

DS2__HW4__REGRESSION__TREE

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

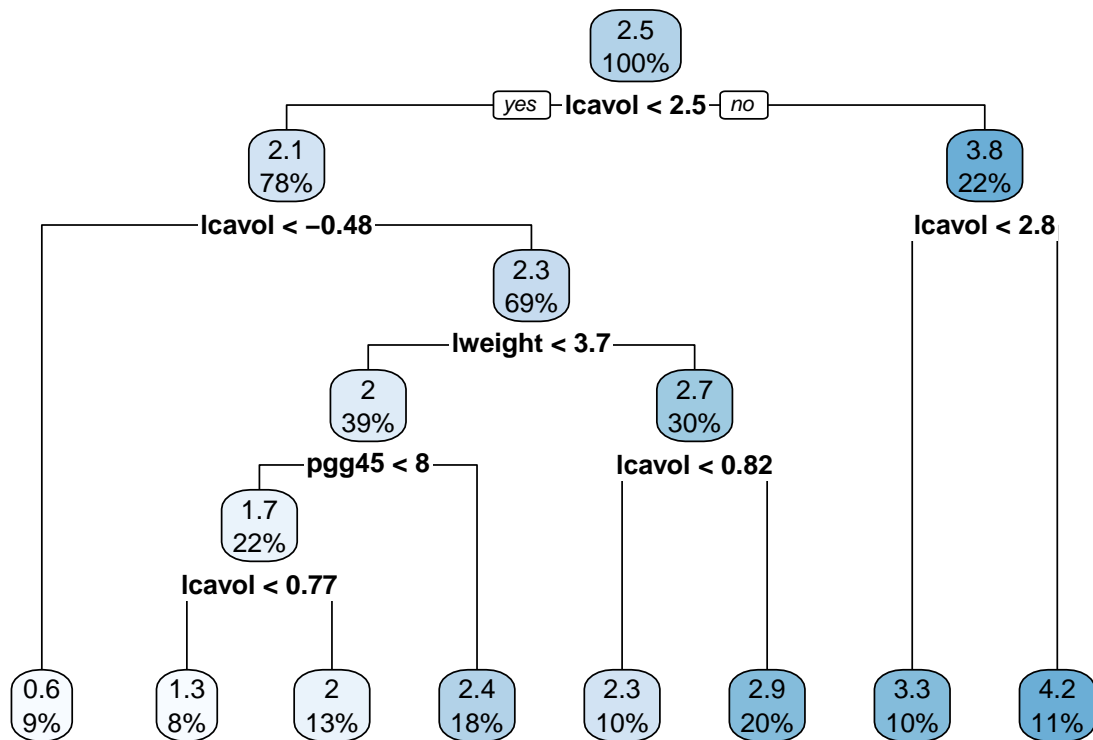
```
##      lcavol  lweight age      lbph svi      lcp gleason pgg45      lpsa
## 1 -0.5798185 2.769459 50 -1.386294 0 -1.386294      6      0 -0.4307829
## 2 -0.9942523 3.319626 58 -1.386294 0 -1.386294      6      0 -0.1625189
## 3 -0.5108256 2.691243 74 -1.386294 0 -1.386294      7     20 -0.1625189
## 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)
ctrl1 = trainControl(method = "cv")
```

1a) Fit a regression tree with `lpsa` as the response; 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?

```
set.seed(1)
rpart.fit = train(lpsa~., Prostate,
                  method = "rpart",
                  tuneGrid = data.frame(cp = exp(seq(-6,-2,length=20))), trControl = ctrl1)
rpart.plot(rpart.fit$finalModel)

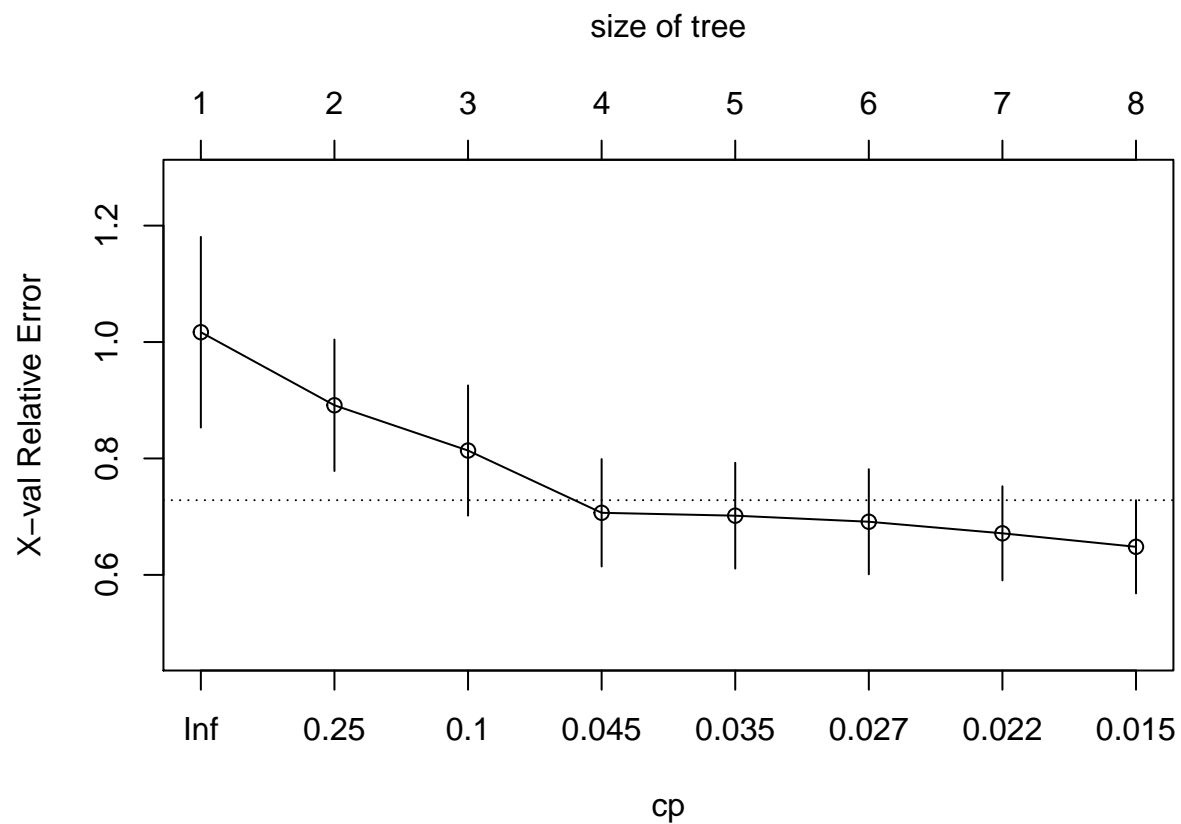
#####
set.seed(1)
tree1 = rpart(formula = lpsa~., data = Prostate)
rpart.plot(tree1)
```



```
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
```

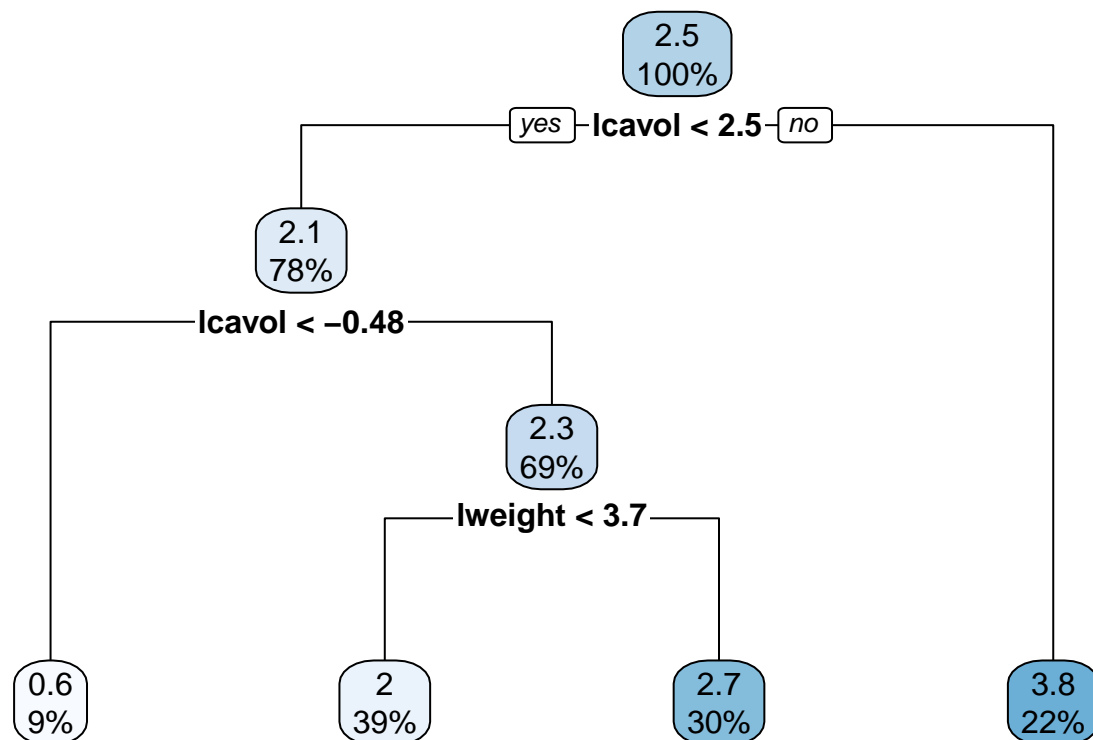
```
plotcp(tree1)
```



```

### tree by minimum 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)

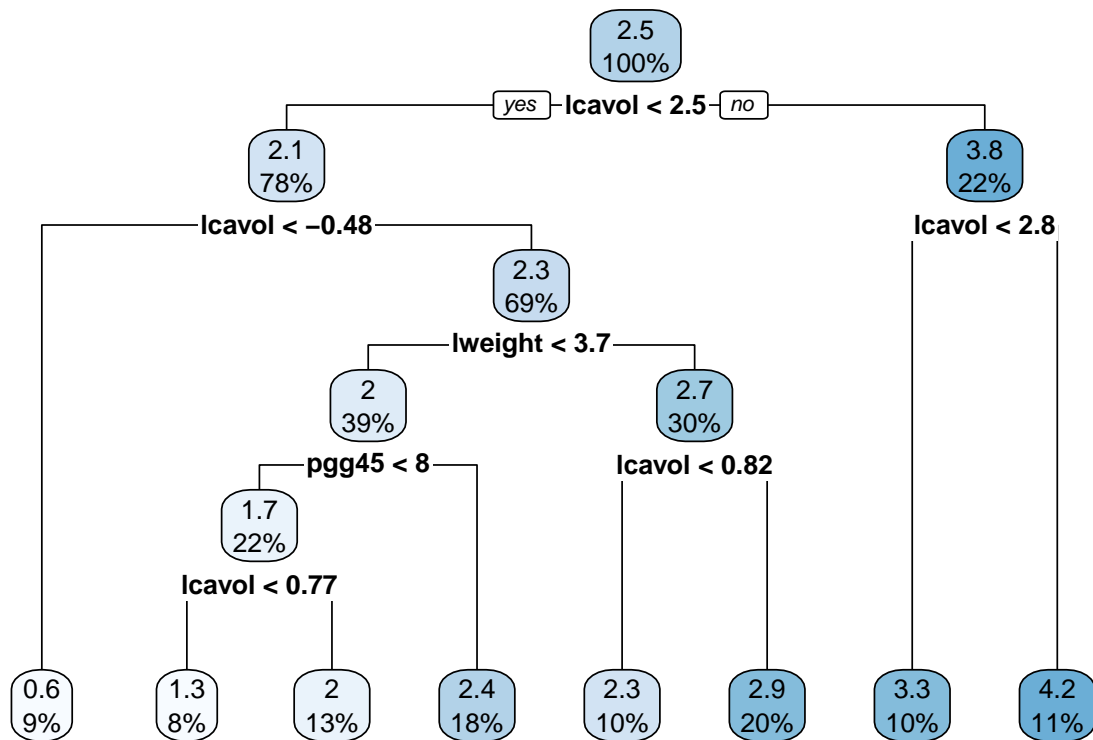
```



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, and interpret the information displayed.

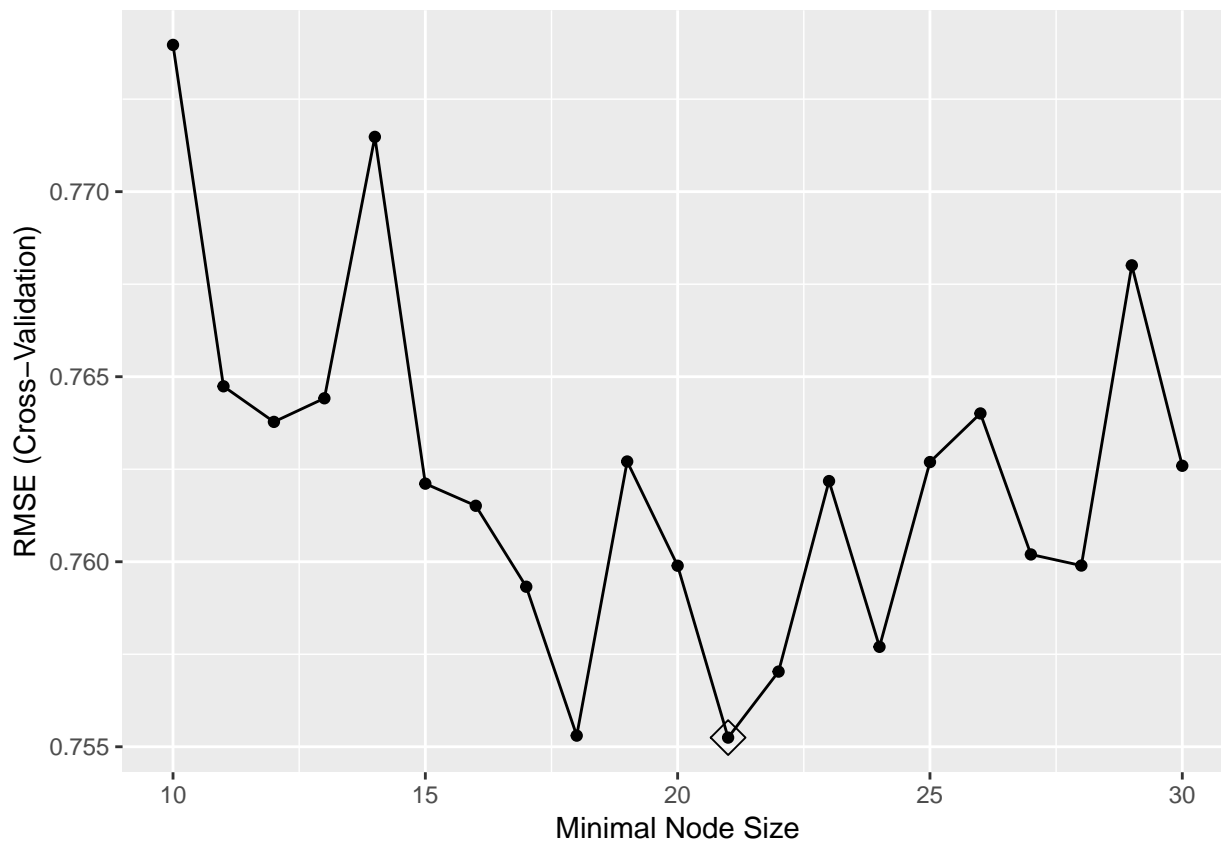
```
rpart.plot(tree2)
```



(c) Perform bagging and report the variable importance.

```

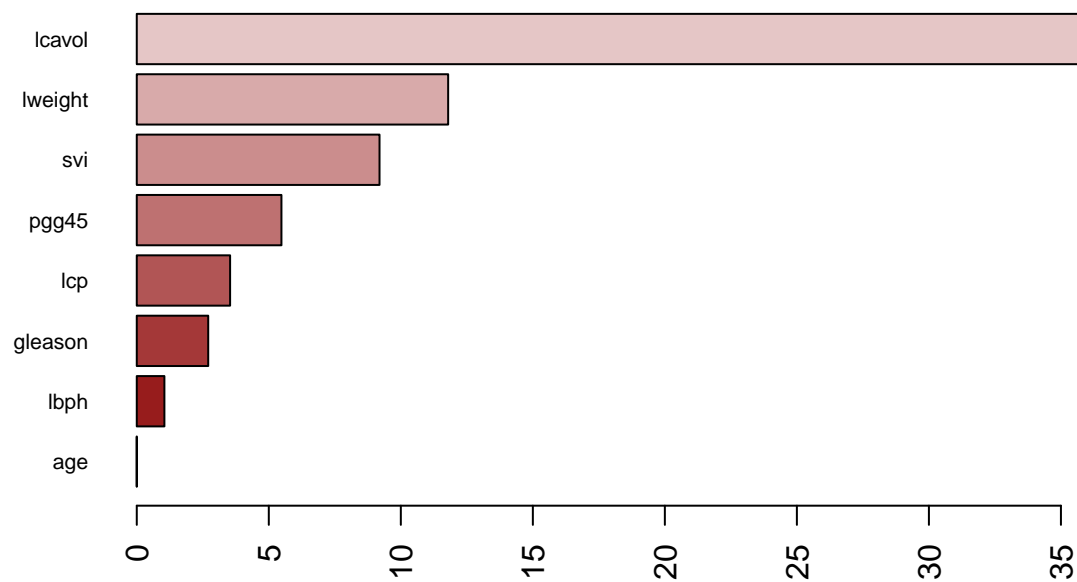
set.seed(2)
rf.grid = expand.grid(mtry = 8,
                      splitrule = "variance",
                      min.node.size = 10:30)
bagging.fit = train(lpsa~., Prostate,
                    method = "ranger",
                    tuneGrid = rf.grid,
                    trControl = ctrl)
ggplot(bagging.fit,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

```

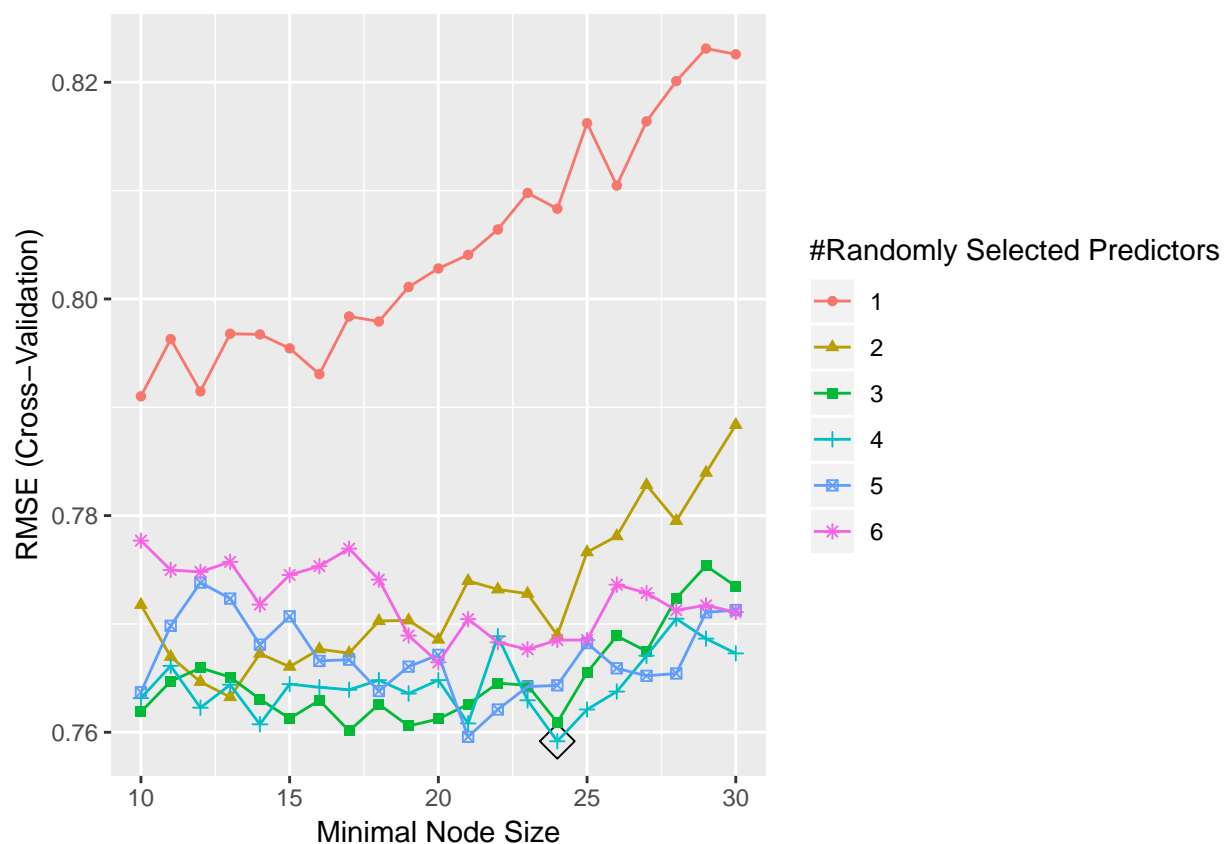


(d) Perform random forests and report the variable importance.

```
### tuning parameter
rf.grid = expand.grid(mtry = 1:6,
                     splitrule = "variance",
                     min.node.size = 10:30)### ?

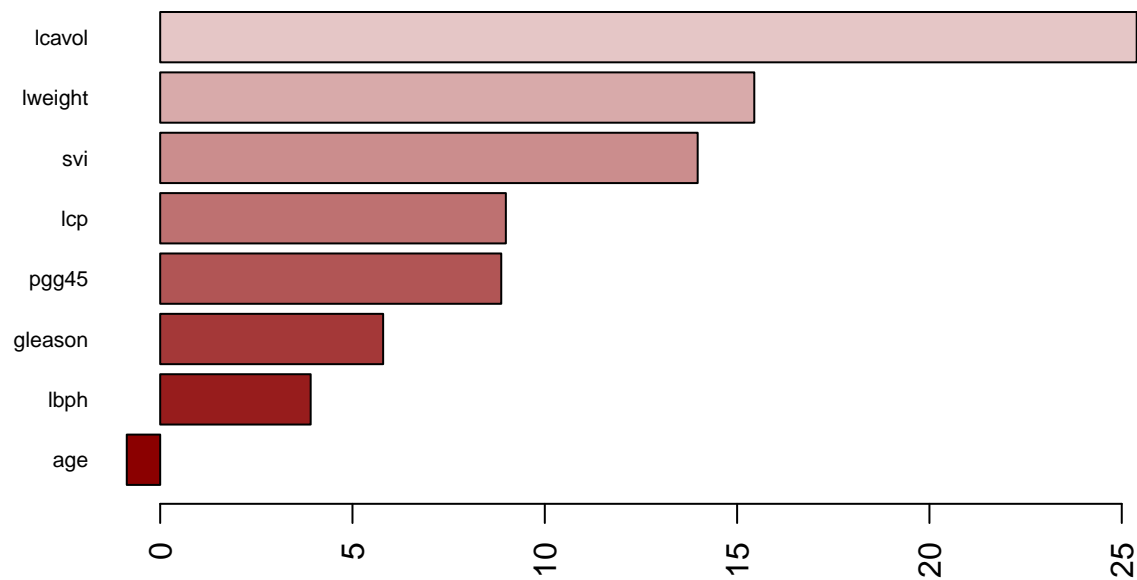
### fit model
set.seed(3)
rf.fit = train(lpsa~., Prostate,
               method = "ranger",
               tuneGrid = rf.grid,
               trControl = ctr1)

### 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)

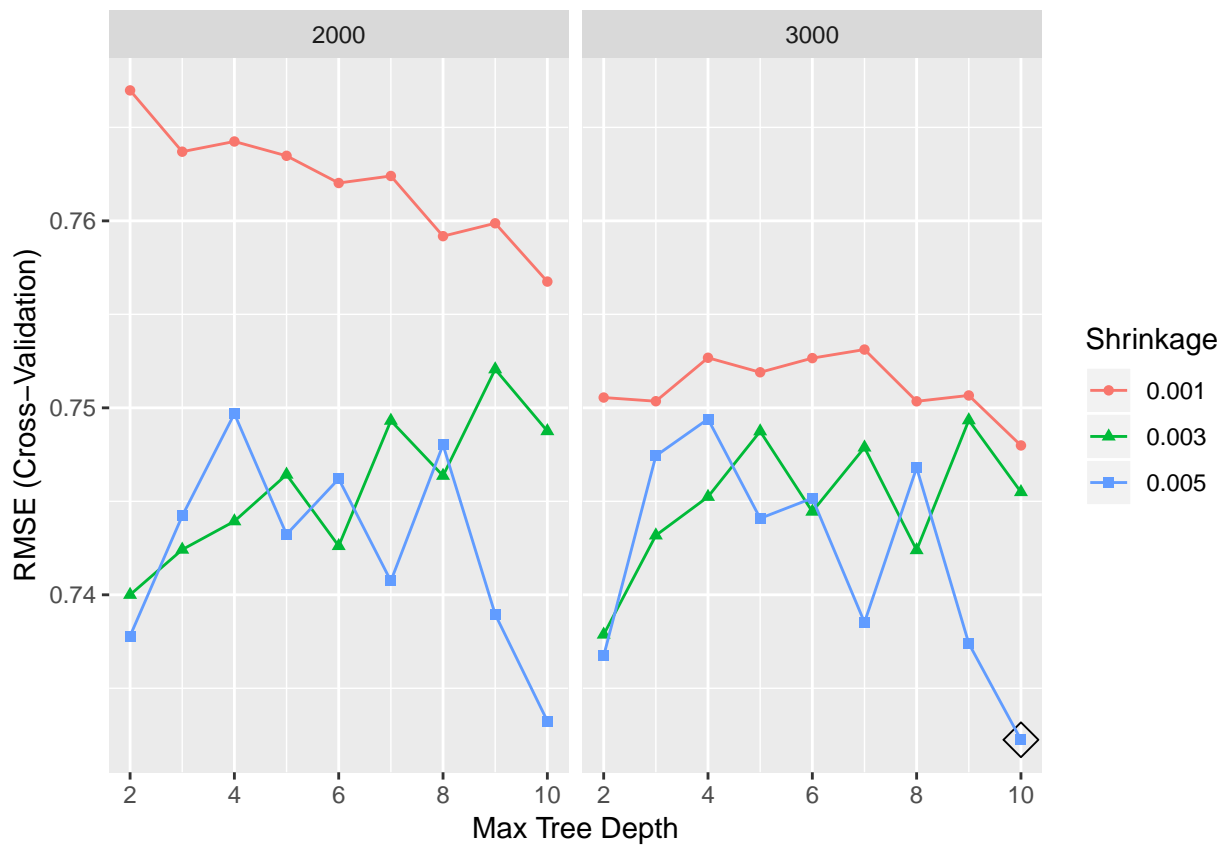
barplot(sort(ranger::importance(rf.final.imp), decreasing = FALSE),
        las = 2, horiz = TRUE, cex.names = 0.7, col = colorRampPalette(colors = c("darkred", "white", "white", "white", "white", "white"))(6))
```



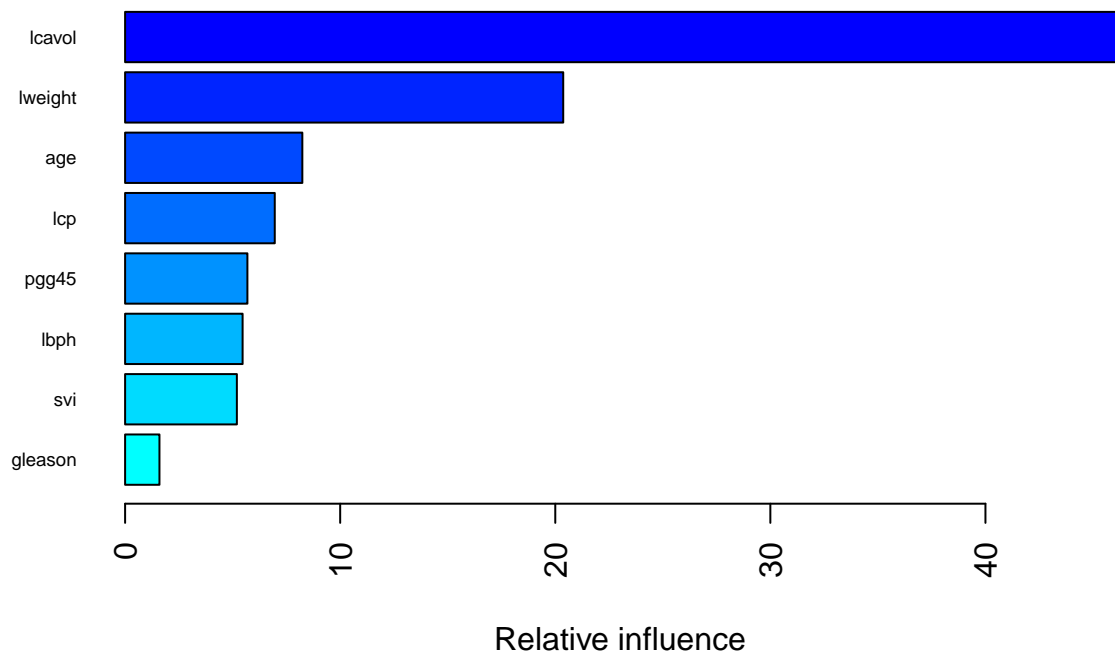
(e) Perform boosting and report the variable importance.

```
### 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 = ctrl1,
               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
```

(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
```

Problem 2

```
data(OJ)
head(OJ)
```

```
##   Purchase WeekofPurchase StoreID PriceCH PriceMM DiscCH DiscMM SpecialCH
## 1      CH              237      1    1.75    1.99    0.00    0.0         0
## 2      CH              239      1    1.75    1.99    0.00    0.3         0
## 3      CH              245      1    1.86    2.09    0.17    0.0         0
## 4      MM              227      1    1.69    1.69    0.00    0.0         0
## 5      CH              228      7    1.69    1.69    0.00    0.0         0
## 6      CH              230      7    1.69    1.99    0.00    0.0         0
```

```
## SpecialMM LoyalCH SalePriceMM SalePriceCH PriceDiff Store7 PctDiscMM
## 1 0 0.500000 1.99 1.75 0.24 No 0.000000
## 2 1 0.600000 1.69 1.75 -0.06 No 0.150754
## 3 0 0.680000 2.09 1.69 0.40 No 0.000000
## 4 0 0.400000 1.69 1.69 0.00 No 0.000000
## 5 0 0.956535 1.69 1.69 0.00 Yes 0.000000
## 6 1 0.965228 1.99 1.69 0.30 Yes 0.000000
## PctDiscCH ListPriceDiff STORE
## 1 0.000000 0.24 1
## 2 0.000000 0.24 1
## 3 0.091398 0.23 1
## 4 0.000000 0.00 1
## 5 0.000000 0.00 0
## 6 0.000000 0.30 0
```

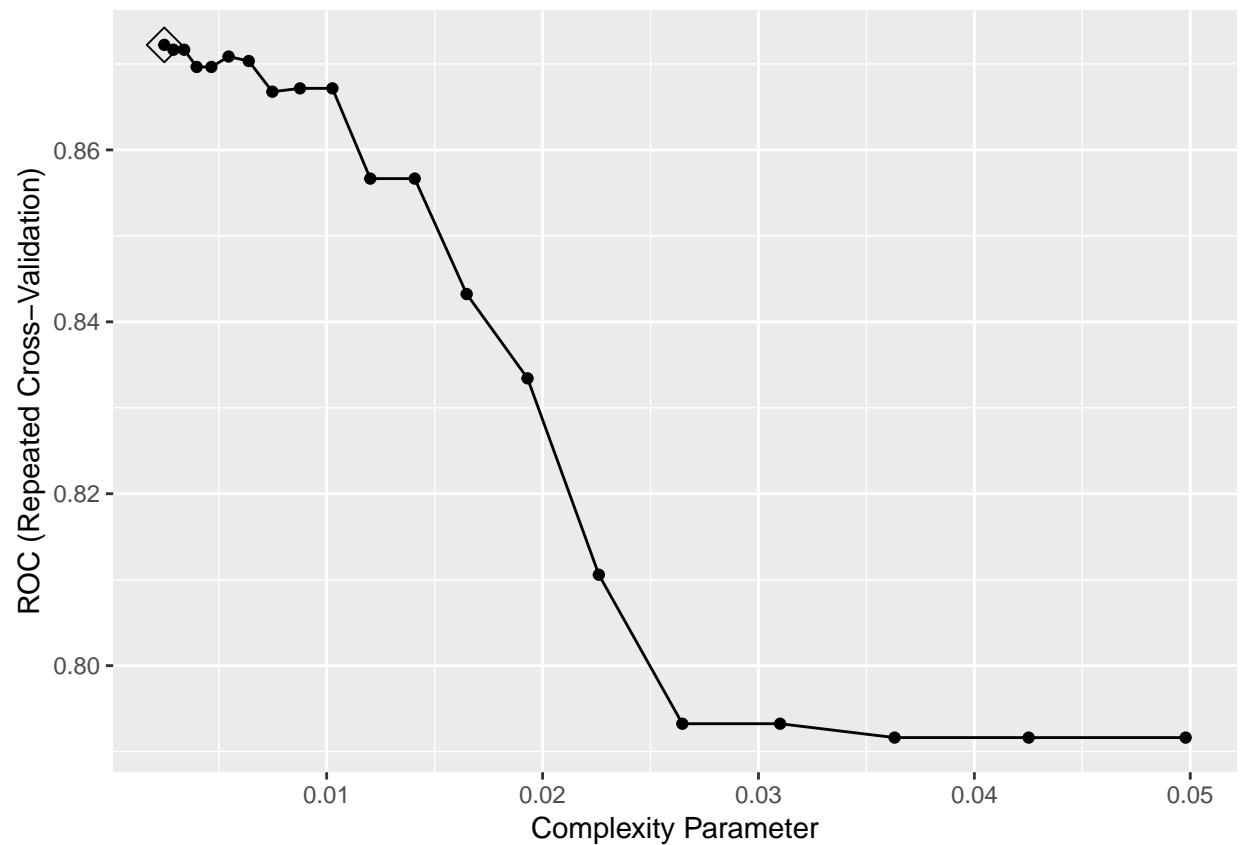
```
levels(OJ$Purchase)
```

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

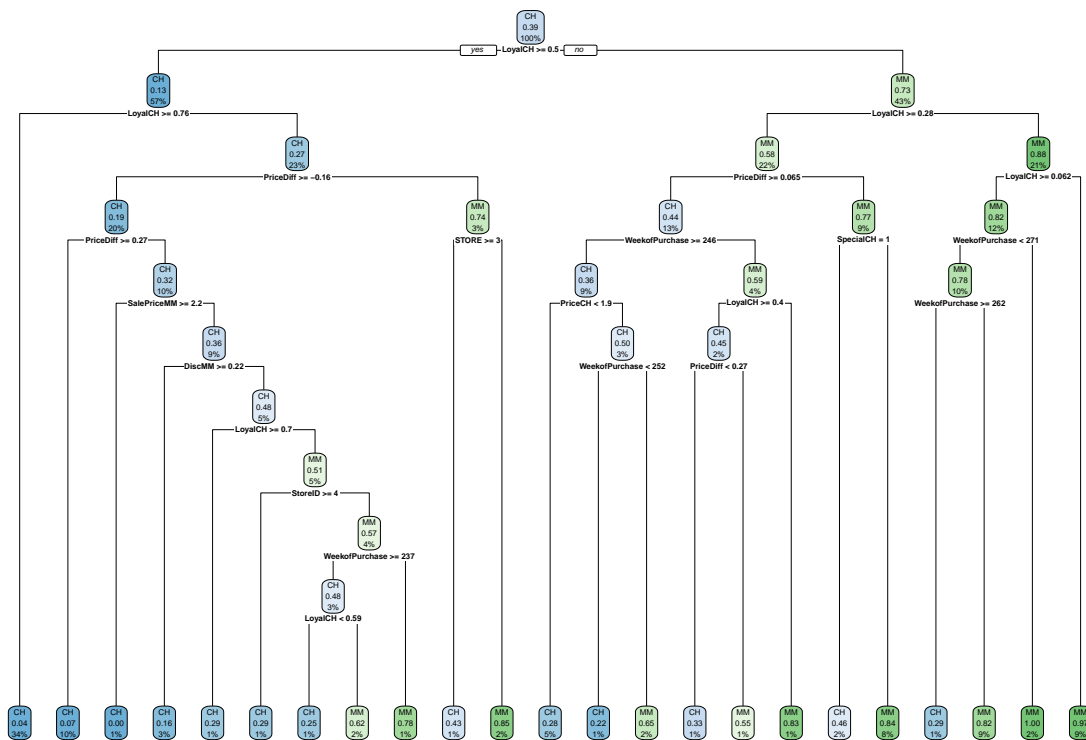
```
rowtrain2 = createDataPartition(y = OJ$Purchase,
                                p = 800/1070,
                                list = FALSE)
```

(a) Fit a classification tree to the training set, 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?

```
ctrl = 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 = ctrl,
                   metric = "ROC")
ggplot(rpart.fit2, highlight = TRUE)
```



```
### 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
```

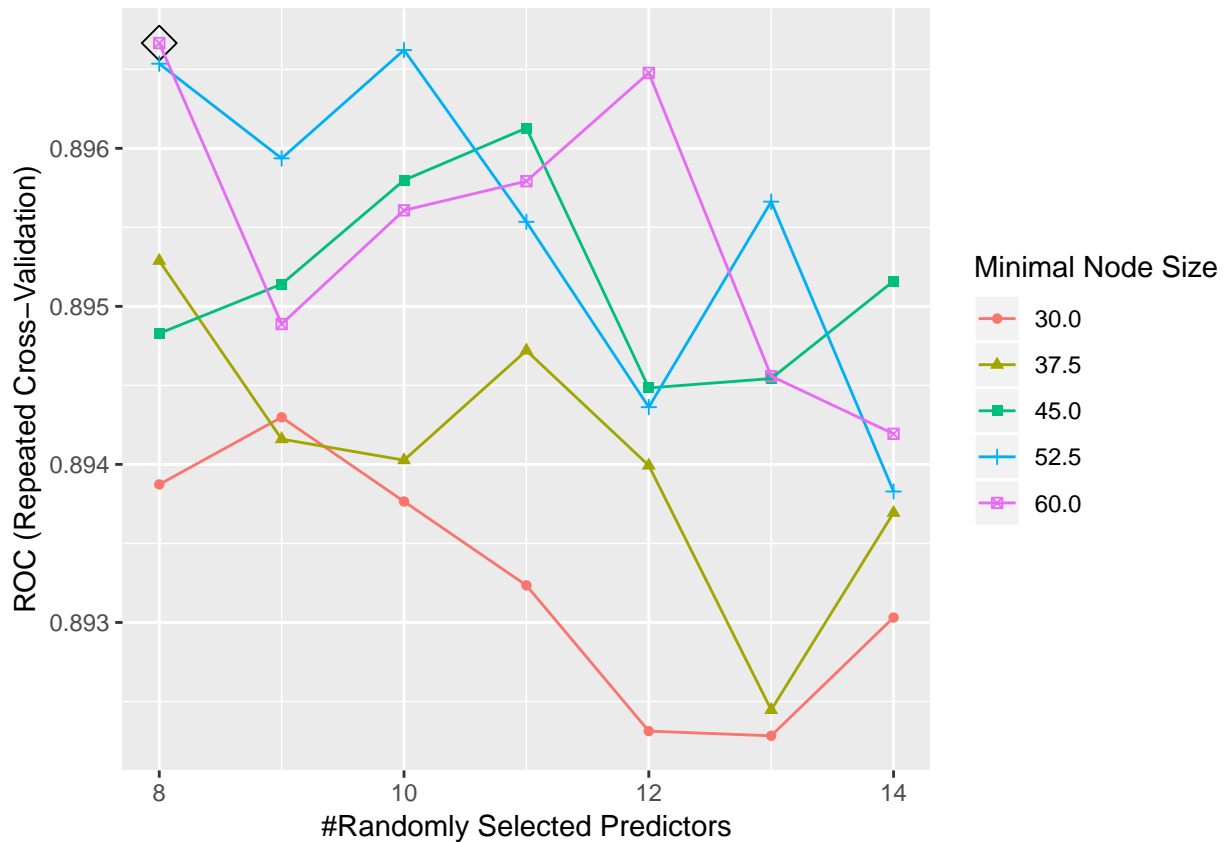
According to cross validation, the optimal tree size is 11.

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

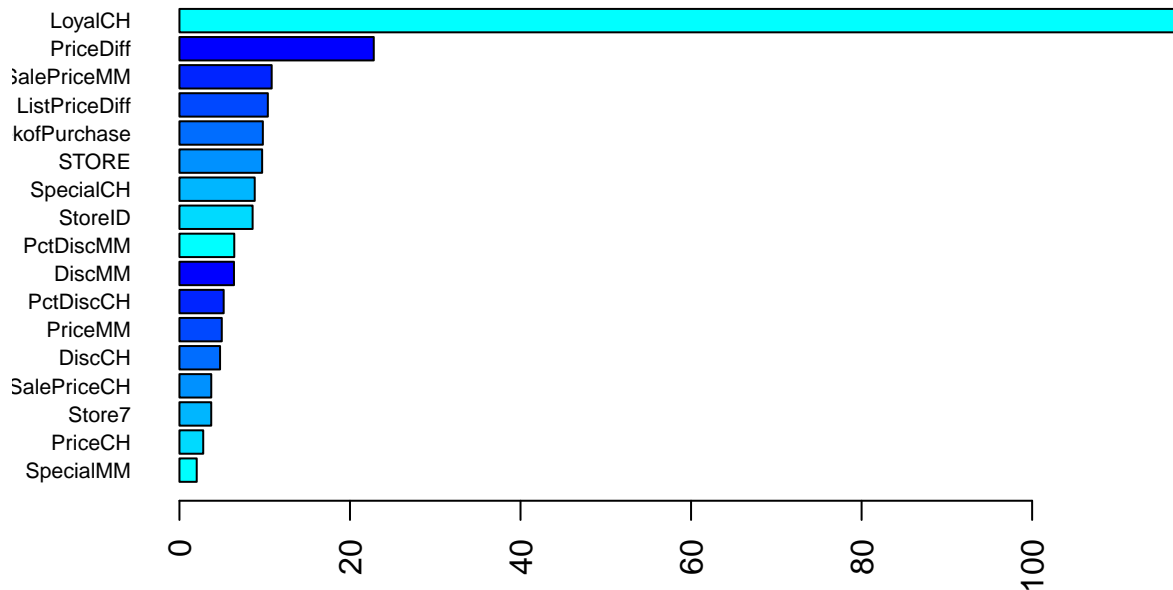
```
rf.grid2 = expand.grid(mtry = 8:14,
                      splitrule = "gini",
                      min.node.size = seq(30,60,length = 5))

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))
```



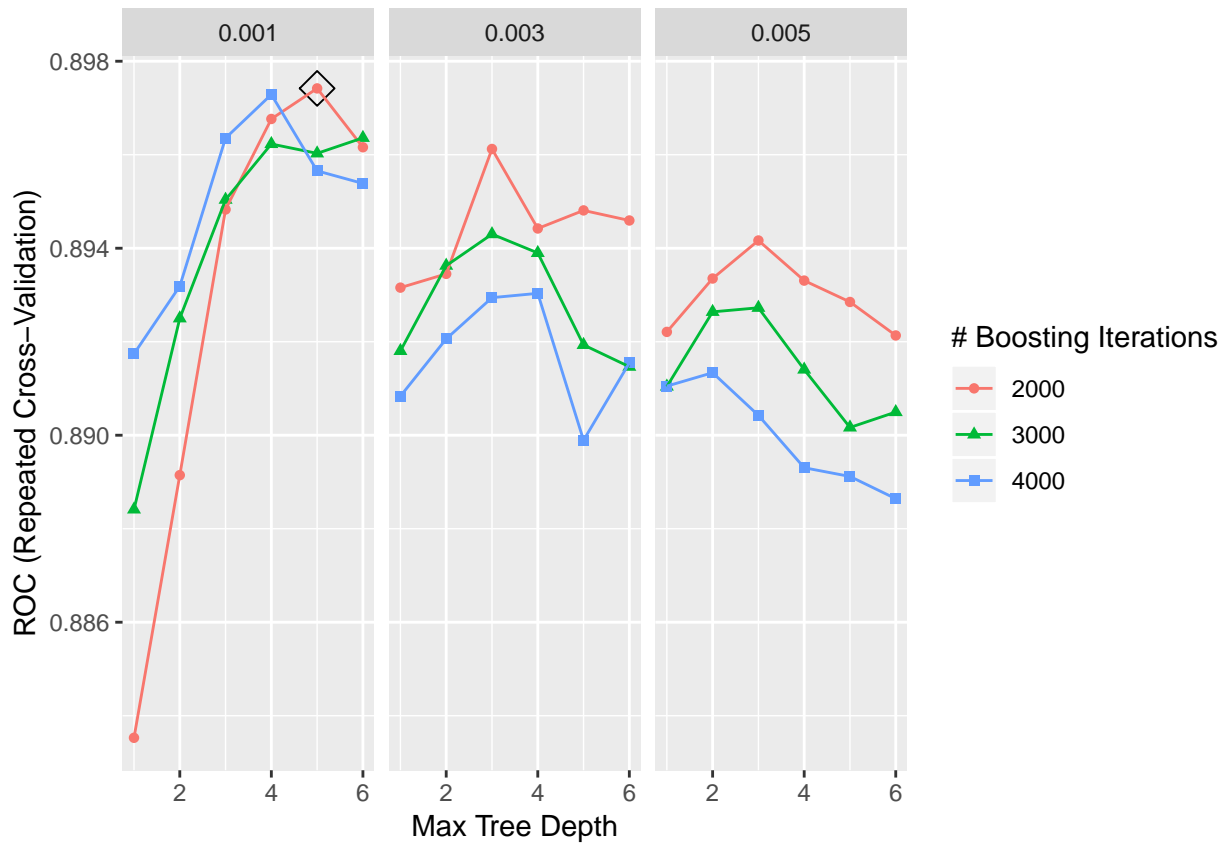
```
### test error rate

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

## [1] 0.1710037
```

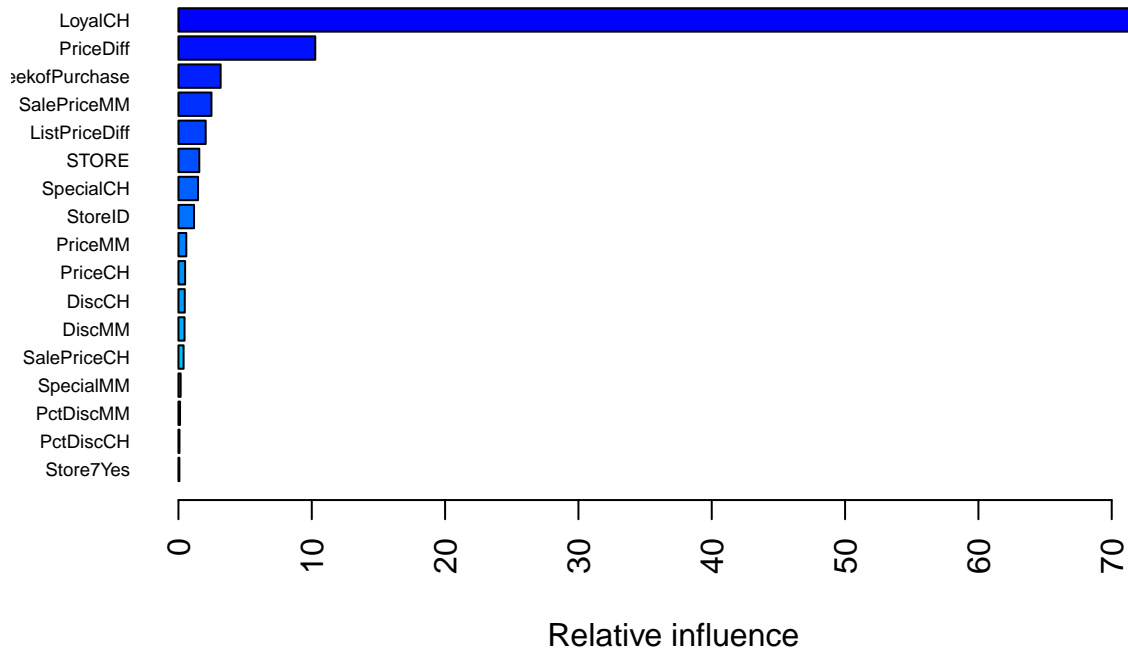
(c) Perform boosting on the training set and report variable importance. What is the test error rate?

```
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 = ctrl,
                 method = "gbm",
                 distribution = "bernoulli",
                 metric = "ROC",
                 verbose = FALSE)
ggplot(gbm2.fit, highlight = 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

```