# Problem set 8

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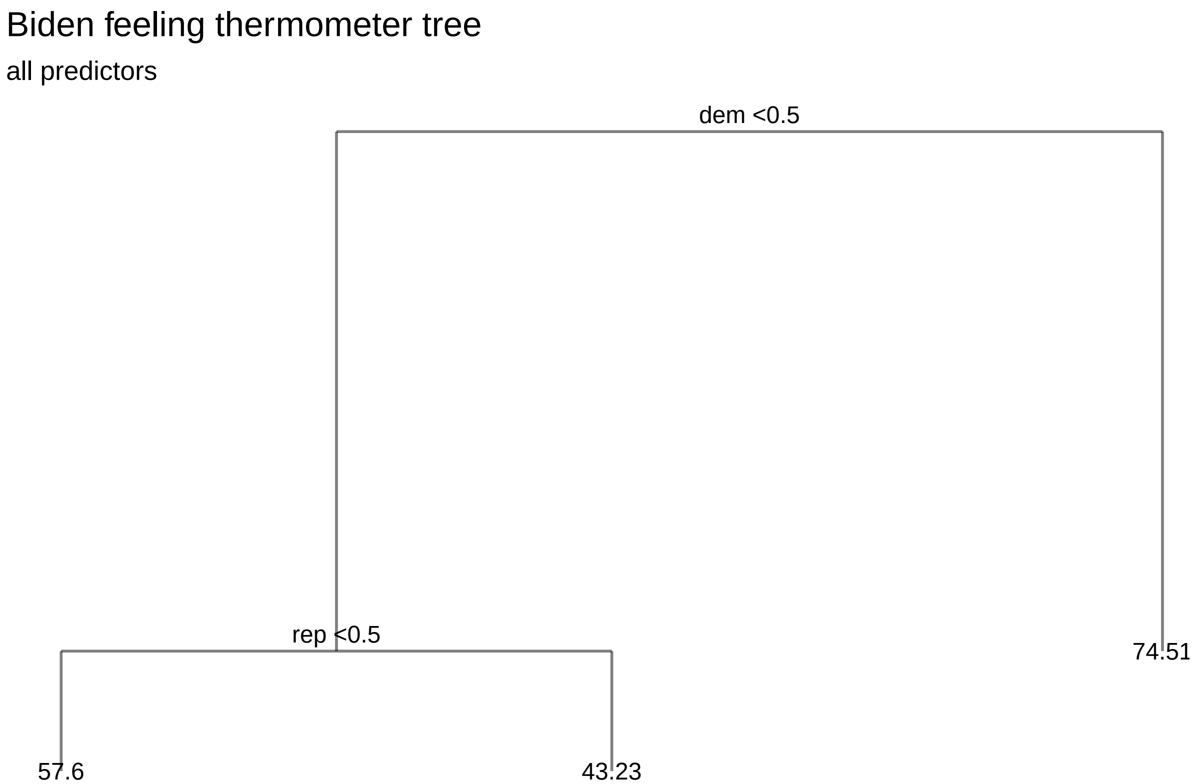
## Part 1: Sexy Joe Biden (redux times two)

### 1. Let's first split the data into a training set and a testing set

```
biden_split <- resample_partition(biden_data, c(test = 0.3, train = 0.7))
```

### 2. Fit a decision tree to the training data, with biden as the response variable and the other variables as predictors. Plot the tree and interpret the results. What is the test MSE?

```
# estimate model
biden_tree1 <- tree(biden ~ ., data = biden_split$train)

#mod <- prune.tree(auto_tree, best = 2)

# plot unpruned tree
mod <- biden_tree1

tree_data <- dendro_data(mod)
ggplot(segment(tree_data)) +
  geom_segment(aes(x = x, y = y, xend = xend, yend = yend),
               alpha = 0.5) +
  geom_text(data = label(tree_data),
            aes(x = x, y = y, label = label_full), vjust = -0.5, size = 3) +
  geom_text(data = leaf_label(tree_data),
            aes(x = x, y = y, label = label), vjust = 0.5, size = 3) +
  theme_dendro() +
  labs(title = "Biden feeling thermometer tree",
       subtitle = "all predictors")
```




```
biden_tree1_mse <- mse(biden_tree1, biden_split$test)
biden_tree1_mse
```

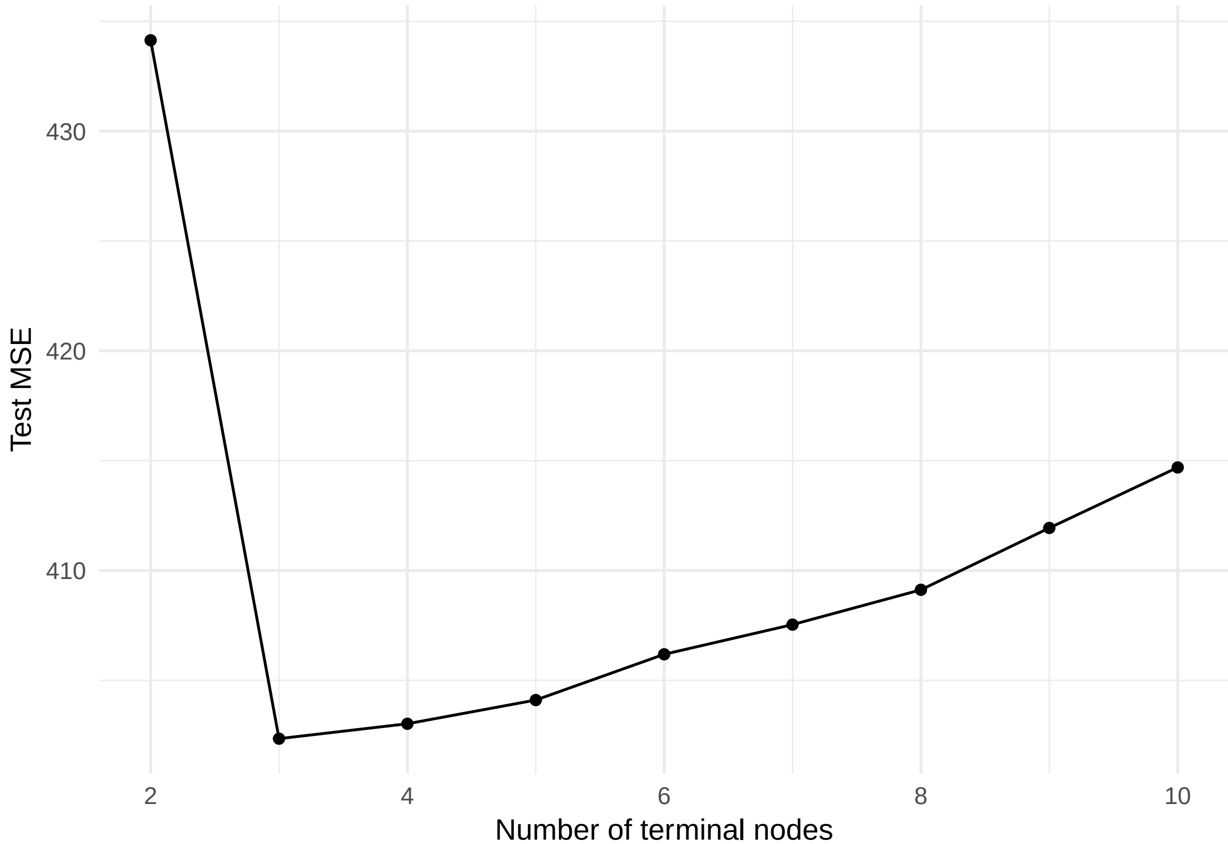
```
## [1] 406
```

Using all other variables as predictors and the default setting for tree(), the decision tree that we've obtained has a mse value of 406 on the test data. This model has three terminal nodes (57.6, 43.23 and 74.51), one internal node (rep<0.5), and three branches. For observations with dem<0.5 and rep<0.5, the person being independent, the model estimates the biden score to be 57.6. For observations with dem<0.5 and rep>=0.5, the person being republican, the model estimates the biden score to be 43.23. For observations with dem>=0.5, the person being democract, the model estimates the biden score to be 74.51.

### 3. Now fit another tree to the training data with the determined list options. Use cross-validation to determine the optimal level of tree complexity, plot the optimal tree, and interpret the results. Does pruning the tree improve the test MSE?

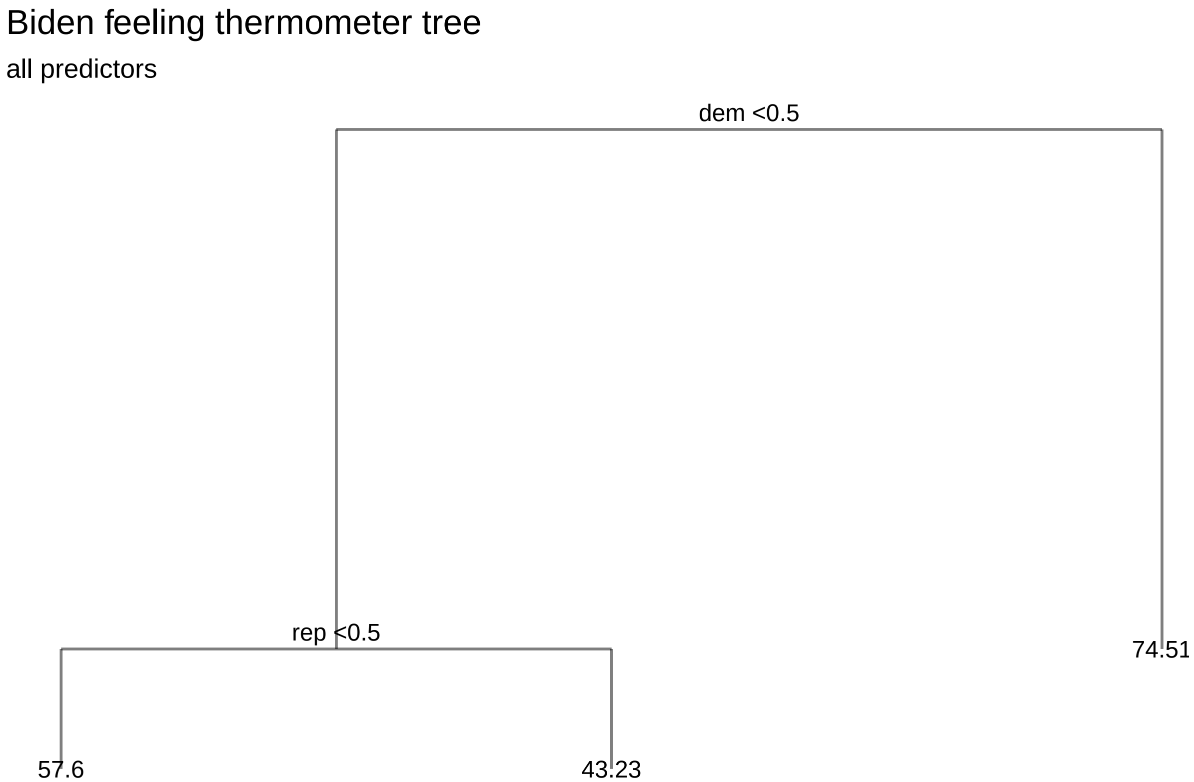
```
# generate 10-fold CV trees
biden_cv <- crossv_kfold(biden_data, k = 10) %>%
  mutate(tree = map(train, ~ tree(biden ~ ., data = ., control = tree.control(nobs = nrow(biden_data) ,

# calculate each possible prune result for each fold
biden_cv <- expand.grid(biden_cv$.id, 2:10) %>%
  as_tibble() %>%
  mutate(Var2 = as.numeric(Var2)) %>%
  rename(.id = Var1,
         k = Var2) %>%
  left_join(biden_cv) %>%
```

```r
  mutate(prune = map2(tree, k, ~ prune.tree(.x, best = .y)),
         mse = map2_dbl(prune, test, mse))

biden_cv %>%
  select(k, mse) %>%
  group_by(k) %>%
  summarize(test_mse = mean(mse),
            sd = sd(mse, na.rm = TRUE)) %>%
  ggplot(aes(k, test_mse)) +
  geom_point() +
  geom_line() +
  labs(x = "Number of terminal nodes",
       y = "Test MSE")
```




```r
#from the plot we see that the optimal number of terminal nodes is 3
# estimate model
biden_tree2 <- tree(biden ~ ., data = biden_split$train, control = tree.control(nobs = nrow(biden_split$

# plot unpruned tree
mod <- prune.tree(biden_tree2, best = 3)

tree_data <- dendro_data(mod)
ggplot(segment(tree_data)) +
  geom_segment(aes(x = x, y = y, xend = xend, yend = yend),
               alpha = 0.5) +
  geom_text(data = label(tree_data),
            aes(x = x, y = y, label = label_full), vjust = -0.5, size = 3) +
```

```
  geom_text(data = leaf_label(tree_data),
            aes(x = x, y = y, label = label), vjust = 0.5, size = 3) +
  theme_dendro() +
  labs(title = "Biden feeling thermometer tree",
       subtitle = "all predictors")
```




```
biden_tree2_mse <- mse(mod, biden_split$test)
biden_tree2_mse
```

```
## [1] 406
```

After using ten fold cross validation, we observe that the number of terminal nodes with lowest test MSE is 3. Thus, we prune the tree to make it only have three terminal nodes. The resulting tree is exactly the same as the previous one, so the mse of this tree is also the same, 406. We may guess that cross validation is implemented for the default setting for the `tree()` function.

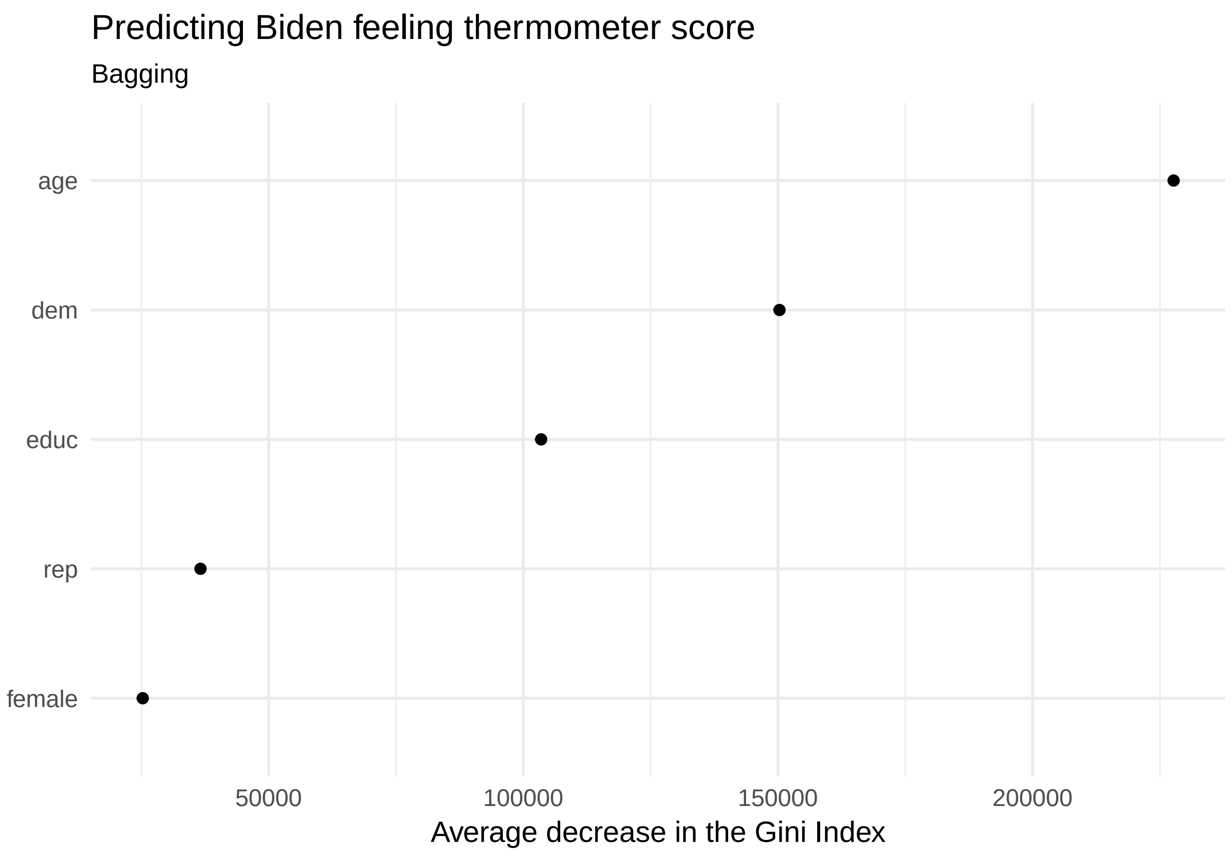
## 4. Use the bagging approach to analyze this data. What test MSE do you obtain? Obtain variable importance measures and interpret the results.

```
#select(-Name, -Ticket, -Cabin, -Sex, -PassengerId) %>%
# biden_rf_data <- biden_data %>%
#     mutate_each(funs(as.factor(female, dem, rep)), age, educ) %>%
#     na.omit

biden_bag <- randomForest(biden ~ ., data = biden_split$train,
                             mtry = 5, ntree = 500)

biden_bag_mse <- mse(biden_bag, biden_split$test)
```

```
biden_bag_mse
```

```
## [1] 485
```

```
data_frame(var = rownames(importance(biden_bag)),
           MeanDecreaseGini = importance(biden_bag)[,1]) %>%
  mutate(var = fct_reorder(var, MeanDecreaseGini, fun = median)) %>%
  ggplot(aes(var, MeanDecreaseGini)) +
  geom_point() +
  coord_flip() +
  labs(title = "Predicting Biden feeling thermometer score",
       subtitle = "Bagging",
       x = NULL,
       y = "Average decrease in the Gini Index")
```




Test MSE of this bagged model is 485, which is larger than that of our precious models, 406. This shows that this bagging model does not perform as well as simple decision tree for this dataset. To interpret the importance of parameters for this model, the larger the average decrease in the Gini Index is, the more important the parameter is. From the plot, we could see that for this bagged biden feeling thermometer model, age, democract or not and education are the three most important parameters, while republican or not and gender are less important.

**5. Use the random forest approach to analyze this data. What test MSE do you obtain? Obtain variable importance measures and interpret the results. Describe the effect of m, the number of variables considered at each split, on the error rate obtained.**

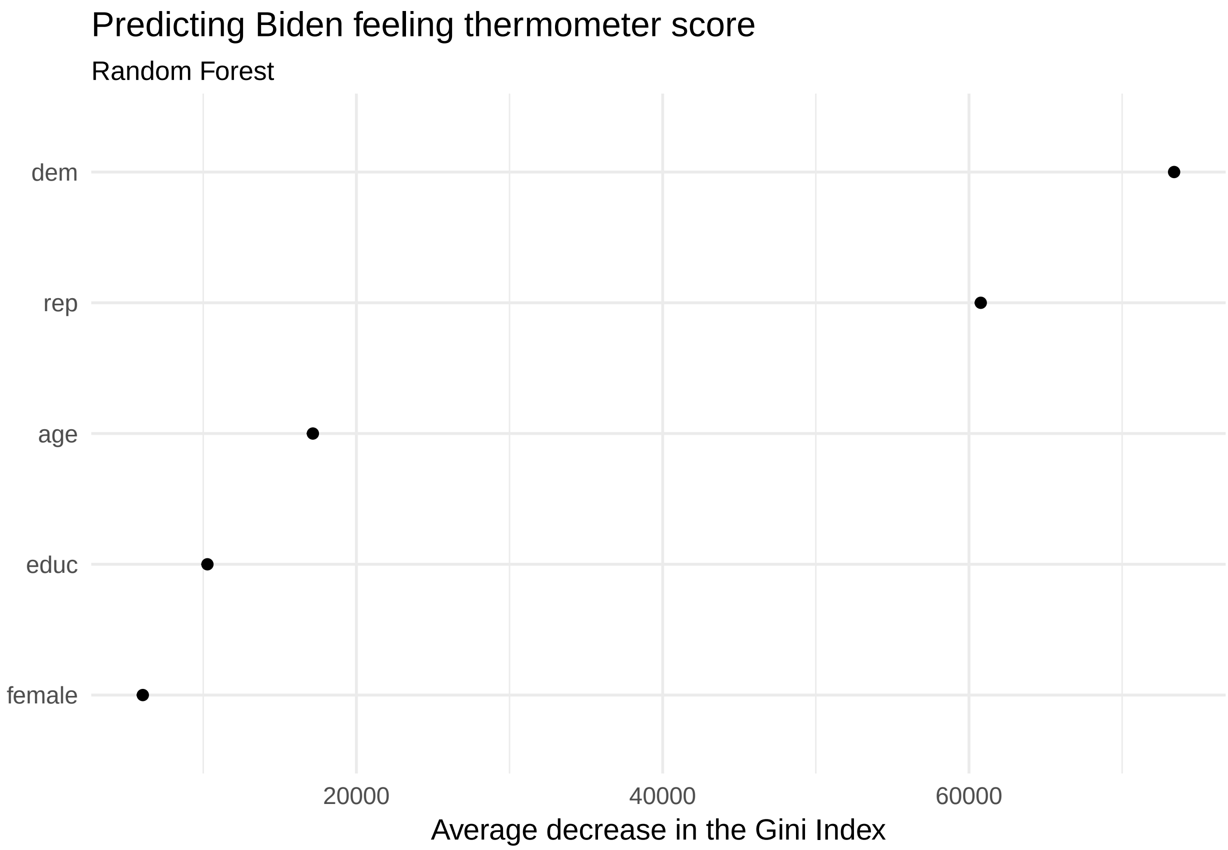
```
biden_rf <- randomForest(biden ~ ., data = biden_split$train, ntree = 500)
biden_rf
```

```
##
## Call:
##  randomForest(formula = biden ~ ., data = biden_split$train, ntree = 500)
##                Type of random forest: regression
##                      Number of trees: 500
## No. of variables tried at each split: 1
##
##           Mean of squared residuals: 406
##                     % Var explained: 25.7
```

```
biden_rf_mse <- mse(biden_rf, biden_split$test)
biden_rf_mse
```

```
## [1] 409
```

```
data_frame(var = rownames(importance(biden_rf)),
           MeanDecreaseGini = importance(biden_rf)[,1]) %>%
  mutate(var = fct_reorder(var, MeanDecreaseGini, fun = median)) %>%
  ggplot(aes(var, MeanDecreaseGini)) +
  geom_point() +
  coord_flip() +
  labs(title = "Predicting Biden feeling thermometer score",
       subtitle = "Random Forest",
       x = NULL,
       y = "Average decrease in the Gini Index")
```




MSE of the random forest model is 409, considerably smaller to that of the bagged model. Importances of parameters are different from bagging. Looking at the average decrease in the Gini Index of each variable, we can tell that `dem` and `rep` are the two most important parameters, which correspond more to the decision tree models that we've obtained previously. Compared to the importance of each parameters of bagging model, the values of this random forest model are much lower. While `age`, the most important variable of bagging model has an average decrease in the Gini Index as 300000, `dem` and `rep`, the two most important variables of random forest model have average decrease in the Gini Index as about 105000 and 80000 respectively. This might be because of the variable restriction imposed when considering splits.

### 6. Use the boosting approach to analyze the data. What test MSE do you obtain? How does the value of the shrinkage parameter influence the test MSE?

```
biden_models <- list("boosting" = gbm(biden ~ ., data = biden_split$train,
                                               n.trees = 10000),
                      "boosting_s1" = gbm(biden ~ ., data = biden_split$train,
                                               n.trees = 10000, shrinkage = 0.1),
                       "boosting_s2" = gbm(biden ~ ., data = biden_split$train,
                                               n.trees = 10000, shrinkage = .01),
                       "boosting_s3" = gbm(biden ~ ., data = biden_split$train,
                                               n.trees = 10000, shrinkage = .005))
```

```
## Distribution not specified, assuming gaussian ...
## Distribution not specified, assuming gaussian ...
## Distribution not specified, assuming gaussian ...
## Distribution not specified, assuming gaussian ...
```

```
mse_boosting <- function(model, data) {
  pred <- predict(model,newdata = as_tibble(data),
                                          n.trees = 10000)
  mean((pred - as_tibble(data)$biden)**2)
}

boosting_mse <- mse_boosting(biden_models$boosting, biden_split$test)
boosting_s1_mse <- mse_boosting(biden_models$boosting_s1, biden_split$test)
boosting_s2_mse <- mse_boosting(biden_models$boosting_s2, biden_split$test)
boosting_s3_mse <- mse_boosting(biden_models$boosting_s3, biden_split$test)

data_frame(shrinkage = c(0.1, 0.01, 0.001, 0.005),
           model = biden_models[c("boosting_s1", "boosting_s2","boosting", "boosting_s3")],
           mse = c(boosting_s1_mse, boosting_s2_mse, boosting_mse, boosting_s3_mse )) %>%
  select(-model) %>%
  knitr::kable(caption = "Influence of shrinkage parameter on the test MSE",
               col.names = c("shrinkage", "MSEs"))
```

Table 1: Influence of shrinkage parameter on the test MSE

| shrinkage | MSEs |
|---|---|
| 0.100 | 420 |
| 0.010 | 407 |
| 0.001 | 400 |
| 0.005 | 404 |

Test MSE of the boosting model with default setting is 399.716, which is only slightly smaller than those of previous models. In order to test the influence of shrinkage parameter on the performance of the model, we fitted three separate boosting models with shrinkage parameters 0.1, 0.01, 0.005 respectively. As the table indicates, as the shrinkage values decreases, the MSE also decreases, meaning that the models have better performance. Since shrinkage parameter controls the rate that boosting learns, this corresponds to the fact that generally statistical learning approaches that learn slowlier tend to perform better.

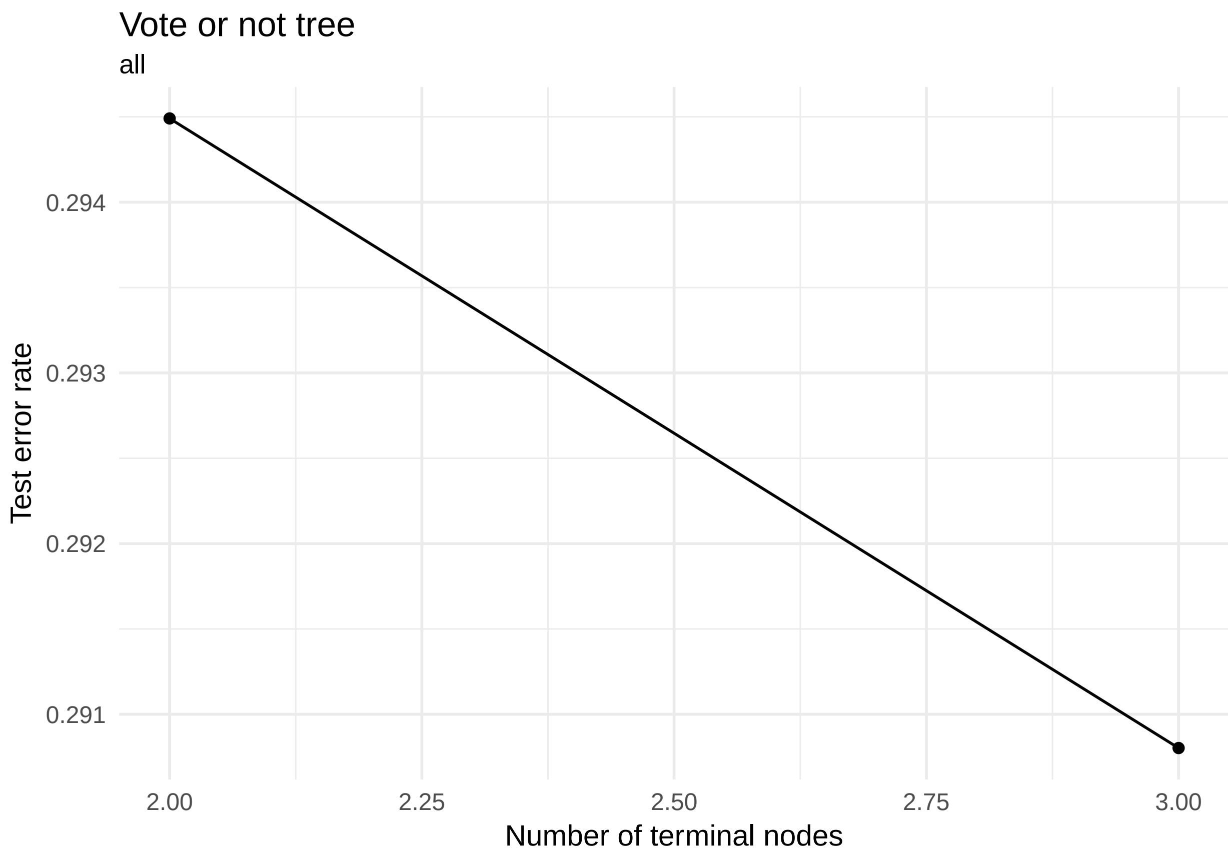
## Part 2: Modeling voter turnout

### 1. Use cross-validation techniques and standard measures of model fit (e.g. test error rate, PRE, ROC curves/AUC) to compare and evaluate at least five tree-based models of voter turnout. Select the best model and interpret the results using whatever methods you see fit (graphs, tables, model fit statistics, predictions for hypothetical observations, etc.)

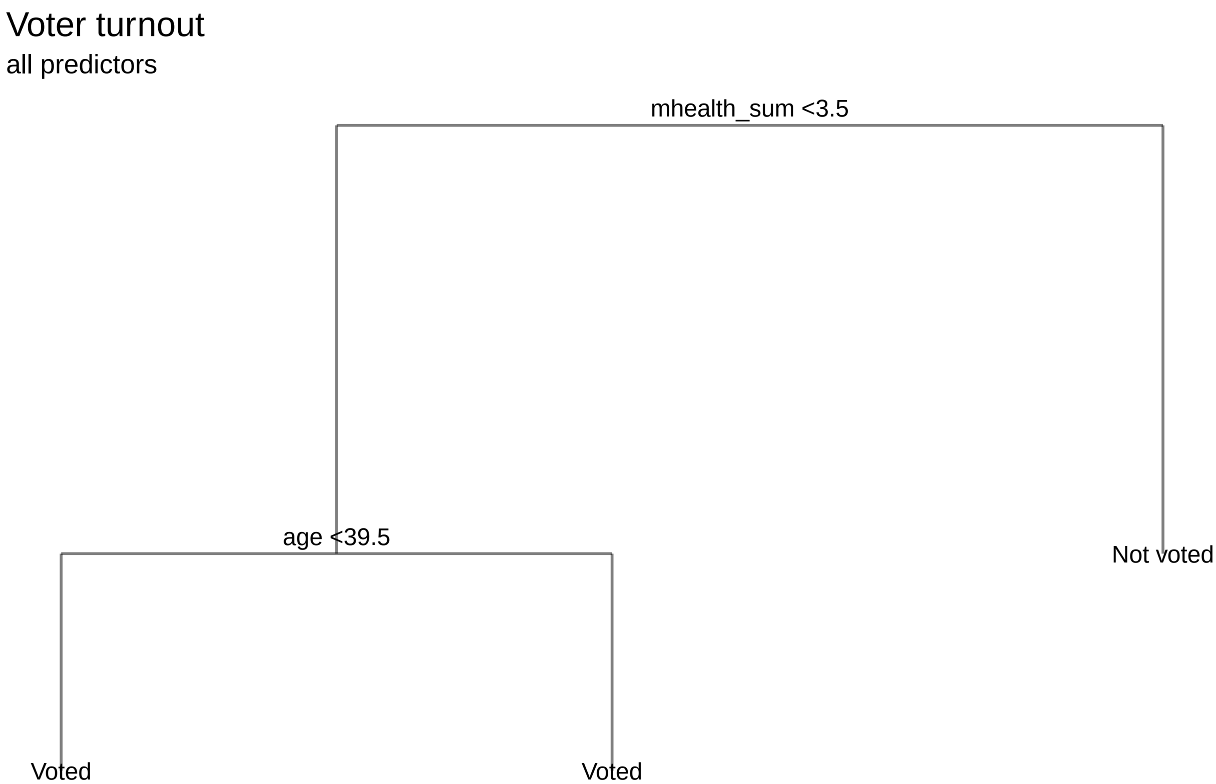
#### Decision tree

```
gss <- gss_data %>%
  as_tibble() %>%
  mutate(Voted = factor(vote96, levels = 0:1, labels = c("Not voted", "Voted")))

gss_split <- resample_partition(gss, c(test = 0.3, train = 0.7))
```

```r
# estimate model
gss_dt <- tree(Voted~ . - vote96, data = gss_split$train , control = tree.control(nobs = nrow(gss_split$

# generate 10-fold CV trees
gss_cv <- as.data.frame(gss_split$train)  %>%
  na.omit() %>%
  crossv_kfold(k = 10) %>%
  mutate(tree = map(train, ~ tree(Voted~ . - vote96, data = . ,
     control = tree.control(nobs = nrow(gss_split$train),
                            mindev = .001))))

# calculate each possible prune result for each fold
gss_cv <- expand.grid(gss_cv$.id,
                          seq(from = 2, to = ceiling(length(mod$frame$yval) / 2))) %>%
  as_tibble() %>%
  mutate(Var2 = as.numeric(Var2)) %>%
  rename(.id = Var1,
         k = Var2) %>%
  left_join(gss_cv) %>%
  mutate(prune = map2(tree, k, ~ prune.misclass(.x, best = .y)),
         mse = map2_dbl(prune, test, err.rate.tree))

gss_cv %>%
  group_by(k) %>%
  summarize(test_mse = mean(mse),
            sd = sd(mse, na.rm = TRUE)) %>%
  ggplot(aes(k, test_mse)) +
  geom_point() +
  geom_line() +
  labs(title = "Vote or not tree",
       subtitle = "all",
       x = "Number of terminal nodes",
       y = "Test error rate")
```




```r
#optimal number of terminal nodes is 3

# plot pruned tree
mod <- prune.tree(gss_dt, best = 3)

tree_data <- dendro_data(mod)
ggplot(segment(tree_data)) +
  geom_segment(aes(x = x, y = y, xend = xend, yend = yend),
               alpha = 0.5) +
  geom_text(data = label(tree_data),
            aes(x = x, y = y, label = label_full), vjust = -0.5, size = 3) +
  geom_text(data = leaf_label(tree_data),
            aes(x = x, y = y, label = label), vjust = 0.5, size = 3) +
  theme_dendro() +
  labs(title = "Voter turnout",
       subtitle = "all predictors")
```




```r
gss_dt_err <- err.rate.tree (mod, gss_split$test)

pred <- predict(mod, newdata = as_tibble(gss_split$test), type = "class")
roc_dt <- roc(response = as.numeric(as_tibble(gss_split$test)$Voted), predictor =as.numeric(pred))
auc_dt <- auc(roc_dt)
```

Performance of this decision tree model Test error rate: `R gss_dt_err` AUC: `R auc_dt`

## Bagging

```r
gss_train <- na.omit(as_tibble(gss_split$train))
gss_test <- na.omit(as_tibble(gss_split$test))

gss_bag <- randomForest(Voted ~ .-vote96, data = gss_train,
                             mtry = 7, ntree = 500)

gss_bag_err <- err.rate.tree (gss_bag, gss_test)
pred <- predict(gss_bag, newdata = gss_test, type = "class")
roc_bag <- roc(response = as.numeric(gss_test$Voted), predictor =as.numeric(pred))
auc_bag <- auc(roc_bag)

# data_frame(var = rownames(importance(biden_bag)),
#            MeanDecreaseGini = importance(biden_bag)[,1]) %>%
#   mutate(var = fct_reorder(var, MeanDecreaseGini, fun = median)) %>%
#   ggplot(aes(var, MeanDecreaseGini)) +
#   geom_point() +
#   coord_flip() +
#   labs(title = "Predicting Biden feeling thermometer score",
```

```r
#         subtitle = "Bagging",
#         x = NULL,
#         y = "Average decrease in the Gini Index")
```

Performance of this bagging model Test error rate: `R gss_bag_err` AUC: `R auc_bag`

## Random forest

```r
gss_rf <- randomForest(Voted ~ .-vote96, data = gss_train, ntree = 500)

gss_rf_err <- err.rate.tree (gss_rf, gss_test)
pred <- predict(gss_rf, newdata = gss_test, type = "class")
roc_rf <- roc(response = as.numeric(gss_test$Voted), predictor =as.numeric(pred))
auc_rf <- auc(roc_rf)
```

Performance of this random forest model Test error rate: `R gss_rf_err` AUC: `R auc_rf`

## Boosting

```r
gss_boosting1 <- gbm(vote96 ~ .-Voted, data = gss_train, n.trees = 10000,
                     interaction.depth = 1, shrinkage = 0.001)
```

```
## Distribution not specified, assuming bernoulli ...
```

```r
pred <- predict(gss_boosting1, newdata = gss_test, n.trees = 10000)

gss_b1_err <- mean((pred - gss_test$vote96)**2)
#pred <- predict(gss_boosting1, newdata = gss_test, type = "class")
roc_b1 <- roc(response = gss_test$vote96, predictor =pred)
auc_b1 <- auc(roc_b1)
```

Performance of this boosting model Test error rate: `R gss_b1_err` AUC: `R auc_b1`

## Boosting

```r
gss_boosting2 <-  gbm(vote96 ~ .-Voted, data = gss_train, n.trees = 10000,
                      interaction.depth = 4, shrinkage = 0.0002)
```

```
## Distribution not specified, assuming bernoulli ...
```

```r
pred <- predict(gss_boosting2, newdata = gss_test, n.trees = 10000)

gss_b2_err <- mean((pred - gss_test$vote96)**2)
roc_b2 <- roc(response = gss_test$vote96, predictor =pred)
auc_b2 <- auc(roc_b2)
```

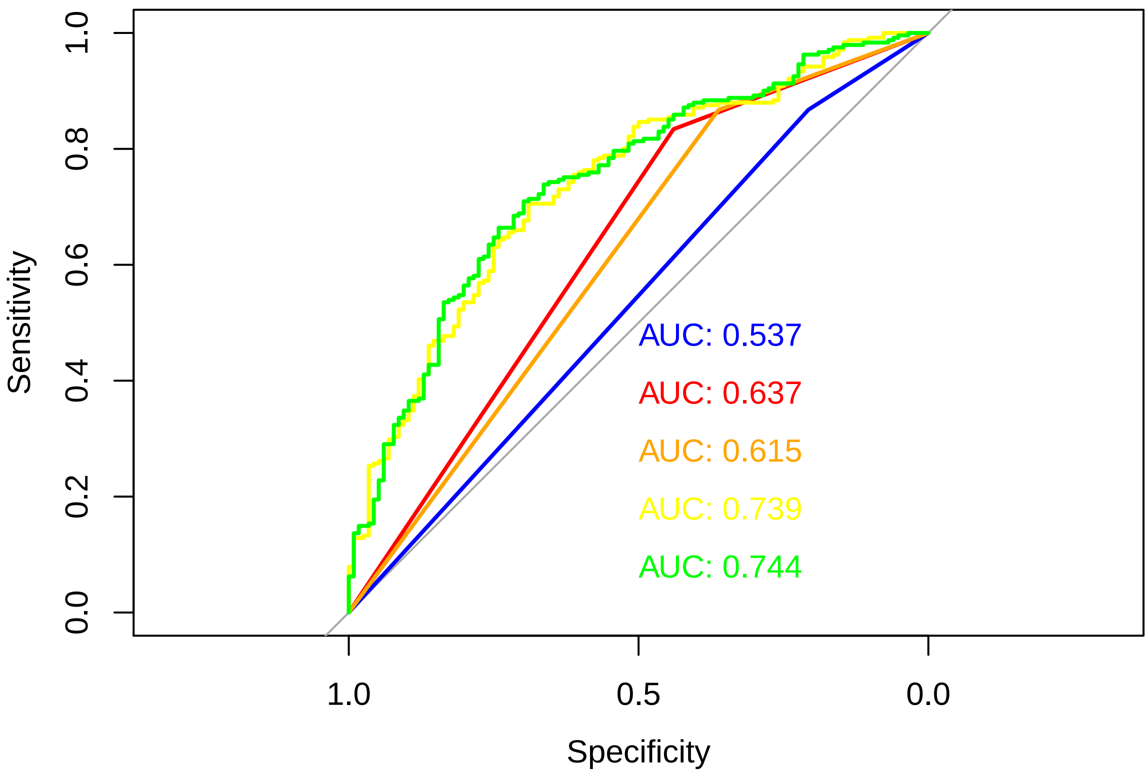
Performance of this boosting model Test error rate: `R gss_b2_err` AUC: `R auc_b2`

```r
data_frame(model = c("Decision tree", "Bagging", "Random forest", "Boosting1", "Boosting2"),
           error_rate = c(gss_dt_err, gss_bag_err, gss_rf_err, gss_b1_err,gss_b2_err),
           auc = c(auc_dt, auc_bag, auc_rf, auc_b1, auc_b2) )%>%
  knitr::kable(caption = "Comparison between five tree-based models",
               col.names = c("Model", "test error rate", "AUC"))
```

Table 2: Comparison between five tree-based models

| Model | test error rate | AUC |
|---|---|---|
| Decision tree | 0.348 | 0.537 |
| Bagging | 0.294 | 0.637 |
| Random forest | 0.297 | 0.615 |
| Boosting1 | 1.020 | 0.739 |
| Boosting2 | 0.549 | 0.744 |

```
plot(roc_dt, print.auc = TRUE, col = "blue")
plot(roc_bag, print.auc = TRUE, col = "red", print.auc.y = .4, add = TRUE)
plot(roc_rf, print.auc = TRUE, col = "orange", print.auc.y = .3, add = TRUE)
plot(roc_b1, print.auc = TRUE, col = "yellow", print.auc.y = .2, add = TRUE)
plot(roc_b2, print.auc = TRUE, col = "green", print.auc.y = .1, add = TRUE)
```




Comparing across all five tree based models, we can see that the one with the highest AUC, 0.744, is the second boosting model; however, the test error rate for this model is as high as 0.549. Since AUC shows the probability that a classifier will rank a randomly chosen positive instance higher than a randomly chosen negative one (assuming 'positive' ranks higher than 'negative'), and is the standard measurement for machine learning community to compare models. Since the test error rate is greatly depend on the split of test and training set, AUC could be a more robust measure. Thus, we will depend on AUC and choose the second boosting as our model. Due to the nature of boosting, it's very hard to interprate, we could only use ROC curve to visualize the performance.

**2. Use cross-validation techniques and standard measures of model fit (e.g. test error rate, PRE, ROC curves/AUC) to compare and evaluate at least five SVM models of voter turnout. Select the best model and interpret the results using whatever methods you see fit (graphs, tables, model fit statistics, predictions for hypothetical observations, etc.)**

```r
set.seed(1234)
#linear kernel with age + educ
gss_tune <- tune(svm, Voted ~ age + educ, data = gss_train,
                     kernel = "linear",
                     range = list(cost = c(.001, .01, .1, 1, 5, 10, 100)))
#summary(gss_tune)
gss_best <- gss_tune$best.model
summary(gss_best)
```

```
##
## Call:
## best.tune(method = svm, train.x = Voted ~ age + educ, data = gss_train,
##     ranges = list(cost = c(0.001, 0.01, 0.1, 1, 5, 10, 100)),
##     kernel = "linear")
##
##
## Parameters:
##    SVM-Type:  C-classification
##  SVM-Kernel:  linear
##        cost:  5
##       gamma:  0.5
##
## Number of Support Vectors:  523
##
##  ( 262 261 )
##
##
## Number of Classes:  2
##
## Levels:
##  Not voted Voted
```

```r
# get predictions for test set
fitted <- predict(gss_best, gss_test, decision.values = TRUE) %>%
  attributes

roc_1 <- roc(gss_test$Voted, fitted$decision.values)
#plot(roc_1)
auc_1 <- auc(roc_1)

# sum_err_1 <- mean(fitted != actual, na.rm = TRUE))
# round(fitted$decision.values)+1
```

```r
set.seed(1234)
#polynomial kernel with age+ educ
gss_poly_tune <- tune(svm, Voted ~ age + educ, data = gss_train,
                     kernel = "polynomial",
                     range = list(cost = c(.001, .01, .1, 1, 5, 10, 100)))
```

```r
#summary(gss_poly_tune)
gss_poly_best <- gss_poly_tune$best.model
summary(gss_poly_best)
```

```
##
## Call:
## best.tune(method = svm, train.x = Voted ~ age + educ, data = gss_train,
##     ranges = list(cost = c(0.001, 0.01, 0.1, 1, 5, 10, 100)),
##     kernel = "polynomial")
##
##
## Parameters:
##    SVM-Type:  C-classification
##  SVM-Kernel:  polynomial
##        cost:  5
##      degree:  3
##       gamma:  0.5
##      coef.0:  0
##
## Number of Support Vectors:  508
##
##  ( 255 253 )
##
##
## Number of Classes:  2
##
## Levels:
##  Not voted Voted
```

```r
# get predictions for test set
fitted <- predict(gss_poly_best, gss_test, decision.values = TRUE) %>%
  attributes

roc_2 <- roc(gss_test$Voted, fitted$decision.values)
#plot(roc_2)
auc_2 <- auc(roc_2)
```

```r
set.seed(1234)
#radical kernel with age+ educ
gss_rad_tune <- tune(svm, Voted ~ age + educ, data = gss_train,
                     kernel = "radial",
                     range = list(cost = c(.001, .01, .1, 1, 5, 10, 100)))

gss_rad_best <- gss_rad_tune$best.model
summary(gss_rad_best)
```

```
##
## Call:
## best.tune(method = svm, train.x = Voted ~ age + educ, data = gss_train,
##     ranges = list(cost = c(0.001, 0.01, 0.1, 1, 5, 10, 100)),
##     kernel = "radial")
##
##
## Parameters:
##    SVM-Type:  C-classification
```

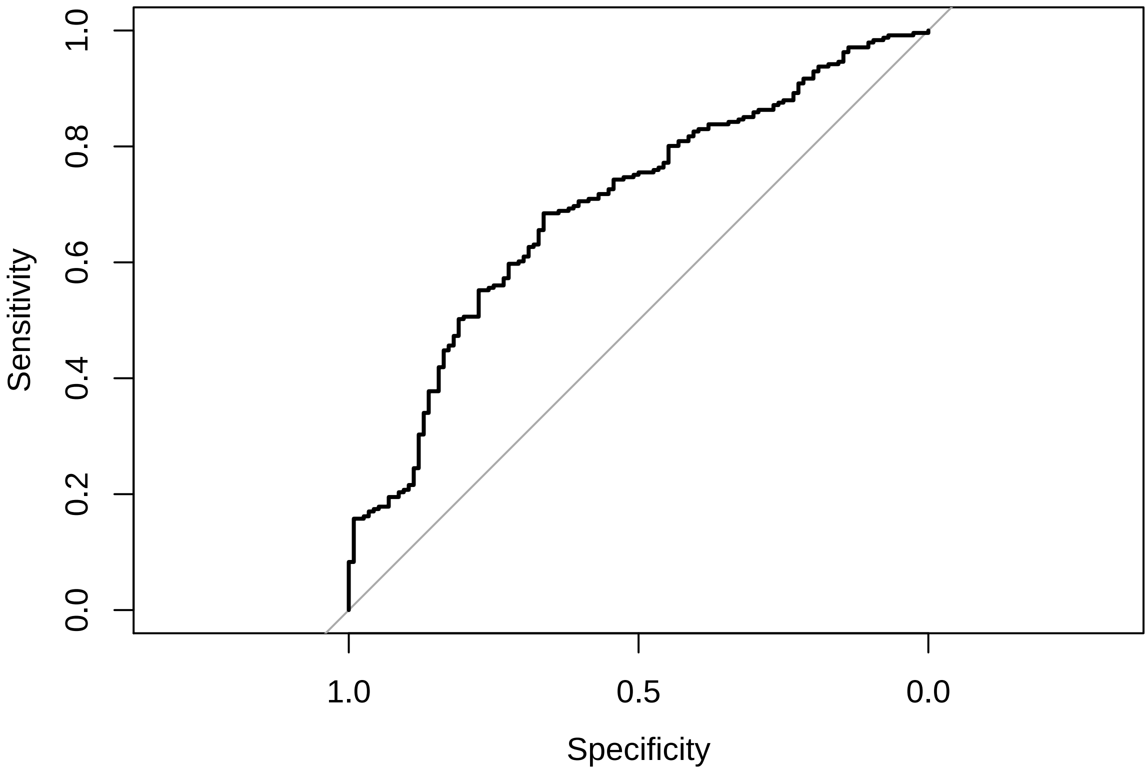
```
##  SVM-Kernel:  radial
##        cost:  5
##       gamma:  0.5
##
## Number of Support Vectors:  496
##
##  ( 260 236 )
##
##
## Number of Classes:  2
##
## Levels:
##  Not voted Voted
```

```r
# get predictions for test set
fitted <- predict(gss_rad_best, gss_test, decision.values = TRUE) %>%
  attributes

roc_3 <- roc(gss_test$Voted, fitted$decision.values)
#plot(roc_3)
auc_3 <- auc(roc_3)
```

```r
set.seed(1234)
#polynomial kernel with age+ educ
gss_poly_tune2 <- tune(svm, Voted ~ .-vote96, data = gss_train,
                     kernel = "polynomial",
                     range = list(cost = c(.001, .01, .1, 1, 5, 10, 100)))
#summary(gss_poly_tune)
gss_poly_best2 <- gss_poly_tune2$best.model
summary(gss_poly_best2)
```

```
##
## Call:
## best.tune(method = svm, train.x = Voted ~ . - vote96, data = gss_train,
##     ranges = list(cost = c(0.001, 0.01, 0.1, 1, 5, 10, 100)),
##     kernel = "polynomial")
##
##
## Parameters:
##    SVM-Type:  C-classification
##  SVM-Kernel:  polynomial
##        cost:  5
##      degree:  3
##       gamma:  0.143
##      coef.0:  0
##
## Number of Support Vectors:  482
##
##  ( 251 231 )
##
##
## Number of Classes:  2
##
## Levels:
##  Not voted Voted
```

```r
# get predictions for test set
fitted <- predict(gss_poly_best2, gss_test, decision.values = TRUE) %>%
  attributes

roc_4 <- roc(gss_test$Voted, fitted$decision.values)
plot(roc_4)
```



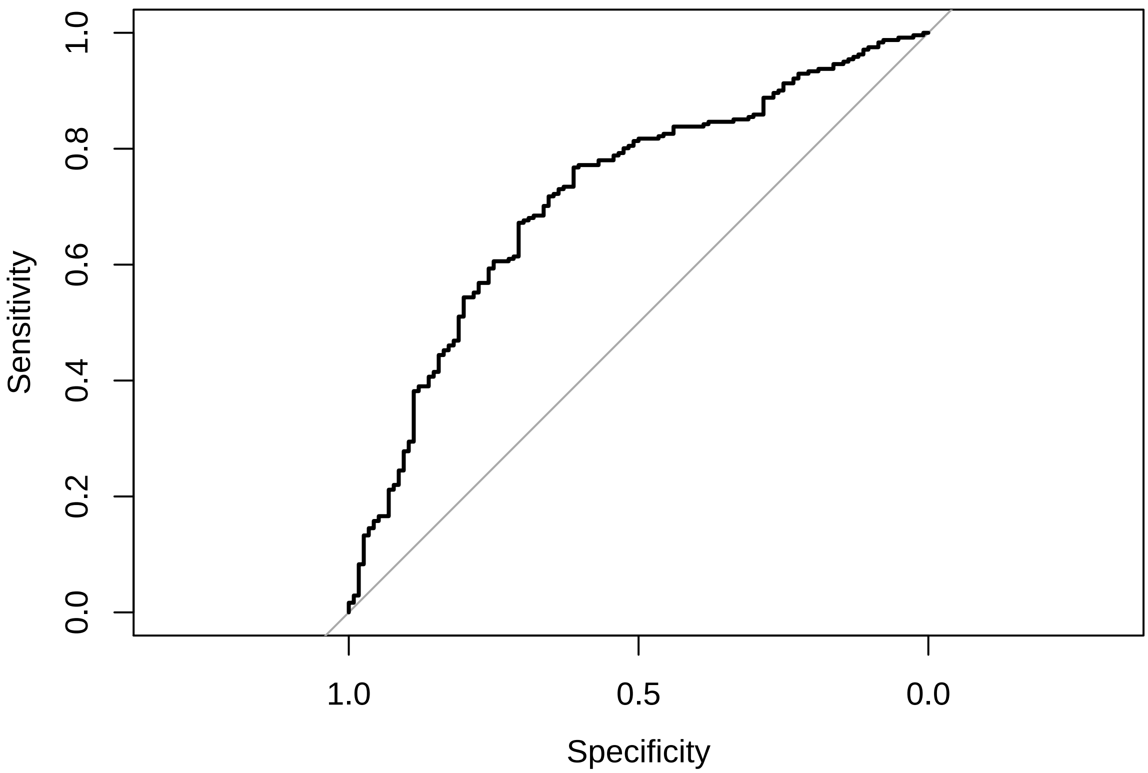

```r
auc_4 <- auc(roc_4)
```

```r
set.seed(1234)
#radical kernel with age+ educ
gss_rad_tune2 <- tune(svm, Voted ~ .-vote96, data = gss_train,
                     kernel = "radial",
                     range = list(cost = c(.001, .01, .1, 1, 5, 10, 100)))

gss_rad_best2 <- gss_rad_tune2$best.model
summary(gss_rad_best2)
```

```
##
## Call:
## best.tune(method = svm, train.x = Voted ~ . - vote96, data = gss_train,
##     ranges = list(cost = c(0.001, 0.01, 0.1, 1, 5, 10, 100)),
##     kernel = "radial")
##
##
## Parameters:
##    SVM-Type:  C-classification
##  SVM-Kernel:  radial
##        cost:  1
##       gamma:  0.143
```

```
##
## Number of Support Vectors:  504
##
##  ( 268 236 )
##
##
## Number of Classes:  2
##
## Levels:
##  Not voted Voted
```

```
# get predictions for test set
fitted <- predict(gss_rad_best2, gss_test, decision.values = TRUE) %>%
  attributes

roc_5 <- roc(gss_test$Voted, fitted$decision.values)
plot(roc_5)
```




```
auc_5 <- auc(roc_5)
```

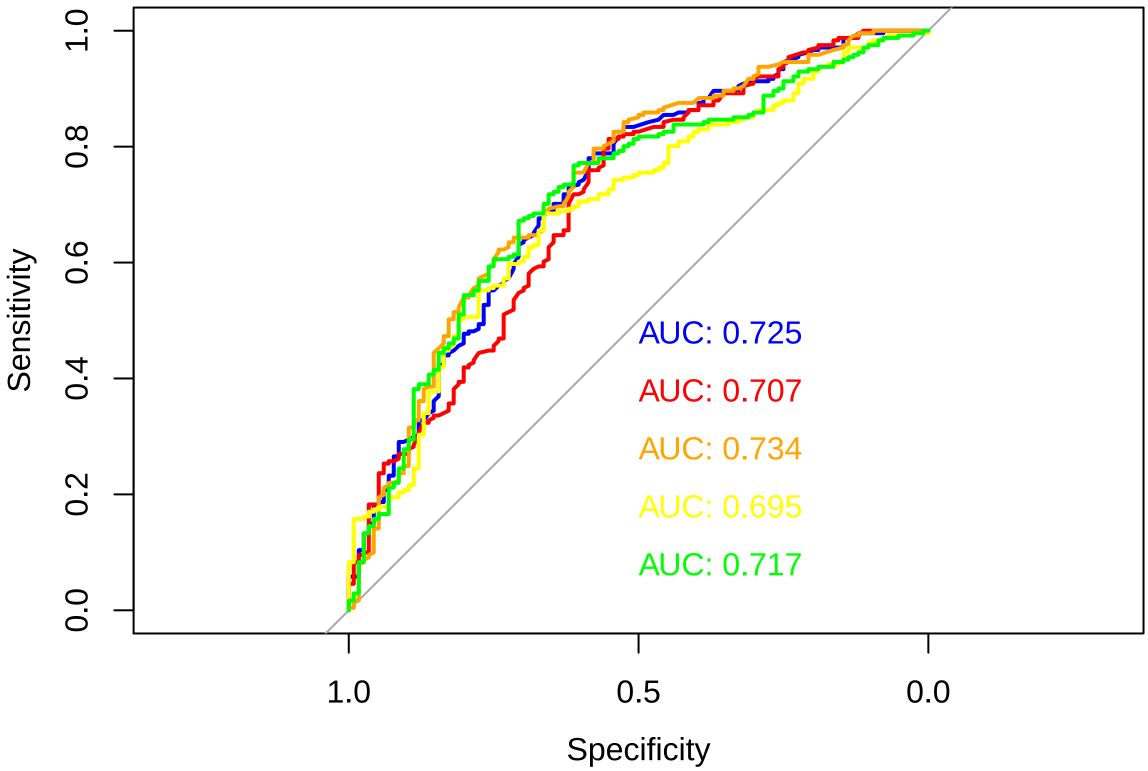
```
data_frame(model = c("Linear with two variables", "Polynomial with two variables", "Radial with two vari
           error_rate = c(gss_dt_err, gss_bag_err, gss_rf_err, gss_b1_err,gss_b2_err),
           auc = c(auc_1, auc_2, auc_3, auc_4, auc_5) )%>%
  knitr::kable(caption = "Comparison between five svm models",
               col.names = c("Model", "test error rate", "AUC"))
```

Table 3: Comparison between five svm models

| Model | test error rate | AUC |
|---|---|---|
| Linear with two variables | 0.348 | 0.725 |

| Model | test error rate | AUC |
|---|---|---|
| Polynomial with two variables | 0.294 | 0.707 |
| Radial with two variables | 0.297 | 0.734 |
| Polynomial with all | 1.020 | 0.695 |
| Radial with all | 0.549 | 0.717 |

```
plot(roc_1, print.auc = TRUE, col = "blue")
plot(roc_2, print.auc = TRUE, col = "red", print.auc.y = .4, add = TRUE)
plot(roc_3, print.auc = TRUE, col = "orange", print.auc.y = .3, add = TRUE)
plot(roc_4, print.auc = TRUE, col = "yellow", print.auc.y = .2, add = TRUE)
plot(roc_5, print.auc = TRUE, col = "green", print.auc.y = .1, add = TRUE)
```




From question 1, we've realized that both age and education are very important parameters to predict voter turnout. Thus, we started training svm models using these two variables. After comparing AUCs of all five models, we can see that the AUC values of these models are very almost the same, all around 0.744. Comparing the test error rate, the SVM model with polynomial kernel using two variables has the smallest value, 0.294. Thus, we will pick this as our best model.

## Part 3: OJ Simpson

### 1. What is the relationship between race and belief of OJ Simpson's guilt? Develop a robust statistical learning model and use this model to explain the impact of an individual's race on their beliefs about OJ Simpson's guilt.

We observe that the two variables that's related to race are `black` and `hispanic`, so we'll use these two variables for different models. Since we want to predict whether individuals believe Simpson to be guilty or not, it is a binary classification problem. Naturally, we would choose to fit a logistic model in "binomial" family.

## Logistic

```
set.seed(1234)
s_split <- resample_partition(s_data, c(test = 0.3, train = 0.7))
s_train <- na.omit(as_tibble(s_split$train))
s_test <- na.omit(as_tibble(s_split$test))

getProb <- function(model, data){
  data <- data %>%
    add_predictions(model) %>%
    mutate(prob = exp(pred) / (1 + exp(pred)),
           pred_bi = as.numeric(prob > .5))
  return(data)
}

 # function to calculate PRE for a logistic regression model
PRE <- function(model){
  # get the actual values for y from the data
  y <- model$y
  # get the predicted values for y from the model
  y.hat <- round(model$fitted.values)
  # calculate the errors for the null model and your model
  E1 <- sum(y != median(y))
  E2 <- sum(y != y.hat)
  # calculate the proportional reduction in error
  PRE <- (E1 - E2) / E1
return(PRE) }


s_logistic <- glm(guilt ~ black + hispanic, data = s_train, family = binomial)
tidy(s_logistic)
```

```
##          term estimate std.error statistic  p.value
## 1 (Intercept)    1.459    0.0938     15.55 1.68e-54
## 2       black   -3.053    0.2169    -14.07 5.64e-45
## 3    hispanic   -0.539    0.2846     -1.89 5.83e-02
```

```
glance(s_logistic)
```

```
##   null.deviance df.null logLik AIC BIC deviance df.residual
## 1          1233     986   -478 963 978      957         984
```

```
s_log_test <- getProb(s_logistic, s_test)

#ROC
roc_1 <- roc(s_log_test$guilt, s_log_test$pred_bi)
auc_1 <- auc(s_log_test$guilt, s_log_test$pred_bi)
auc_1
```

```
## Area under the curve: 0.744
```

```
pre_1 <- PRE(s_logistic)
pre_1
```

```
## [1] 0.399
```

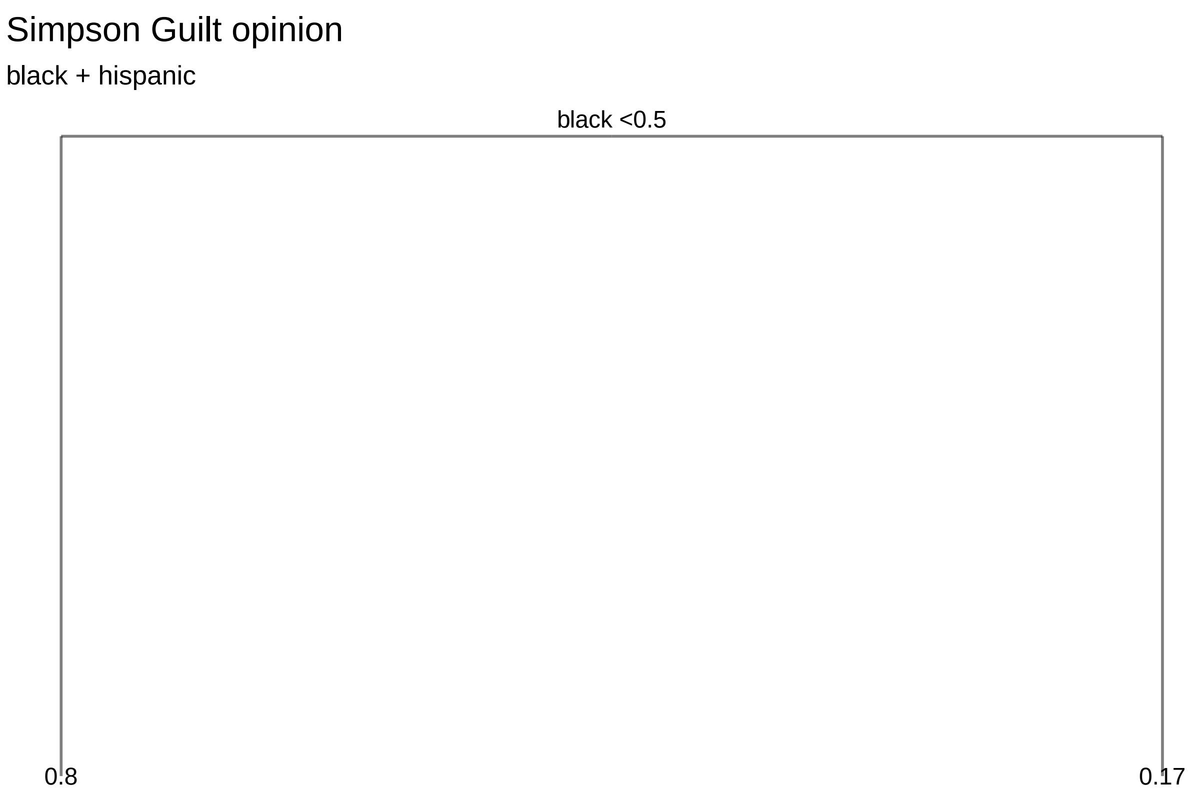
```
err_1 <- 1- mean(s_log_test$guilt == s_log_test$pred_bi, na.rm = TRUE)
err_1
```

```
## [1] 0.17
```

Since tree-based method and SVMs are all classic methods for classification in machine learning, we could try to fit decision trees and SVMs using these two variables. I choose decision tree as the second model because it's very easy to interpret compared to boosting.

### Decision tree

```
set.seed(1234)
s_dt <- tree(guilt ~ black + hispanic, data = s_train)

# plot pruned tree
mod <- s_dt

tree_data <- dendro_data(mod)
ggplot(segment(tree_data)) +
  geom_segment(aes(x = x, y = y, xend = xend, yend = yend),
               alpha = 0.5) +
  geom_text(data = label(tree_data),
            aes(x = x, y = y, label = label_full), vjust = -0.5, size = 3) +
  geom_text(data = leaf_label(tree_data),
            aes(x = x, y = y, label = label), vjust = 0.5, size = 3) +
  theme_dendro() +
  labs(title = "Simpson Guilt opinion",
       subtitle = "black + hispanic")
```




```
pred <- predict(s_dt, newdata = s_test, n.trees = 10000)

err_2 <- 1- mean(s_test$guilt == round(pred))


roc_2 <- roc(response = s_test$guilt, predictor = pred)
auc_2 <- auc(roc_2)
```

The third model that I'm trying to use is boosting because even though it's like a black box and hard to interpret, it has given me the highest AUC values from Question 2. Maybe it will work great here as well.

### Boosting

```
set.seed(1234)
s_boosting <-  gbm(guilt ~  black + hispanic, data = s_train, n.trees = 10000, interaction.depth = 4, sh
```

```
## Distribution not specified, assuming bernoulli ...
```

```
pred <- predict(s_boosting, newdata = s_test, n.trees = 10000)

err_3 <- 1- mean(s_test$guilt == round(pred))
roc_3 <- roc(response = s_test$guilt, predictor =pred)
auc_3 <- auc(roc_3)
```

The last two models that I'm trying are the SVM with a linear kernel with both `age` and `educ` and SVM with polynomial kernel with both variables. Since we've learnt that these two variables are very important from the previous models, we can safely depend on them.

### SVM with linear kernel

```r
set.seed(1234)
#polynomial kernel with age+ educ
s_linear_tune <- tune(svm, guilt ~ black + hispanic, data = s_train,
                     kernel = "linear",
                     range = list(cost = c(.001, .01, .1, 1, 5, 10, 100)))
#summary(gss_poly_tune)
s_linear_best <- s_linear_tune$best.model
summary(s_linear_best)
```

```
##
## Call:
## best.tune(method = svm, train.x = guilt ~ black + hispanic, data = s_train,
##     ranges = list(cost = c(0.001, 0.01, 0.1, 1, 5, 10, 100)),
##     kernel = "linear")
##
##
## Parameters:
##    SVM-Type:  eps-regression
##  SVM-Kernel:  linear
##        cost:  1
##       gamma:  0.5
##     epsilon:  0.1
##
##
## Number of Support Vectors:  378
```

```r
# get predictions for test set
fitted <- predict(s_linear_best, s_test, decision.values = TRUE) %>%
  attributes

err_4 <- 1- mean(s_test$guilt == round(fitted$decision.values))
roc_4 <- roc(s_test$guilt, fitted$decision.values)
#plot(roc_5)
auc_4 <- auc(roc_4)
```

### SVM with polynomial kernel

```r
set.seed(1234)
#polynomial kernel with age+ educ
s_poly_tune <- tune(svm, guilt ~ black + hispanic, data = s_train,
                     kernel = "polynomial",
                     range = list(cost = c(.001, .01, .1, 1, 5, 10, 100)))
#summary(gss_poly_tune)
s_poly_best <- s_poly_tune$best.model
summary(s_poly_best)
```

```
##
## Call:
## best.tune(method = svm, train.x = guilt ~ black + hispanic, data = s_train,
##     ranges = list(cost = c(0.001, 0.01, 0.1, 1, 5, 10, 100)),
##     kernel = "polynomial")
```

```
##
##
## Parameters:
##    SVM-Type:  eps-regression
##  SVM-Kernel:  polynomial
##        cost:  0.1
##      degree:  3
##       gamma:  0.5
##      coef.0:  0
##     epsilon:  0.1
##
##
## Number of Support Vectors:  382
```

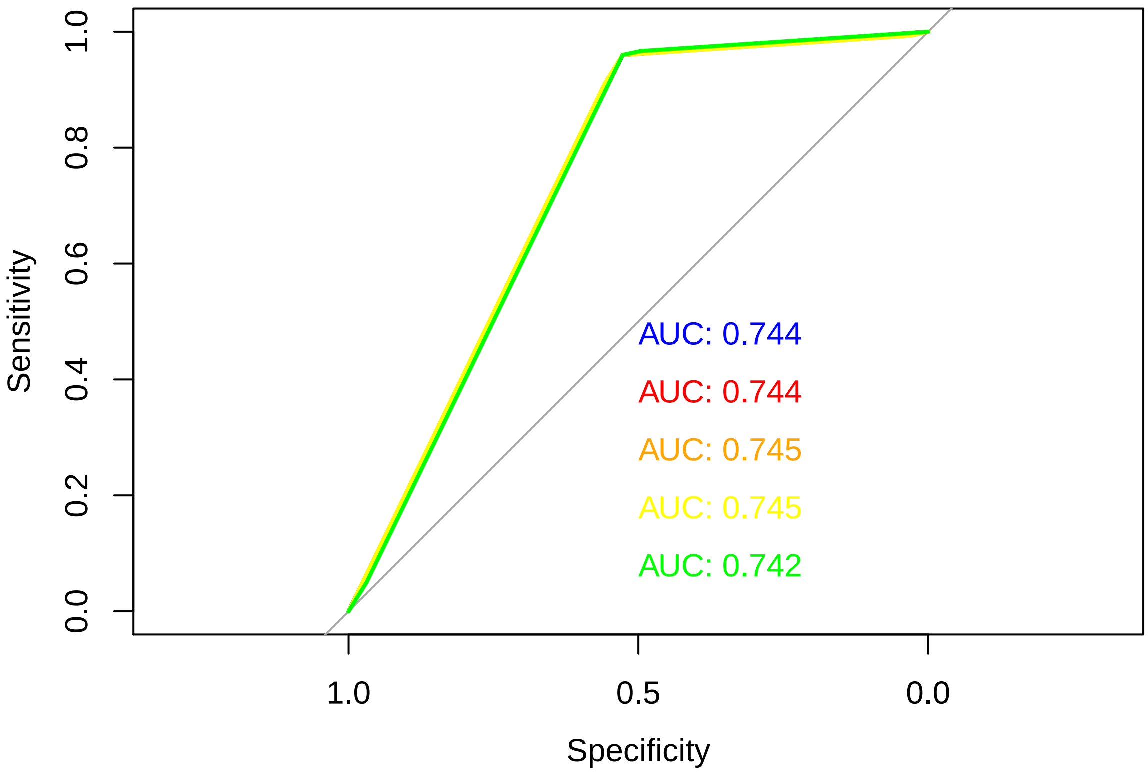
```
# get predictions for test set
fitted <- predict(s_poly_best, s_test, decision.values = TRUE) %>%
  attributes

err_5 <- 1- mean(s_test$guilt == round(fitted$decision.values))
roc_5 <- roc(s_test$guilt, fitted$decision.values)
#plot(roc_5)
auc_5 <- auc(roc_5)
```

```
data_frame(model = c("Logistic", "Decision Tree", "Boosting", "SVM with linear kernel", "SVM with radial
           error_rate = c(err_1, err_2, err_3, err_4, err_5),
           auc = c(auc_1, auc_2, auc_3, auc_4, auc_5) )%>%
  knitr::kable(caption = "Comparison between five models",
               col.names = c("Model", "test error rate", "AUC"))
```

Table 4: Comparison between five models

| Model | test error rate | AUC |
|---|---|---|
| Logistic | 0.170 | 0.744 |
| Decision Tree | 0.170 | 0.744 |
| Boosting | 0.329 | 0.745 |
| SVM with linear kernel | 0.329 | 0.745 |
| SVM with radial kernel | 0.329 | 0.742 |

```
plot(roc_1, print.auc = TRUE, col = "blue")
plot(roc_2, print.auc = TRUE, col = "red", print.auc.y = .4, add = TRUE)
plot(roc_3, print.auc = TRUE, col = "orange", print.auc.y = .3, add = TRUE)
plot(roc_4, print.auc = TRUE, col = "yellow", print.auc.y = .2, add = TRUE)
plot(roc_5, print.auc = TRUE, col = "green", print.auc.y = .1, add = TRUE)
```




Just like the previous question, we get very similar AUC values for all five models. All are around 0.744. Among the five, both logistic and decision tree have a test error rate of 0.17, which is pretty impressive given the simplicity of these models. This might show us that when we do not have a huge dataset, simpler algorithms could work just fine or even better than fancy algorithms.

We could choose decision tree as our best model due to it's simplicity. From the tree, we observe that `black` is the only parameter that's used. If an individual is black, he/she will believe that Simpson is not guilty; otherwise, he/she will believe that he's not guity.

## 2. How can you predict whether individuals believe OJ Simpson to be guilty of these murders? Develop a robust statistical learning model to predict whether individuals believe OJ Simpson to be either probably guilty or probably not guilty and demonstrate the effectiveness of this model using methods we have discussed in class.

### Logistic

```
s_2_log <- glm(guilt ~ ., data = s_train, family = binomial)
tidy(s_2_log)
```

```
##                                  term estimate std.error statistic
## 1                         (Intercept)   0.9784    0.4270    2.2912
## 2                                 dem   0.1200    0.2699    0.4448
## 3                                 rep   0.5283    0.2820    1.8737
## 4                                 age   0.0182    0.0053    3.4297
## 5                   educHIGH SCHOOL GRAD  -0.3389    0.2302   -1.4723
## 6                educNOT A HIGH SCHOOL GRAD  -1.2756    0.3517   -3.6267
## 7                         educREFUSED  13.6738  572.4217    0.0239
```

```
## 8  educSOME COLLEGE(TRADE OR BUSINESS)  -0.2520    0.2372   -1.0625
## 9                              female  -0.1972    0.1757   -1.1218
## 10                              black  -2.8875    0.2285  -12.6373
## 11                           hispanic  -0.3725    0.2969   -1.2548
## 12               income$30,000-$50,000  -0.2924    0.2313   -1.2644
## 13               income$50,000-$75,000  -0.0182    0.3059   -0.0596
## 14                  incomeOVER $75,000   0.3750    0.3741    1.0026
## 15              incomeREFUSED/NO ANSWER  -1.3029    0.3706   -3.5157
## 16                 incomeUNDER $15,000  -0.2716    0.2929   -0.9273
##     p.value
## 1  2.20e-02
## 2  6.56e-01
## 3  6.10e-02
## 4  6.04e-04
## 5  1.41e-01
## 6  2.87e-04
## 7  9.81e-01
## 8  2.88e-01
## 9  2.62e-01
## 10 1.31e-36
## 11 2.10e-01
## 12 2.06e-01
## 13 9.52e-01
## 14 3.16e-01
## 15 4.39e-04
## 16 3.54e-01
```

```r
glance(s_2_log)
```

```
##   null.deviance df.null logLik AIC  BIC deviance df.residual
## 1          1233     986   -450 932 1011      900         971
```

```r
s_log_test <- getProb(s_2_log, s_test)

#ROC
roc2_1 <- roc(s_log_test$guilt, s_log_test$pred_bi)
auc2_1 <- auc(s_log_test$guilt, s_log_test$pred_bi)
auc2_1
```

```
## Area under the curve: 0.75
```

```r
pre2_1 <- PRE(s_2_log)
pre2_1
```

```
## [1] 0.415
```

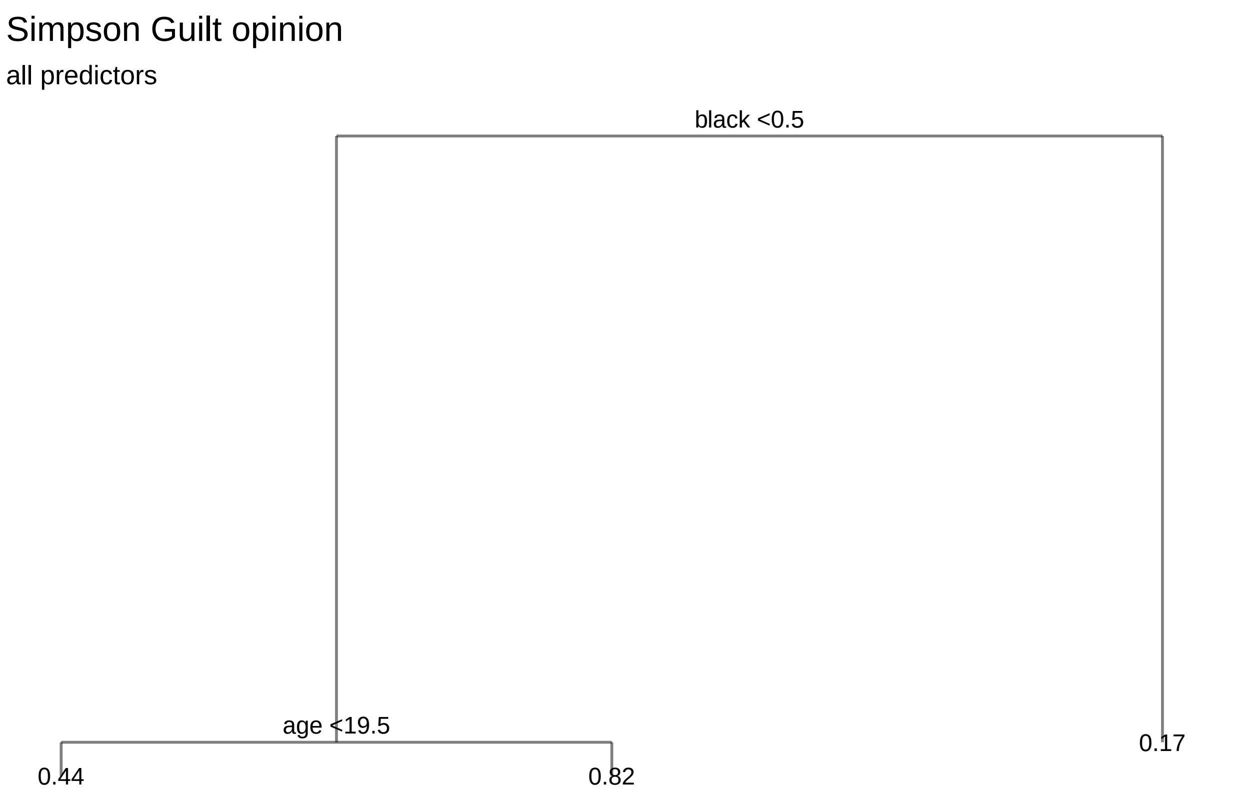
```r
err2_1 <- 1- mean(s_log_test$guilt == s_log_test$pred_bi, na.rm = TRUE)
err2_1
```

```
## [1] 0.17
```

## Decision Tree

```r
set.seed(1234)
s_2_dt <- tree(guilt ~ ., data = s_train)
```

```r
# plot pruned tree
mod <- s_2_dt

tree_data <- dendro_data(mod)
ggplot(segment(tree_data)) +
  geom_segment(aes(x = x, y = y, xend = xend, yend = yend),
               alpha = 0.5) +
  geom_text(data = label(tree_data),
            aes(x = x, y = y, label = label_full), vjust = -0.5, size = 3) +
  geom_text(data = leaf_label(tree_data),
            aes(x = x, y = y, label = label), vjust = 0.5, size = 3) +
  theme_dendro() +
  labs(title = "Simpson Guilt opinion",
       subtitle = "all predictors")
```




```r
pred <- predict(s_2_dt, newdata = s_test, n.trees = 10000)

err2_2 <- 1- mean(s_test$guilt == round(pred))


roc2_2 <- roc(response = s_test$guilt, predictor = pred)
auc2_2 <- auc(roc2_2)
```

### Boosting

```r
set.seed(1234)
s_2_boosting <-  gbm(guilt ~  ., data = s_train, n.trees = 10000)
```

```
## Distribution not specified, assuming bernoulli ...
```

```
pred <- predict(s_2_boosting, newdata = s_test, n.trees = 10000)

err2_3 <- 1- mean(s_test$guilt == round(pred))
roc2_3 <- roc(response = s_test$guilt, predictor =pred)
auc2_3 <- auc(roc2_3)
```

### SVM with linear kernel

```
set.seed(1234)
s_2_linear_tune <- tune(svm, guilt ~ black + age, data = s_train,
                       kernel = "linear",
                       range = list(cost = c(.001, .01, .1, 1, 5, 10, 100)))
#summary(gss_poly_tune)
s_2_linear_best <- s_2_linear_tune$best.model
summary(s_2_linear_best)
```

```
##
## Call:
## best.tune(method = svm, train.x = guilt ~ black + age, data = s_train,
##     ranges = list(cost = c(0.001, 0.01, 0.1, 1, 5, 10, 100)),
##     kernel = "linear")
##
##
## Parameters:
##    SVM-Type:  eps-regression
##  SVM-Kernel:  linear
##        cost:  10
##       gamma:  0.5
##     epsilon:  0.1
##
##
## Number of Support Vectors:  384
```

```
# get predictions for test set
fitted <- predict(s_2_linear_best, s_test, decision.values = TRUE) %>%
  attributes

err2_4 <- 1- mean(s_test$guilt == round(fitted$decision.values))
roc2_4 <- roc(s_test$guilt, fitted$decision.values)
auc2_4 <- auc(roc2_4)
```

### SVM with polynomial kernel

```
set.seed(1234)
#polynomial kernel
s_2_poly_tune <- tune(svm, guilt ~ black + age, data = s_train,
                     kernel = "polynomial",
                     range = list(cost = c(.001, .01, .1, 1, 5, 10, 100)))
#summary(gss_poly_tune)
s_2_poly_best <- s_2_poly_tune$best.model
```

```r
summary(s_2_poly_best)
```

```
##
## Call:
## best.tune(method = svm, train.x = guilt ~ black + age, data = s_train,
##     ranges = list(cost = c(0.001, 0.01, 0.1, 1, 5, 10, 100)),
##     kernel = "polynomial")
##
##
## Parameters:
##    SVM-Type:  eps-regression
##  SVM-Kernel:  polynomial
##        cost:  0.1
##      degree:  3
##       gamma:  0.5
##      coef.0:  0
##     epsilon:  0.1
##
##
## Number of Support Vectors:  390
```

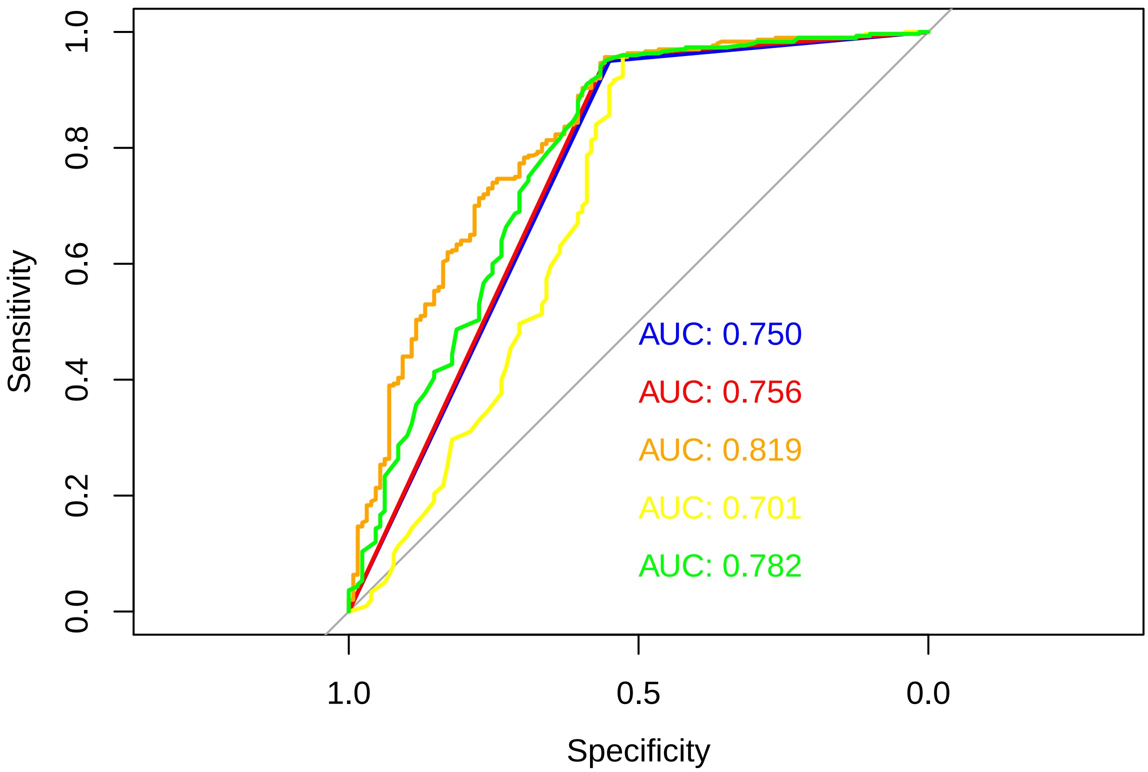
```r
# get predictions for test set
fitted <- predict(s_2_poly_best, s_test, decision.values = TRUE) %>%
  attributes

err2_5 <- 1- mean(s_test$guilt == round(fitted$decision.values))
roc2_5 <- roc(s_test$guilt, fitted$decision.values)
#plot(roc_5)
auc2_5 <- auc(roc2_5)
```

```r
data_frame(model = c("Logistic", "Decision Tree", "Boosting", "SVM with linear kernel", "SVM with radial
           error_rate = c(err2_1, err2_2, err2_3, err2_4, err2_5),
           auc = c(auc2_1, auc2_2, auc2_3, auc2_4, auc2_5) )%>%
  knitr::kable(caption = "Comparison between five models",
               col.names = c("Model", "test error rate", "AUC"))
```

Table 5: Comparison between five models

| Model | test error rate | AUC |
|---|---|---|
| Logistic | 0.170 | 0.750 |
| Decision Tree | 0.168 | 0.756 |
| Boosting | 0.748 | 0.819 |
| SVM with linear kernel | 0.329 | 0.701 |
| SVM with radial kernel | 0.329 | 0.782 |

```r
plot(roc2_1, print.auc = TRUE, col = "blue")
plot(roc2_2, print.auc = TRUE, col = "red", print.auc.y = .4, add = TRUE)
plot(roc2_3, print.auc = TRUE, col = "orange", print.auc.y = .3, add = TRUE)
plot(roc2_4, print.auc = TRUE, col = "yellow", print.auc.y = .2, add = TRUE)
plot(roc2_5, print.auc = TRUE, col = "green", print.auc.y = .1, add = TRUE)
```




For same reasons as question1, we've chosen logistic, tree-based models and svms for this question. Since we've observed that both black and age are the most important variables for this question, we decided to use these two variables for SVMs instead of using all variables to avoid long running time.

We could observe from the ROC curve that the model with highest AUC is the boosting model and its AUC is as high as 0.819; however, it also has an incredibly high test rate as 0.748. We would choose the decision tree as our best model for this case, since it has a reasonably high AUC, 0.756 compared to the other models. It also has the lowest test error rate, 0.748. More importantly, we're able to easily interprate the result.

According to the tree, individuals that are not black but are youger than 19.5 would believe that Simpson is not guilty. Individuals that are not black but are older than 19.5 would believe that Simpson is guilty. Individuals that are black would believe that Simpson is not guilty. Interpreting this finding, we could see that being black or not is almost deterministic for the opinion of individuals.