Homework 4

Yanhao Li

Contents

```
library(tidyverse)
library(ISLR)
library(lasso2)
library(ISLR)
library(rpart)
library(rpart.plot)
library(randomForest)
library(ranger)
library(caret)
library(gbm)
```

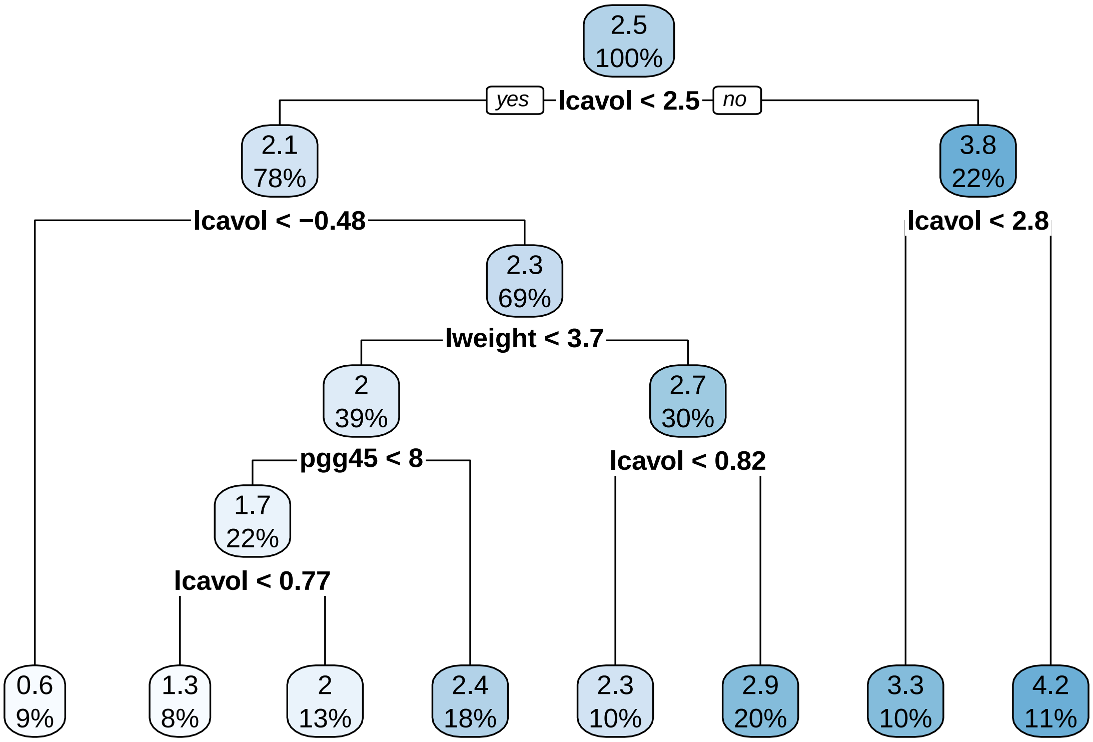
Question 1

Load, clean, and tidy data

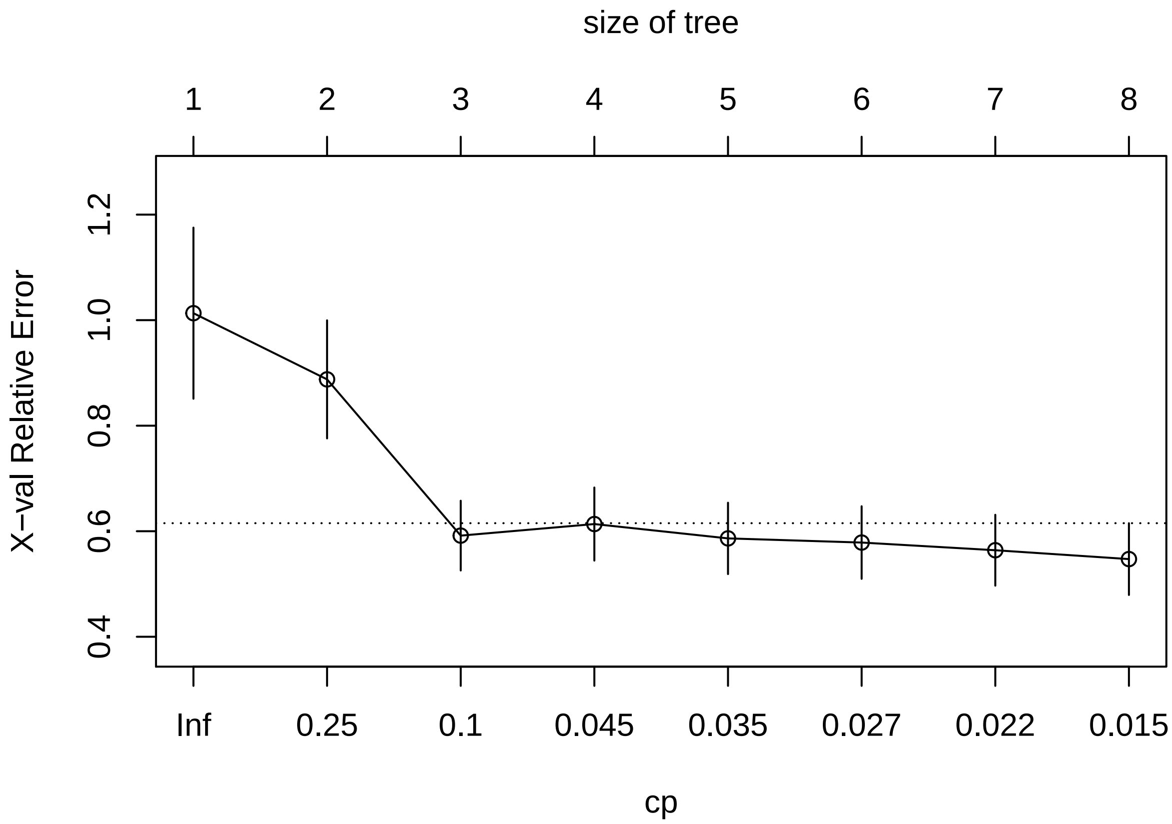
```
data("Prostate")

prostate = Prostate %>%
  janitor::clean_names()
```

Question a

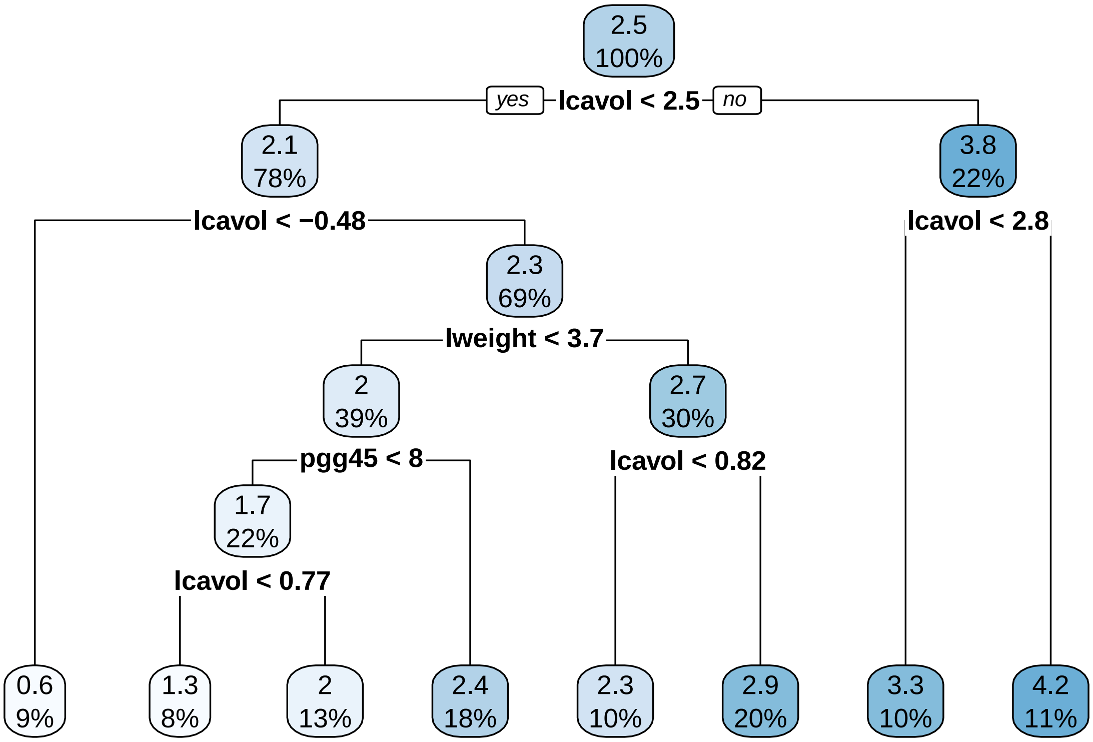
```
set.seed(1)

tree1 = rpart(formula = lpsa ~ .,
              data = prostate)

rpart.plot(tree1)
```



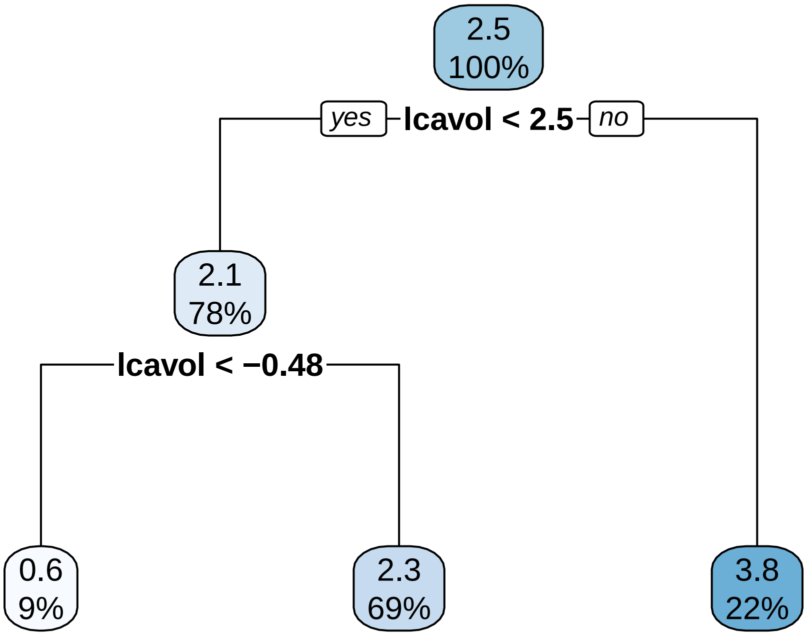
```
cpTable <- tree1$cptable

plotcp(tree1)
```



```r
# minimum cross-validation error
minErr <- which.min(cpTable[,4])

tree2 <- prune(tree1, cp = cpTable[minErr,1])

rpart.plot(tree2)
```



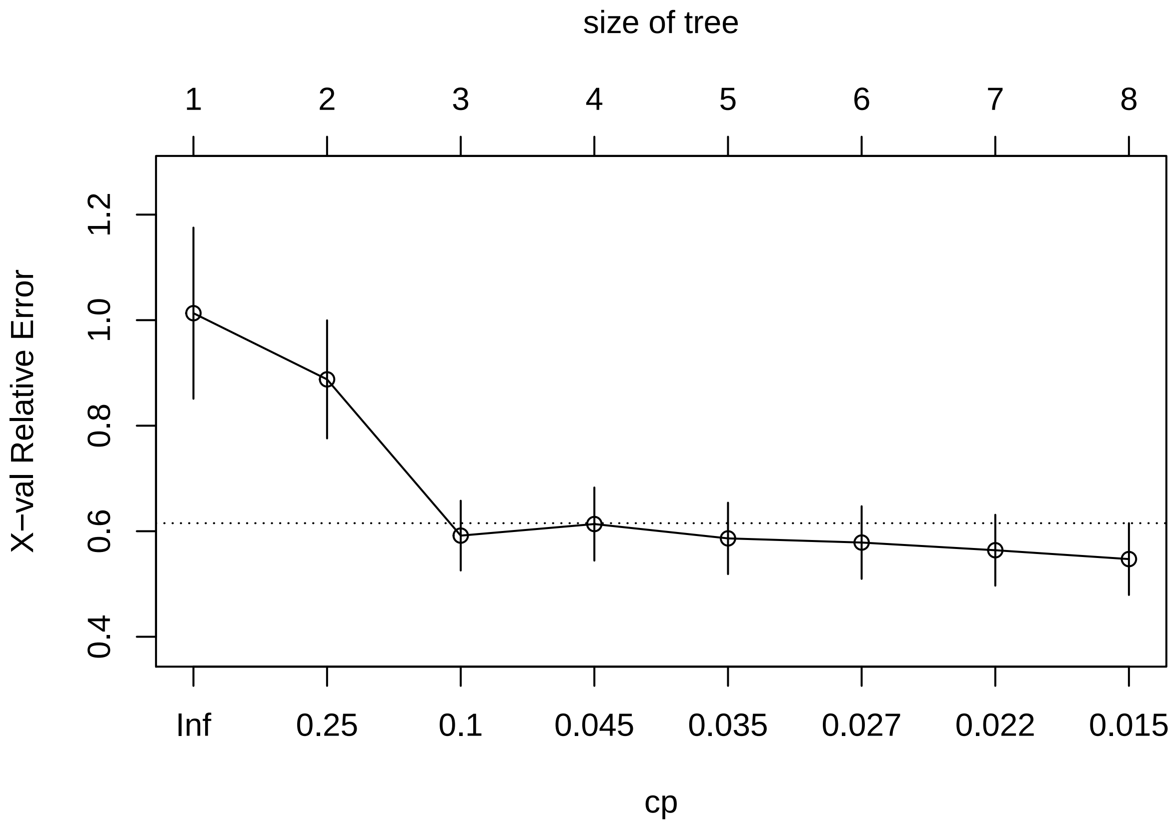
```
# 1SE rule
tree3 <- prune(tree1, cp = cpTable[cpTable[,4] < cpTable[minErr,4] + cpTable[minErr,5],1][1])

rpart.plot(tree3)
```



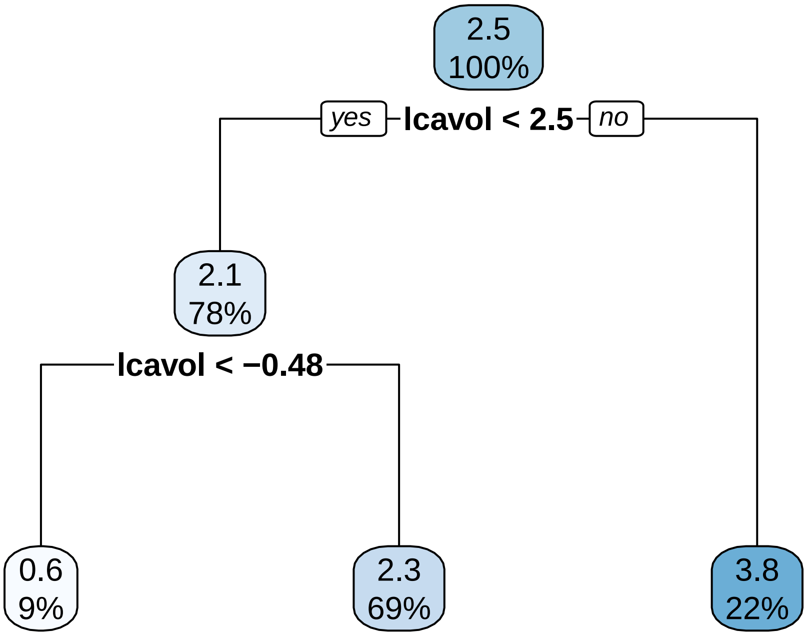
Tree size corresponds to the lowest cross-validation error is 8. It is different from the tree size obtained using the 1 SE rule, which is 3.

Question b

```
plotcp(tree1)
```



```
set.seed(1)

tree4 <- rpart(formula = lpsa ~ .,
               data = prostate,
               control = rpart.control(cp = 0.1))

rpart.plot(tree4)
```

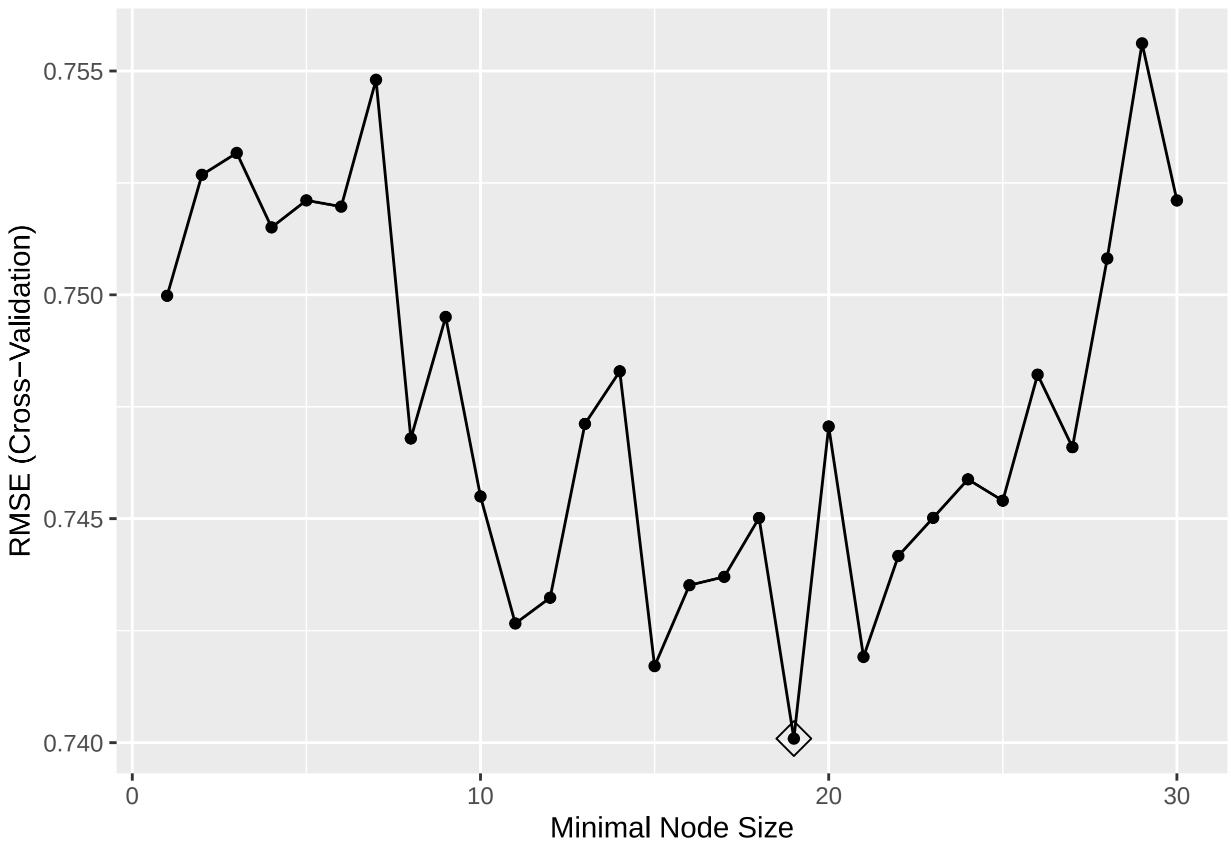


A good choice of cp for pruning is often the leftmost value for which the mean lies below the horizontal line. According to the plot, I choose cp equals to 0.1 and size of tree equals to 3.

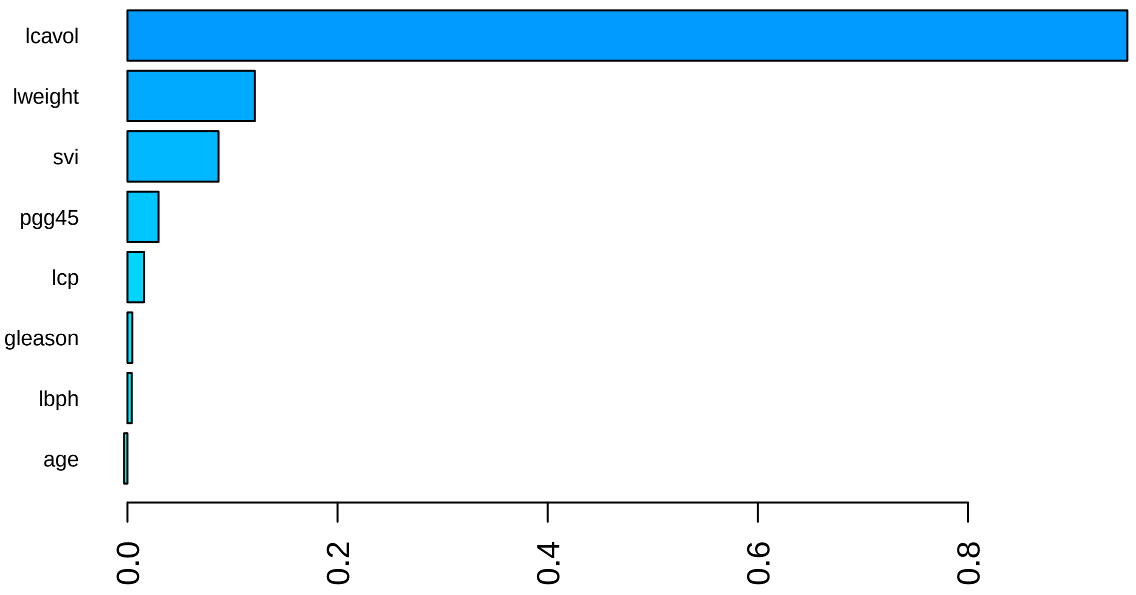
In terminal node where lcvol is less than -0.48, the mean lpsa is 0.6. This node contains 9% of the sample.

Question c

```
ctrl <- trainControl(method = "cv")

bag.grid <- expand.grid(mtry = 8,
                        splitrule = "variance",
                        min.node.size = 1:30)

set.seed(1)

bag.fit <- train(lpsa~.,
                 Prostate,
                 method = "ranger",
                 tuneGrid = bag.grid,
                 trControl = ctrl,
                 importance = "permutation")

ggplot(bag.fit, highlight = TRUE)
```



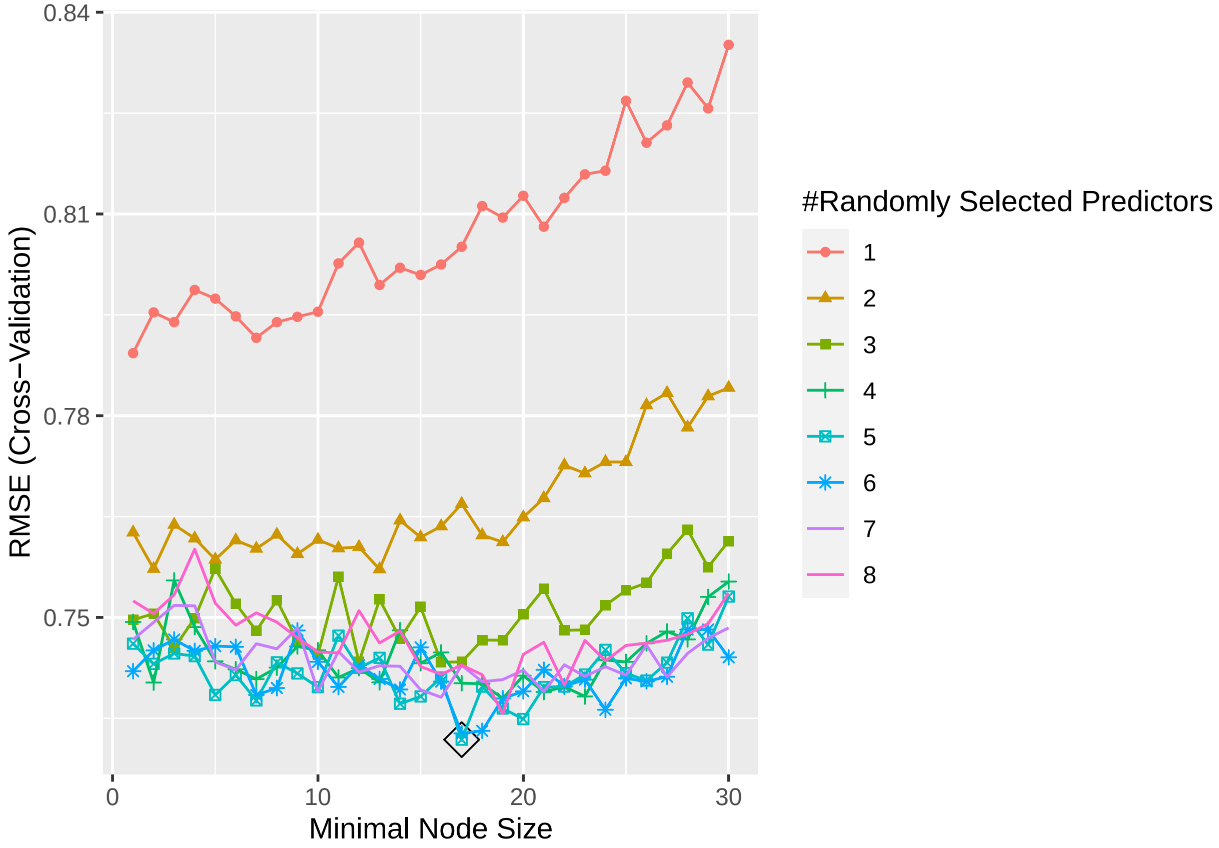
```
barplot(sort(ranger::importance(bag.fit$finalModel), decreasing = FALSE),
        las = 2, horiz = TRUE, cex.names = 0.7,
        col = colorRampPalette(colors = c("cyan","blue"))(19))
```



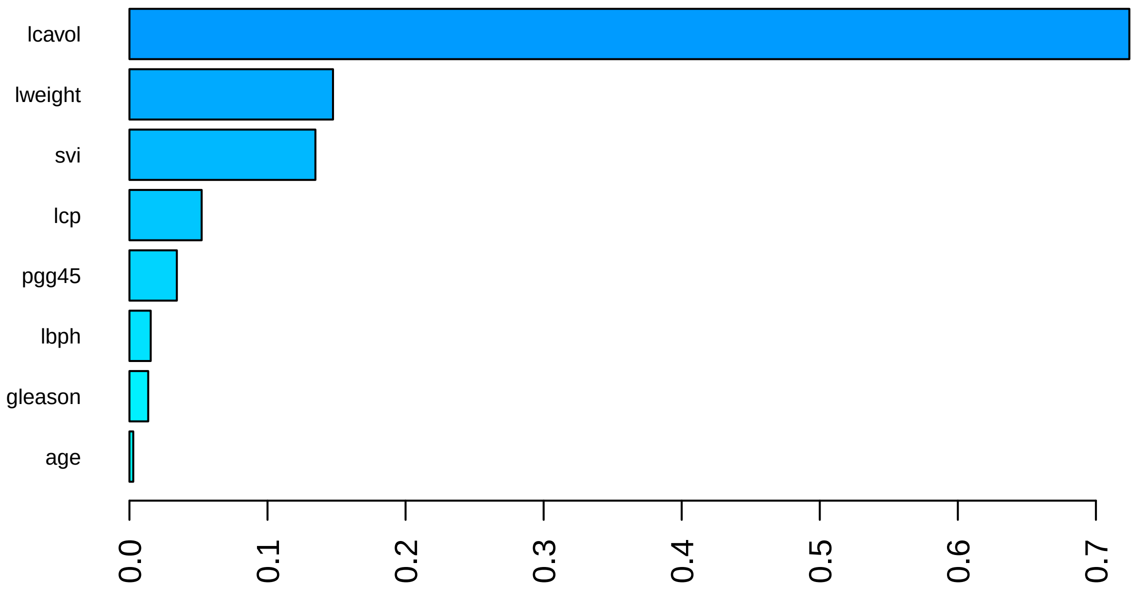
According to the plot, variable importance from highest to lowest is lcavol, lweight, svi, pgg45, lcp, gleason, lbph, and age.

Question d

```
rf.grid <- expand.grid(mtry = 1:8,
                       splitrule = "variance",
                       min.node.size = 1:30)

set.seed(1)

rf.fit <- train(lpsa ~ . ,
                prostate,
                method = "ranger",
                tuneGrid = rf.grid,
                trControl = ctrl,
                importance = "permutation")

ggplot(rf.fit, highlight = TRUE)
```



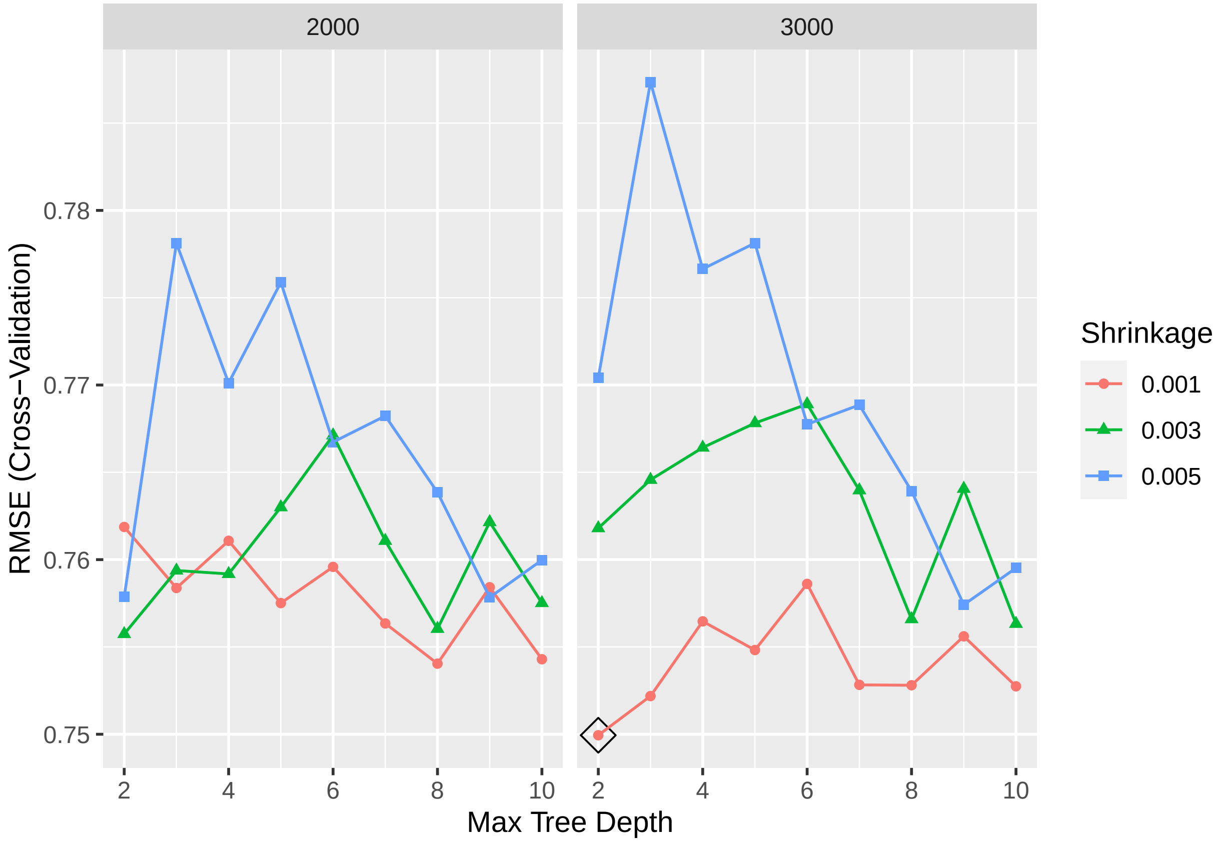
```
barplot(sort(ranger::importance(rf.fit$finalModel), decreasing = FALSE),
        las = 2, horiz = TRUE, cex.names = 0.7,
        col = colorRampPalette(colors = c("cyan","blue"))(19))
```



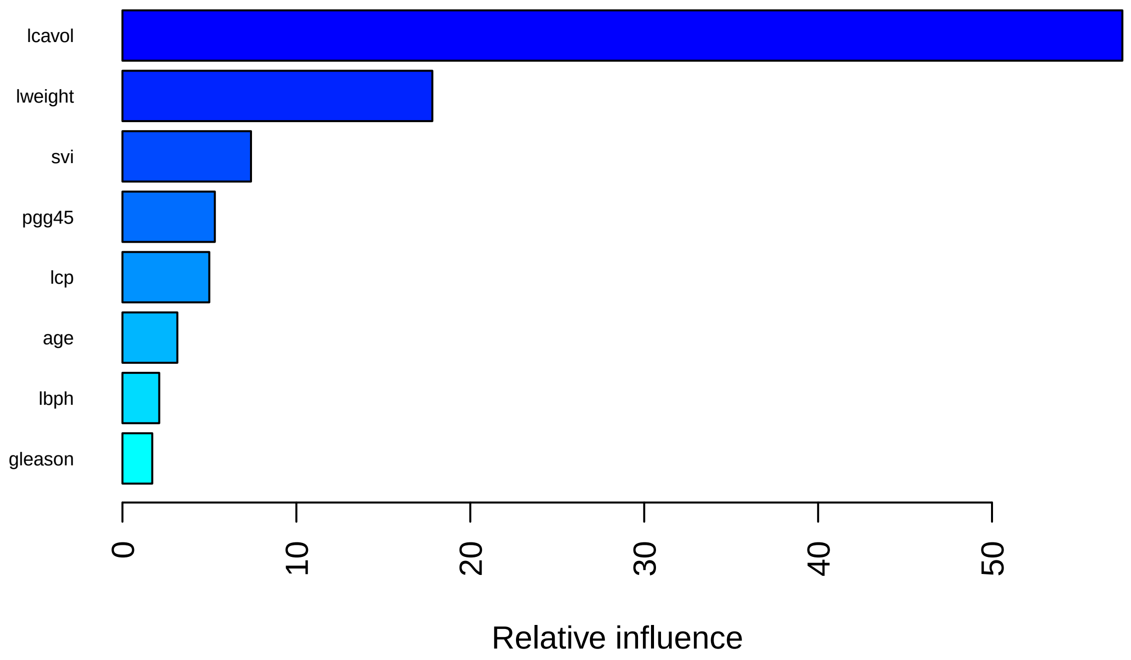
According to the plot, variable importance from highest to lowest is lcavol, lweight, svi, lcp, pgg45, lbph, gleason, and age.

Question e

```r
gbm.grid <- expand.grid(n.trees = c(2000,3000),
                        interaction.depth = 2:10,
                        shrinkage = c(0.001,0.003,0.005),
                        n.minobsinnode = 1)

set.seed(1)

gbm.fit <- train(lpsa ~ . ,
                 prostate,
                 method = "gbm",
                 tuneGrid = gbm.grid,
                 trControl = ctrl,
                 verbose = FALSE)

ggplot(gbm.fit, highlight = TRUE)
```



```
summary(gbm.fit$finalModel, las = 2, cBars = 19, cex.names = 0.6)
```



```
##             var   rel.inf
## lcavol   lcavol 57.494112
## lweight lweight 17.818879
## svi         svi  7.392286
## pgg45     pgg45  5.312763
## lcp         lcp  4.994192
## age         age  3.157564
## lbph       lbph  2.115772
## gleason gleason  1.714432
```

According to the plot, variable importance from highest to lowest is lcavol, lweight, svi, pgg45, lcp, age, lbph, and gleason.

Question f

```
resamp <- resamples(list(bag = bag.fit, rf = rf.fit, bst = gbm.fit))

summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
##
```

```
## Models: bag, rf, bst
## Number of resamples: 10
##
## MAE
##          Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## bag 0.4616225 0.5496355 0.6181923 0.6041023 0.6575394 0.7234704    0
## rf  0.4570936 0.5415374 0.6148593 0.6000239 0.6699930 0.7046284    0
## bst 0.4988605 0.5382599 0.6238535 0.6060614 0.6541746 0.7189084    0
##
## RMSE
##          Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## bag 0.5421937 0.6587298 0.7315537 0.7400910 0.8227738 0.9183309    0
## rf  0.5406496 0.6394524 0.7253799 0.7318267 0.8257673 0.9340790    0
## bst 0.6127814 0.6613586 0.7369285 0.7499428 0.8330904 0.9285269    0
##
## Rsquared
##          Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## bag 0.4337901 0.5292513 0.6201345 0.6193841 0.6972059 0.7870307    0
## rf  0.3511685 0.5449248 0.6009057 0.6156774 0.7326923 0.7714574    0
## bst 0.3912307 0.4940316 0.6253058 0.6103438 0.7211938 0.8171347    0
```

According to the table, random forest has lower mean RMSE. Consequently, I will choose random forest.

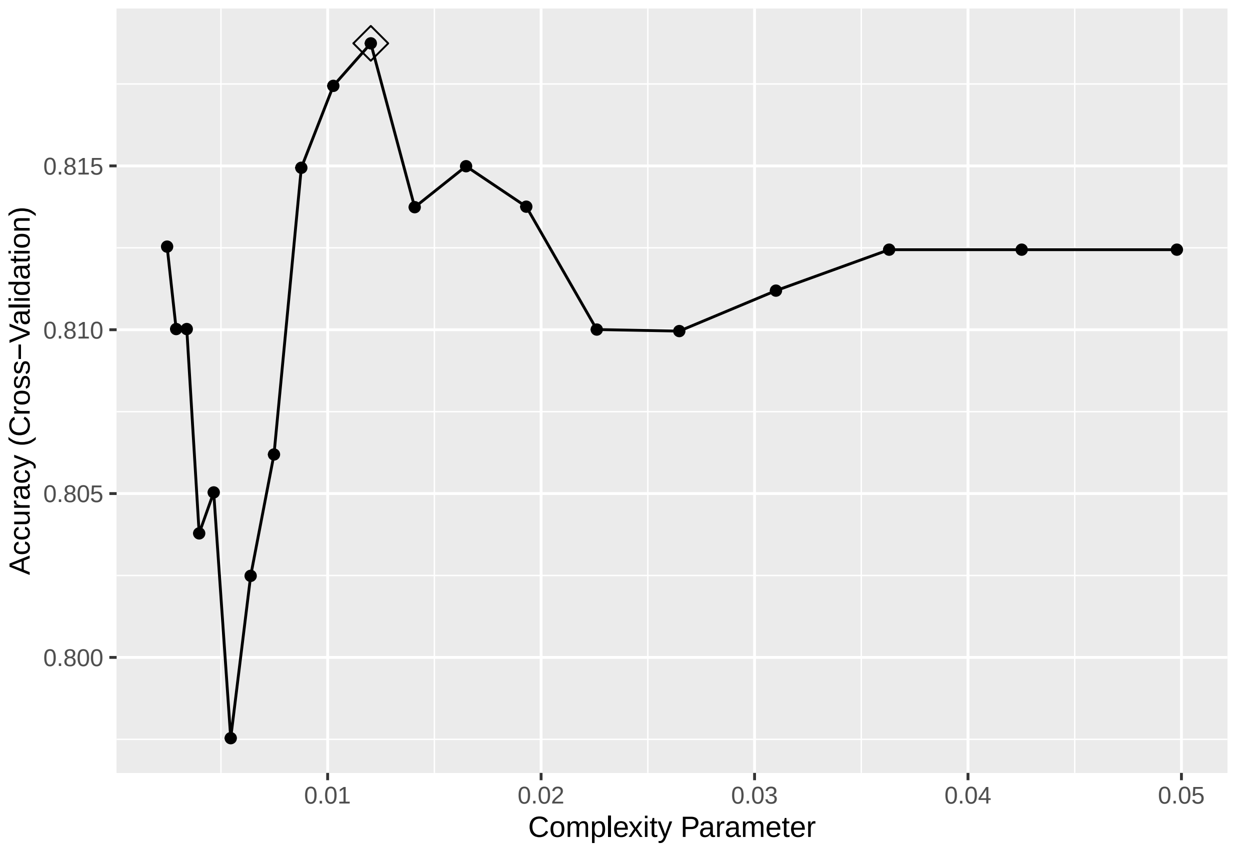
Question 2

Load, clean, and tidy data

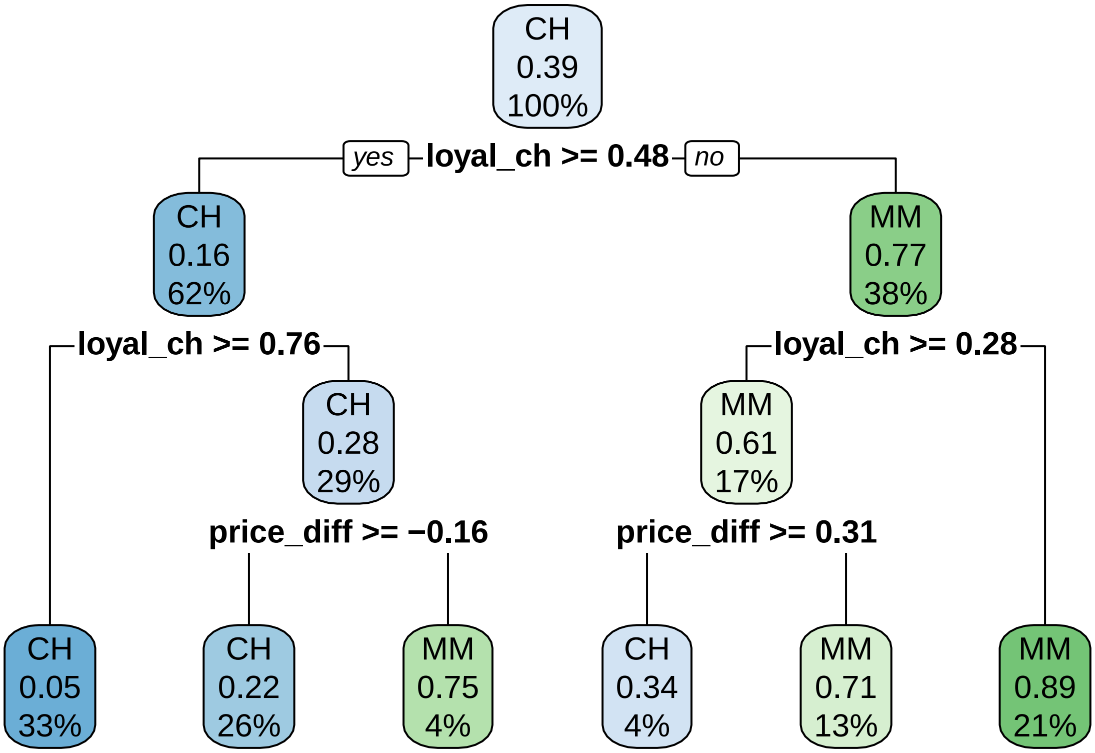
```r
data("OJ")

oj <- OJ %>%
  janitor::clean_names()

set.seed(1)

rowTrain = createDataPartition(y = oj$purchase,
                               p = 799/1070,
                               list = FALSE)
```

Question a

```r
rpart.fit <- train(purchase~.,
                   oj,
                   subset = rowTrain,
                   method = "rpart",
                   tuneGrid = data.frame(cp = exp(seq(-6,-3, len = 20))),
                   trControl = ctrl)

ggplot(rpart.fit, highlight = TRUE)
```



```
rpart.plot(rpart.fit$finalModel)
```



```r
rpart.pred <- predict(rpart.fit, newdata = oj[-rowTrain,])

mean(rpart.pred != oj$purchase[-rowTrain])
```

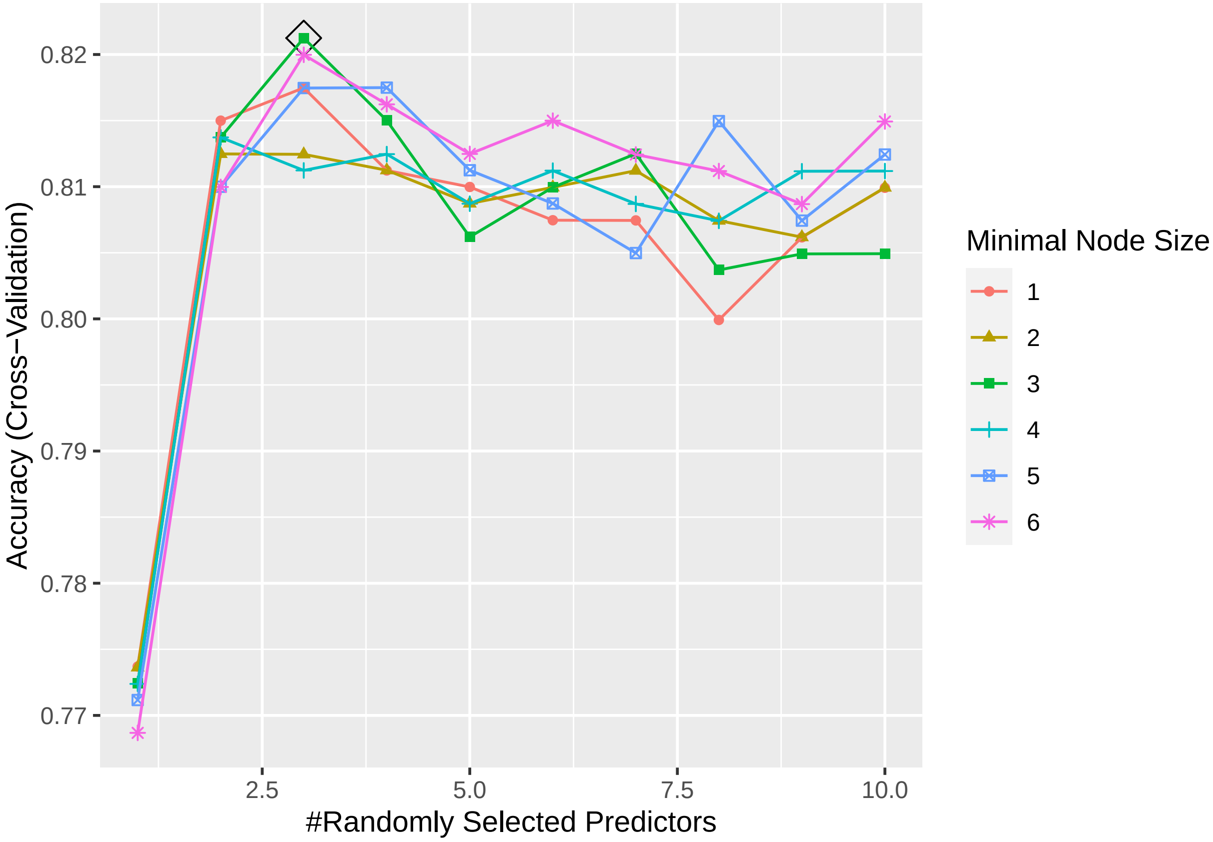
```
## [1] 0.1740741
```

The test classification error rate is 17.4%.

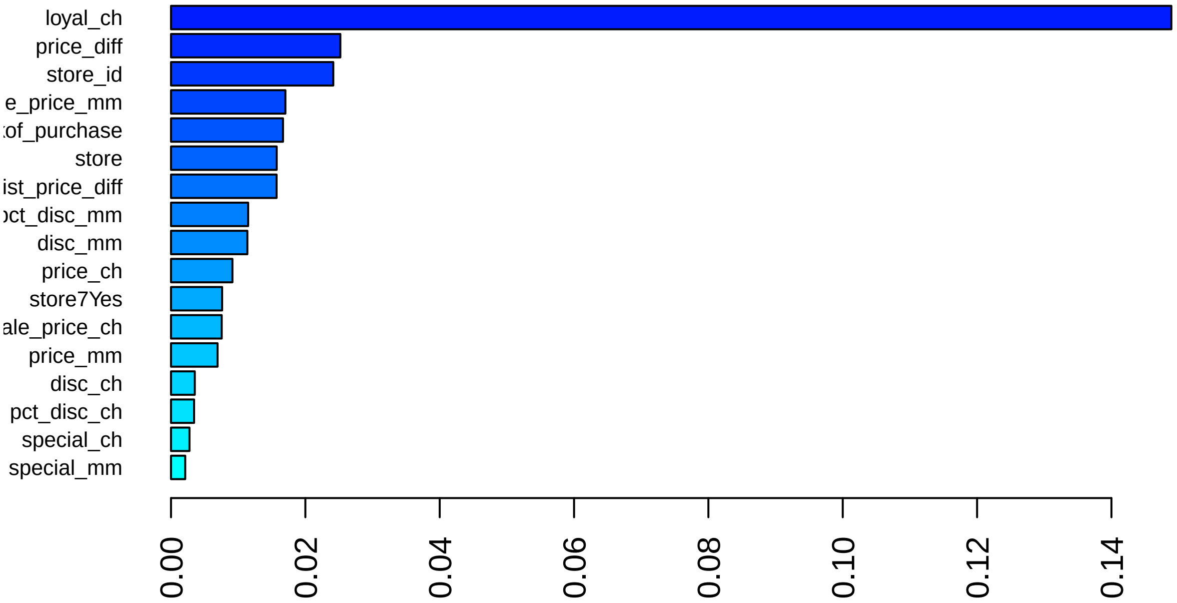
Question b

```r
rf.grid2 <- expand.grid(mtry = 1:10,
                       splitrule = "gini",
                       min.node.size = 1:6)

set.seed(1)

rf.fit2 <- train(purchase~.,
                oj,
                subset = rowTrain,
                method = "ranger",
                tuneGrid = rf.grid2,
                trControl = ctrl,
                importance = "permutation")
```

```r
ggplot(rf.fit2, highlight = TRUE)
```



```r
barplot(sort(ranger::importance(rf.fit2$finalModel), decreasing = FALSE),
        las = 2, horiz = TRUE, cex.names = 0.7,
        col = colorRampPalette(colors = c("cyan","blue"))(19))
```



```r
rf.pred <- predict(rf.fit2, newdata = oj[-rowTrain,])

mean(rf.pred != oj$purchase[-rowTrain])
```

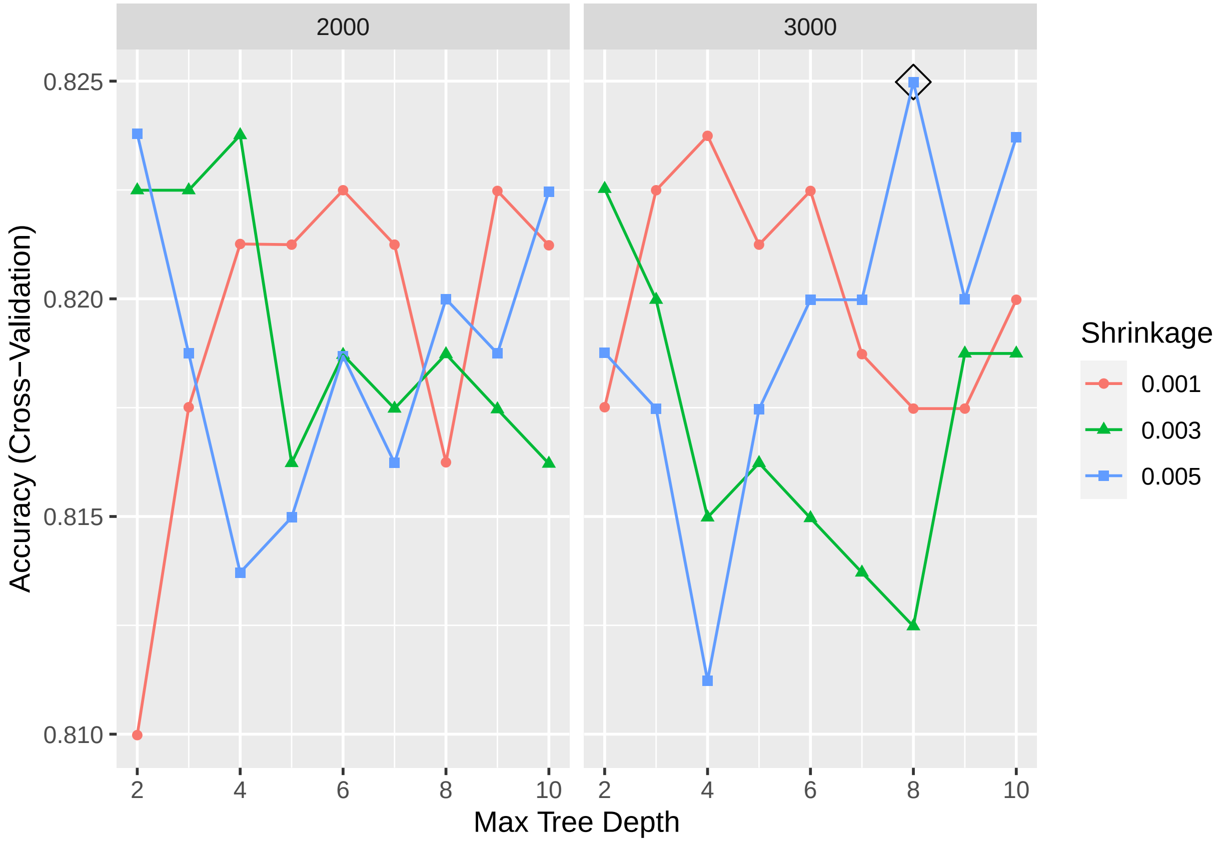
```
## [1] 0.2
```

According to the plot, variable importance rank from highest to lowest.

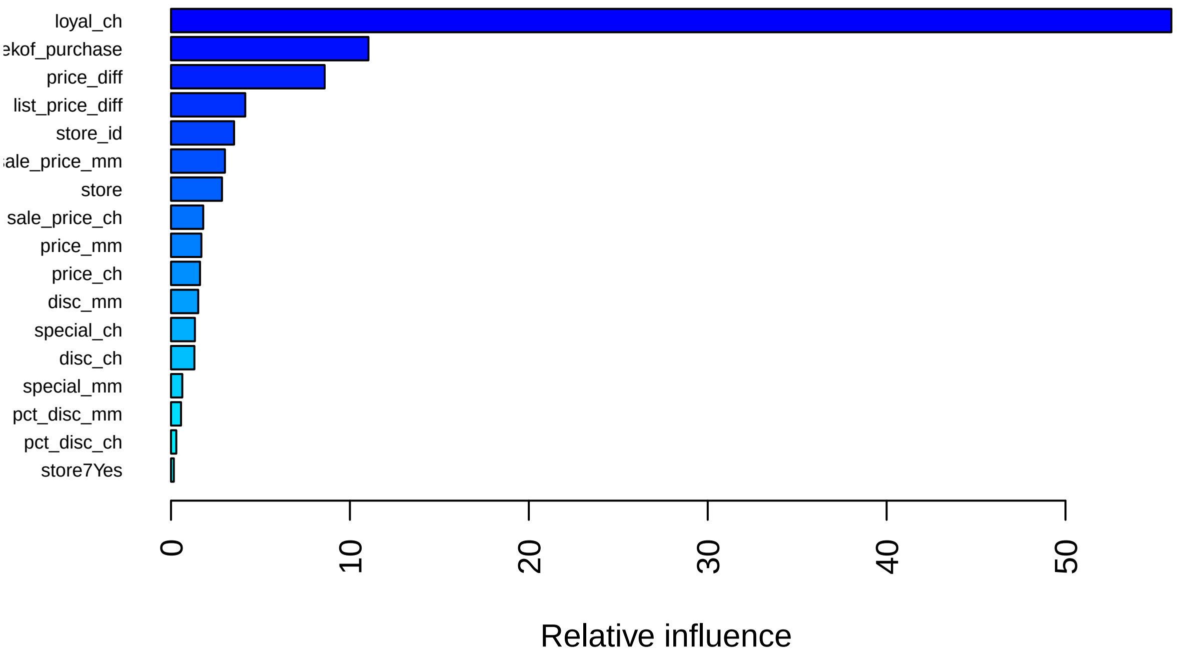
The test classification error rate is 20%.

Question c

```r
gbm.grid2 <- expand.grid(n.trees = c(2000,3000),
                         interaction.depth = 2:10,
                         shrinkage = c(0.001,0.003,0.005),
                         n.minobsinnode = 1)

set.seed(1)

gbm.fit2 <- train(purchase~.,
                  oj,
                  subset = rowTrain,
                  tuneGrid = gbm.grid2,
                  trControl = ctrl,
                 method = "gbm",
                 verbose = FALSE)

ggplot(gbm.fit2, highlight = TRUE)
```



```
summary(gbm.fit2$finalModel, las = 2, cBars = 19, cex.names = 0.6)
```



```
##                                 var    rel.inf
## loyal_ch                   loyal_ch 55.9164601
## weekof_purchase weekof_purchase 11.0343364
## price_diff               price_diff  8.5857250
## list_price_diff list_price_diff  4.1499793
## store_id                   store_id  3.5246670
## sale_price_mm         sale_price_mm  3.0143621
## store                         store  2.8499466
## sale_price_ch         sale_price_ch  1.8007158
## price_mm                   price_mm  1.6976583
## price_ch                   price_ch  1.6213438
## disc_mm                     disc_mm  1.5214530
## special_ch               special_ch  1.3350196
## disc_ch                     disc_ch  1.3058032
## special_mm               special_mm  0.6309374
## pct_disc_mm             pct_disc_mm  0.5597987
## pct_disc_ch             pct_disc_ch  0.2947931
## store7Yes                 store7Yes  0.1570006
```

```
gbm.pred <- predict(gbm.fit2, newdata = oj[-rowTrain,])

mean(gbm.pred != oj$purchase[-rowTrain])
```

```
## [1] 0.1925926
```

According to the plot, variable importance rank from highest to lowest.

The test classification error rate is 19.3%.