p8106_hw4_yg2625

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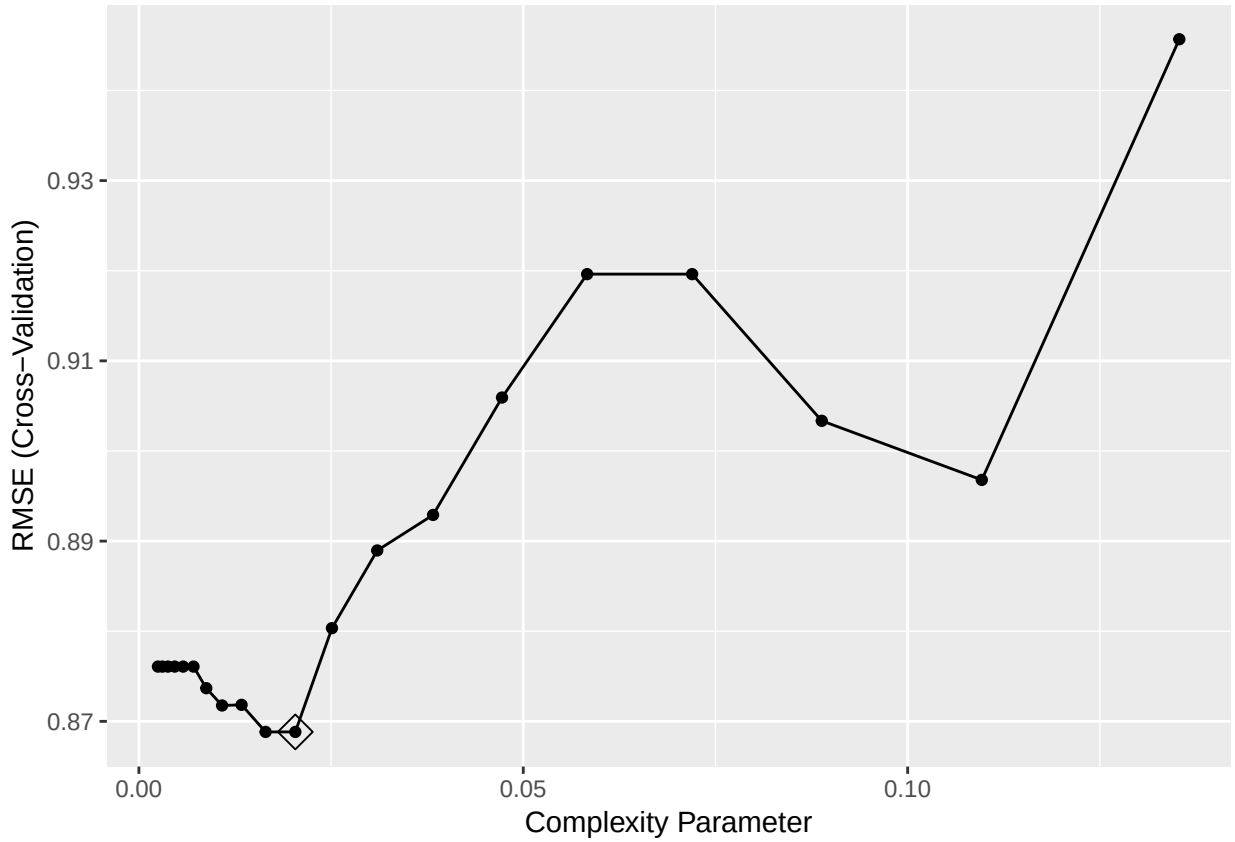
1. This problem involves the Prostate data in the lasso2 package (see L5.Rmd). Use set.seed() for reproducible results.

load data

```
data("Prostate")
pros_data = Prostate%>%
  janitor::clean_names()
```

(a) Fit a regression tree with lpsa as the response and the other variables as predictors. Use cross-validation to determine the optimal tree size. Which tree size corresponds to the lowest cross-validation error? Is this the same as the tree size obtained using the 1 SE rule?

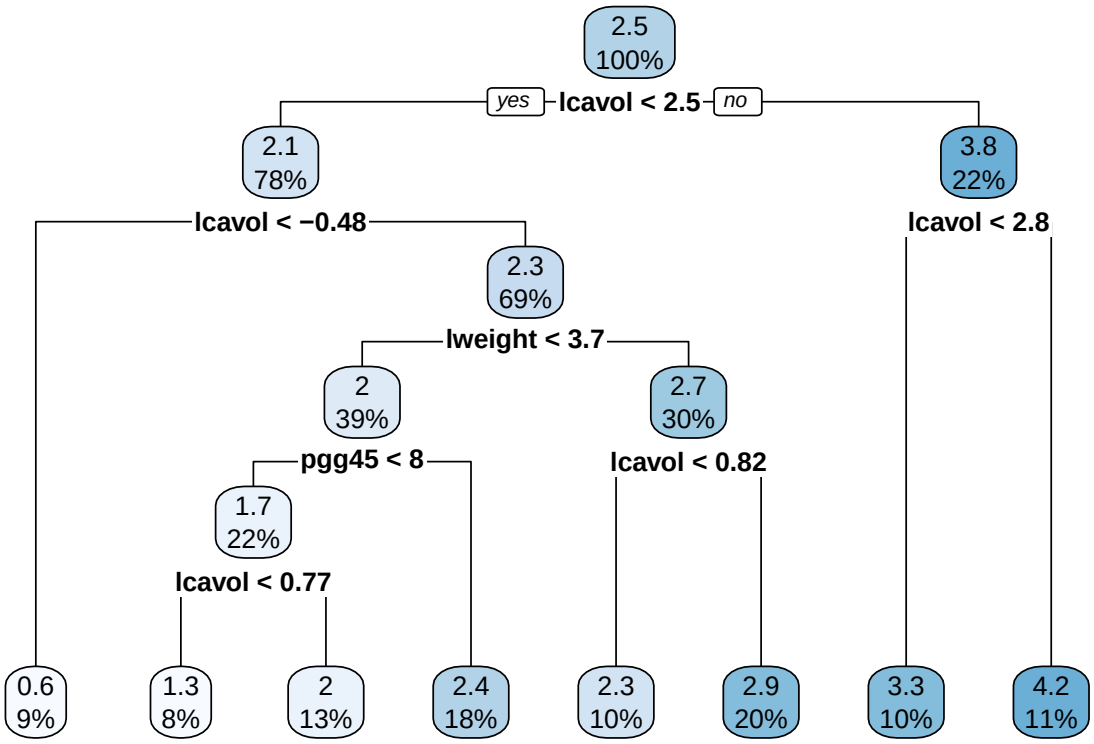
```
# use cross-validation through caret
ctrl <- trainControl(method = "cv")

# tune over cp, method = "rpart"
rpart.fit1 <- train(lpsa ~ ., pros_data,
                    method = "rpart",
                    tuneGrid = data.frame(cp = exp(seq(-6,-2, length = 20))),
                    trControl = ctrl)
ggplot(rpart.fit1, highlight = TRUE)
```




```
# cptable showed that the optimal tree size is 8
rpart.fit1$finalModel$cptable
```

```
##           CP nsplit rel error
## 1 0.34710828      0 1.0000000
## 2 0.18464743      1 0.6528917
## 3 0.05931585      2 0.4682443
## 4 0.03475635      3 0.4089284
## 5 0.03460901      4 0.3741721
## 6 0.02156368      5 0.3395631
## 7 0.02146995      6 0.3179994
## 8 0.00000000      7 0.2965295
```

```
rpart.plot(rpart.fit1$finalModel)
```



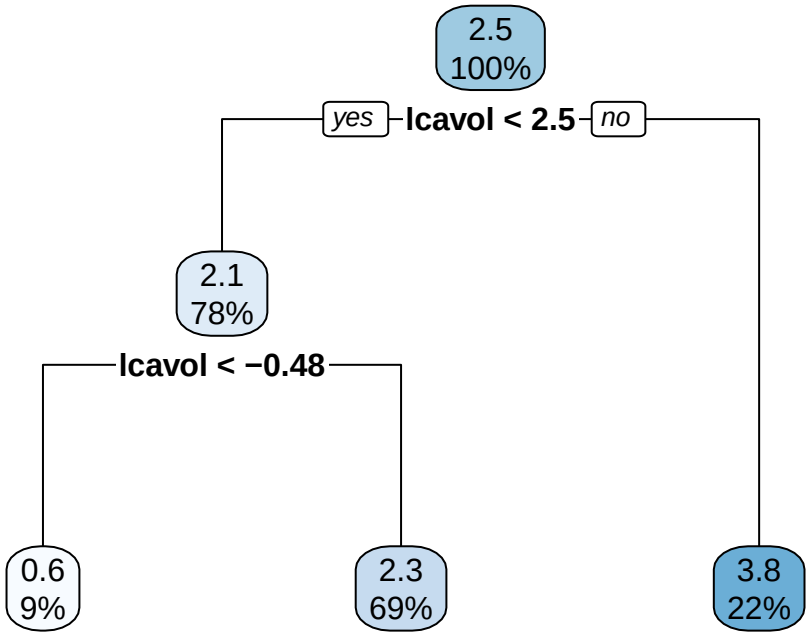

```
# use 1SE through caret
rpart.fit2 <- train(lpsa ~ ., pros_data,
                    method = "rpart",
                    tuneGrid = data.frame(cp = exp(seq(-6,-2, length = 20))),
                    trControl = trainControl(method = 'cv',
                                             number = 10,
                                             selectionFunction = 'oneSE'))
```

```
## Warning in nominalTrainWorkflow(x = x, y = y, wts = weights, info =
## trainInfo, : There were missing values in resampled performance measures.
```

```
# cptable showed that the optimal tree size is 3
rpart.fit2$finalModel$cptable
```

```
##           CP nsplit rel error
## 1 0.34710828      0 1.0000000
## 2 0.18464743      1 0.6528917
## 3 0.08882807      2 0.4682443
```

```
rpart.plot(rpart.fit2$finalModel)
```



Based on the result, cross-validation showed that the optimal tree size is 8 while 1SE obtained optimal tree size as 3. Hence, 1SE rule generates tree with smaller size.

(b) Create a plot of the final tree you choose. Pick one of the terminal nodes, and interpret the information displayed.

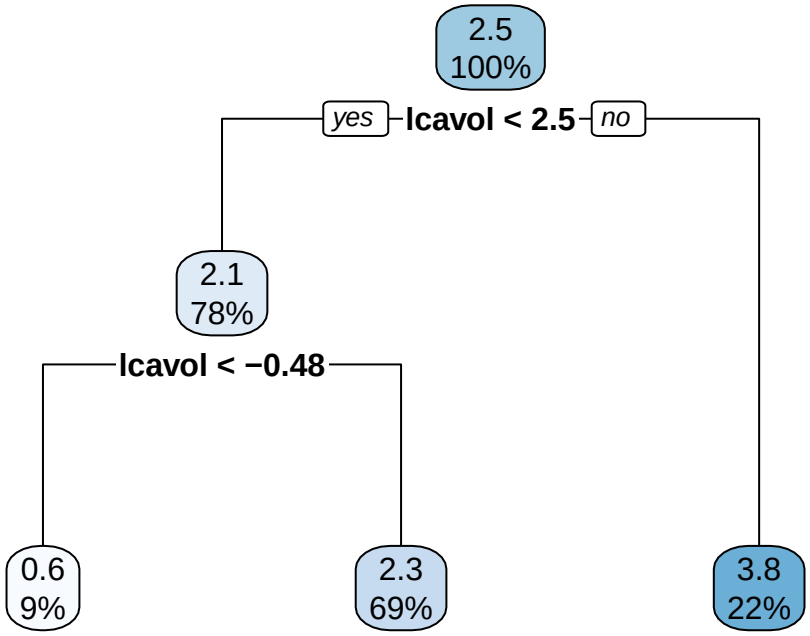
```
resamp = resamples(list(minErr = rpart.fit1, min_1se = rpart.fit2))
summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: minErr, min_1se
## Number of resamples: 10
##
## MAE
##              Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## minErr  0.6029257 0.6833061 0.7132861 0.7481058 0.7878006 1.0108929    0
## min_1se 0.5640925 0.6790613 0.7081498 0.7305603 0.7886243 0.8963087    0
##
## RMSE
##              Min.   1st Qu.    Median      Mean   3rd Qu.     Max. NA's
## minErr  0.6940977 0.7916380 0.8659767 0.8688293 0.9202064 1.116127    0
## min_1se 0.7171773 0.8096023 0.8513418 0.8740592 0.9689131 1.015270    0
```

```
##
## Rsquared
##                Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## minErr  0.10742511 0.4435906 0.5507225 0.4869429 0.5676906 0.6732530    0
## min_1se 0.08493423 0.4242442 0.4933295 0.4436730 0.5761213 0.5981874    1
```

Since two regression generates similar RMSE. Following principle of parsimony, we choose the simpler model with tree using 1SE principle. And the plot is shown below:

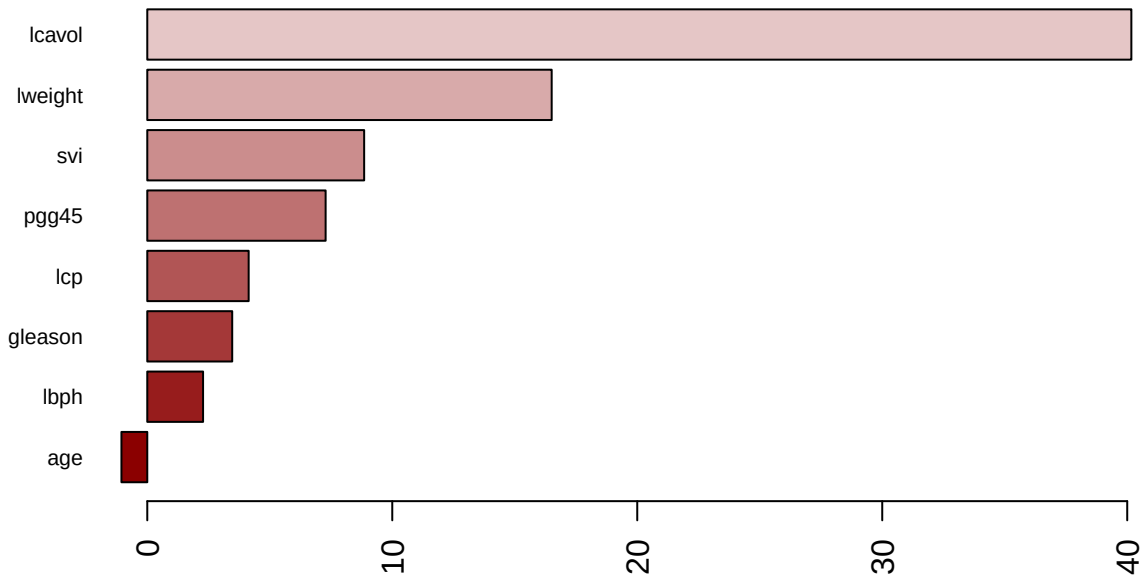
```
rpart.plot(rpart.fit2$finalModel)
```



Interpretation: The regression tree pruned by 1SE rule has size as 3. When log(cancer volume)(lcavol) is greater than 2.5, the log(prostate specific antigen) is predicted to be 3.8, which contains 22% of the trainning observations.

(c) Perform bagging and report the variable importance.

```
bagging <- ranger(lpsa ~., pros_data,
                          mtry = 8, splitrule = "variance",
                          min.node.size = 30,
                          importance = "permutation",
                          scale.permutation.importance = TRUE)

barplot(sort(ranger::importance(bagging), decreasing = FALSE),
        las = 2, horiz = TRUE, cex.names = 0.7,
        col = colorRampPalette(colors = c("darkred","white","darkblue"))(19))
```



Based on the output, variable importance ranking: lcavol>lweight>svi>pgg45>lcp>gleason>lbph>age.

(d) Perform random forests and report the variable importance.

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

rf.fit <- train(lpsa ~ ., pros_data,
                method = "ranger",
                tuneGrid = rf.grid,
                trControl = ctrl)
# get best tuning parameter alpha = 5
rf.fit$bestTune
```

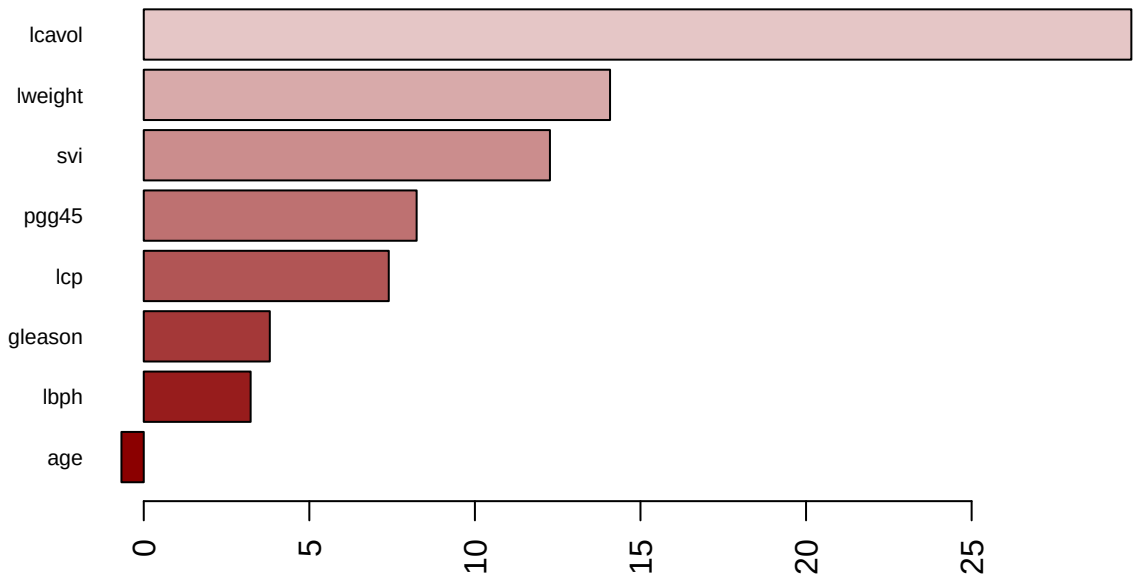
```
##     mtry splitrule min.node.size
## 141    5  variance            21
```

```
# random forests plot
ggplot(rf.fit, highlight = TRUE)
```

```
## Warning: The shape palette can deal with a maximum of 6 discrete values
## because more than 6 becomes difficult to discriminate; you have 8.
## Consider specifying shapes manually if you must have them.
```

```
## Warning: Removed 60 rows containing missing values (geom_point).
```

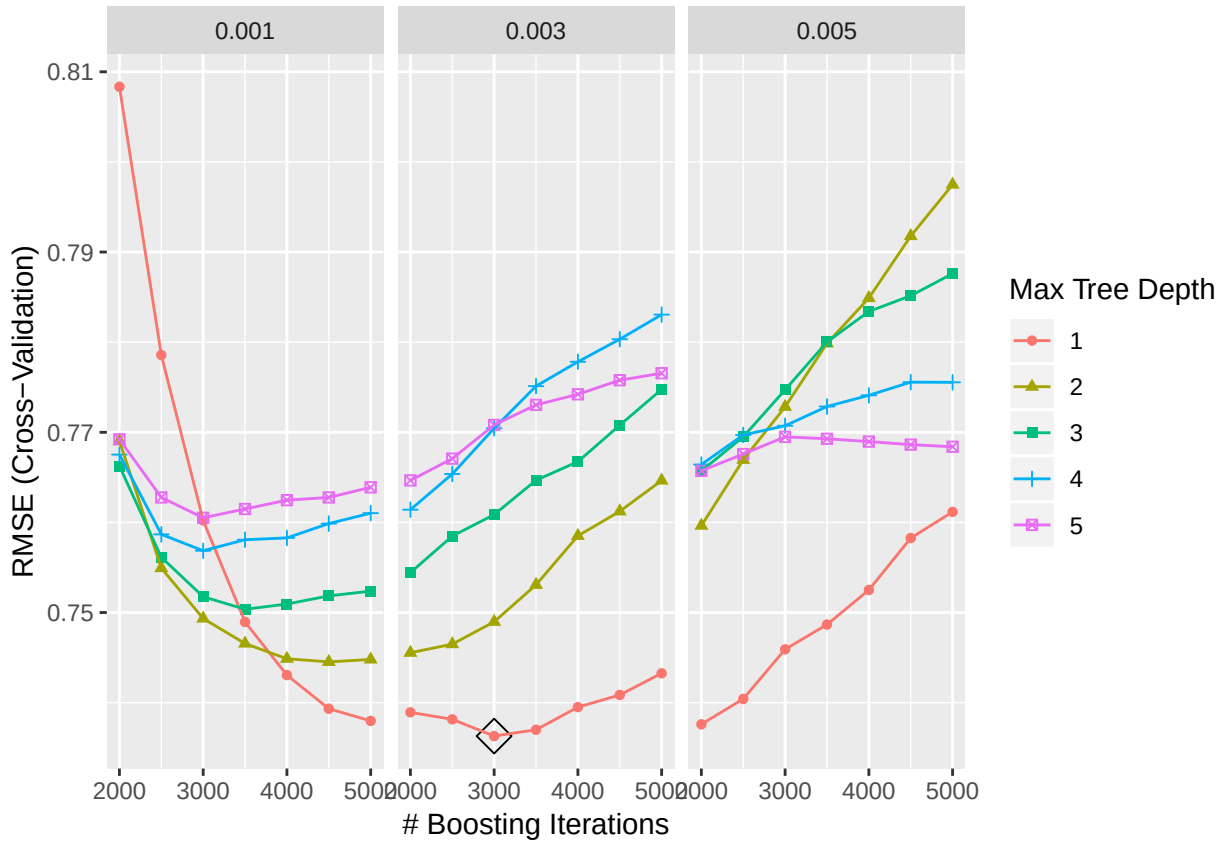

```
# fit random forest model using best tuning parameter
rf <- ranger(lpsa ~., pros_data,
                        mtry = 5, splitrule = "variance",
                        min.node.size = 30,
                        importance = "permutation",
                        scale.permutation.importance = TRUE)

barplot(sort(ranger::importance(rf), decreasing = FALSE),
        las = 2, horiz = TRUE, cex.names = 0.7,
        col = colorRampPalette(colors = c("darkred","white","darkblue"))(19))
```



Based on the output, variable importance ranking: lcavol>lweight>svi>pgg45>lcp>gleason>lbph>age.

(e) Perform boosting and report the variable importance.

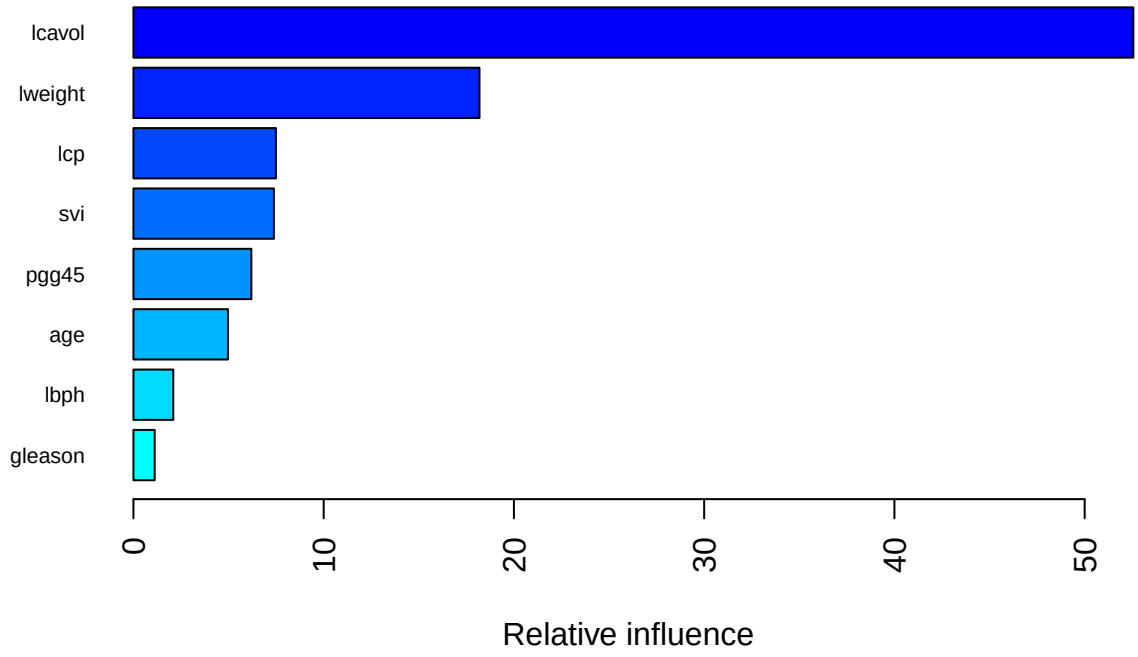
```
set.seed(1)
gbm.grid <- expand.grid(n.trees = c(2000,2500,3000,3500,4000,4500,5000),
                        interaction.depth = 1:5,
                        shrinkage = c(0.001,0.003,0.005),
                        n.minobsinnode = 1)

gbm.fit <- train(lpsa ~ ., pros_data,
                 tuneGrid = gbm.grid,
                 trControl = ctrl,
                 method = "gbm",
                 verbose = FALSE)
# boosting plot
ggplot(gbm.fit, highlight = TRUE)
```




```
# best tunning parameter alpha = 38
gbm.fit$bestTune
```

```
##    n.trees interaction.depth shrinkage n.minobsinnode
## 38    3000                 1     0.003              1
```

```
# summary output
summary(gbm.fit, las = 2, cex.names = 0.7)
```




```
##             var   rel.inf
## lcavol   lcavol 52.559738
## lweight lweight 18.189924
## lcp         lcp  7.489362
## svi         svi  7.382924
## pgg45     pgg45  6.198291
## age         age  4.968294
## lbph       lbph  2.094587
## gleason gleason  1.116880
```

Based on the result, variable importance ranking: lcavol>lweight>svi>lcp>pgg45>age>lbph>gleason.

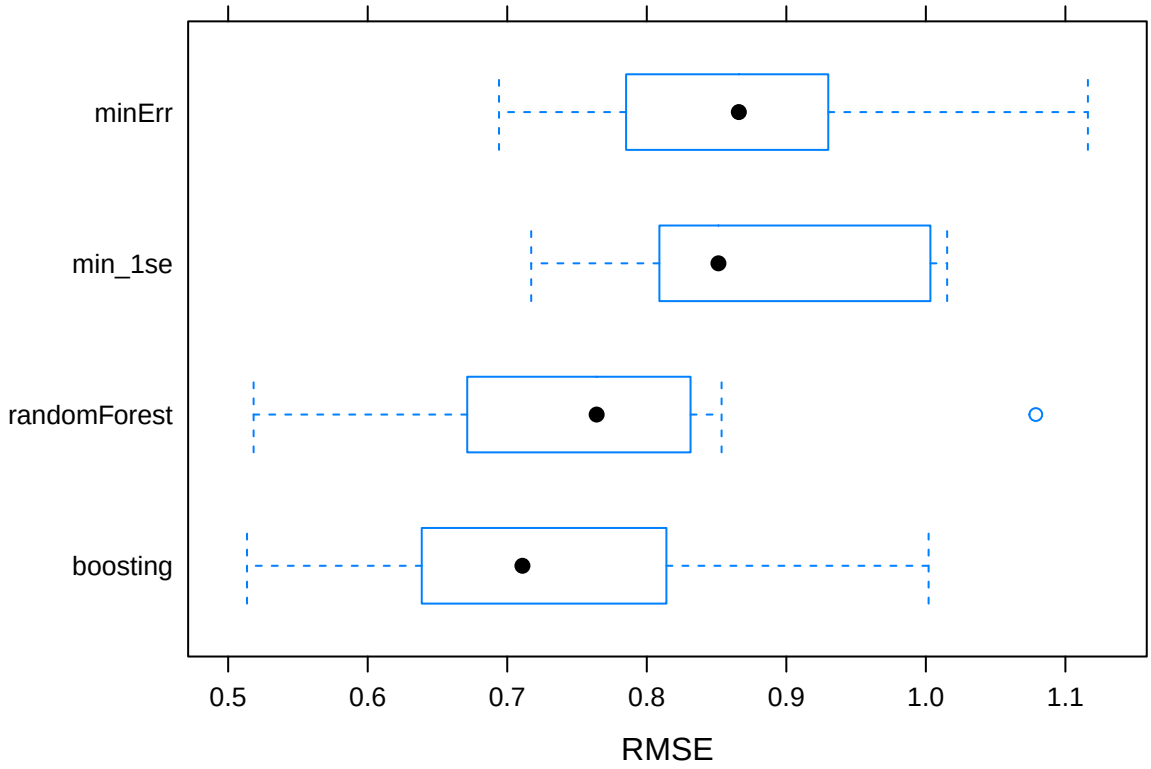
(f) Which of the above models will you select to predict PSA level? Explain.

```
resamp2 = resamples(list(minErr = rpart.fit1,
                         min_1se = rpart.fit2,
                         randomForest = rf.fit,
                         boosting = gbm.fit))

summary(resamp2)
```

```
##
## Call:
## summary.resamples(object = resamp2)
```

```
##
## Models: minErr, min_1se, randomForest, boosting
## Number of resamples: 10
##
## MAE
##                   Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
## minErr       0.6029257 0.6833061 0.7132861 0.7481058 0.7878006 1.0108929
## min_1se      0.5640925 0.6790613 0.7081498 0.7305603 0.7886243 0.8963087
## randomForest 0.4391181 0.5799877 0.5927113 0.6231634 0.6411043 0.9684338
## boosting     0.4199595 0.4948608 0.5521303 0.6014267 0.6682515 0.8755513
##              NA's
## minErr          0
## min_1se         0
## randomForest    0
## boosting        0
##
## RMSE
##                   Min.   1st Qu.    Median      Mean   3rd Qu.     Max.
## minErr       0.6940977 0.7916380 0.8659767 0.8688293 0.9202064 1.116127
## min_1se      0.7171773 0.8096023 0.8513418 0.8740592 0.9689131 1.015270
## randomForest 0.5182232 0.6775767 0.7640668 0.7500340 0.8232725 1.078782
## boosting     0.5134918 0.6555081 0.7108809 0.7362931 0.7893717 1.001967
##              NA's
## minErr          0
## min_1se         0
## randomForest    0
## boosting        0
##
## Rsquared
##                    Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
## minErr       0.10742511 0.4435906 0.5507225 0.4869429 0.5676906 0.6732530
## min_1se      0.08493423 0.4242442 0.4933295 0.4436730 0.5761213 0.5981874
## randomForest 0.23616569 0.6109251 0.6770639 0.6289637 0.7185763 0.7342918
## boosting     0.37577693 0.5852946 0.6866416 0.6439764 0.7348701 0.7897067
##              NA's
## minErr          0
## min_1se         1
## randomForest    0
## boosting        0
```

```
bwplot(resamp2, metric = "RMSE")
```



Based on the output, simple regression trees method including minimum CV error and 1SE principle methods generates model with larger RMSE than ensemble methods(bagging, random forest, boosting). And bagging being a special case of random forest selecting 8 predictors(mtry = 8) without tunning, violated principle of parsimony compared to random forest and boosting methods. Boosting generates model with smaller RMSE than randomForest. Hence, boosting model is most preferrable.

2. This problem involves the OJ data in the ISLR package. The data contains 1070 purchases where the customers either purchased Citrus Hill or Minute Maid Orange Juice. A number of characteristics of customers and products are recorded. Create a training set containing a random sample of 800 observations, and a test set containing the remaining observations. Use set.seed() for reproducible results.

load data

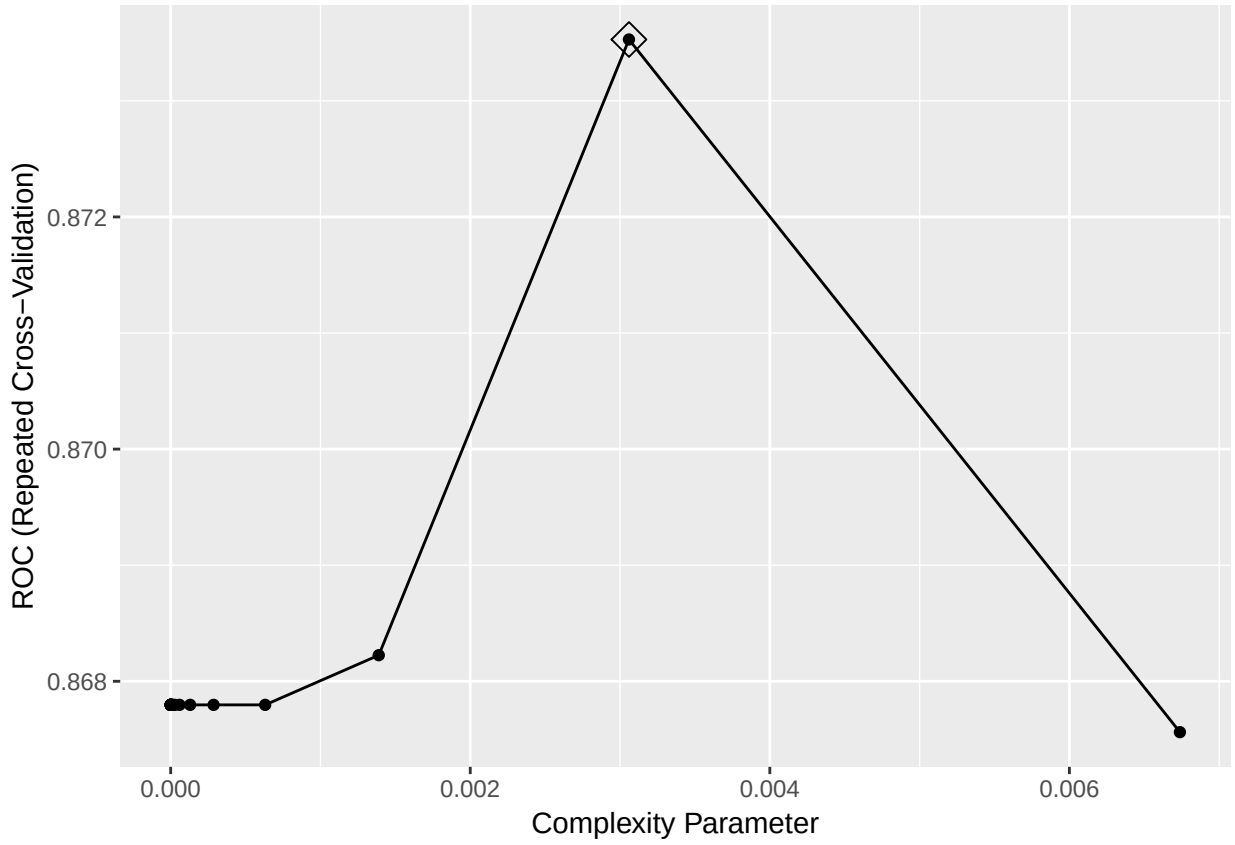
```
data(OJ)
oj_data = OJ %>%
  janitor::clean_names()

# create a training set containing 800 obs
set.seed(1)
rowTrain = createDataPartition(y = oj_data$purchase,
                               p = 799/1070,
                               list = F)

train_data = oj_data[rowTrain, ]
test_data = oj_data[-rowTrain, ]
# check whether there is 800 obs
```

```r
dim(train_data)
```

```
## [1] 800  18
```

(a) Fit a classification tree to the training set, with Purchase as the response and the other variables as predictors. Use cross-validation to determine the tree size and create a plot of the final tree. Predict the response on the test data. What is the test classification error rate?

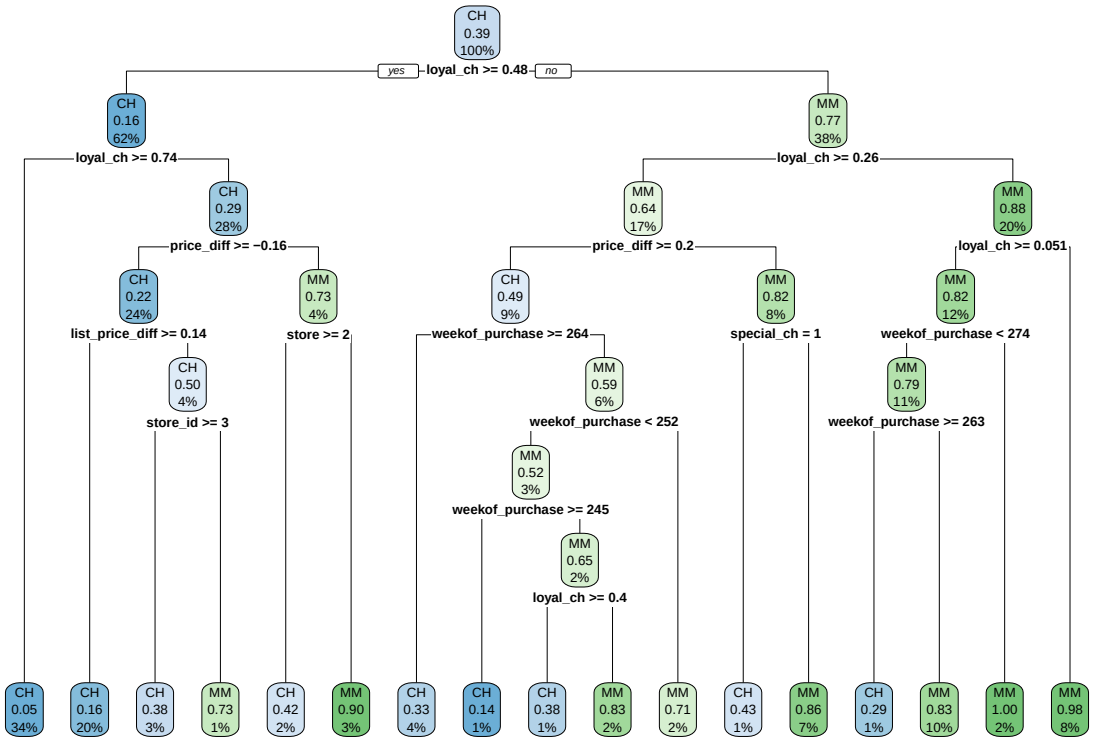
```r
ctrl2 <- trainControl(method = "repeatedcv",
                      summaryFunction = twoClassSummary,
                      classProbs = TRUE)

set.seed(1)
rpart.fit_oj <- train(purchase ~ ., train_data,
                  method = "rpart",
                  tuneGrid = data.frame(cp = exp(seq(-20,-5, len = 20))),
                  trControl = ctrl2,
                  metric = "ROC")

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



```
# optimal tree size is 17 with smallest CV error
rpart.fit_oj$finalModel$cptable
```

```
##            CP nsplit rel error
## 1 0.525641026      0 1.0000000
## 2 0.024038462      1 0.4743590
## 3 0.010683761      3 0.4262821
## 4 0.008012821      6 0.3942308
## 5 0.006410256     10 0.3621795
## 6 0.003205128     12 0.3493590
## 7 0.003059592     16 0.3365385
```

```
# plot of tree
rpart.plot(rpart.fit_oj$finalModel)
```




```
# predict response on test data
pred = predict(rpart.fit_oj, newdata = test_data,
               type = "raw");pred
```

```
##   [1] CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH
##  [24] CH CH CH CH CH CH CH CH CH CH MM MM CH CH CH CH CH CH CH CH CH CH CH CH
##  [47] CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH
##  [70] CH CH CH CH MM MM MM MM MM MM MM CH MM MM CH CH CH MM MM CH CH CH CH
##  [93] CH CH CH CH MM MM MM MM CH MM MM CH MM CH CH CH MM MM CH CH CH CH CH
## [116] CH CH CH MM CH CH CH CH CH CH CH MM MM MM MM CH CH CH CH CH CH CH MM
## [139] CH CH MM MM MM MM MM MM MM MM MM CH MM MM CH CH CH MM CH CH CH CH CH
## [162] CH CH CH CH MM CH CH CH MM CH CH CH CH CH CH CH MM MM MM CH MM MM MM
```

```
## [185] MM MM MM MM MM MM MM CH CH CH MM MM CH CH MM CH MM MM CH CH CH CH CH
## [208] CH CH MM CH MM MM CH CH CH CH CH CH CH CH CH CH MM CH CH CH CH CH MM
## [231] CH CH CH MM MM MM MM CH MM MM MM MM MM MM MM MM MM MM MM CH MM MM MM
## [254] MM MM MM CH CH CH CH CH CH CH CH CH CH CH CH CH MM CH
## Levels: CH MM
```

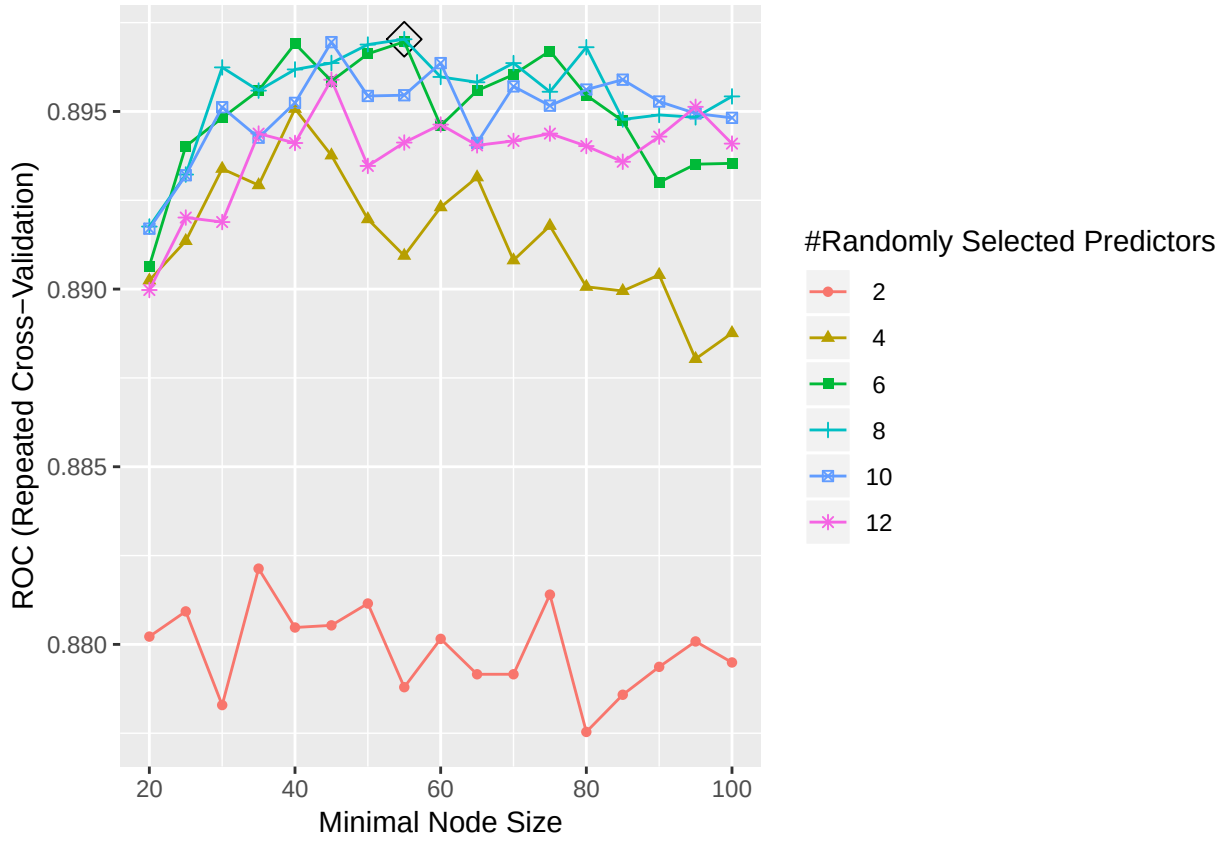
```
# test classification error rate
1 - mean(test_data$purchase == pred)
```

```
## [1] 0.2074074
```

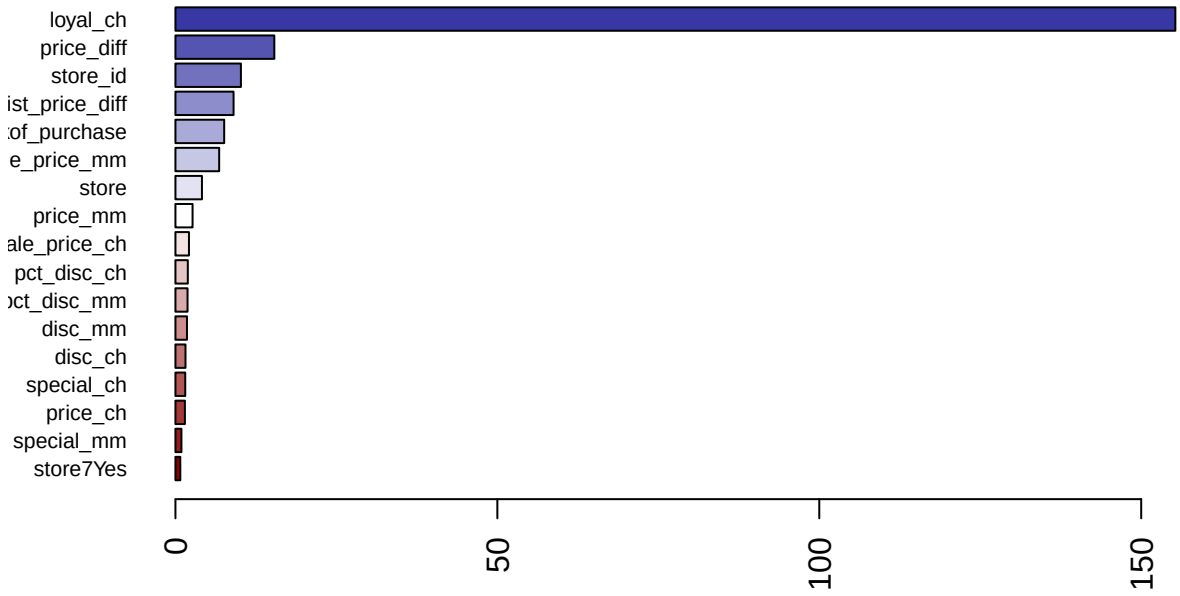
Hence, the optimal tree size is 17 and the test classification error rate is 0.207.

(b) Perform random forests on the training set and report variable importance. What is the test error rate?

```
rf.grid_oj <- expand.grid(mtry = seq(2,12,2),
                          splitrule = "gini",
                          min.node.size = seq(20,100,5))
set.seed(1)
rf.fit_oj <- train(purchase ~ ., train_data,
                   method = "ranger",
                   tuneGrid = rf.grid_oj,
                   metric = "ROC",
                   importance = "impurity",
                   trControl = ctrl2)
# rf plot
ggplot(rf.fit_oj, highlight = TRUE)
```




```
# compare variable importance
barplot(sort(ranger::importance(rf.fit_oj$finalModel), decreasing = FALSE),
        las = 2, horiz = TRUE, cex.names = 0.7,
        col = colorRampPalette(colors = c("darkred","white","darkblue"))(19))
```




```
# predict on test data
pred2 = predict(rf.fit_oj, newdata = test_data,
                type = "raw");pred
```

```
##   [1] CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH
##  [24] CH CH CH CH CH CH CH CH CH CH MM MM CH CH CH CH CH CH CH CH CH CH CH CH
##  [47] CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH
##  [70] CH CH CH CH MM MM MM MM MM MM MM CH MM MM CH CH CH MM MM CH CH CH CH
##  [93] CH CH CH CH MM MM MM MM CH MM MM CH MM CH CH CH MM MM CH CH CH CH CH
## [116] CH CH CH MM CH CH CH CH CH CH CH MM MM MM MM CH CH CH CH CH CH CH MM
## [139] CH CH MM MM MM MM MM MM MM MM MM CH MM MM CH CH CH MM CH CH CH CH CH
## [162] CH CH CH CH MM CH CH CH MM CH CH CH CH CH CH CH MM MM MM CH MM MM MM
## [185] MM MM MM MM MM MM MM CH CH CH MM MM CH CH MM CH MM MM CH CH CH CH CH
## [208] CH CH MM CH MM MM CH CH CH CH CH CH CH CH CH CH MM CH CH CH CH CH MM
## [231] CH CH CH MM MM MM MM CH MM MM MM MM MM MM MM MM MM MM CH MM MM MM
## [254] MM MM MM CH CH CH CH CH CH CH CH CH CH CH CH MM CH
## Levels: CH MM
```

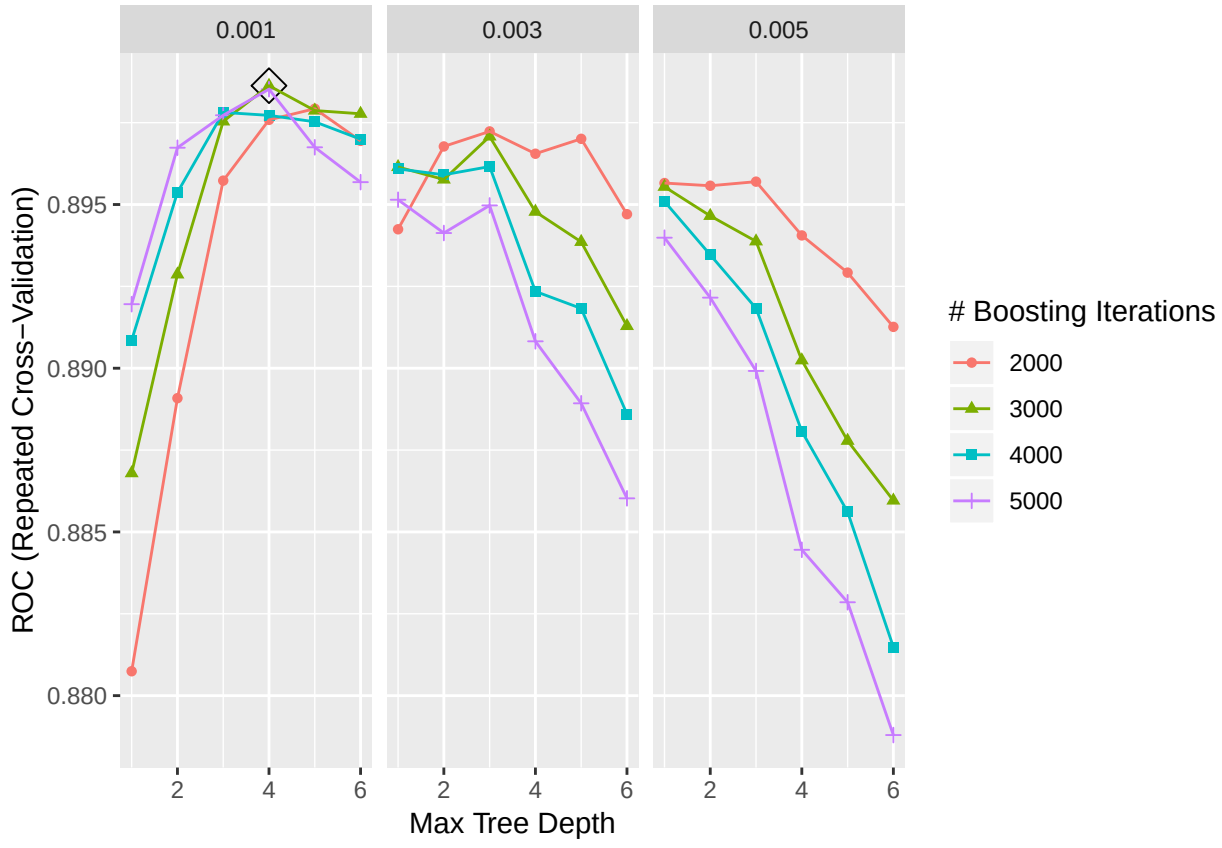
```
# test error rate
1 - mean(test_data$purchase == pred2)
```

```
## [1] 0.1851852
```

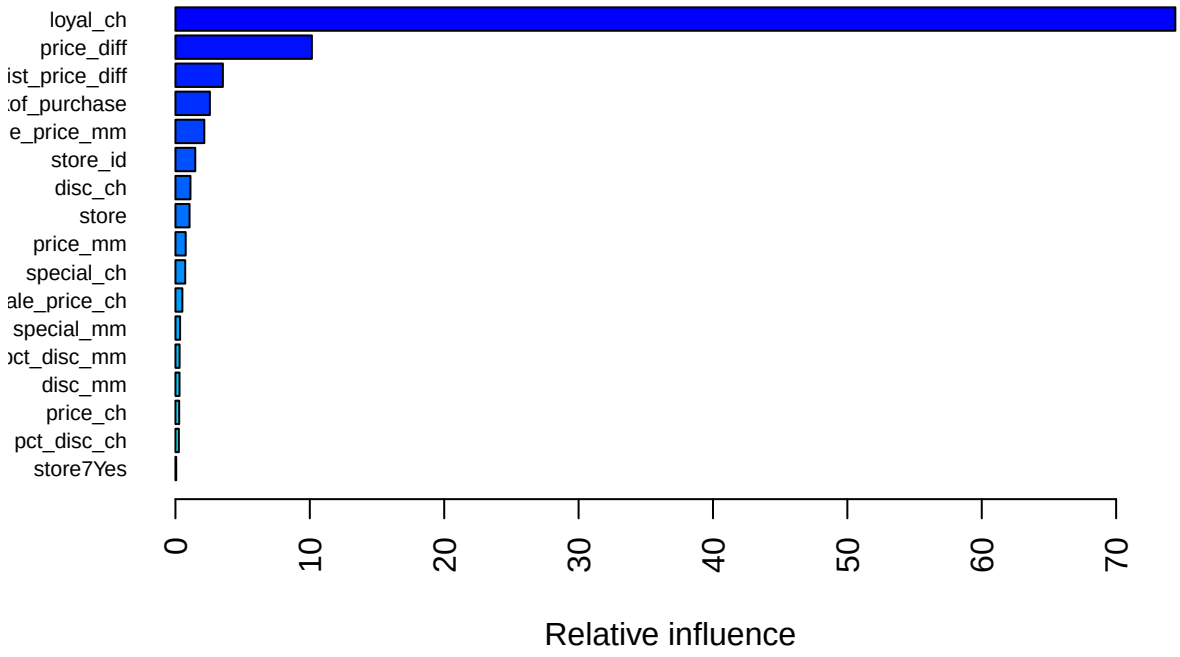
Based on the result, variable importance ranking top 5(based on impurity): loyal_ch > price_diff > store_id > list_price_diff > week_of_purchase, and store7Yes has least importance. The test error rate is 0.185.

(c) Perform boosting on the training set and report variable importance. What is the test error rate?

```
set.seed(1)
gbm.grid_oj <- expand.grid(n.trees = seq(2000,5000,1000),
                           interaction.depth = 1:6,
                           shrinkage = c(0.001,0.003,0.005),
                           n.minobsinnode = 1)

gbm.fit_oj <- train(purchase ~ ., train_data,
                    tuneGrid = gbm.grid_oj,
                    trControl = ctrl2,
                    method = "gbm",
                    distribution = "bernoulli",
                    metric = "ROC",
                    verbose = FALSE)
# boosting plot
ggplot(gbm.fit_oj, highlight = TRUE)
```




```
# showing boosting output to compare variable importance
summary(gbm.fit_oj, las = 2, cex.names = 0.7)
```




```
##                              var     rel.inf
## loyal_ch               loyal_ch 74.40696463
## price_diff           price_diff 10.15330714
## list_price_diff list_price_diff  3.53011611
## weekof_purchase weekof_purchase  2.56357515
## sale_price_mm     sale_price_mm  2.14822889
## store_id               store_id  1.47539447
## disc_ch                 disc_ch  1.11626896
## store                     store  1.04910068
## price_mm               price_mm  0.76460598
## special_ch           special_ch  0.72884720
## sale_price_ch     sale_price_ch  0.51509395
## special_mm           special_mm  0.34477001
## pct_disc_mm         pct_disc_mm  0.30903481
## disc_mm                 disc_mm  0.30450219
## price_ch               price_ch  0.27852532
## pct_disc_ch         pct_disc_ch  0.25457303
## store7Yes             store7Yes  0.05709149
```

```
# predict on test data
pred3 = predict(gbm.fit_oj, newdata = test_data,
                type = "raw");pred
```

```
##   [1] CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH
##  [24] CH CH CH CH CH CH CH CH CH CH MM MM CH CH CH CH CH CH CH CH CH CH CH CH
##  [47] CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH CH
##  [70] CH CH CH CH MM MM MM MM MM MM MM CH MM MM CH CH CH MM MM CH CH CH CH
```

```
##  [93] CH CH CH CH MM MM MM MM CH MM MM CH MM CH CH CH MM MM CH CH CH CH CH
## [116] CH CH CH MM CH CH CH CH CH CH CH MM MM MM MM CH CH CH CH CH CH CH MM
## [139] CH CH MM MM MM MM MM MM MM MM MM CH MM MM CH CH CH MM CH CH CH CH CH
## [162] CH CH CH CH MM CH CH CH MM CH CH CH CH CH CH CH MM MM MM CH MM MM MM
## [185] MM MM MM MM MM MM MM CH CH CH MM MM CH CH MM CH MM MM CH CH CH CH CH
## [208] CH CH MM CH MM MM CH CH CH CH CH CH CH CH CH CH MM CH CH CH CH CH MM
## [231] CH CH CH MM MM MM MM CH MM MM MM MM MM MM MM MM MM MM MM CH MM MM MM
## [254] MM MM MM CH CH CH CH CH CH CH CH CH CH CH CH MM CH
## Levels: CH MM
```

```r
# test error rate
1 - mean(test_data$purchase == pred3)
```

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

Based on the output, variable importance ranking top 5: loyal_ch > price_diff > list_price_diff > week_of_purchase > sale_price_mm, and store7Yes has least importance. The test error rate is 0.193.