

# Project 6: Randomization and Matching

## Introduction

In this project, you will explore the question of whether college education causally affects political participation. Specifically, you will use replication data from *Who Matches? Propensity Scores and Bias in the Causal Effects of Education on Participation* by former Berkeley PhD students John Henderson and Sara Chatfield. Their paper is itself a replication study of *Reconsidering the Effects of Education on Political Participation* by Cindy Kam and Carl Palmer. In their original 2008 study, Kam and Palmer argue that college education has no effect on later political participation, and use the propensity score matching to show that pre-college political activity drives selection into college and later political participation. Henderson and Chatfield in their 2011 paper argue that the use of the propensity score matching in this context is inappropriate because of the bias that arises from small changes in the choice of variables used to model the propensity score. They use genetic matching (at that point a new method), which uses an approach similar to optimal matching to optimize Mahalanobis distance weights. Even with genetic matching, they find that balance remains elusive however, thus leaving open the question of whether education causes political participation.

You will use these data and debates to investigate the benefits and pitfalls associated with matching methods. Replication code for these papers is available online, but as you'll see, a lot has changed in the last decade or so of data science! Throughout the assignment, use tools we introduced in lab from the tidyverse and the MatchIt packages. Specifically, try to use dplyr, tidyr, purrr, stringr, and ggplot instead of base R functions. While there are other matching software libraries available, MatchIt tends to be the most up to date and allows for consistent syntax.

## Data

The data is drawn from the Youth-Parent Socialization Panel Study which asked students and parents a variety of questions about their political participation. This survey was conducted in several waves. The first wave was in 1965 and established the baseline pre-treatment covariates. The treatment is whether the student attended college between 1965 and 1973 (the time when the next survey wave was administered). The outcome is an index that calculates the number of political activities the student engaged in after 1965. Specifically, the key variables in this study are:

- **college**: Treatment of whether the student attended college or not. 1 if the student attended college between 1965 and 1973, 0 otherwise.
- **ppnscale**: Outcome variable measuring the number of political activities the student participated in. Additive combination of whether the student voted in 1972 or 1980 (`student_vote`), attended a campaign rally or meeting (`student_meeting`), wore a campaign button (`student_button`), donated money to a campaign (`student_money`), communicated with an elected official (`student_communicate`), attended a demonstration or protest (`student_demonstrate`), was involved with a local community event (`student_community`), or some other political participation (`student_other`)

Otherwise, we also have covariates measured for survey responses to various questions about political attitudes. We have covariates measured for the students in the baseline year, covariates for their parents in the baseline year, and covariates from follow-up surveys. **Be careful here.** In general, post-treatment covariates will be clear from the name (i.e. `student_1973Married` indicates whether the student was married in the 1973 survey). Be mindful that the baseline covariates were all measured in 1965, the treatment occurred between 1965 and 1973, and the outcomes are from 1973 and beyond. We will distribute the Appendix from Henderson

and Chatfield that describes the covariates they used, but please reach out with any questions if you have questions about what a particular variable means.

```
# Load tidyverse and MatchIt
# Feel free to load other libraries as you wish
library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.2 --
## v ggplot2 3.4.1      v purrr   1.0.1
## v tibble  3.2.1      v dplyr   1.1.0
## v tidyr   1.3.0      v stringr 1.5.0
## v readr   2.1.3      v forcats 1.0.0
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()

library(MatchIt)
library(ggplot2)
library(cobalt)

## cobalt (Version 4.5.1, Build Date: 2023-04-27)
##
## Attaching package: 'cobalt'
##
## The following object is masked from 'package:MatchIt':
##
##     lalonde

library(WeightIt)
library(gridExtra)

##
## Attaching package: 'gridExtra'
##
## The following object is masked from 'package:dplyr':
##
##     combine

library(dplyr)

setwd("/Users/alexadia/Documents/GitHub/Computational-Social-Science-Projects/Project 6")

# Load ypsps data
ypsps <- read_csv('data/ypsps.csv')

## Rows: 1254 Columns: 174
## -- Column specification -----
## Delimiter: ","
## dbf (174): interviewid, college, student_vote, student_meeting, student_othe...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.

head(ypsps)

## # A tibble: 6 x 174
##   interviewid college student_vote student_meeting student_other student_button
##         <dbl>   <dbl>         <dbl>         <dbl>         <dbl>         <dbl>
```

```
## 1      1      1      1      0      0      0
## 2      2      1      1      1      1      1
## 3      3      1      1      0      0      1
## 4      4      0      0      0      0      0
## 5      5      1      1      1      0      0
## 6      6      1      1      0      0      0
## # i 168 more variables: student_money <dbl>, student_communicate <dbl>,
## #   student_demonstrate <dbl>, student_community <dbl>, student_ppnscale <dbl>,
## #   student_PubAff <dbl>, student_Newspaper <dbl>, student_Radio <dbl>,
## #   student_TV <dbl>, student_Magazine <dbl>, student_FamTalk <dbl>,
## #   student_FrTalk <dbl>, student_AdultTalk <dbl>, student_PID <dbl>,
## #   student_SPID <dbl>, student_GovtOpinion <dbl>, student_GovtCrook <dbl>,
## #   student_GovtWaste <dbl>, student_TrGovt <dbl>, student_GovtSmart <dbl>, ...
```

## Randomization

Matching is usually used in observational studies to approximate random assignment to treatment. But could it be useful even in randomized studies? To explore the question do the following:

1. Generate a vector that randomly assigns each unit to either treatment or control
2. Choose a baseline covariate (for either the student or parent). A binary covariate is probably best for this exercise.
3. Visualize the distribution of the covariate by treatment/control condition. Are treatment and control balanced on this covariate?
4. Simulate the first 3 steps 10,000 times and visualize the distribution of treatment/control balance across the simulations.

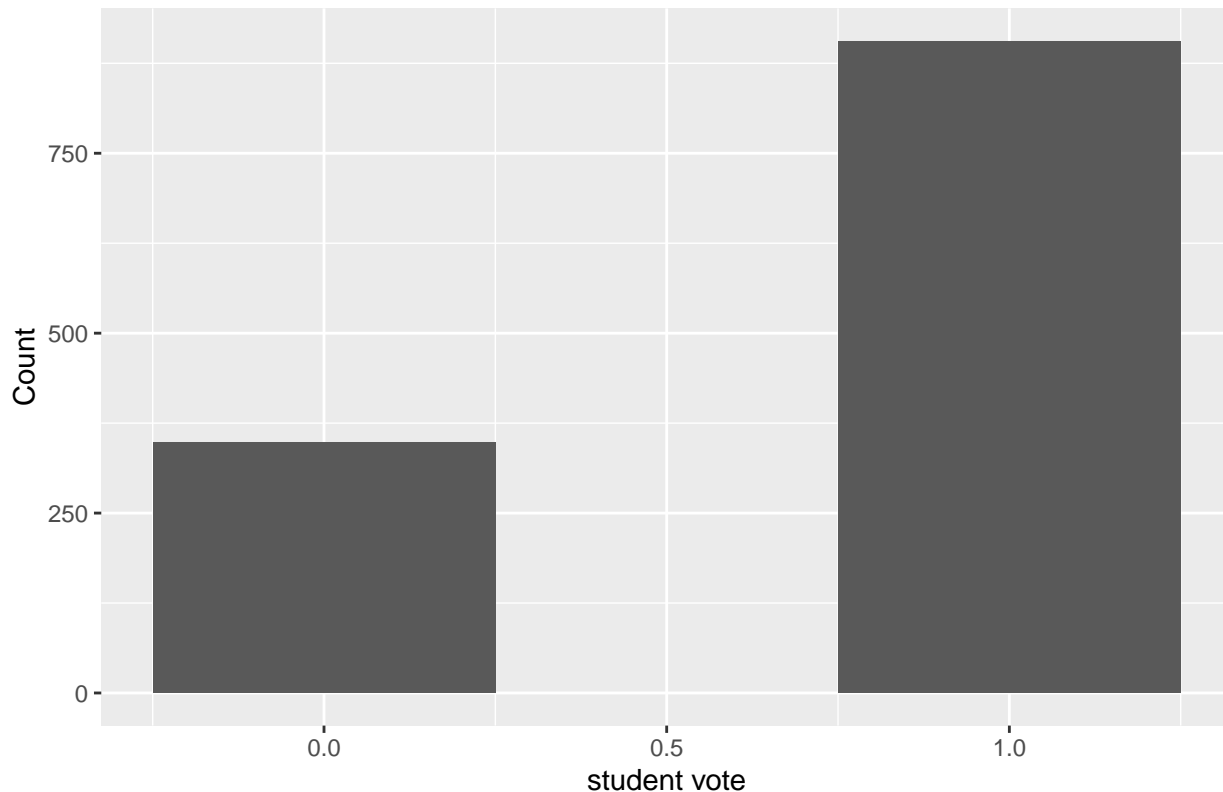
```
# Generate a vector that randomly assigns each unit to treatment/control
set.seed(6)
n_obs <- 1254
#1 is treatment and 0 is control
assignment <- sample(c(0, 1), n_obs, replace = TRUE)

# Choose a baseline covariate (use dplyr for this)
#Let's go with student vote

# Visualize the distribution by treatment/control (ggplot)
visualize_df <- data.frame(assignment, ypsps$student_vote)
ggplot(visualize_df, aes(x = ypsps.student_vote, fill = assignment)) +
  geom_bar(position = "dodge", width = 0.5) +
  labs(x = "student vote", y = "Count", fill = "Assignment") +
  ggtitle("Distribution of Student Vote Covariate by Treatment/Control Condition")
```

```
## Warning: The following aesthetics were dropped during statistical transformation: fill
## i This can happen when ggplot fails to infer the correct grouping structure in
##   the data.
## i Did you forget to specify a `group` aesthetic or to convert a numerical
##   variable into a factor?
```

Distribution of Student Vote Covariate by Treatment/Control Condition



```
# Simulate this 10,000 times (monte carlo simulation - see R Refresher for a hint)
# Function to simulate data and calculate balance
simulate_balance <- function() {
  # Random assignment of treatment/control (1 for treatment, 0 for control)
  assignment <- sample(c(0, 1), n_obs, replace = TRUE)

  # Choose a baseline covariate using dplyr
  # For simplicity, I'll generate a random distribution of 'college' here
  college <- sample(c("Yes", "No"), n_obs, replace = TRUE)

  # Calculate balance
  balance <- table(assignment, college)
  prop_treatment_yes <- balance[2, "Yes"] / sum(balance[2, ])
  prop_control_yes <- balance[1, "Yes"] / sum(balance[1, ])

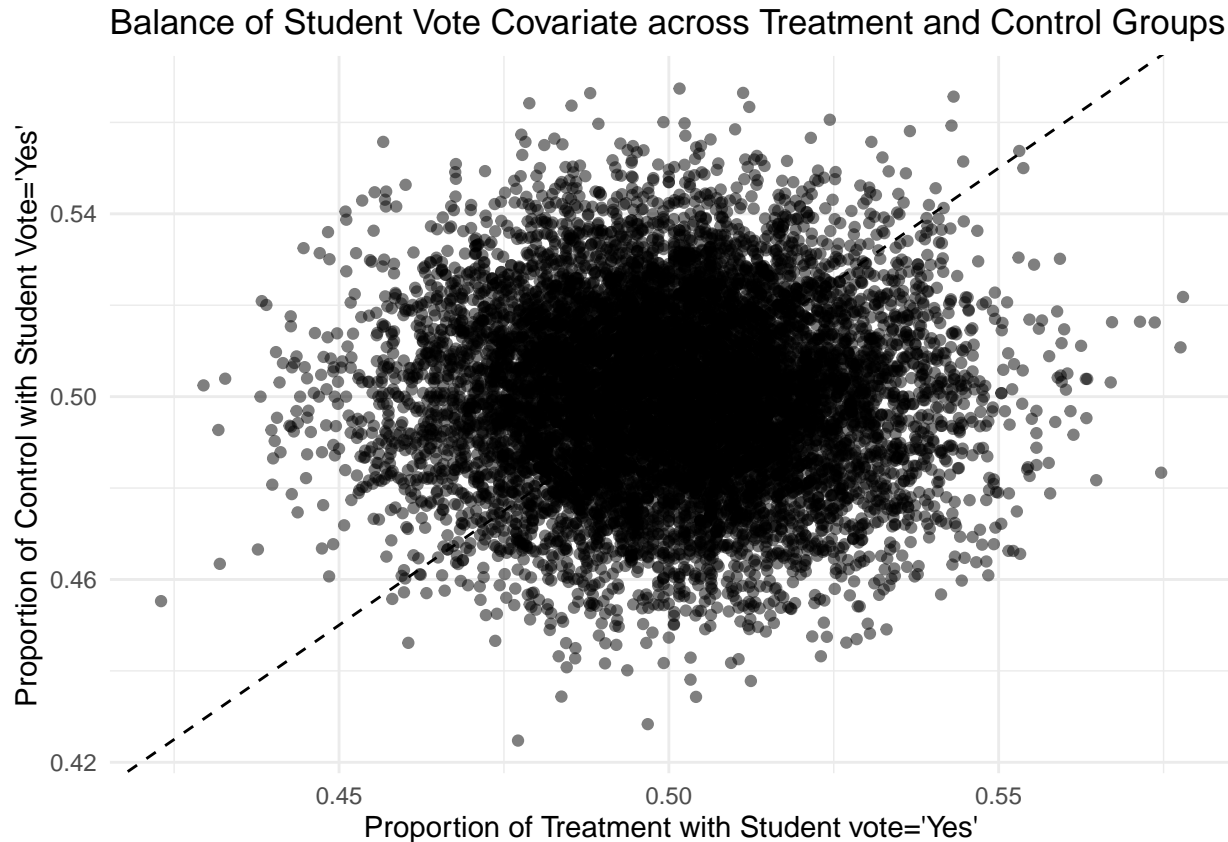
  return(c(prop_treatment_yes = prop_treatment_yes, prop_control_yes = prop_control_yes))
}

# Simulate 10,000 times
simulations <- replicate(10000, simulate_balance())

# Convert results to a data frame for visualization
balance_df <- data.frame(t(simulations))

# Visualize the distribution of treatment/control balance
ggplot(balance_df, aes(x = prop_treatment_yes, y = prop_control_yes)) +
  geom_point(alpha = 0.5) +
```

```
geom_abline(intercept = 0, slope = 1, linetype = "dashed") +
labs(x = "Proportion of Treatment with Student vote='Yes'",
     y = "Proportion of Control with Student Vote='Yes'",
     title = "Balance of Student Vote Covariate across Treatment and Control Groups") +
theme_minimal()
```



## Questions

1. What do you see across your simulations? Why does independence of treatment assignment and baseline covariates not guarantee balance of treatment assignment and baseline covariates?

While there is general clustering around the middle (the expected 50/50 odds), there are many times where there is variation that creates an imbalance across the student vote covariate between treatment and control. Therefore, even if independence exists, it only guarantees that, on average, treatment and control groups will be balanced. However, this does NOT guarantee that any given world state is balanced across these groups because of the influence of chance.

## Propensity Score Matching

### One Model

Select covariates that you think best represent the “true” model predicting whether a student chooses to attend college, and estimate a propensity score model to calculate the Average Treatment Effect on the Treated (ATT). Plot the balance of the top 10 (or fewer if you select fewer covariates). Report the balance of the p-scores across both the treatment and control groups, and using a threshold of standardized mean difference of p-score  $\leq .1$ , report the number of covariates that meet that balance threshold.

```

# Select covariates that represent the "true" model for selection, fit model
select_df<-ypsp$%>%select(student_LifeWish, student_GPA, student_Race, student_Knowledge, student_SchCl
select_covs<-select_df%>%select(-college)
select_model<-glm(college ~ ., data = select_df, family = binomial)
# Plot the balance for the top 10 covariates
balance_stats <- bal.tab(select_covs, treat=select_df$college)

```

```
## Note: `s.d.denom` not specified; assuming pooled.
```

```

# Report the overall balance and the proportion of covariates that meet the balance threshold
balance_stats

```

```

## Balance Measures
##
## student_LifeWish  Contin. -0.1721
## student_GPA      Contin. -0.5205
## student_Race     Contin. -0.0362
## student_Knowledge Contin.  0.9156
## student_SchClub  Contin.  0.3445
## parent_HHInc     Contin.  0.6362
## parent_EducHH    Contin.  0.8859
## parent_EducW     Contin.  0.7202
## parent_Knowledge  Contin.  0.6449
## parent_OwnHome   Binary   0.1015
##
## Sample sizes
##      Control Treated
## All      451      803

```

## Simulations

Henderson/Chatfield argue that an improperly specified propensity score model can actually *increase* the bias of the estimate. To demonstrate this, they simulate 800,000 different propensity score models by choosing different permutations of covariates. To investigate their claim, do the following:

- Using as many simulations as is feasible (at least 10,000 should be ok, more is better!), randomly select the number of and the choice of covariates for the propensity score model.
- For each run, store the ATT, the proportion of covariates that meet the standardized mean difference  $\leq .1$  threshold, and the mean percent improvement in the standardized mean difference. You may also wish to store the entire models in a list and extract the relevant attributes as necessary.
- Plot all of the ATTs against all of the balanced covariate proportions. You may randomly sample or use other techniques like transparency if you run into overplotting problems. Alternatively, you may use plots other than scatterplots, so long as you explore the relationship between ATT and the proportion of covariates that meet the balance threshold.
- Finally choose 10 random models and plot their covariate balance plots (you may want to use a library like gridExtra to arrange these)

**Note:** There are lots of post-treatment covariates in this dataset (about 50!)! You need to be careful not to include these in the pre-treatment balancing. Many of you are probably used to selecting or dropping columns manually, or positionally. However, you may not always have a convenient arrangement of columns, nor is it fun to type out 50 different column names. Instead see if you can use dplyr 1.0.0 functions to programatically drop post-treatment variables (here is a useful tutorial).

Note: I tried for hours to do this mean percent improvement stuff but couldn't figure it out. Sorry!

```

sim_df<-ypsp$%>%
  select(-starts_with("student_1973"))%>%select(-starts_with("student_1982"))%>%select(-interviewid, -p

starter_df<-sim_df%>%select(-student_ppnscale)

available_covariates <- sim_df%>%select(-college, -student_ppnscale)

num_simulations<-1000 #will rerun this weekend with correct sims

#I did try to get the pre-smd scores to figure out the percentages
means_treatment_orig <- colMeans(starter_df[starter_df$college == 1, -1])
means_control_orig <- colMeans(starter_df[starter_df$college == 0, -1])
sds_treatment_orig <- apply(starter_df[starter_df$college == 1, -1], 2, sd)
sds_control_orig <- apply(starter_df[starter_df$college == 0, -1], 2, sd)

smd_before <- (means_treatment_orig - means_control_orig) / sqrt((sds_treatment_orig^2 + sds_control_or
smd_before <- as.data.frame(smd_before)

# Create an empty data frame to store results
results <- data.frame(ATT = numeric(num_simulations), Prop_Cov=numeric(num_simulations))

# get simulations
for (i in 1:num_simulations) {
  # Set seed for reproducibility, incrementing by i
  set.seed(6 + i)

  # Randomly select 5 covariates
  selected_covariates <- sample(available_covariates, 5)

  # Create formula for matchit
  formula <- as.formula(paste("college ~", paste(selected_covariates, collapse = "+")))

  # Perform propensity score matching
  matched_data <- matchit(formula, data = sim_df, method = "nearest", replace=TRUE)

  #extract the matched data - need this because it's actually kind of difficult to get the differences
  postmatch_data<-match.data(matched_data)

  #manually calculate the ATT because I can't figure out how to do it the elegant way
  treated <- postmatch_data$student_ppnscale[postmatch_data$college==1]
  control <- postmatch_data$student_ppnscale[postmatch_data$college==0]
  ATT <- mean(treated)-mean(control)

  means_treatment <- colMeans(postmatch_data[postmatch_data$college == 1, -1])
  means_control <- colMeans(postmatch_data[postmatch_data$college == 0, -1])
  sds_treatment <- apply(postmatch_data[postmatch_data$college == 1, -1], 2, sd)
  sds_control <- apply(postmatch_data[postmatch_data$college == 0, -1], 2, sd)

  # Calculate standardized mean differences
  smd <- (means_treatment - means_control) / sqrt((sds_treatment^2 + sds_control^2) / 2)
  smd<-as.data.frame(smd)%>%head(-2)

```

```

abs_smd <- abs(smd)
#proportion of covariates
count <- sum(abs_smd$smd < 0.1)
total<-nrow(abs_smd)
prop_cov<-count/total

# Store results in the data frame
results[i, "ATT"] <- ATT
results[i, "Prop_Cov"] <- prop_cov
}

```

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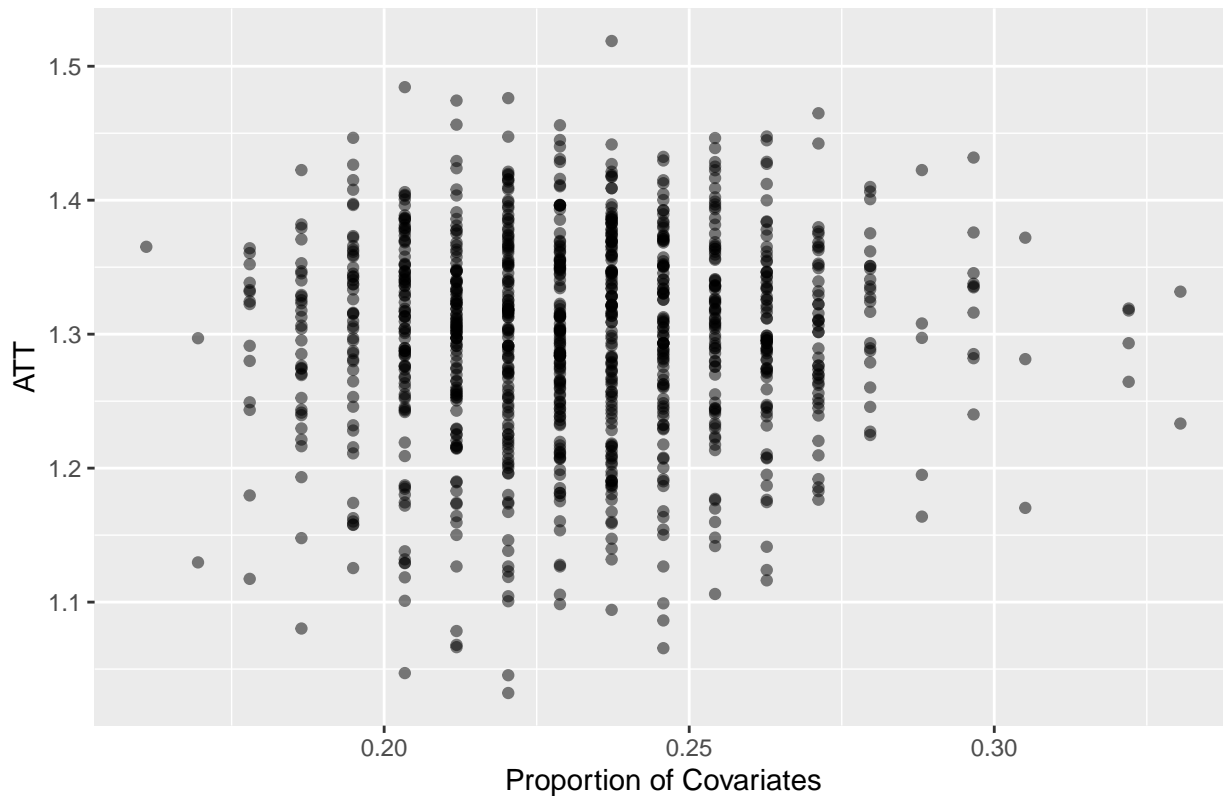
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```

```
#plot
ggplot(results, aes(x = Prop_Cov, y = ATT)) +
  geom_point(alpha = 0.5) + # Add transparency to avoid overplotting
  labs(x = "Proportion of Covariates", y = "ATT") + # Label axes
  ggtitle("Scatterplot of ATTs vs. Balanced Covariate Proportions") # Title of the plot
```

Scatterplot of ATTs vs. Balanced Covariate Proportions



```
#simulation graphs
graph_sims<-10

graph_list <- list()

for (i in 1:graph_sims) {
  # Set seed for reproducibility, incrementing by i
  set.seed(6 + i)
  # Randomly select 5 covariates
  selected_covariates <- sample(available_covariates, 5)

  # Create formula for matchit
  formula <- as.formula(paste("college ~", paste(selected_covariates, collapse = "+")))

  # Perform propensity score matching
  matched_data <- matchit(formula, data = sim_df, method = "nearest", replace=TRUE)

  m.out<-match.data(matched_data)

  graph<-love.plot(m.out, treat=m.out$college, binary = "std", thresholds = c(m = .1))
  graph_list[[i]] <- graph
}
```

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## Note: `s.d.denom` not specified; assuming pooled.

## Warning in sqrt(Reduce("+", lapply(unique.treats, function(t) col.w.v(mat[treat
## == : NaNs produced

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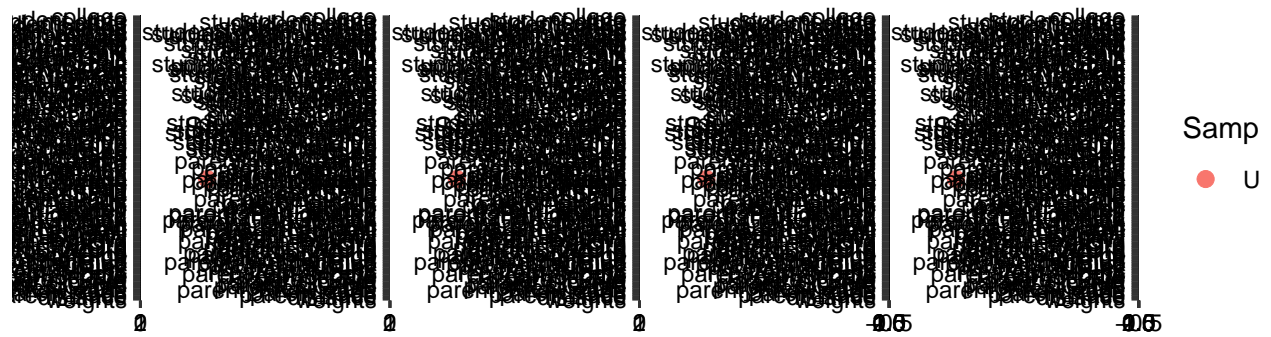
## Note: `s.d.denom` not specified; assuming pooled.

## Warning in sqrt(Reduce("+", lapply(unique.treats, function(t) col.w.v(mat[treat
## == : NaNs produced

grid.arrange(grobs = graph_list, nrow = 2)

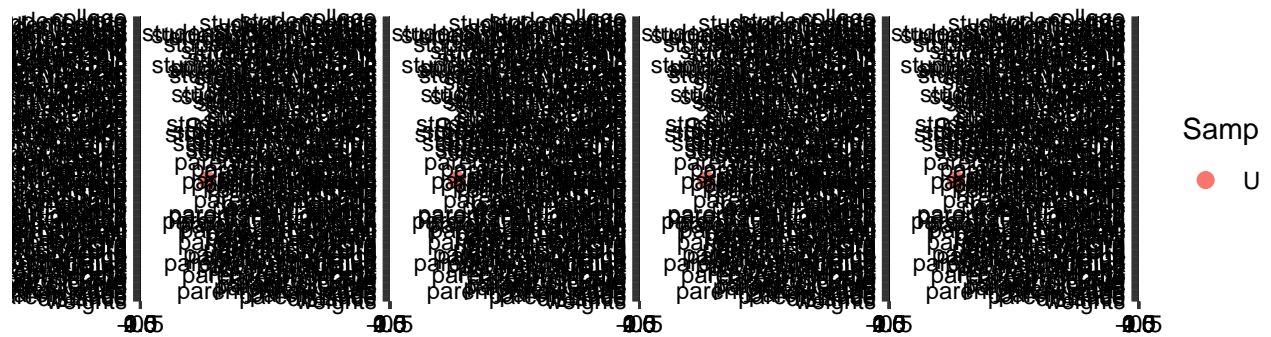
```

Covariate Balance Covariate Balance Covariate Balance Covariate Balance Covariate Balance



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Covariate Balance Covariate Balance Covariate Balance Covariate Balance Covariate Balance



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## Questions (Note: Answering theoretically for some because I didn't do very well with the code this time)

1. **How many simulations resulted in models with a higher proportion of balanced covariates? Do you have any concerns about this?**
2. **Your Answer:** There are going to be multiple simulations where models will not necessarily have a higher proportion of balanced covariates. I would guess this is partly due to the fact that the matching covariates can be incorrectly specified and thus yields suboptimal results the further the matched covariates are from the "true" set of covariates that should feed into the match.
3. **Analyze the distribution of the ATTs. Do you have any concerns about this distribution?**
4. **Your Answer:** Yes, the ATTs can highly depend on which set of covariates are selected as part of the
5. **Do your 10 randomly chosen covariate balance plots produce similar numbers on the same covariates? Is it a concern if they do not?**
6. **Your Answer:** Not necessarily! This is concerning, because it means the end-covariate balancing is dependent on which covariates are selected as the ones to use to match the data. I believe this can probably be addressed by the use of doubly robust methods (at least in a way that is better than just matching).

## Matching Algorithm of Your Choice

### Simulate Alternative Model

Henderson/Chatfield propose using genetic matching to learn the best weights for Mahalanobis distance matching. Choose a matching algorithm other than the propensity score (you may use genetic matching if you wish, but it is also fine to use the greedy or optimal algorithms we covered in lab instead). Repeat the same steps as specified in Section 4.2 and answer the following questions:

```

# Remove post-treatment covariates
sim_df<-ypsp$%>%
  select(-starts_with("student_1973"))%>%select(-starts_with("student_1982"))%>%select(-interviewid, -p

starter_df<-sim_df%>%select(-student_ppnscale)

available_covariates <- sim_df%>%select(-college, -student_ppnscale)

# Create an empty data frame to store results
results <- data.frame(ATT = numeric(num_simulations), Prop_Cov=numeric(num_simulations))

# get simulations
for (i in 1:num_simulations) {
  # Set seed for reproducibility, incrementing by i
  set.seed(206 + i)

  # Randomly select 5 covariates
  selected_covariates <- sample(available_covariates, 5)

  # Create formula for matchit
  formula <- as.formula(paste("college ~", paste(selected_covariates, collapse = "+")))

  # Perform propensity score matching
  matched_data <- matchit(formula, data = sim_df, method = "nearest", replace=TRUE)

  #extract the matched data - need this because it's actually kind of difficult to get the differences
  postmatch_data<-match.data(matched_data)

  #manually calculate the ATT because I can't figure out how to do it the elegant way
  treated <- postmatch_data$student_ppnscale[postmatch_data$college==1]
  control <- postmatch_data$student_ppnscale[postmatch_data$college==0]
  ATT <- mean(treated)-mean(control)

  means_treatment <- colMeans(postmatch_data[postmatch_data$college == 1, -1])
  means_control <- colMeans(postmatch_data[postmatch_data$college == 0, -1])
  sds_treatment <- apply(postmatch_data[postmatch_data$college == 1, -1], 2, sd)
  sds_control <- apply(postmatch_data[postmatch_data$college == 0, -1], 2, sd)

  # Calculate standardized mean differences
  smd <- (means_treatment - means_control) / sqrt((sds_treatment^2 + sds_control^2) / 2)
  smd<-as.data.frame(smd)%>%head(-2)
  abs_smd <- abs(smd)
  #proportion of covariates
  count <- sum(abs_smd$smd < 0.1)
  total<-nrow(abs_smd)
  prop_cov<-count/total

  # Store results in the data frame
  results[i, "ATT"] <- ATT
  results[i, "Prop_Cov"] <- prop_cov
}

```

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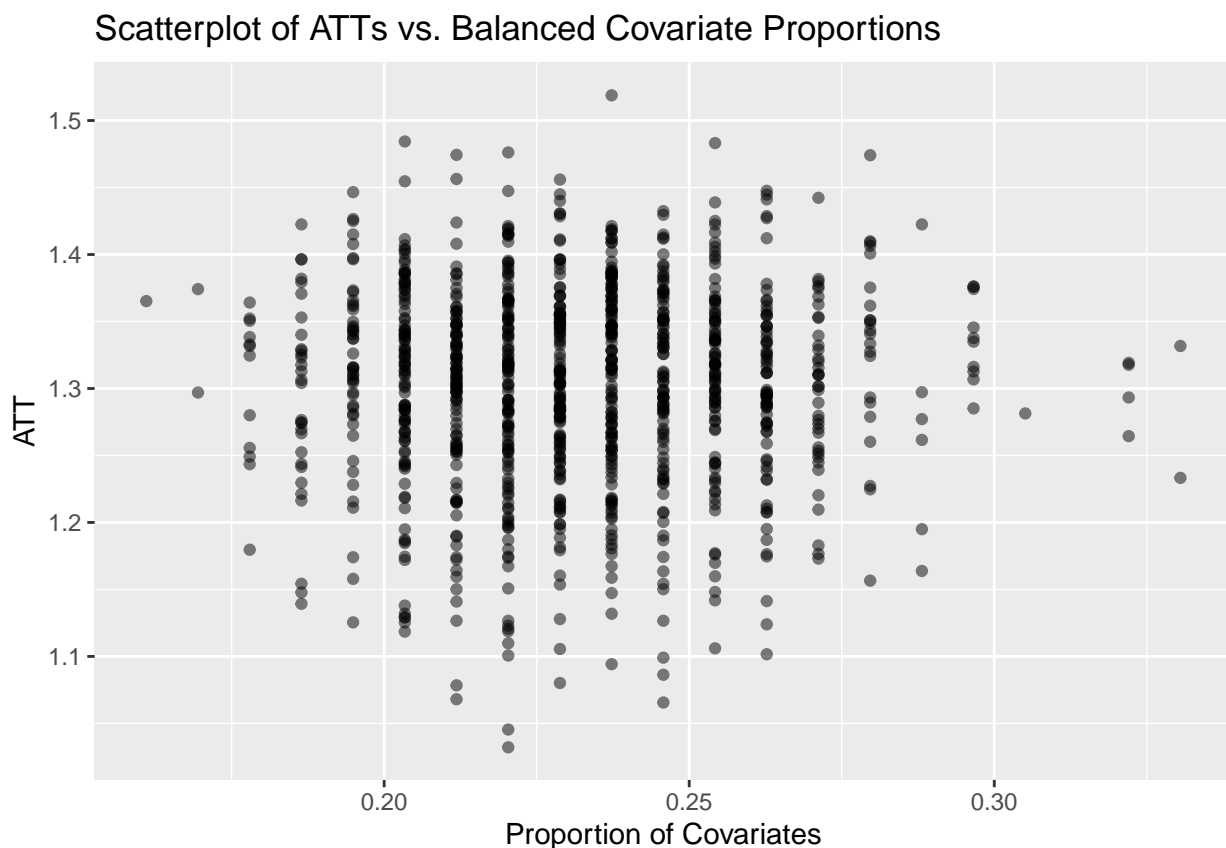
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```
#plot
ggplot(results, aes(x = Prop_Cov, y = ATT)) +
  geom_point(alpha = 0.5) + # Add transparency to avoid overplotting
  labs(x = "Proportion of Covariates", y = "ATT") + # Label axes
  ggtitle("Scatterplot of ATTs vs. Balanced Covariate Proportions") # Title of the plot
```



```
#simulation graphs
graph_sims<-10

graph_list <- list()

for (i in 1:graph_sims) {
  # Set seed for reproducibility, incrementing by i
  set.seed(6 + i)
  # Randomly select 5 covariates
  selected_covariates <- sample(available_covariates, 5)
```

```

# Create formula for matchit
formula <- as.formula(paste("college ~", paste(selected_covariates, collapse = "+")))

# Perform propensity score matching
matched_data <- matchit(formula, data = sim_df, method = "genetic", replace=TRUE)

m.out<-match.data(matched_data)

graph<-love.plot(m.out, treat=m.out$college, binary = "std", thresholds = c(m = .1))

graph_list[[i]] <- graph
}

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## page and https://www.jsekhon.com

## Note: `s.d.denom` not specified; assuming pooled.

## Warning in sqrt(Reduce("+", lapply(unique.treats, function(t) col.w.v(mat[treat
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## Note: `s.d.denom` not specified; assuming pooled.

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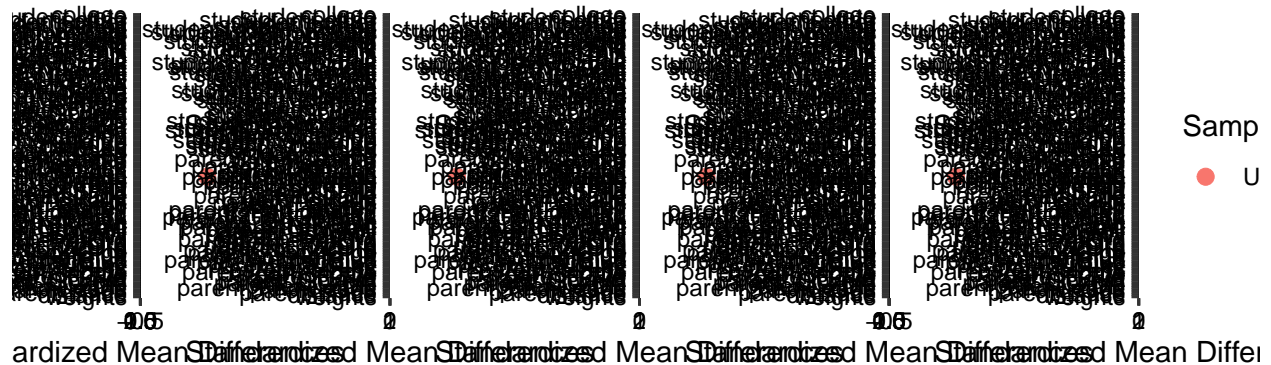
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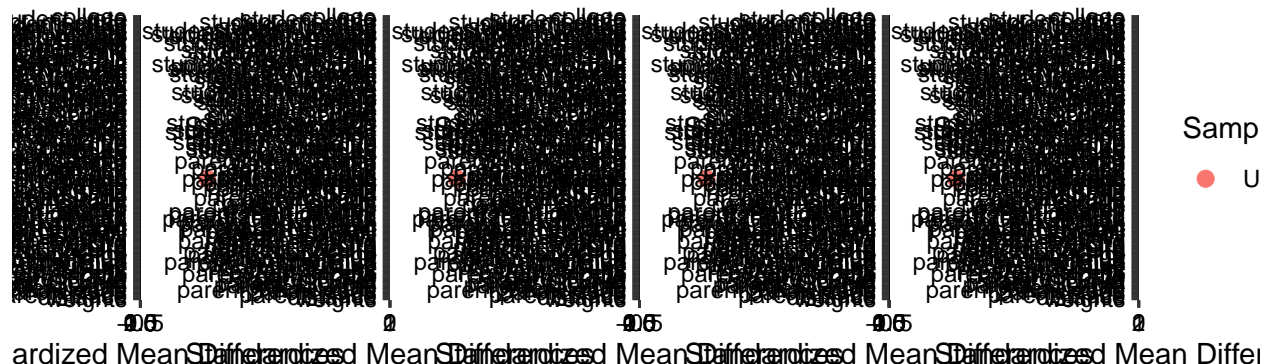
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```
grid.arrange(grobs = graph_list, nrow = 2)
```

Covariate BalanceCovariate BalanceCovariate BalanceCovariate BalanceCovariate Balance



Covariate BalanceCovariate BalanceCovariate BalanceCovariate BalanceCovariate Balance



## Questions

1. Does your alternative matching method have more runs with higher proportions of balanced covariates?
2. **Your Answer:** I would expect genetic matching to provide more potential "upside" in terms of getting more balanced covariates than simple nearest neighbor.
3. Use a visualization to examine the change in the distribution of the percent improvement in balance in propensity score matching vs. the distribution of the percent improvement in balance in your new method. Which did better? Analyze the results in 1-2 sentences.
4. **Your Answer:** I would expect the genetic matching to improve balance more often than nearest neighbor propensity score matching, again aligning with the findings from the paper. Genetic matching allows some complexity in the distance calculation than simple nearest neighbor analysis does not.

**Optional:** Looking ahead to the discussion questions, you may choose to model the propensity score using an algorithm other than logistic regression and perform these simulations again, if you wish to explore the second discussion question further.

## Discussion Questions

1. Why might it be a good idea to do matching even if we have a randomized or as-if-random design?
2. **Your Answer:** Even with randomization, there are differences that may arise in covariate balance simply because of chance; randomization may again guarantee balance on average but not balance in any iteration we observe (including in a given trial). Matching (or some other adjustment technique) is still useful for achieving balance to address the by-chance variation in balance that can arise even with randomization (or pseudo-randomization).
3. The standard way of estimating the propensity score is using a logistic regression to estimate probability of treatment. Given what we know about the curse of dimensionality, do you think there might be advantages to using other machine learning algorithms (decision trees, bagging/boosting forests, ensembles, etc.) to estimate propensity scores instead?
4. **Your Answer:** Using a logistic regression with a set number of covariates would generate a propensity score using user-selected covariates (or every covariate). Obviously, not every covariate may actually be important in matching observations, and researcher-selected covariates may be assumed to be important when they actually aren't. Machine learning methods can take data-driven approaches to the selection of matching covariates in a way that optimizes the generation of propensity scores in a way the traditional methods do not.