Machine Learning Hw4

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```
library(ISLR)
library(caret)
library(rpart)
library(rpart.plot)
library(party)
library(partykit)
library(randomForest)
library(ranger)
library(gbm)
library(plotmo)
library(pdp)
library(lime)
library(lasso2)
```

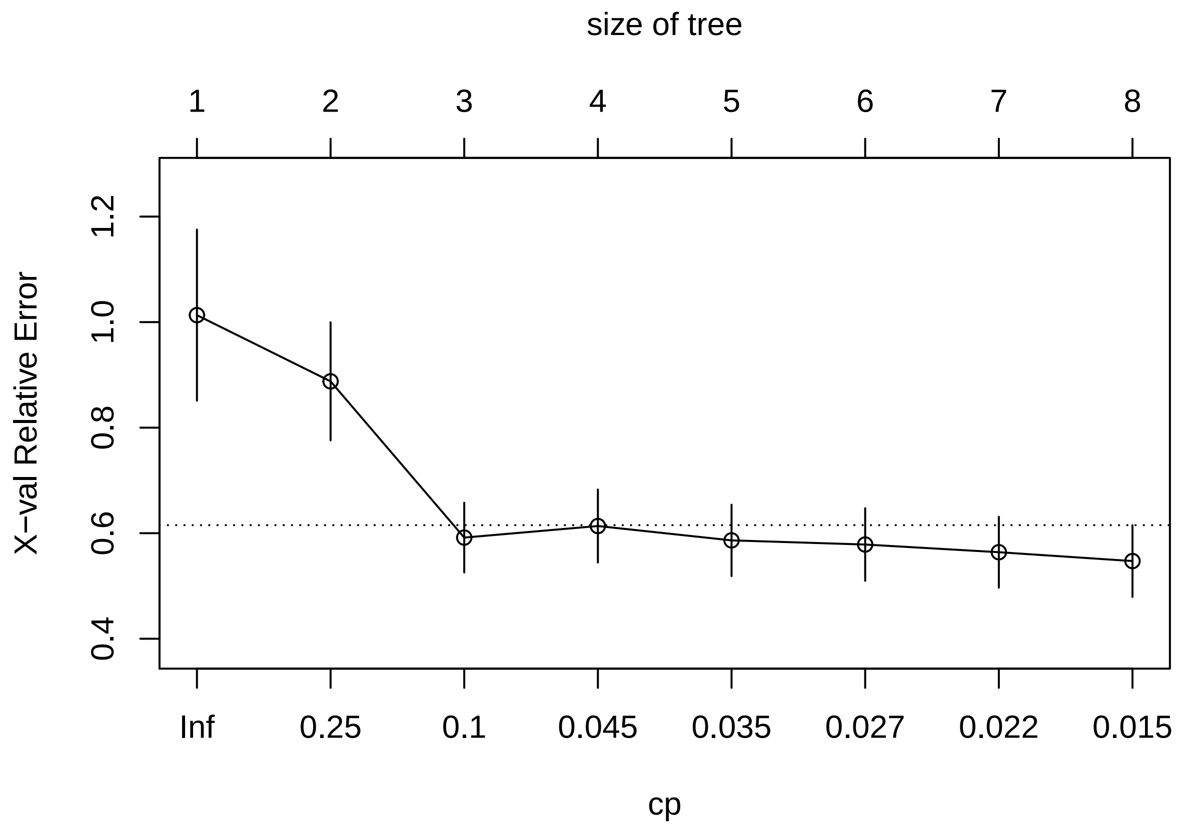
(a) Fit a regression tree with lpsa as the response and the other variables as predictors. Use cross-validation to determine the optimal tree size. Which tree size corresponds to the lowest cross-validation error? Is this the same as the tree size obtained using the 1 SE rule?

```
set.seed(1)
data("Prostate")
ctrl <- trainControl(method = "cv")
```

```
set.seed(1)
tree <- rpart(formula = lpsa~., data = Prostate,
               control = rpart.control(cp = 0.01))
cpTable <- printcp(tree)
```

```
##
## Regression tree:
## rpart(formula = lpsa ~ ., data = Prostate, control = rpart.control(cp = 0.01))
##
## 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 1.01323 0.162162
## 2 0.184647      1   0.65289 0.88779 0.111915
## 3 0.059316      2   0.46824 0.59168 0.066102
## 4 0.034756      3   0.40893 0.61359 0.069269
## 5 0.034609      4   0.37417 0.58640 0.067630
## 6 0.021564      5   0.33956 0.57853 0.068772
## 7 0.021470      6   0.31800 0.56398 0.067155
## 8 0.010000      7   0.29653 0.54721 0.068034
```

```
plotcp(tree)
```



```
minErr <- which.min(cpTable[,4])
minErr
```

```
## 8
## 8
```

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

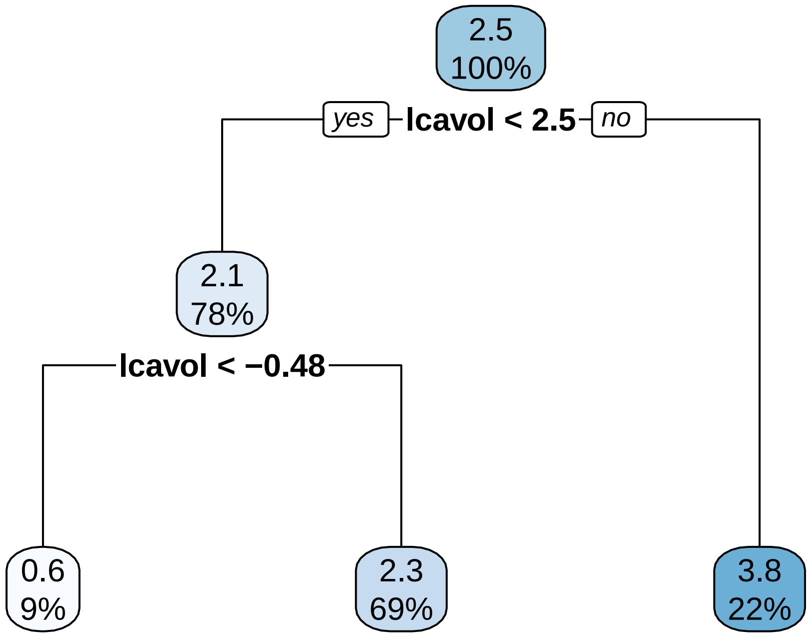
```
cpTable[cpTable[,4] < cpTable[minErr,4] + cpTable[minErr,5],1][1]
```

```
##          3
## 0.05931585
```

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

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

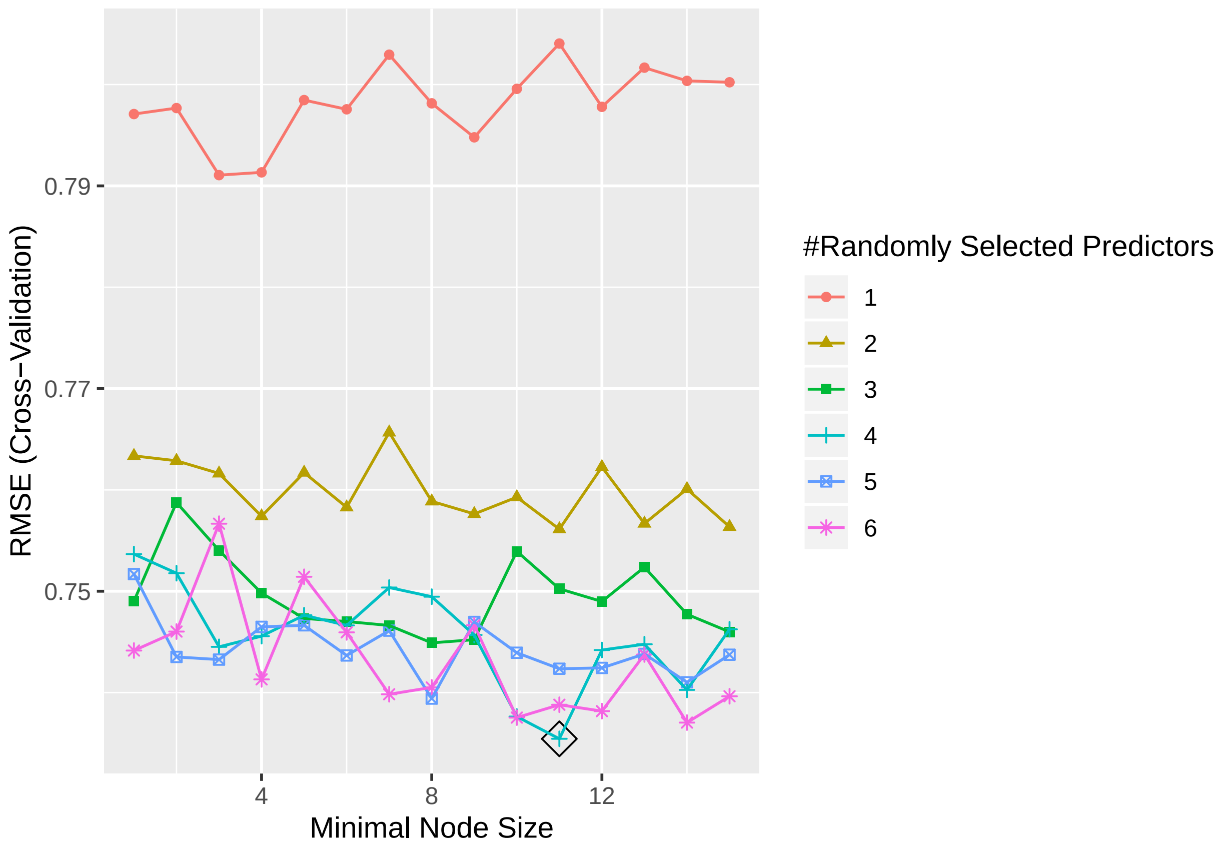
```
tree_a = prune(tree, cp = cpTable[cpTable[,4] < cpTable[minErr,4] + cpTable[minErr,5], 1][1])
rpart.plot(tree_a)
```



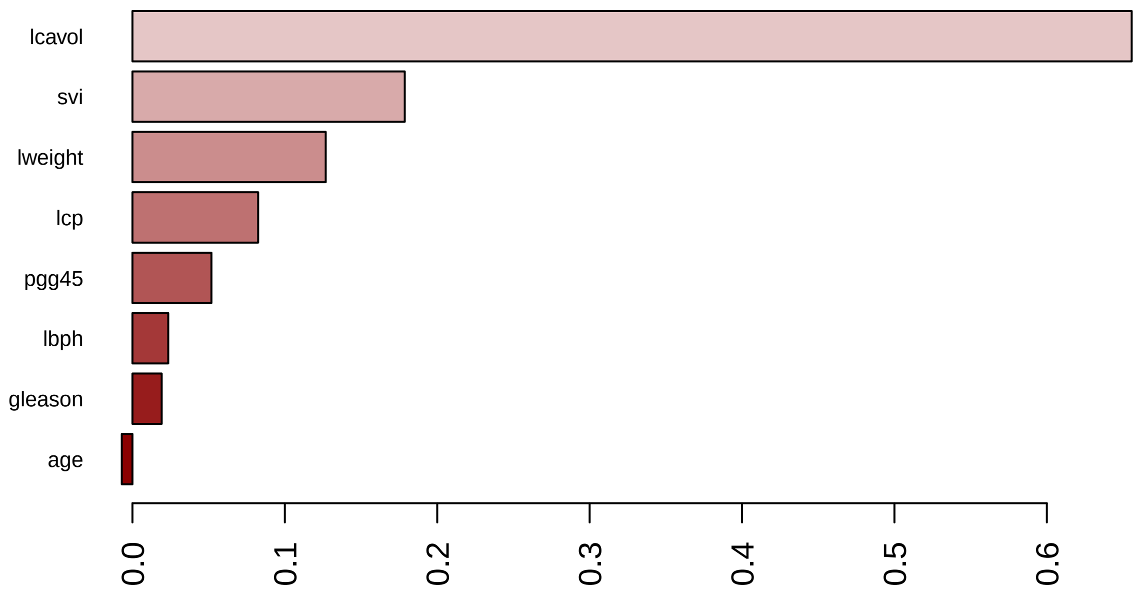
(c) Perform bagging and report the variable importance

```
bagging.grid <- expand.grid(mtry = 1:6,
                       splitrule = "variance",
                       min.node.size = 1:15)
set.seed(1)
bagging <- train(lpsa~., Prostate,
                method = "ranger",
                tuneGrid = bagging.grid,
                trControl = ctrl,
                importance = "permutation")

ggplot(bagging, highlight = TRUE)
```



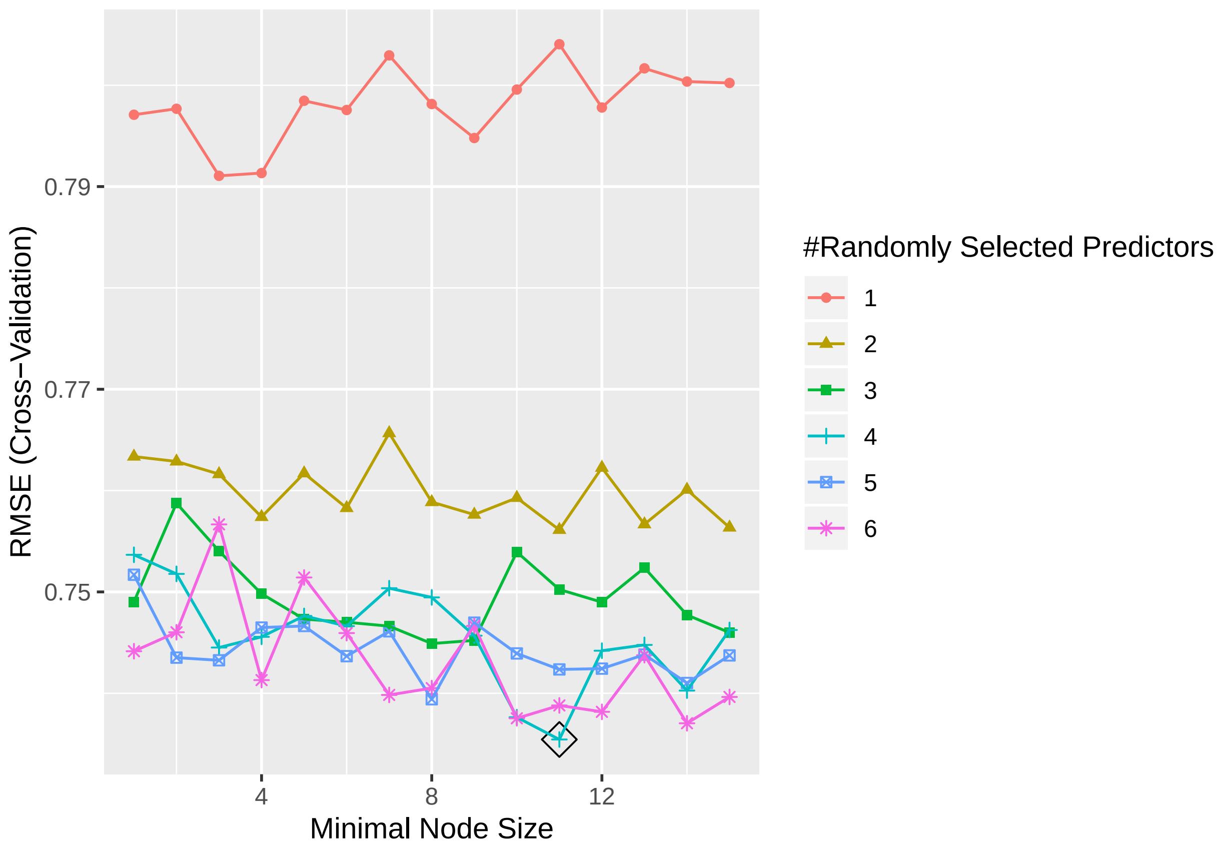
```r
barplot(sort(ranger::importance(bagging$finalModel), decreasing = FALSE),
        las = 2, horiz = TRUE, cex.names = 0.7,
        col = colorRampPalette(colors = c("darkred","white","darkblue"))(19))
```



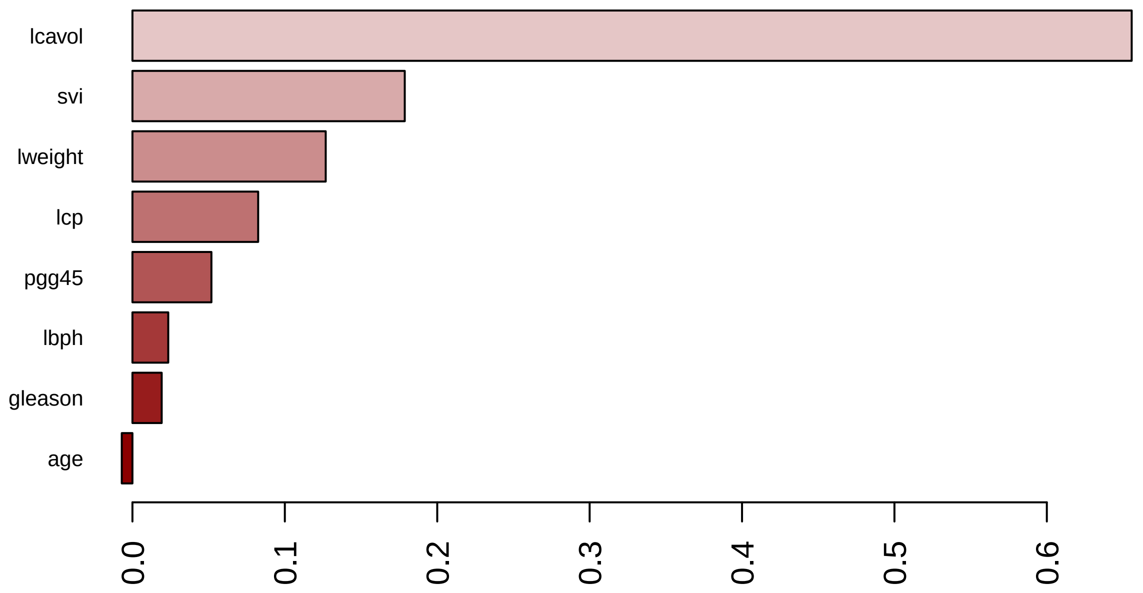
The important variables are : lcavol, lweight, svi

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

```r
rf.grid = expand.grid(mtry = 1:6,
                      splitrule = "variance",
                      min.node.size = 1:15)
set.seed(1)
rf.fit = train(lpsa~., Prostate,
               method = "ranger",
               tuneGrid = rf.grid,
               trControl = ctrl,
               importance = 'permutation')
ggplot(rf.fit, highlight = TRUE)
```



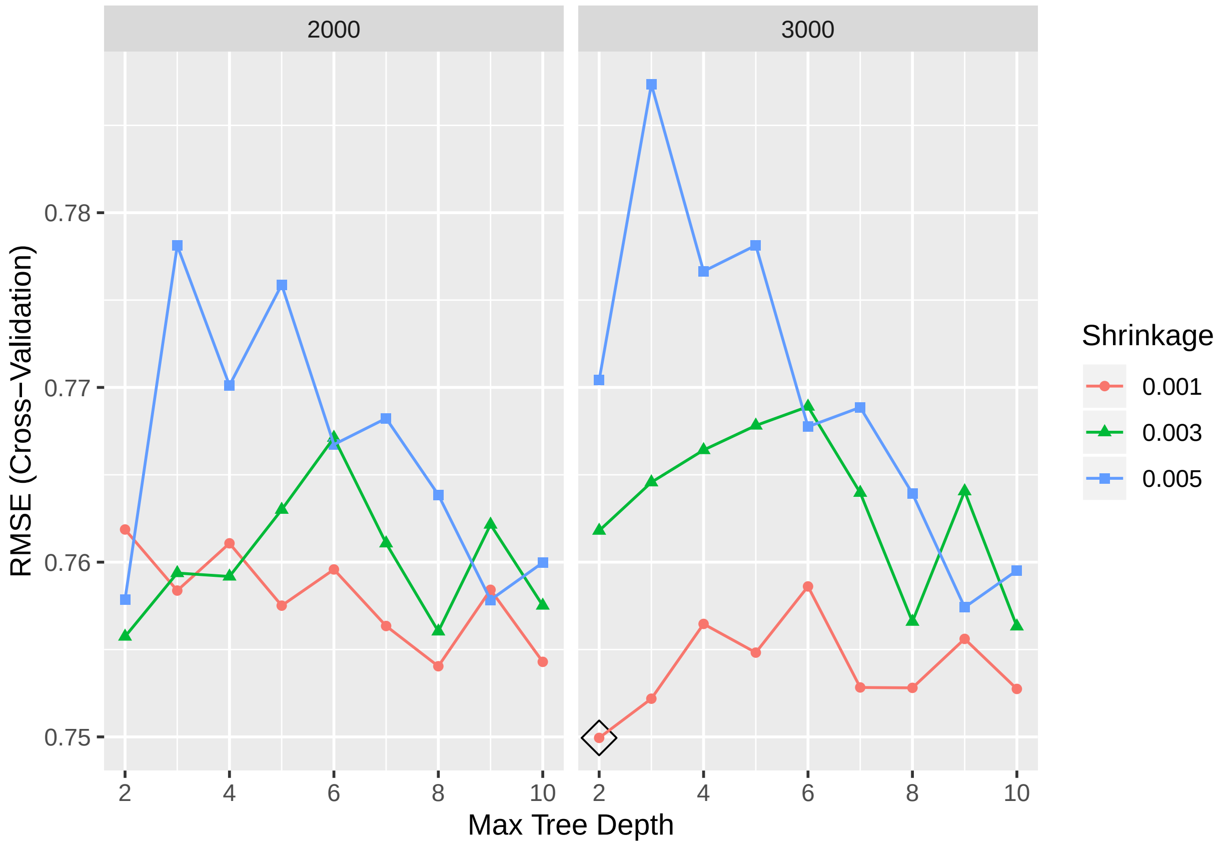
```r
barplot(sort(ranger::importance(rf.fit$finalModel), decreasing = FALSE),
        las = 2, horiz = TRUE, cex.names = 0.7,
        col = colorRampPalette(colors = c("darkred","white","darkblue"))(19))
```



(e) Perform boosting and report the variable importance.

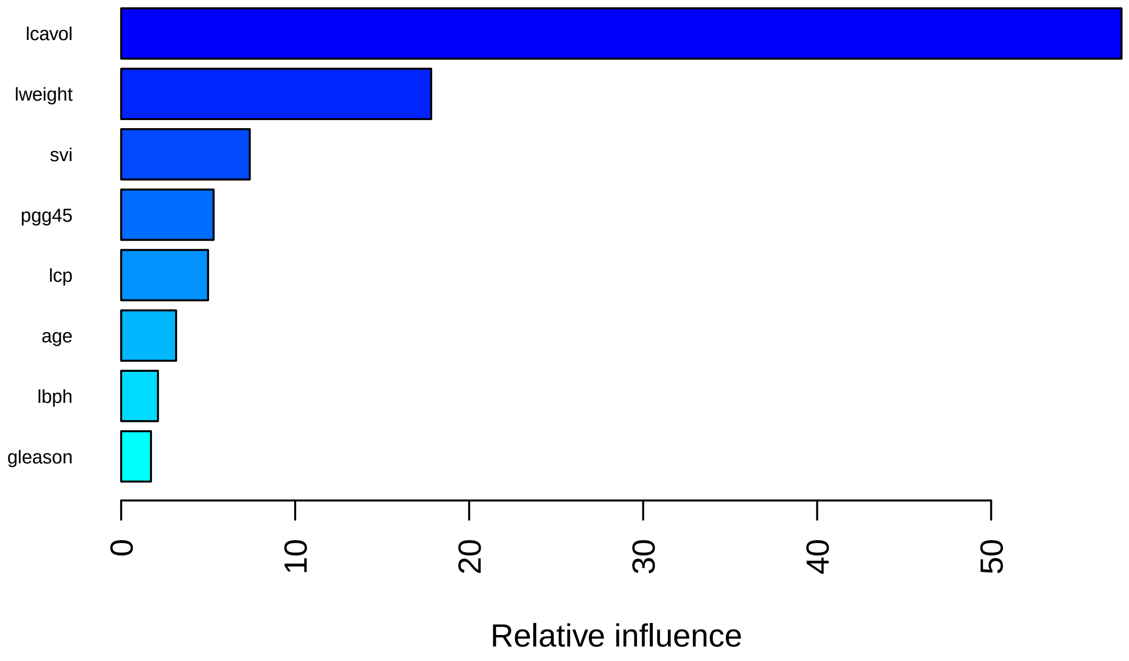
```
gbm.grid <- expand.grid(n.trees = c(2000,3000),
                        interaction.depth = 2:10,
                        shrinkage = c(0.001,0.003,0.005),
                        n.minobsinnode = 1)
set.seed(1)
gbm.fit <- train(lpsa~., Prostate,
                 method = "gbm",
                 tuneGrid = gbm.grid,
                 trControl = ctrl,
                 verbose = FALSE)

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



Variable importance from boosting can be obtained using the `summary()` function.

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



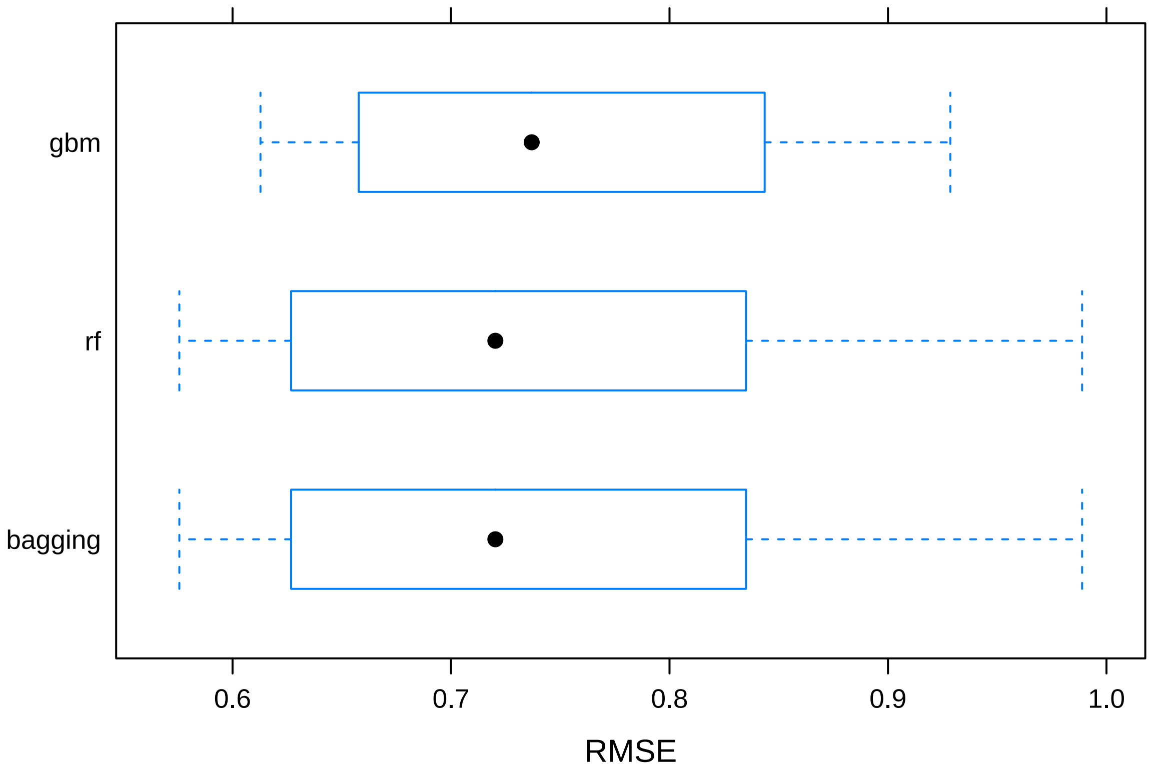
```
##              var   rel.inf
## lcavol   lcavol 57.494112
## lweight lweight 17.818879
## svi         svi  7.392286
## pgg45     pgg45  5.312763
## lcp         lcp  4.994192
## age         age  3.157564
## lbph       lbph  2.115772
## gleason gleason  1.714432
```

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

```r
resamp <- resamples(list(bagging = bagging, rf = rf.fit, gbm = gbm.fit))
summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: bagging, rf, gbm
## Number of resamples: 10
##
## MAE
##              Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## bagging 0.4794948 0.5357349 0.6115087 0.5980269 0.6632726 0.7001466    0
## rf      0.4794948 0.5357349 0.6115087 0.5980269 0.6632726 0.7001466    0
## gbm     0.4988605 0.5382599 0.6238535 0.6060614 0.6541746 0.7189084    0
##
## RMSE
##              Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## bagging 0.5756510 0.6319992 0.7202955 0.7354396 0.8235912 0.9888492    0
## rf      0.5756510 0.6319992 0.7202955 0.7354396 0.8235912 0.9888492    0
## gbm     0.6127814 0.6613586 0.7369285 0.7499428 0.8330904 0.9285269    0
##
## Rsquared
##              Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## bagging 0.3250728 0.5203503 0.6199793 0.6083602 0.7499733 0.7763990    0
## rf      0.3250728 0.5203503 0.6199793 0.6083602 0.7499733 0.7763990    0
## gbm     0.3912307 0.4940316 0.6253058 0.6103438 0.7211938 0.8171347    0
```

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

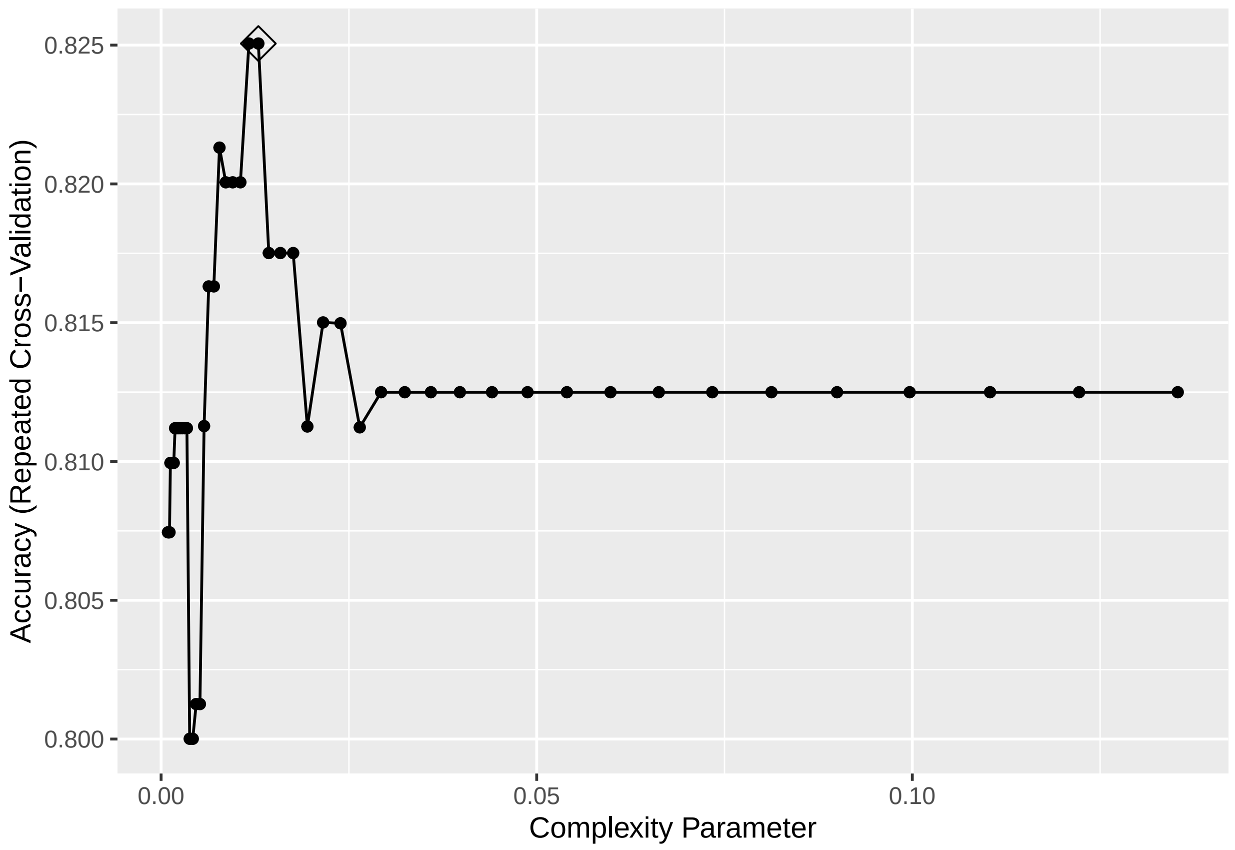


2. This problem involves the OJ data in the ISLR package. The data contains 1070 purchases where the customers either purchased Citrus Hill or Minute Maid Orange Juice. A number of characteristics of customers and products are recorded. Create a training set containing a random sample of 800 observations,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

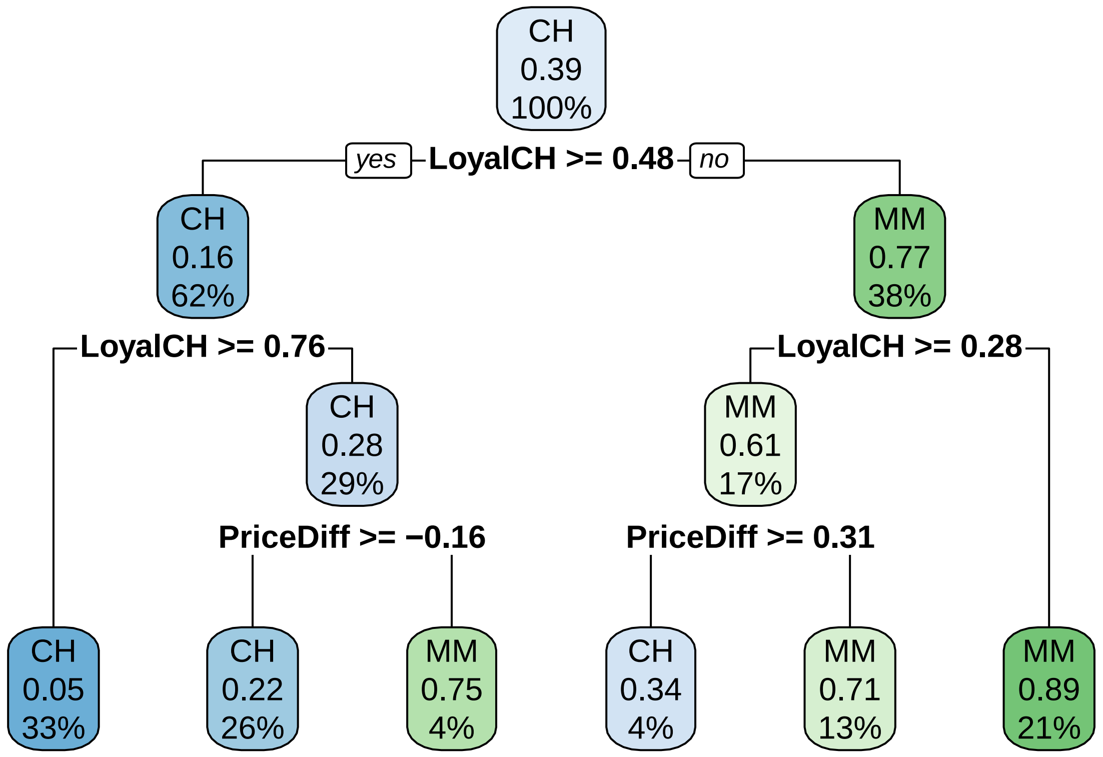
```
data("OJ")
set.seed(1)
rowTrain = createDataPartition(y = OJ$Purchase,
                               p = 0.747,
                               list = FALSE)
ctrl <- trainControl(method = "repeatedcv")
```

(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?

```
set.seed(1)
rpart.class <- train(Purchase ~., OJ,
                   subset = rowTrain,
                   method = "rpart",
                   tuneGrid = data.frame(cp = exp(seq(-7,-2, len = 50))),
                   trControl = ctrl,
                   metric = "Accuracy")
ggplot(rpart.class, highlight = T)
```



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



```
rpart.class$bestTune
```

```
##            cp
## 27 0.01294638
```

```
rpart.pred <- predict(rpart.class, newdata = OJ[-rowTrain,])
confusionMatrix(rpart.pred,
                reference = OJ$Purchase[-rowTrain])
```

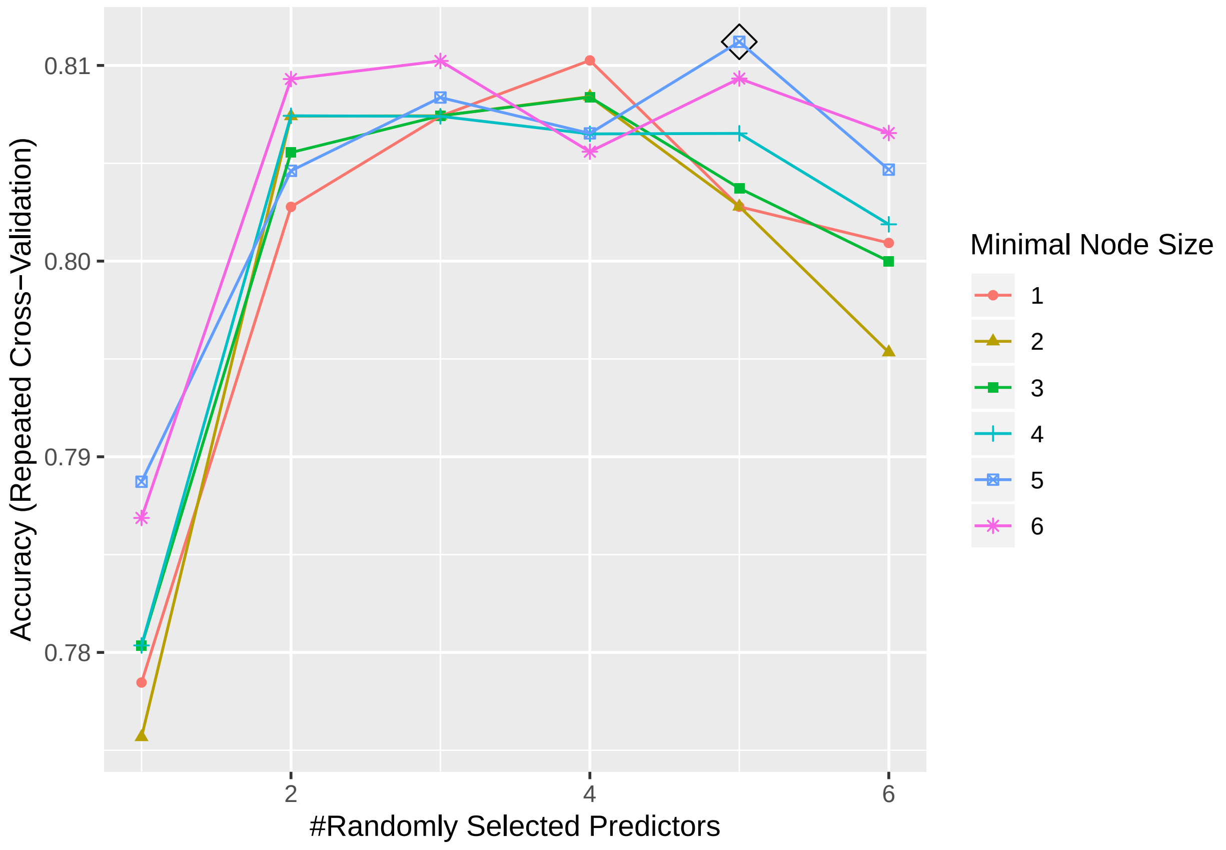
```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  CH  MM
##         CH 142  24
##         MM  23  81
##
##                Accuracy : 0.8259
##                  95% CI : (0.7753, 0.8692)
##     No Information Rate : 0.6111
##     P-Value [Acc > NIR] : 1.626e-14
##
##                   Kappa : 0.6331
##
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.8606
##             Specificity : 0.7714
##          Pos Pred Value : 0.8554
##          Neg Pred Value : 0.7788
##              Prevalence : 0.6111
##          Detection Rate : 0.5259
##    Detection Prevalence : 0.6148
##       Balanced Accuracy : 0.8160
##
##        'Positive' Class : CH
##
```

```
# Error rate
error_rate = mean(rpart.pred != OJ$Purchase[-rowTrain]) * 100
cat(c("The error rate for the classification tree is", error_rate, '%'))
```

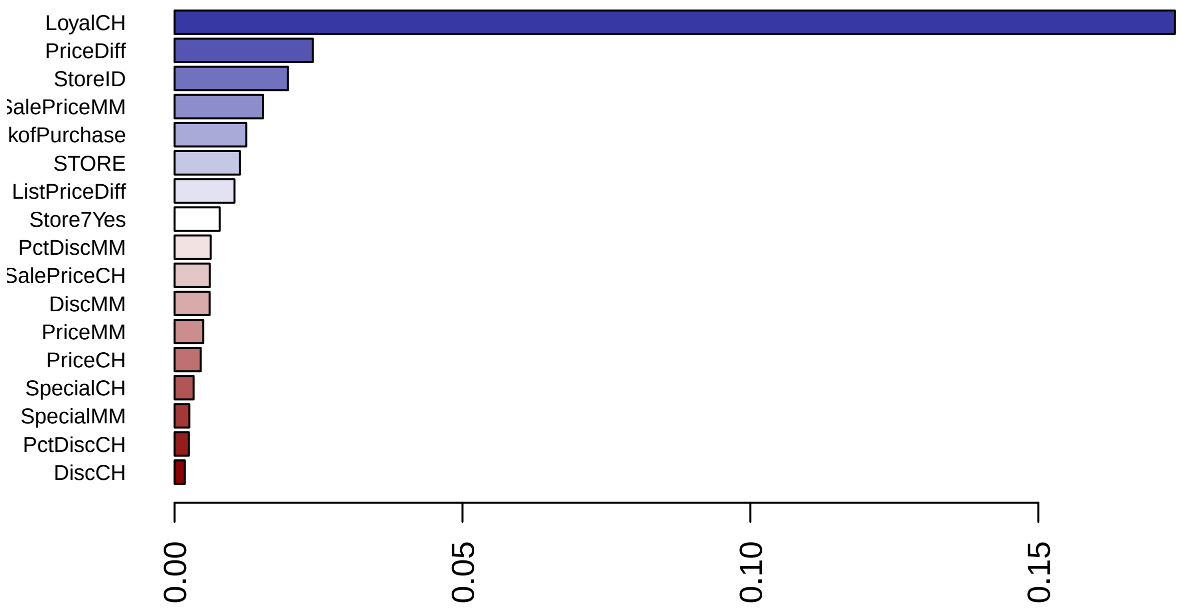
```
## The error rate for the classification tree is 17.4074074074074 %
```

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

```
rf.grid1 = expand.grid(mtry = 1:6,
                       splitrule = "gini",
                       min.node.size = 1:6)
set.seed(1)
rf.fit1 = train(Purchase~., OJ,
                 method = "ranger",
                 tuneGrid = rf.grid1,
                 trControl = ctrl,
                 importance = 'permutation')
ggplot(rf.fit1, highlight = TRUE)
```

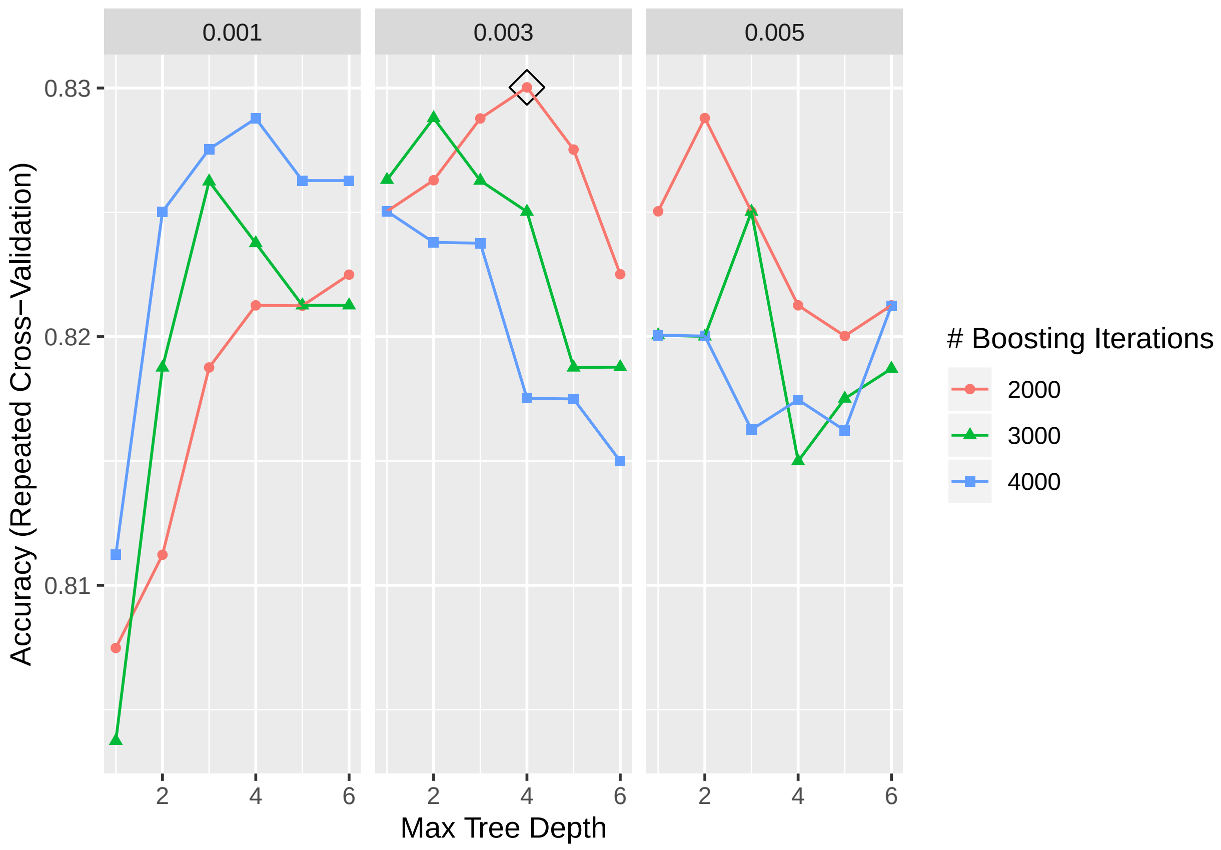


```
barplot(sort(ranger::importance(rf.fit1$finalModel), decreasing = FALSE),
        las = 2, horiz = TRUE, cex.names = 0.7,
        col = colorRampPalette(colors = c("darkred","white","darkblue"))(19))
```



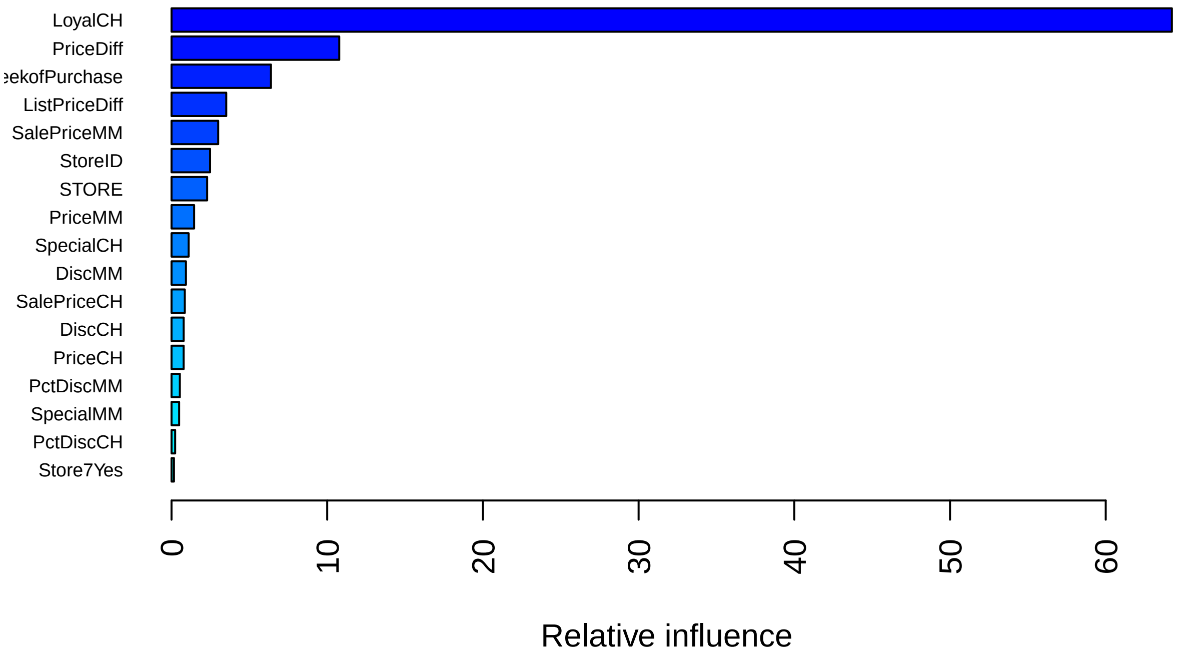
(c) Perform boosting on the training set and report variable importance. What is the test error rate?

```r
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)
set.seed(1)
gbm2.fit <- train(Purchase ~., OJ,
                 subset = rowTrain,
                 tuneGrid = gbm2.grid,
                 trControl = ctrl,
                 method = "gbm",
                 distribution = "adaboost",
                 metric = "Accuracy",
                 verbose = FALSE)
ggplot(gbm2.fit, highlight = TRUE)
```



The selected model had a maximum tree depth of 3 and learning rate of 0.003 with 3000 boosting iterations.

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



```
##                                      var     rel.inf
## LoyalCH               LoyalCH 64.2497567
## PriceDiff           PriceDiff 10.7738464
## WeekofPurchase WeekofPurchase  6.3868678
## ListPriceDiff   ListPriceDiff  3.5154509
## SalePriceMM       SalePriceMM  2.9987268
## StoreID               StoreID  2.4774727
## STORE                   STORE  2.2892477
## PriceMM               PriceMM  1.4530011
## SpecialCH           SpecialCH  1.1007800
## DiscMM                 DiscMM  0.9273452
## SalePriceCH       SalePriceCH  0.8540572
## DiscCH                 DiscCH  0.7788827
## PriceCH               PriceCH  0.7777353
## PctDiscMM           PctDiscMM  0.5350004
## SpecialMM           SpecialMM  0.4903835
## PctDiscCH           PctDiscCH  0.2340908
## Store7Yes           Store7Yes  0.1573546
```