HW4 Propensity Scores and IPTW: Answers

We are both submitting this assignment on NYU Classes.

Question 1: Load the data and choose confounders (Step 1)

```
### Answer 1
load("hw4.Rdata")
hw4 <- subset(hw4, bw<3000)
#remove white and college to avoid multicolinearity, don't add momed and state indicators
df <- data.frame(ppvtr.36=hw4$ppvtr.36, treat=hw4$treat, subset(hw4, select=c(bw, bwg, hispanic, black,
covariates <- colnames(df)[3:length(colnames(df))]
covariates
```

```
##  [1] "bw"       "bwg"      "hispanic" "black"    "b.marr"   "lths"
##  [7] "hs"       "ltcoll"   "work.dur" "prenatal" "booze"    "cig"
## [13] "sex"      "first"    "preterm"  "momage"   "dayskidh" "income"
```

```
### Answer 2
fit <- glm(treat ~ bw + bwg + hispanic + black + b.marr + lths + hs +
ltcoll + work.dur + prenatal + booze + cig + sex + first + preterm + momage + dayskidh + income,
family=binomial(link="logit"), data=df)
#pscores <- predict(fit, type='response') #same as line below
pscores <- fit$fitted.values
df$pscores <- pscores #unnecessary
```

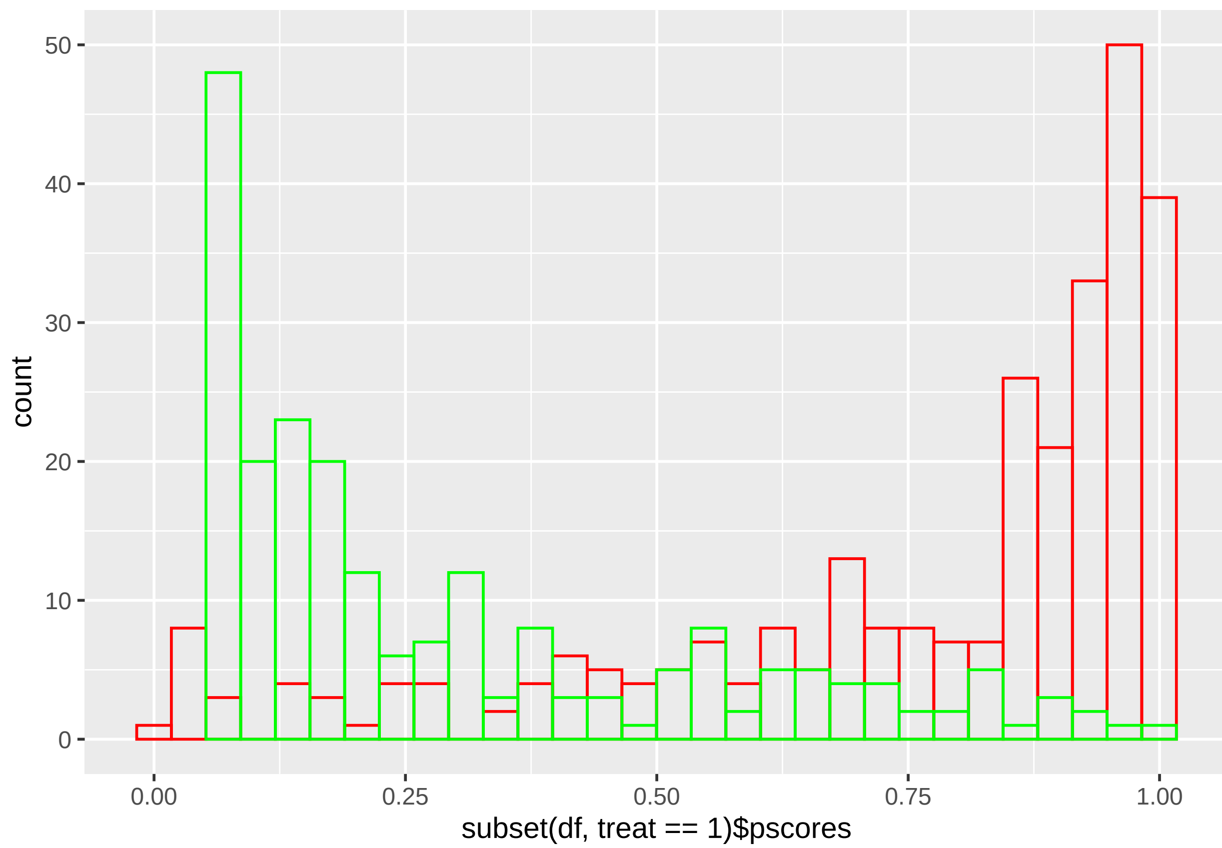
```
### Answer 3(a): We are interested in ATT
# because the research question asks about the children that did receive treatment.
```

```
### Answer 3(b)
matches <- matching(z=df$treat, score=pscores, replace=TRUE)
weight <- c(rep(1,sum(df$treat==1)),matches$cnts)
#weight <- ifelse(df$treat == 0, matches$cnts, 1)

#saving weight as a unique variable for later
weight1 <- weight
```

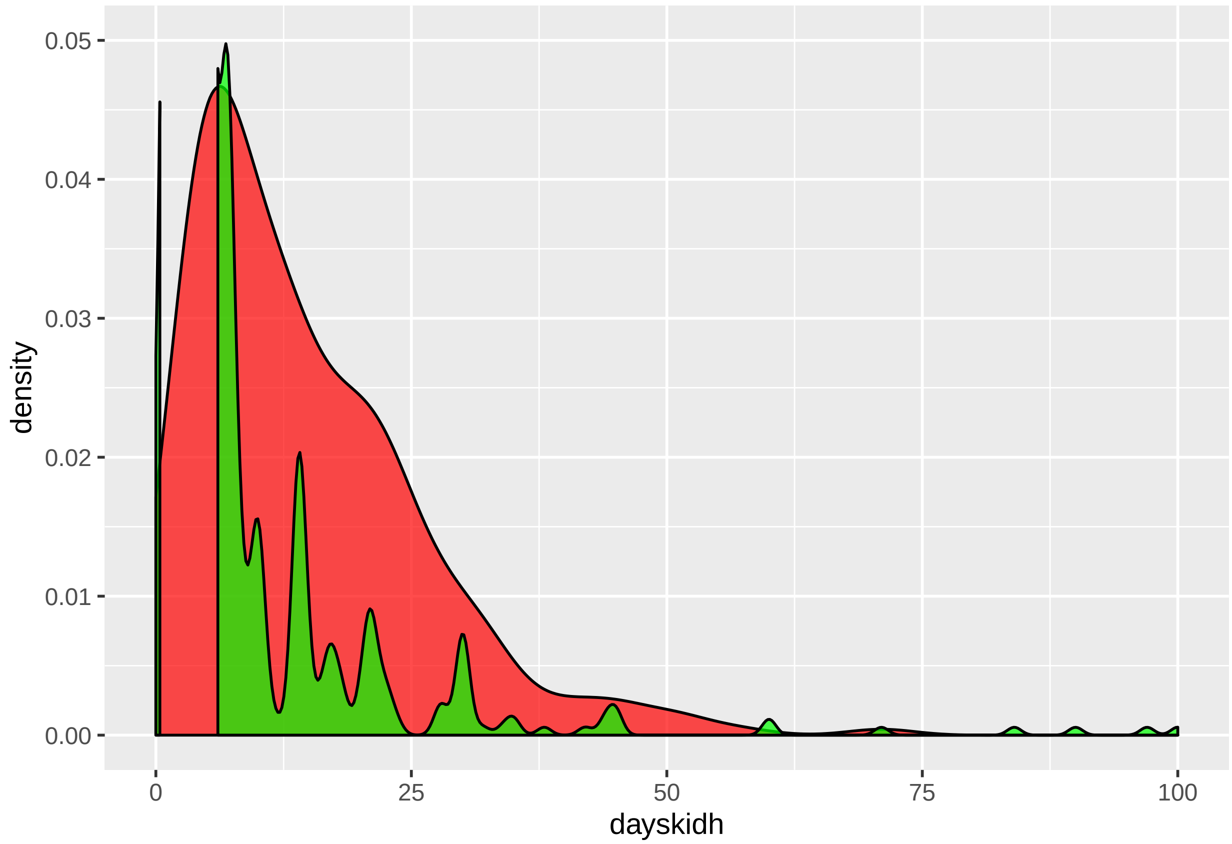
```
### Answer 4(a)

require(ggplot2)
plot <- ggplot() + geom_histogram(aes(subset(df, treat==1)$pscores), color="red", alpha=0) + geom_histo
plot
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

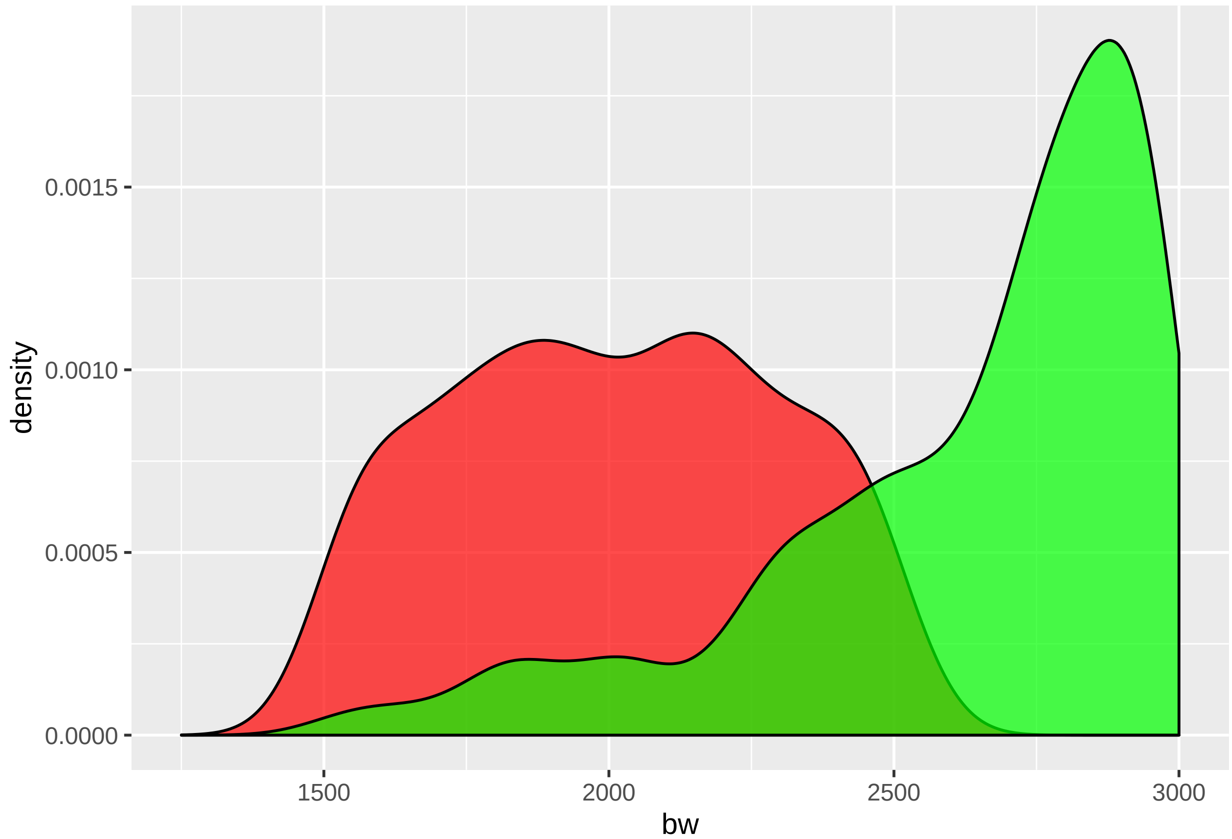
```
## Warning: Removed 2 rows containing missing values (geom_bar).
```




```
plot <- ggplot(data = df, aes(x = dayskidh)) + geom_density(data = subset(df, treat == 1), fill = "red"
plot
```




```
plot <- ggplot(data = df, aes(x = bw)) + geom_density(data = subset(df, treat == 1), fill = "red", alpha
plot
```




```
### Answer 4(b)
# The overlap on pscores is not perfect. Even though
# there exist "empirical counterfactuals" for all
# treated when pscore = 1 we will need to match many
# treated to the same control unit. In control group,
# kids stay in average less time in the hospital, but
# there are enough units to create empirical
# counterfactuals for all treated. In bw, there are empirical
# caunterfactuals for all treated except for the 1250 to 1500 range where
# there is no overlap. I include the low birthwight treated in my analysis
# because I don't want to piroritize bw in my analysis.
# Note, that if we were estimating ATC bw would be more problematic,
# because there are no counterfactuals for many
# healthy controls.
# To summarize, there exist empirical copunterfactuals
# for all treated and therefore we are not violating asusmptions.
```

```
### Answer 4(c)

balance.function <- function(data, cov, weights){

  balance <- data.frame(covariate = numeric(0), mn1 = numeric(0), mn0 = numeric(0),mn1.m= numeric(0), mn

  for(i in cov){
```

```r
    mean_unmatched_control <- round(mean(subset(data, treat == 0)[,i]),3)
    mean_unmatched_treated <- round(mean(subset(data, treat == 1)[,i]),3)

    mean_matched_control <- round(weighted.mean(data[data$treat==0, i], weights[data$treat==0]),3)
    mean_matched_treated <- round(weighted.mean(data[data$treat==1, i], weights[data$treat==1]),3)

    unmatched_mean_difference <- round(ifelse(1 == range(data[,i])[2], mean_unmatched_treated - mean_unm
    matched_mean_difference <- round(ifelse(1 == range(data[,i])[2], mean_matched_treated - mean_matched

    unmatched_sd_ratio <- round(ifelse(1 == range(data[,i])[2],0, sd(subset(data, treat == 0)[,i]) / sd

    matched_sd_ratio <- ifelse(1 == range(data[,i])[2] , 0, round(sqrt(wtd.var(data[data$treat==0, i], w

    output <- list(i, mean_unmatched_treated, mean_unmatched_control,  mean_matched_treated, mean_matche
    balance[nrow(balance) + 1,] <- output
#    print(output)
  }
return(balance)
}

first_balance <- balance.function(df, covariates, weight)
first_balance
```

```
##    covariate       mn1       mn0     mn1.m     mn0.m   diff diff.m ratio
## 1         bw  2008.648  2629.482  2008.648  1951.542 -2.191  0.202 1.175
## 2        bwg     0.490     0.928     0.490     0.507 -0.438 -0.017 0.000
## 3   hispanic     0.093     0.185     0.093     0.138 -0.092 -0.045 0.000
## 4      black     0.503     0.377     0.503     0.490  0.126  0.013 0.000
## 5     b.marr     0.431     0.595     0.431     0.472 -0.164 -0.041 0.000
## 6       lths     0.434     0.341     0.434     0.269  0.093  0.165 0.000
## 7         hs     0.283     0.422     0.283     0.466 -0.139 -0.183 0.000
## 8     ltcoll     0.166     0.187     0.166     0.079 -0.021  0.087 0.000
## 9   work.dur     0.590     0.578     0.590     0.690  0.012 -0.100 0.000
## 10  prenatal     0.955     0.976     0.955     1.000 -0.021 -0.045 0.000
## 11     booze     0.124     0.778     0.124     0.131 -0.654 -0.007 0.000
## 12       cig     0.352     0.428     0.352     0.334 -0.076  0.018 0.000
## 13       sex     0.507     0.544     0.507     0.624 -0.037 -0.117 0.000
## 14     first     0.483     0.448     0.483     0.469  0.035  0.014 0.000
## 15   preterm     6.072     2.406     6.072     5.451  1.907  0.323 1.295
## 16    momage    24.445    23.541    24.445    24.969  0.154 -0.089 0.552
## 17  dayskidh    14.686     6.021    14.686    14.563  0.768  0.011 0.794
## 18    income 21347.394 27330.257 21347.394 17218.172 -0.287  0.198 3.822
##    ratio.m
## 1    1.272
## 2    0.000
## 3    0.000
## 4    0.000
## 5    0.000
## 6    0.000
## 7    0.000
## 8    0.000
## 9    0.000
## 10   0.000
```

```
## 11   0.000
## 12   0.000
## 13   0.000
## 14   0.000
## 15   1.272
## 16   0.486
## 17   1.408
## 18   0.937
```

(d) How do you interpret the resulting balance? In particular what are your concerns with regard to covariates that are not well balanced (3-4 sentences at most).

```
### Answer 4(d)

# I think the above balance is sufficient. I am worried about
# the high ratio of standard deviation of dayskidh which might
# reflect the matching of many treated to same control. Other
# variables that are concerning are work.dur, income, momage, and dayskidh.
# Income could be a confounder and predict the parent treating the child
# to high quality care independent of the study, but the difference
# in incomes between the groups doesn't seem to be large enough to
# restructure the dataset.
```

```
### 4(e) -- test
df.test <- subset(data.frame(ppvtr.36=hw4$ppvtr.36, treat=hw4$treat, subset(hw4, select=c("bw", "b.marr
covariates.test <- colnames(df)[3:length(colnames(df))]
test.fit <- glm(treat ~ bw + b.marr,family=binomial(link="logit"), data=df)
pscores.test <- test.fit$fitted.values
matches.t <- matching(z=df$treat, score=pscores.test, replace=TRUE)
#weight.test <- ifelse(df.test$treat == 0, matches.test$cnts, 1)
weight.test <- c(rep(1,sum(df.test$treat==1)),matches.t$cnts)
temp <-balance.function(df.test, c("bw", "b.marr"), weights=weight.test)
temp
```

```
##   covariate      mn1      mn0    mn1.m    mn0.m   diff diff.m ratio
## 1        bw 2008.648 2629.482 2008.648 2001.838 -2.191  0.024 1.175
## 2    b.marr    0.431    0.595    0.431    0.486 -0.164 -0.055 0.000
##   ratio.m
## 1   1.044
## 2   0.000
```

```
             mn1       mn0     mn1.m     mn0.m    diff   diff.m   ratio   ratio.m
bw      2008.648  2629.482  2008.648  2001.838  -2.191    0.024   1.175     1.044
b.marr     0.431     0.595     0.431     0.486  -0.164   -0.055   0.000     0.000
```

```
### Answer 5

# without replacement
matches <- matching(z=df$treat, score=pscores, replace=FALSE)
weight2 <- ifelse(matches$matched!=0, 1, 0)
balance2 <- balance.function(df, covariates, weight2)
#balance2
```

```r
# using matchit
rownames(df) <- NULL
match <- matchit(data = df, formula = treat ~ bw + bwg + hispanic + black + b.marr + lths + hs +
ltcoll + work.dur + prenatal + booze + cig + sex + first + preterm + momage + dayskidh + income, method
```

```
## Warning in optmatch::fullmatch(d, min.controls = ratio, max.controls = ratio, : Without 'data' argume
##     to be the same as your original data.
```

```r
weight3 <- rep(0,nrow(df))
weight3[as.numeric(match$match.matrix)] <- 1
weight3[df$treat==1] <- 1
balance3 <- balance.function(df, covariates, weight3)
#balance3

# different covariates. I add the indicator for states where the RCT
# was conducted and I treat square of bw as a covariate.
df <- data.frame(ppvtr.36=hw4$ppvtr.36, treat=hw4$treat, subset(hw4, select=c(bw, bwg, hispanic, black,
df$bw2 <- (df$bw)^2
covariates_sq <- colnames(df)[3:length(colnames(df))]
fit <- glm(treat ~ bw + I(bw^2) + bwg + hispanic + black + b.marr + lths + hs +
ltcoll + work.dur + prenatal + booze + cig + sex + first + preterm + momage + dayskidh + income+ st9 + s
family=binomial(link="logit"), data=df)
#pscores <- predict(fit, type='response') #same as line below
pscores <- fit$fitted.values
matches <- matching(z=df$treat, score=pscores, replace=TRUE)
weight4 <- c(rep(1,sum(df$treat==1)),matches$cnts)
balance4 <- balance.function(df, covariates_sq, weight4)
balance4
```

```
##    covariate       mn1       mn0     mn1.m     mn0.m   diff diff.m
## 1         bw  2008.648  2629.482  2008.648  1995.651 -2.191  0.046
## 2        bwg     0.490     0.928     0.490     0.276 -0.438  0.214
## 3   hispanic     0.093     0.185     0.093     0.593 -0.092 -0.500
## 4      black     0.503     0.377     0.503     0.190  0.126  0.313
## 5     b.marr     0.431     0.595     0.431     0.783 -0.164 -0.352
## 6       lths     0.434     0.341     0.434     0.721  0.093 -0.287
## 7         hs     0.283     0.422     0.283     0.245 -0.139  0.038
## 8     ltcoll     0.166     0.187     0.166     0.031 -0.021  0.135
## 9   work.dur     0.590     0.578     0.590     0.807  0.012 -0.217
## 10  prenatal     0.955     0.976     0.955     1.000 -0.021 -0.045
## 11     booze     0.124     0.778     0.124     0.090 -0.654  0.034
## 12       cig     0.352     0.428     0.352     0.166 -0.076  0.186
## 13       sex     0.507     0.544     0.507     0.255 -0.037  0.252
## 14     first     0.483     0.448     0.483     0.128  0.035  0.355
## 15   preterm     6.072     2.406     6.072     6.272  1.907 -0.104
## 16    momage    24.445    23.541    24.445    22.797  0.154  0.281
## 17  dayskidh    14.686     6.021    14.686    18.299  0.768 -0.320
## 18    income 21347.394 27330.257 21347.394 20447.440 -0.287  0.043
## 19       st9     0.134     0.021     0.134     0.576  0.113 -0.442
## 20      st12     0.100     0.054     0.100     0.052  0.046  0.048
## 21      st25     0.114     0.015     0.114     0.010  0.099  0.104
## 22      st36     0.117     0.041     0.117     0.110  0.076  0.007
```

```
## 23      st42       0.145       0.039       0.145       0.017  0.106  0.128
## 24      st48       0.114       0.071       0.114       0.028  0.043  0.086
## 25      st53       0.138       0.011       0.138       0.069  0.127  0.069
## 26       bw2 4114652.738 7024897.142 4114652.738 4021682.103 -2.552  0.082
##    ratio ratio.m
## 1  1.175   0.699
## 2  0.000   0.000
## 3  0.000   0.000
## 4  0.000   0.000
## 5  0.000   0.000
## 6  0.000   0.000
## 7  0.000   0.000
## 8  0.000   0.000
## 9  0.000   0.000
## 10 0.000   0.000
## 11 0.000   0.000
## 12 0.000   0.000
## 13 0.000   0.000
## 14 0.000   0.000
## 15 1.295   0.887
## 16 0.552   0.491
## 17 0.794   1.945
## 18 3.822   0.815
## 19 0.000   0.000
## 20 0.000   0.000
## 21 0.000   0.000
## 22 0.000   0.000
## 23 0.000   0.000
## 24 0.000   0.000
## 25 0.000   0.000
## 26 1.417   0.711
```

```
### Answer 6
fit <- glm(treat ~ bw + bwg + hispanic + black + b.marr + lths + hs +
ltcoll + work.dur + prenatal + booze + cig + sex + first + preterm + momage + dayskidh + income,
family=binomial(link="logit"), data=df)
#pscores <- predict(fit, type='response') #same as line below
pscores <- fit$fitted.values

pscores_c <- pscores[df$treat==0]
pscores_c <- pscores_c/mean(pscores_c)

weight_IPTW <- c(rep(1,sum(df$treat==1)), pscores_c)
balance_IPTW <- balance.function(df, covariates, weight_IPTW)
```

```
### Answer 7
comp_table <- data.frame(first_balance[,c(7,9)], balance2[,c(7,9)], balance3[,c(7,9)], balance4[c(1:18)
colnames(comp_table) <- c("diff.m 1", "ratio.m 1", "diff.m 2", "ratio.m 2", "diff.m 3", "ratio.m 3", "di
comp_table
```

```
##          diff.m 1 ratio.m 1 diff.m 2 ratio.m 2 diff.m 3 ratio.m 3 diff.m 4
## bw          0.202     1.272   -1.096     1.350   -1.094     1.348    0.046
## bwg        -0.017     0.000   -0.282     0.000   -0.282     0.000    0.214
```

```
## hispanic   -0.045     0.000   -0.035     0.000   -0.038     0.000   -0.500
## black       0.013     0.000    0.075     0.000    0.075     0.000    0.313
## b.marr     -0.041     0.000   -0.066     0.000   -0.069     0.000   -0.352
## lths        0.165     0.000    0.037     0.000    0.037     0.000   -0.287
## hs         -0.183     0.000   -0.086     0.000   -0.086     0.000    0.038
## ltcoll      0.087     0.000   -0.003     0.000   -0.003     0.000    0.135
## work.dur   -0.100     0.000   -0.013     0.000   -0.013     0.000   -0.217
## prenatal   -0.045     0.000   -0.024     0.000   -0.021     0.000   -0.045
## booze      -0.007     0.000   -0.355     0.000   -0.355     0.000    0.034
## cig         0.018     0.000   -0.082     0.000   -0.079     0.000    0.186
## sex        -0.117     0.000   -0.003     0.000   -0.007     0.000    0.252
## first       0.014     0.000    0.076     0.000    0.076     0.000    0.355
## preterm     0.323     1.272    0.953     1.505    0.950     1.502   -0.104
## momage     -0.089     0.486    0.090     0.561    0.092     0.562    0.281
## dayskidh    0.011     1.408    0.439     1.216    0.442     1.216   -0.320
## income      0.198     0.937   -0.327     4.501   -0.333     4.503    0.043
##          ratio.m 4 diff.m IPTW ratio.m IPTW
## bw           0.699       -0.537         1.298
## bwg          0.000       -0.173         0.000
## hispanic     0.000       -0.021         0.000
## black        0.000        0.072         0.000
## b.marr       0.000       -0.099         0.000
## lths         0.000        0.078         0.000
## hs           0.000       -0.119         0.000
## ltcoll       0.000        0.019         0.000
## work.dur     0.000       -0.003         0.000
## prenatal     0.000       -0.031         0.000
## booze        0.000       -0.242         0.000
## cig          0.000       -0.064         0.000
## sex          0.000       -0.025         0.000
## first        0.000        0.036         0.000
## preterm      0.887        0.542         1.535
## momage       0.491        0.038         0.561
## dayskidh     1.945        0.264         1.372
## income       0.815       -0.129         3.090
```

```r
# I would choose my first propensity score model
# or IPTW because they have the best balance. First
# model has better balance but matches many control units
# to one treated unit. As I explained in 4(c) the difference
# in means and ratio of standard deviations remains big for income
# dayskidh and momage but they are still better than the other models.
#
```

```r
### Answer 8
effect1 <- lm(ppvtr.36 ~ treat, data=df, weights = weight1)$coefficients[2]
effect2 <- lm(ppvtr.36 ~ treat, data=df, weights = weight2)$coefficients[2]
effect3 <- lm(ppvtr.36 ~ treat, data=df, weights = weight3)$coefficients[2]
effect4 <- lm(ppvtr.36 ~ treat, data=df, weights = weight4)$coefficients[2]
#effect5 <- lm(ppvtr.36 ~ treat, data=df, weights = weight5)$coefficients[2]
effect_IPTW <- lm(ppvtr.36 ~ treat, data=df, weights = weight_IPTW)$coefficients[2]
treatment_effect <- c(effect1, effect2, effect3, effect4, effect_IPTW)
names(treatment_effect) <- c("effect1", "effect2","effect3","effect4", "effect_IPTW")
treatment_effect
```

```
##     effect1     effect2     effect3     effect4 effect_IPTW
##    6.260002   10.837432   10.906397   -1.815980    8.250768
```

```
### Answer 9

# (1) ignorability
## We have measured all confounders and therefore we can
## ignore the effects of the unobserved factors.

# (2) sufficient overlap (positivity)
## We can make inferences about treatment effect on the
## treated or controls only  over the area of common
## support. We have satisfied this asusmption when we
## have empirical counterfactuals for all treated (for ATT)
## or all controls (for ATC)

# (3) appropriate specification of the propensity score model
## We know the matching based on the propensity score
## model is appropriate when there is balance between
## the comparison groups

# (4) Stable Unit Treatment Value Assumption
## The assumption that the effect of treatment is independent
## of the composition of treatment selection

# Parametric (5)
## On the area of common support linearity holds.
```

```
### Answer 10

# Causal interpretation for my original propensity score estimate (effect1):
# The average treatment effect on the treated (ATT) was 6.26 IQ
# points. In the counterfactual case without treatment, we would
# observe IQ scores 6.26 points lower on average after three years.
# We conclude that the treatment had causally contributed to a
# significant increase in children's IQ scores.
```

Question 11: Comparison to linear regression

Fit a regression of your outomes to the treatment indicator and covariates. (a) Report your estimate and standard error. (b) Interpret your results non-causally. (c) Why might we prefer the results from the propensity score approach to the linear regression results in terms of identifying a causal effect?

```
### Answer 11
fit <- lm(ppvtr.36 ~ treat + bw + bwg + hispanic + black + b.marr + lths + hs +
ltcoll + work.dur + prenatal + booze + cig + sex + first + preterm + momage + dayskidh + income, data=di
# (a)
summary(fit)$coefficients[2,][1:2]
```

```
##   Estimate Std. Error
##  10.986261   1.669124
```

```
# (b)
## Treatment is correlated with an IQ test score increase of 10.98.
# Children who received treatment score better on the IQ test by an average of 10.98.

# (c)
## Linear regression violates the overlap assumption
## and therefore cannot be used to identify causal effects.
## The treatment and control groups are not sufficiently simillar
## to one another to warrant counterfactual inferences.
```