Li_Hengle_hw5

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Conceptual: Cost functions for classification trees

1. (15 points) Consider the Gini index, classification error, and cross-entropy in simple classification settings with two classes. Of these three possible cost functions, which would be best to use when growing a decision tree? Which would be best to use when pruning a decision tree? Why?

- The Gini index is the best in growing a decision tree in a setting with two classes. The algorithm of the decision tree aims to find the feature and splitting value that leads to the largest information gain. In a two-class case, say 4 balls of either red color or blue color, the information gain is: `IG = I(D0) - (N1/N0)*I(D1) - (N2/N0)*I(D2)`, where I can be entropy, Gini index, or classification error, and D0, D1, D2 are the dataset of the parent and children nodes. The information gain for classification error is the same whether one slipts the 4 balls by 2:2 or 1:3, while entropy and Gini index will point to 1:3. Between the latter two, repeating the same experiment would show that Gini index can produce a higher information gain than entropy.
- Classification error rate is the best in pruning a decision tree. The goal of pruning is to simplify decision trees that overfit the data. In this respect, classification error rate is more sensitive to overfitting than the other two measures, which makes it more preferable.

Application: Predicting attitudes towards racist college professors

In this problem set, you are going to predict attitudes towards racist college professors, using the GSS survey data. Specifically, each respondent was asked "Should a person who believes that Blacks are genetically inferior be allowed to teach in a college or university?" Given the kerfuffle over Richard J. Herrnstein and Charles Murray's *The Bell Curve* and the ostracization of Nobel laureate James Watson over his controversial views on race and intelligence, this analysis will provide further insight into the public debate over this issue.

`gss_*.csv` contain a selection of features from the 2012 GSS. The outcome of interest `colrac` is a binary variable coded as either `ALLOWED` or `NOT ALLOWED`, where 1 = the racist professor should be allowed to teach, and 0 = the racist professor should **not** be allowed to teach. Documentation for the other predictors (if the variable is not clearly coded) can be viewed here. Some data pre-processing has been done in advance for you to ease your model fitting: (1) Missing values have been imputed; (2) Categorical variables with low-frequency classes had those classes collapsed into an "other" category; (3) Nominal variables with more than two classes have been converted to dummy variables; and (4) Remaining categorical variables have been converted to integer values, stripping their original labels

Your mission is to bring trees into the context of other classification approaches, thereby constructing a series of models to accurately predict an individual's attitude towards permitting racist professors to teach. The learning objectives of this exercise are:

```
1. Implement a battery of learners (including trees)
2. Tune hyperparameters
```

3. Substantively evaluate models

2. (35 points; 5 points/model) Estimate the following models, predicting `colrac` using the training set (the training `.csv`) with 10-fold CV:

   - Logistic regression
   - Naive Bayes
   - Elastic net regression
   - Decision tree (CART)
   - Bagging
   - Random forest
   - Boosting

Tune the relevant hyperparameters for each model as necessary. Only use the tuned model with the best performance for the remaining exercises. **Be sure to leave sufficient time for hyperparameter tuning.** Grid searches can be computationally taxing and take quite a while, especially for tree-aggregation methods.

```
library(tidyverse)
library(tidymodels)
library(rcfss)
library(margins)
library(rsample)
library(caret)
library(glmnet)
library(yardstick)
library(tree)
library(randomForest)
library(ranger)
library(pROC)
library(iml)

set.seed(6758)
```

```
gss_test <- read_csv("data/gss_test.csv")
gss_train <- read_csv("data/gss_train.csv")
```

```
#spliting the training set for model fitting
spliting <- initial_split(gss_train)
gss_train_train <- training(spliting)
gss_train_test <- testing(spliting)

#naive Bayesian in train() requires categorical values
gss_train_cat <- gss_train_train %>%
  mutate(colrac_cat = ifelse(colrac == 1, "Allowed", "Not allowed"))

gss_train_cat2 <- gss_train_test %>%
  mutate(colrac_cat = ifelse(colrac == 1, "Allowed", "Not allowed"))

#10-fold CV
gss_train_cv <- gss_train_train %>% vfold_cv(v = 10)
```

```r
#set up X and Y for models
X <- gss_train_train %>%
  dplyr::select(-colrac)

Y <- gss_train_train$colrac

#categorical values for naive Bayesian
Y_cat <- gss_train_cat$colrac_cat

#for elastic net
X_cv <- model.matrix(colrac ~ ., data = gss_train_train)[, -1]
X_cv_test <- model.matrix(colrac ~ ., data = gss_train_test)[, -1]
```

Logistic regression

```r
#define control method to k-fold CV
cv_10 <- trainControl(method = "cv", number = 10)

#construct model
glm_gss <- train(
  x = X,
  y = Y,
  method = "glm",
  trControl = cv_10,
  family = "binomial"
)
```

```r
#make predictions and present results
glm_result <- tibble(truth = gss_train_test$colrac,
                     pred = round(predict(glm_gss, newdata = gss_train_test))) %>%
  count(truth == pred) %>%
  spread("truth == pred", n) %>%
  mutate(err_rate = 100* `FALSE` / (`FALSE` + `TRUE`))

glm_result$err_rate
```

```
## [1] 20.59621
```

Naive Bayesian

```r
#construct model
nb_gss <- train(
  x = X,
  y = Y_cat,
  method = "nb",
  trControl = cv_10
)
```

```r
#accuracy through confusionMatrix()
confusionMatrix(nb_gss)
```

```
## Cross-Validated (10 fold) Confusion Matrix
##
## (entries are percentual average cell counts across resamples)
##
##              Reference
## Prediction    Allowed Not allowed
##   Allowed        39.3        11.9
##   Not allowed    14.5        34.3
##
##  Accuracy (average) : 0.7362
```

```r
#error rate by direct calculations
nb_result <- tibble(truth = gss_train_cat2$colrac_cat,
                    pred = predict(nb_gss, newdata = gss_train_test)) %>%
  count(truth == pred) %>%
  spread("truth == pred", n) %>%
  mutate(err_rate = 100* `FALSE` / (`FALSE` + `TRUE`),
         accuracy = 100* `TRUE` / (`FALSE` + `TRUE`))

#accuracy
nb_result$accuracy
```

```
## [1] 72.35772
```

```r
#error rate
nb_result$err_rate
```

```
## [1] 27.64228
```

Elastic net

```r
#randomize which fold among the 10 to use for training
folds <- sample(1:10, size = length(Y), replace = TRUE)

#create a grid for entries of lambda and MSE
#using lambda.1se here as in the previous two models
tuning <- tibble(alpha = seq(0, 1, by = .1),
                 mse_1se = NA,
                 lambda_1se = NA
                 )

#fill in the grid with values
#for each alpha, there is a corresponding lambda
for(i in seq_along(tuning$alpha)){
  filling <- cv.glmnet(x = X_cv,
                   y = Y,
                   alpha = tuning$alpha[i],
```

```
                    foldid = folds)
  tuning$mse_1se[i] <- filling$cvm[filling$lambda == filling$lambda.1se]
  tuning$lambda_1se[i] <- filling$lambda.1se
}

#create another grid for the calculated lambda and possible alpha
testing <- expand.grid(alpha = seq(0, 1, by = 0.1),
                       lambda_1se = tuning$lambda_1se)
```

```
#a grid for all models and their testing MSE
models_enet <- tibble(alpha = testing$alpha,
                      lambda_1se = testing$lambda_1se,
                      err_rate = NA)

#use a function to make predictions
very_fancy <- function(al, bi){
  #reproduce the model with corresponding alpha
  dumb <- glmnet(
    x = X_cv,
    y = Y,
    alpha = al
    )
  mid_filler <- tibble(truth = gss_train_train$colrac,
                       pred = round(predict(dumb,
                                    s = bi,
                                    newx = X_cv))) %>%
    #calculate error rates
    count(truth == pred) %>%
    spread("truth == pred", n) %>%
    mutate(err_rate = 100* `FALSE` / (`FALSE` + `TRUE`))
  mid_filler$err_rate
}
```

```
#execute the calculations
for(i in seq_along(models_enet$alpha)) {
  models_enet$err_rate[i] <- very_fancy(models_enet$alpha[i],
                                    models_enet$lambda_1se[i])
}

#present the results
models_enet
```

```
## # A tibble: 121 x 3
##    alpha lambda_1se err_rate
##    <dbl>      <dbl>    <dbl>
##  1   0        0.357     19.2
##  2   0.1      0.357     22.7
##  3   0.2      0.357     22.5
##  4   0.3      0.357     22.5
##  5   0.4      0.357     21.5
##  6   0.5      0.357     21.8
##  7   0.6      0.357     26.4
##  8   0.7      0.357     46.3
```

```
##  9   0.8      0.357     46.3
## 10   0.9      0.357     46.3
## # ... with 111 more rows
```

```
#find the combination where MSE is smallest
elas_meters <- models_enet[which.min(models_enet$err_rate),]
elas_meters
```

```
## # A tibble: 1 x 3
##   alpha lambda_1se err_rate
##   <dbl>      <dbl>    <dbl>
## 1     0     0.0391     17.2
```

```
#tune glmnet based on the results
elas_gss <- glmnet(
  x = X_cv,
  y = Y,
  alpha = elas_meters$alpha
  )

elas_result <- tibble(truth = gss_train_test$colrac,
                      pred = round(predict(elas_gss,
                                           s = elas_meters$lambda_1se,
                                           newx = X_cv_test))) %>%
  count(truth == pred) %>%
  spread("truth == pred", n) %>%
  mutate(err_rate = 100* `FALSE` / (`FALSE` + `TRUE`))

elas_result$err_rate
```

```
## [1] 20.59621
```

Decision tree

```
rac_tree <- vfold_cv(gss_train_train, v = 10) %>%
  mutate(tree = map(splits, ~ tree(colrac ~ .,
                                   data = analysis(.x),
                                   control = tree.control(nobs = nrow(gss_train_train),
                                                          mindev = 0))))
```

```
# generate 10-fold CV trees
colrac_cv <- vfold_cv(gss_train_train, v = 10) %>%
  #a full tree for each split
  mutate(tree = map(splits, ~ tree(colrac ~ ., data = analysis(.x),
                                   control = tree.control(nobs = nrow(gss_train_train),
                                                          mindev = 0))))

# calculate each possible prune result for each fold
colrac_prune <- expand.grid(rac_tree$id, 2:50) %>%
  as_tibble() %>%
  mutate(Var2 = as.numeric(Var2)) %>%
```

```
  rename(id = Var1,
         k = Var2) %>%
  left_join(colrac_cv) %>%
  mutate(prune = map2(tree, k, ~ prune.tree(.x, best = .y)),
         estimate = map2(prune, splits, ~ predict(.x, newdata = assessment(.y))),
         truth = map(splits, ~ assessment(.x)$colrac)) %>%
  unnest(estimate, truth) %>%
  #round estimates for comparison
  mutate(estimate = round(estimate)) %>%
  group_by(k) %>%
  count(truth == estimate) %>%
  spread("truth == estimate", n) %>%
  mutate(err_rate = 100* `FALSE` / (`FALSE` + `TRUE`))
```

```
#locate the tree with the smallest error rate
tree_meters <- colrac_prune[which.min(colrac_prune$err_rate),]

tree_meters
```

```
## # A tibble: 1 x 4
## # Groups:   k [1]
##       k `FALSE` `TRUE` err_rate
##   <dbl>   <int>  <int>    <dbl>
## 1    12     241    866     21.8
```

```
#name the tree
tree_gss <- tree(colrac ~ .,
                 data = gss_train_train,
                 control = tree.control(nobs = nrow(gss_train_train),
                                        mindev = 0)) %>%
  prune.tree(best = tree_meters$k)
```

```
#make complete predictions with the tree
tree_result <- tibble(truth = gss_train_test$colrac,
                      pred = predict(tree_gss, newdata = gss_train_test)) %>%
  mutate(pred = round(pred)) %>%
  count(truth == pred) %>%
  spread("truth == pred", n) %>%
  mutate(err_rate = 100* `FALSE` / (`FALSE` + `TRUE`))

#present the error rate
tree_result$err_rate
```

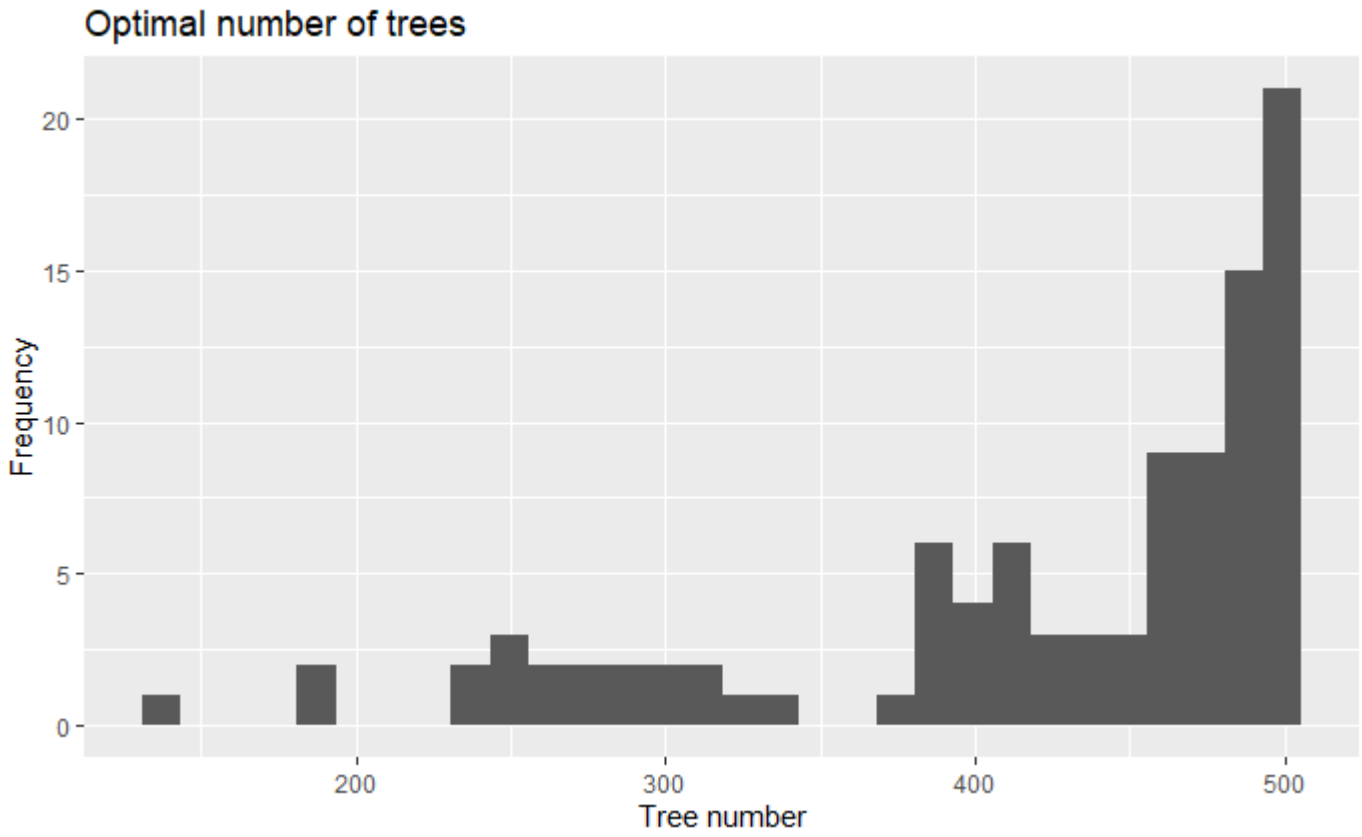
```
## [1] 27.64228
```

Number of trees

The following codes can produce the graph below, but it takes a long time to run. Note that here comparisons are about MSE rather than error rates. Even though they are not the same thing, both can reflect the accuracy of a model, since predictions are numbers between 0 and 1. The codes here use MSE to save time. The point is, out-of-bag MSE reaches minimum around 500, which is the reason why we will be setting tree numbers to be 500 in the following models.

```
treecount <- vector(mode = "numeric", length = 100)

for(i in seq_along(treecount)) {
  tree_num <- randomForest(
    formula = colrac ~ .,
    data = gss_train)

  treecount[i] <- which.min(tree_num$mse)
}

many_trees <- tibble(number = treecount)

many_trees %>%
  ggplot(aes(x = number)) +
  geom_histogram() +
  labs(title = "Optimal number of trees",
       x = "Tree number",
       y = "Frequency")
```

```
knitr::include_graphics('manytrees.png')
```



Bagging

```
#create a grid for mtry, min.node.size, sample.fraction
bag_grid <- expand.grid(
  node_size = seq(1, 9, by = 1),
  sample_size = c(0.2, 0.4, 0.6, 0.8),
  err_rate = NA
)

#a list to identify which split from the CV to use
id <- sample(1:10, size = 36, replace = TRUE)

#join the grid with fold id's
bag_grid <- bind_cols(bag_grid, id = id)

#10-fold split data and assign ids
split_grid <- tibble(gss_train_cv$splits, 1:10) %>%
  rename("splits" = `gss_train_cv$splits`,
         "id" = `1:10`)

#set up the grid
bag_grid <- left_join(bag_grid, split_grid)
```

```
for(i in 1:nrow(bag_grid)) {
  # train bagging model
  model <- randomForest(
    formula = colrac ~ .,
    data = analysis(bag_grid$splits[[i]]),
    num.trees = 500,
    mtry = ncol(analysis(bag_grid$splits[[i]])) - 1,
    replace = FALSE,
    samplesize = bag_grid$sample_size[i] * nrow(analysis(bag_grid$splits[[i]])),
    min.node.size = bag_grid$node_size[i]
  )
  # extract testing data
  truth_ext <- assessment(bag_grid$splits[[i]])
  # make predictions and calulate error rates
  model_result <- tibble(truth = truth_ext$colrac,
                         pred = round(predict(model, newdata = truth_ext))) %>%
    count(truth == pred) %>%
    spread("truth == pred", n) %>%
    mutate(err_rate = 100* `FALSE` / (`FALSE` + `TRUE`))
  #insert error rates
  bag_grid$err_rate[i] <- model_result$err_rate
}
```

```
# find the parameters with the lowest error rate
bag_meters <- bag_grid[which.min(bag_grid$err_rate),] %>%
  dplyr::select(-splits, -id)

bag_meters
```

```
##    node_size sample_size err_rate
```

```
## 10         1         0.4 10.90909
```

```
# fit model
bag_gss <- randomForest(
    formula = colrac ~ .,
    data = gss_train_train,
    num.trees = 500,
    mtry = ncol(gss_train_train) - 1,
    replace = FALSE,
    samplesize = bag_meters$sample_size * nrow(gss_train_train),
    min.node.size = bag_meters$node_size
    )
```

```
#using predict() on bag_gss will take incredibly long
#fortunately bag_gss already has predictions
bag_result <- tibble(truth = gss_train_test$colrac,
                     pred = round(predict(bag_gss, newdata = gss_train_test))) %>%
  mutate(pred = round(pred)) %>%
  count(truth == pred) %>%
  spread("truth == pred", n) %>%
  mutate(err_rate = 100* `FALSE` / (`FALSE` + `TRUE`))

#present the error rate
bag_result$err_rate
```

```
## [1] 24.11924
```

Random forest

```
#create a grid for mtry, min.node.size, sample.fraction
rf_grid <- expand.grid(
  mtry = seq(20, 30, by = 2),
  node_size = seq(1, 9, by = 1),
  sample_size = c(0.2, 0.4, 0.6, 0.8),
  err_rate = NA
)

#a list to identify which split from the CV to use
id <- sample(1:10, size = nrow(rf_grid), replace = TRUE)

#join the grid with fold id's
rf_grid <- bind_cols(rf_grid, id = id)

#set up the grid
rf_grid <- left_join(rf_grid, split_grid)
```

```
for(i in 1:nrow(rf_grid)) {
  # train bagging model
  model <- ranger(
    formula = colrac ~ .,
    data = analysis(rf_grid$splits[[i]]),
```

```
    num.trees = 500,
    mtry = rf_grid$mtry[i],
    replace = FALSE,
    sample.fraction = rf_grid$sample_size[[i]],
    min.node.size = rf_grid$node_size[i]
  )
  # extract testing data
  truth_ext <- assessment(rf_grid$splits[[i]])
  # make predictions, note that here in the predict function
  #new data is "data", not "newdata"
  tatakai <- predict(model, data = truth_ext)
  # calculate error rates
  model_result <- tibble(truth = truth_ext$colrac,
                         pred = round(tatakai$predictions)) %>%
    count(truth == pred) %>%
    spread("truth == pred", n) %>%
    mutate(err_rate = 100* `FALSE` / (`FALSE` + `TRUE`))
  #insert error rates
  rf_grid$err_rate[i] <- model_result$err_rate
}
```

```
# find the parameters with the lowest error rate
rf_meters <- rf_grid[which.min(rf_grid$err_rate),] %>%
  dplyr::select(-splits, -id)

rf_meters
```

```
##     mtry node_size sample_size err_rate
## 187   20         5         0.8 9.090909
```

```
# fit model
rf_gss <- ranger(
    formula = colrac ~ .,
    data = gss_train_train,
    num.trees = 500,
    mtry = rf_meters$mtry,
    replace = FALSE,
    sample.fraction = rf_meters$sample_size,
    min.node.size = rf_meters$node_size
  )
```

```
#make predictions with the tuned model
rf_ttk <- predict(rf_gss, data = gss_train_test)
#insert values and calculate error rates
rf_result <- tibble(truth = gss_train_test$colrac,
                    pred = round(rf_ttk$predictions)) %>%
  mutate(pred = round(pred)) %>%
  count(truth == pred) %>%
  spread("truth == pred", n) %>%
  mutate(err_rate = 100* `FALSE` / (`FALSE` + `TRUE`))

#present the error rate
rf_result$err_rate
```

```
## [1] 21.40921
```

Boosting

```
boost_gss <- train(colrac ~ .,
                   data = gss_train_train,
                   method = "gbm",
                   trControl = cv_10,
                   verbose = 0)
```

```
#make predictions and present results
boost_result <- tibble(truth = gss_train_test$colrac,
                       pred = round(predict(boost_gss, newdata = gss_train_test))) %>%
  count(truth == pred) %>%
  spread("truth == pred", n) %>%
  mutate(err_rate = 100* `FALSE` / (`FALSE` + `TRUE`))

boost_result$err_rate
```

```
## [1] 22.22222
```

Evaluate the models

3. (20 points) Compare and present each model's (training) performance based on

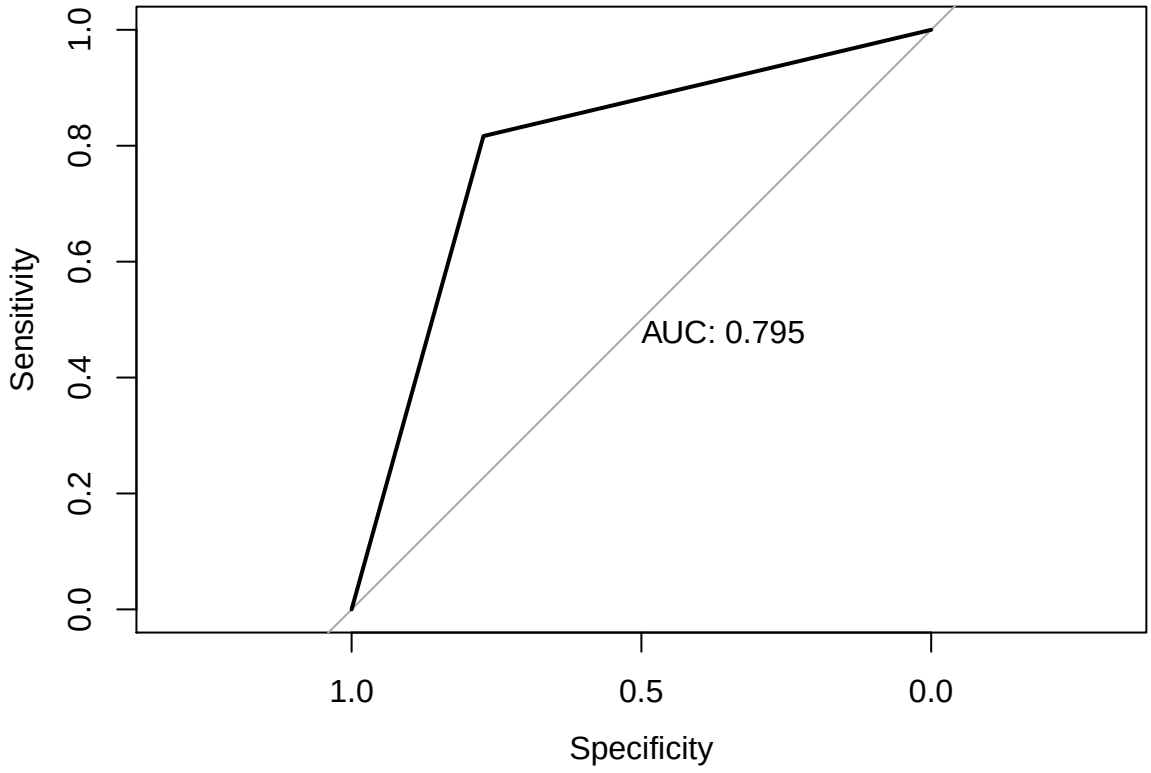
    - Cross-validated error rate
    - ROC/AUC

```
error_rates <- tibble("Logistic regression" = glm_result$err_rate,
                      "Naive Bayesian" = nb_result$err_rate,
                      "Elastic net" = elas_result$err_rate,
                      "Decision tree" = tree_result$err_rate,
                      "Bagging" = bag_result$err_rate,
                      "Random forest" = rf_result$err_rate,
                      "Boosting" = boost_result$err_rate
                      )

error_rates <- data.frame(t(error_rates))
colnames(error_rates) <- c("Error rate")
error_rates
```

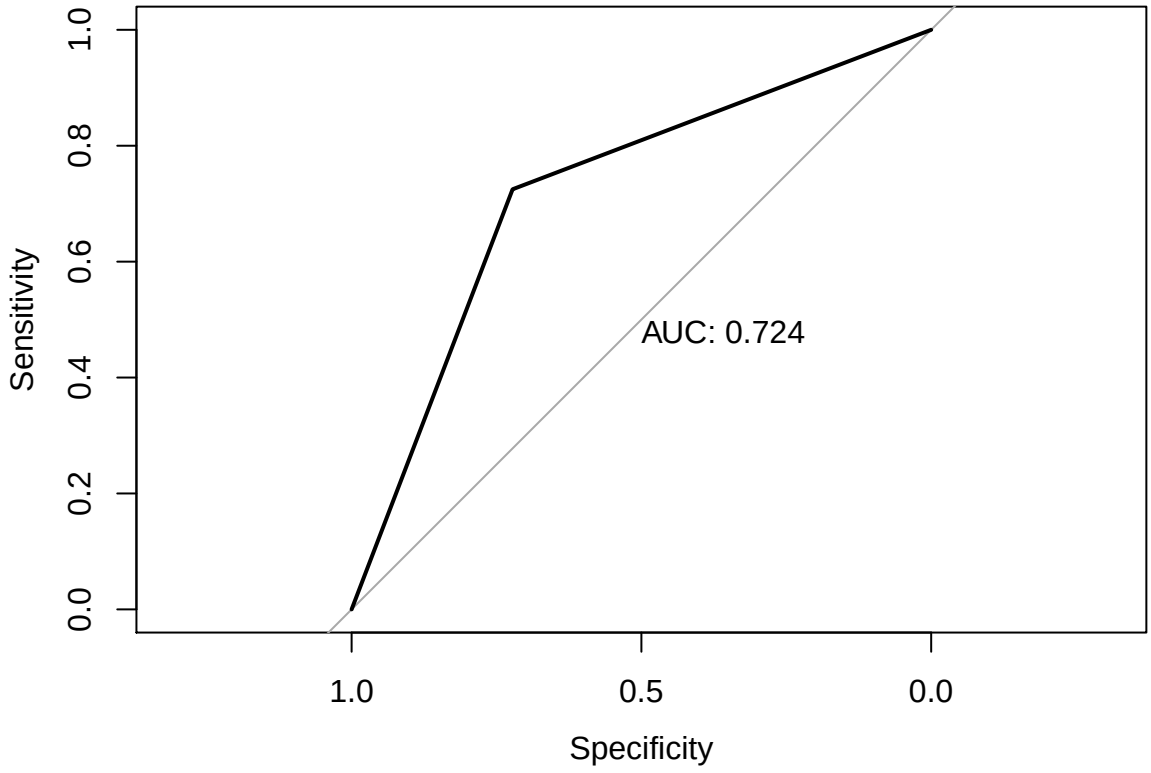
```
##                     Error rate
## Logistic regression   20.59621
## Naive Bayesian        27.64228
## Elastic net           20.59621
## Decision tree         27.64228
## Bagging               24.11924
## Random forest         21.40921
## Boosting              22.22222
```

```r
#glm
glm_pred <- tibble(truth = gss_train_test$colrac,
                   pred = round(predict(glm_gss, newdata = gss_train_test)))

#nb
nb_pred <- tibble(truth = gss_train_cat2$colrac_cat,
                   pred = predict(nb_gss, newdata = gss_train_test))

#elastic net
elas_pred <- tibble(truth = gss_train_test$colrac,
                     pred = round(predict(elas_gss,
                                          s = elas_meters$lambda_1se,
                                          newx = X_cv_test)))

#decision tree
tree_pred <- tibble(truth = gss_train_test$colrac,
                     pred = predict(tree_gss, newdata = gss_train_test))

#bagging
bag_pred <- tibble(truth = gss_train_test$colrac,
                     pred = round(predict(bag_gss, newdata = gss_train_test)))

#random forest
rf_pred <- tibble(truth = gss_train_test$colrac,
                     pred = round(rf_ttk$predictions))

#boosting
boost_pred <- tibble(truth = gss_train_test$colrac,
                   pred = round(predict(boost_gss, newdata = gss_train_test)))
```

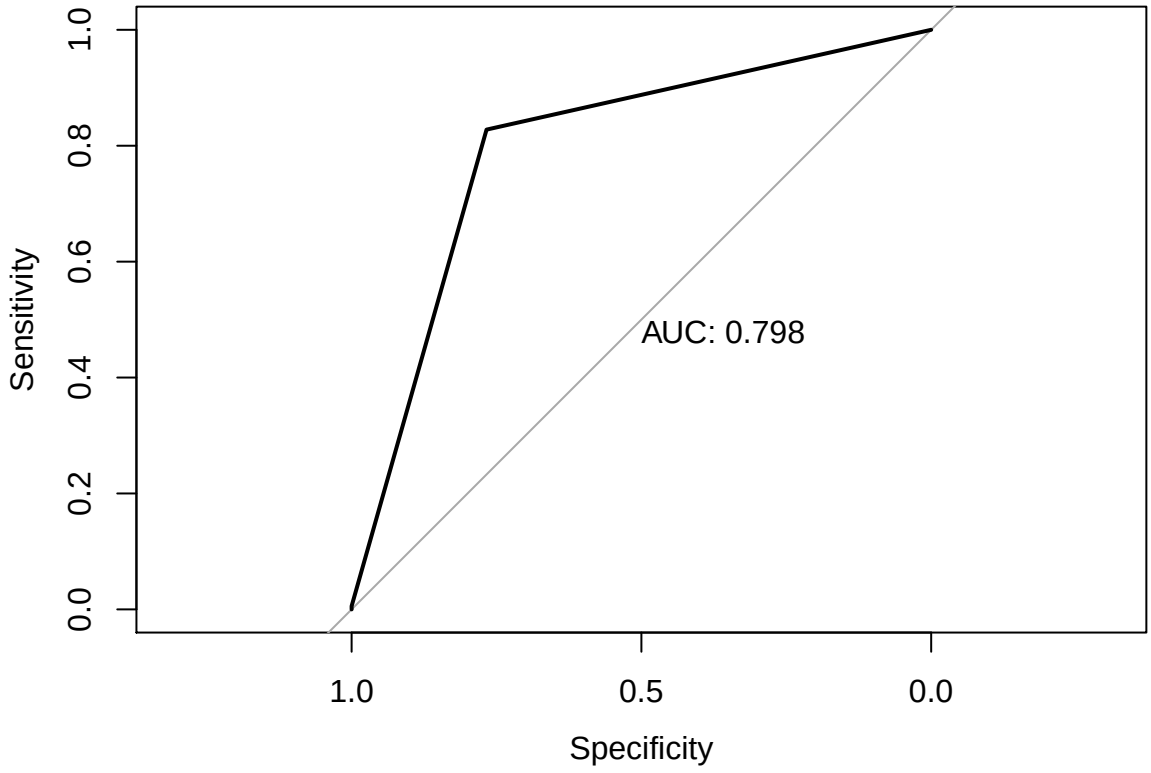
```r
#glm
glm_roc <- roc(response = glm_pred$truth,
               predictor =  as.numeric(glm_pred$pred),
               plot = TRUE,
               print.auc=TRUE)
```



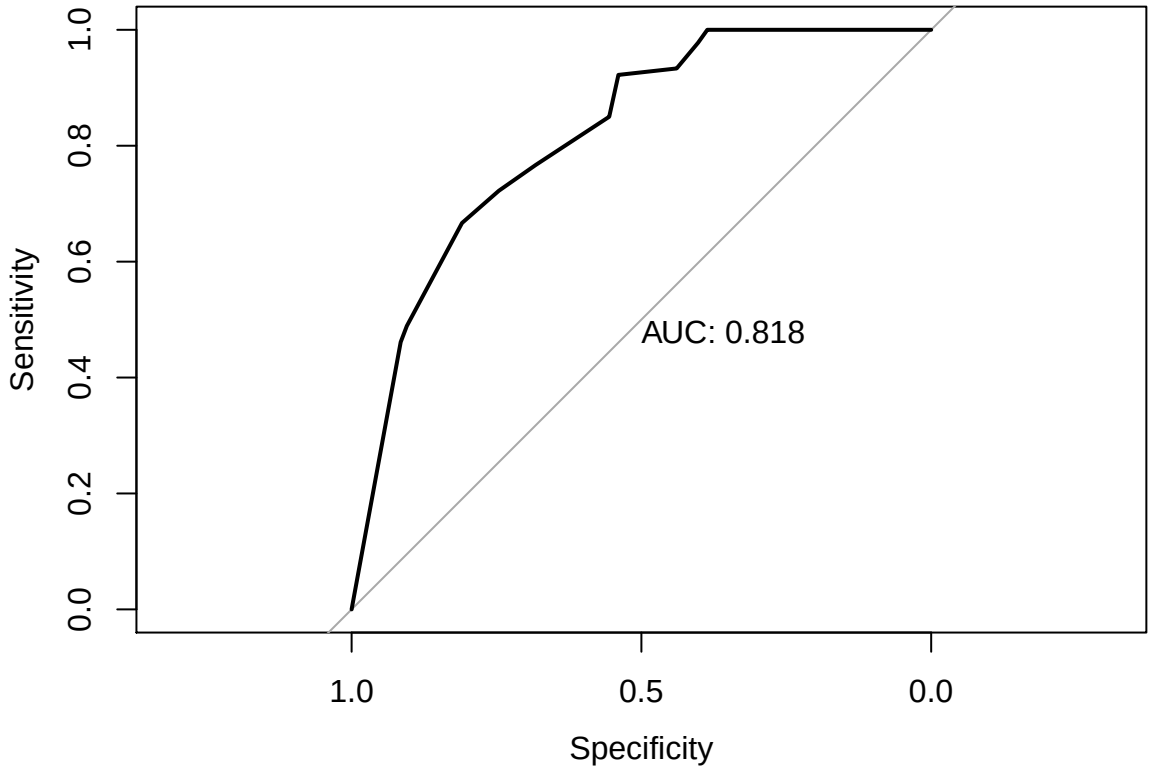

```
#nb
nb_roc <- roc(response = nb_pred$truth,
              predictor =  as.numeric(nb_pred$pred),
              plot = TRUE,
              print.auc=TRUE)
```



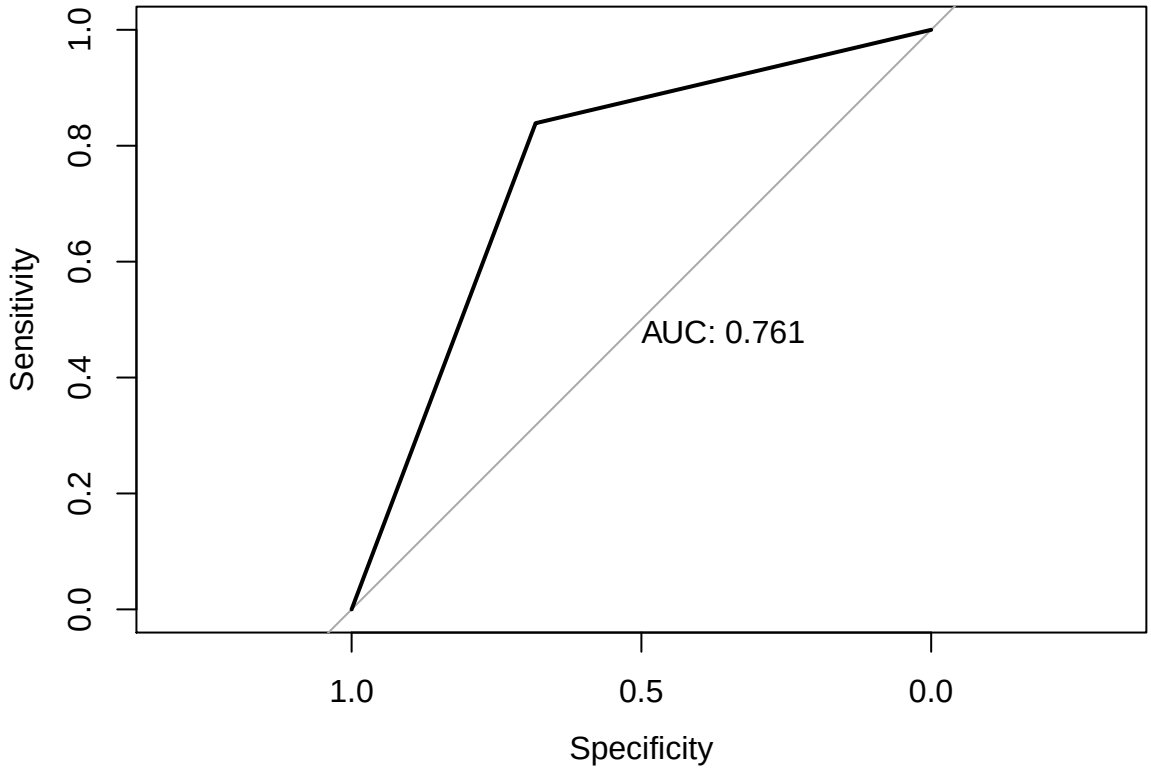

```
#elastic net
elas_roc <- roc(response = elas_pred$truth,
                predictor =  as.numeric(elas_pred$pred),
                plot = TRUE,
                print.auc=TRUE)
```



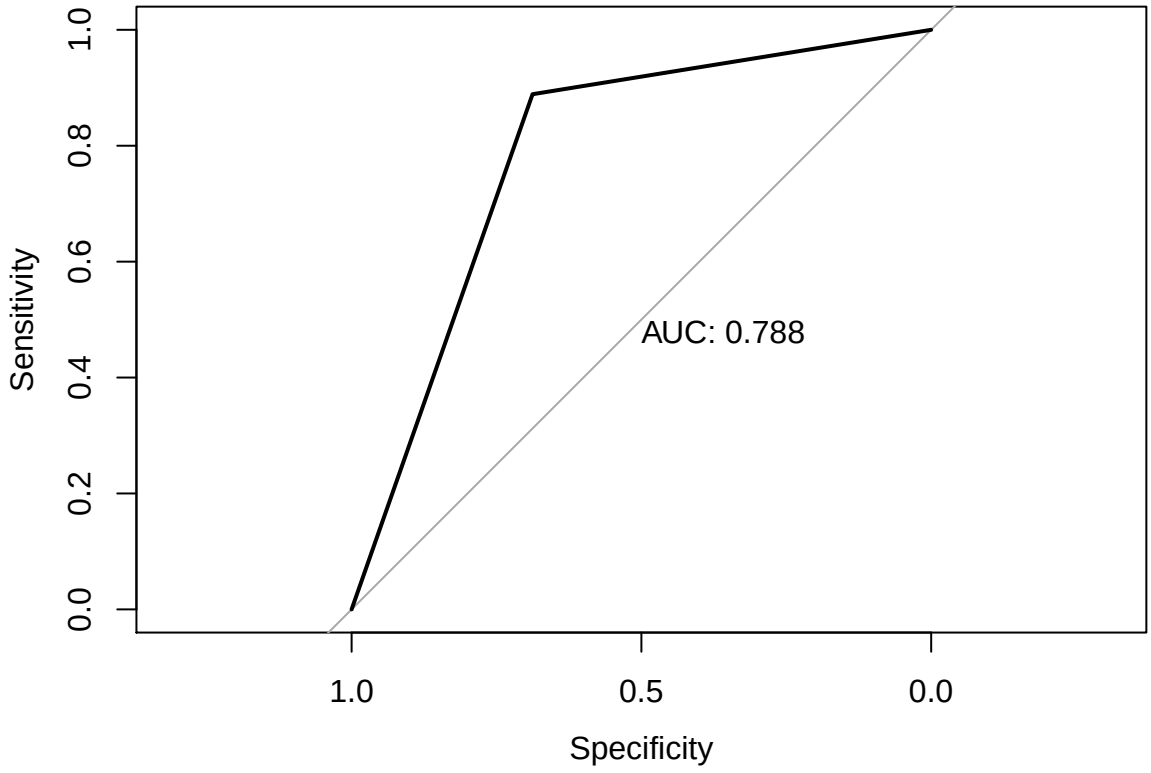

```
#decision tree
dtree <- roc(response = tree_pred$truth,
             predictor =  as.numeric(tree_pred$pred),
             plot = TRUE,
             print.auc=TRUE)
```



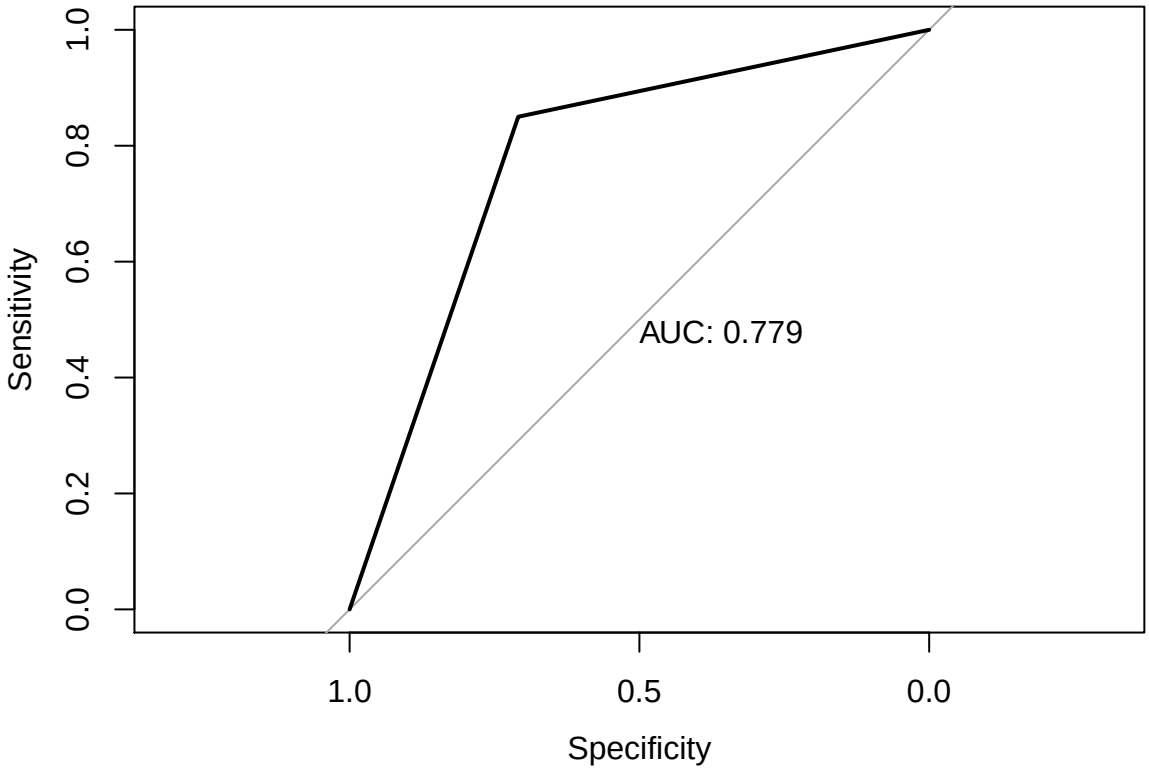

```
#bagging
bag_roc <- roc(response = bag_pred$truth,
               predictor =  as.numeric(bag_pred$pred),
               plot = TRUE,
               print.auc=TRUE)
```




```
#random forest
rf_roc <- roc(response = rf_pred$truth,
              predictor =  as.numeric(rf_pred$pred),
              plot = TRUE,
              print.auc=TRUE)
```




```
#boosting
bost_roc <- roc(response = boost_pred$truth,
                predictor =  as.numeric(boost_pred$pred),
                plot = TRUE,
                print.auc=TRUE)
```



4. (15 points) Which is the best model? Defend your choice.

- The best model is the logistic regression model.
- When we compare cross-validated error rates, two models have the lowest number, the logistic regression model (20.596206), and the elastic net model (20.596206). It should be noted that if not specified for binomial response, the error rate of the logistic model will increase by around 2%. Also, if specified for binomial response, the error rate of the elastic net model will be over 50%. We need to compare AUROC to decided which model is better.
- By defition, ROC is plotted with sensitivity (true positive rate) against false positive rate (1 - specificity). Therefore, the higher AUC is, the more accurate a model is in predicting outcomes. Moreover, 1 - AUC is the probability of Type 1 and Type 2 errors. Here, the three highest AUCs belong to logistic regression (0.795), elastic net (0.798), and decision tree (0.818).
- Decision tree is not an option here. When we train the models through cross validation and compare their error rates, it appears decision tree and naive Bayesian have the highest error rate. That means, decision tree is probably doing a bad job in predicting negative outcomes, which produces a high error rate for it.
- The difference between their AUROC is very small (0.003). In this sense, the elastic net model is slightly more accurate than the logistic model in training performance. However, good training performance sometimes means overfitting, and leads to worse testing performance. To prove which model is better, we need to fit both to the testing set.

Evaluate the *best* model

5. (15 points) Evaluate the *final*, best model's (selected in 4) performance on the test set (the test `.csv`) by calculating and presenting the classification error rate and AUC. Compared to the fit evaluated on

the training set in questions 3-4, does the "best" model generalize well? Why or why not? How do you know?

```
X_test <- model.matrix(colrac ~ ., data = gss_test)[, -1]

elas_test <- tibble(truth = gss_test$colrac,
                    pred = round(predict(elas_gss,
                                         s = elas_meters$lambda_1se,
                                         newx = X_test)))

elas_test_err <- elas_test %>%
  count(truth == pred) %>%
  spread("truth == pred", n) %>%
  mutate(err_rate = 100* `FALSE` / (`FALSE` + `TRUE`))

elas_test_err$err_rate
```

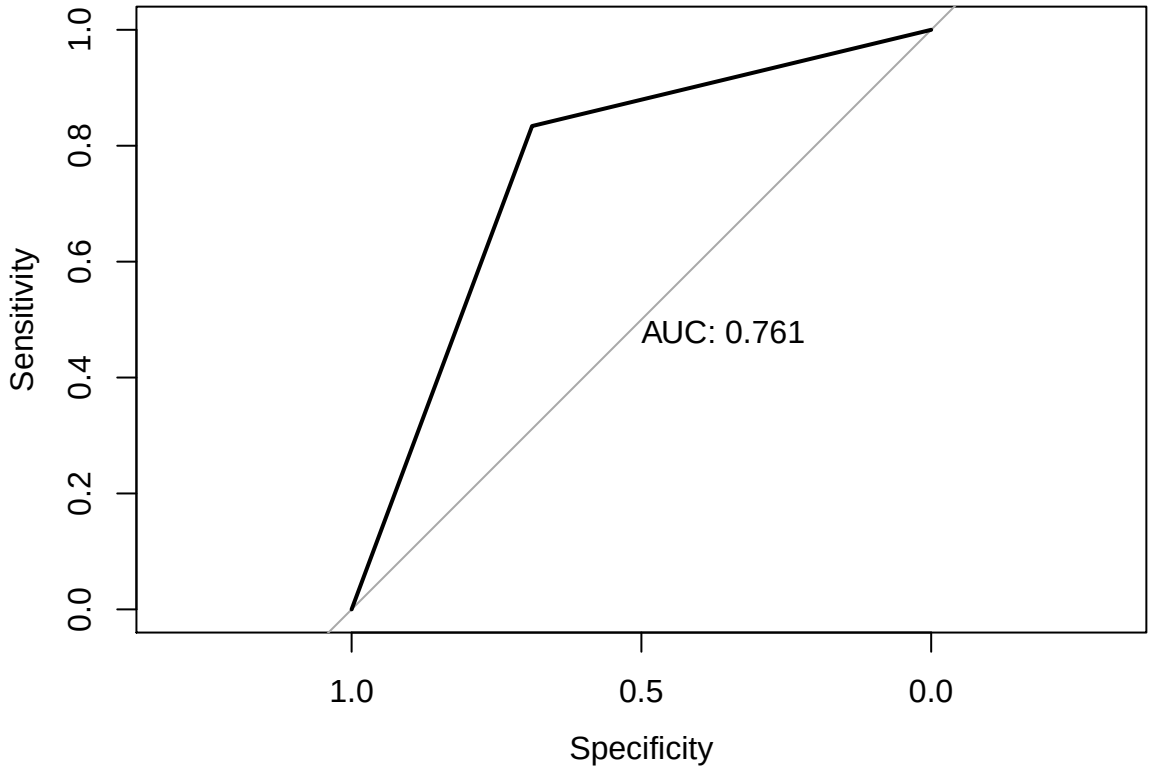
```
## [1] 23.32657
```

```
glm_test <- tibble(truth = gss_test$colrac,
                   pred = round(predict(glm_gss, newdata = gss_test)))

glm_test_err <- glm_test %>%
  count(truth == pred) %>%
  spread("truth == pred", n) %>%
  mutate(err_rate = 100* `FALSE` / (`FALSE` + `TRUE`))

glm_test_err$err_rate
```

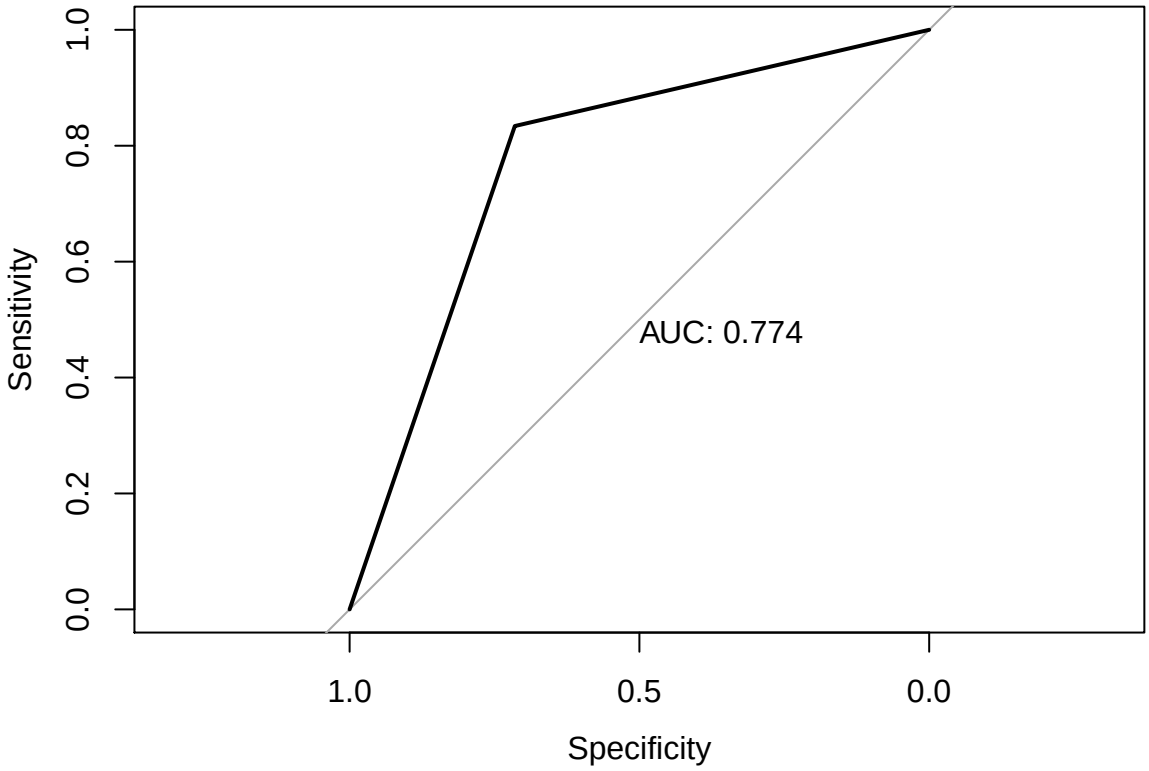
```
## [1] 22.10953
```

Here, the logistic regression model has a lower error rate than the elastic net model.

```
test_elas_roc <- roc(response = elas_test$truth,
                predictor =  as.numeric(elas_test$pred),
                plot = TRUE,
                print.auc=TRUE)
```




```
test_glm_roc <- roc(response = glm_test$truth,
                    predictor =  as.numeric(glm_test$pred),
                    plot = TRUE,
                    print.auc=TRUE)
```



Again, the logistic regression model outperforms the elastic net model in AUROC, by 0.013. Although the difference is still small, it does appear that the logistic regression model is slightly better, and therefore the best among the 7 models.

- The logistic regression model performs well on the test set data.
- Its error rate is 22.1095335, which is still lower than 4 out of the 6 remaining models' training error rate. That is, the model testing performance is even better than those model's training performance.
- Moreover, the AUC is 0.774. Compared with its training AUC 0.795, it dropped by 0.021, less than 5%. Considering that the performance is run on a test set, this drop is reasonably small.

Bonus: PDPs/ICE

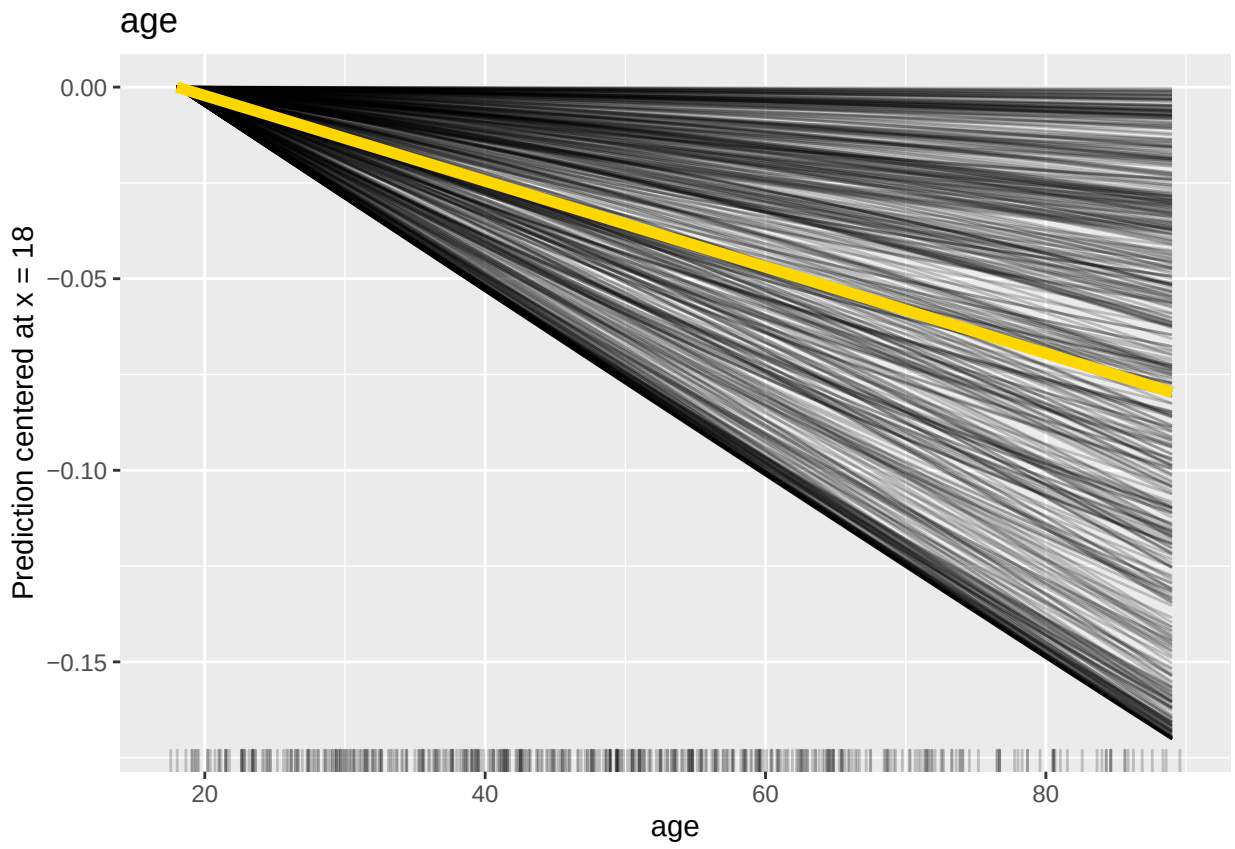
6. (Up to 5 extra points) Present and substantively interpret the "best" model (selected in question 4) using PDPs/ICE curves over the range of: `tolerance` and `age`. Note, interpretation must be more than simple presentation of plots/curves. You must sufficiently describe the changes in *probability* estimates over the range of these two features. You may earn *up to* 5 extra points, where partial credit is possible if the solution is insufficient along some dimension (e.g., technically/code, interpretation, visual presentation, etc.).

Age

```
#separate features from the outcome
features <- gss_test %>%
```

```
  dplyr::select(-colrac)

response <- gss_test$colrac

#enter the model and values
predictor.glm <- Predictor$new(
  model = glm_gss,
  data = features,
  y = response,
  predict.fun = predict,
  class = "classification"
)
```

```
#set up for age
glm.age <- Partial$new(predictor.glm, "age", ice = TRUE)

#set ICE centered on min age
glm.age$center(min(features$age))

#graph ICE plot for age
plot(glm.age) +
  ggtitle("age")
```

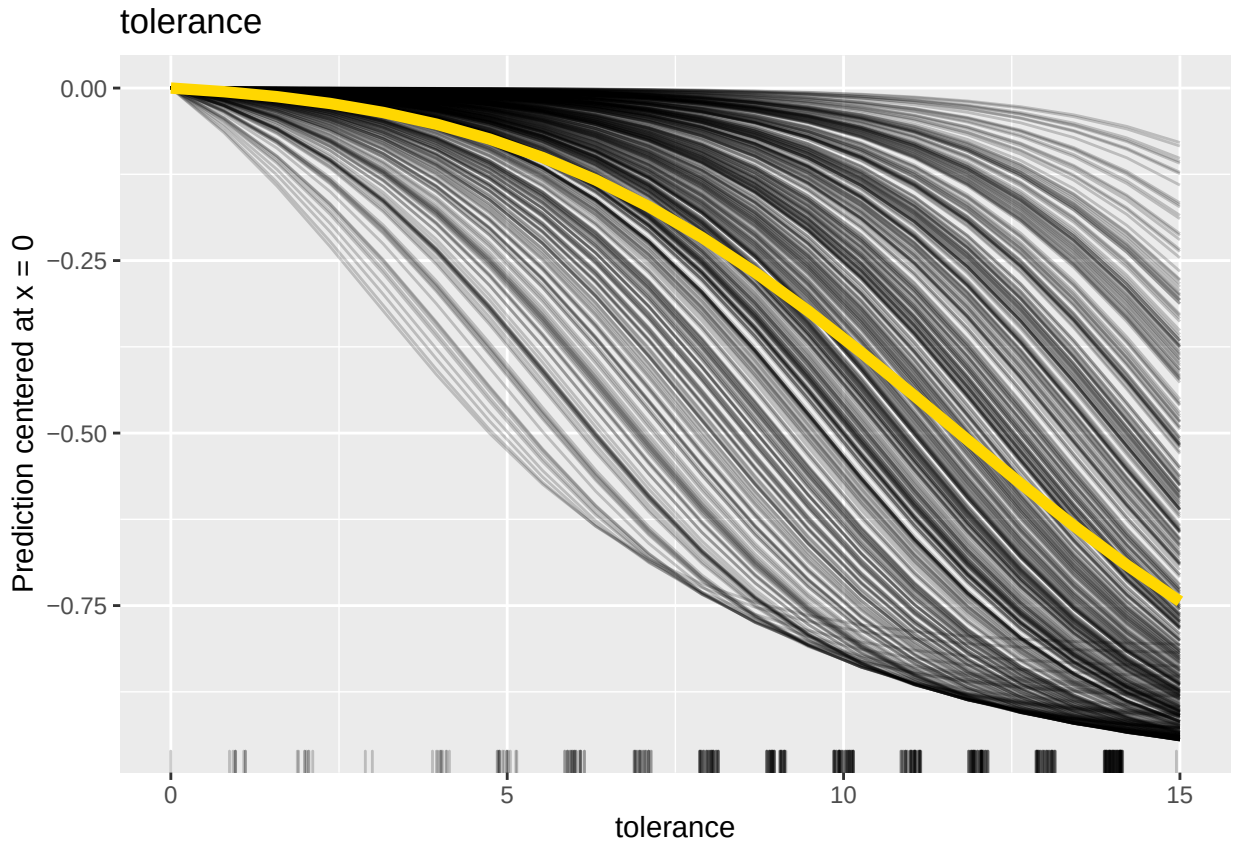


The ICE plot centered on min `age`(18) for age shows that in the logistic regression model, `age` is generally negatively associated with the probability of one agreeing to let a racist professor teach in college. The

yellow line in the plot (PDP) is the average effect of age on the prediction. Its slope is negative, but very close to 0, which means the impact of `age` on the prediction of `colrac` is very limited.

Tolerance

```
#set up for tolerance
glm.tol <- Partial$new(predictor.glm, "tolerance", ice = TRUE)

#set ICE to be centered on min tolerance
glm.tol$center(min(features$tolerance))

#graph ICE plot
plot(glm.tol) +
  ggtitle("tolerance")
```



- The variable `tolerance` is an index based on one's answers to GSS's battery of questions about political tolerance. It is negatively associate with one's tolerance level, i.e., the higher `tolerance` score one has, the less tolerant towards political outgroups the person is.
- In this light, it's no surprise that `tolerance` is negatively associated with the probability of one allowing a racist professor to teach in college. (In fact, `colrac` itself is used to calculate `tolerance`) It's natural that the higher one scores in `tolerance`, the less tolerant he/she is towards outgroups, and the less likely he/she will agree to let a racist professor to teach in college.
- However, the impact of `tolerance` on `colrac` in the model is much stronger than `age`, as we can see by comparing the y-axises. The slope of the yellow line (PDP) in the `tolerance` ICE plot increases

as `tolerance` increases. (It's a matter of course, since `colrac` is used to calculate `tolerance`, but not `age`).

- On the other hand, we can see that the majority of `tolerance` scores are between 5 and 14, as shown on the plot. That implies the general population itself is not very "tolerant".