Homework 2

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```
library(tidyverse)
library(knitr)
library(PSweight)
```

Part 1

Question 1

```
hsr <- read.table("data/hw2/HSR.txt", header = TRUE)
#p_z = P(Y(z)==1)
#target estimand is ATE p_1 - p_2
X <- apply(hsr[,c(1,3,4,5,6,7,8,12)], MARGIN = 2, factor)
Z <- factor(hsr$pg)
Y <- hsr$i_aqoc
```

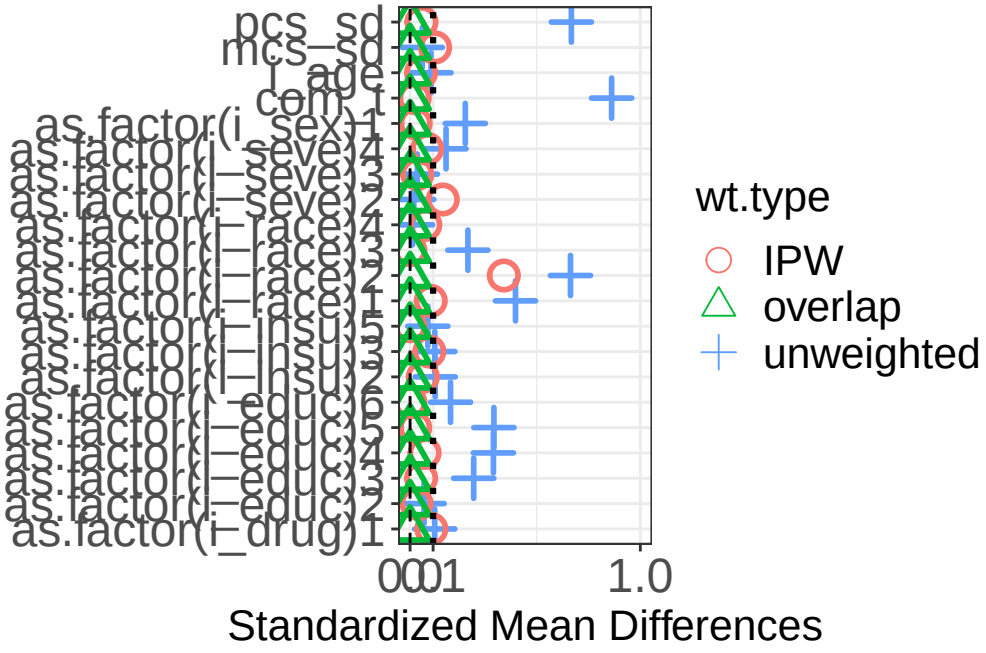
a)

```
ps_formula <- as.factor(pg) ~ i_age + as.factor(i_sex) + as.factor(i_race) + as.factor(i_e

prop_scores <- glm(ps_formula, family = "binomial"
                   , data = hsr)$fitted.values

prop_score_summary <- SumStat(ps.formula = ps_formula
                              , weight = c('IPW','overlap')
                              ,data = hsr)
```

```
#Estimated propensity Scores
cat(prop_scores)
```

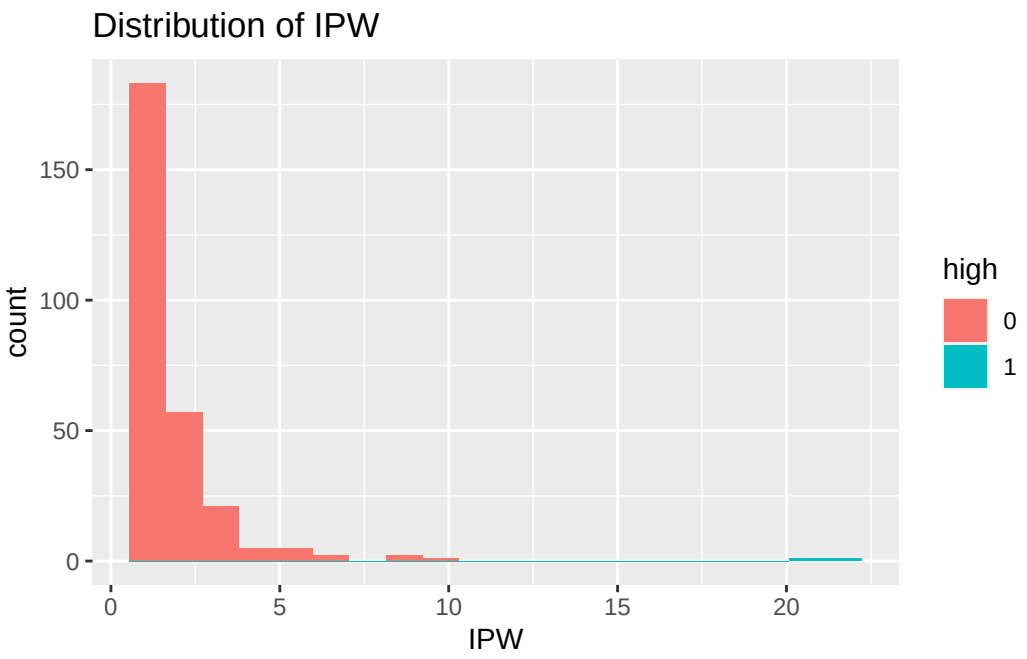
```
0.3666097 0.4691487 0.5608349 0.8235156 1.73677e-07 0.2859149 0.6462016 0.841273 0.3948395 0
```

```
#checking balance via ASD
plot(prop_score_summary, metric = "ASD")
```



From the love plot we see that most of the covariates have an ASD above 0.1 when unweighted but perform much better with IPW. mcs_sd and severity2 are slightly above 0.1 and race2 is around 0.35 under IPW. The covariates are perfected balanced with overlap weighing.

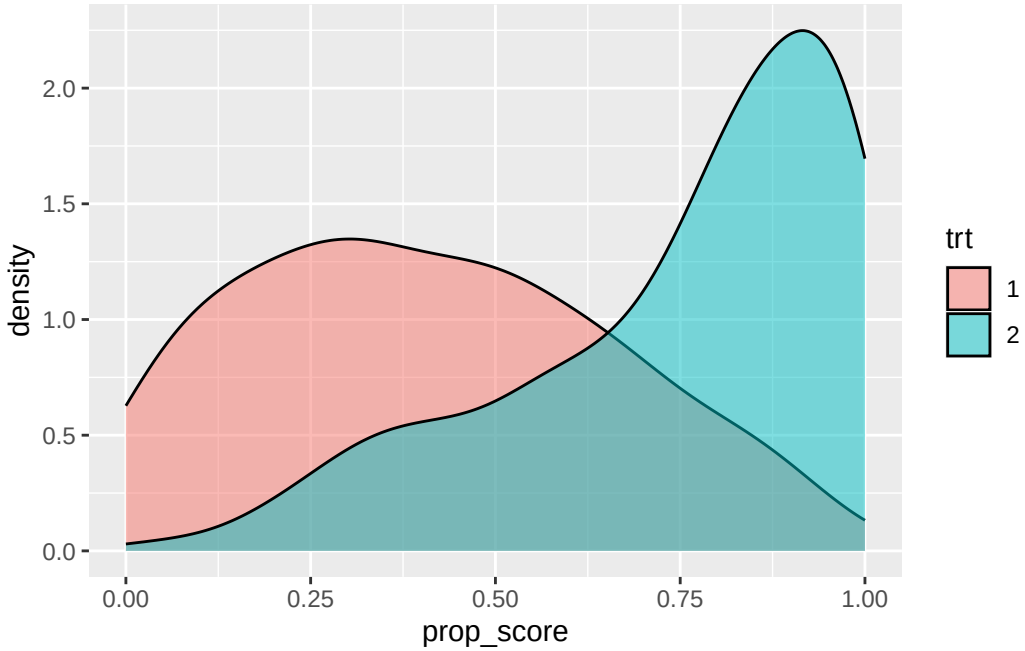
```
#Inverse Probability Weights
IPW_weights <- ifelse(Z == 2, 1/prop_scores,1/(1-prop_scores))

#Normalized IPW
IPW_weights_norm <- numeric(length(IPW_weights))
IPW_weights_norm[Z==2] = IPW_weights[Z==2]/sum(IPW_weights[Z==2])
IPW_weights_norm[Z==1] = IPW_weights[Z==1]/sum(IPW_weights[Z==1])
ggplot(data.frame(weights = IPW_weights
                  ,high=as.factor(ifelse(IPW_weights>15,1,0)))
       , aes(x = weights, fill = high)) +
  geom_histogram(bins = 20) +
  labs(title = "Distribution of IPW", x = "IPW")
```



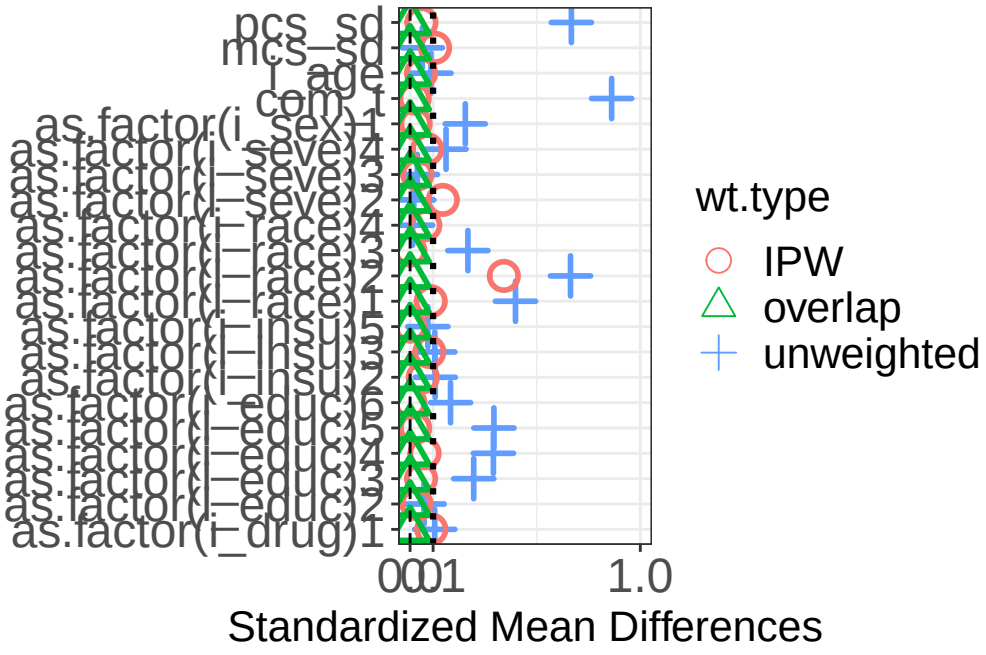
Looking at he distribution of IPW there are 2 observations with high weights relative to the sample.

b)

```
tibble(
  prop_score = prop_scores,
  trt = Z
) |>
  ggplot(aes(x = prop_score, fill = trt)) +
  geom_density(alpha = 0.5)
```




```
plot(prop_score_summary, metric = "ASD")
```



From the density plot of propensity scores by group, there is good overlap. The love plot shows good balance with overlap weighting and IPW weighting.

c)

```
unweighted <- prop_score_summary$unweighted.sumstat[,1:2]
colnames(unweighted) <- c("unweighted.trt1", "unweighted.trt2")

ipw_weighted <- prop_score_summary$IPW.sumstat[,1:2]
colnames(ipw_weighted) <- c("IPW.trt1", "IPW.trt2")

overlap_weighted <- prop_score_summary$overlap.sumstat[,1:2]
colnames(overlap_weighted) <- c("overlap.trt1", "overlap.trt2")

tab1 <- cbind(unweighted, ipw_weighted, overlap_weighted) |> round(4)
tab1 |>
  kable()
```

	unweighted.trt1	unweighted.trt2	IPW.trt1	IPW.trt2	overlap.trt1	overlap.trt2
i_age	40.4571	39.6532	41.5684	41.1479	41.1248	41.1248
as.factor(i_sex)1	0.7619	0.6532	0.7181	0.7071	0.7152	0.7152
as.factor(i_race)1	0.8381	0.6416	0.7601	0.7205	0.8236	0.8236
as.factor(i_race)2	0.0095	0.2197	0.0269	0.1371	0.0200	0.0200
as.factor(i_race)3	0.0571	0.0116	0.0374	0.0372	0.0380	0.0380
as.factor(i_race)4	0.0667	0.0694	0.0765	0.0597	0.0752	0.0752
as.factor(i_educ)2	0.0190	0.0116	0.0145	0.0114	0.0165	0.0165
as.factor(i_educ)3	0.0952	0.0289	0.0561	0.0455	0.0608	0.0608
as.factor(i_educ)4	0.3905	0.2254	0.2862	0.3152	0.3064	0.3064
as.factor(i_educ)5	0.2571	0.4277	0.3621	0.3514	0.3213	0.3213
as.factor(i_educ)6	0.2286	0.3064	0.2771	0.2765	0.2950	0.2950
as.factor(i_insu)2	0.2571	0.3064	0.2515	0.2761	0.2535	0.2535
as.factor(i_insu)3	0.0000	0.0058	0.0000	0.0035	0.0000	0.0000
as.factor(i_insu)5	0.0571	0.0405	0.0309	0.0307	0.0254	0.0254
as.factor(i_drug)1	0.9905	0.9769	0.9941	0.9846	0.9925	0.9925
as.factor(i_seve)2	0.2381	0.2312	0.2176	0.2794	0.2508	0.2508
as.factor(i_seve)3	0.4667	0.4509	0.3963	0.4118	0.4453	0.4453
as.factor(i_seve)4	0.1905	0.1329	0.1755	0.1478	0.1587	0.1587
com_t	2.9143	1.7168	2.4733	2.4398	2.3778	2.3778
pcs_sd	41.4148	48.2981	46.1089	46.6206	45.3764	45.3764
mcs_sd	48.9392	48.4198	48.1294	46.9954	48.4299	48.4299

d)

```
Z <- ifelse(Z == 1,0,1)
ps.hsr <- as.factor(pg) ~ i_age + as.factor(i_sex) + as.factor(i_race) + as.factor(i_educ)

ate.ipw.norm <- PSweight(ps.formula = ps.hsr, yname = "i_aqoc", data = hsr
                    , weight = "IPW")
ato.overlap <- PSweight(ps.formula = ps.hsr, yname = "i_aqoc", data = hsr
                    , weight = "overlap")
ate.ipw.nonnorm <- summary(lm(i_aqoc ~ pg, data = hsr, weights = IPW_weights))$coefficient
results.ate <- rbind(summary(ate.ipw.norm, type = "DIF", contrast = c(1,-1))$estimates[,1:
      summary(ato.overlap, type = "DIF", contrast = c(1,-1))$estimates[,1:2],
      ate.ipw.nonnorm)
```

```
rownames(results.ate) <- c("ATE IPW Normalized", "ATO Overlap", "ATE NonNormalized")
results.ate |> round(4)
```

```
                  Estimate Std.Error
ATE IPW Normalized   0.1455    0.0562
ATO Overlap          0.1272    0.0607
ATE NonNormalized   -0.1455    0.0527
```

Question 2

a)

```
ps_formula <- as.factor(pg) ~ i_age + as.factor(i_sex) + as.factor(i_race) + as.factor(i_e

prop_scores <- glm(ps_formula, family = "binomial"
                    , data = hsr)$fitted.values

hsr_subsetted <- subset(hsr, i_sex == 1) |> mutate(across(1:11, scale))
hsr_subsetted$ipw_weights <- ifelse(hsr_subsetted$pg == 1, 1/prop_scores,1/(1-prop_scores)
att.subgroup <- summary(lm(i_aqoc ~ pg + i_age  + as.factor(i_race) + as.factor(i_educ) +

att.subgroup
```

```
   Estimate  Std. Error
-0.11791118  0.05743876
```

b)

```
ps_formula <- as.factor(pg) ~ i_age + as.factor(i_race) + as.factor(i_educ) + as.factor(i_

prop_scores <- glm(ps_formula, family = "binomial"
                   , data = hsr)$fitted.values

hsr_subsetted <- subset(hsr, i_sex == 1)
hsr_subsetted$ipw_weights <- ifelse(hsr_subsetted$pg == 1, 1/prop_scores,1/(1-prop_scores)

hsr_subsetted <- hsr_subsetted |> mutate(across(1:11, scale))
att.subgroup <- summary(lm(i_aqoc ~ pg + i_age  + as.factor(i_race) + as.factor(i_educ) +
att.subgroup
```

```
   Estimate  Std. Error
-0.09025359  0.04397855
```

c)

```
hsr_subsetted <- subset(hsr, i_sex == 1) |>mutate(across(1:11, scale))
ps.hsr <- as.factor(pg) ~ i_age + as.factor(i_race) + as.factor(i_educ) + as.factor(i_insu


summary(PSweight(ps.formula = ps.hsr, yname = "i_aqoc", data = hsr_subsetted
                   , weight = "IPW"))$estimates[,1:2]
```

```
   Estimate   Std.Error
-0.13034248  0.06778558
```

Option (c) is most likely the best way to estimate $E[Y(1)|V=1)] - E[Y(2)|V=1]$ because it adjusts the propensity score estimation to the subgroup. This helps with incorporating information specific to V=1

Question 3

a)

```
Z <- ifelse(hsr$pg == 1, 1,0)
X <- scale(as.matrix(hsr[,2:11]))
```

```r
Y <- hsr$i_aqoc
delta <- summary(glm(Y~X + Z + X*Z, family = "binomial"))$coefficients["Z",1]
Q <- exp(delta)
Q
```

```
[1] 2.928333
```

b)

```r
model <- glm(Y~X + Z + X*Z, family = "binomial")
p <- predict(model, type = "response")

phat_1 <- mean(p[Z ==1])
phat_2 <- mean(p[Z ==0])
Q <- (phat_1*(1-phat_2))/(phat_2*(1-phat_1))
Q
```

```
[1] 2.253486
```

c)

```r
new_dat1 <-  model[["model"]] |> mutate(Z = rep(1,length(Y)))
new_dat2 <-  model[["model"]] |> mutate(Z = rep(0,length(Y)))

p1 <- predict(model, type = "response",newdata = new_dat1)
p2 <- predict(model, type = "response",newdata = new_dat2)
phat_1 <- mean(p1)
phat_2 <- mean(p2)
Q <- (phat_1*(1-phat_2))/(phat_2*(1-phat_1))
Q
```

```
[1] 1.948134
```

d)

```r
prop_score = glm(Z ~ X, family = binomial)$fitted.values

q.prop_score = quantile(prop_score, c(0.2,0.4,0.6,0.8))
```

```r
stratas = cut(prop_score, breaks = c(0,q.prop_score,1), labels = 1:5)
dat <- tibble(
  z = Z,
  x = X,
  y = Y,
  strat = stratas
)

estimates <- numeric(length = 5)
for (s in 1:5) {
  strat_dat <- dat[dat$strat==s,]
  mod <- glm(y~x + z + x*z, data = strat_dat, family = "binomial")
  estimates[s] = summary(mod)$coefficients[2,1]
}
mean(exp(estimates))
```

```
[1] 1.170579
```

e)

```r
estimates <- numeric(5)
for (s in 1:5) {
  strat_dat <- dat[dat$strat==s,]
  mod <- glm(y~x + z + x*z, data = strat_dat, family = "binomial")
  p <- predict(mod, type = "response")
  phat_1 <- mean(p[strat_dat$z ==1])
  phat_2 <- mean(p[strat_dat$z ==0])
  estimates[s] = (phat_1*(1-phat_2))/(phat_2*(1-phat_1))
}
estimates
```

```
[1] 2.800000e+00 8.138248e+07 8.478261e-01 2.062500e+00 2.000000e+00
```

```r
mean(estimates)
```

```
[1] 16276498
```

Part 2

```r
brscn <- read.table("data/hw2/brscn.txt", header = TRUE)
#brscn <- brscn |>
#  mutate(across(2:12,as.factor))
str(brscn)
```

```
'data.frame':   56480 obs. of  14 variables:
 $ obs        : num  39021 39022 39023 39024 39025 ...
 $ group      : int  7 7 7 7 7 7 7 7 7 7 ...
 $ brscn      : int  1 1 0 1 1 1 1 0 1 1 ...
 $ agecat     : int  0 0 0 0 0 0 0 0 0 0 ...
 $ female     : int  0 0 0 0 0 0 0 0 0 0 ...
 $ mcaid      : int  0 0 0 0 0 0 0 0 0 0 ...
 $ poor       : int  0 0 0 0 0 0 0 0 0 0 ...
 $ black      : int  0 0 0 0 0 0 0 0 0 0 ...
 $ cendivis   : int  1 1 1 1 1 1 1 1 1 1 ...
 $ model      : int  2 2 2 2 2 2 2 2 2 2 ...
 $ taxstat    : int  0 0 0 0 0 0 0 0 0 0 ...
 $ affil      : int  0 0 0 0 0 0 0 0 0 0 ...
 $ blprop     : num  0.17 0.17 0.17 0.17 0.17 ...
 $ blproplogit: num  -1.59 -1.59 -1.59 -1.59 -1.59 ...
```

Question 1

```r
form <- black ~ agecat + mcaid + poor + cendivis + model + taxstat + affil + blprop + blpr

#test <- PSweight_cl(form, yname = "brscn", data = brscn)
test <- summary(glm(form, family = "binomial", data = brscn))#$fitted.values
#glmar ; weighted average for each cluster
test$coefficients
```

```
               Estimate  Std. Error    z value      Pr(>|z|)
(Intercept)  0.97636668 0.196670077   4.964490  6.888174e-07
agecat       0.14333149 0.113719761   1.260392  2.075279e-01
mcaid        1.21701100 0.053069543  22.932381 2.209085e-116
poor         1.11747583 0.046116157  24.231764 1.029559e-129
cendivis    -0.07363049 0.005707975 -12.899581  4.525491e-38
model       -0.07372071 0.023180858  -3.180241  1.471528e-03
taxstat     -0.12453270 0.034153656  -3.646248  2.660973e-04
```

```
affil       -0.25049461 0.017764882 -14.100550  3.768202e-45
blprop      -0.89859918 0.485182830  -1.852084  6.401381e-02
blproplogit  1.12243765 0.058893266  19.058845  5.548569e-81
```