P8106_hw4_xh2395

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Homework 4 problem 1 Description

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

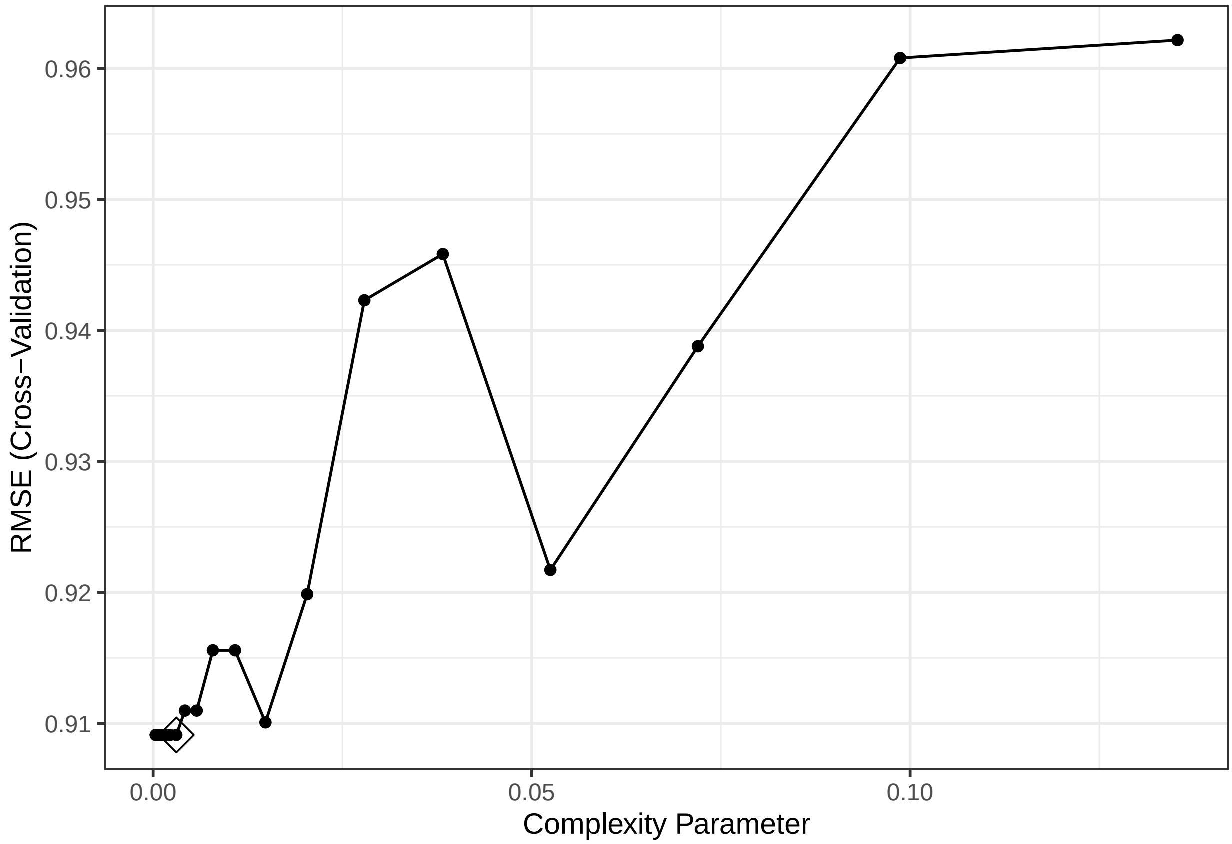
Problem 1

a) Fit a regression tree

The lowest cross-validation error

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

```
set.seed(2020)

tree_fit = train(lpsa~.,
             data = Prostate,
             method = "rpart",
             tuneGrid = data.frame(cp =exp(seq(-8,-2, length = 20))),
             trControl = ctrl)

ggplot(tree_fit, highlight = TRUE)
```



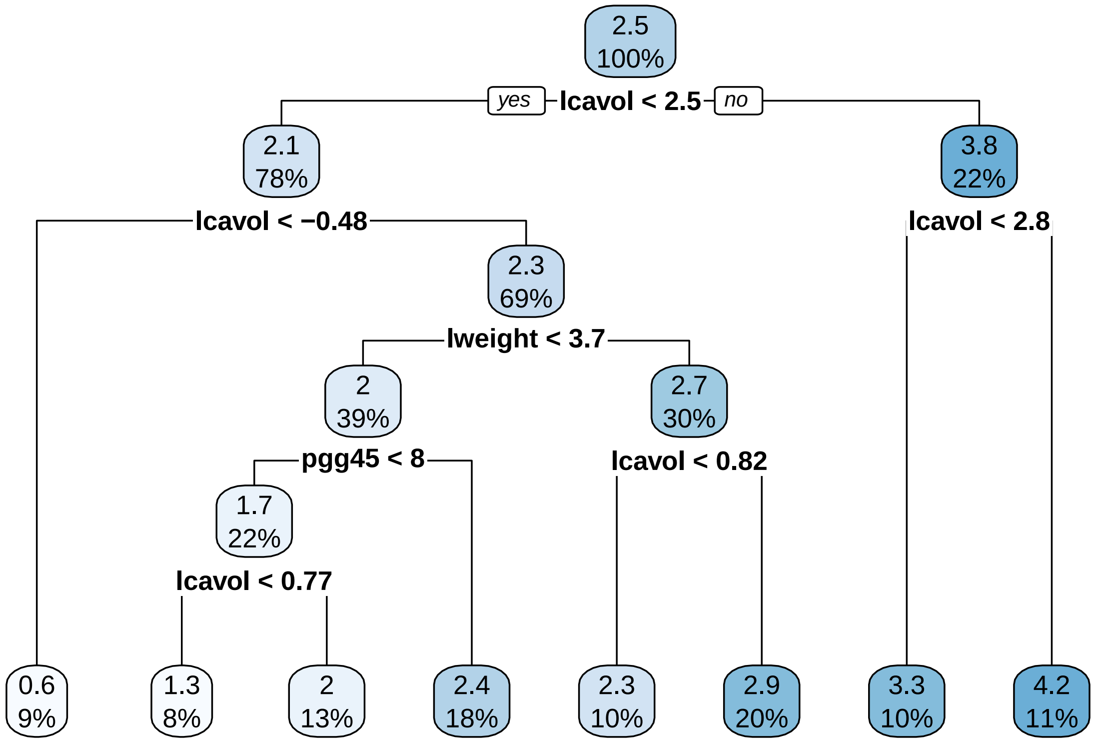

```r
tree_fit$bestTune
```

```
##             cp
## 8 0.003059592
```

```r
tree_fit$finalModel$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
```

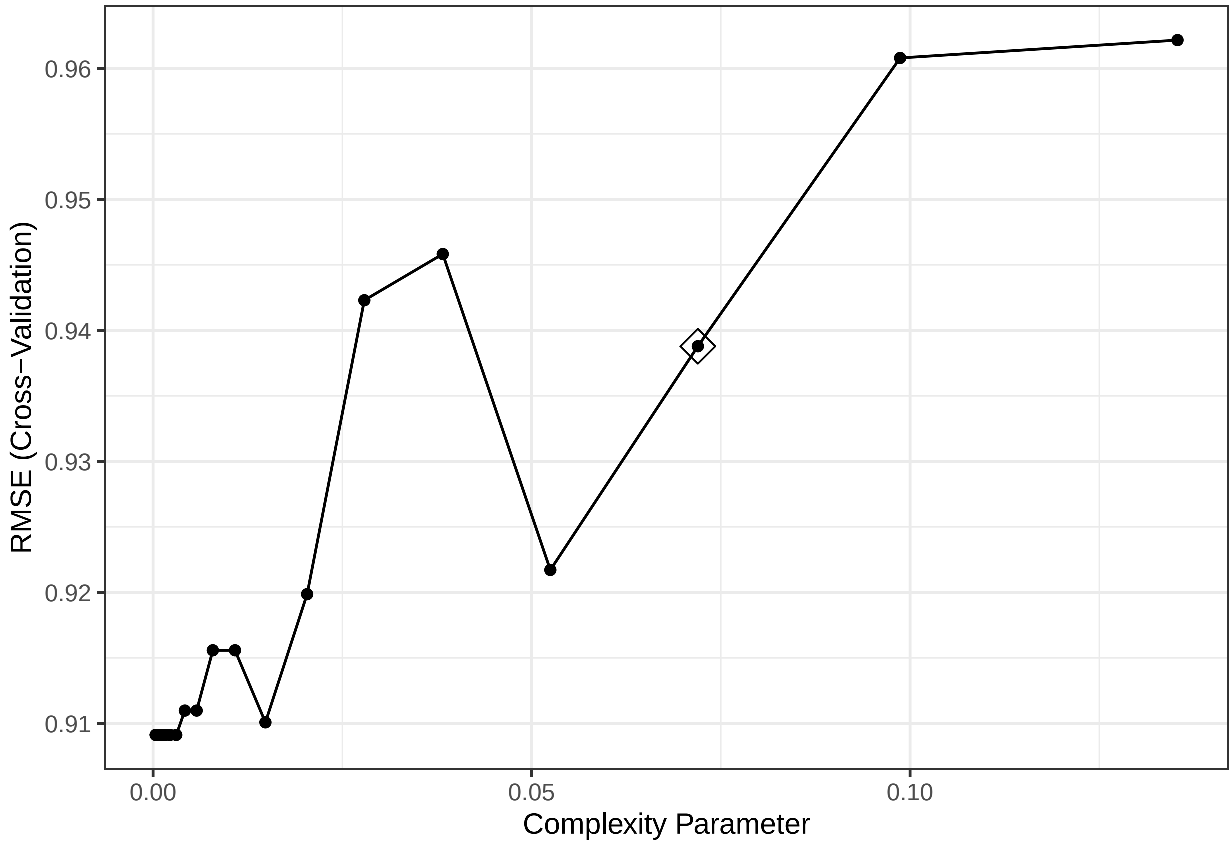
```r
rpart.plot(tree_fit$finalModel)
```



The tree size corresponds to the lowest cross-validation error is 8.

The 1 SE rule

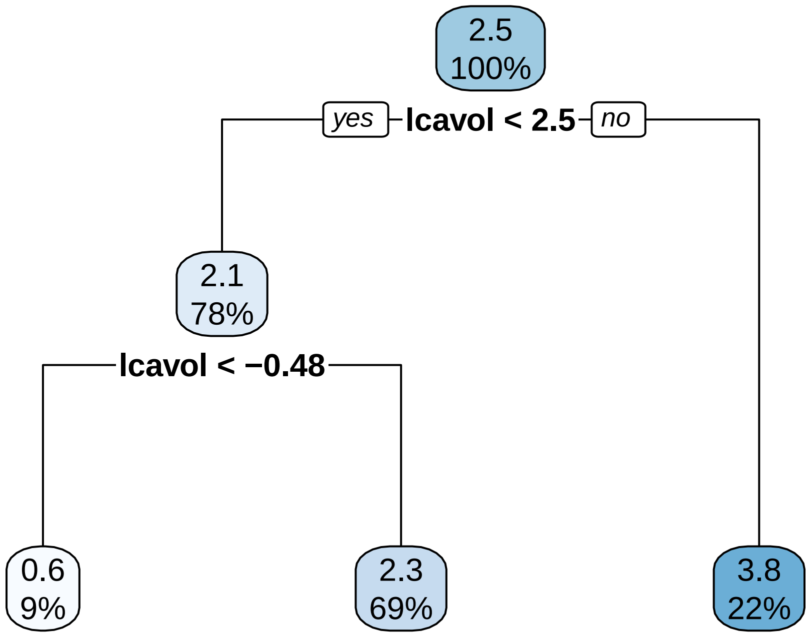
```
set.seed(2020)

tree_fit_2 = train(lpsa~.,
            data = Prostate,
            method = "rpart",
            tuneGrid = data.frame(cp =exp(seq(-8,-2, length = 20))),
            trControl = trainControl(method = "cv",
                                     number = 10,
                                     selectionFunction = "oneSE"))

ggplot(tree_fit_2, highlight = TRUE)
```




```
tree_fit_2$finalModel$cptable
```

```
##           CP nsplit rel error
## 1 0.34710828      0 1.0000000
## 2 0.18464743      1 0.6528917
## 3 0.07196474      2 0.4682443
```

```
rpart.plot(tree_fit_2$finalModel)
```

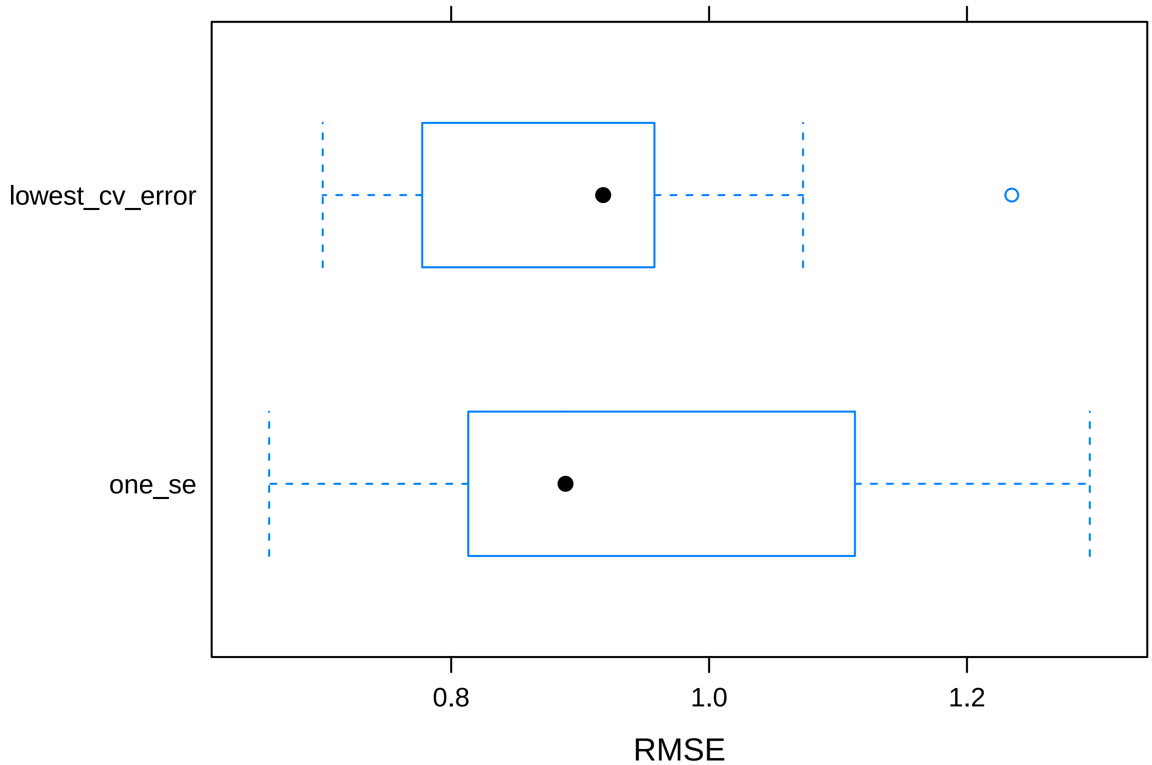


The tree size obtained using the 1 SE rule is 3.

The two tree sizes obtained by different selection functions are different.

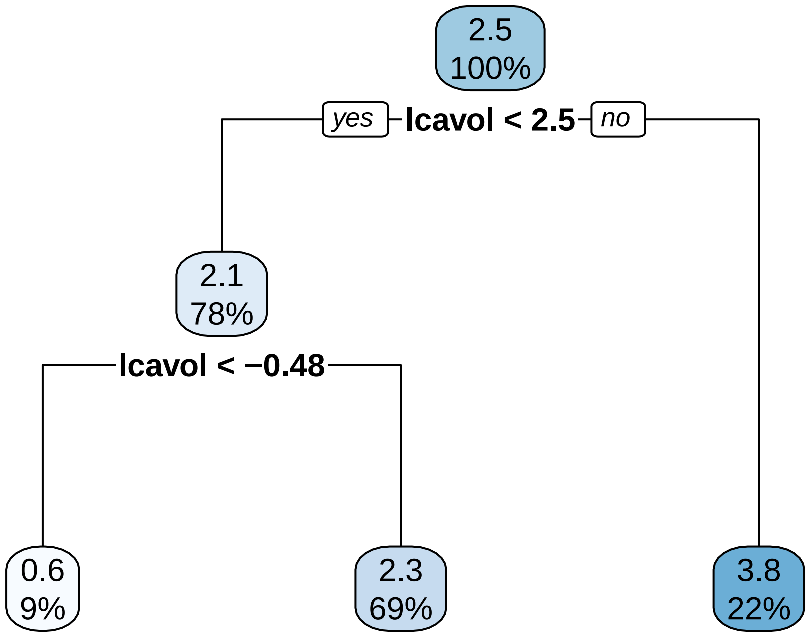
b) Choose one decision tree model

```
resamp = resamples(list(lowest_cv_error = tree_fit,
                        one_se = tree_fit_2
                        ))

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



I choosed tree size 3 as it has a similar performance with size 8 and it is simpler.

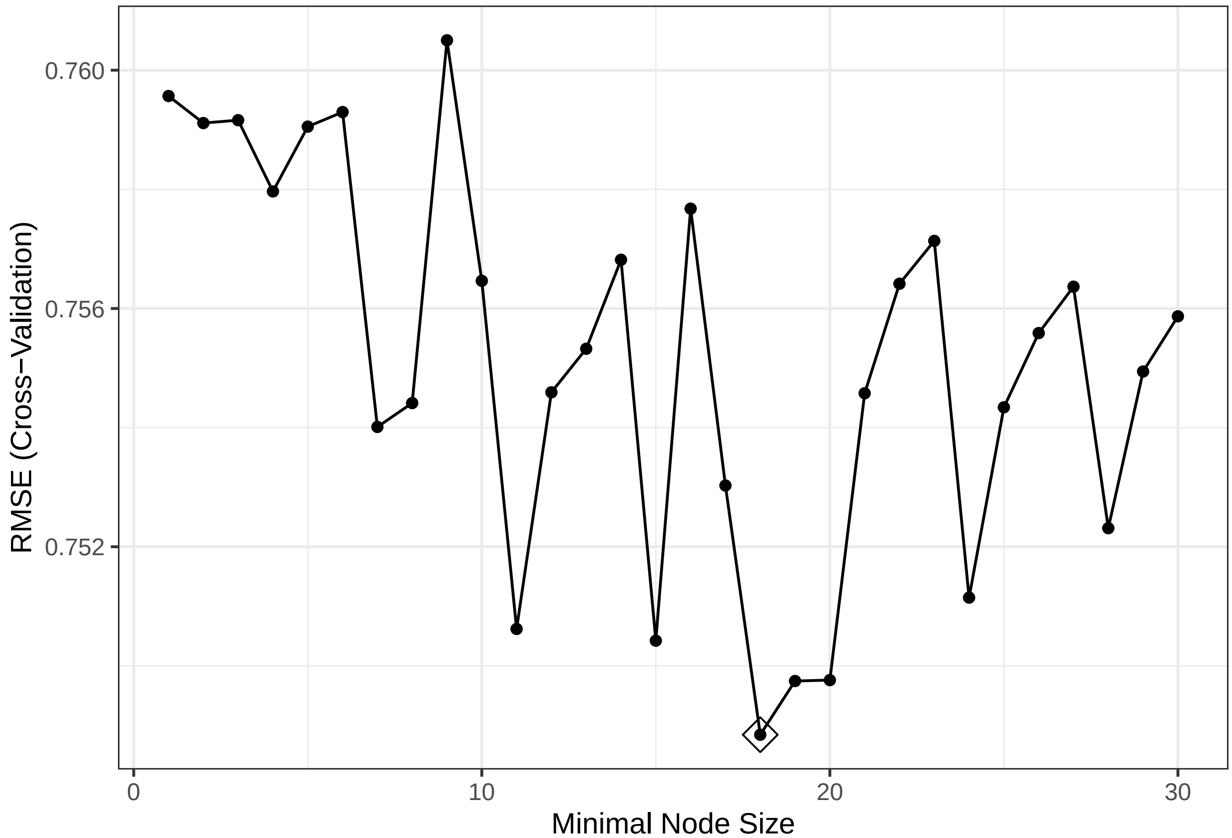
```
rpart.plot(tree_fit_2$finalModel)
```



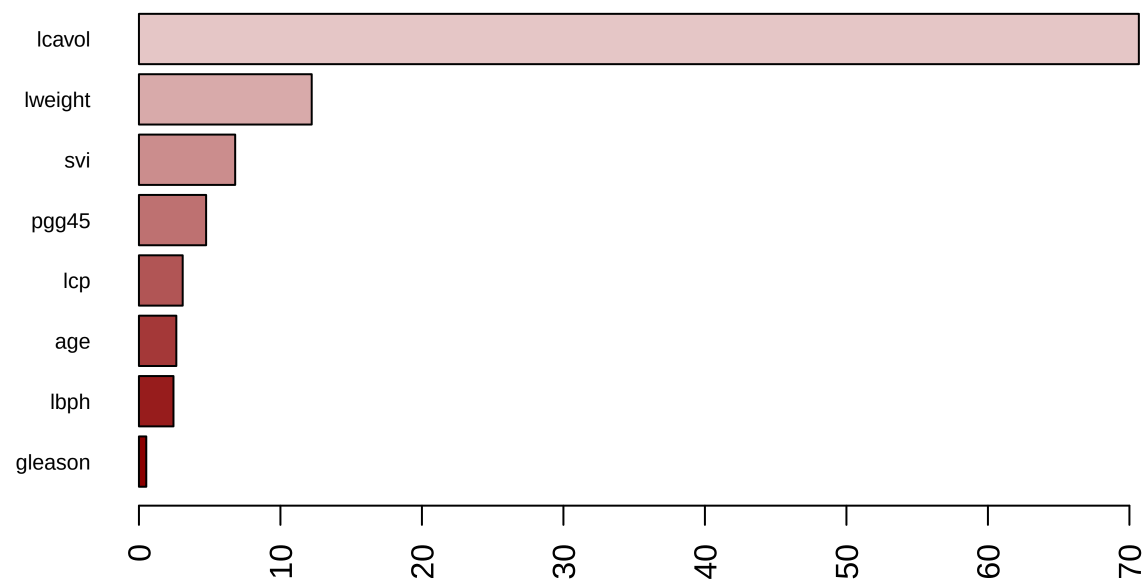
The first terminal node in the plot: When the lcavol is smaller than -0.48 (firstly smaller than 2.5), the predicted value (or the mean of observations in this terminal node) is 0.6. This terminal node contains 9% training data observations.

c) Bagging

```
set.seed(2020)

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

bag_fit = train(lpsa~.,
                data = Prostate,
                method = "ranger",
                tuneGrid = bagging.grid,
                importance = "impurity",
                trControl = ctrl)

ggplot(bag_fit, highlight = T)
```




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

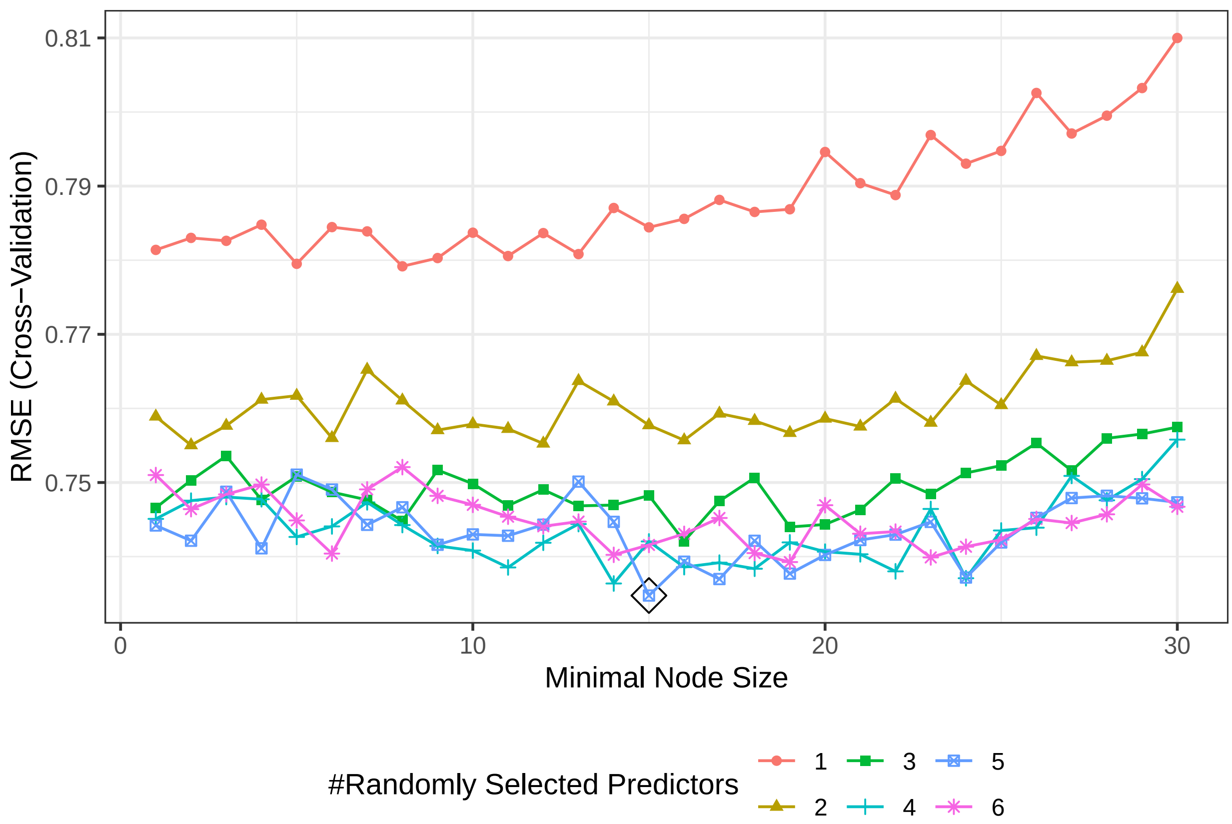


The lcavol is the most important variable in this bagging model.

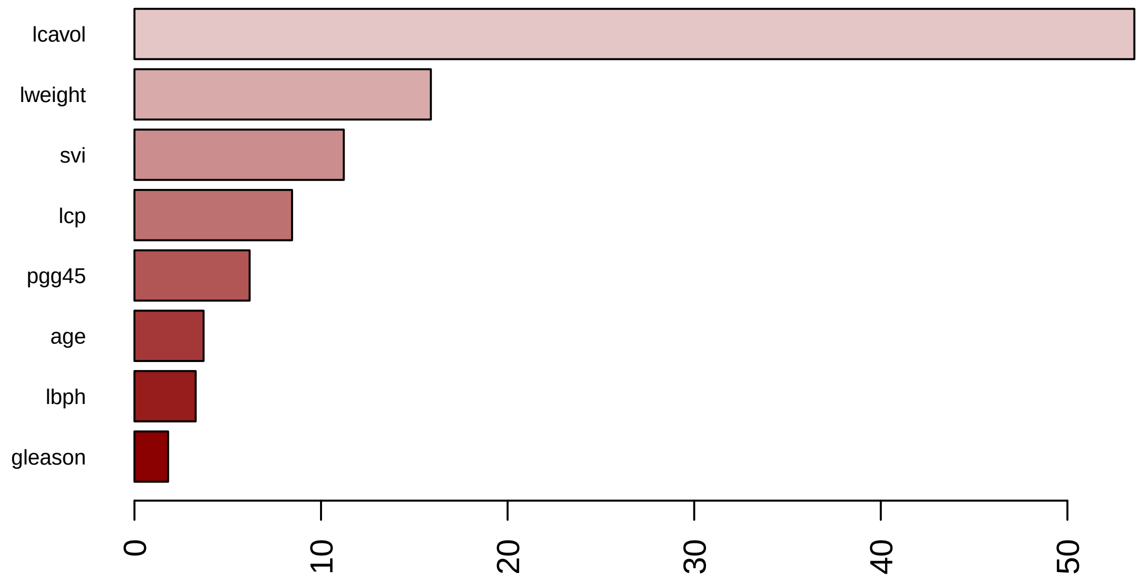
Importance: lcavol > lweight > svi > pgg45 > lcp > age > lbph > gleason

d) Random Forests

```
set.seed(2020)

rf.grid = expand.grid(mtry = 1:6,
                      splitrule = "variance",
                      min.node.size = 1:30
                      )

rf_fit = train(lpsa~.,
               data = Prostate,
               method = "ranger",
               tuneGrid = rf.grid,
               importance = "impurity",
               trControl = ctrl)

ggplot(rf_fit, highlight = T)
```




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

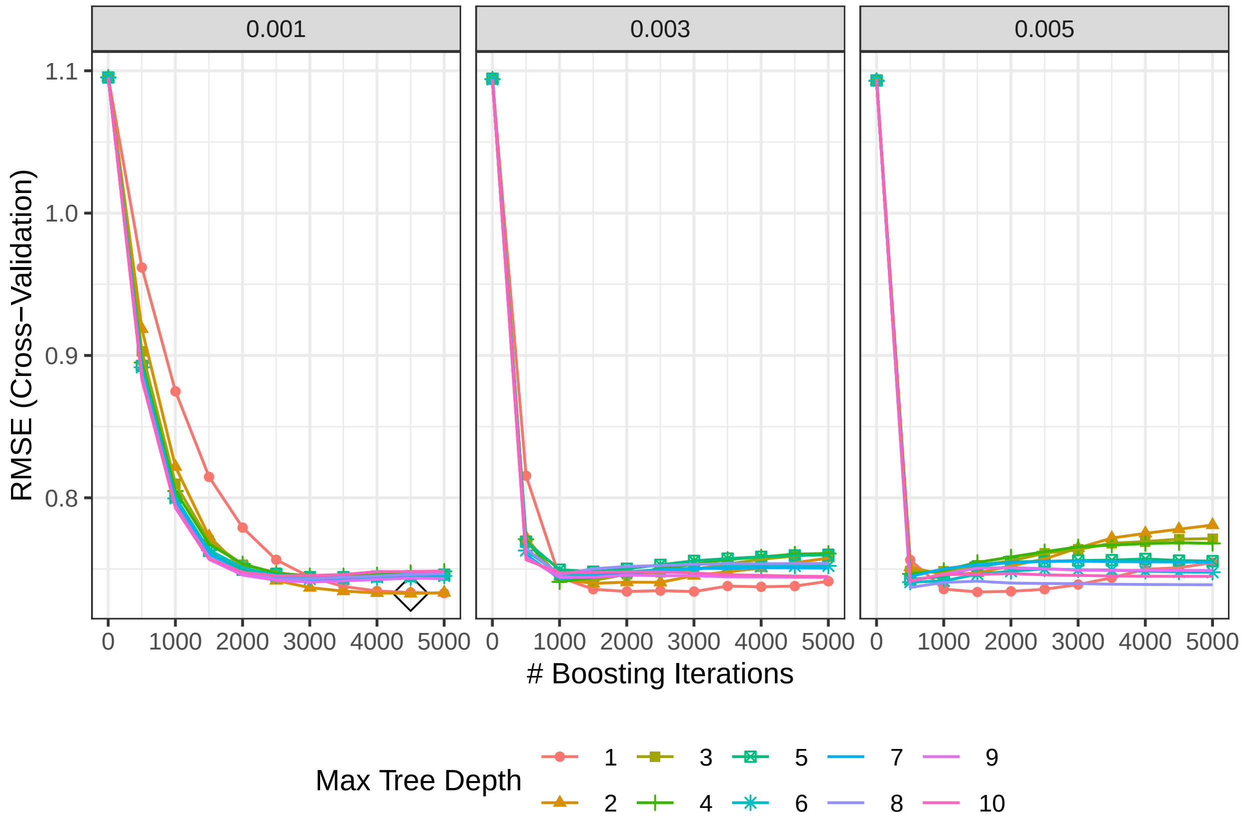


The lcavol is the most important variable in this random forests model.

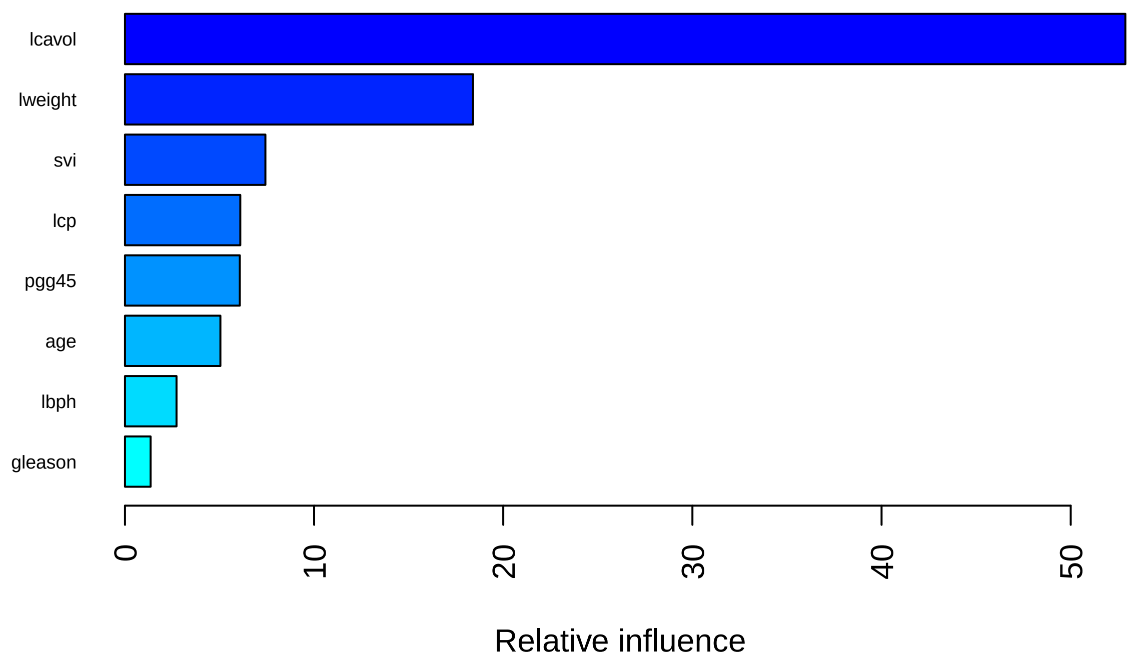
Importance: lcavol > lweight > svi > lcp > pgg45 > age > lbph > gleason

e) Boosting

```
set.seed(2020)

gbm.grid = expand.grid(
    n.trees = seq(1,5001, by = 500),
    interaction.depth = 1:10,
    shrinkage = c(0.001, 0.003, 0.005),
    n.minobsinnode = 1
    )

gbm_fit = train(lpsa~.,
                data = Prostate,
                method = "gbm",
                tuneGrid = gbm.grid,
                trControl = ctrl,
                verbose = FALSE)

ggplot(gbm_fit, highlight = T)
```




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




```
##              var   rel.inf
## lcavol    lcavol 52.889150
## lweight lweight 18.401589
## svi          svi  7.423689
## lcp          lcp  6.096547
## pgg45      pgg45  6.069915
## age          age  5.043442
## lbph        lbph  2.722959
## gleason gleason  1.352709
```

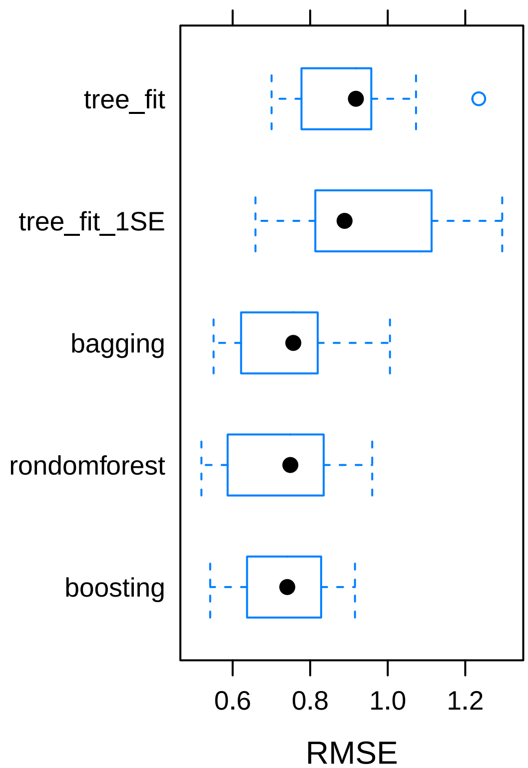
The lcavol is the most important variable in this boosting model.

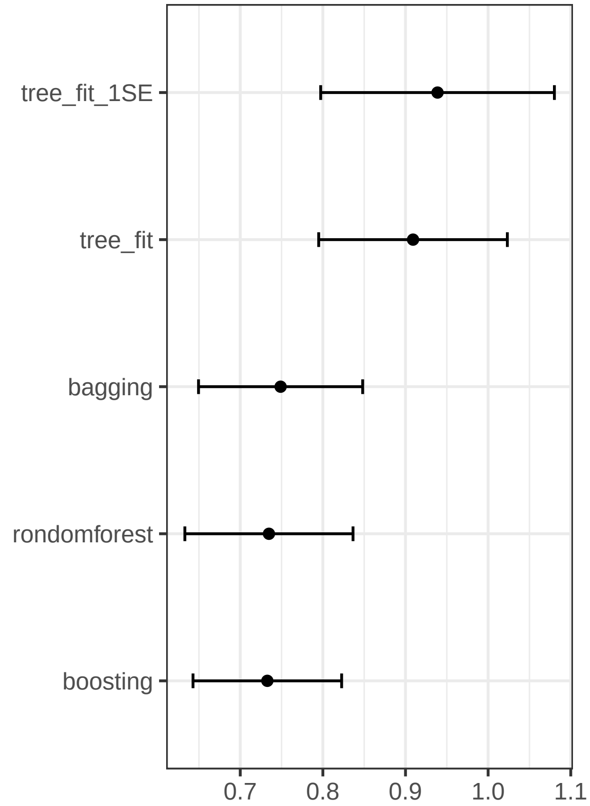
Importance: lcavol > lweight > svi > lcp > pgg45 > age > lbph > gleason

f) Compare Models

```
resamp2 = resamples(list(tree_fit = tree_fit,
                         tree_fit_1SE = tree_fit_2,
                         bagging = bag_fit,
                         rondomforest = rf_fit,
                         boosting = gbm_fit
                         ))
a = bwplot(resamp2, metric = "RMSE")
b = ggplot(resamp2, metric = "RMSE")
```

```r
gridExtra::grid.arrange(a,b,ncol = 2,nrow = 1)
```





From the boxplots of RMSE in the cross-vaildation, we can see that ensemble methods (bagging, random forerst and boosting) have a better performance in the cross-vaildation than the simple decision tree model. Comparing means of RMSE of different models in the cross-vaildation, we choose the boosting model to predict PSA level as it has the lowest mean.

Homework 4 problem 2 Description

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.

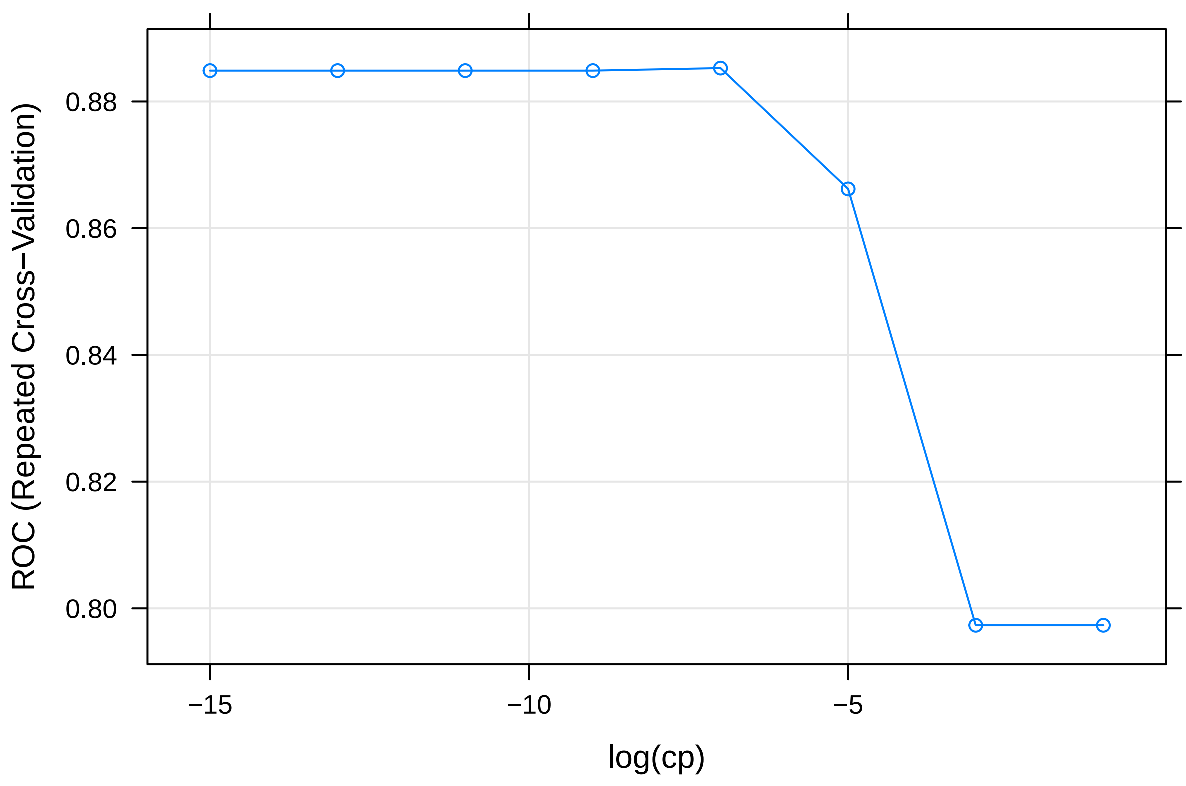
Problem 2

a) Decision Tree

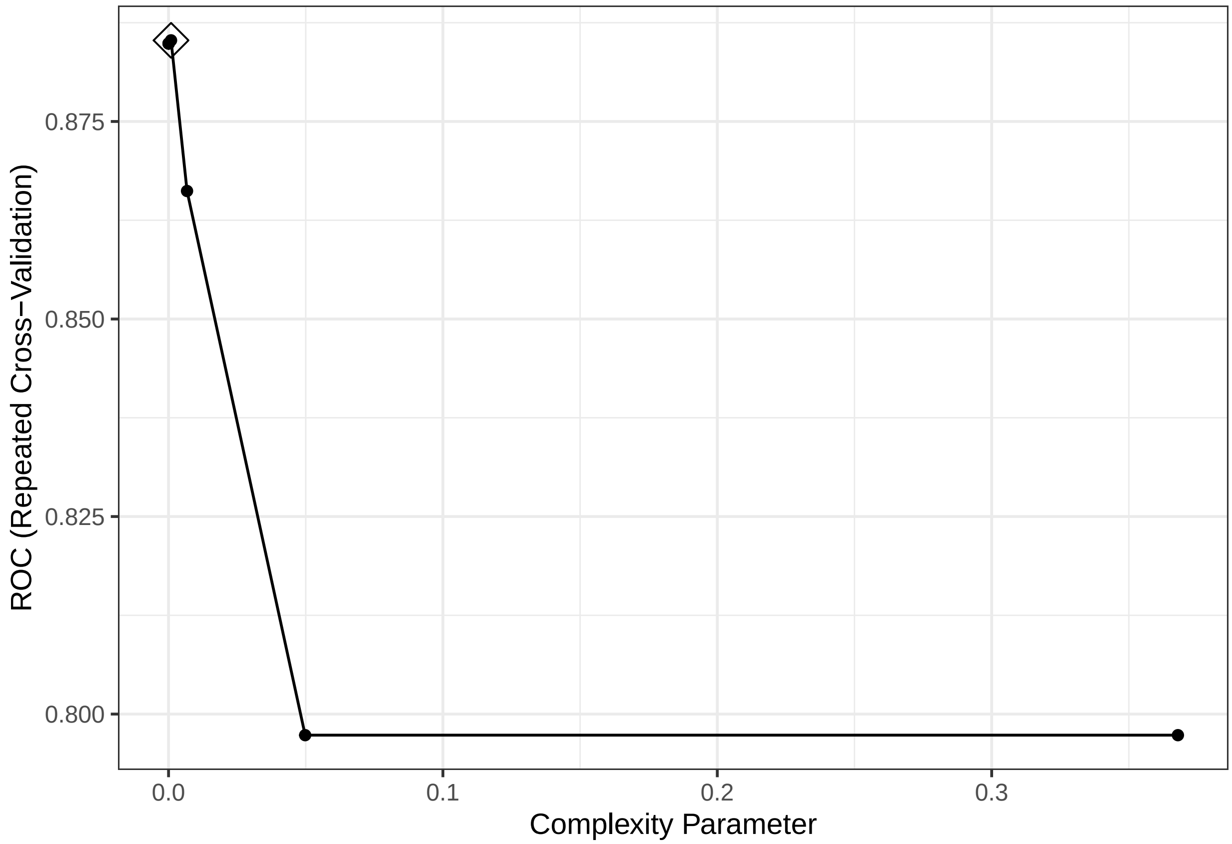
```r
set.seed(2020)

train_ind = sample(seq_len(nrow(OJ)), size = 800)
```

```r
training = OJ[train_ind, ]
test = OJ[-train_ind, ]
```

```r
set.seed(2020)

ctrl2 = trainControl(method = "repeatedcv",
                     summaryFunction = twoClassSummary,
                     classProbs = TRUE)

tree_fit_c = train(Purchase~.,
                   data = training,
                   method = "rpart",
                   tuneGrid = data.frame(cp = exp(seq(-15,0, by = 2))),
                   trControl = ctrl2,
                   metric = "ROC"
                   )

plot(tree_fit_c, xTrans = function(x)log(x), xlab = "log(cp)")
```




```r
ggplot(tree_fit_c, highlight = T)
```




```r
tree_fit_c$bestTune
```

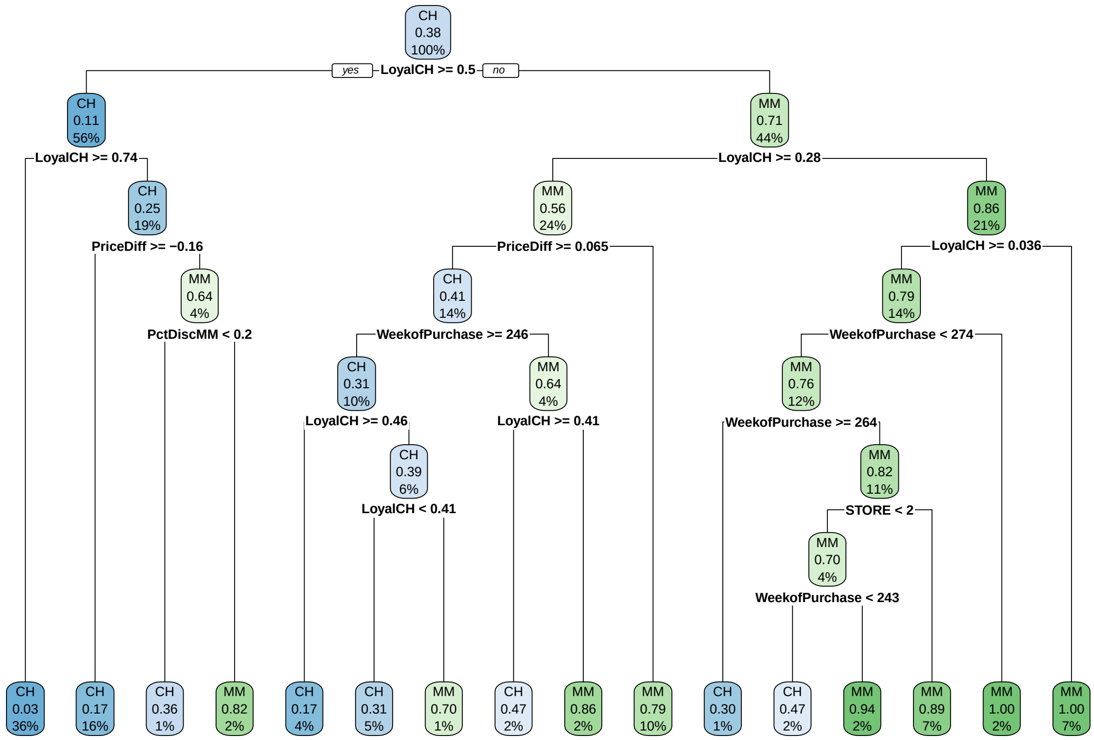
```
##            cp
## 5 0.000911882
```

```r
tree_fit_c$finalModel$cptable
```

```
##              CP nsplit rel error
## 1  0.486666667      0 1.0000000
## 2  0.035000000      1 0.5133333
## 3  0.030000000      3 0.4433333
## 4  0.013333333      4 0.4133333
## 5  0.010000000      6 0.3866667
## 6  0.006666667      7 0.3766667
## 7  0.004444444      9 0.3633333
## 8  0.003333333     12 0.3500000
## 9  0.001666667     13 0.3466667
## 10 0.000911882     15 0.3433333
```

The plot of the final tree

```r
rpart.plot(tree_fit_c$finalModel)
```



Predict the response on the test data

```r
tree.pred = predict(tree_fit_c, newdata = test, type = "raw")

1 - sum(tree.pred == test$Purchase) / length(test$Purchase)
```

```
## [1] 0.2222222
```

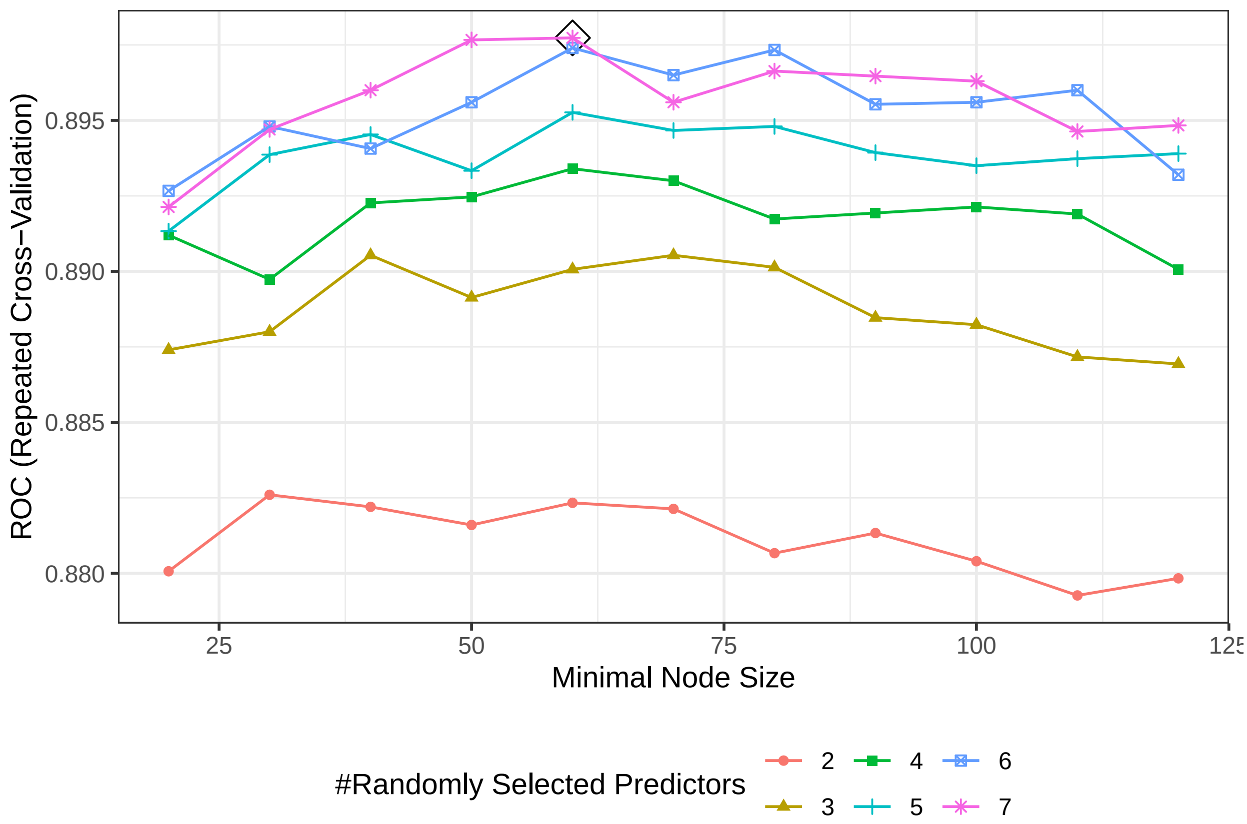
Test classification error rate

The tree size is 16. The test classification error rate is 22.22% for this tree model.

b)Random forests

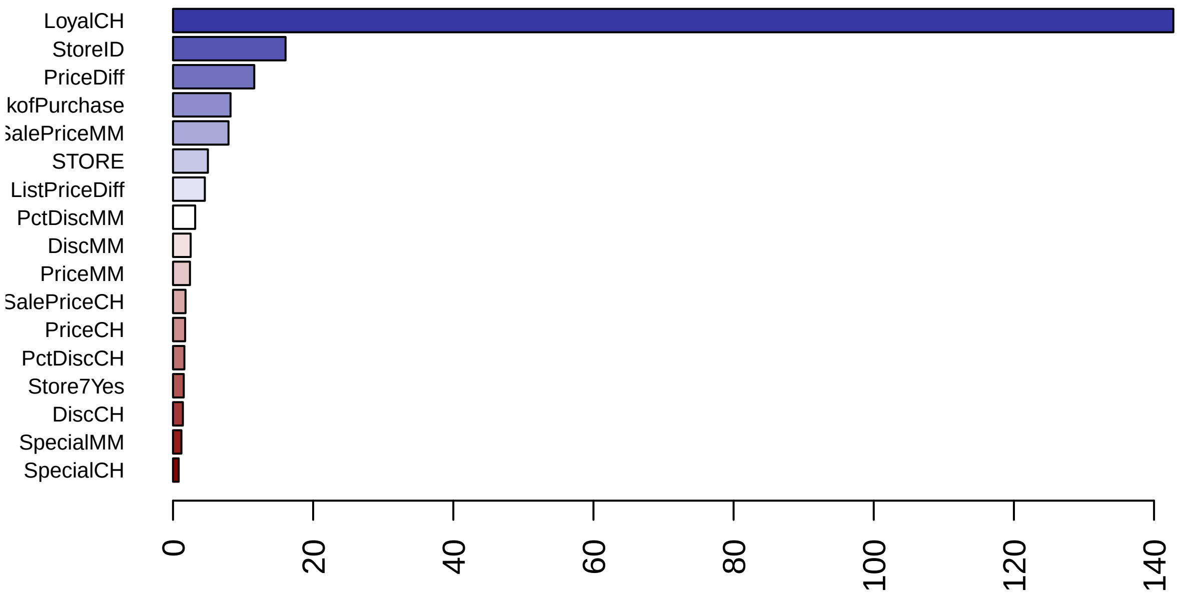
```r
set.seed(2020)

rf.grid2 = expand.grid(mtry = 2:7,
                       splitrule = "gini",
                       min.node.size = seq(20,120, by = 10))

rf_fit_c = train(Purchase~.,
```

```
                 data = training,
                 method = "ranger",
                 tuneGrid = rf.grid2,
                 metric = "ROC",
                 trControl = ctrl2,
                 importance = "impurity")

ggplot(rf_fit_c, highlight = T)
```



Report variable importance

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



The loyalCH is the most important variable in this random forest model.

The top 5 most important variables: LoyalCH > StoreID > PriceDiff > WeekofPurchase > SalePriceMM

Predict the response on the test data

```
rf.pred = predict(rf_fit_c, newdata = test, type = "raw")

1 - sum(rf.pred == test$Purchase) / length(test$Purchase)
```

```
## [1] 0.1888889
```

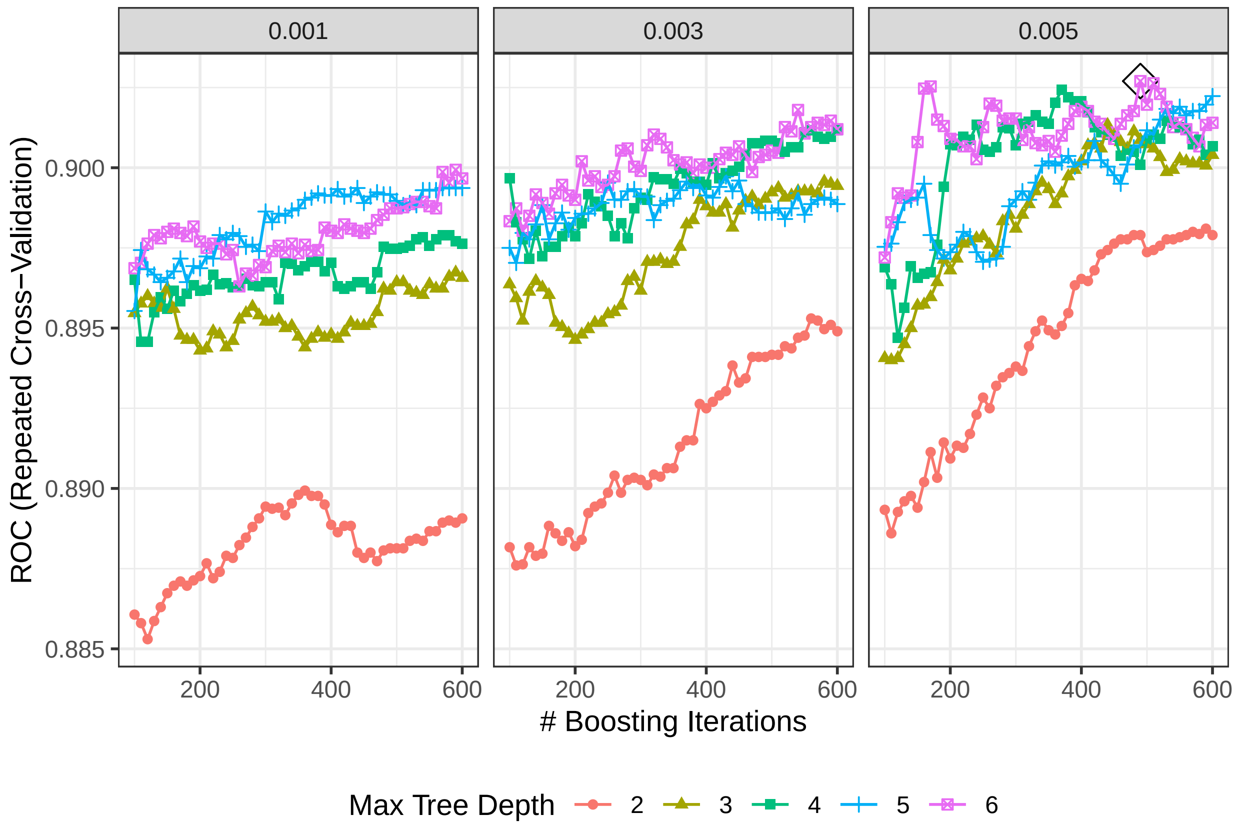
Test classification error rate

The test classification error rate is 18.89% for this random forest model.

c) Boosting

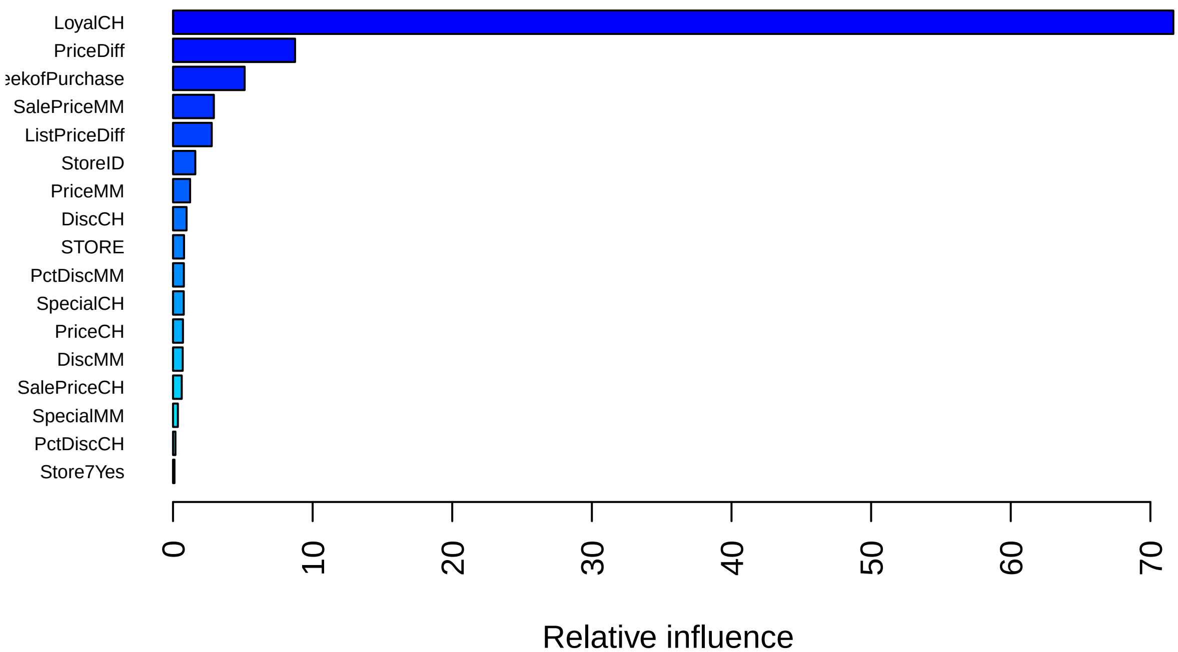
```
set.seed(2020)

gbm.grid2 = expand.grid(n.trees = seq(100, 600, by = 10),
                        interaction.depth = 2:6,
```

```
                        shrinkage = c(0.001, 0.003, 0.005),
                        n.minobsinnode = 1)

gbm_fit_c = train(Purchase~.,
                data = training,
                method = "gbm",
                trControl = ctrl2,
                distribution = "bernoulli",
                metric = "ROC",
                tuneGrid = gbm.grid2,
                verbose = F
                )

ggplot(gbm_fit_c, highlight = T)
```



Report variable importance

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




```
##                           var    rel.inf
## LoyalCH               LoyalCH 71.6453345
## PriceDiff           PriceDiff  8.7405234
## WeekofPurchase WeekofPurchase  5.1302524
## SalePriceMM       SalePriceMM  2.9255109
## ListPriceDiff   ListPriceDiff  2.7745226
## StoreID               StoreID  1.5965679
## PriceMM               PriceMM  1.2252798
## DiscCH                 DiscCH  0.9690714
## STORE                   STORE  0.7891423
## PctDiscMM           PctDiscMM  0.7772935
## SpecialCH           SpecialCH  0.7691108
## PriceCH               PriceCH  0.7125856
## DiscMM                 DiscMM  0.6929432
## SalePriceCH       SalePriceCH  0.6244650
## SpecialMM           SpecialMM  0.3479619
## PctDiscCH           PctDiscCH  0.1737719
## Store7Yes           Store7Yes  0.1056629
```

The loyalCH is the most important variable in this boosting model.

The top 5 most important variables: LoyalCH > PriceDiff > WeekofPurchase > SalePriceMM > ListPriceDiff

Predict the response on the test data

```r
gbm.pred = predict(gbm_fit_c, newdata = test, type = "raw")
1 - sum(gbm.pred == test$Purchase) / length(test$Purchase)
```

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

Test classification error rate

The test classification error rate is 18.52% for this boosting model.