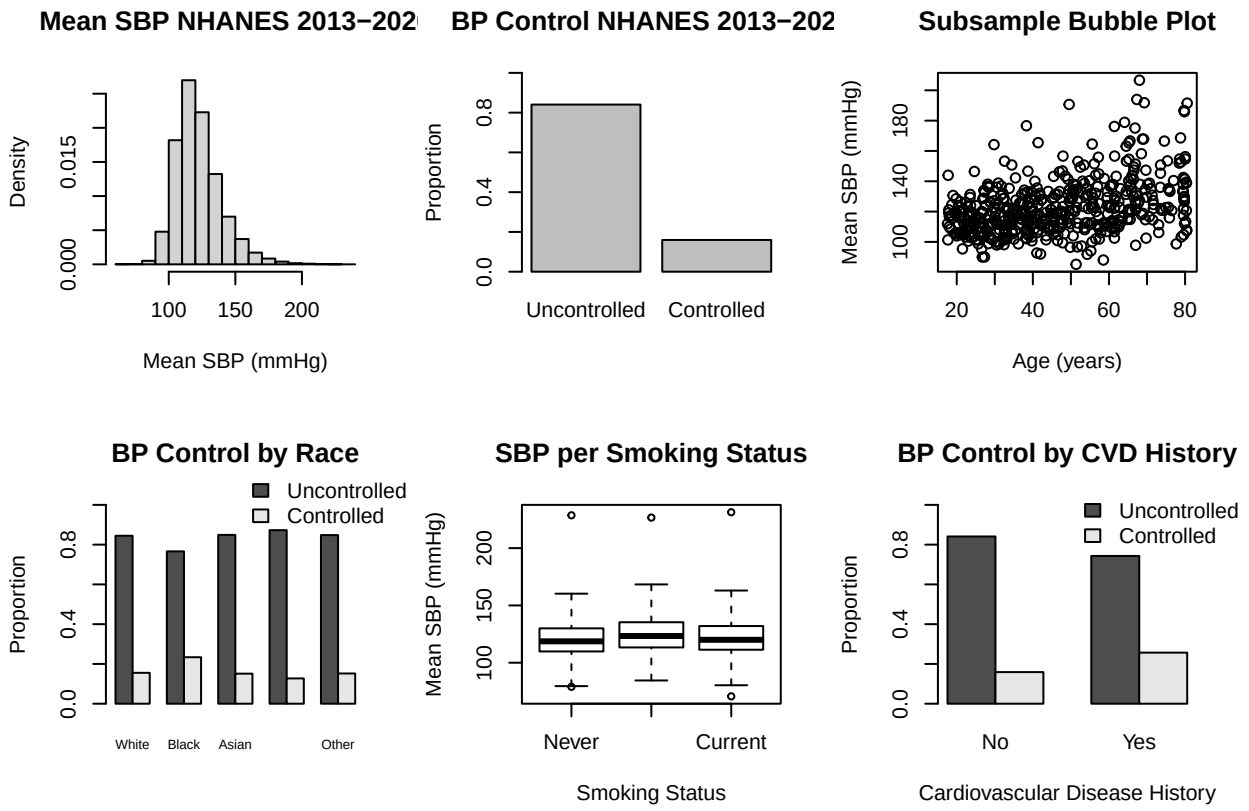
Characteristic	**No**, N = 110,019,543	**Yes**, N = 579,490,999
Cardiovascular Disease, n (%)	15,856,616 (14%)	40,856,909 (7.1%)
BP Medication Use, n (%)	51,549,103 (47%)	111,273,973 (19%)
Total Cholesterol, Median (IQR)	192 (163, 222)	183 (158, 211)
Unknown	63,100,407	325,591,825
HDL, Median (IQR)	52 (42, 65)	52 (43, 63)
Unknown	63,100,407	325,591,825
LDL, Median (IQR)	112 (88, 139)	109 (86, 133)
Unknown	63,221,679	325,731,647
Triglycerides, Median (IQR)	105 (72, 155)	89 (61, 135)
Unknown	63,221,679	325,731,647
Cholesterol Medication Use, n (%)	16,391,227 (34%)	47,895,434 (19%)
Unknown	62,505,218	323,610,642

Possible Figure 1:

I made a six-panel figure that could serve as our single Figure 1, feel free to change these plots to different things or remove ones we might not need. - Will

```
par(mfrow = c(2, 3))

svyhist(~bp_sys_mean, htsub2, main = "Mean SBP NHANES 2013-2020", xlab = "Mean SBP (mmHg)")

prop <- svymean(~bp_uncontrolled_140_90, htsub2, na.rm=TRUE)

barplot(prop,
        ylim=c(0, 1.0),
        main="BP Control NHANES 2013-2020", names.arg = c("Uncontrolled", "Controlled"),
        ylab = "Proportion")

 svyplot(bp_sys_mean~demo_age_years, htsub2, style = "subsample", xlab = "Age (years)", ylab = "Mean SBP

 race <- svyby(~bp_uncontrolled_140_90, ~factor(demo_race), htsub2, svymean, na.rm=TRUE)

barplot(race,
        legend.text=c("Uncontrolled", "Controlled"),
        ylim=c(0, 1.0),
        args.legend = list(x = "topright", bty = "n", inset = c(-0.20, -0.2)),
        main="BP Control by Race",
        ylab = "Proportion",
        names.arg = c("White", "Black", "Asian", "Hispanic", "Other"),
        cex.names = 0.6)

svyboxplot(bp_sys_mean~factor(cc_smoke), htsub2, na.rm=TRUE, xlab = "Smoking Status", ylab = "Mean SBP

cvd <- svyby(~bp_uncontrolled_140_90, ~factor(cc_cvd_chd), htsub2, na.rm = T, svymean)

barplot(cvd,
        legend.text=c("Uncontrolled", "Controlled"),
        ylim=c(0, 1.0),
        args.legend = list(x = "topright", bty = "n", inset = c(-0.20, -0.1)),
        main="BP Control by CVD History",
```

```
        xlab = "Cardiovascular Disease History",
        ylab = "Proportion")
```



Regression models - really don't know which variables to select

using the **bp_uncontrolled_140_90** variable instead of bp_control for regression

```
m1 <- svyglm(bp_uncontrolled_140_90 ~ demo_age_cat + demo_race + demo_gender + cc_smoke + cc_bmi+ cc_dia

#need to set BMI reference value to normal level rather than underweight

summary(m1)
```

```
##
## Call:
## svyglm(formula = bp_uncontrolled_140_90 ~ demo_age_cat + demo_race +
##     demo_gender + cc_smoke + cc_bmi + cc_diabetes + cc_ckd +
##     cc_cvd_any + chol_trig + chol_ldl + chol_hdl, design = htsub2,
##     family = quasibinomial())
##
## Survey design:
## subset(htsub, svy_year == "2013-2014" | svy_year == "2015-2016" |
##     svy_year == "2017-2020")
##
```

```
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 -4.2784289  0.2847878 -15.023  < 2e-16 ***
## demo_age_cat45 to 64         1.1528233  0.1252890   9.201 5.47e-11 ***
## demo_age_cat65 to 74         1.7627753  0.1598648  11.027 4.28e-13 ***
## demo_age_cat75+              2.4495017  0.1681808  14.565  < 2e-16 ***
## demo_raceNon-Hispanic Black  0.8670093  0.1173396   7.389 1.02e-08 ***
## demo_raceNon-Hispanic Asian  0.3999404  0.1137010   3.517 0.001199 **
## demo_raceHispanic            0.1559047  0.1091321   1.429 0.161743
## demo_raceOther               0.0207119  0.2431672   0.085 0.932594
## demo_genderWomen            -0.3087733  0.1070130  -2.885 0.006566 **
## cc_smokeFormer               0.0729305  0.1250743   0.583 0.563463
## cc_smokeCurrent              0.2004411  0.1685633   1.189 0.242179
## cc_bmi25 to <30             -0.0215815  0.1116762  -0.193 0.847849
## cc_bmi30 to <35              0.2261152  0.1130356   2.000 0.053045 .
## cc_bmi35+                    0.7023231  0.1345164   5.221 7.63e-06 ***
## cc_diabetesYes               0.3421597  0.1262108   2.711 0.010214 *
## cc_ckdYes                    0.6520772  0.1190915   5.475 3.49e-06 ***
## cc_cvd_anyYes               -0.0273710  0.1208875  -0.226 0.822158
## chol_trig                    0.0017308  0.0003819   4.533 6.21e-05 ***
## chol_ldl                     0.0052070  0.0012622   4.125 0.000209 ***
## chol_hdl                     0.0061692  0.0032180   1.917 0.063190 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 0.9486429)
##
## Number of Fisher Scoring iterations: 5
```

```
#need to look into subset of high cholesterol and hypertension?
```

Modeling medication use with bp_uncontrolled_140_90 outcome

Model is limited to survey design subset of hypertension patients from 2013-2020. We selected medication variables concerning self-reported blood pressure medication use (yes/no), the number of antihypertensive medication pills taken per day, the use of vasodilators (yes/no), alpha and beta blockers (yes/no), the use of angiotensin receptor blockers, and the use of statins or other cholesterol medication for cholesterol control (yes/no). These variables were selected based on their prior association with blood pressure levels in existing clinical trials and research studies.

```
meds_binary <- svyglm(bp_uncontrolled_140_90 ~ bp_med_use + bp_med_n_pills + bp_med_vasod + bp_med_alpha
```

Use of blood pressure medications, number of antihypertensive pills (1-4+), and angiotensin receptor blockers, were significantly associated with having uncontrolled blood pressure. The use of vasodilators, statins or other cholesterol medication, alpha and beta blockers, had non-statistically significant associations with having uncontrolled blood pressure.

Modeling medication use with bp_sys_mean outcome

We now model the continuous outcome of the average systolic blood pressure with the same medication covariates among those with hypertension from 2013-2020.

```
meds_continuous <- svyglm(bp_sys_mean ~ bp_med_use + bp_med_n_pills + bp_med_vasod + bp_med_alpha + bp_
```

The use of blood pressure medications, number of antihypertensive pills (1), and angiotensin receptor blockers were significantly associated with mean systolic blood pressure levels in those with hypertension from 2013-2020. The use of (2-4+) antihypertensive pills per day, vasodilators, alpha and beta blockers, and statins and other cholesterol medications, had non-statistically significant associations with mean systolic blood pressure levels in those with hypertension from 2013-2020.

Nested Models

Level One Demographic Characteristics.

```
model_1 <- svyglm(bp_uncontrolled_140_90 ~ demo_age_cat + demo_race + demo_gender, #demographics
                  design = htsub2, family=quasibinomial())

summary(model_1)
```

```
##
## Call:
## svyglm(formula = bp_uncontrolled_140_90 ~ demo_age_cat + demo_race +
##     demo_gender, design = htsub2, family = quasibinomial())
##
## Survey design:
## subset(htsub, svy_year == "2013-2014" | svy_year == "2015-2016" |
##     svy_year == "2017-2020")
##
## Coefficients:
##                              Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 -2.92319    0.09320 -31.364  < 2e-16 ***
## demo_age_cat45 to 64         1.41571    0.07074  20.014  < 2e-16 ***
## demo_age_cat65 to 74         2.01652    0.07848  25.696  < 2e-16 ***
## demo_age_cat75+              2.70181    0.10722  25.200  < 2e-16 ***
## demo_raceNon-Hispanic Black  0.86309    0.07301  11.822  1.1e-15 ***
## demo_raceNon-Hispanic Asian  0.26243    0.07708   3.405  0.00136 **
## demo_raceHispanic            0.23525    0.07650   3.075  0.00350 **
## demo_raceOther               0.27350    0.17971   1.522  0.13474
## demo_genderWomen            -0.21386    0.06224  -3.436  0.00124 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 0.9818051)
##
## Number of Fisher Scoring iterations: 5
```

Level Two Health-related Characteristics

```
model_2 <- svyglm(bp_uncontrolled_140_90 ~ demo_age_cat + demo_race + demo_gender + #demographics
                    cc_smoke + cc_bmi+ cc_diabetes + cc_ckd + cc_cvd_any + chol_trig + chol_ldl + chol_
                  design = htsub2, family=quasibinomial())
summary(model_2)
```

```
##
## Call:
## svyglm(formula = bp_uncontrolled_140_90 ~ demo_age_cat + demo_race +
##     demo_gender + cc_smoke + cc_bmi + cc_diabetes + cc_ckd +
##     cc_cvd_any + chol_trig + chol_ldl + chol_hdl, design = htsub2,
##     family = quasibinomial())
##
## Survey design:
## subset(htsub, svy_year == "2013-2014" | svy_year == "2015-2016" |
##     svy_year == "2017-2020")
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 -4.2784289  0.2847878 -15.023  < 2e-16 ***
## demo_age_cat45 to 64         1.1528233  0.1252890   9.201 5.47e-11 ***
## demo_age_cat65 to 74         1.7627753  0.1598648  11.027 4.28e-13 ***
## demo_age_cat75+              2.4495017  0.1681808  14.565  < 2e-16 ***
## demo_raceNon-Hispanic Black  0.8670093  0.1173396   7.389 1.02e-08 ***
## demo_raceNon-Hispanic Asian  0.3999404  0.1137010   3.517 0.001199 **
## demo_raceHispanic            0.1559047  0.1091321   1.429 0.161743
## demo_raceOther               0.0207119  0.2431672   0.085 0.932594
## demo_genderWomen            -0.3087733  0.1070130  -2.885 0.006566 **
## cc_smokeFormer               0.0729305  0.1250743   0.583 0.563463
## cc_smokeCurrent              0.2004411  0.1685633   1.189 0.242179
## cc_bmi25 to <30             -0.0215815  0.1116762  -0.193 0.847849
## cc_bmi30 to <35              0.2261152  0.1130356   2.000 0.053045 .
## cc_bmi35+                    0.7023231  0.1345164   5.221 7.63e-06 ***
## cc_diabetesYes               0.3421597  0.1262108   2.711 0.010214 *
## cc_ckdYes                    0.6520772  0.1190915   5.475 3.49e-06 ***
## cc_cvd_anyYes               -0.0273710  0.1208875  -0.226 0.822158
## chol_trig                    0.0017308  0.0003819   4.533 6.21e-05 ***
## chol_ldl                     0.0052070  0.0012622   4.125 0.000209 ***
## chol_hdl                     0.0061692  0.0032180   1.917 0.063190 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 0.9486429)
##
## Number of Fisher Scoring iterations: 5
```

Level Three Medication Use

```
model_3 <- svyglm(bp_uncontrolled_140_90 ~ demo_age_cat + demo_race + demo_gender + #demographics
                    cc_smoke + cc_bmi+ cc_diabetes + cc_ckd + cc_cvd_any + chol_trig + chol_ldl + chol_
                    bp_med_use + bp_med_n_pills + bp_med_vasod + bp_med_alpha + #medication
                    bp_med_beta + bp_med_angioten + chol_med_statin + chol_med_use, #medication
                  design = htsub2, family=quasibinomial())
summary(model_3)
```

```
##
## Call:
## svyglm(formula = bp_uncontrolled_140_90 ~ demo_age_cat + demo_race +
```

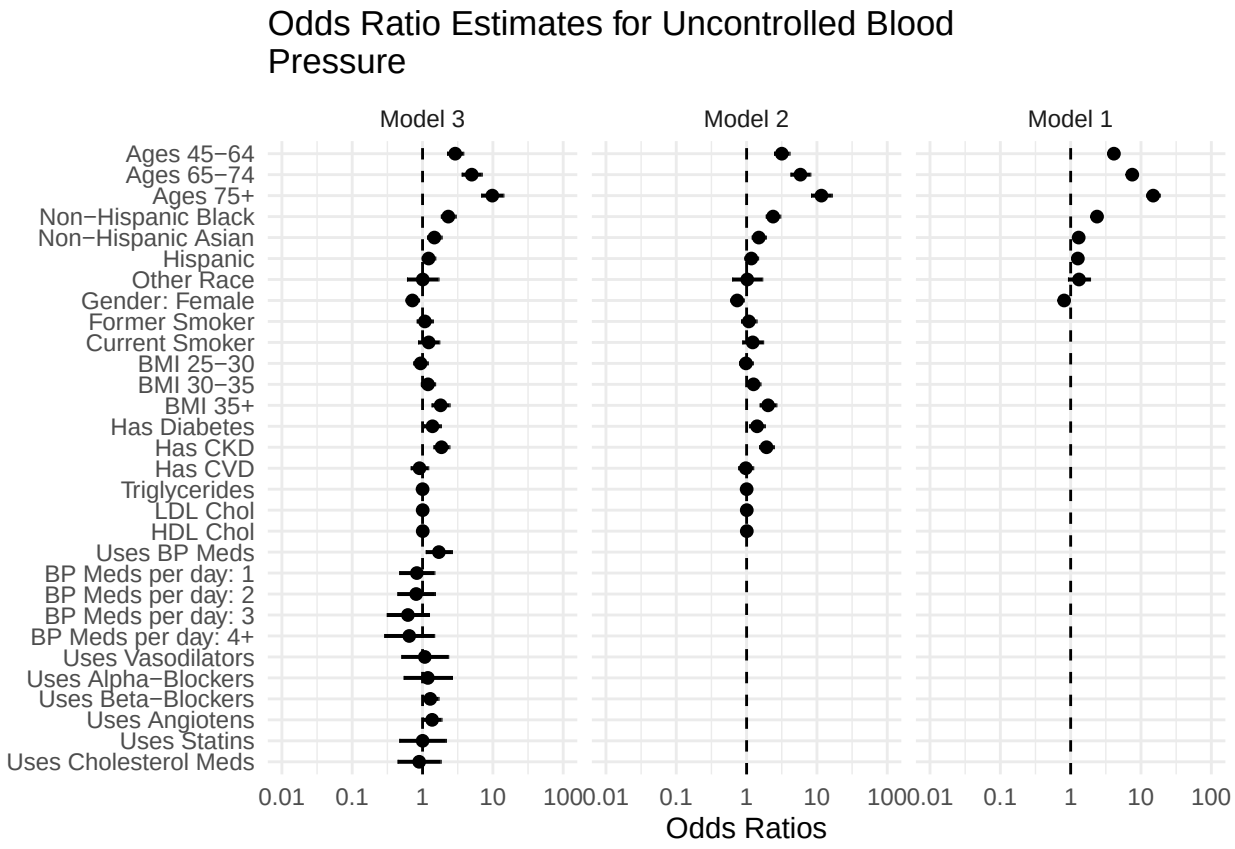
```
##     demo_gender + cc_smoke + cc_bmi + cc_diabetes + cc_ckd +
##     cc_cvd_any + chol_trig + chol_ldl + chol_hdl + bp_med_use +
##     bp_med_n_pills + bp_med_vasod + bp_med_alpha + bp_med_beta +
##     bp_med_angioten + chol_med_statin + chol_med_use, design = htsub2,
##     family = quasibinomial())
##
## Survey design:
## subset(htsub, svy_year == "2013-2014" | svy_year == "2015-2016" |
##     svy_year == "2017-2020")
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 -4.2354978  0.2697846 -15.700 1.86e-14 ***
## demo_age_cat45 to 64         1.0690468  0.1288047   8.300 1.19e-08 ***
## demo_age_cat65 to 74         1.6111371  0.1594032  10.107 2.58e-10 ***
## demo_age_cat75+              2.2844522  0.1762558  12.961 1.35e-12 ***
## demo_raceNon-Hispanic Black  0.8434587  0.1182782   7.131 1.79e-07 ***
## demo_raceNon-Hispanic Asian  0.3873648  0.1161263   3.336 0.002659 **
## demo_raceHispanic            0.1973600  0.1073986   1.838 0.078030 .
## demo_raceOther               0.0066420  0.2505540   0.027 0.979062
## demo_genderWomen            -0.3324135  0.1055494  -3.149 0.004206 **
## cc_smokeFormer               0.0752089  0.1281457   0.587 0.562533
## cc_smokeCurrent              0.2019008  0.1687557   1.196 0.242761
## cc_bmi25 to <30             -0.0631372  0.1149384  -0.549 0.587664
## cc_bmi30 to <35              0.1786980  0.1134249   1.575 0.127718
## cc_bmi35+                    0.5917701  0.1431533   4.134 0.000351 ***
## cc_diabetesYes               0.3255830  0.1337452   2.434 0.022397 *
## cc_ckdYes                    0.6201295  0.1265869   4.899 4.84e-05 ***
## cc_cvd_anyYes               -0.0996443  0.1392883  -0.715 0.481002
## chol_trig                    0.0016698  0.0003928   4.252 0.000259 ***
## chol_ldl                     0.0050071  0.0012360   4.051 0.000434 ***
## chol_hdl                     0.0063284  0.0032239   1.963 0.060870 .
## bp_med_useYes                0.5344699  0.2079053   2.571 0.016488 *
## bp_med_n_pillsOne           -0.1874577  0.2794390  -0.671 0.508476
## bp_med_n_pillsTwo           -0.2084591  0.2981528  -0.699 0.490901
## bp_med_n_pillsThree         -0.4789832  0.3351850  -1.429 0.165378
## bp_med_n_pillsFour or more  -0.4355646  0.3967429  -1.098 0.282731
## bp_med_vasodYes              0.0736384  0.3720228   0.198 0.844692
## bp_med_alphaYes              0.1738527  0.3837901   0.453 0.654464
## bp_med_betaYes               0.2530225  0.1310938   1.930 0.065016 .
## bp_med_angiotenYes           0.3140413  0.1492004   2.105 0.045525 *
## chol_med_statinYes           0.0018895  0.3706140   0.005 0.995973
## chol_med_useYes             -0.1105545  0.3425864  -0.323 0.749602
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 0.941334)
##
## Number of Fisher Scoring iterations: 5
```

I added the nested models based on three levels. Should we also make figures based on the significant variables from these models? If these models look good, I will proceed making the table two - Harry

Figure 2: Forest plot of estimates from models 1-3

This plots estimates and 95% CI for odds ratios from models 1-3 and can be our figure 2 - Will

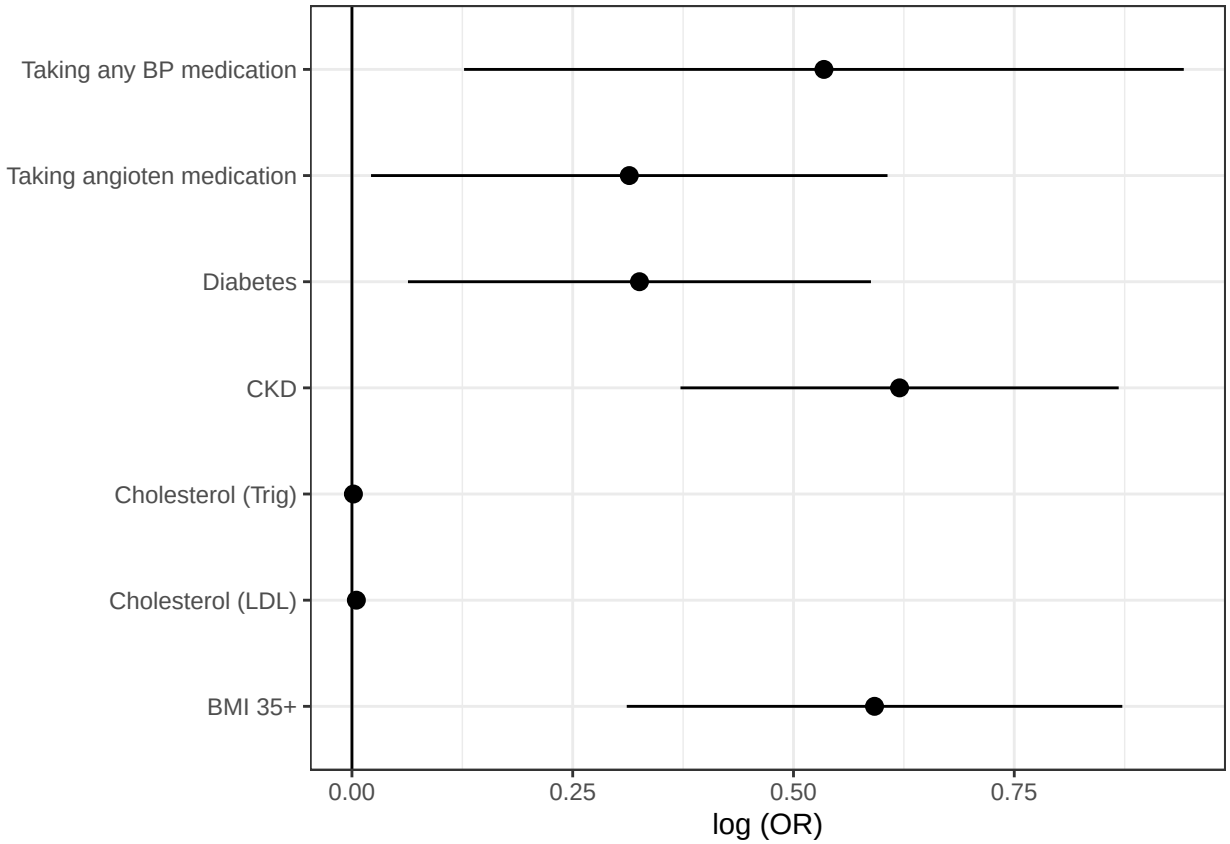
```
plot_models(model_1, model_2, model_3, transform = "exp", legend.title = "", show.p = T, grid = T, show
```



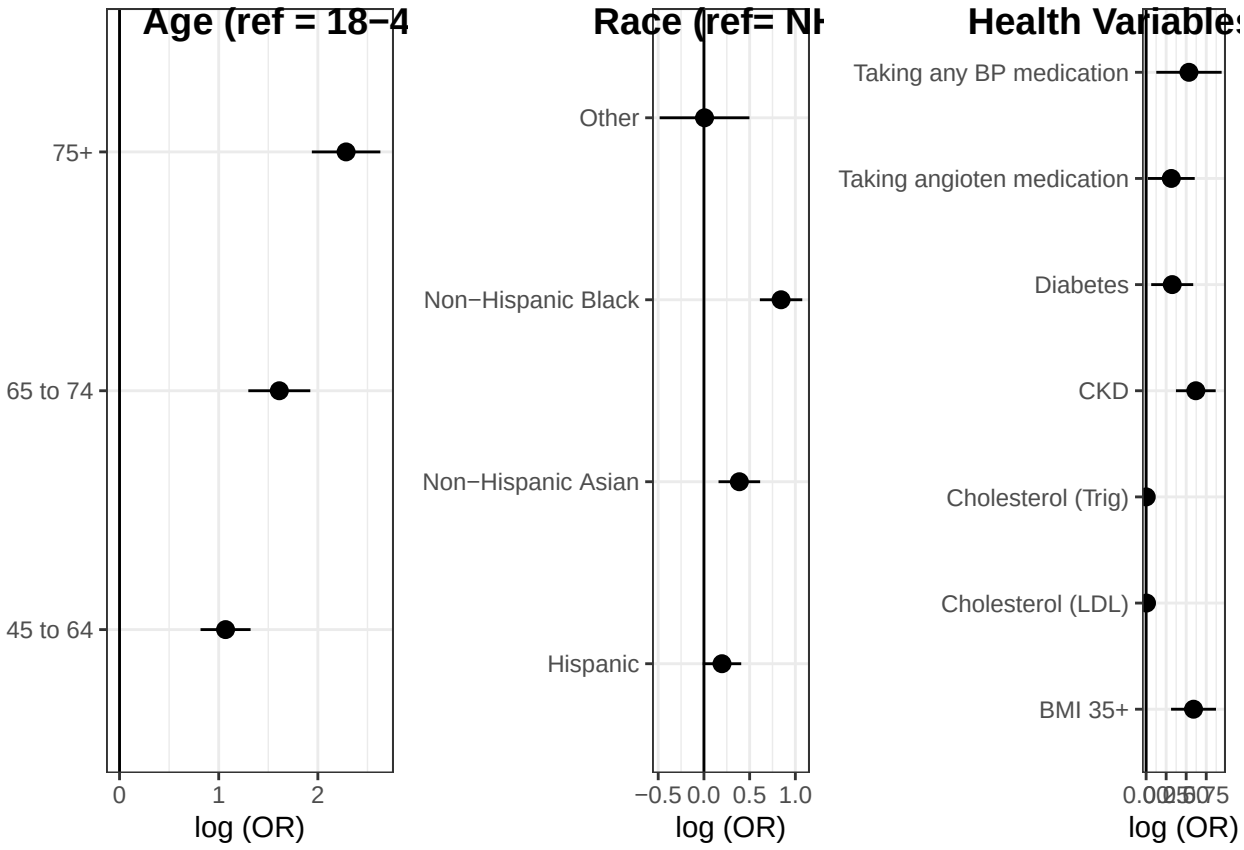
Farizah's code for plotting forest plot of model 3, I don't think it's outputting correctly:

```
#age
reg_age <- matrix(c(1.0690468, 1.6111371, 2.2844522, 0.1288047, 0.1594032, 0.1762558), byrow=FALSE, nco

colnames(reg_age) <- c("log_or", "se")

reg_age <- reg_age %>% as_tibble()
reg_age$age <- c("45 to 64", "65 to 74", "75+" )
reg_age$l95 <- reg_age$log_or-1.96*reg_age$se
reg_age$u95 <- reg_age$log_or+1.96*reg_age$se

age_plot <- ggplot(reg_age, aes(x = log_or, y = age)) + geom_point() + geom_pointrange(aes(xmin = l95, 
#race

reg_race <- matrix(c(0.8434587, 0.3873648, 0.1973600, 0.0066420, 0.1182782, 0.1161263, 0.1073986, 0.250
colnames(reg_race) <- c("log_or", "se")

reg_race <- reg_race %>% as_tibble()
reg_race$race <- c("Non-Hispanic Black", "Non-Hispanic Asian", "Hispanic", "Other" )
```

```r
reg_race$l95 <- reg_race$log_or-1.96*reg_race$se
reg_race$u95 <- reg_race$log_or+1.96*reg_race$se

race_plot <- ggplot(reg_race, aes(x = log_or, y = race)) + geom_point() + geom_pointrange(aes(xmin = l95

#health

reg_health <- matrix(c(0.5917701, 0.3255830, 0.6201295, 0.0016698, 0.0050071, 0.5344699, 0.3140413, 0.14

colnames(reg_health) <- c("log_or", "se")


reg_health <- reg_health %>% as_tibble()
reg_health$Variable <- c("BMI 35+", "Diabetes", "CKD", "Cholesterol (Trig)", "Cholesterol (LDL)", "Takin

reg_health$l95 <- reg_health$log_or-1.96*reg_health$se
reg_health$u95 <- reg_health$log_or+1.96*reg_health$se

health_plot <- ggplot(reg_health, aes(x = log_or, y = Variable)) + geom_point() + geom_pointrange(aes(xm

health_plot
```




```r
library(ggpubr)
ggarrange(age_plot, race_plot, health_plot, ncol =3, nrow=1, labels = c("Age (ref = 18-44)", "Race (ref=
```


Age (ref = 18−4
75+
65 to 74
45 to 64
0
1
2
log (OR)
Race (ref= NH
Other
Non−Hispanic Black
Non−Hispanic Asian
Hispanic
−0.5
0.0
0.5
1.0
log (OR)
Health Variables
Taking any BP medication
Taking angioten medication
Diabetes
CKD
Cholesterol (Trig)
Cholesterol (LDL)
BMI 35+
log (OR)