DS2_HW4_REGRESSION_TREE

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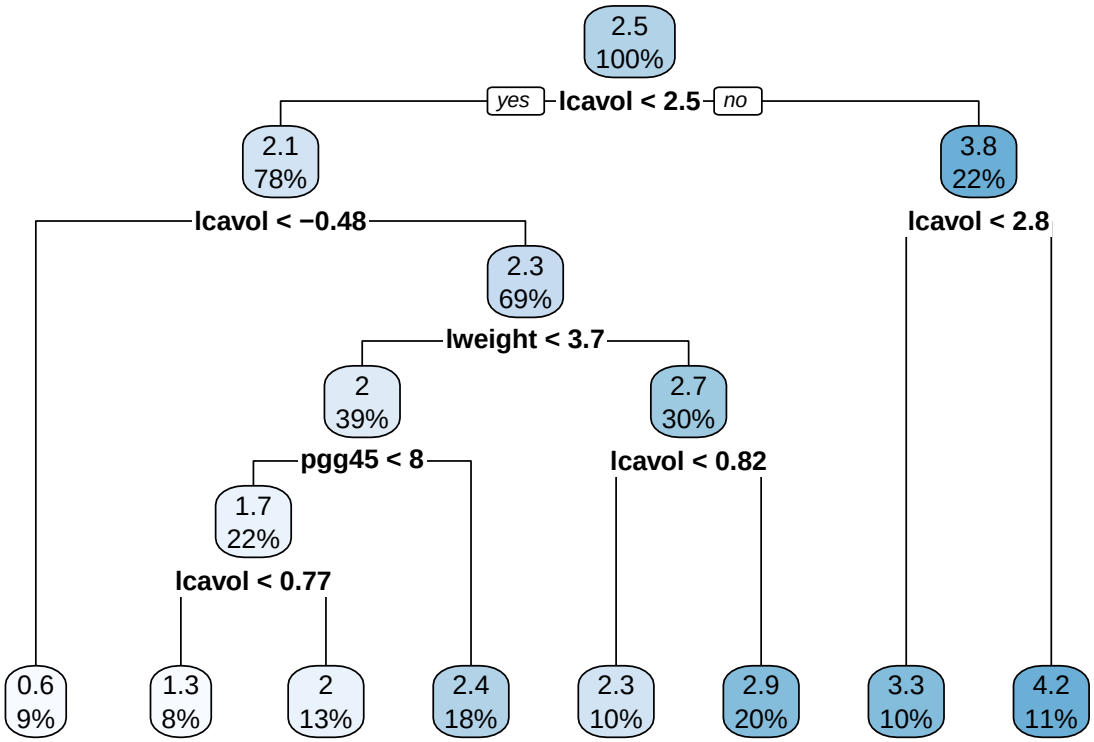
```
data(Prostate)
head(Prostate)
```

```
##       lcavol  lweight age      lbph svi       lcp gleason pgg45       lpsa
## 1 -0.5798185 2.769459  50 -1.386294   0 -1.386294       6     0 -0.4307829
## 2 -0.9942523 3.319626  58 -1.386294   0 -1.386294       6     0 -0.1625189
## 3 -0.5108256 2.691243  74 -1.386294   0 -1.386294       7    20 -0.1625189
## 4 -1.2039728 3.282789  58 -1.386294   0 -1.386294       6     0 -0.1625189
## 5  0.7514161 3.432373  62 -1.386294   0 -1.386294       6     0  0.3715636
## 6 -1.0498221 3.228826  50 -1.386294   0 -1.386294       6     0  0.7654678
```

```
set.seed(1)
rowtrain = createDataPartition(y = Prostate$lpsa,
                               p = 0.75,
                               list = FALSE)
ctr1 = trainControl(method = "cv")
```

1a) Fit a regression tree withlpsaas the response;Use cross-validation to determine the optimal tree size. Which tree size correspondsto the lowest cross-validation error? Is this the same as the tree size obtained usingthe 1 SE rule?

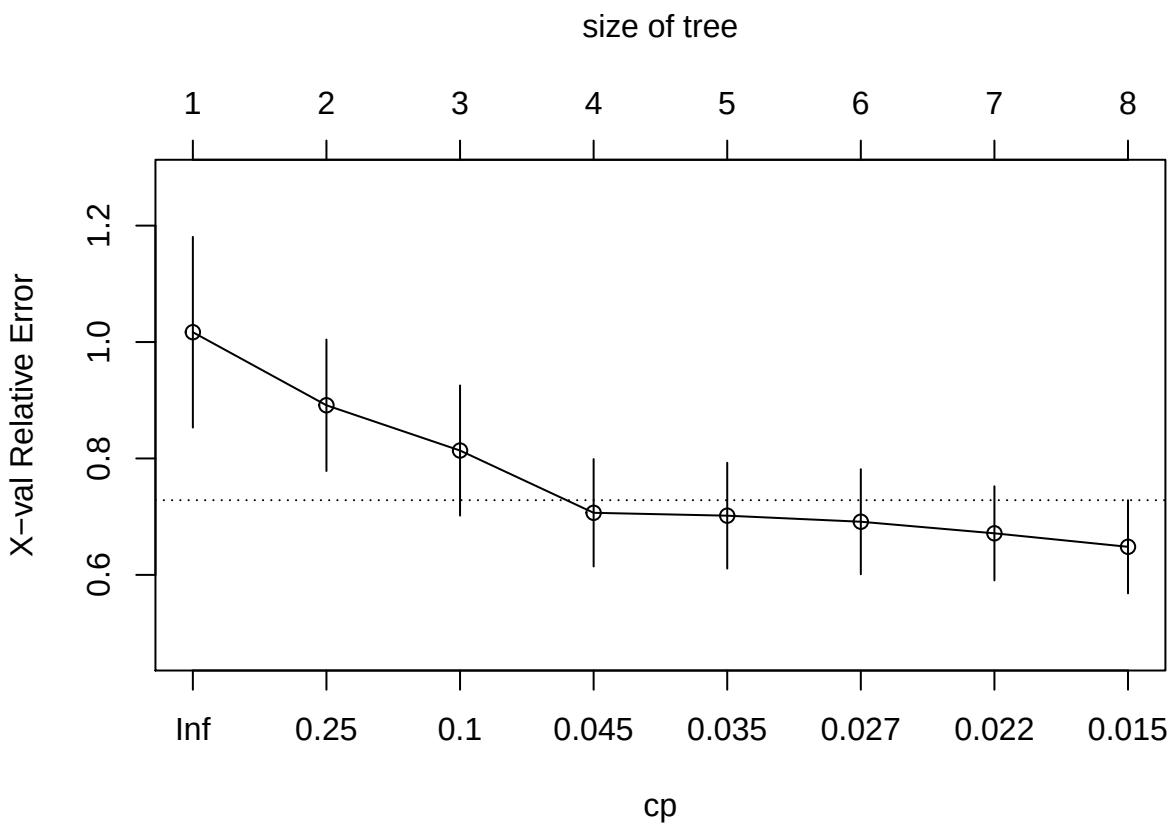
```
set.seed(1)
rpart.fit = train(lpsa~., Prostate,
                  method = "rpart",
                  tuneGrid = data.frame(cp = exp(seq(-6,-2,length=20))), trControl = ctr1)
rpart.plot(rpart.fit$finalModel)

#####
set.seed(1)
tree1 = rpart(formula = lpsa~., data = Prostate)
rpart.plot(tree1)
```



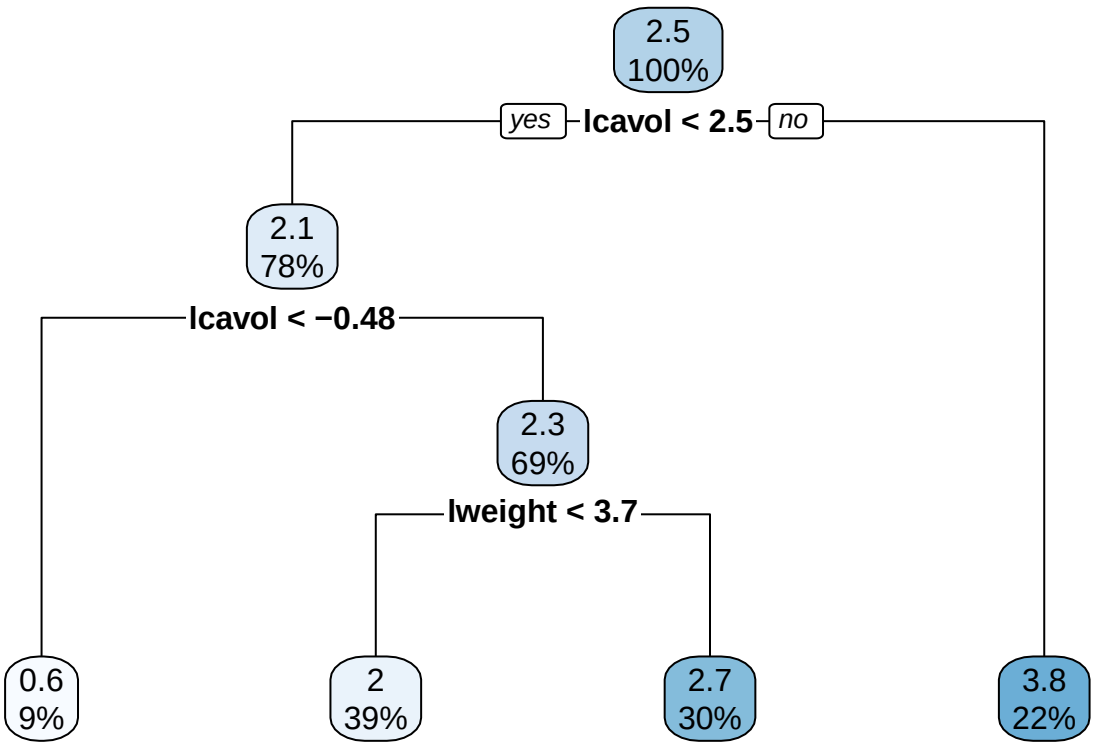

```
cp_table = printcp(tree1)### cross validation built in rpart; large cp give smaller tree
```

```
##
## Regression tree:
## rpart(formula = lpsa ~ ., data = Prostate)
##
## Variables actually used in tree construction:
## [1] lcavol  lweight pgg45
##
## Root node error: 127.92/97 = 1.3187
##
## n= 97
##
##         CP nsplit rel error  xerror     xstd
## 1 0.347108      0   1.00000 1.01687 0.163742
## 2 0.184647      1   0.65289 0.89137 0.112926
## 3 0.059316      2   0.46824 0.81363 0.111838
## 4 0.034756      3   0.40893 0.70667 0.092263
## 5 0.034609      4   0.37417 0.70171 0.090879
## 6 0.021564      5   0.33956 0.69128 0.090257
## 7 0.021470      6   0.31800 0.67139 0.080849
## 8 0.010000      7   0.29653 0.64826 0.080048
```

```
plotcp(tree1)
```



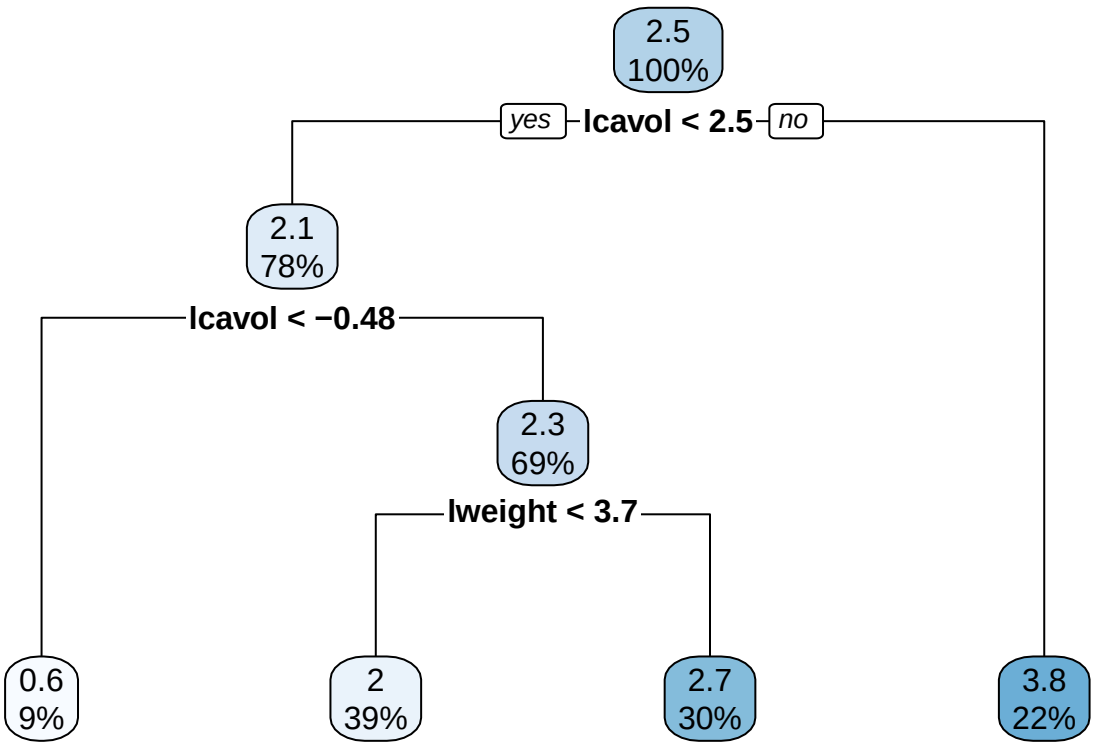

```
### tree by minimium cross validation error
minerror = which.min(cp_table[,4])
tree2 = prune(tree1, cp = cp_table[minerror,1])
### 1SE rule- simplest model with error smaller than the line
tree3 = prune(tree1, cp = cp_table[cp_table[,4]<cp_table[minerror,4]+cp_table[minerror,5],1][1])
# split 3
rpart.plot(tree3)
```



According to the plot. the optimal tree size is 7+1 = 8 by cross validation. According to 1SE rule, the optimal split is 3. Therefore, the tree size are different.

2 Create a plot of the final tree you choose. Pick one of the terminal nodes, andinterpret the information displayed.

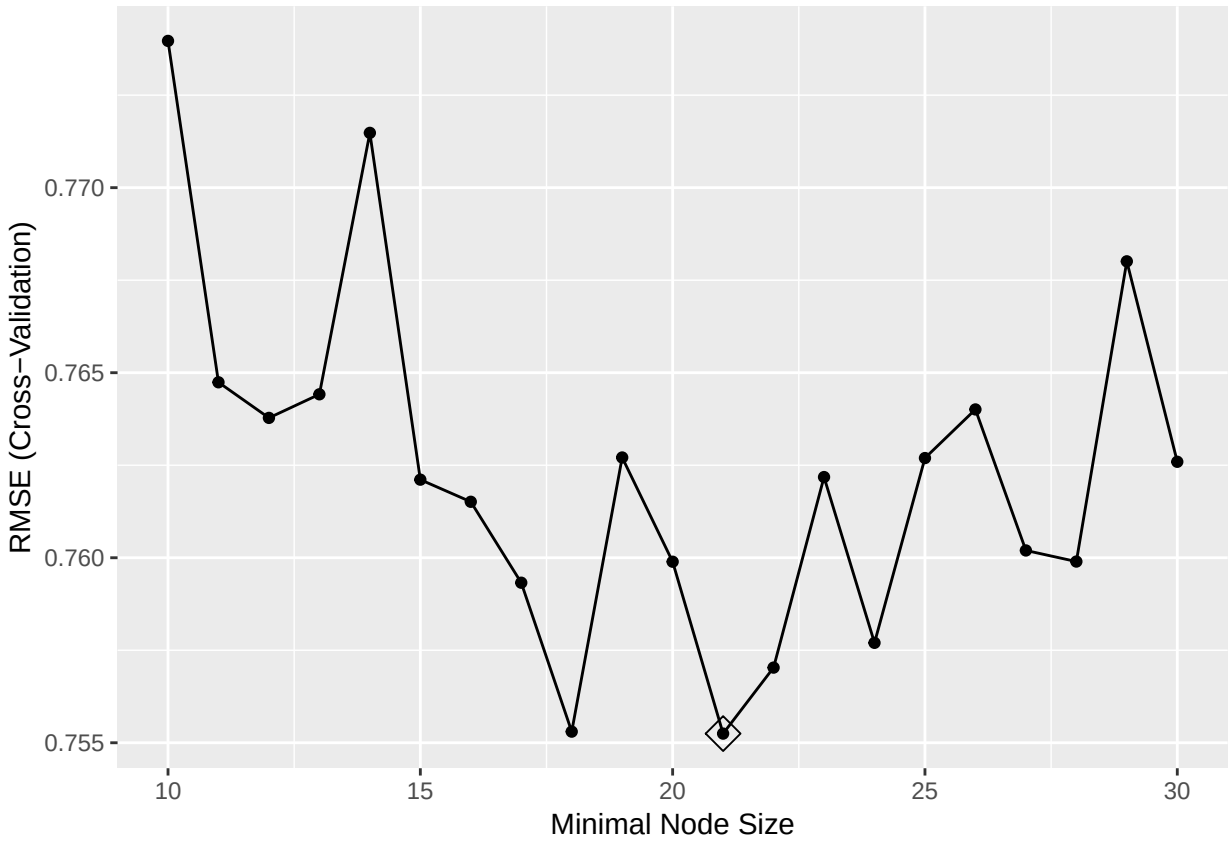
```
rpart.plot(tree3)
```



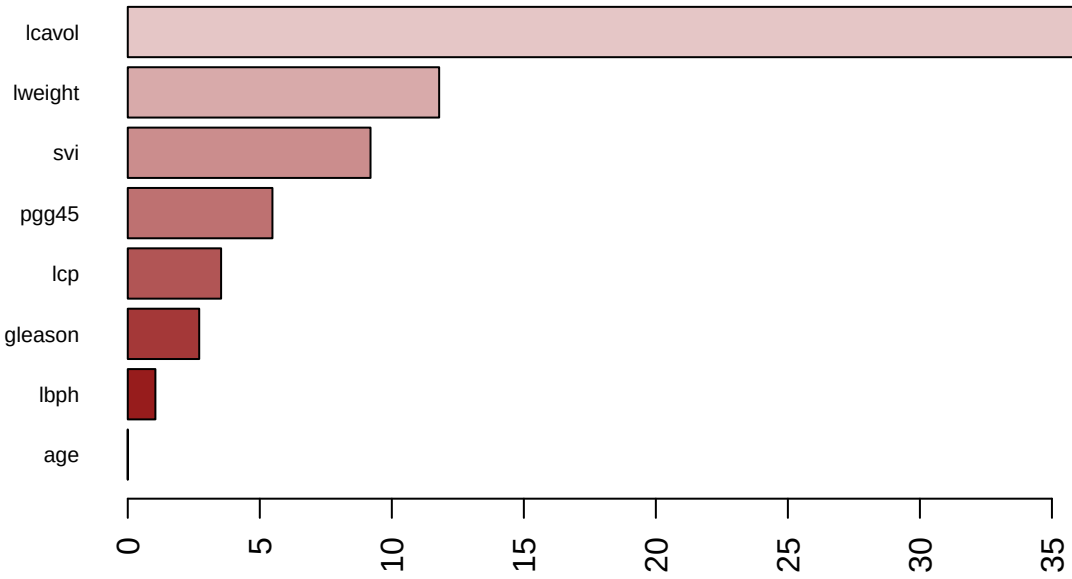
Since both models have similar cross validation error. We should choose the simpler model which is 1 SE model. Node 3.8 interpretation: when the log cancer volumn is greater 2.5. the log mean of log prostate specific antigen is 3.8. The nodes include 22% response of training dataset.

(c) Perform bagging and report the variable importance.

```
set.seed(2)
rf.grid = expand.grid(mtry = 8,
                      splitrule = "variance",
                     min.node.size = 10:30)
bagging.fit = train(lpsa~., Prostate,
                    method = "ranger",
                    tuneGrid = rf.grid,
                    trControl = ctr1)
ggplot(bagging.fit , highlight = TRUE)
```



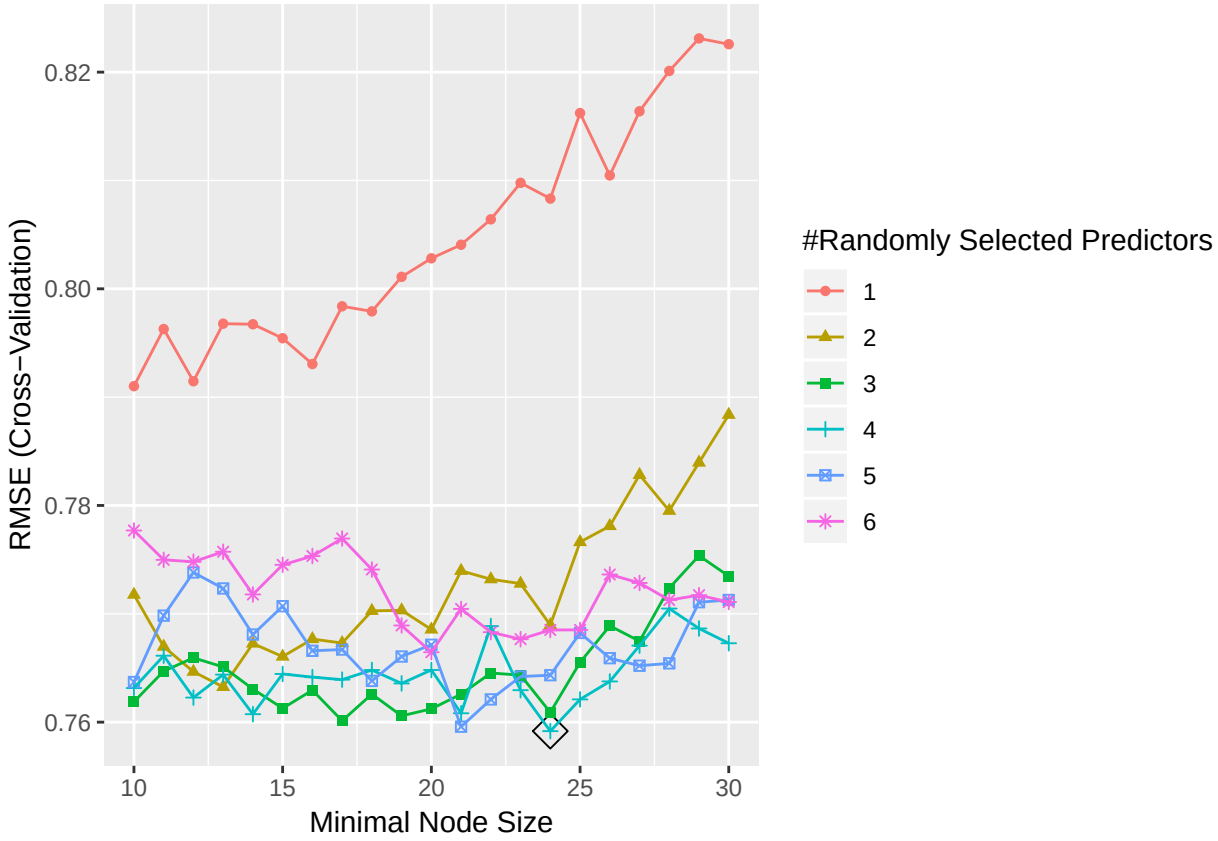

```
bagging.imp = ranger(lpsa~., Prostate,
                     mtry = 8,
                     splitrule = "variance",
                     min.node.size = 11,
                     importance = "permutation",
                     scale.permutation.importance = TRUE)
barplot(sort(ranger::importance(bagging.imp), decreasing = FALSE),
        las = 2, horiz = TRUE, cex.names = 0.7, col = colorRampPalette(colors = c("darkred", "white", "
```



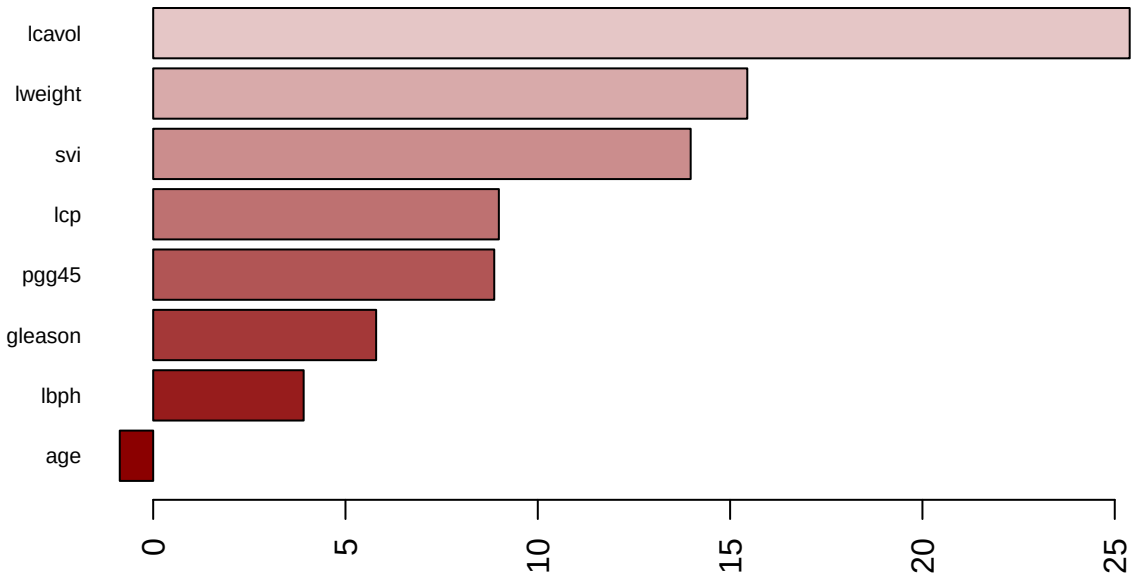
Based on the plot above, the variable importance is lcavol > lweight > svi > pgg45 > lcp > gleason > lbph > age.

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

```
### tuning parameter
rf.grid = expand.grid(mtry = 1:6,
                      splitrule = "variance",
                      min.node.size = 10:30)### ?
### fit model
set.seed(3)
rf.fit = train(lpsa~., Prostate,
               method = "ranger",
               tuneGrid = rf.grid,
               trControl = ctr1)
### tuning parameter choosen
ggplot(rf.fit, highlight = TRUE)
```



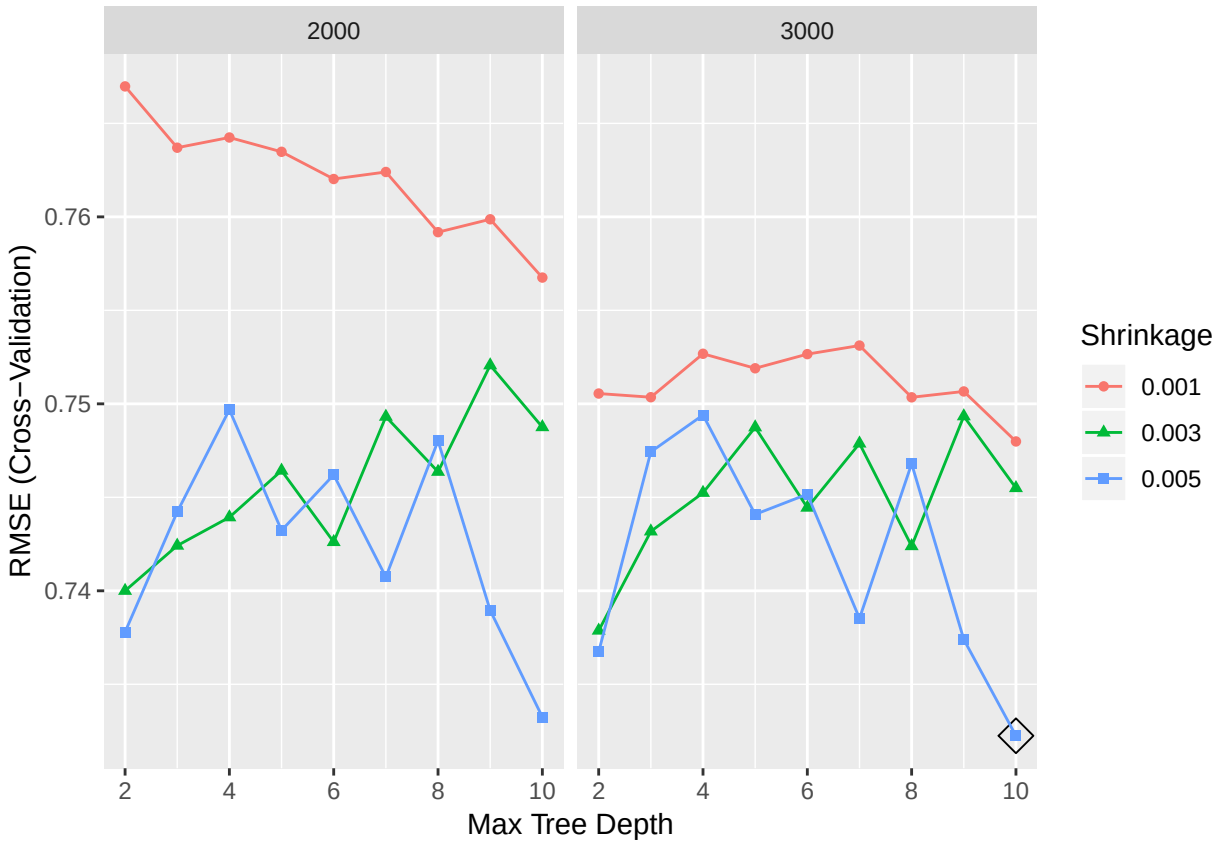

```
### variable importance.
rf.final.imp = ranger(lpsa~., Prostate,
                      mtry = 4, splitrule = "variance",
                      min.node.size = 24,
                      importance = "permutation",
                      scale.permutation.importance = TRUE)
barplot(sort(ranger::importance(rf.final.imp), decreasing = FALSE),
        las = 2, horiz = TRUE, cex.names = 0.7, col = colorRampPalette(colors = c("darkred", "white", "
```



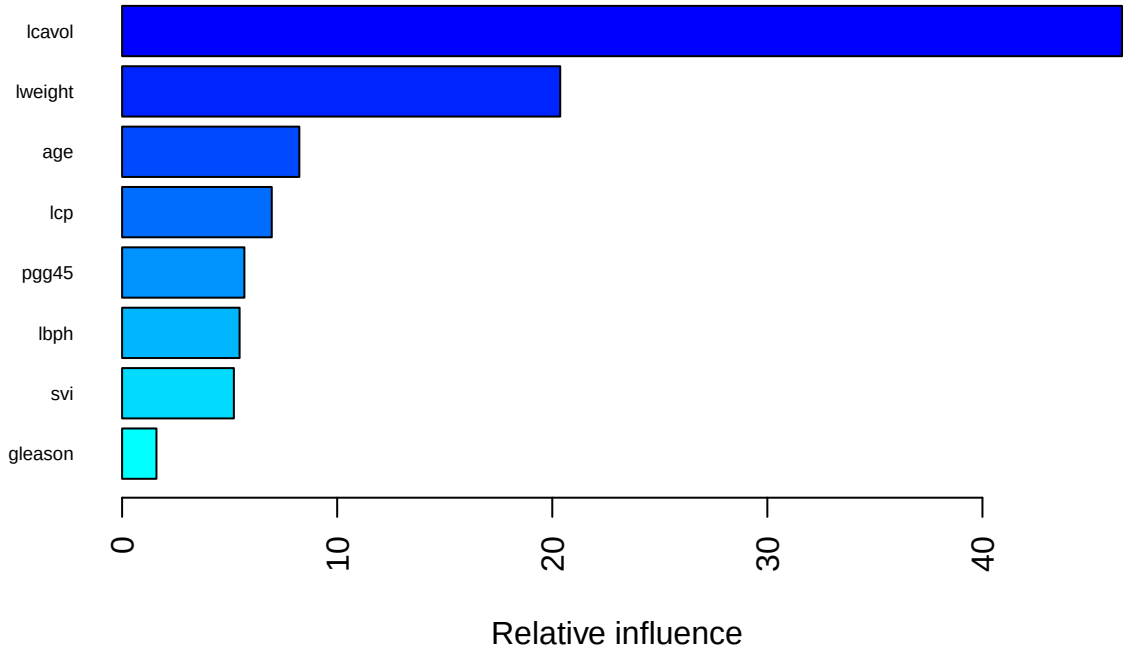
Based on the plot above, the variable importance is lcavol > lweight > svi > lcp > pgg45 > gleason > lbph > age.

(e) Perform boosting and report the variable importance.

```
### tuning parameter
gbm.grid = expand.grid(n.trees = c(2000,3000),
                       interaction.depth = 2:10,
                       shrinkage = c(0.001, 0.003, 0.005),
                       n.minobsinnode = 1)
### fit model
gbm.fit = train(lpsa~.,Prostate,
                method = "gbm",
                tuneGrid = gbm.grid,
                trControl = ctr1,
                verbose = FALSE)
ggplot(gbm.fit, highlight = TRUE)
```




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




```
##             var   rel.inf
## lcavol   lcavol 46.491222
## lweight lweight 20.369375
## age         age  8.239670
```

```
## lcp         lcp  6.957807
## pgg45     pgg45  5.685430
## lbph       lbph  5.463286
## svi         svi  5.195660
## gleason gleason  1.597550
```

Based on the plot above, the variable importance is lcavol > lweight > lcp > age > svi > pgg45 > lbph > gleason

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

```
resamp = resamples(list(rpart = rpart.fit, bagging = bagging.fit, rf = rf.fit, gbm = gbm.fit))
summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: rpart, bagging, rf, gbm
## Number of resamples: 10
##
## MAE
##              Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## rpart   0.6029257 0.6833061 0.7132861 0.7481058 0.7878006 1.0108929    0
## bagging 0.4132455 0.5733499 0.6171783 0.6242907 0.6717655 0.8203720    0
## rf      0.3207104 0.4336260 0.6678633 0.6367605 0.7578791 1.0413658    0
## gbm     0.4073739 0.5278648 0.5467414 0.5822022 0.6558448 0.8031722    0
##
## RMSE
##              Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## rpart   0.6940977 0.7916380 0.8659767 0.8688293 0.9202064 1.1161271    0
## bagging 0.5690718 0.6507318 0.7658300 0.7552480 0.8558485 0.9142573    0
## rf      0.3852574 0.5493899 0.8002497 0.7591698 0.9212254 1.1998445    0
## gbm     0.4994624 0.6739685 0.7284938 0.7322453 0.7914498 0.9575104    0
##
## Rsquared
##               Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## rpart   0.10742511 0.4435906 0.5507225 0.4869429 0.5676906 0.6732530    0
## bagging 0.30582778 0.5199532 0.6269879 0.6297696 0.7633807 0.9030913    0
## rf      0.05163731 0.4903155 0.6836592 0.5723541 0.7337990 0.8431251    0
## gbm     0.18153923 0.4188219 0.6308190 0.5685605 0.7310841 0.7685486    0
```

Boosting model is selected because the cross validation error of boosting model is smallest among these models.

Problem 2

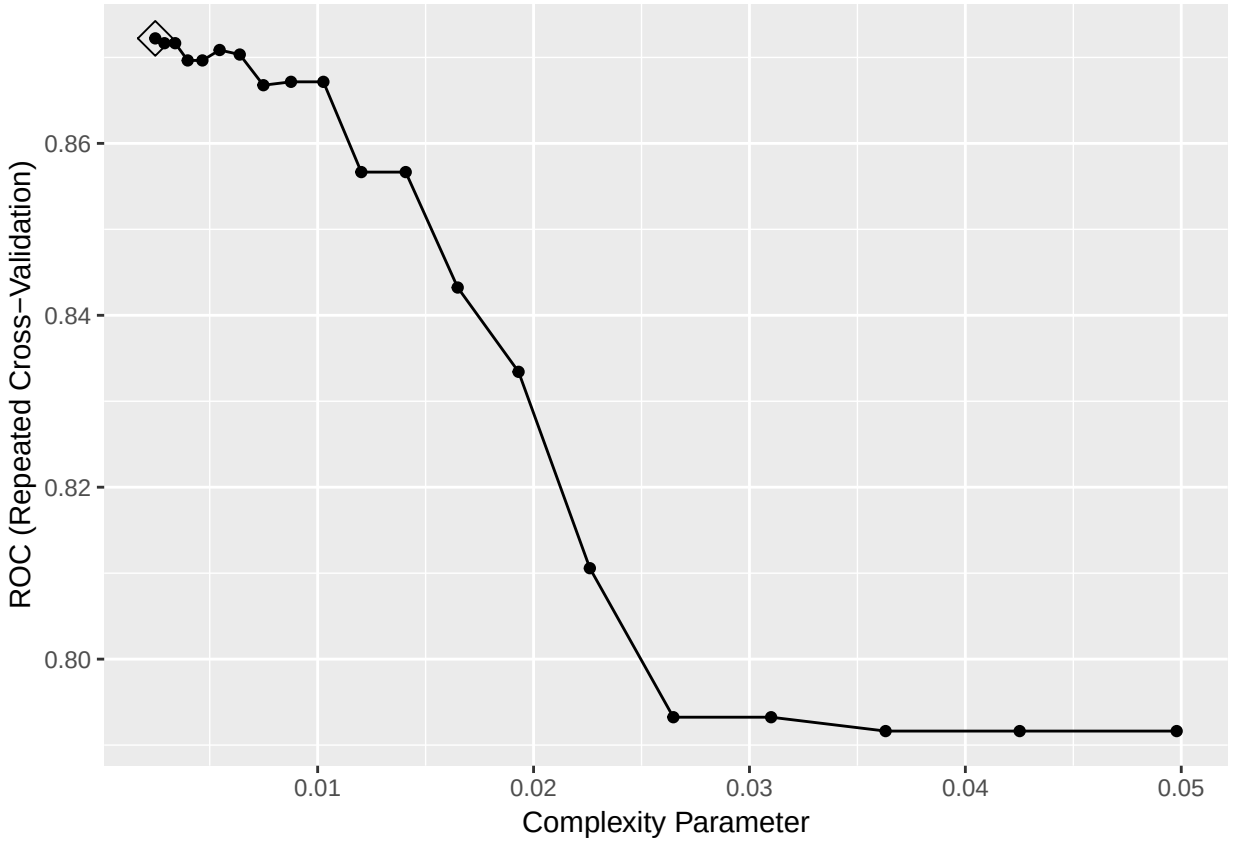
```
data(OJ)
levels(OJ$Purchase)
```

```
## [1] "CH" "MM"
```

```
rowtrain2 = createDataPartition(y = OJ$Purchase,
                                p = 800/1070,
                                list = FALSE)
```

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

```
ctr1 = trainControl(method = "repeatedcv",
                    summaryFunction = twoClassSummary,
                    classProbs = TRUE)
set.seed(1)
rpart.fit2 = train(Purchase~.,OJ,
                   subset = rowtrain2,
                   method = "rpart",
                   tuneGrid = data.frame(cp = exp(seq(-6,-3,len=20))),
                   trControl = ctr1,
                   metric = "ROC")
ggplot(rpart.fit2, highlight = TRUE)
```

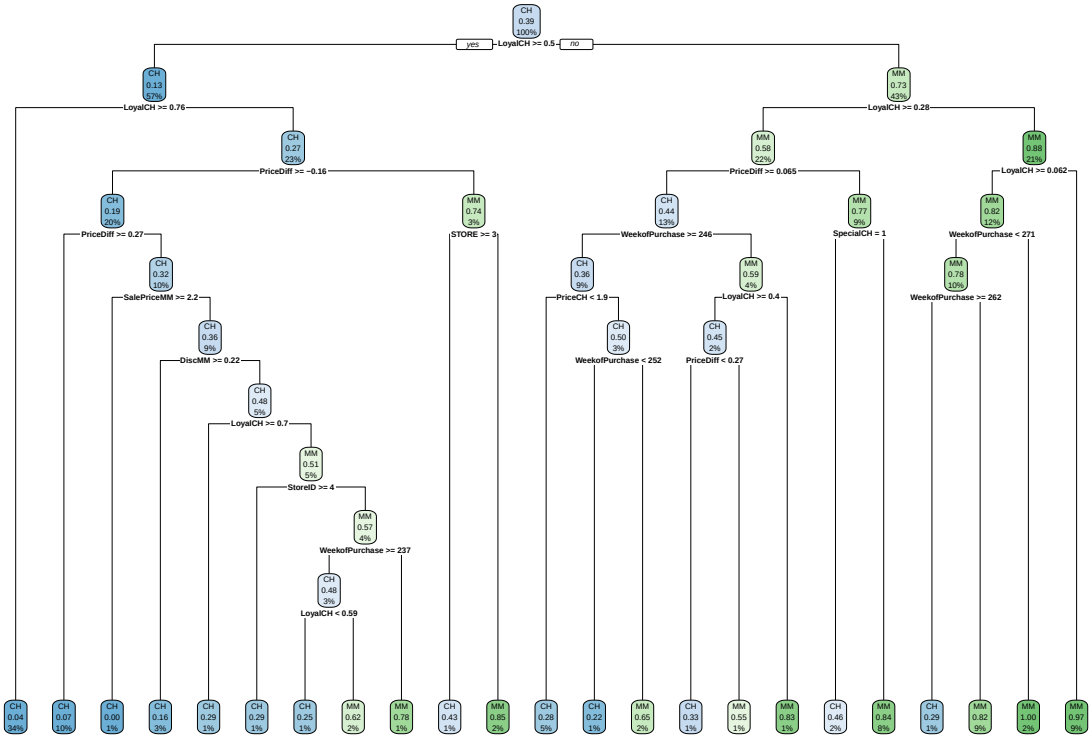



```
rpart.fit2$finalModel$cptable
```

```
##            CP nsplit rel error
## 1 0.503205128      0 1.0000000
## 2 0.020833333      1 0.4967949
## 3 0.019230769      5 0.4134615
```

```
## 4 0.008012821      6 0.3942308
## 5 0.006410256      8 0.3782051
## 6 0.003205128      9 0.3717949
## 7 0.002564103     15 0.3525641
## 8 0.002478752     22 0.3269231
```

```
### plot of final tree
rpart.plot(rpart.fit2$finalModel)
```




```
### predict
pred = predict(rpart.fit2, newdata = OJ[-rowtrain2,])
### test classification error rate
mean(pred != OJ[-rowtrain2,]$Purchase)
```

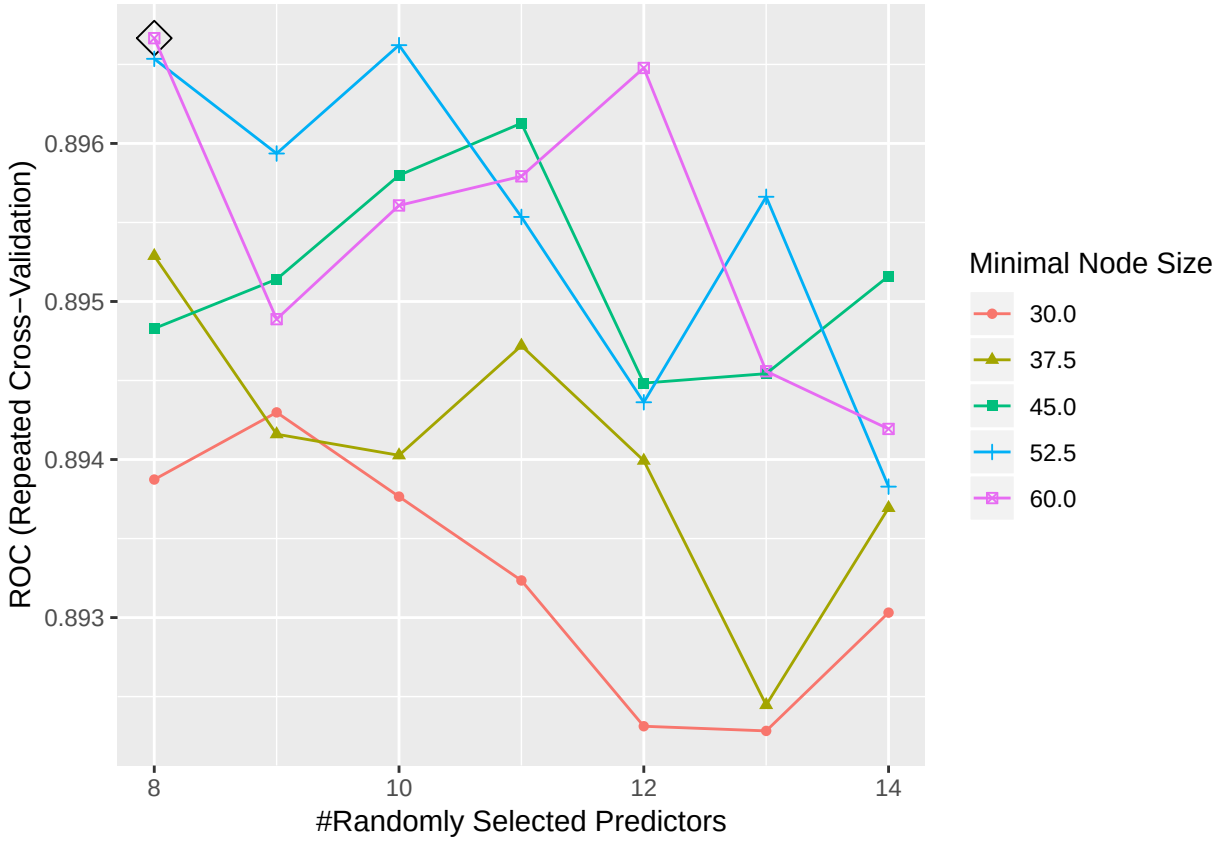
```
## [1] 0.1821561
```

According to cross validation, the number of split is 10 and the optimal tree size is 11.The test classification error rate is 0.1858736.

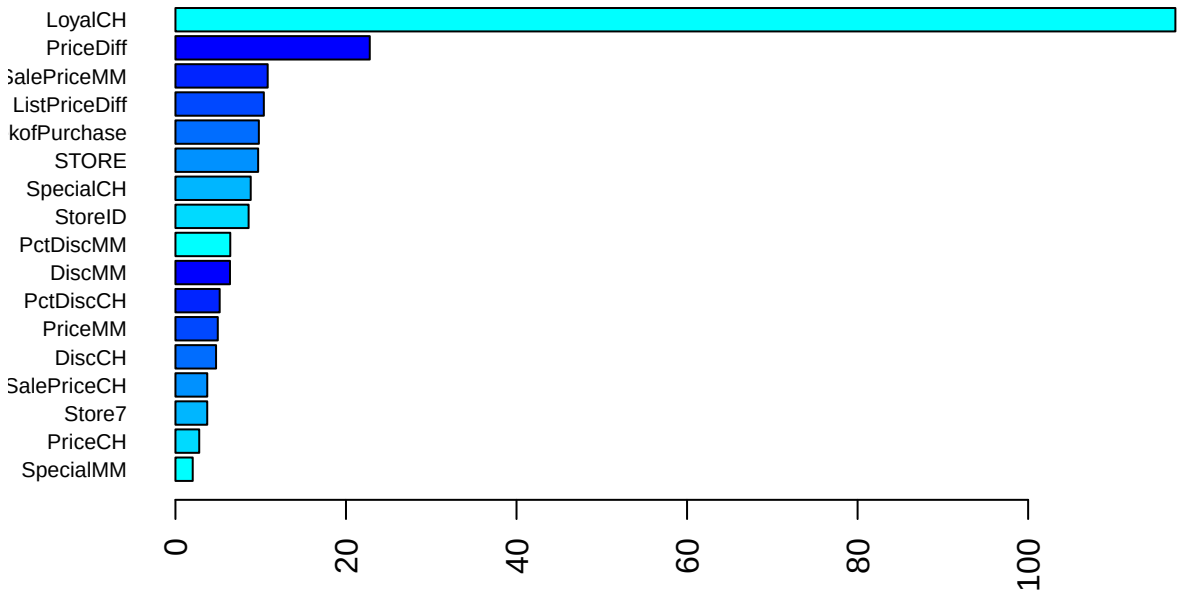
(b) Perform random forests on the training set and report variable importance. What isthe test error rate?

```
rf.grid2 = expand.grid(mtry = 8:14,
                       splitrule = "gini",
                       min.node.size = seq(30,60,length = 5))
set.seed(1)
rf.fit2 = train(Purchase~., OJ,
                subset = rowtrain2,
                method = "ranger",
                tuneGrid =  rf.grid2,
                metric = "ROC",
```

```
                trControl = ctr1)

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




```
### VARIABLE IMPORTANCE
rf2.final.imp = ranger(Purchase~., OJ[rowtrain2,],
                       mtry = 9 ,
                       min.node.size = 45,
                        splitrule = "gini",
                       importance = "permutation",
                       scale.permutation.importance = TRUE)
barplot(sort(ranger::importance(rf2.final.imp), decreasing = FALSE),
        las = 2, hori = TRUE, cex.names = 0.7,
        col = colorRampPalette(colors = c("cyan","blue"))(8))
```




```
### test error rate

pred_rf = predict(rf.fit2, newdata = OJ[-rowtrain2,])
mean(pred_rf!= OJ[-rowtrain2,]$Purchase)
```

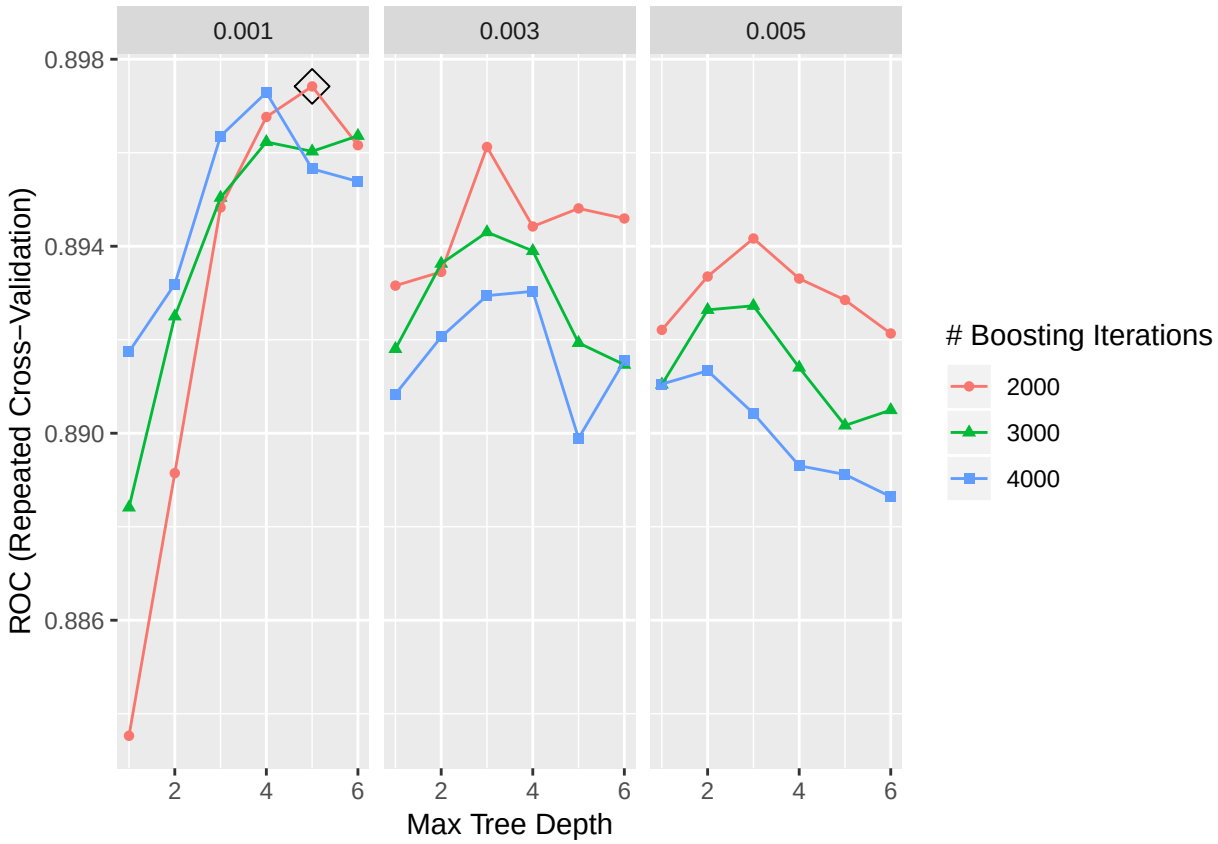
```
## [1] 0.1710037
```

The importance of variable was shown above.

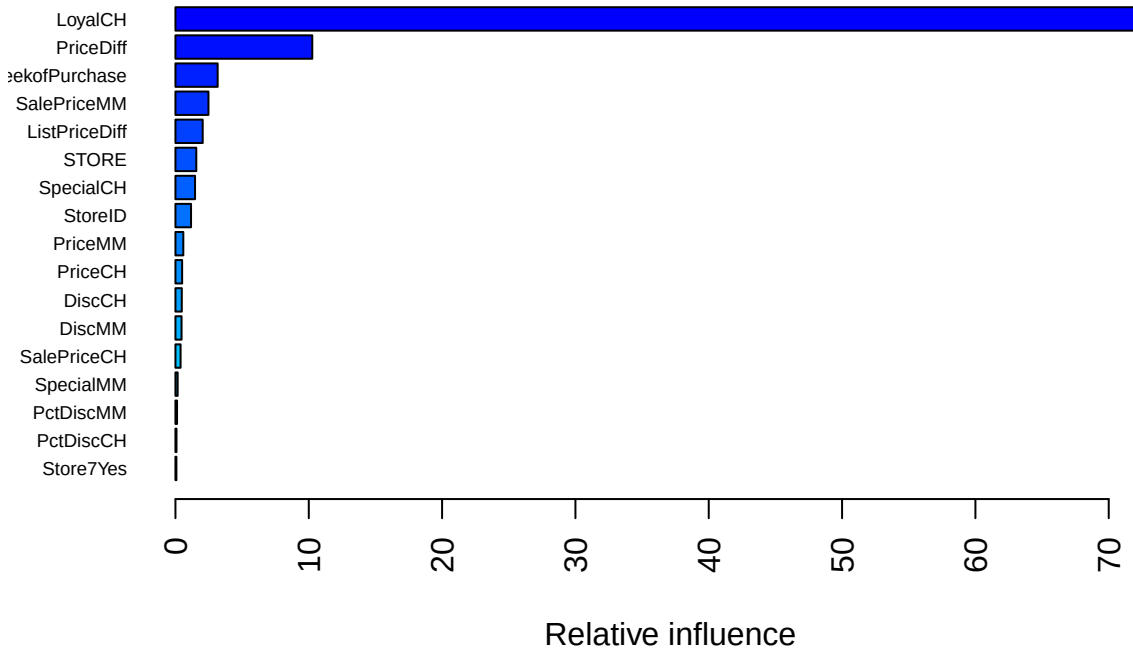
The test classification error rate is 0.1821561.

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

```
gbm2.grid = expand.grid(n.trees = c(2000, 3000, 4000),
                        interaction.depth = 1:6,
                        shrinkage = c(0.001,0.003,0.005),
                        n.minobsinnode = 1)
gbm2.fit = train(Purchase~., OJ[rowtrain2,],
                 tuneGrid = gbm2.grid,
                 trControl = ctr1,
                 method = "gbm",
                 distribution = "bernoulli",
                 metric = "ROC",
                 verbose = FALSE)
ggplot(gbm2.fit, highligh = TRUE)
```




```
### important variable
summary(gbm2.fit$finalModel, las = 2, cBars = 19, cex.names = 0.6)
```




```
##                              var     rel.inf
## LoyalCH                  LoyalCH 75.00017781
## PriceDiff              PriceDiff 10.26319526
```

```
## WeekofPurchase WeekofPurchase  3.16546239
## SalePriceMM       SalePriceMM  2.47592453
## ListPriceDiff   ListPriceDiff  2.04450990
## STORE                   STORE  1.56394329
## SpecialCH           SpecialCH  1.46930112
## StoreID               StoreID  1.17043846
## PriceMM               PriceMM  0.59068255
## PriceCH               PriceCH  0.50269348
## DiscCH                 DiscCH  0.47539396
## DiscMM                 DiscMM  0.45799764
## SalePriceCH       SalePriceCH  0.38504642
## SpecialMM           SpecialMM  0.16546476
## PctDiscMM           PctDiscMM  0.12021707
## PctDiscCH           PctDiscCH  0.07733877
## Store7Yes           Store7Yes  0.07221257
```

```
### test error rate
pred_gbm2 = predict(gbm2.fit, newdata = OJ[-rowtrain2,])
mean(pred_gbm2!=OJ[-rowtrain2,]$Purchase)
```

```
## [1] 0.1710037
```

The importance of variable was shown above. The test classification error rate is 0.1747212.