POLS 207

Problem Set 3[*]

Villaseñor-Derbez, J.C.

Problem 1: NSW experiment and observational comparison

```r
# Load packages
suppressPackageStartupMessages({
  library(startR)
  library(Matching)
  library(ebal)
  library(foreign)
  library(here)
  library(tidyverse)
})

# Load data
nsw_dat <- read.dta("nsw_exper.dta")
```

a) Using the experimental data, obtain a simple unbiased estimate of the ATE of NSW on 1978 earnings, its SE and a 95% confidence interval.

Because this is experimental data, the difference in means is an unbiased estimate of the ATE.

```r
# Simple unbiased estimate of the ATE
# Calculate group-level means
mT <- mean(nsw_dat$re78[nsw_dat$nsw == 1], na.rm = T)
mC <- mean(nsw_dat$re78[nsw_dat$nsw == 0], na.rm = T)

# Difference in means
ATE <- mT - mC
```

```r
# Calculate standard errors
# Get variances
sigma_y1 <- var(nsw_dat$re78[nsw_dat$nsw == 1], na.rm = T)
sigma_y0 <- var(nsw_dat$re78[nsw_dat$nsw == 0], na.rm = T)

# Get sample sizes
N1 <- sum(nsw_dat$nsw == 1, na.rm = T)
N0 <- sum(nsw_dat$nsw == 0, na.rm = T)

# Calculate Standard Errors
SE <- sqrt((sigma_y1 / N1) + (sigma_y0 / N0))
```

```r
# Calculate 95% CIs
CI_h <- ATE + (1.96 * SE)
CI_l <- ATE - (1.96 * SE)
```

The $A\hat{T}E = 1794.343$, with $SE = 670.99$ and $CI_{95} = (479.18, 3109.49)$.

[*] Available on GitHUb: https://github.com/jcvdav/POLS207/blob/master/ps3/ps3.pdf

b) With the experimental data, use OLS to estimate the ATE controlling for age, education, race, ethnicity, marital status, and employment and earnings in 1974 and 1975. Report the estimate and its SE. Compare it to the one obtained in (a), explaining the reason for any similarities or differences.

The table below shows the coefficient estimates for the stated regression. The $A\hat{T}E_{OLS} = 1672.042$. The previous estimate was slightly higher ($A\hat{T}E = 1794.343$), but the OLS estimate is within the 95% CIs calculated before. The OLS estimate represents the conditional-variance weighted estimate.

```r
# Fit model and report in stargazer tables with HC2 SEs
lm(re78 ~ nsw + age + educ + black + hisp + married + re74 + re75 + u74 + u75,
   data = nsw_dat) %>%
  stargazer::stargazer(.,
                       se = estimatr::starprep(., se_type = "HC2"),
                       t.auto = T,
                       p.auto = T,
                       header = F,
                       title = "Estimate of the Sample Average Treatment Effect.",
                       single.row = T)
```

Table 1: Estimate of the Sample Average Treatment Effect.

	Dependent variable:
	re78
nsw	1,672.042** (663.722)
age	53.668 (40.567)
educ	402.947** (163.077)
black	−2,039.466* (1,048.241)
hisp	424.649 (1,443.157)
married	−146.662 (870.023)
re74	0.124 (0.133)
re75	0.019 (0.144)
u74	1,380.999 (1,571.072)
u75	−1,071.817 (1,411.349)
Constant	221.429 (2,864.634)
Observations	445
R^2	0.058
Adjusted R^2	0.037
Residual Std. Error	6,509.273 (df = 434)
F Statistic	2.683*** (df = 10; 434)
Note:	*p<0.1; **p<0.05; ***p<0.01

c) File `nsw_psid_withtreated.dta` contains treated units taken from the experiment, but control units replaced by the non-experimental sample from the PSID.

```
# Read non-experimental sample
psid_dat <- read.dta("nsw_psid_withtreated.dta")
```

Check the covariate balance in this merged dataset. Decide on a few sensible balance statistics and report them in a table.

The following table shows the covariate balance for non-experimental data. Student's t test of difference in menas suggests that all covariates (except for `hisp`) are unbalanced, and that differences between treated and control groups exist. The Kolmogorov-Smirnov test shows that the data within each group also come from different distributions.

```
balance <- psid_dat %>%
  drop_na() %>%
  MatchBalance(nsw ~ age + educ + black + hisp + married + re74 + re75 + u74 + u75,
               data = .,
               print.level = 0) %>%
  baltest.collect(var.names = c("age", "educ", "black", "hisp", "married", "re74", "re75", "u74", "u75"
                  after = F) %>%
  as_tibble(rownames = "Covariate") %>%
  dplyr::select(-contains("qq"), -contains("pooled")) %>%
  mutate_at(.vars = vars(-Covariate), round, 2)

knitr::kable(balance,
             booktabs = T,
             col.names = c("Covariate",
                           "Mean (Treatment)",
                           "Mean (Control)",
                           "Standardized difference",
                           "Variance ratio",
                           "T p-value",
                           "KS p-value"),
             caption = "Pre-matching balance of covariates for non-experimental data."
)
```

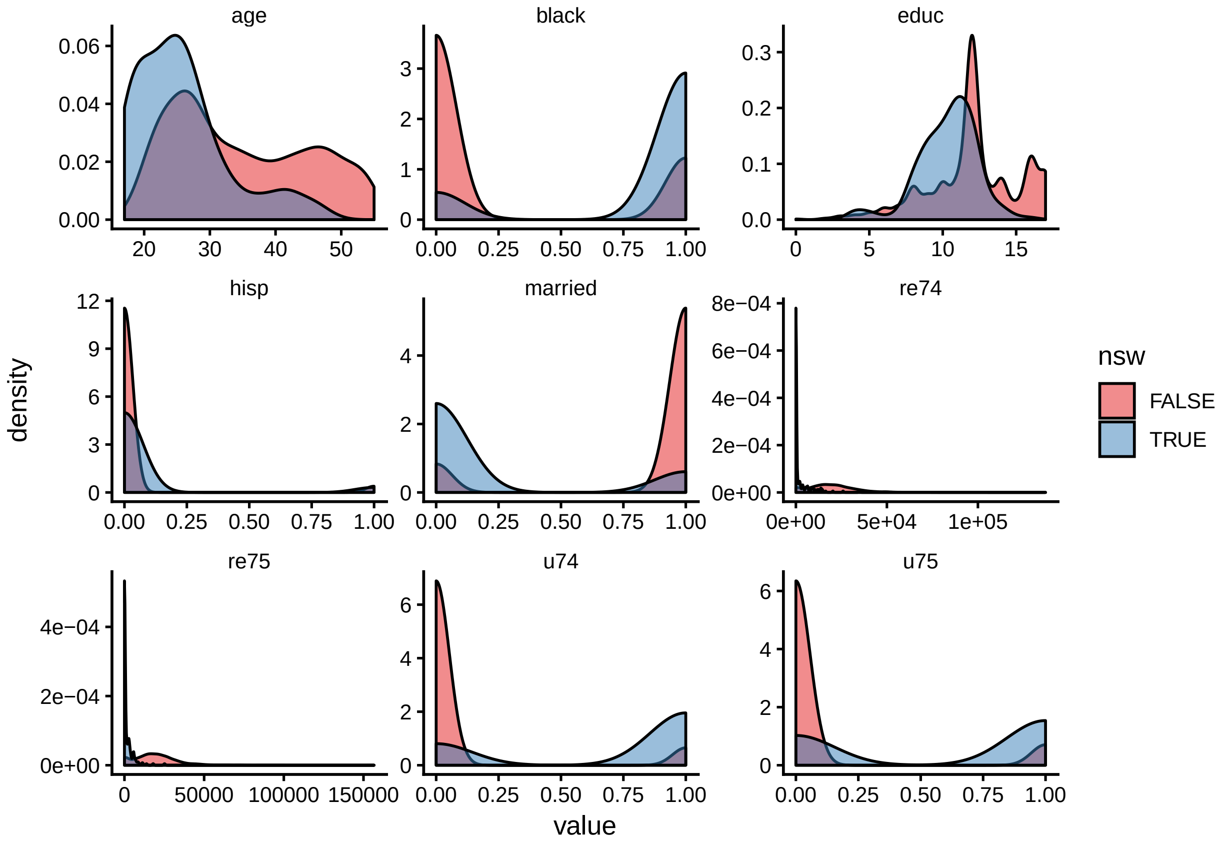
Table 2: Pre-matching balance of covariates for non-experimental data.

Covariate	Mean (Treatment)	Mean (Control)	Standardized difference	Variance ratio	T p-value	KS p-value
age	25.82	34.85	-126.27	0.47	0.00	0
educ	10.35	12.12	-88.08	0.43	0.00	0
black	0.84	0.25	162.56	0.71	0.00	NA
hisp	0.06	0.03	11.36	1.79	0.13	NA
married	0.19	0.87	-172.41	1.33	0.00	NA
re74	2095.57	19428.75	-354.71	0.13	0.00	0
re75	1532.06	19063.34	-544.58	0.06	0.00	0
u74	0.71	0.09	136.39	2.63	0.00	NA
u75	0.60	0.10	101.79	2.68	0.00	NA

How do the treatment and control group differ?

The treatment group has younger people, with less education, a greater percentage of black and hispanics, and most people are single. The treatment group has lower average real earnings and a greater proportion of unemployment. The figure below shows the density distributions for each covariate in the dataset.

```r
psid_dat %>%
  select(-c(re78, u78)) %>%
  gather(variable, value, -c(nsw)) %>%
  mutate(nsw = nsw == 1) %>%
  ggplot(aes(x = value, fill = nsw, group = nsw)) +
  geom_density(alpha = 0.5) +
  facet_wrap(~variable, scales = "free") +
  ggtheme_plot() +
  scale_fill_brewer(palette = "Set1")
```



Among the observed covariates, what seem to be the most important factors that determine selection into the program (the "treatment")?

The data suggest that your real earnings and employment status for 1974 and 1975 lead to selection into treatment. This can (and will) be further identified by estimating propensity scores with a binary logistic regression.

Estimate the (naive) ATE of the program on 1978 earnings without adjusting for any of the covariates. Report the estimate and a standard error.

```
# Simple unbiased estimate of the ATE for psid data
mTpsid <- mean(psid_dat$re78[psid_dat$nsw == 1], na.rm = T)
mCpsid <- mean(psid_dat$re78[psid_dat$nsw == 0], na.rm = T)

ATEpsid <- mTpsid - mCpsid
```

```
# Calculate standard errors
# Get variances
sigma_y1psid <- var(psid_dat$re78[psid_dat$nsw == 1], na.rm = T)
sigma_y0psid <- var(psid_dat$re78[psid_dat$nsw == 0], na.rm = T)

# Get sample sizes
N1psid <- sum(psid_dat$nsw == 1, na.rm = T)
N0psid <- sum(psid_dat$nsw == 0, na.rm = T)

# Calculate Standard Errors
SEpsid <- sqrt((sigma_y1psid / N1psid) + (sigma_y0psid / N0psid))
```

In this case, the naive ATE estimate for 1978 earnigns appears to be $ATE = -15204.78$, suggesting that the program reduces the average earnings. The standard error is now $SE = 657.07$

d) Repeat (b) using the non-experimental data. Does the estimate of the ATE change? Why or why not?

The table below shows a drastic change in my ATE. By including covariates, the sign and magnitude of the ATE changes. This, however, still produces an estimate lower to the one obtaines with experimental data.

```
# Fit naive lm and calculate HC2 SE into stargazer
lm(re78 ~ nsw + age + educ + black + hisp + married + re74 + re75, data = psid_dat) %>%
  stargazer::stargazer(.,
                       se = estimatr::starprep(., se_type = "HC2"),
                       t.auto = T, p.auto = T, header = F, single.row = T,
                       title = "Estimate of the Sample Average Treatment Effect using the non-experimen
```

Table 3: Estimate of the Sample Average Treatment Effect using the non-experimental data.

	Dependent variable:
	re78
nsw	859.769 (768.537)
age	−81.537*** (20.719)
educ	528.024*** (88.743)
black	−542.706 (442.463)
hisp	2,165.572* (1,227.276)
married	1,220.269** (496.886)
re74	0.278*** (0.062)
re75	0.568*** (0.067)
Constant	776.729 (1,489.169)
Observations	2,675
R^2	0.586
Adjusted R^2	0.585
Residual Std. Error	10,070.410 (df = 2666)
F Statistic	472.194*** (df = 8; 2666)
Note:	*p<0.1; **p<0.05; ***p<0.01

e) Using the non-experimental data, condition (only) on the marital status of individuals, and manually compute the subclassification estimator of the ATT.

```r
# Get treated and control outcomes for married
married_treated <- psid_dat$re78[psid_dat$nsw == 1 & psid_dat$married == 1]
married_control <- psid_dat$re78[psid_dat$nsw == 0 & psid_dat$married == 1]

# Get treated and control outcomes for single
single_treated <- psid_dat$re78[psid_dat$nsw == 1 & psid_dat$married == 0]
single_control <- psid_dat$re78[psid_dat$nsw == 0 & psid_dat$married == 0]

# Get ATT by strata
married_ATT <- mean(married_treated) - mean(married_control)
single_ATT <- mean(single_treated) - mean(single_control)

# Number of treated individuals
n_treated <- sum(psid_dat$nsw == 1)
# Number of treated indivuduals who are married
n_treated_married <- sum(psid_dat$nsw == 1 & psid_dat$married == 1)
# Proportion of married individuals in treated population
pr_married_treated <- n_treated_married / n_treated
# Proportion of single individuals in treated population
pr_single_treated <- 1 - pr_married_treated

# Weighted ATT estimate
ATT_married <- (pr_single_treated * single_ATT) + (pr_married_treated * married_ATT)
```

The subclassification ATT conditioning on marital status is $ATT = -11124.4$.

f) Repeat the above, this time conditioning (only) on Unemployment status in 1975 using a sub-classification estimator of the ATT.

```r
# Get treated and control outcomes for unemployed
unemployed_treated <- psid_dat$re78[psid_dat$nsw == 1 & psid_dat$u75 == 1]
unemployed_control <- psid_dat$re78[psid_dat$nsw == 0 & psid_dat$u75 == 1]

# Get treated and control outcomes of employed
employed_treated <- psid_dat$re78[psid_dat$nsw == 1 & psid_dat$u75 == 0]
employed_control <- psid_dat$re78[psid_dat$nsw == 0 & psid_dat$u75 == 0]

# Calculate strata-level difference in menas
unemployed_ATT <- mean(unemployed_treated) - mean(unemployed_control)
employed_ATT <- mean(employed_treated) - mean(employed_control)

# Number of unemployed people in the treated group
n_treated_unemployed <- sum(psid_dat$nsw == 1 & psid_dat$u75 == 1)
# Proportion of unemployed people in treated population
pr_unemployed_treated <- n_treated_unemployed / n_treated
# Proportion of employed people in treated population
pr_employed_treated <- 1 - pr_unemployed_treated

# Subclassification ATT for employment status
```

```
ATT_u75 <- (pr_employed_treated * employed_ATT) + (pr_unemployed_treated * unemployed_ATT)
```

The subclassification ATT conditioning on employment status is $ATT = -6244.687$.

Problem 2: Matching on NSW

a) With the non-experimental data, show the balance on the data. Then match, using the following covariates: "age", "educ", "black", "hisp", "married", "re74", "re75", "u74", and "u75". Show the new balance tables, and estimate the ATT.

The table below shows post-matching balance, where balance is achieved for most of the covariates (not for education or earnings in 1975). Estimating the ATT with bias adjustment, we obtain ($ATT = 2415$; $t_{184} = 1.432; p = 0.15$)

```
# Create matrix with covariates
X <- psid_dat %>%
  select(-c(nsw, re78, u78)) %>%
  as.matrix()

# Match
matched <- Match(Y = psid_dat$re78,
                 Tr = psid_dat$nsw,
                 X = X, M = 1,
                 estimand = "ATT",
                 BiasAdjust = T)

# Check balance
balance_matched <- MatchBalance(
  match.out = matched,
  formul = nsw ~ age + educ + black + hisp + married + re74 + re75 + u74 + u75,
  data = psid_dat,
  print.level = 0) %>%
  baltest.collect(
    var.names = c("age", "educ", "black", "hisp", "married", "re74", "re75", "u74", "u75"),
    after = T
  ) %>%
  as_tibble(rownames = "Covariate") %>%
  dplyr::select(-contains("qq"), -contains("pooled"))

# Report into table
knitr::kable(balance_matched,
             booktabs = T,
             col.names = c(
               "Covariate",
               "Mean (Treatment)",
               "Mean (Control)",
               "Standardized difference",
               "Variance ratio",
               "T p-value",
               "KS p-value"),
             caption = "Pre-matching balance of covariates.")
```

Table 4: Pre-matching balance of covariates.

Covariate	Mean (Treatment)	Mean (Control)	Standardized difference	Variance ratio	T p-value	KS p-value
age	25.8162162	26.0774775	-3.651440	0.9240888	0.6010652	0.000
educ	10.3459459	10.6522523	-15.234191	1.3120104	0.0024980	0.002
black	0.8432432	0.8432432	0.000000	1.0000000	1.0000000	NA
hisp	0.0594595	0.0594595	0.000000	1.0000000	1.0000000	NA
married	0.1891892	0.1891892	0.000000	1.0000000	1.0000000	NA
re74	2095.5740112	2173.7482894	-1.599761	0.9734941	0.4333570	0.500
re75	1532.0556149	2095.3161514	-17.496633	0.7448871	0.0010229	0.068
u74	0.7081081	0.7081081	0.000000	1.0000000	1.0000000	NA
u75	0.6000000	0.6000000	0.000000	1.0000000	1.0000000	NA

b) What is the importance of the bias adjustment? When is it most important to use the bias adjustment?

If balance is not achieved for some variables, these might be influencing selection into treatment. If there is a consistent discrepancy between groups, it is unlikely to average-out by increasing sample size. In stead, bias adjustment allows us to correct for this. Bias adjustemnt should be used if covariate balance is not reached even after matching.

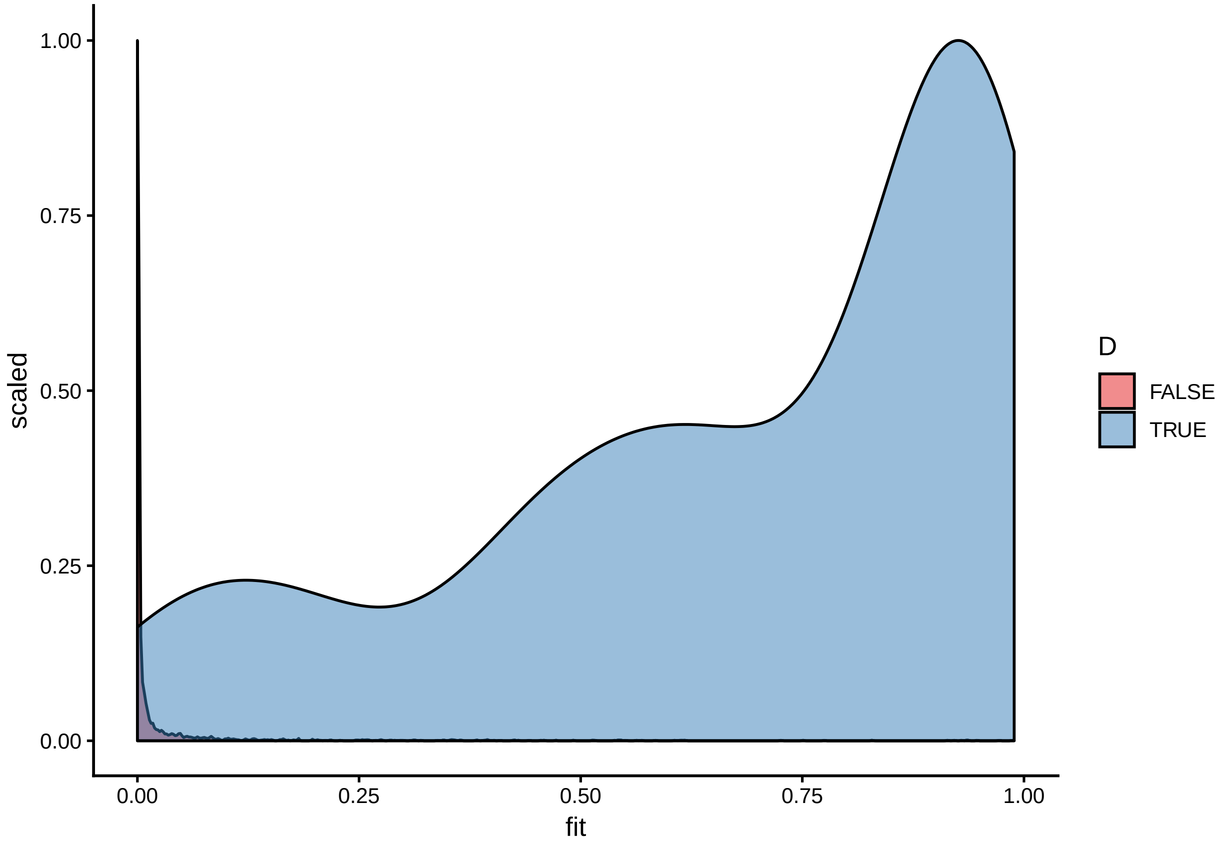
c) In the non-experimental sample, compare the number of treated to untreated units. Comment on the result, and whether it is good or bad in your view.

The non-experimental data has 13-times more observations. This larger sample size likely covers a wider range of covariate values, which might help obtain better matches.

d) In the non-experimental sample, estimate propensity scores using a logistic regression. Report the distributions of propensity scores for treated and control groups and comment on the overlap.

The figure below shows the distribuion of fitted values after performing a logistic regression. It is clear that the covariates in treatment and control groups significantly predict treatment status.

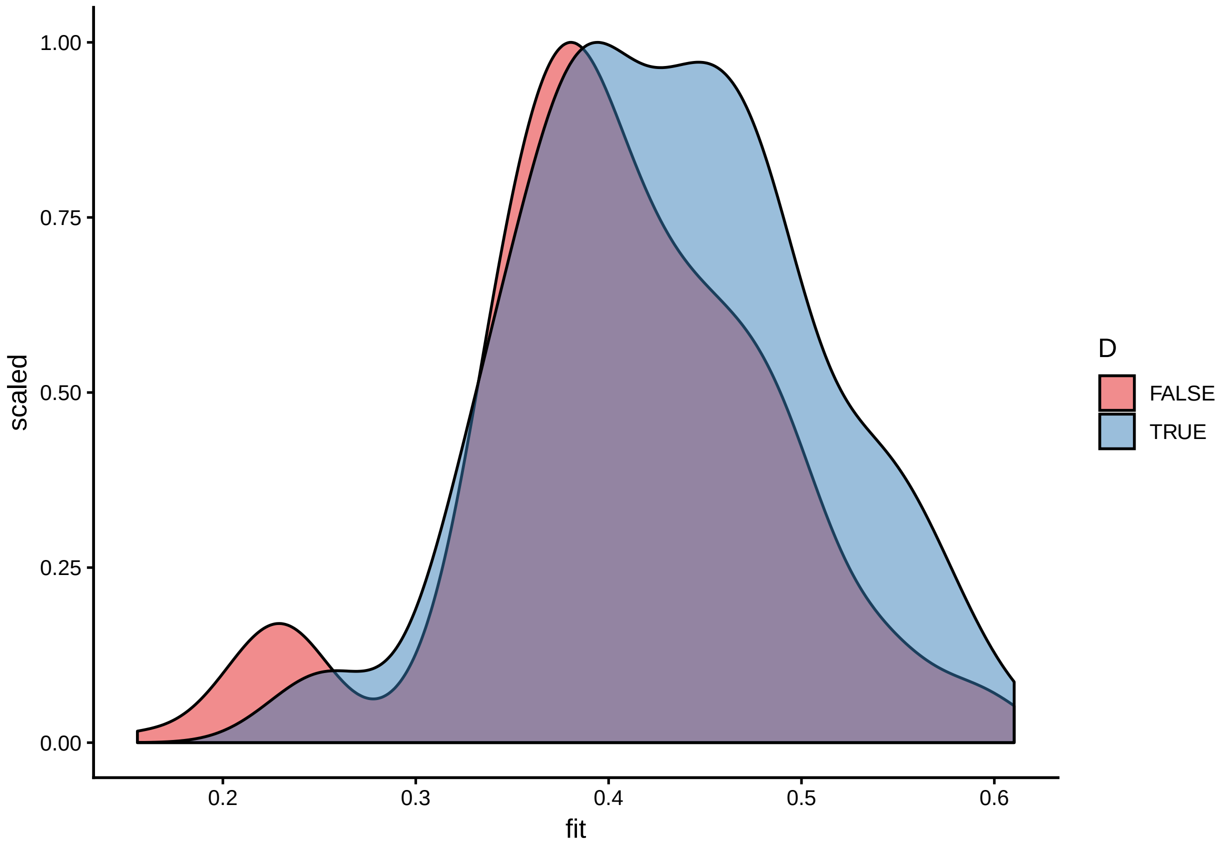
```r
glm_fit <- glm(nsw ~ age + educ + black + hisp + married + re74 + re75 + u74 + u75,
               data = psid_dat,
               family = "binomial")

fit <- glm_fit$fit

D <- psid_dat$nsw == 1

tibble(D = D, fit = fit) %>%
  ggplot(aes(x  = fit, y = ..scaled.., group = D, fill = D)) +
  geom_density(alpha = 0.5) +
  ggtheme_plot() +
  scale_fill_brewer(palette = "Set1")
```



e) Now using the experimental sample, estimate propensity scores. Compare distributions of the propensity scores for treated and control groups here. What do you observe? Compare your results with part (d).

However, wen we repeat the process with the experimental data we observe a better overlap. While it seems like treated units (blue) have a greater probability of being selected into treatment, these show similar distribution and descriptive statistics.

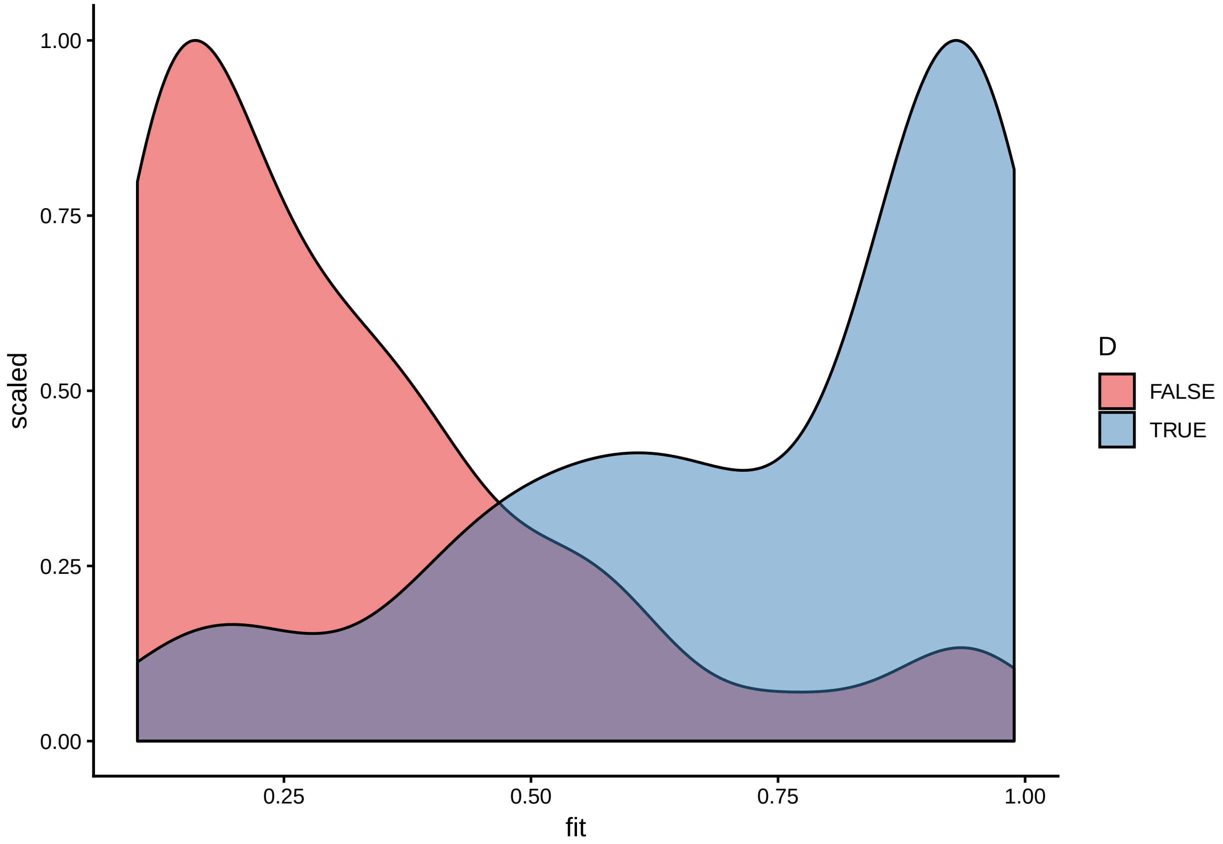
```
glm_fit_exp <- glm(nsw ~ age + educ + black + hisp + married + re74 + re75 + u74 + u75,
               data = nsw_dat,
               family = "binomial" (link=logit))

fit_exp <- glm_fit_exp$fit

D_exp <- nsw_dat$nsw == 1

tibble(D = D_exp, fit = fit_exp) %>%
  ggplot(aes(x  = fit, y = ..scaled.., group = D, fill = D)) +
  geom_density(alpha = 0.5) +
  ggtheme_plot() +
  scale_fill_brewer(palette = "Set1")
```



f) Back to the non-experimental sample. Trim off observations that have propensity scores lower than 0.1. Then report balance statistics for the trimmed data. Compare the results to the balance you initially saw for this dataset. Do the results differ, and why or why not?

Removing propensit scores lower than 0.1 modifies the fit, but it still shows a clear difference between treated and control groups, with treated individuals having higher propensity scores. Results differ in that there is more overlap. However, there is still an unbalance in propensity scores between the groups.

```r
tibble(D = D, fit = fit) %>%
  filter(fit > 0.1) %>%
  ggplot(aes(x  = fit, y = ..scaled.., group = D, fill = D)) +
  geom_density(alpha = 0.5) +
  ggtheme_plot() +
  scale_fill_brewer(palette = "Set1")
```



g) In the non-experimental sample, match on the estimated propensity scores (from part d) using `Match()` to obtain an estimator of the average effect of the treatment on the treated for the NSW program.

```
matched_PS <- Match(Y = psid_dat$re78,
                    Tr = psid_dat$nsw,
                    X = fit,
                    M = 1,
                    estimand = "ATT",
                    BiasAdjust = T)

summary(matched_PS)
```

```
##
## Estimate...  2145.8
## AI SE......  1554
## T-stat.....  1.3808
## p.val......  0.16733
##
## Original number of observations..............  2675
## Original number of treated obs...............  185
## Matched number of observations...............  185
## Matched number of observations  (unweighted).  1997
```

h) Compare the various results and tests above and discuss. For example, do the results differ for the experimental and non-experimental data? Why? Can you replicate the experimental results? How?

The table shows all ATT and ATE estimates obtained. Estimates obtained from experimental data show less discrepancy. Estimates of non-experimental data are sensitive to model specification, and have a wider range of variation. Non-experimental data yields biased estimates because treatment was not assigned at random, and we are effectively comparing to distinct populations. Experimental data, instead, uses random assignment.

source	estimation	value
Exp	Diff	1794.343
Exp	OLS	1672.042
Non-exp	Diff	-15204.780
Non-exp	OLS	859.769
Non-exp	Diff (married)	-11124.400
Non-exp	Diff (unemployed)	-6244.687
Non-exp	Matching	2415.500
Non-exp	PS matching	2145.800

I don't think experimental results can be replicated with non-experimental data. However, there is certainly room to reduce bias in the estimate. I think a next step would be to try inverse-weighted propensity scores or different matching techniques to obtain a better group of counterfactuals that better represent the untreated outcomes of the treated group.