Project 4: Causal Inference Algorithms Evaluation

Group 8

03/31/2021

Setup

First, we set working directories as needed, install required libraries and import the data.

Introduction

In this project, we are looking for the best algorithm for causal inference of propensity scores to see how close the estimated average treatment effects (ATEs) are to the true ATEs. For the estimation of propensity scores, we use regression trees. The algorithms we use to estimate ATEs in this project are propensity matching, stratification and weighted regression. We also compare the run times of different algorithms and propensity score estimations across both data sets.

About the Data

There are two attached data sets for this project, named *highDim_data set* and *lowDim_data set*, which were from the Atlantic Causal Inference Conference (ACIC) Data Challenge. For the high dimensional data, there are 2000 observations, 185 variables ($V1$-$V185$), 1 treatment indicator variable (A) and 1 continuous response variable (Y). For the low dimensional data, there are 475 observations, 22 variables ($V1$-$V22$), 1 treatment indicator variable (A) and 1 continuous response variable (Y).

```
## [1] "High Dimensional Data"
```

```
##
##      0      1
## 0.6785 0.3215
```

```
## [1] "Low Dimensional Data"
```

```
##
##     0     1
## 0.788 0.212
```

From the tables above, we see that the control groups are not balanced for both data sets. For the high dimension data, the treated group consists of 67.85% of the samples. For the low dimension data, the treated group consists of 78.8% of the samples.

For the purpose of comparing the different algorithms, we chose to add weights to the observations while estimating the propensity scores using classification/regression trees.

Background

Regression Trees

The mathematical formula for a regression tree is shown below.

$$\hat{f}(x) = \sum_{m=1}^{M} c_m I\{x \in R_m\}$$

Here, R_m is a specific region, M is the number of regions, and c_m is the value associated with a region.

The way regression trees work is that the space is split into multiple regions based on some set of decisions. This process keeps repeating until a stopping rule is applied. In regression, we use **squared error loss** to find the optimal tree model, but in classification, as with the case for estimating propensity scores, we use a measure of impurity. In our case, we use one called the **Gini index**. In R, we use "rpart" library to run the regression tree algorithm. The parameters of the function includes **minsplit**, **minbucket** and **cp**. The parameter of **cp** indicates the complexity of the model, we get more complex trees with lower values of "cp".

We can visualize the tree and the decision rules at each split, using the **plot.rpart** function in R. The decision rules help to determine which variables are of the highest importance when estimating the propensity scores.

Propensity Scores

The propensity score is defined as follows:

$$e(x) = Pr(T = 1|X = x),\ 0 < e(x) < 1$$

Based on the formula above, given the (multiple) covariates (x), the propensity score is the probability that the observation is in the treatment group (in our case, observations where $A = 1$). Since, our data is based on observational studies, we can use propensity scores to make causal inferences.

Average Treatment Effect (ATE)

The average treatment effect is defined as follows:

$$\Delta_t = E(Y_1 - Y_0|T = 1)$$

ATE is defined as the difference in the average outcomes between observations assigned to treatment group and the control group. This allows us to measure the effect a treatment had on each group.

Cross-Validation

We perform five fold cross-validation for the high dimension and low dimension data sets. The main objective of the cross validation is to tune the "cp" parameter to avoid overfitting.

Step 1: Set Controls and Establish Hyperparameters

We set up the controls to start the the cross validation process

```r
K <- 5  # number of CV folds
sample.reweight <- TRUE # run sample reweighting in model training

# setting the following to false loads data generated from a previous run
# this data is the same in each run due to a set seed

run.cv.trees_high <- TRUE # run cross-validation on the training set for trees on high dim data

run.cv.trees_low <- TRUE # run cross-validation on the training set for trees on low dim data
```

We choose a set of “cp” values here to cross validate in order to find the optimal “cp” value for each data set; here we choose to do powers of two.

```r
# hyperparameters for trees
hyper_grid_trees <- expand.grid(
  maxdepth = c(1, 5, 10, 15, 20, 25, 30)
)
```

Step 2: Cross-Validate the Hyperparameters

We source the library functions that we created to help cross validate the “cp” hyperparamter.

```r
# data pre-processing

# features are the predictors: V1 - Vp
# column 1 is the response Y
# column 2 is the treatment A

feature_train_high = df_high[, -1:-2]
label_train_high = df_high[, 2]

feature_train_low = df_low[, -1:-2]
label_train_low = df_low[, 2]
```

High Dimensional Data We run the cross validation algorithm on the high dimensional data.

```r
set.seed(5243)

if(run.cv.trees_high){
  res_cv_trees_high <- matrix(0, nrow = nrow(hyper_grid_trees), ncol = 4)
  for(i in 1:nrow(hyper_grid_trees)){
    cat("complexity = ", hyper_grid_trees$cp[i], "\n", sep = "")
    res_cv_trees_high[i,] <- cv.function(features = feature_train_high,
                                       labels = label_train_high,
                                       maxdepth = hyper_grid_trees$maxdepth[i],
                                       K, reweight = sample.reweight)
  save(res_cv_trees_high, file = "../output/res_cv_trees_high.RData")
  }
} else{
  load("../output/res_cv_trees_high.RData")
}
```

```
## complexity =
## complexity =
## complexity =
## complexity =
## complexity =
## complexity =
## complexity =
```

Low Dimensional Data We run the cross validation algorithm on the high dimensional data.

```
set.seed(5243)

if(run.cv.trees_low){
  res_cv_trees_low <- matrix(0, nrow = nrow(hyper_grid_trees), ncol = 4)
  for(i in 1:nrow(hyper_grid_trees)){
    cat("complexity = ", hyper_grid_trees$cp[i], "\n", sep = "")
    res_cv_trees_low[i,] <- cv.function(features = feature_train_low,
                                        labels = label_train_low,
                                        maxdepth = hyper_grid_trees$maxdepth[i],
                                        K, reweight = sample.reweight)
  save(res_cv_trees_low, file="../output/res_cv_trees_low.RData")
  }
}else{
  load("../output/res_cv_trees_low.RData")
}
```

```
## complexity =
## complexity =
## complexity =
## complexity =
## complexity =
## complexity =
## complexity =
```

Step 3: Visualize CV Error and AUC

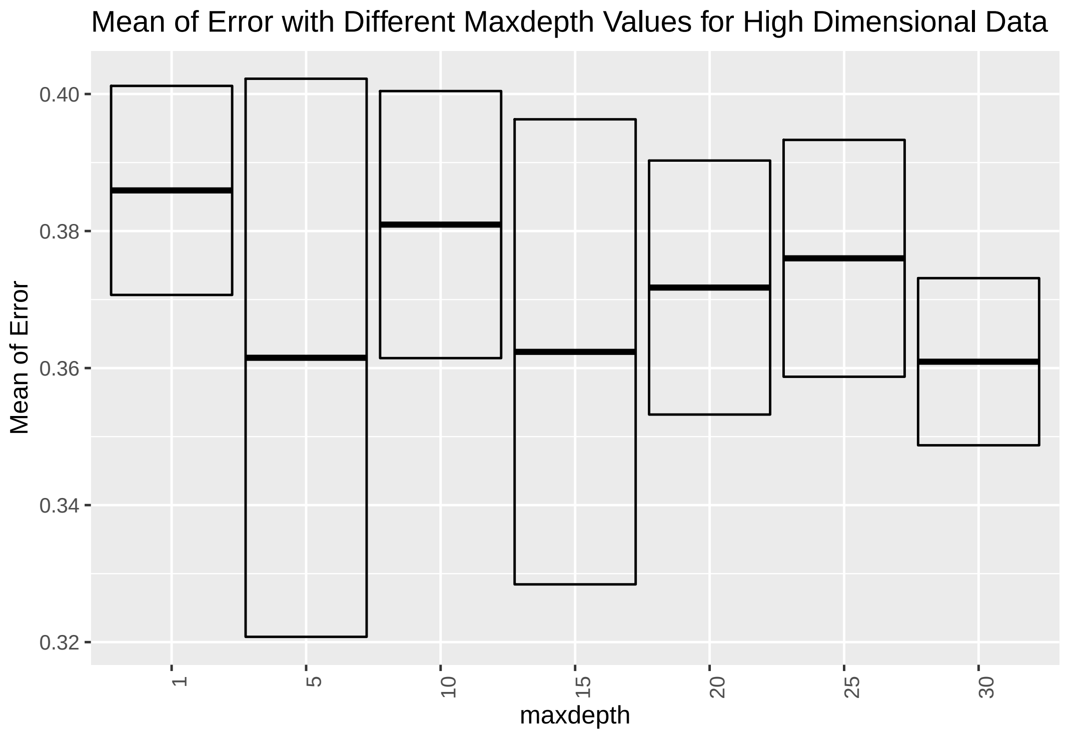
After cross validating, we obtain the mean error and the AUC values for each potential "maxdepth" value for both data sets. We display these values and associated standard errors in the plots below.

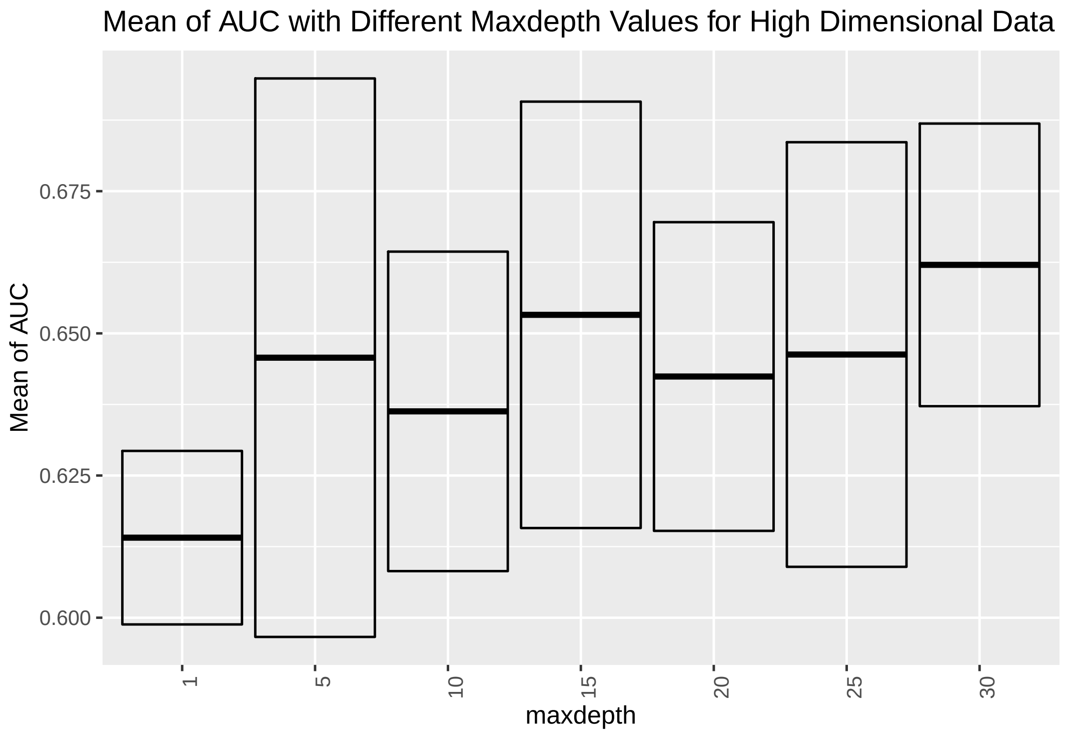
Because of the imbalances in the groups for both datasets, we choose to not only weigh our observations, but to also focus on mean AUC when selecting the optimal hyperparameter.

High Dimensional Data Based on the plots and table below, we find that the model with the highest mean AUC value has a "maxdepth" value of 5.

```
# create data frame to organize results
res_cv_trees_high <- as.data.frame(res_cv_trees_high)
colnames(res_cv_trees_high) <- c("mean_error", "sd_error", "mean_AUC", "sd_AUC")
cv_results_trees_high = data.frame(hyper_grid_trees, res_cv_trees_high)

# look at top 5 models with highest AUC
cv_results_trees_high[order(cv_results_trees_high$mean_AUC, decreasing = TRUE), ][1:5, ]
```

```
##   maxdepth mean_error   sd_error  mean_AUC     sd_AUC
## 7       30  0.3609282 0.01219715 0.6620405 0.02484604
## 4       15  0.3623673 0.03393795 0.6532559 0.03749102
## 6       25  0.3760187 0.01728488 0.6462752 0.03733310
## 2        5  0.3615023 0.04072998 0.6457202 0.04910346
## 5       20  0.3717513 0.01853577 0.6424085 0.02714165
```





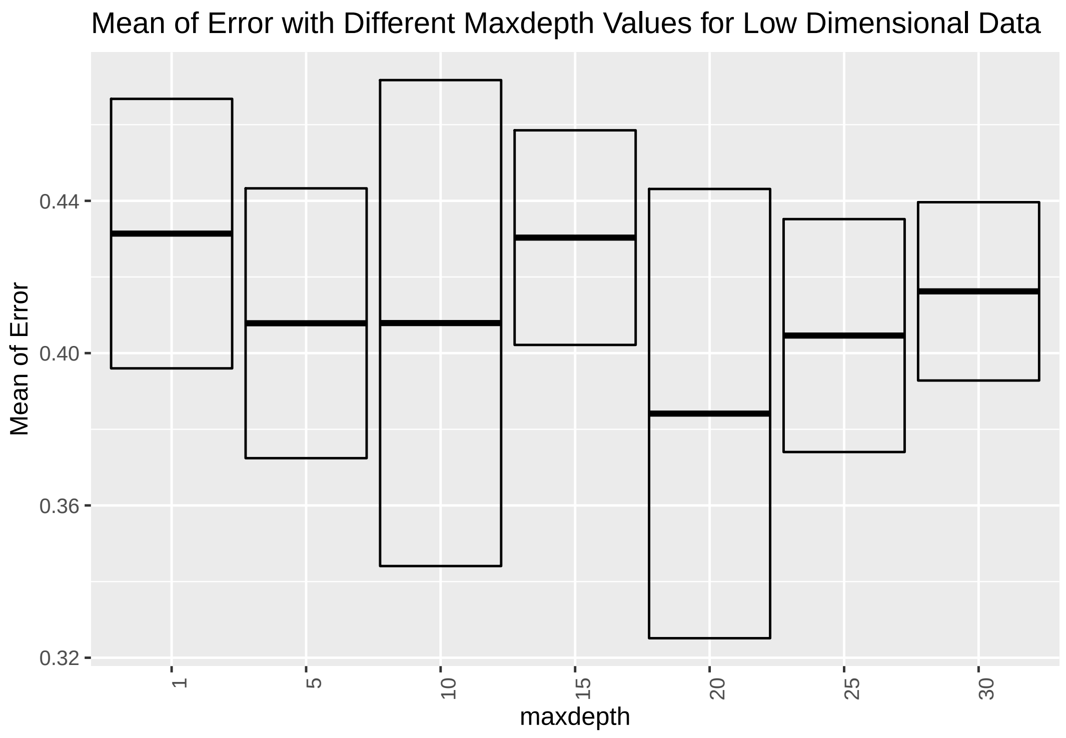
```r
best_maxdepth_high <- cv_results_trees_high$maxdepth[cv_results_trees_high$mean_AUC ==
                                                     max(cv_results_trees_high$mean_AUC)]

best_maxdepth_high
```

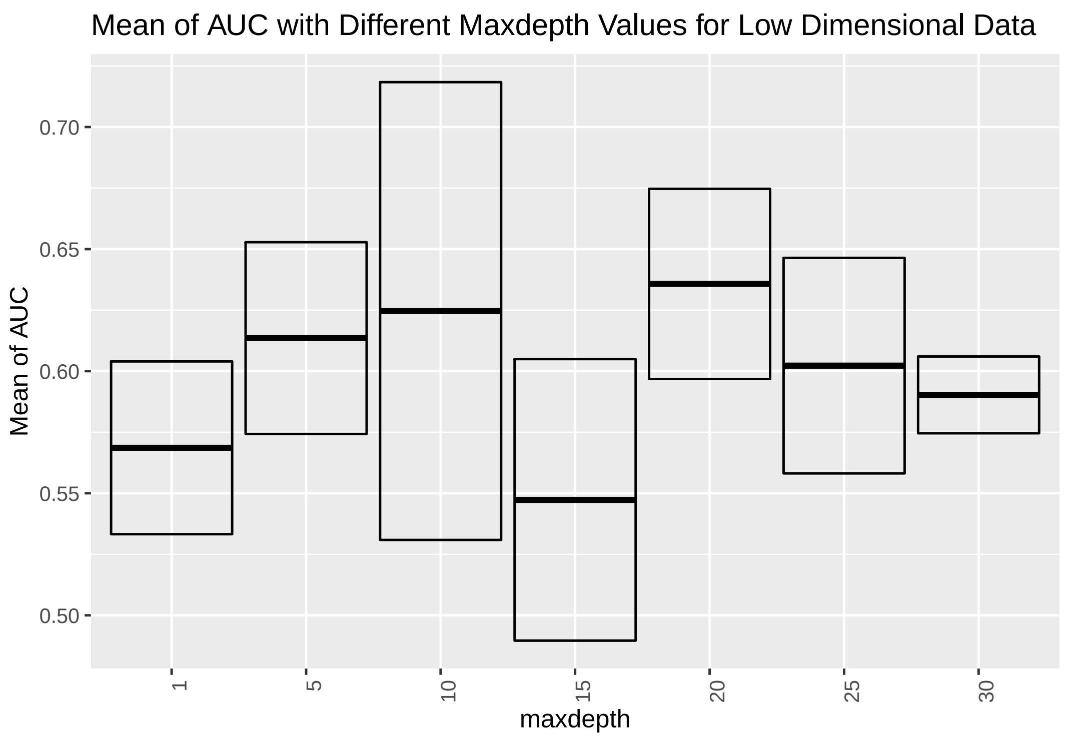
```
## [1] 30
```

Low Dimensional Data Based on the plots and table below, we find that the model with the highest mean AUC value has a "maxdepth" value of 25.

```r
# create data frame to organize results
res_cv_trees_low <- as.data.frame(res_cv_trees_low)
colnames(res_cv_trees_low) <- c("mean_error", "sd_error", "mean_AUC", "sd_AUC")
cv_results_trees_low = data.frame(hyper_grid_trees, res_cv_trees_low)

# look at top 5 models with lowest AUC
cv_results_trees_low[order(cv_results_trees_low$mean_AUC, decreasing = TRUE), ][1:5, ]
```

```
##   maxdepth mean_error   sd_error  mean_AUC     sd_AUC
## 5       20  0.3841200 0.05899462 0.6357454 0.03894949
## 3       10  0.4078955 0.06381304 0.6246288 0.09375529
## 2        5  0.4078461 0.03543237 0.6135589 0.03927286
## 6       25  0.4046125 0.03058485 0.6022665 0.04414551
## 7       30  0.4162237 0.02341654 0.5902807 0.01572384
```





```r
best_maxdepth_low <- cv_results_trees_low$maxdepth[cv_results_trees_low$mean_AUC ==
                                         max(cv_results_trees_low$mean_AUC)]
best_maxdepth_low
```

```
## [1] 20
```

Propensity Score Estimation

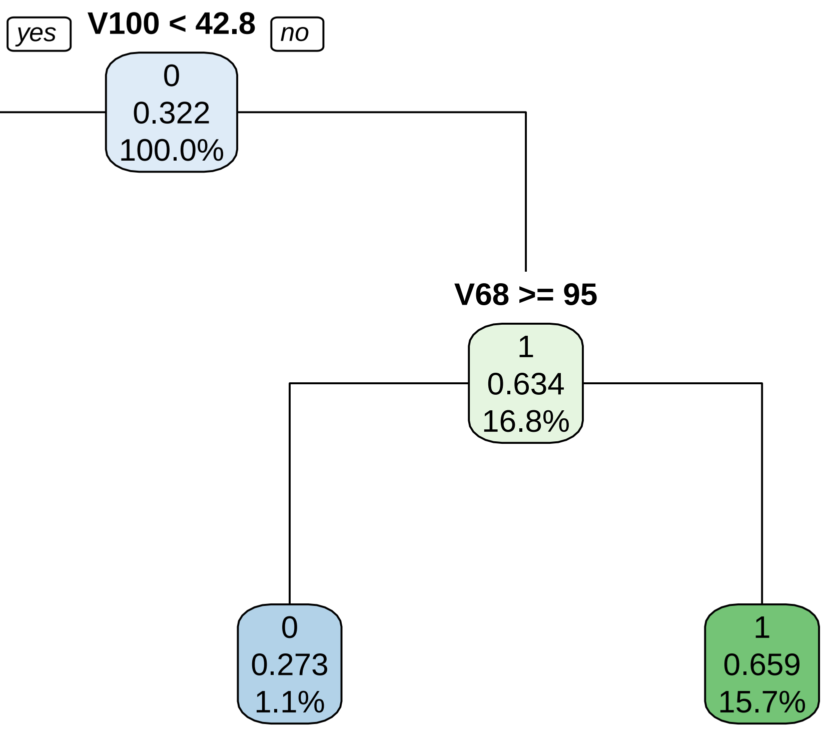
With the optimal "maxdepth" parameters for each dataset, we now estimate the propensity scores using a weighted classification tree model.

```r
# imbalanced dataset requires weights
# to be used in the trained model

weights_high <- rep(NA, length(df_high$A))
for (v in unique(df_high$A)){
  weights_high[df_high$A == v] = 0.5 * length(df_high$A) / length(df_high$A[df_high$A == v])
}


weights_low <- rep(NA, length(df_low$A))
for (v in unique(df_low$A)){
  weights_low[df_low$A == v] = 0.5 * length(df_low$A) / length(df_low$A[df_low$A == v])
}
```

```r
start.time_propensity_score_high <- Sys.time()

# create tree model for high dimensional data with best cp parameter
tree_high <- rpart(A ~ . - Y, method = "class", data = df_high, maxdepth = best_maxdepth_high)

# calculate propensity scores
prop_score_high <- predict(tree_high, newdata = df_high[, -2], type = "prob")[, 2]

end.time_propensity_score_high <- Sys.time()
time_propensity_score_high <- end.time_propensity_score_high - start.time_propensity_score_high
time_propensity_score_high
```

High Dimensional Data

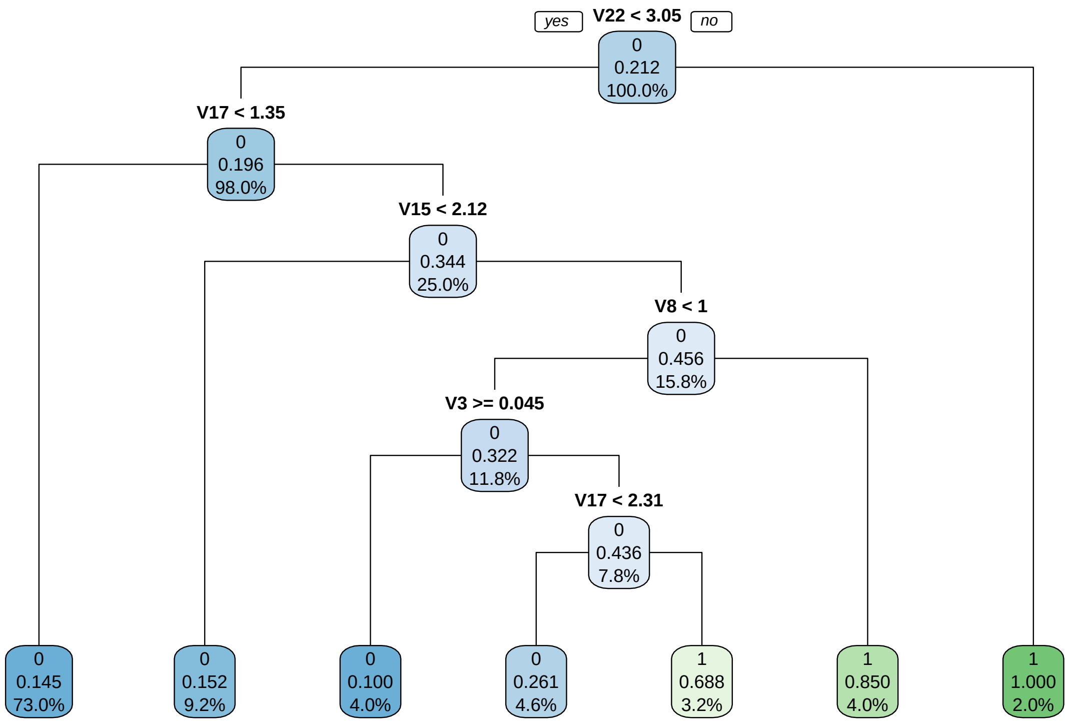
```
## Time difference of 0.8556349 secs
```



```r
start.time_propensity_score_low <- Sys.time()

# create tree model for low dimensional data with best cp parameter
tree_low <- rpart(A ~ . - Y, method = "class", data = df_low, maxdepth = best_maxdepth_low)

# calculate propensity scores
prop_score_low <- predict(tree_low, newdata = df_low[, -2], type = "prob")[, 2]

end.time_propensity_score_low <- Sys.time()
time_propensity_score_low <- end.time_propensity_score_low - start.time_propensity_score_low
time_propensity_score_low
```

Low Dimensional Data

```
## Time difference of 0.03090096 secs
```



ATE Estimation

With the estimated propensity scores on hand, we propose, explain, and discuss the pros and cons of three different ATE estimation algorithms: propensity matching, stratificationand weighted regression.

Propensity Matching using Propensity Score from Regression Trees (Full Matching)

Full matching creates a series of matched sets, where each matched set contains at least one treated individual and at least one control individual (and each matched set may have many from either group). Full matching forms these matched sets in an optimal way, such that treated individuals who have many comparison individuals who are similar (on the basis of the propensity score) will be grouped with many comparison individuals, whereas treated individuals with few similar comparison individuals will be grouped with relatively fewer comparison individuals.(See Stuart (2010))

Our group is assigned the task of using propensity score for Full Matching. The distance of Propensity Score is defined as:

$$D_{ij} = \mid e_i - e_j \mid$$

where e_k is the propensity score for individual k.

After the matched sets are obtained, calculate a "subclass effects" for each matched set/subclass, and then estimate overall ATE by an weighted average of the subclass effects where weights would be the number of individuals in each subclass.

```
source("../lib/propensity_matching.R")
match_High_Dim <- get_match_obj(read.csv(highDim_csv))
```

Getting the Data Loaded for High and Low Dimension Data

```
## Full matching...
## Calculating matching weights... Done.
```

```
match_Low_Dim <- get_match_obj(read.csv(lowDim_csv))
```

```
## Full matching...
## Calculating matching weights... Done.
```

```
# Timing the process -- start
start.time_propensity_matching_low <- Sys.time()
start.time_propensity_matching_high <- Sys.time()

# creates a dataset with one row per unit. It will be identical to the dataset supplied except
# that several new columns will be added containing information related to the matching
g.matches_high <- match.data(match_High_Dim, data = read.csv(highDim_csv), distance = "prop_score")
g.matches_low <- match.data(match_Low_Dim, data = read.csv(lowDim_csv), distance = "prop_score")


# Timing the process -- ends
end.time_propensity_matching_low <- Sys.time()
time_propensity_matching_low <- end.time_propensity_matching_low - start.time_propensity_matching_low
time_propensity_matching_low
```

```
## Time difference of 0.103174 secs
```

```
end.time_propensity_matching_high <- Sys.time()
time_propensity_matching_high <- end.time_propensity_matching_high - start.time_propensity_matching_hig
time_propensity_matching_high
```

```
## Time difference of 0.1051009 secs
```

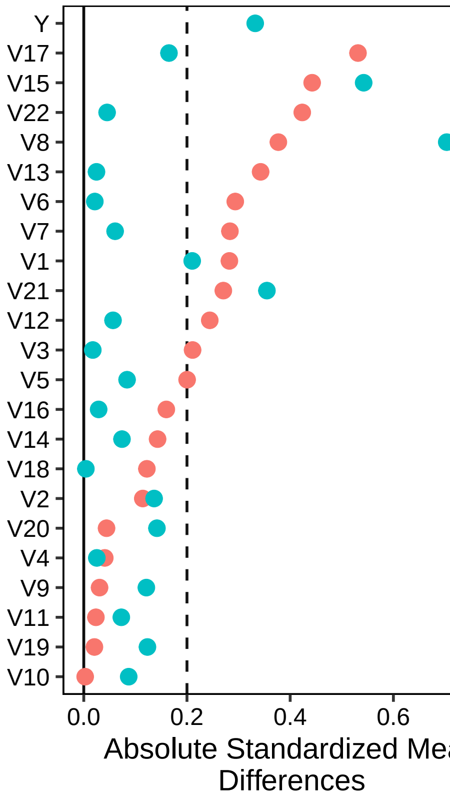
Estimating Effects After Matching We diagnose the quality of the resulting matched samples. We would would like the treatment to be unrelated to the covariates such that:

$$\tilde{p}(X|T = 1) = \tilde{p}(X|T = 0)$$

where $\tilde{p}$ denotes the empirical distribution.

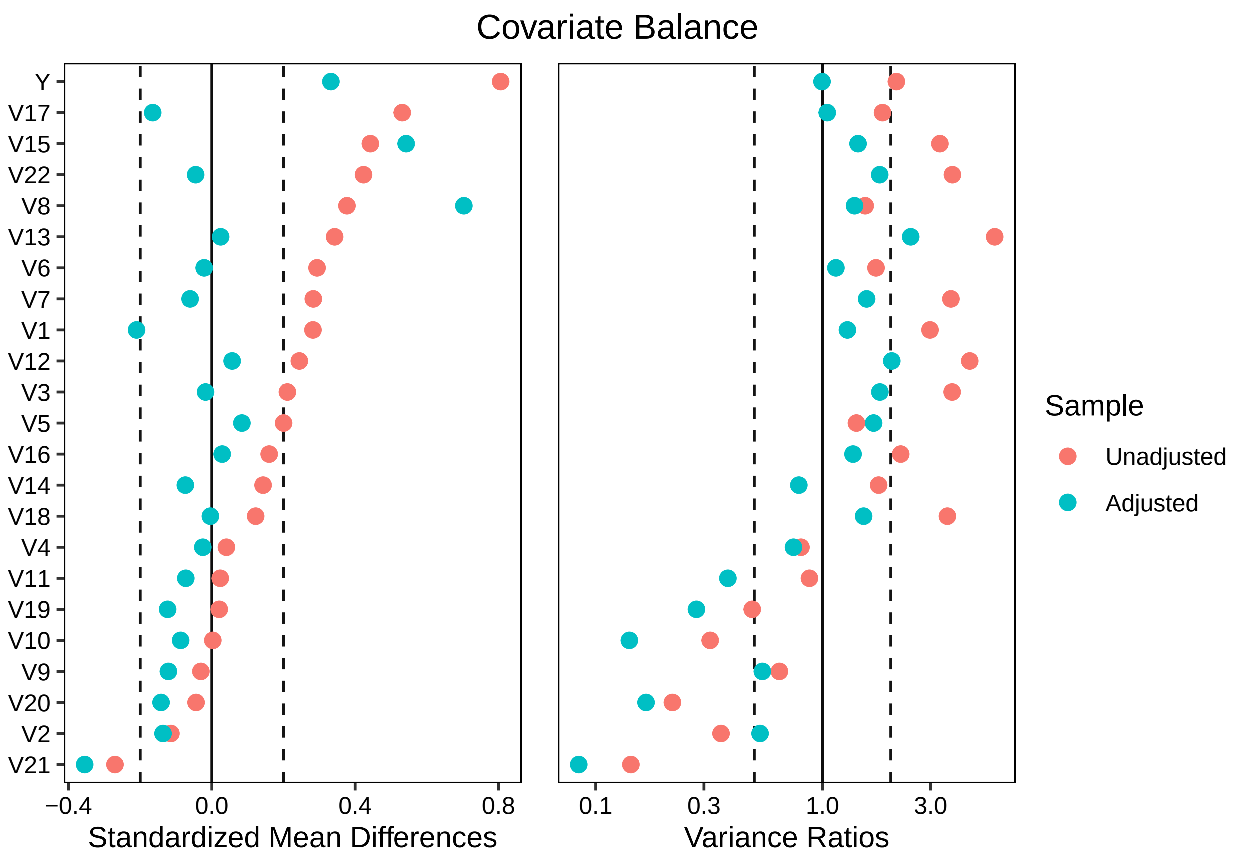
A plot of the standardized differences of means, gives us a quick overview of whether balance has improved for individual covariates.

```
love.plot(match_Low_Dim,stats = c("mean.diffs", "variance.ratios"), binary = "std",drop.distance = TRUE
          var.order = "unadjusted",
          abs = TRUE,
          thresholds = c(m = .2, v = 2))
```



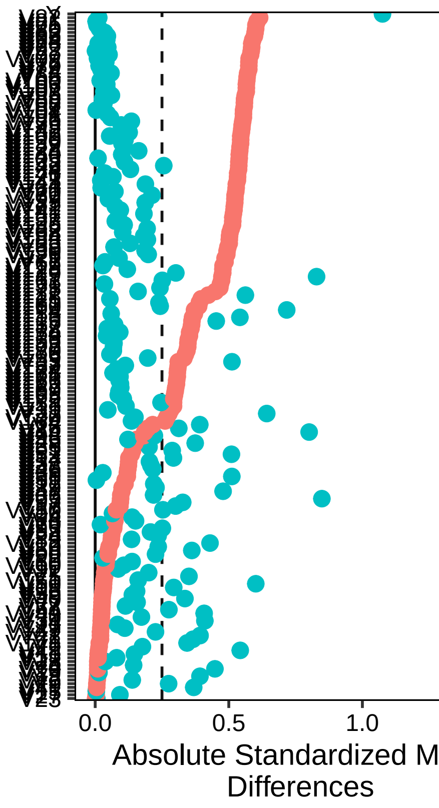
Standardized Differences of Means After Matching Low Dimensional Data

```
love.plot(match_Low_Dim,stats = c("mean.diffs", "variance.ratios"), binary = "std",drop.distance = TRUE
          var.order = "unadjusted",
          abs = FALSE,
          thresholds = c(m = .2, v = 2))
```



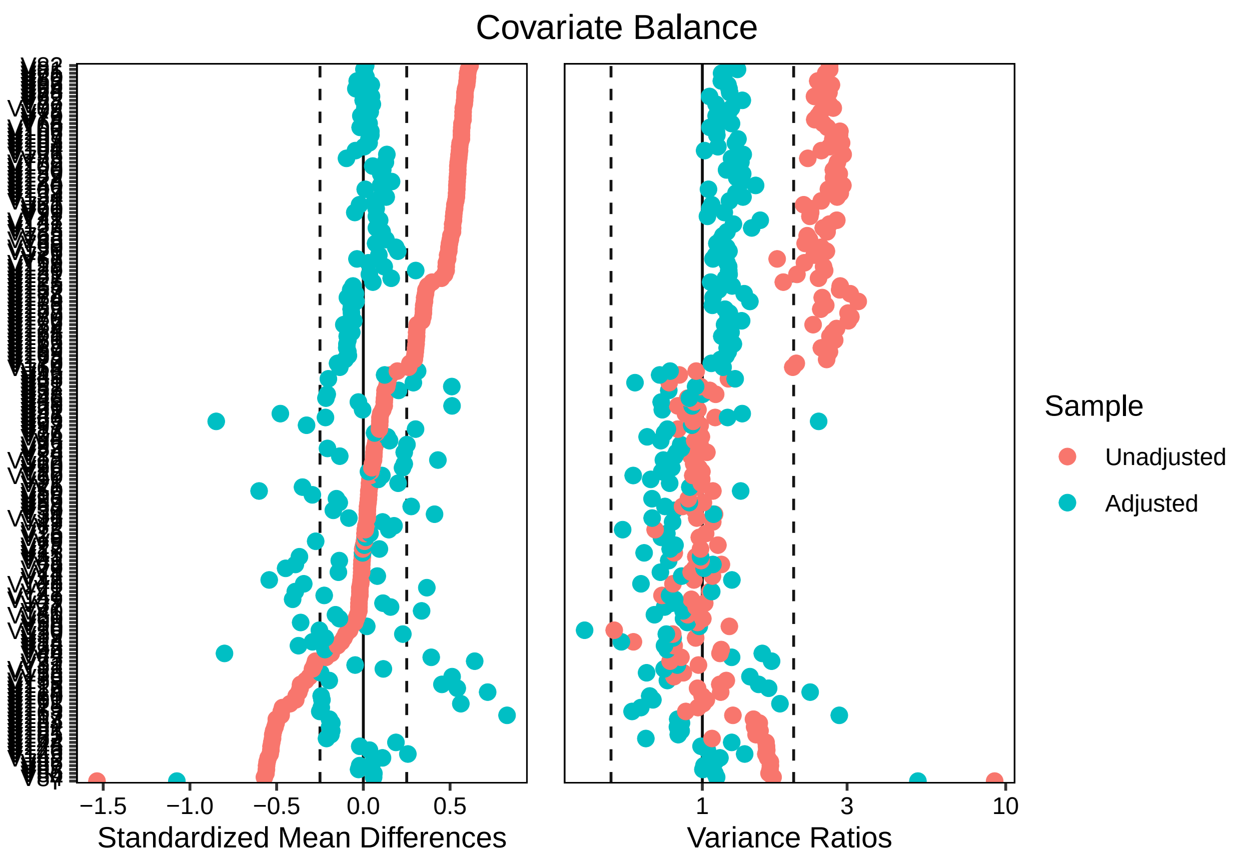
From these plots we see that balance was quite poor prior to matching, but full matching improved balance on all covariates

```
love.plot(match_High_Dim,stats = c("mean.diffs", "variance.ratios"), binary = "std",drop.distance = TRU
          var.order = "unadjusted",
          abs = TRUE,
          thresholds = c(m = .25, v = 2))
```



Standardized Differences of Means After Matching High Dimensional Data

```
love.plot(match_High_Dim,stats = c("mean.diffs", "variance.ratios"), binary = "std",drop.distance = TRUI
          var.order = "unadjusted",
          abs = FALSE,
          thresholds = c(m = .25, v = 2))
```

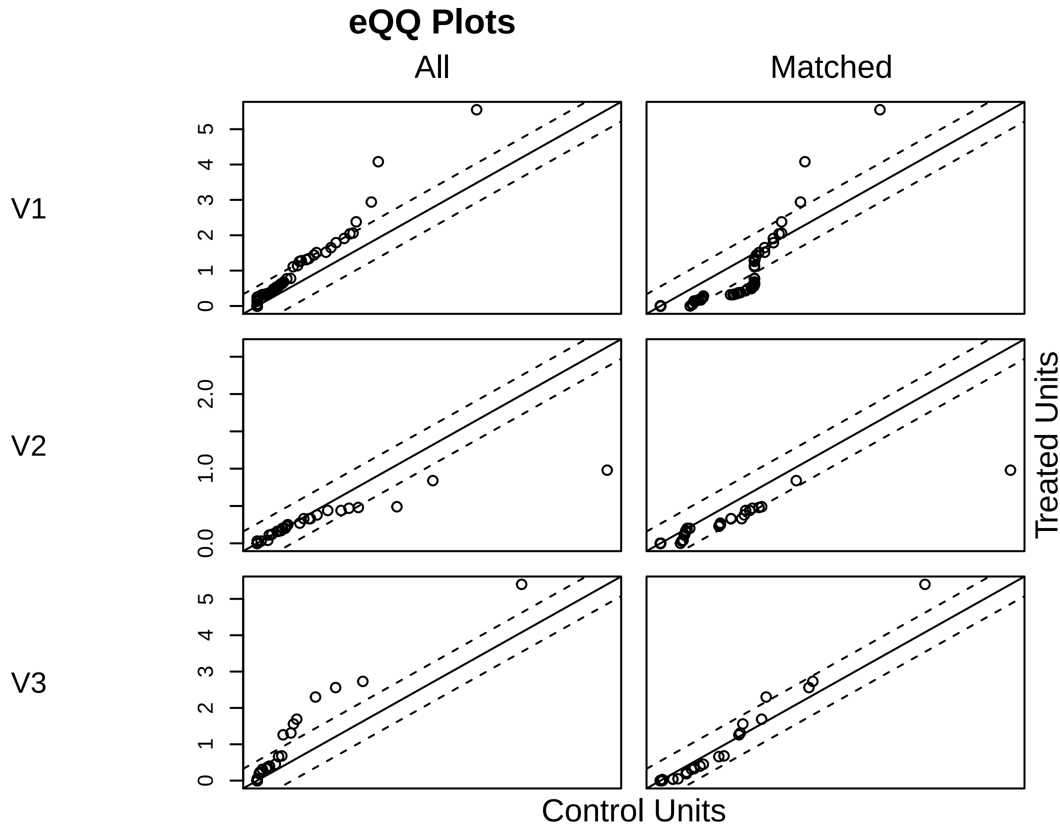


```
# list1 <- seq(1, 200, by=1)
# empty_vec <- rep("", 200)
#
# #empty_vec=vector(length =  200, " ")
# list1=paste0("V",list1)
#
# v <- data.frame(old = list1,
#                 new = empty_vec)
#
# love.plot(match_High_Dim, binary = "std",drop.distance = TRUE,
#           var.order = "unadjusted",
#           abs = TRUE,
#           thresholds = c(m = .25), var.names = v) #line = TRUE
```

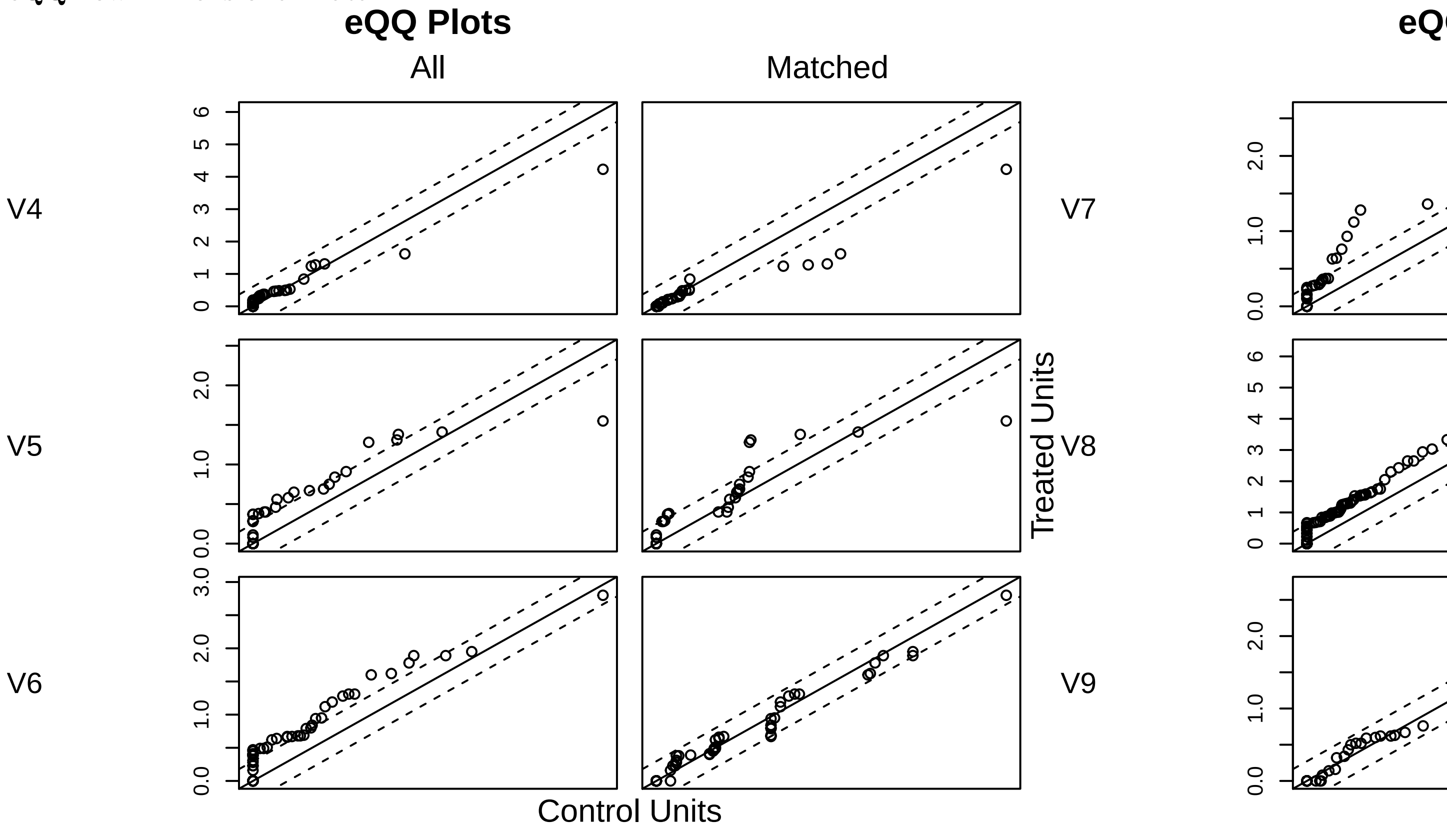
the standardized difference of means of each covariate has decreased after matching.

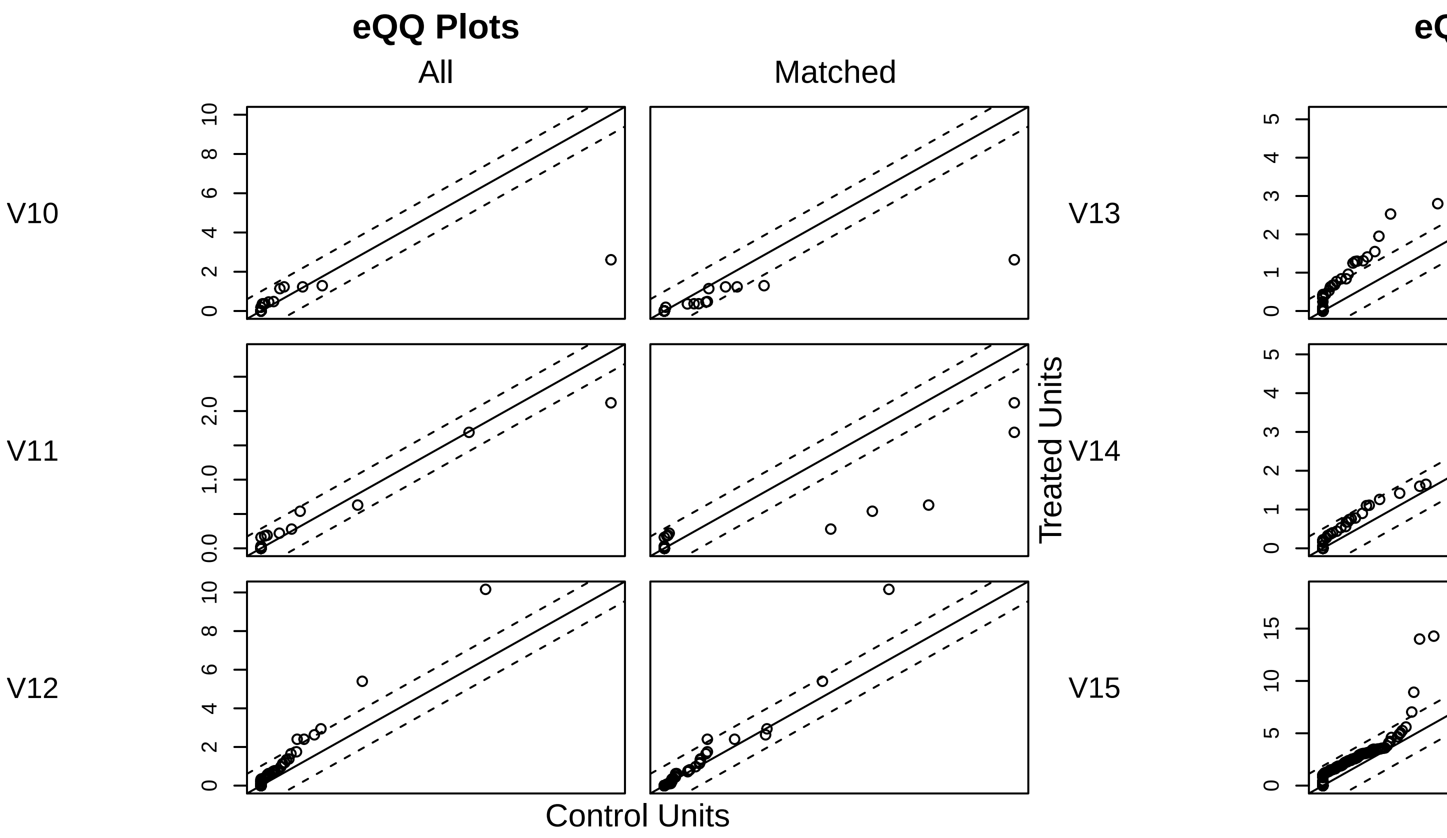
For continuous covariates, we can also examine quantile–quantile (QQ) plots, which compare the empirical distributions of each variable. QQ plots compare the quantiles of a variable in the treatment group against the corresponding quantiles in the control group. If the two groups have identical empirical distributions, all points would lie on the 45 degree line.

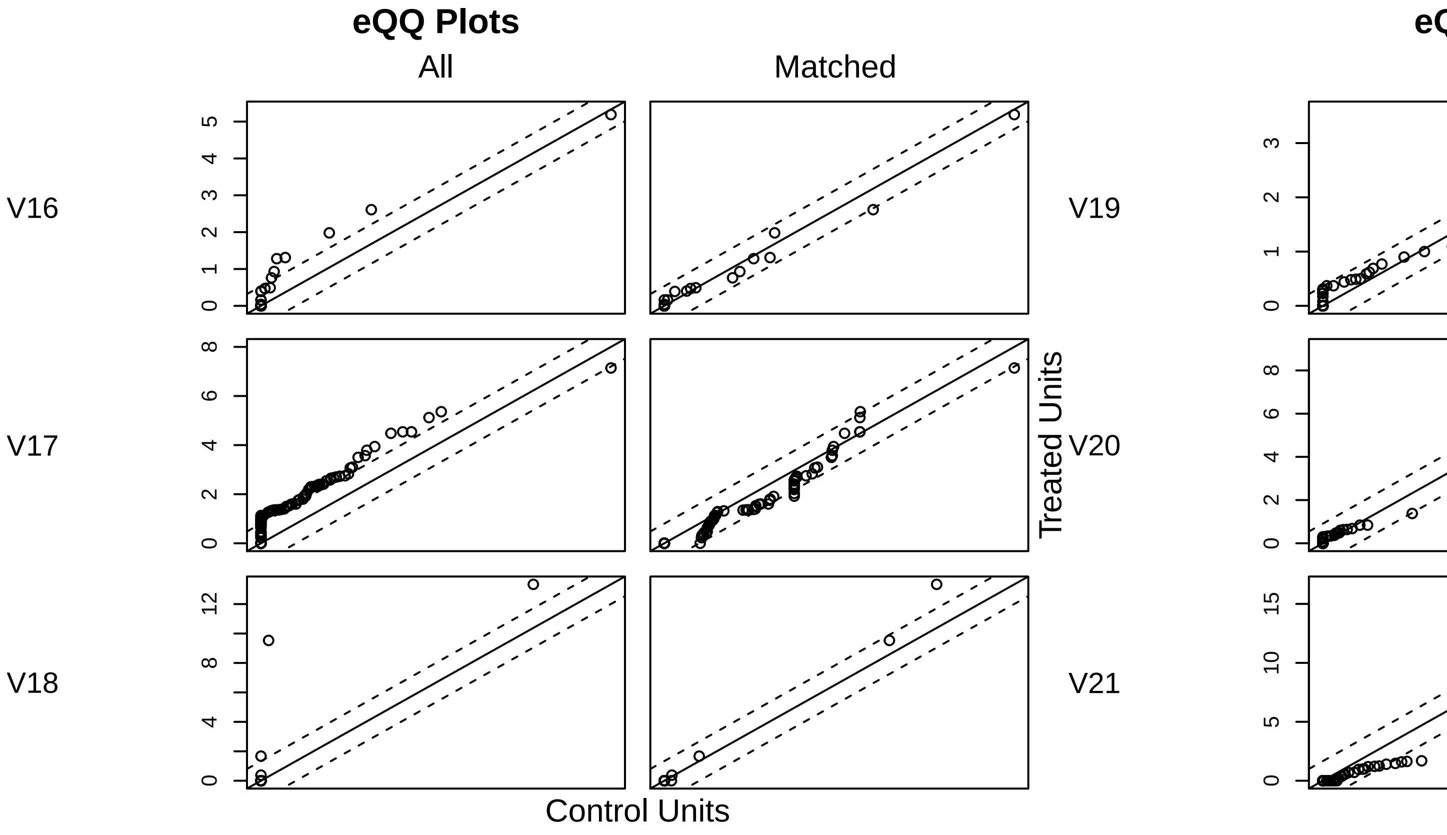
```
#eQQ plot
plot(match_Low_Dim, type = "qq", interactive = FALSE)
```

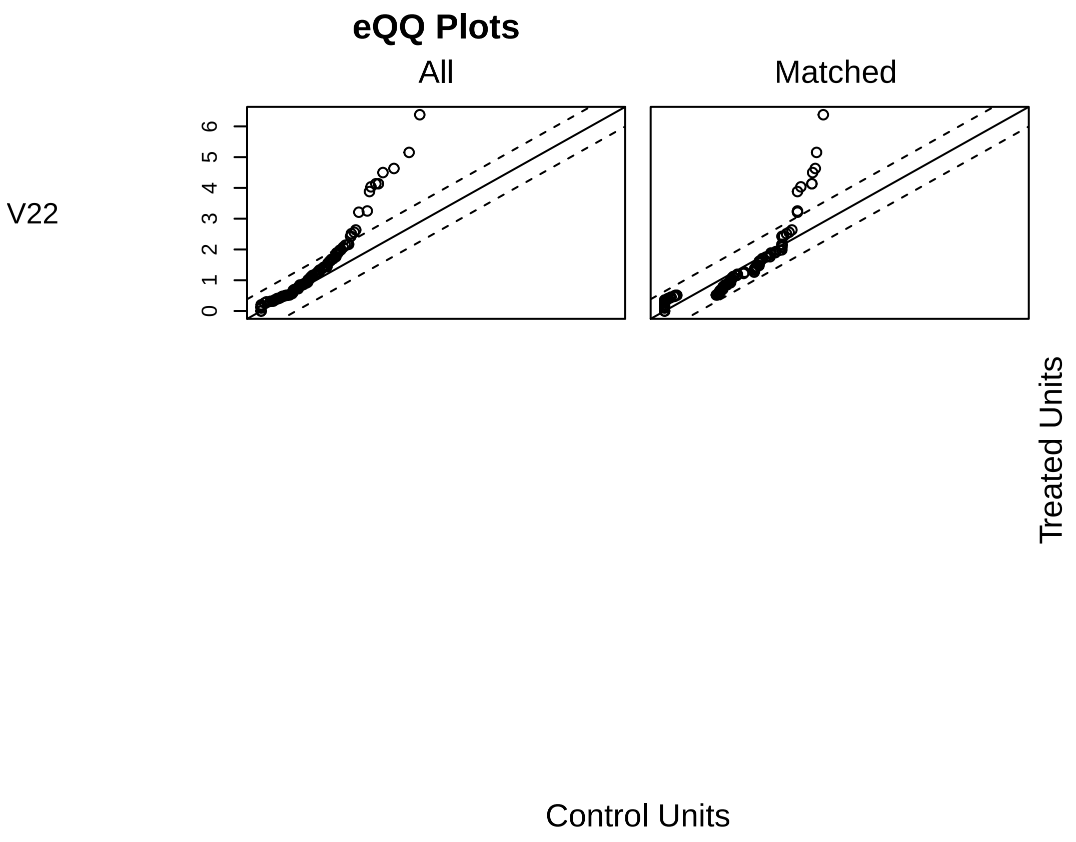


eQQ Low Dimensional Data

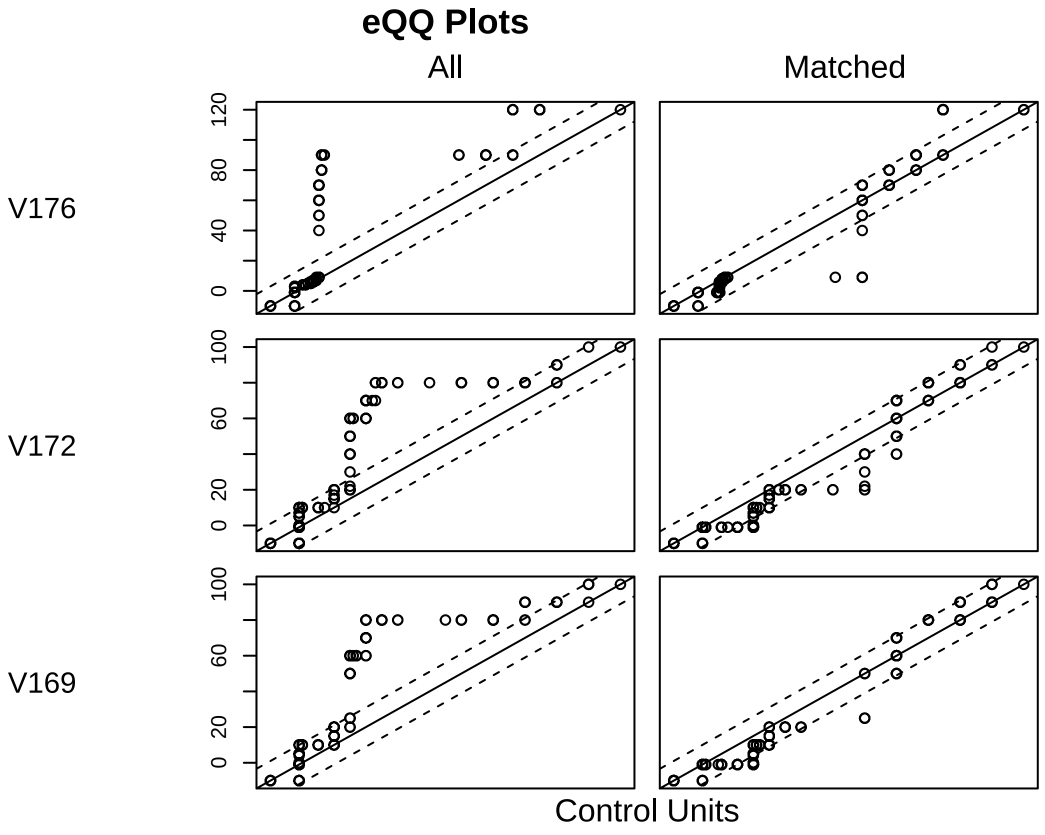



eQQ Plots
All
Matched
V10
V11
V12
V13
V14
V15
Treated Units
Control Units

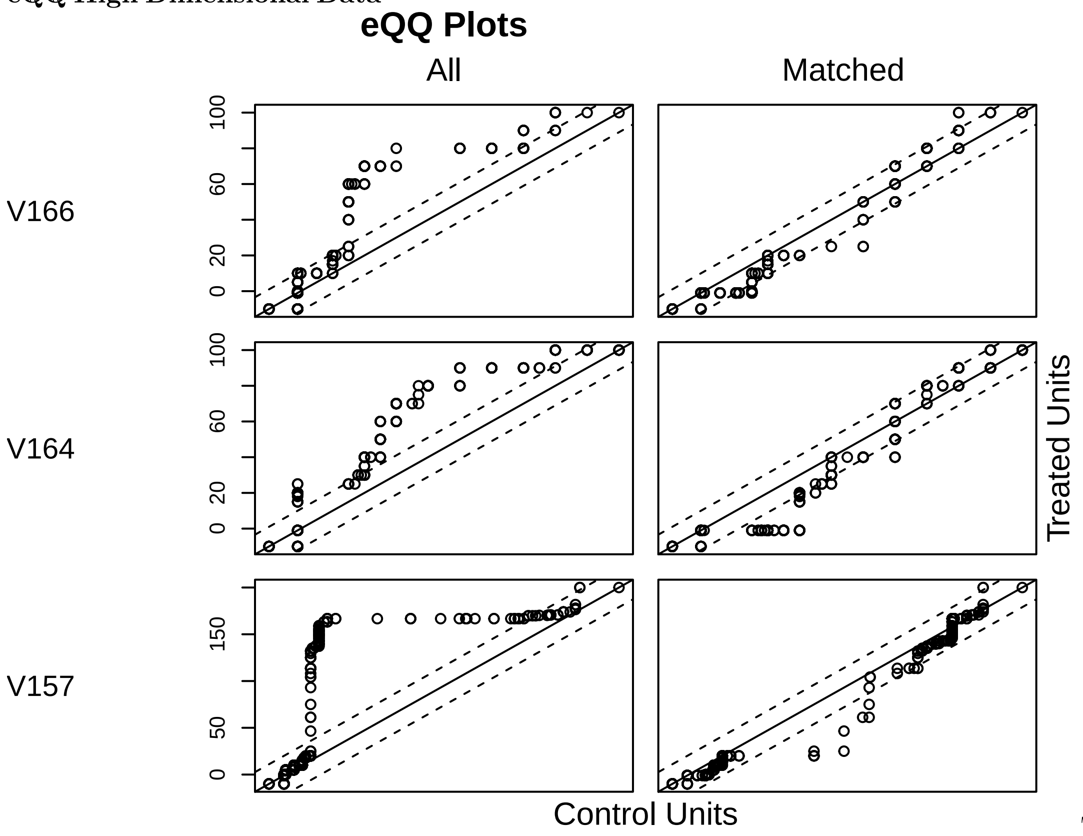

eQQ Plots
All
Matched
V16
V17
V18
V19
V20
V21
Treated Units
Control Units



```
#eQQ plot
plot(match_High_Dim, type = "qq", interactive = FALSE, which.xs = c("V176","V172", "V169", "V166", "V16
```



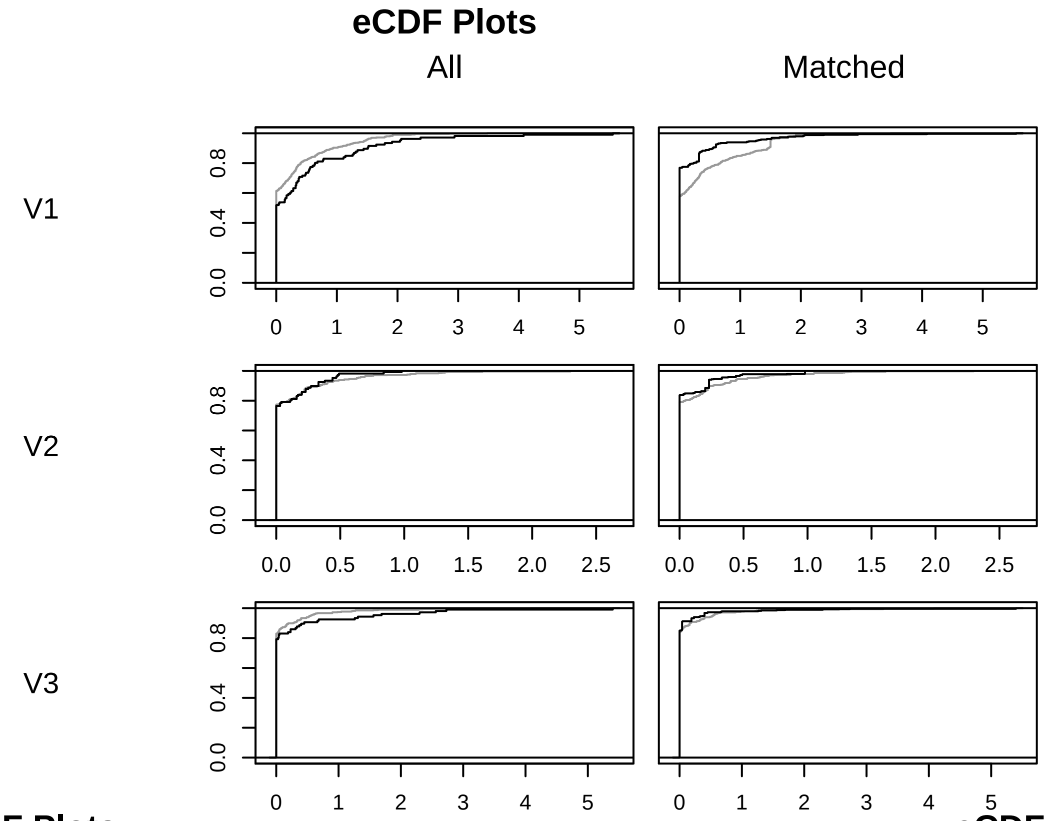
eQQ High Dimensional Data



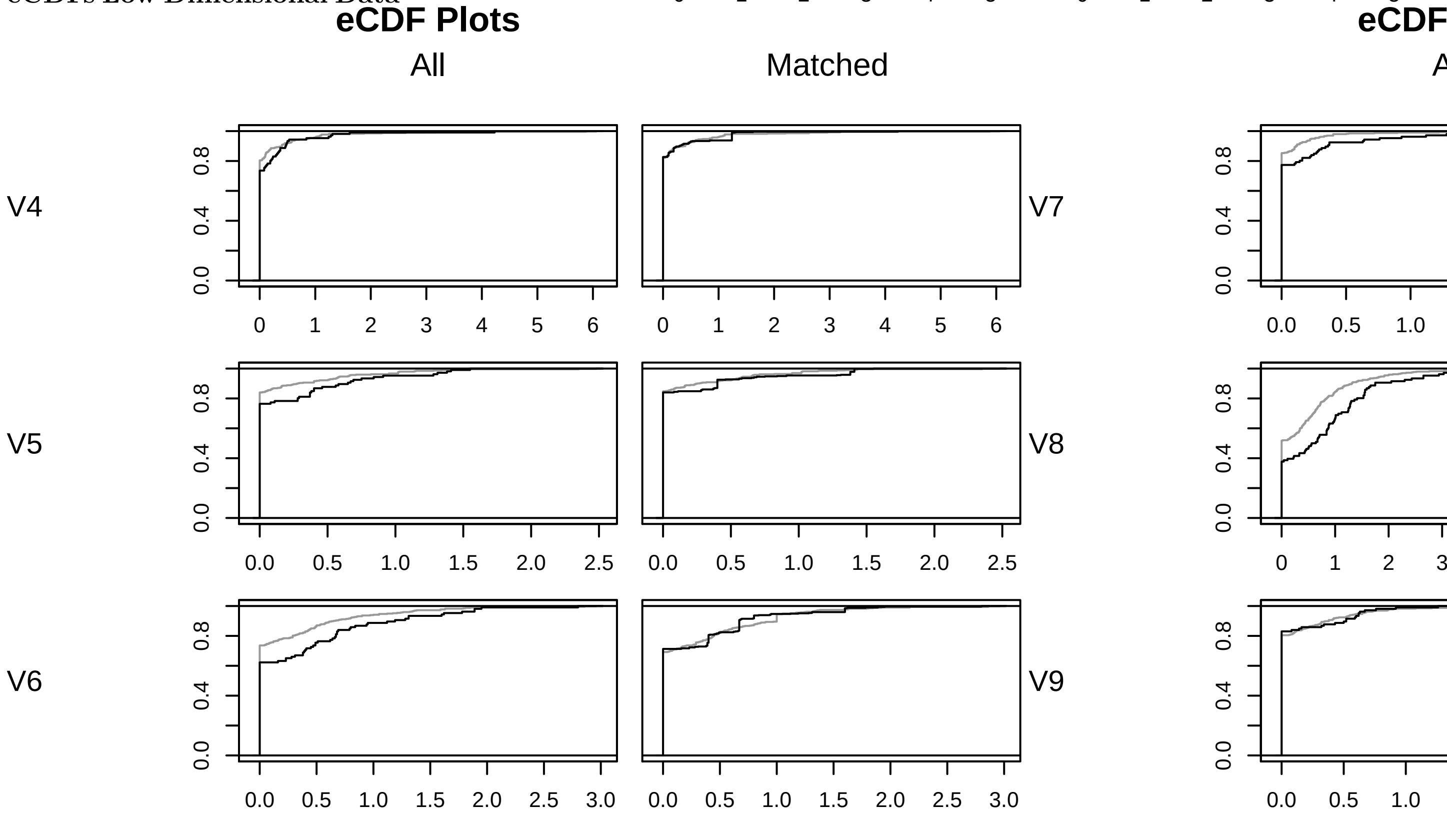
The y-axis displays the value of the covariate for the treated units, and the x-axis displays the the value of the covariate at the corresponding quantile in the control group. When values fall on the 45 degree line, the groups are balanced. We can see that some covariates remain somewhat imbalanced, but other covariates have much better balance after matching than before.

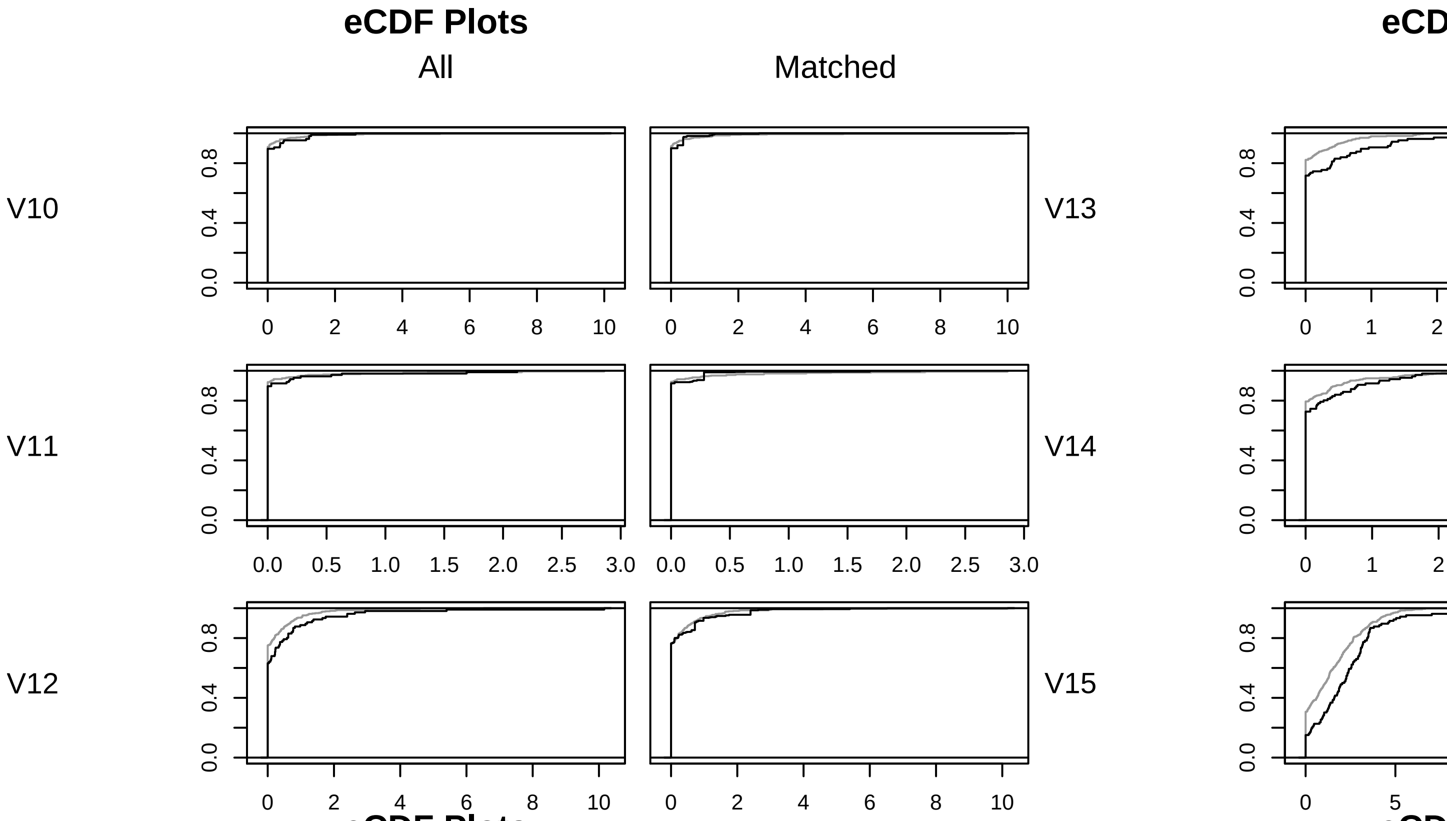
Statistics related to the difference in the empirical cumulative density functions (eCDFs) of each covariate between groups allow assessment of imbalance across the entire covariate distribution of that covariate rather than just its mean or variance.

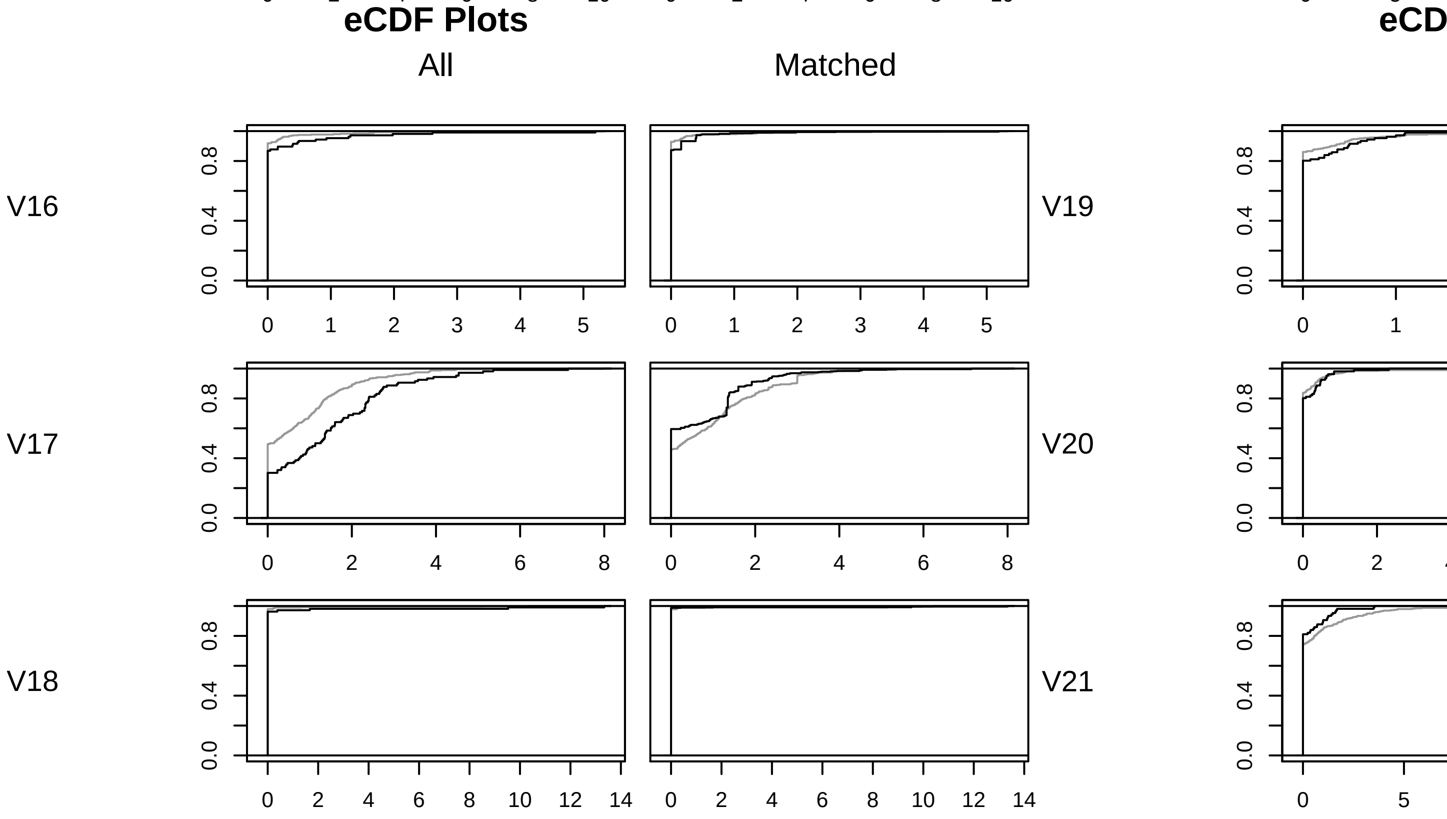
```
plot(match_Low_Dim, type = "ecdf", interactive = FALSE)
```

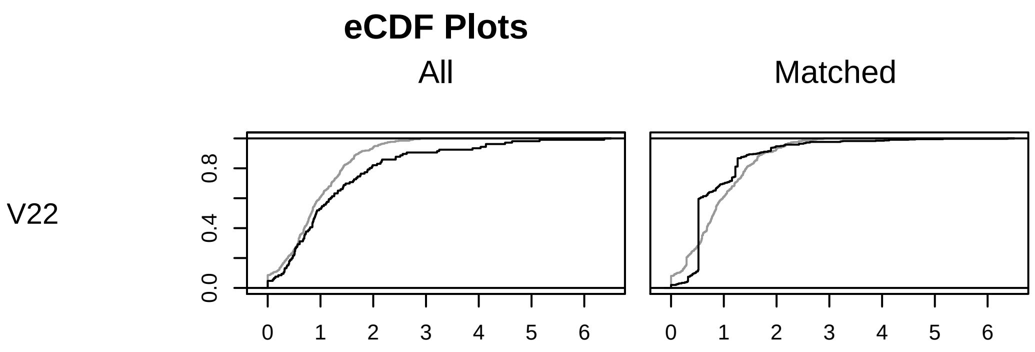


eCDFs Low Dimensional Data

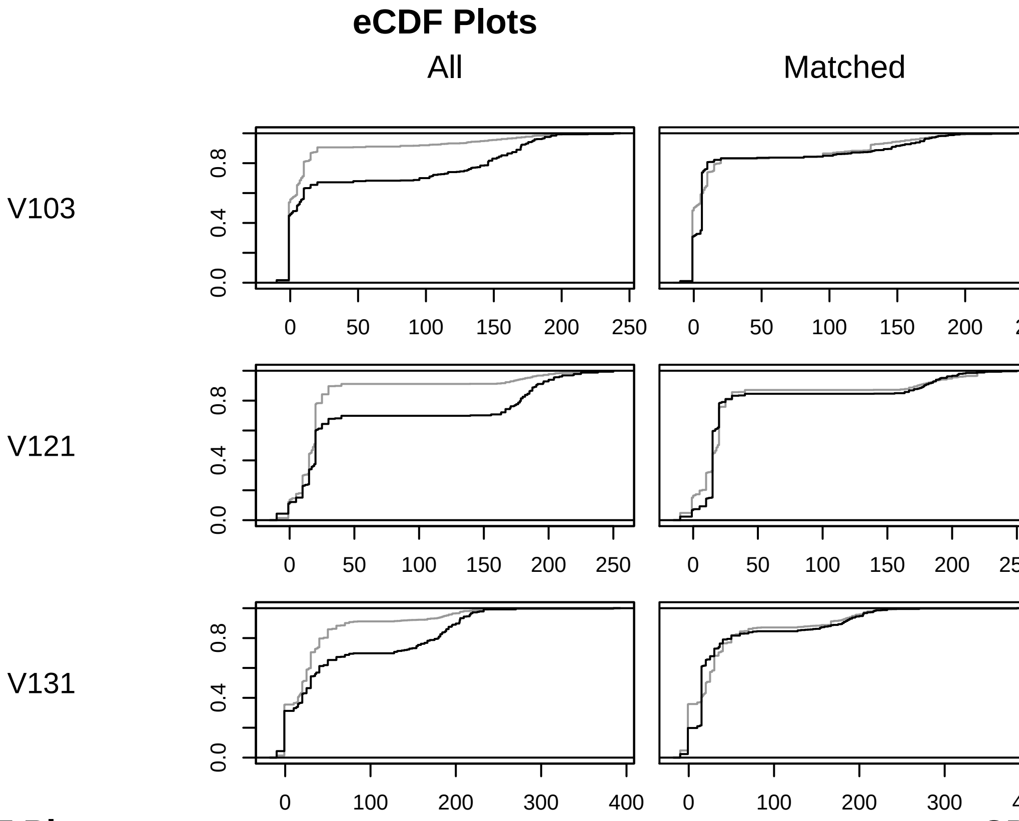



eCDF Plots
All
Matched
eCD
V10
V11
V12
V13
V14
V15
0.0
0.4
0.8

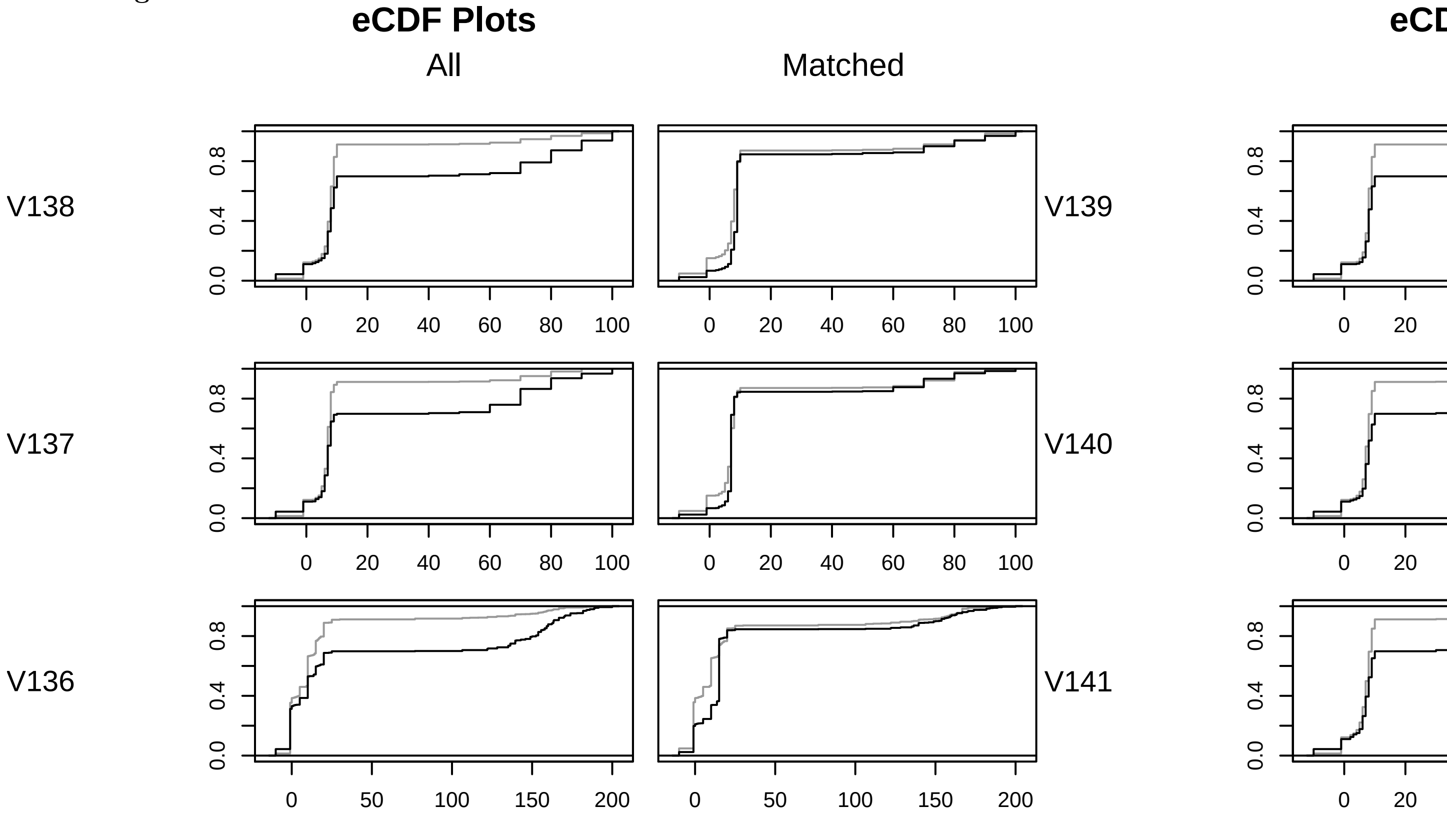

eCDF Plots
All
Matched
eCD
V16
V17
V18
V19
V20
V21
0.0
0.4
0.8



```
plot(match_High_Dim, type = "ecdf", interactive = FALSE, which.xs = c("V103","V121","V131","V138","V137
```



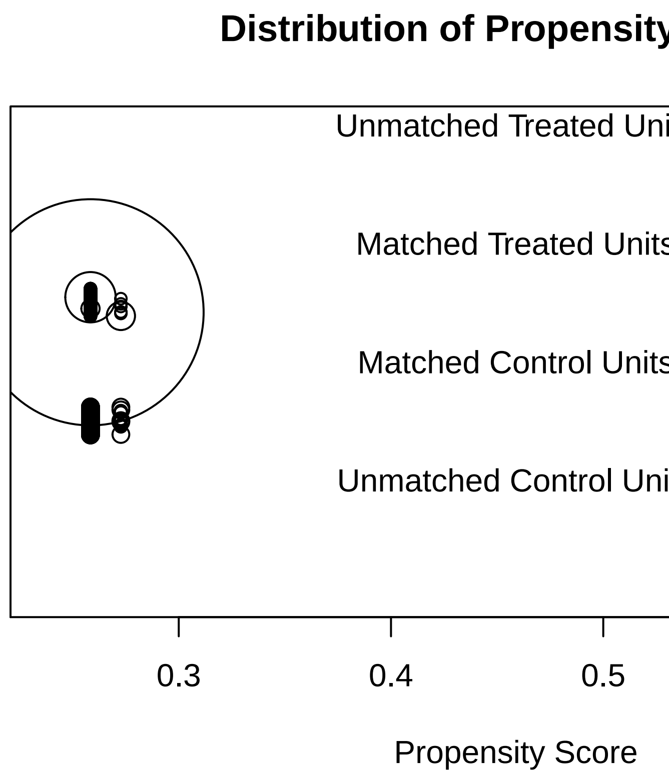
eCDFs High Dimensional Data



The x-axis display the covariate values and the y-axis display the proportion of the sample at or less than that covariate value. Perfectly overlapping lines indicate good balance. The black line corresponds to the treated group and the gray line to the control group.

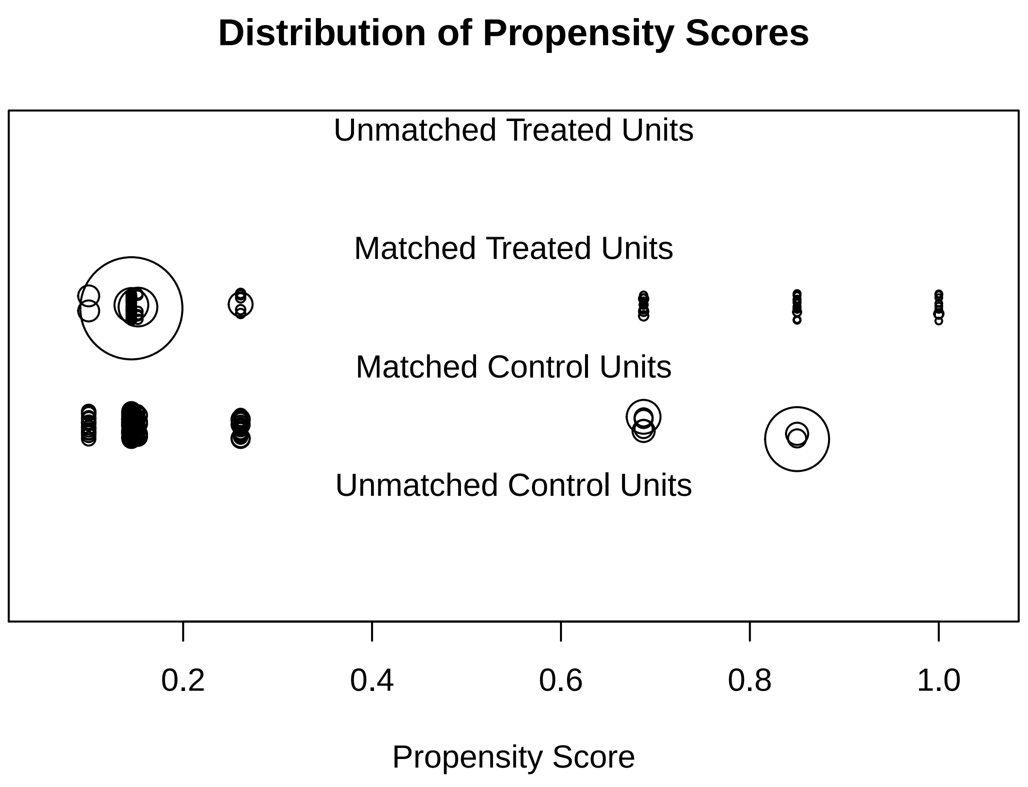
We see adequate overlap of the propensity scores, with a good control match for each treated individual. For weighting or subclassification, plots such as the ones below show the dots with their size proportional to their weight.

```r
plot(match_High_Dim, type = "jitter", interactive = FALSE)
```



Distribution of Propensity Scores High Dimensional Data
#### Distribution of Propensity Scores Low Dimensional Data

```r
plot(match_Low_Dim, type = "jitter", interactive = FALSE)
```



Calculating the ATE after Full matching Including interactions between the treatment and covariates can be beneficial when effect modification by the covariates may be present. In order to interpret the coefficient on treatment as a marginal effect estimate, we need to center the covariates at their means in the target population. Below we use the strategy of centering the covariates at their means.

```
md_cen <- g.matches_high
ATE_fullmatching_high_fit <- get_ATE_using_treatment_covariate_interactions(g.matches_high,185)

#Only output the intercept and coefficient on treatment
result_ATE_high<-coeftest(ATE_fullmatching_high_fit, vcov. = vcovCL, cluster = ~subclass)[1:2,]


ATE_fullmatching_high <- result_ATE_high[2][1]
ATE_fullmatching_high
```

```
## [1] -57.49297
```

```
md_cen <- g.matches_low
ATE_fullmatching_low_fit <- get_ATE_using_treatment_covariate_interactions(g.matches_low,22)

#Only output the intercept and coefficient on treatment
result_ATE_low<-coeftest(ATE_fullmatching_low_fit, vcov. = vcovCL, cluster = ~subclass)[1:2,]

ATE_fullmatching_low <- result_ATE_low[2][1]
ATE_fullmatching_low
```

```
## [1] 2.073773
```

Stratification

In the stratification method, we aim at dividing the data set into strata such that the propensity scores in each stratum are close enough. For choosing number of strata, K, five (5) was advocated by Rosenbaum and Rubin (1984). However, the propensity scores generated by CART are discrete numbers that are not proportional to the quantiles. If we divide the data into five strata by quantiles, each having roughly 20% of the total number of objects, the propensity scores in each stratum might not be similar.

Therefore, we divided the low dimensional data set into 6 stratum, and the high dimensional data set into 2 stratum, where propensity score in each strata is either uniform or significantly close.

The following formula was used to calculate the ATE:

$$\hat{\Delta}_S = \sum_{j=1}^{K} \frac{N_j}{N} \{N_{1j}^{-1} \sum_{i=1}^{N} T_i Y_i I(\hat{e}_i \in \hat{Q}_j) - N_{0j}^{-1} \sum_{i=1}^{N} (1 - T_i) Y_i I(\hat{e}_i \in \hat{Q}_j)\}$$

where K is the number of strata, $\hat{e}$ is the estimated propensity score, Y is the response for each observation, and T is the treatment variable (either 0 or 1). N_j is the number of individuals in stratum j. N_{1j} is the number of "treated" individuals in stratum j, while N_{0j} is the number of "controlled" individuals in stratum j. $\hat{Q}_j = (\hat{q_{j-1}}, \hat{q}_j]$ where $\hat{q}_j$ is the jth sample quantile of the estimated propensity scores.

```r
# Timing the process -- start
start.time_stratification_low <- Sys.time()

prop_score <- g.matches_low$prop_score
df_low <- cbind(df_low, prop_score)
df_strat_low <- df_low[,c("Y","A","prop_score")]

strata_low_1 <- df_strat_low[df_strat_low$prop_score <= 0.125, ]
sum_strata_low_1 <- strata_low_1 %>%
  group_by(A) %>%
  summarise(Avg_Y = mean(Y))

strata_low_2 <- df_strat_low[0.125 < df_strat_low$prop_score & df_strat_low$prop_score <= 0.250, ]
sum_strata_low_2 <- strata_low_2 %>%
  group_by(A) %>%
  summarise(Avg_Y = mean(Y))

strata_low_3 <- df_strat_low[0.250 < df_strat_low$prop_score & df_strat_low$prop_score <= 0.5, ]
sum_strata_low_3 <- strata_low_3 %>%
  group_by(A) %>%
  summarise(Avg_Y = mean(Y))

strata_low_4 <- df_strat_low[0.5 < df_strat_low$prop_score & df_strat_low$prop_score <= 0.75, ]
sum_strata_low_4 <- strata_low_4 %>%
  group_by(A) %>%
  summarise(Avg_Y = mean(Y))

strata_low_5 <- df_strat_low[0.75 < df_strat_low$prop_score & df_strat_low$prop_score <= 0.875, ]
sum_strata_low_5 <- strata_low_5 %>%
  group_by(A) %>%
  summarise(Avg_Y = mean(Y))
```

```
strata_low_6 <- df_strat_low[0.875 < df_strat_low$prop_score, ]
sum_strata_low_6 <- strata_low_6 %>%
  group_by(A) %>%
  summarise(Avg_Y = mean(Y))

ATE_Stratification_low <- as.double(((sum_strata_low_1[2,2] - sum_strata_low_1[1,2])*nrow(strata_low_1)
(sum_strata_low_3[2,2] - sum_strata_low_3[1,2])*nrow(strata_low_3) +
(sum_strata_low_4[2,2] - sum_strata_low_4[1,2])*nrow(strata_low_4) +
(sum_strata_low_5[2,2] - sum_strata_low_5[1,2])*nrow(strata_low_5) +
(sum_strata_low_6[1,2])*nrow(strata_low_6))/nrow(df_strat_low))
ATE_Stratification_low
```

Low Dimensional Data

```
## [1] 4.388841
```

```
# Timing the process -- ends
end.time_stratification_low <- Sys.time()
time_stratification_low <- end.time_stratification_low - start.time_stratification_low
time_stratification_low
```

```
## Time difference of 0.06098986 secs
```

The ATE of low dimensional data calculated by stratification is 4.388841.

```
# Timing the process -- start
start.time_stratification_high <- Sys.time()

prop_score <- g.matches_high$prop_score

df_high <- cbind(df_high, prop_score)
df_strat_high <- df_high[,c("Y","A","prop_score")]

strata_high_1 <- df_strat_high[df_strat_high$prop_score <= 0.3, ]
sum_strata_high_1 <- strata_high_1 %>%
  group_by(A) %>%
  summarise(Avg_Y = mean(Y))

strata_high_2 <- df_strat_high[0.3 < df_strat_high$prop_score, ]
sum_strata_high_2 <- strata_high_2 %>%
  group_by(A) %>%
  summarise(Avg_Y = mean(Y))

ATE_Stratification_high <- as.double(((sum_strata_high_1[2,2] - sum_strata_high_1[1,2])*nrow(strata_high
ATE_Stratification_high
```

High Dimensional Data

```
## [1] -61.93289
```

```r
# Timing the process -- ends
end.time_stratification_high <- Sys.time()
time_stratification_high <- end.time_stratification_high - start.time_stratification_high
time_stratification_high
```

```
## Time difference of 0.01782799 secs
```

The ATE of low dimensional data calculated by stratification is -61.93289.

Weighted Regression

Weighted least square estimation of the regression function:

$$Y_i = \alpha_0 + \tau * T_i + \alpha_1^{'} * Z_i + \alpha_2^{'} * (Z_i - \bar{Z}) * T_i + \varepsilon_i$$

The weights are the same as the ones of "Inverse Propensity Weighting". The Z_i are a subset of the covariates X_i; with sample average $\bar{Z}$. τ is an estimate for ATE. For the method of selecting Z, we get the estimation using linear regressions:

$$Y_i = \beta_{k0} + \beta_{k1} * T_i + \beta_{k2} * X_{ik} + \varepsilon_i$$

We calculate the t-statistic for the test of the null hypothesis that the slope coefficient β_{k2} is equal to zero in each of these regressions, and now select for Z all the covariates with a t-statistic larger in absolute value than t_{reg}. Thus, we include in the final regression all covariates which have substantial correlation with the outcome conditional on the treatment. (See Hirano and Imbens (2001))

Loading the Data and Data Preprocessing

```r
# timing starts
start.time_weighted_regression_low <- Sys.time()
start.time_weighted_regression_high <- Sys.time()


#The weight will be used for the weighted least square estimation of the regression function. (formula
# prop_score_low<-g.matches_low$prop_score
# prop_score_high<-g.matches_high$prop_score

weight_low <- cbind(as.numeric(A_low), prop_score_low) %>%
  as_tibble %>%
  mutate(weights = (V1/prop_score_low + (1-V1)/(1-prop_score_low)))
```

Finding weights and regression

```
## Warning: The `x` argument of `as_tibble.matrix()` must have unique column names if `.name_repair` is
## Using compatibility `.name_repair`.
```

```r
weight_low = weight_low[,"weights"]
weight_high <- cbind(as.numeric(A_high), prop_score_low) %>%
  as_tibble %>%
  mutate(weights = (V1/prop_score_high + (1-V1)/(1-prop_score_high)))
weight_high = weight_high[,"weights"]

#### Linear regression for selecting covarites
#Calculate the t-statistic
#we select for Z all the covariates with t-statsitic larger in absolute value than t reg (formula 2)

filter_low <- summary(lm(Y~., data = df_low))$coef[,4][3:24]<0.05
Z_low <- cbind(A_low, X_low[,filter_low])

filter_high <- summary(lm(Y~., data = df_high))$coef[,4][3:ncol(X_high)]<0.05
Z_high <- cbind(A_high, X_high[,filter_high])

#### Modify the data
Z_low <- Z_low %>% apply(2, as.numeric)
Z_high <- Z_high %>% apply(2, as.numeric)

#### Final Regression for ATE
Y_low <- df_low$Y
Y_high <- df_high$Y


#fit the weighted regression model and pick the coefficient of the treatment since ATE is the coeff of
#  lowdim
weighted_low <- lm(Y_low ~ Z_low, weights = as.numeric(unlist(weight_low)))
ATE_weightedreg_low <- coef(weighted_low)[2]


# timing ends
end.time_weighted_regression_low <- Sys.time()
time_weighted_regression_low <- end.time_weighted_regression_low - start.time_weighted_regression_low
time_weighted_regression_low
```

```
## Time difference of 0.172893 secs
```

```r
#  highdim
weighted_high <- lm(Y_high ~ Z_high, weights = as.numeric(unlist(weight_high)))
ATE_weightedreg_high <- coef(weighted_high)[2]

# timing ends
end.time_weighted_regression_high <- Sys.time()
time_weighted_regression_high <- end.time_weighted_regression_high - start.time_weighted_regression_hig
time_weighted_regression_high
```

```
## Time difference of 0.1801081 secs
```

```r



ATE_weightedreg_low
```

Summarizing Final Results

```
##    Z_low
## 2.305857
```

```
ATE_weightedreg_high
```

```
##    Z_high
## -57.16409
```

Results

We compare the accuracy and performance of the three ATE Estimation procedures below.

ATE Results

We are provided the true ATE values of -54.8558 for the high dimensional data and 2.0901 for the low dimensional data.

```
##                      High Dimensional Data Low Dimensional Data
## True                            -54.855800             2.090100
## Stratification                  -61.932886             4.388841
## Propensity Matching             -57.492971             2.073773
## Weighted Regression             -57.164089             2.305857
```

From the table above, we see that regression adjustment performed the best for the high dimensional data and stratification performed the best for the low dimensional data.

Run Time Results

```
##                              High Dimensional Data Low Dimensional Data
## Propensity Score Estimation             0.85563493           0.03090096
## Stratification                          0.01782799           0.06098986
## Propensity Matching                     0.10510087           0.10317397
## Weighted Regression                     0.18010807           0.17289305
```

Given the nature of trees, propensity score estimations are quickly calculated once we have the proper hyper-parameters selected from cross-validation–even for the high dimensional data, propensity score estimations did not take more than two seconds.

Given the size of the two datasets, the stratification is the fastest method. However, descriptions of run times are device dependant and we are making conclusions based on average run times we saw through numerous iterations.

Conclusion

Overall, we believe that using classification/regression trees for propensity scores was not the ideal approach for either dataset. While we cross-validated the hyperparameter of maxdepth, to help avoid with overfitting, the mean error of choosing different parameters didn't vary much, which means that the tree model yields similar propensity score estimation regardless of the model complexity.

The results were relatively consistent among all three methods. The propensity matching and weighted regression are getting quite satisfactory results. But the stratification's estimation is more deviated from the true values. Specifically, the weighted regression yields the best ATE estimation for the high dimensional dataset, while the propensity matching yields the best ATE estimation for the low dimensional dataset. While we might not completely trust the estimation of these methods, they show a fast and easy way to get a general sense of the average treatment effect.

References

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- Lunceford, Jared K, and Marie Davidian. 2004. "Stratification and Weighting via the Propensity Score in Estimation of Causal Treatment Effects a Comparative Study." Statistics in Medicine 23 (19): 2937–60.
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