Data Analysis 2

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```r
## libraries
libs <- c("tidyverse", "haven", "bibtex", "psych", "knitr", "pastecs", "kableExtra","survey", "cobalt",

sapply(libs, require, character.only = TRUE)
```

```
##    tidyverse        haven       bibtex        psych        knitr      pastecs
##         TRUE         TRUE         TRUE         TRUE         TRUE         TRUE
##   kableExtra       survey       cobalt randomForest        ipred        rpart
##         TRUE         TRUE         TRUE         TRUE         TRUE         TRUE
##     baguette      parsnip    SimDesign    bartCause         lme4          grf
##         TRUE         TRUE         TRUE         TRUE         TRUE         TRUE
##    GenericML          car
##         TRUE         TRUE
```

```r
covariateNames <- c(
    "X1RTHETK1",
    "X1MTHETK1",
    "X1TCHAPP",
    "X1TCHCON",
    "X1TCHPER",
    "X1TCHEXT",
    "X1TCHINT",
    "X1ATTNFS",
    "X1INBCNT",
    "X12MOMAR",
    "X1NUMSIB",
    "P1OLDMOM",
    "P1CHLDBK",
    "P2DISTHM",
    "P1NUMPLA",
    "T2PARIN",
    "X12PAR1ED_I",
    "X12PAR2ED_I",
    "X2INCCAT_I",
    "X1PAR1EMP",
    "S2LUNCH",
    "X2KRCETH",
    "S2NGHBOR",
    "S2OUTSID",
    "S2USDABR",
    "S2PUBSOC",
```

```
    "X1LOCALE",
    "S1_ID",
    "W1_2P0PSU",
    "prop.missing")

covariateNamesBART <- c(
    "X1RTHETK1",
    "X1MTHETK1",
    "X1TCHAPP",
    "X1TCHCON",
    "X1TCHPER",
    "X1TCHEXT",
    "X1TCHINT",
    "X1ATTNFS",
    "X1INBCNT",
    "X12MOMAR",
    "X1NUMSIB",
    "P1OLDMOM",
    "P1CHLDBK",
    "P2DISTHM",
    "P1NUMPLA",
    "T2PARIN",
    "X12PAR1ED_I",
    "X12PAR2ED_I",
    "X2INCCAT_I",
    "X1PAR1EMP",
    "S2LUNCH",
    "X2KRCETH",
    "S2NGHBOR",
    "S2OUTSID",
    "S2USDABR",
    "S2PUBSOC",
    "X1LOCALE")

## directory path (assignment_2 as current working directory)

data_dir <- file.path(".", "data")

## loading data
load(file.path(data_dir, "chapter_10_data_cleaned_and_imputed.Rdata"))
```

In this paper, we explore heterogeneity of treatment using three different methods; CausalBART, GenericML, and CausalForest. We will explore the heterogeneity (answer the assginment questions) separately for each model before concluding and comparing the findings at the conclusion of the paper.

```
psFormula <- paste(covariateNames, collapse="+")
psFormula <- formula(paste("treated~", psFormula, sep=""))
print(psFormula)
```

```
## treated ~ X1RTHETK1 + X1MTHETK1 + X1TCHAPP + X1TCHCON + X1TCHPER +
##     X1TCHEXT + X1TCHINT + X1ATTNFS + X1INBCNT + X12MOMAR + X1NUMSIB +
##     P1OLDMOM + P1CHLDBK + P2DISTHM + P1NUMPLA + T2PARIN + X12PAR1ED_I +
##     X12PAR2ED_I + X2INCCAT_I + X1PAR1EMP + S2LUNCH + X2KRCETH +
```

```
##     S2NGHBOR + S2OUTSID + S2USDABR + S2PUBSOC + X1LOCALE + S1_ID +
##     W1_2P0PSU + prop.missing
```

BART

```r
# credit to Matt, esp for the covs matrices!
train <- data %>%
  sample_frac(size = 0.5)
test <- anti_join(data, train)

matrix_covsBART <- as.matrix(train %>% select(covariateNamesBART) %>%
                           mutate(across(.fns = as.numeric)))

matrix_covsBART_2 <- as.matrix(test %>% select(covariateNamesBART) %>%
                           mutate(across(.fns = as.numeric)))

# estimating conditional average treatment effects (CATEs) using BART

bart <- bartc(response = train$X2MTHETK1,
             treatment = as.numeric(as.character(train$treated)),
             confounders = matrix_covsBART,
             method.rsp = "bart",
             method.trt = "glm",
             keepTrees = TRUE,
             estimand = "ate")
```

```
## fitting treatment model via method 'glm'
## fitting response model via method 'bart'
```

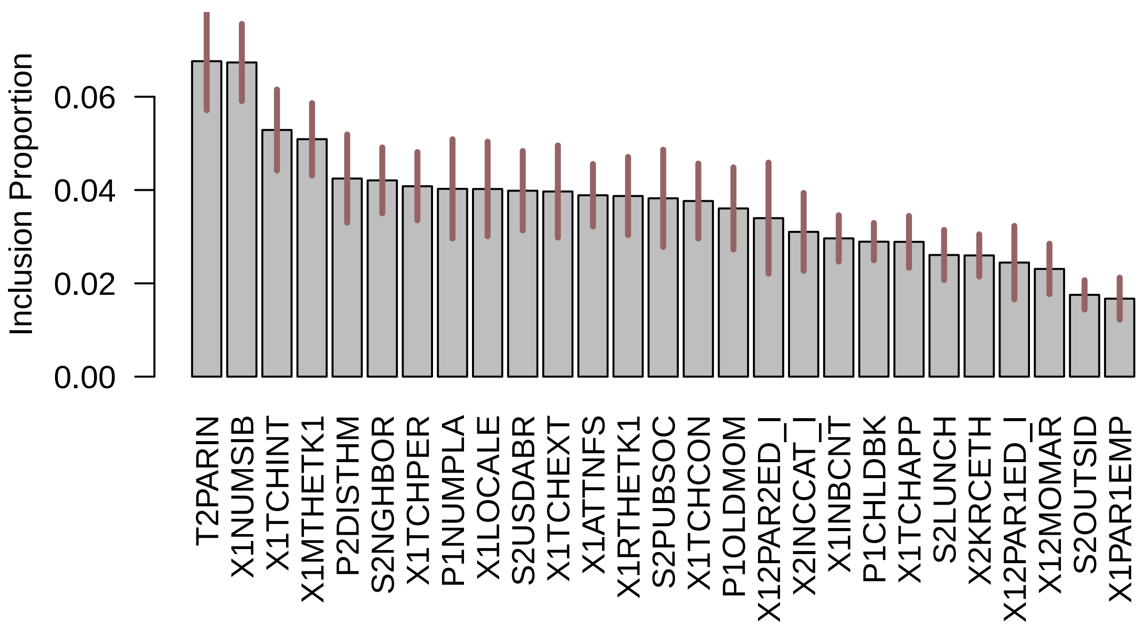
```r
cate <- predict(bart,
               newdata = matrix_covsBART_2,
               type = "icate")

cate_m <- apply(cate, 2, mean)


library(bartMachine)

bart_machine <- bartMachine(X=as.data.frame(matrix_covsBART),
                            y=cate_m,
                            serialize = T,
                            mem_cache_for_speed = F)
```

```
## bartMachine initializing with 50 trees...
## bartMachine vars checked...
## bartMachine java init...
## bartMachine factors created...
## bartMachine before preprocess...
## bartMachine after preprocess... 27 total features...
## bartMachine sigsq estimated...
```

```
## bartMachine training data finalized...
## Now building bartMachine for regression...
## evaluating in sample data...done
## serializing in order to be saved for future R sessions...done
```

```r
var.importance <- investigate_var_importance(bart_machine,
                                             num_replicates_for_avg = 25)
```

```
## .........................
```




```r
#select variables whose importance is greater than the median
important.vars = names(var.importance$avg_var_props)[
  var.importance$avg_var_props > median(var.importance$avg_var_props)]

test <- test %>% mutate(across(.fns = as.numeric))
test$treated <- test$treated - 1

bart2 <- bartc(response = test$X2MTHETK1,
              treatment = test$treated,
              confounders = data.frame(test[,important.vars]),
              method.rsp = "bart",
              method.trt = "glm",
              estimand = "ate",
              keepTrees = T)
```

```
## fitting treatment model via method 'glm'
## fitting response model via method 'bart'
```

```r
cate2 <- predict(bart2,
                newdata = data.frame(test[,important.vars]),
                type = "icate")

test$cate2 <- apply(cate2, 2, mean)

model <- paste(important.vars, collapse="+")
model <- paste(c("cate2",model), collapse="~")
model.cate <- lm(model,data = test)
summary(model.cate)
```

```
##
## Call:
## lm(formula = model, data = test)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.06939 -0.01188 -0.00292  0.00619  0.37797
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  5.592e-03  3.564e-03   1.569   0.1167
## T2PARIN      7.610e-04  4.401e-04   1.729   0.0838 .
## X1NUMSIB    -2.006e-04  2.904e-04  -0.691   0.4897
## X1TCHINT     2.822e-03  6.986e-04   4.039 5.42e-05 ***
## X1MTHETK1   -1.923e-02  5.610e-04 -34.283  < 2e-16 ***
## P2DISTHM     1.135e-04  8.378e-05   1.355   0.1754
## S2NGHBOR    -1.912e-05  9.891e-06  -1.933   0.0532 .
## X1TCHPER    -2.526e-03  6.318e-04  -3.998 6.46e-05 ***
## P1NUMPLA    -8.282e-05  2.883e-04  -0.287   0.7739
## X1LOCALE    -1.738e-03  2.849e-04  -6.103 1.10e-09 ***
## S2USDABR     5.051e-04  7.864e-04   0.642   0.5207
## X1TCHEXT     8.748e-03  6.351e-04  13.773  < 2e-16 ***
## X1ATTNFS     2.746e-04  3.162e-04   0.869   0.3851
## X1RTHETK1    3.929e-03  5.917e-04   6.639 3.42e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02561 on 6328 degrees of freedom
## Multiple R-squared:  0.3321, Adjusted R-squared:  0.3308
## F-statistic: 242.1 on 13 and 6328 DF,  p-value: < 2.2e-16
```

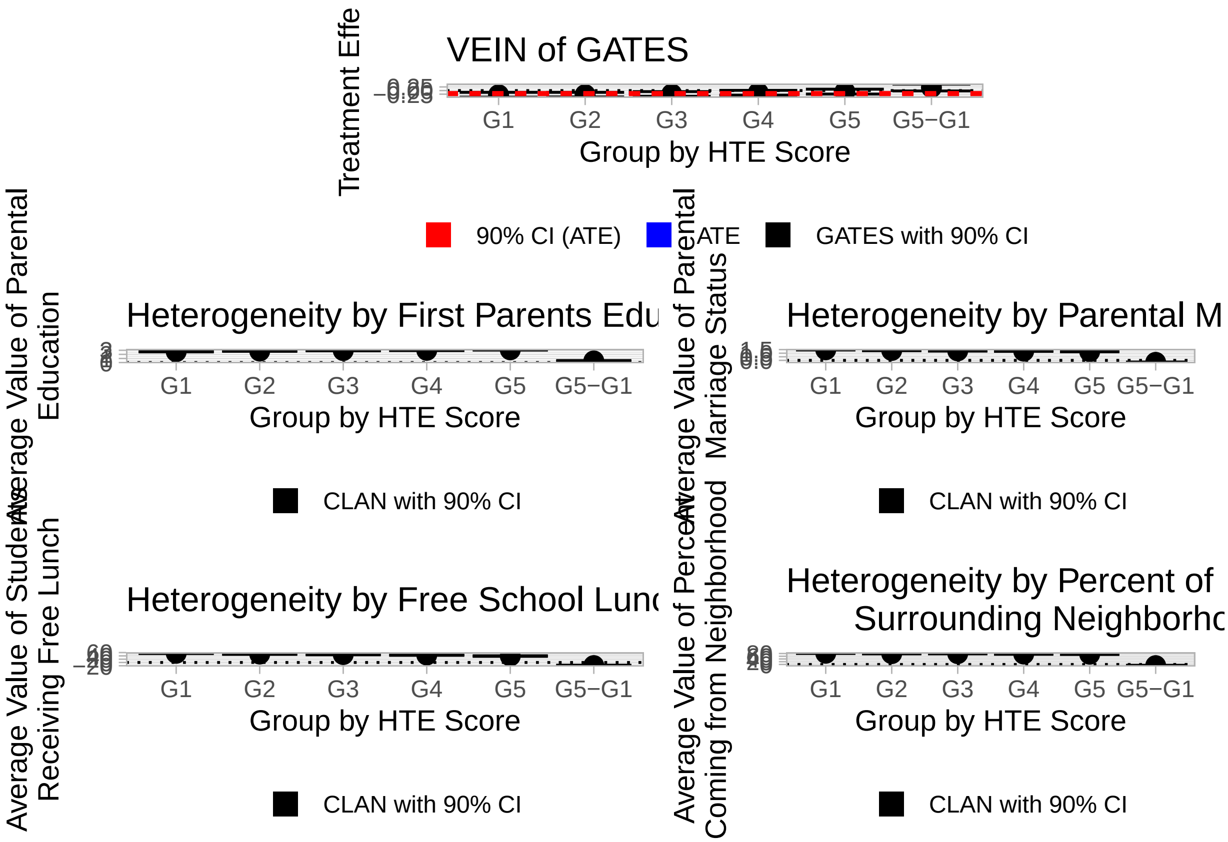
```r
# correlation matrix


# qqplot
```

GenericML

```r
##' @Matt
learners <- c("random_forest", "lasso")
matrix_covs <- as.matrix(data %>% select(all_of(covariateNames)) %>%
                           mutate(across(.fns = as.numeric)))
X1 <- setup_X1(funs_Z = c("B", "S"))
               #fixed_effects = vil_pair)
vcov <- setup_vcov(estimator = "vcovHC")
                   #arguments = list(cluster = demi_paire))


library(parsnip)
ps_nnet <- mlp(mode = "classification",
               engine = "nnet",
hidden_units = 20) %>%
  fit(psFormula,
      data = data)
data$ps_nnet <- predict(ps_nnet,
                      new_data = data,
                      type = "prob")[,2]
data$ps_nnet <- data$ps_nnet$.pred_1 ## remove the $column.name


genML <- GenericML(
  Z = matrix_covs, #covariates
  D = as.numeric(as.character(data$treated)), #treatment
  Y = as.numeric(data$T2TTABS), #outcome
  learners_GenericML = learners,  # learners specified above
  learner_propensity_score = as.numeric(data$ps_nnet), #as.numeric(data$ps)  #ps
  num_splits = 10,                          # number splits of the data
  quantile_cutoffs = c(0.2, 0.4, 0.6, 0.8), # grouping for CATEs
  significance_level = 0.05,                # significance level
  X1_BLP = X1, X1_GATES = X1,               # regression setup
  vcov_BLP = vcov, vcov_GATES = vcov,       # covariance setup
  parallel = F, #num_cores = 6L, # parallelization
  seed = 20220621)                         # RNG seed
best <- get_best(genML)
## random_forest is best, becomes the default for all future GenML functions
base <- get_BLP(genML)
## significant indicating treatment heterogeneity
a <- get_GATES(genML) %>%
  plot()
# Plot parental education
b <- get_CLAN(genML,
         variable = "X12PAR1ED_I") %>%
  plot() +
  labs(title = "Heterogeneity by First Parents Education",
       y = str_wrap("Average Value of Parental Education", 25))
# Plot family marriage status
c <- get_CLAN(genML,
         variable = "X12MOMAR") %>%
  plot() +
```

```
  labs(title = "Heterogeneity by Parental Marriage Status",
       y = str_wrap("Average Value of Parental Marriage Status", 25))
# Plot lunch variable
d <- get_CLAN(genML,
         variable = "S2LUNCH") %>%
  plot() +
  labs(title = "Heterogeneity by Free School Lunch",
       y = str_wrap("Average Value of Students Receiving Free Lunch", 25))
# Plot percent coming from neighborhood
e <- get_CLAN(genML,
         variable = "S2NGHBOR") %>%
  plot() +
  labs(title = "Heterogeneity by Percent of School coming from
       Surrounding Neighborhood",
       y = str_wrap("Average Value of Percent Coming from Neighborhood", 25))
library(patchwork)
layout <- c("#AA#
            BBCC
            DDEE")
genMLplot<- a + b + c + d + e +
  plot_layout(design = layout)
```

```
genMLplot
```



VEIN of GATES
Treatment Effe
G1
G2
G3
G4
G5
G5−G1
Group by HTE Score
90% CI (ATE)
ATE
GATES with 90% CI
Heterogeneity by First Parents Edu
Average Value of Parental
Education
Group by HTE Score
CLAN with 90% CI
Heterogeneity by Parental M
Average Value of Parental
Marriage Status
Group by HTE Score
CLAN with 90% CI
Heterogeneity by Free School Lunc
Average Value of Students
Receiving Free Lunch
Group by HTE Score
CLAN with 90% CI
Heterogeneity by Percent of
Surrounding Neighborhc
Average Value of Percent
Coming from Neighborhood
Group by HTE Score
CLAN with 90% CI

Causal Forests

```r
#the grf package only takes numeric covariates
data2 <- data
#So convert those factor variables to be the numeric class
for (i in 1:length(covariateNames)) {
  if(class(data2[,covariateNames[i]])=="factor"){
    data2[, covariateNames[i]] <- as.numeric(as.character(data2[,covariateNames[i]]))
  }
}

#Step 1: Split data into training data set and testing data set
#In this case, we split it to be 50/50
set.seed(123)
train_index <- sample(1:nrow(data2), nrow(data2)/2)
train_index <- train_index[order(train_index)]

train_data <- data2[train_index,]
test_data <- data2[-train_index,]

#Step 2: model fit, using causal forest
#Tuning mtry and min.node.size parameters by setting tune.parameters
train.forest = causal_forest(X=train_data[,covariateNames],
                             Y = train_data$X2MTHETK1, num.trees = 5000,
                             W = as.numeric(as.character(train_data$treated)),
                             W.hat = train_data$ps,
                             tune.parameters = c("mtry", "min.node.size"),
                             seed = 0)

train.forest[["tuning.output"]]
```

```
## Tuning status: tuned.
## This indicates tuning found parameters that are expected to perform better than default.
##
## Predicted debiased error: 0.192038999006511
##
## Tuned parameters:
## mtry: 4
##  min.node.size: 1
##
## Average error by 5-quantile:
##
##     mtry     error
##    [1,6] 0.1933593
##   (6,11] 0.1933223
##  (11,16] 0.1933650
##  (16,21] 0.1933936
##  (21,26] 0.1932969
##
##  min.node.size     error
##          [1,2] 0.1922627
##          (2,9] 0.1928078
```

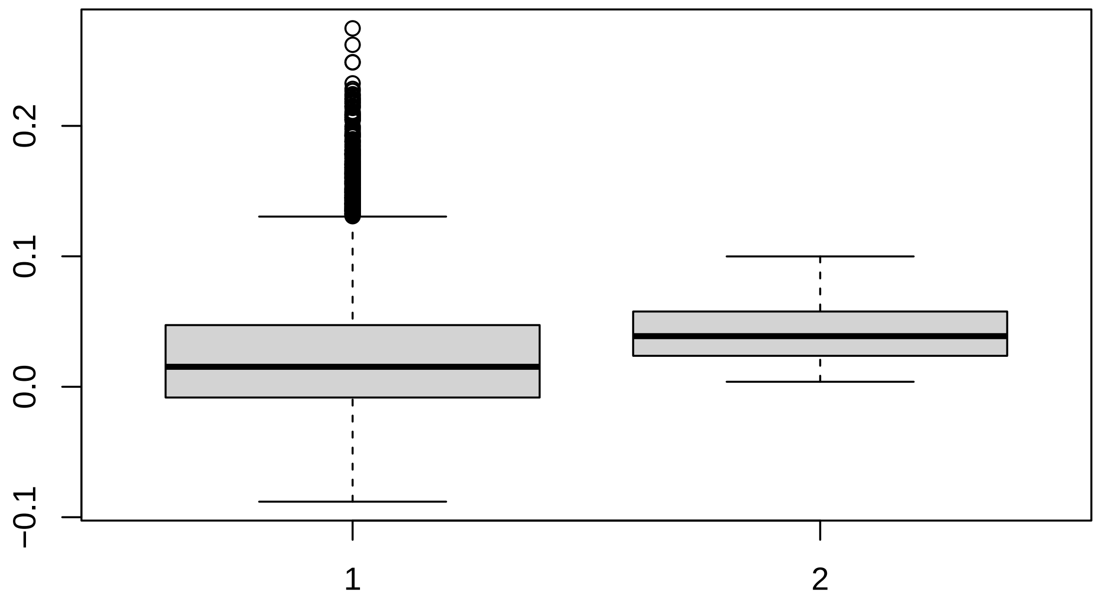
```
##       (9,32.4] 0.1933650
##     (32.4,124] 0.1939739
##      (124,393] 0.1944002
```

```r
#The results showed that mtry = 16 and min.node.size = 1 perform better than the default setting

#Step 3: Obtain estimates of the conditional average treatment effect (CATE)
#with standard errors
tau.hat = predict(train.forest,X= test_data[,covariateNames], estimate.variance = T)
CATE_causalForest = tau.hat$predictions
```

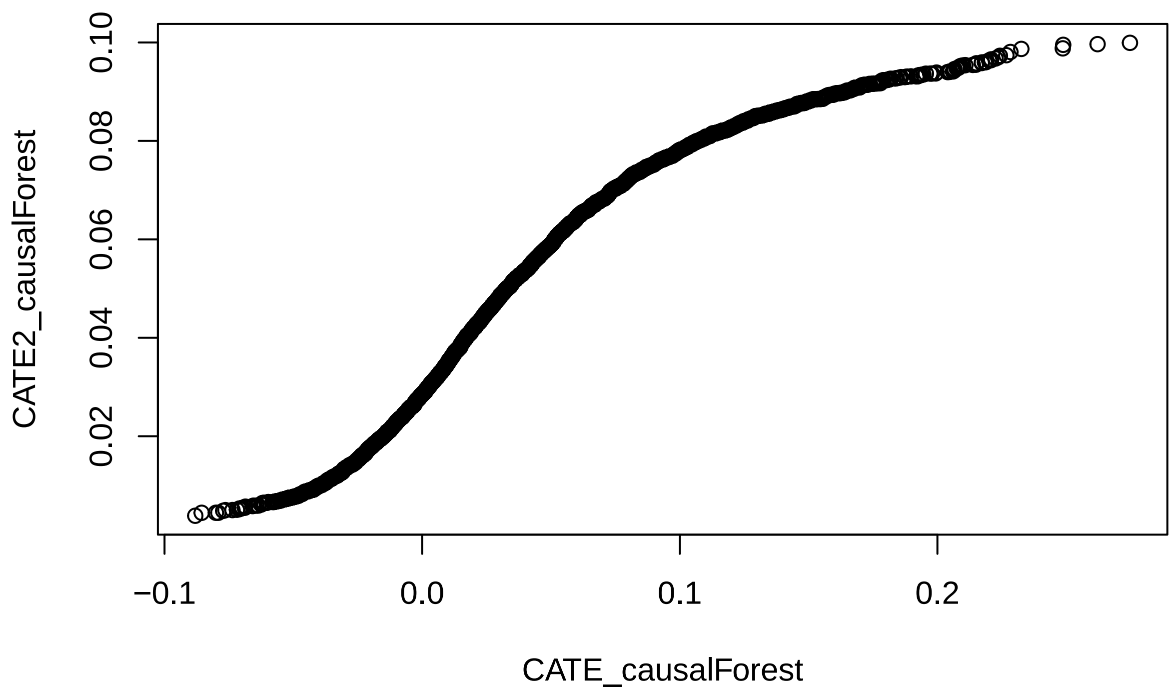
```r
# Causal Forests
#1. correlation matrix
#causal forest only output the best tunning parameters' model fit outcomes
#To answer Q2, I run one more model fit with mtry = 4 and min.node.size = 50
train.forest2 = causal_forest(X=train_data[,covariateNames],
                              Y = train_data$X2MTHETK1, num.trees = 5000,
                              W = as.numeric(as.character(train_data$treated)),
                              W.hat = train_data$ps,
                              mtry = 4, min.node.size = 50,
                              seed = 0)
tau.hat2 = predict(train.forest2,X= test_data[,covariateNames], estimate.variance = T)
CATE2_causalForest = tau.hat2$predictions

cor(CATE_causalForest, CATE2_causalForest)
```

```
## [1] 0.819073
```

```r
#2.box plot
boxplot(CATE_causalForest, CATE2_causalForest)
```




```
#3.QQ plot
qqplot(CATE_causalForest, CATE2_causalForest)
```



Determine Best Linear Projection of CATE/Variable Importance

```
#Causal Forests
#Step 1: Subset important variables
importance_cf = variable_importance(train.forest)
rownames(importance_cf) = names(train_data[,covariateNames])

#select variables above the median of importance of the aggregated importances
#across imputed datasets
important.var_cf = rownames(importance_cf)[importance_cf>median(importance_cf)]

#Step 2
#run test forest
test.forest = causal_forest(X = test_data[,important.var_cf],
                            Y = test_data$X2MTHETK1,
                            W = as.numeric(as.character(test_data$treated)),
                            W.hat = test_data$ps,
                            mtry = 16, num.trees=5000,
                            min.node.size = 1, seed = 0)

#Step 3: Predict the conditional average treatment effect (CATE)
tau.hat = predict(test.forest,X= test_data[,important.var_cf], estimate.variance = T)
CATE_test = tau.hat$predictions
summary(CATE_test)
```

```
##      Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
## -0.173870 -0.017321  0.009734  0.007724  0.035261  0.265324
```

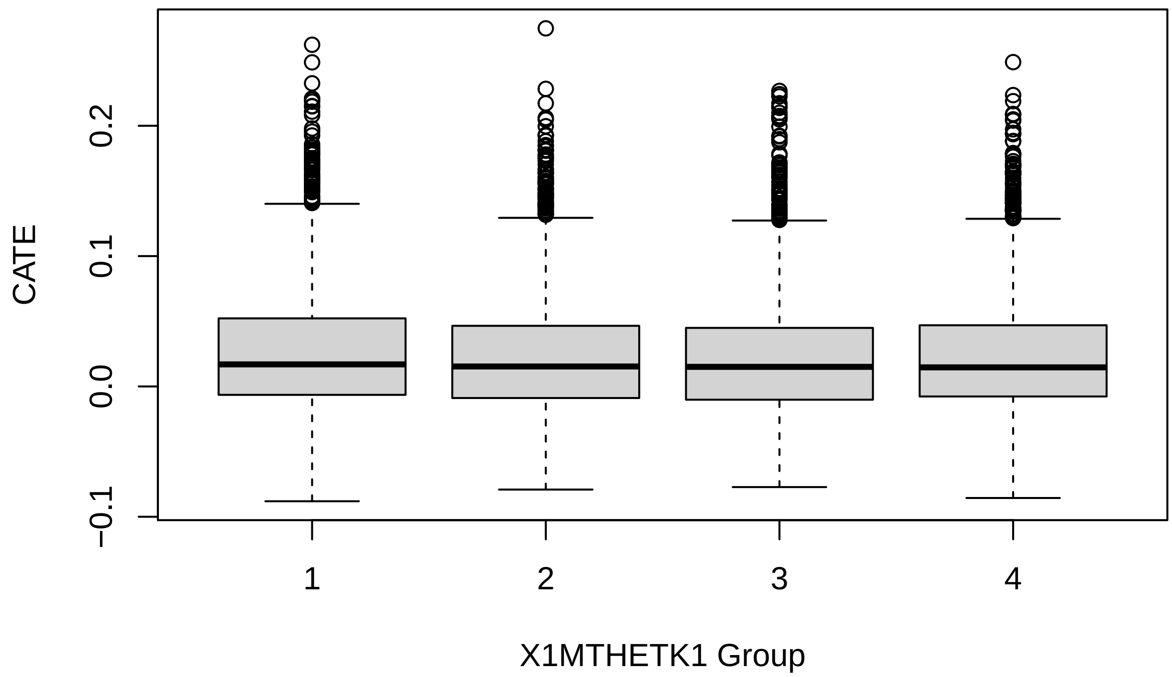
```
#When using the test data set and fitting the important variables,
 #the conditional ATE was small, which ranges from -0.401 to 0.254 with a mean of 0.018.

test_calibration(test.forest)
```

```
##
## Best linear fit using forest predictions (on held-out data)
## as well as the mean forest prediction as regressors, along
## with one-sided heteroskedasticity-robust (HC3) SEs:
##
##                                Estimate Std. Error t value Pr(>t)
## mean.forest.prediction          1.41762    1.68005  0.8438 0.1994
## differential.forest.prediction  0.17620    0.39979  0.4407 0.3297
```

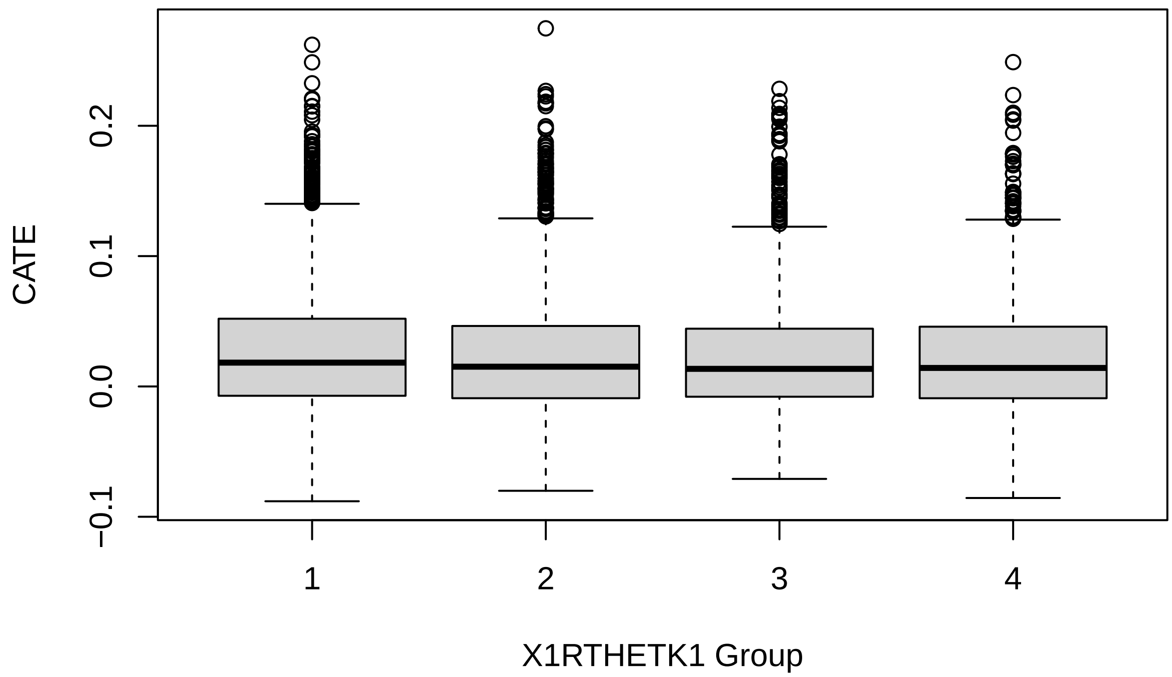
```
#The outcomes showed that the coefficient of the mean forest prediction was 1
 #which indicated the mean forest prediction was correct.
#Also, the results indicated no heterogeneity been detected.
```

Two most important CATE predictors (For each method), plot CATE/predictor relationship

```
#Causal Forests
#The most two predictors are
Top2predictors <- importance_cf[order(importance_cf, decreasing = T),][1:2]

#Predictor 1
groupX1MTHETK1 <- quantile(test_data[, names(Top2predictors)[1]])
test_data$groupX1M <- ifelse(test_data$X1MTHETK1 >= groupX1MTHETK1[4], 4,
                             ifelse(test_data$X1MTHETK1>=groupX1MTHETK1[3] & test_data$X1MTHETK1<groupX
                                    ifelse(test_data$X1MTHETK1>=groupX1MTHETK1[2] & test_data$X1MTHETK1
                                           1)))
test_data$groupX1M <- factor(test_data$groupX1M)
boxplot(CATE_causalForest ~ test_data$groupX1M, xlab = "X1MTHETK1 Group", ylab = "CATE")
```




```
#Predictor 2
groupX1R <- quantile(test_data[, names(Top2predictors)[2]])
test_data$groupX1R <- ifelse(test_data$X1RTHETK1 >= groupX1R[4], 4,
                            ifelse(test_data$X1RTHETK1>=groupX1R[3] & test_data$X1RTHETK1<groupX1R[4],
                                   ifelse(test_data$X1RTHETK1>=groupX1R[2] & test_data$X1RTHETK1<group
                                          1)))
test_data$groupX1R <- factor(test_data$groupX1R)
boxplot(CATE_causalForest ~ test_data$groupX1R, xlab = "X1RTHETK1 Group", ylab = "CATE")
```



Method Comparisons and Conclusion

Insert BART conclusion

Insert GenericML conclusion

Insert Causal Forest conclusion

Comparison

In summary,