Assignment 4

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Objective

This assignment will give you the opportunity to practice several different propensity score approaches to causal inference. In addition, you will be asked to interpret the resulting output and discuss the assumptions necessary for causal inference.

Problem Statement

In this assignment will use data from a constructed observational study. The data and an associated data dictionary are available in this folder. The treatment group for the study that the data are drawn from is the group of children who participated in the IHDP intervention discussed in class. The research question of interest focuses on the effect of the IHDP intervention on age 3 IQ scores for the children that participated in it. The data for the comparison sample of children was pulled from the National Longitudinal Study of Youth during a similar period of time that the data were collected for the IHDP study.

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

Load the data. You can use the load command since the data are in a .Rdata file; this will create a data frame called hw4. Choose the covariates you want to use as confounders. To make life easier you may want to choose binary indicators of unordered categorical variables (rather than a variable labeled e.g. as 1, 2, 3 for different levels of a categorical variable).

Create a new data frame for analysis that includes the outcome in the 1st column, the treatment indicator in the 2nd column, and the covariates in the remaining columns. Be thoughtful about your choices with respect to the nature of the covariates (e.g. is an unordered categorical being represented as such) and timing (don't control for post-treatment variables!). Provide your code and a list of the variable names for the confounder variables chosen.

Also reduce that data frame to include only observations for children whose birth weight is less than 3000 grams.

Solutions.

List of selected confounder variables:

- **"momage": mother's age at time of birth**
- **"momed_recode": recoded mother's education variable, 1 indicates some college or more, 0 indicates high school or less**
- **"prenatal": indicator for whether mom received prenatal care**
- **"cig": indicator for whether mom smoked cigarettes while pregnant**
- **"booze": indicator for whether mom drank alcohol while pregnant**
- **"first": indicator for whether child was the first born for the mother**
- **"bw": child's birth weight**
- **"preterm": number of weeks preterm child was born**
- **"black", "hispanic": indicators for child's race/ethnicity**

```r
library(dplyr)
library(arm)
library(MatchIt)

# load the data
load("hw4.Rdata")

# select children with birth wright less than 3000 grams
hw4_bw <- hw4[hw4$bw < 3000,]

# explore the data
hw4_bw %>% group_by(treat) %>%
          summarise(n_children = n(),
                    ppvtr36_avg = mean(ppvtr.36),
                    ppvtr36_sd = sd(ppvtr.36)/sqrt(n_children))
## # A tibble: 2 x 4
##   treat n_children ppvtr36_avg ppvtr36_sd
##   <dbl>      <int>       <dbl>      <dbl>
## 1     0       1030        83.0      0.650
## 2     1        290        92.1      0.976

t.test(ppvtr.36 ~ treat, data = hw4_bw)
##  Welch Two Sample t-test
## data:  ppvtr.36 by treat
## t = -7.7556, df = 570.75, p-value = 4.067e-14
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -11.402587  -6.794175
## sample estimates:
## mean in group 0 mean in group 1
##        83.01541        92.11379

table(sum(hw4_bw$hispanic, hw4_bw$black, hw4_bw$white)) #check race variables
##
## 1320
##    1
# create a new mother's education binary variable: some college or more= 1,
high school or less = 0
hw4_bw$momed_recode <- ifelse(hw4_bw$momed > 2, 1, 0)
table(hw4_bw$momed_recode, hw4_bw$momed, useNA = "ifany")
##
##       1   2   3   4
##   0 477 517   0   0
##   1   0   0 241  85


# select confounder variables and create a new data set for use
confounders <- c("momage","momed_recode","prenatal","cig","booze","first","bw
","preterm", "black","hispanic")
new <- hw4_bw[,c("ppvtr.36", "treat", confounders)]
```

```r
# check the covariates
new %>% group_by(treat) %>% select(one_of(confounders)) %>%
       summarise_all(funs(mean(., na.rm = T)))
```

```
# Adding missing grouping variables: `treat`
# A tibble: 2 x 11
treat momage momed_recode prenatal cig booze first bw preterm black Hispanic
 <dbl> <dbl>  <dbl>     <dbl>   <dbl> <dbl> <dbl>  <dbl>  <dbl>  <dbl> <dbl>
##  0  23.5   0.237     0.976  0.428  0.778  0.448  2629.  2.41 0.377  0.185
##  1  24.4   0.283     0.955  0.352  0.124  0.483  2009.  6.07 0.503  0.0931
```

Question 2: Estimate the propensity score (Step 2)

Estimate the propensity score. That is, fit a propensity score model and save predicted scores.

Solutions.

```r
# use logistic regression to estimate the propensity score
log.fit <- glm (treat ~ ., data = new[, -1], family = binomial)
summary(log.fit)
```

```
## Call:
## glm(formula = treat ~ ., family = binomial, data = new[, -1])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.82067  -0.25319  -0.07845  -0.02917   3.05339
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)   6.4674665  1.5182007   4.260 2.04e-05 ***
## momage        0.0792188  0.0292925   2.704  0.00684 **
## momed_recode  0.0376455  0.2872872   0.131  0.89575
## prenatal     -1.2292527  0.7238609  -1.698  0.08947 .
## cig           0.6658664  0.2456463   2.711  0.00671 **
## booze        -3.6150372  0.2871809 -12.588  < 2e-16 ***
## first         0.6545039  0.2421043   2.703  0.00686 **
## bw           -0.0039016  0.0004031  -9.680  < 2e-16 ***
## preterm       0.2924527  0.0549464   5.323 1.02e-07 ***
## black         0.6897167  0.2637392   2.615  0.00892 **
## hispanic     -0.6583353  0.3679009  -1.789  0.07354 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##     Null deviance: 1390.02  on 1319  degrees of freedom
## Residual deviance:  517.95  on 1309  degrees of freedom
## AIC: 539.95
## Number of Fisher Scoring iterations: 7
```

```r
# save the predicted propensity scores
pscore_log <- data.frame (pscores = predict(log.fit, type = "response"),
                          treat = log.fit$model$treat)
```

Question 3: Restructure your data through matching. [Or at least create the weights variable that will let you to do so in the following steps] (Step 3)

(a) The first thing you need to be clear on before restructuring your data is the estimand. Given the description above about the research question, what is the estimand of interest?

Solutions.

The estimand of interest is the average treatment effect on the treated (ATT).

(b) First please perform *one-to-one nearest neighbor matching with replacement* using your estimated propensity score from Question 2. Perform this matching using the matching command in the arm package. The "cnts" variable in the output reflects the number of times each control observation was used as a match (the length is equal to the number of control observations). Use the output of this function to create a weight variable that 1) equals one for treated observations and 2) equals the number of times used as a match for non- treated observations.

Solutions.

```
# one-to-one nearest neighbor matching with replacement
match_log <- matching(z = new$treat, score = pscore_log$pscores, replace = T)

# create "weight" variable
wts_log <- data.frame(treat = new$treat, weight = NA)

wts_log[wts_log$treat == 0, ]$weight <- match_log$cnts
wts_log[wts_log$treat == 1, ]$weight <- 1

table(wts_log$weight, wts_log$treat, useNA = "ifany")
```

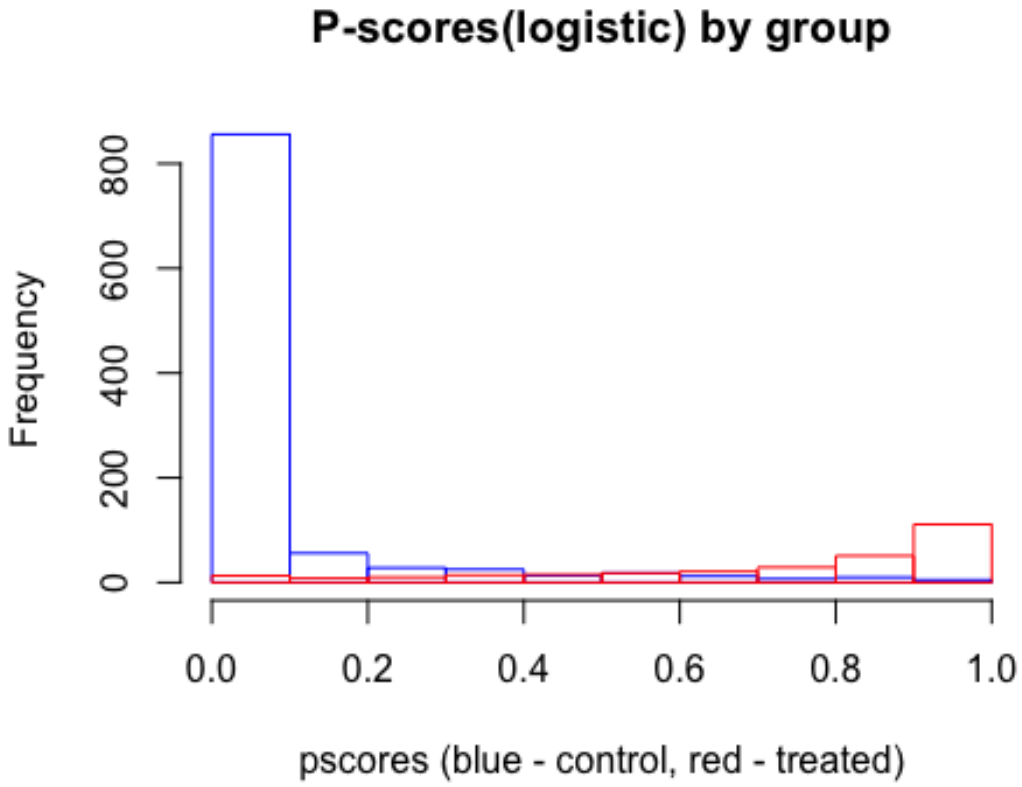
```
##
##        0   1
##   0  944   0
##   1   47 290
##   2   15   0
##   3    5   0
##   4    3   0
##   5    2   0
##   6    2   0
##   7    3   0
##   8    1   0
##   9    2   0
##   11   1   0
##   13   1   0
##   16   1   0
##   18   1   0
##   21   1   0
##   38   1   0
```

Question 4: Check overlap and balance. (Step 4)

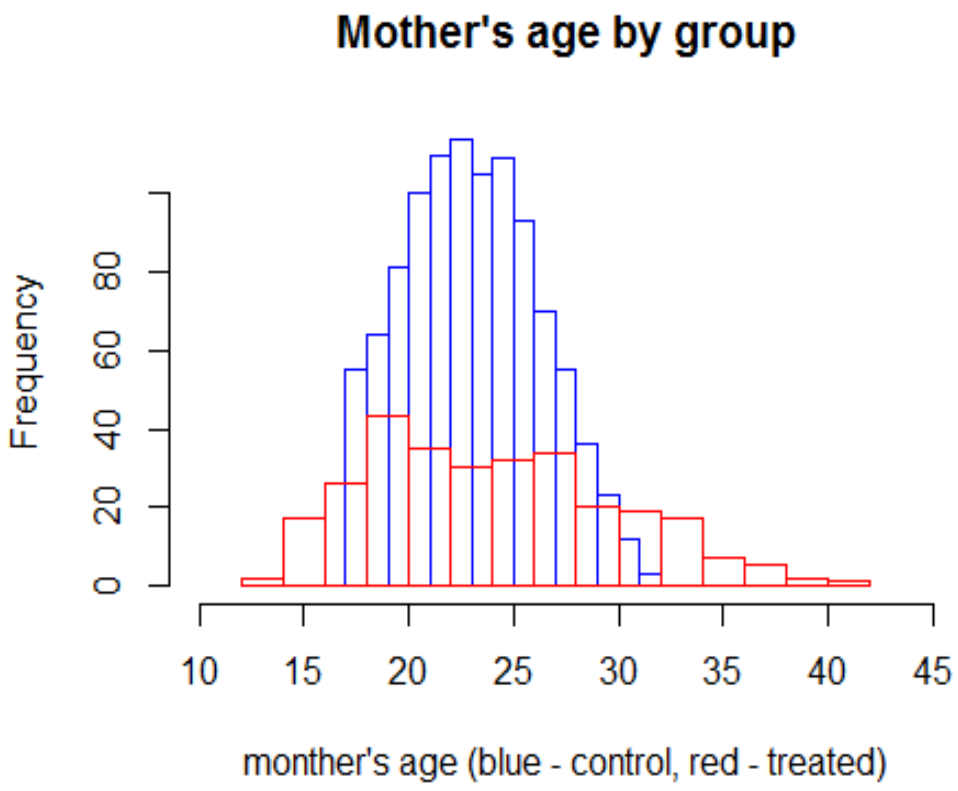
(a) Examining Overlap. Check overlap on the *unmatched* data using some diagnostic plots. Check overlap for the propensity scores as well as two other covariates. Note that it may be necessary to exclude some observations from the plots if they are being obscured in ways similar to the example discussed in class on 10/5.

Solutions.

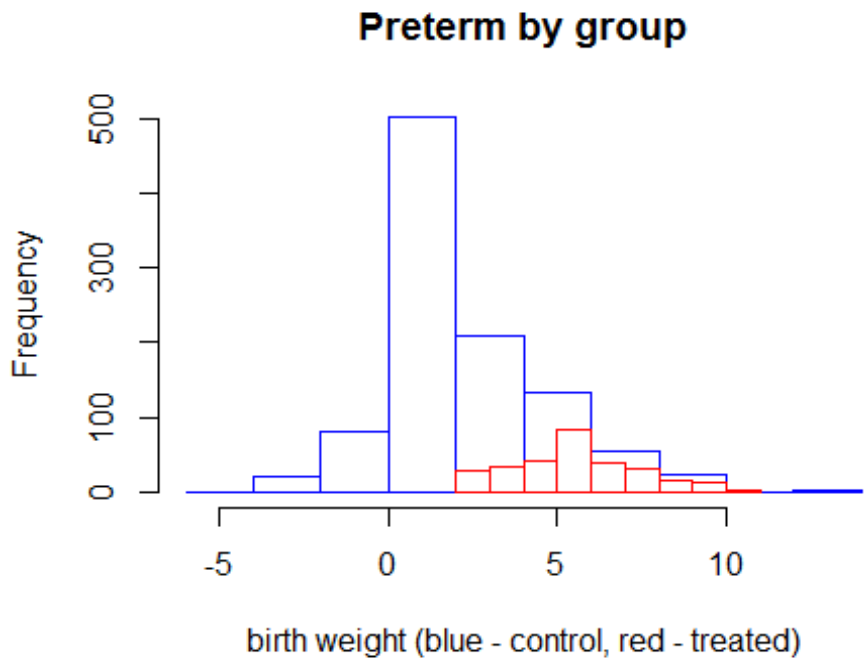
```
# examining the overlap by propensity scores
hist(pscore_df[pscore_df$treat == 0, ]$pscores, border = "blue", main = "P-sc
ores(logistic) by group", xlab = "pscores (blue - control, red - treated)")
hist(pscore_df[pscore_df$treat == 1, ]$pscores, border = "red", add =T)
```




```
# examining the overlap by mother's age (momage)
hist(new[new$treat == 0,]$momage, border = "blue", main = "Mother's age by gr
oup", xlab = "monther's age (blue - control, red - treated)", xlim=c(10, 45))
hist(new[new$treat == 1,]$momage, border = "red", add = T)
```




```
# examining the overlap by preterm
hist(new[new$treat == 0,]$preterm, border = "blue", main = "Preterm by group"
,xlab = "birth weight (blue - control, red - treated)")
hist(new[new$treat == 1,]$preterm, border = "red", add = T)
```



(b) Interpreting Overlap. What do these plots reveal about the overlap required to estimate our estimand of interest?

Solutions.

In terms of the overlaid histograms shown in 4(a):

- **For the logit model propensity scores, the graph shows sufficient overlap between the control and treated group;**
- **For mother's age, we see great overlap between two groups, however, mother's age in the treated group ranges beyond the control group, we may consider removing the out-range observations from the treated group;**
- **For preterm, we see partial overlap, which indicate possible significant differences between the two groups.**

(c) Examining Balance. You will build your own function to check balance! This function should take as inputs (at least) the data frame created in Question 1, the vector with the covariate names chosen in Question 1, and the weights created in Question 2. It should output the following:

1) Mean in the unmatched treatment group
2) Mean in the unmatched control group
3) Mean in the matched treatment group*
4) Mean in the matched control group
5) Unmatched mean difference (standardized for continuous variables, not standardized for binary variables)
6) Matched mean difference (standardized for continuous variables, not standardized for binary variables)
7) Ratio of standard deviations across unmatched groups (control/treated)
8) Ratio of standard deviations across matched groups (control/treated)

Solutions.

```
# my balance checking function
check_balance <- function(df, covs, wts_df){

   treated <- df[df$treat == 1, ]
   control <- df[df$treat == 0, ]

   treated_wts<- wts_df[wts_df$treat == 1, "weight"]
   control_wts<- wts_df[wts_df$treat == 0, "weight"]

   bi_var <- ifelse(sapply(covs, function(x) length(unique(df[, x]))) == 2, "
Y", "N") # identify binary variable
   weighted_sd <- function(x, w) sqrt(sum(w*(x - weighted.mean(x, w))^2)/sum(
w)) # weighted sd function

  mn1 <- sapply(covs, function(x) mean(treated[, x]))
  mn0 <- sapply(covs, function(x) mean(control[, x]))
```

```
  mn1.m <- sapply(covs, function(x) weighted.mean(treated[, x], treated_wts))
  mn0.m <- sapply(covs, function(x) weighted.mean(control[, x], control_wts))

  diff <- ifelse(bi_var == "Y", mn1-mn0, (mn1-mn0)/sapply(covs, function(x) s
d(treated[, x])))
  diff.m <- ifelse(bi_var == "Y", mn1.m-mn0.m, (mn1.m-mn0.m)/sapply(covs, fun
ction(x) sd(treated[, x])))

  ratio <- ifelse(bi_var == "N", sapply(covs, function(x) sd(control[, x])) /
 sapply(covs, function(x) sd(treated[, x])), NA)
  ratio.m <- ifelse(bi_var == "N", sapply(covs, function(x) weighted_sd(contr
ol[, x], control_wts)) / sapply(covs, function(x) weighted_sd(treated[, x], t
reated_wts)), NA)

  data.frame(mn1, mn0, mn1.m,mn0.m, diff, diff.m, ratio, ratio.m)
}

round(check_balance(new, confounders, wts_log),2)
```

```
##                  mn1     mn0   mn1.m   mn0.m  diff diff.m ratio ratio.m
## momage         24.44   23.54   24.44   24.71  0.15  -0.05  0.55    0.46
## momed_recode    0.28    0.24    0.28    0.21  0.05   0.07    NA      NA
## prenatal        0.96    0.98    0.96    0.99 -0.02  -0.04    NA      NA
## cig             0.35    0.43    0.35    0.38 -0.08  -0.03    NA      NA
## booze           0.12    0.78    0.12    0.13 -0.65   0.00    NA      NA
## first           0.48    0.45    0.48    0.51  0.04  -0.03    NA      NA
## bw           2008.65 2629.48 2008.65 1989.15 -2.19   0.07  1.18    1.29
## preterm         6.07    2.41    6.07    5.54  1.91   0.28  1.29    1.34
## black           0.50    0.38    0.50    0.52  0.13  -0.02    NA      NA
## hispanic        0.09    0.19    0.09    0.12 -0.09  -0.03    NA      NA
```

(d) How do you interpret the resulting balance? In particular what are your concerns with regard to covariates that are not well balanced (Write about 5 or 6 sentences).

Solutions.

According to the balance result from 4(c), not all covariate variables achieved a balance after the matching. For example, "momage", "momed_recode", "bw", "preterm" still need to be further balanced. Specially, for the birth weight covariate, because all 290 observations in the treated group are low-weighted (less than 2500 grams), and there are only 300 observations with birth weight less than 2500 grams in the control group, it might be difficult to obtain a well balance in the "bw" variable. In contrast, since mother's ages are not significantly different in treated and control groups, although the ratio of standard deviations across matched groups is not close to 1, in practical, the difference might not be considered significant.

(e) Unit test. Show the results of your balance function on a simple example with the same sample as above (that is, limited to children with birth weight less than 3000) where the propensity score is fit using logistic regression on "bw" and "b.marr" and the matching is performed using 1-1 nearest neighbor matching with replacement.

Solutions.

```
# Unit test
covs_unit <- c("bw", "b.marr")
unit_df <- hw4_bw[,c("ppvtr.36", "treat", covs_unit)]
unit_pscore <- predict(glm (treat ~ bw + b.marr, data = unit_df, family = bin
omial(link = "logit")))
unit_match <- matching(z = unit_df$treat, score = unit_pscore, replace = T)

wts_unit <- data.frame(treat = unit_df$treat, weight = NA)
wts_unit[wts_unit$treat == 0,"weight"] <- unit_match$cnts
wts_unit[wts_unit$treat == 1, "weight"] <- 1

round(check_balance(unit_df, covs_unit, wts_unit),3)
```

```
##             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    NA      NA
```

Question 5: Repeat steps 2-4 within the matching framework.

What to do: It is rare that your first specification of the propensity score model or choice of matching method is the best. Try at least *3* new approaches. Try to achieve better balance! For continuous variables strive for standardized mean differences less than .1. Try to get ratios of standard deviation closer to 1 than they are for the unmatched data (it may be difficult for some covariates to get the ratio close to 1). For binary variables strive for difference in means (equivalently difference in percentages) less than .05.

Ideas for trying something new in Step 2. You could try a new propensity score specification and then find the corresponding matched sample and calculate balance and overlap. For instance, you could change the inputs to the model (add quadratic terms, transformed versions of variables, or interactions, or delete predictors) or the model/algorithm used to estimate propensity scores (try probit or GAM or GBM or something else!). Alternately you could try a different matching method. A simple switch would be to switch from matching without replacement to matching with replacement. You could try k-1 matching or caliper matching or optimal matching though this will require using another package such as MatchIt. You could also try eliminating observations from the dataset. Importantly though if you eliminate observations from the group that we are trying to make inferences about you will need to profile those who have been removed. If you remove control observations from the comparison group (for instance those in states not represented by the IHDP observations) you do not need to do this. Save your results (weights and balance) for reporting later.

Solutions.

- **Method 1: Probit regression with all confounder variables for estimating the propensity score, and k-1 matching without replacement, no observations dropped;**
- **Method 2: Optimal matching using logit distance, less confounder variables as predictor (***treat ~ momage + cig + booze + first + black + hispanic***), no observations dropped;**

- **Method 3: Generalized additive models (GAM) with less confounder variables and interaction (***treat ~ momage + cig + booze + first + bw:preterm + black + hispanic***) for estimating the propensity score, and k-1 matching with replacement; observations of the treated group with mother's age out of the range of the control group were dropped (***17 <= momage of control <=32, 13 <= momage of treated <= 41***).**

Question 6: Repeat steps 2-4, but this time using IPTW.

Save your results (weights and balance) -- do not display them here. Make sure that you use weights specific to the effect of the treatment on the treated. In this section report only your code for estimating the propensity scores and your code for creating the IPTW weights.

Solutions.

```
# logistic propensity score model, no observation dropped
log.fit2 <- glm (treat ~ momage:hispanic + cig + booze + first + bw + preterm
 + black, data = new, family = binomial(link = "logit"))
summary(log.fit2)

pscore_log2 <- data.frame (pscores = predict(log.fit2, type = "response"), tr
eat = log.fit2$model$treat)

# creating iptw weights for ATT
wts_iptw <- pscore_log2
wts_iptw$weight_raw <- ifelse(wts_iptw$treat == 0, wts_iptw$pscores / (1 - wt
s_iptw$pscores), 1)
wts_iptw[wts_iptw$weight_raw > 50,]$weight_raw <- 50 #adjust extreme weights

# normalize the weights
t_sum <- sum(wts_iptw[wts_iptw$treat == 1,]$weight_raw)
c_sum <- sum(wts_iptw[wts_iptw$treat == 0,]$weight_raw)
wts_iptw$weight <- ifelse(wts_iptw$treat == 0, wts_iptw$weight_raw*t_sum/c_su
m, wts_iptw$weight_raw)
```

Question 7: Comparative balance table

Create a table with columns 6 and 8 from your function for each of the matching and weighting methods performed above. Which approach would you choose and why? (1-2 paragraphs at most)

Solutions.

The balance table is shown as Table 1.

- **Method 1: Logit regression with all confounder variables for estimating propensity scores and k-1 with replacement matching;**
- **Method 2: Probit regression with all confounder variables for propensity score estimation, and k-1 no replacement matching;**
- **Method 3: Optimal matching** *(treat ~ momage + cig + booze + first + black + hispanic)* **with logit distance;**

- **Method 4: GAM regression** *(treat ~ momage + cig + booze + first + bw:preterm + black + hispanic)* **for propensity score estimation, k-1 with replacement matching, observations dropped in treated group;**
- **Method 5: Logit regression** *(treat ~ momage:hispanic + cig + booze + first + bw + preterm + black)* **for propensity score estimation, and normalized IPTW ATT weights.**

Covariates	Method 1		Method 2		Method 3		Method 4		Method 5	
	diff.m	ratio.m	diff.m	ratio.m	diff.m	ratio.m	diff.m	ratio.m	diff.m	ratio.m
momage	-0.05	0.46	0.06	0.54	0.01	0.54	-0.14	0.79	0.01	0.51
momed_recode	0.07	NA	0.03	NA	0	NA	-0.04	NA	0.06	NA
prenatal	-0.04	NA	-0.01	NA	-0.03	NA	-0.03	NA	-0.04	NA
cig	-0.03	NA	-0.08	NA	-0.04	NA	0.03	NA	0.04	NA
booze	0	NA	-0.26	NA	-0.09	NA	0	NA	-0.04	NA
first	-0.03	NA	0.08	NA	0	NA	-0.02	NA	0.02	NA
bw	0.07	1.29	-1.23	1.48	-2.32	1.1	-1.89	1.11	0.26	1.29
preterm	0.28	1.34	1.05	1.55	2.01	1.16	0.55	1.01	0.07	1.29
black	-0.02	NA	0.09	NA	0.02	NA	0.13	NA	0.01	NA
hispanic	-0.03	NA	-0.03	NA	-0.02	NA	-0.02	NA	-0.05	NA

Table 1: Balance table

According to the balance results, we would choose Method 5 (Logit regression with IPTW ATT weights) as it achieved the best balance. After matching, almost all 7 binary variables have a difference in means *(diff.m)* **less than or very close to .05** *(momed_recode is .06).* **As for the continuous variables, mother's age** *(momage)* **and preterm weeks (preterm) both obtained a standardized mean difference less than .1, however, their ratios of standard deviation are not really close to 1. Specially, for birth weight** *(bw)***, we already know from the raw data that it is going to be difficult to reach a well balance because there are not enough similar data points for matching in the control group** *(only 300 observations with bw less than 2500 grams),* **and Method 5 obtained the smallest difference in means for the bw variable** *(diff.m = 0.26).*

Question 8: Estimate the treatment effect for the restructured dataset simplied by Questions 4-6 (Step 5)

Estimate the effect of the treatment on the treated for each of your five approaches by fitting a regression with weights equal to the number of times each observation appears in the matched sample (that is, use your weights variable from above) or using IPTW weights. Report the treatment effect and standard error for each approach.

Solutions.

	Unmatched	Method 1	Method 2	Method 3	Method 4	Method 5
Treatment effect	**9.10**	**8.77**	**9.48**	**8.24**	**8.88**	**8.81**
Standard error	**-**	**1.353**	**1.663**	**1.663**	**1.534**	**1.353**

```
# Estimate the treatment effect for restructured datasets
m1.data <- cbind(new, pscores = pscore_log$pscores, weight = wts_log$weight)
m2.data <- cbind(new, pscores = pscore_probit$pscores, weight = wts_probit$weight)
m3.data <- cbind(new, pscores = pscore_opt$pscores, weight = wts_opt$weight)
m4.data <- cbind(new_age, pscores = pscore_gam$pscores, weight = wts_gam$weight)
m5.data <- cbind(new, pscores = pscore_log2$pscores, weight = wts_iptw$weight)

summary(lm(ppvtr.36 ~ factor(treat) + weight, data = m1.data))
summary(lm(ppvtr.36 ~ factor(treat) + weight, data = m2.data))
summary(lm(ppvtr.36 ~ factor(treat) + weight, data = m3.data))
summary(lm(ppvtr.36 ~ factor(treat) + weight, data = m4.data))
summary(lm(ppvtr.36 ~ factor(treat) + weight, data = m5.data))
```

Question 9: Assumptions

What assumptions are necessary to interpret the estimates from the propensity score approaches causally? List and describe ***briefly***.

Solutions.

The necessary assumptions to interpret estimates from propensity score approaches include:

- **Ignorability:** *there are no other confounding variables except the selected 10 potential confounders;*
- **Sufficient overlap:** *there is enough overlap in the estimated propensity scores of the treated and control group;*
- **Appropriate balance achieved from the propensity score model***: the 10 potential confounders should achieve a good balance through the selected best propensity score estimation model;*
- **SUTVA** *(Stable Unit Treatment Value Assumption).*

Question 10: Causal Interpretation

Provide a causal interpretation of *one* of your estimates above. Remember to specify the counterfactual and to be clear about whom you are making inferences. Also make sure to use causal (counterfactual) language.

Solutions.

In terms of the estimate from Method 5, the causal interpretation is:

<u>For children who participated in the IHDP intervention among the analysis sample, their age 3 IQ scores were about 8.81 points higher than had they not received the IHDP intervention.</u>

```
# Method 5: logit regression with IPTW ATT weight
m5.data <- cbind(new, pscores=pscore_log2$pscores, weight=wts_iptw$weight)
summary(lm(ppvtr.36 ~ factor(treat) + weight, data = m5.data))
Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept)     82.9016     0.6309 131.403  < 2e-16 ***
factor(treat)1   8.8080     1.3526   6.512 1.05e-10 ***
weight           0.4041     0.3389   1.192    0.233
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
Residual standard error: 20.01 on 1317 degrees of freedom
Multiple R-squared: 0.03529, Adjusted R-squared: 0.03383
F-statistic: 24.09 on 2 and 1317 DF, p-value: 5.296e-11
```

Question 11: Comparison to linear regression

Fit a regression of your outcomes 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?

Solutions.

(a) According to the linear regression output, the estimated treatment effect is 9.72, and the standard error is 1.679.

(b) Controlling other variables, on average, children who participated in the IHDP intervention would score about 9.7 points higher in age 3 IQ scores than those who did not participate in the intervention.

(c) Compared with multiple linear regression that has a risk of extrapolation, the propensity score approach provided a more straightforward way to determine the range over which comparisons can be supported (*checking the overlap or common support via estimated propensity scores***). Moreover, if covariate balance is achieved and no further regression adjustment is needed, propensity score approach does not rely on the assumption of the relationship between the outcome and covariates (i.e., linearity or log linearity); when additional regression adjustment is used to adjust the remaining covariate imbalances, such adjustments are relatively robust against violations of the linear model in the matched samples.**

```
lm.fit <- lm(ppvtr.36 ~ ., data = new)
summary(lm.fit)
Call: lm(formula = ppvtr.36 ~ ., data = new)
Residuals:
    Min      1Q  Median      3Q     Max
-55.777 -10.246   1.004  11.346  51.964
Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept)   64.975167   6.682969   9.723  < 2e-16 ***
treat          9.719150   1.679203   5.788 8.91e-09 ***
momage         0.358728   0.131005   2.738  0.00626 **
momed_recode   7.118611   1.191113   5.976 2.94e-09 ***
prenatal       2.741787   2.820353   0.972  0.33116
cig            0.706575   1.010459   0.699  0.48451
booze         -0.990936   1.177211  -0.842  0.40007
first          6.810685   0.995543   6.841 1.20e-11 ***
bw             0.004188   0.001708   2.453  0.01431 *
preterm        0.381531   0.235262   1.622  0.10510
black        -17.391480   1.083517 -16.051  < 2e-16 ***
hispanic     -14.698127   1.406093 -10.453  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
Residual standard error: 16.92 on 1308 degrees of freedom
Multiple R-squared:  0.3156,     Adjusted R-squared:  0.3099
F-statistic: 54.84 on 11 and 1308 DF,  p-value: < 2.2e-16
```