

# 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)
```

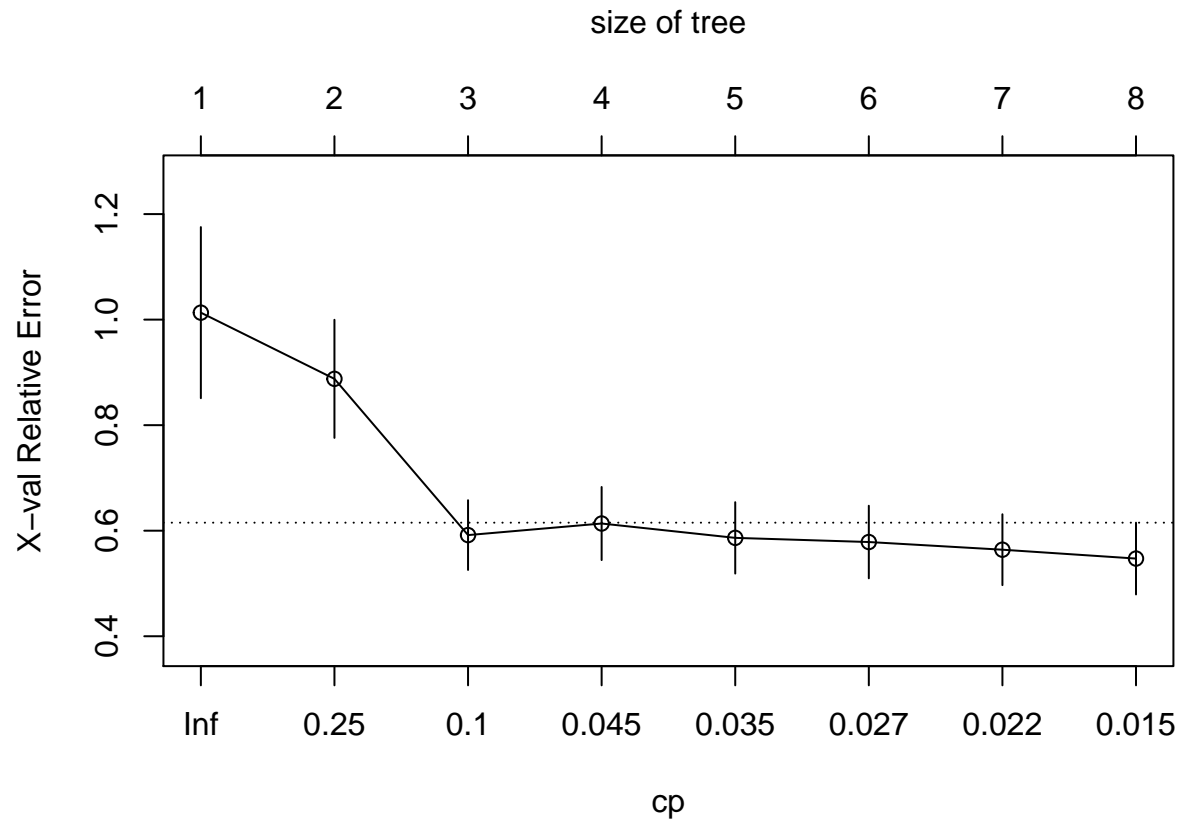
- (a) Fit a regression tree with lpsa as the response and the other variables as predictors. Use cross-validation to determine the optimal tree size. Which tree size corresponds to the lowest cross-validation error? Is this the same as the tree size obtained using the 1 SE rule?

```
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.

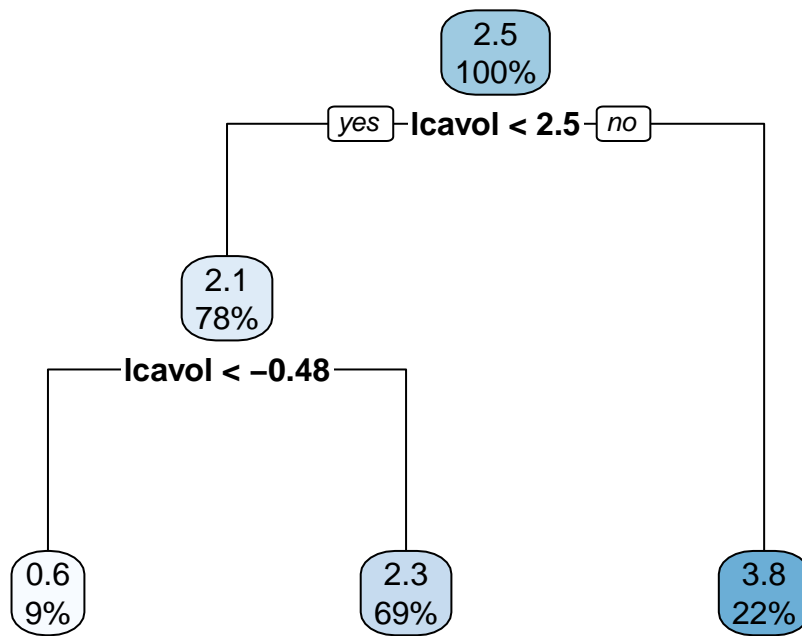
```
cpTable[cpTable[,4] < cpTable[minErr,4] + cpTable[minErr,5],1][1]
```

```
##      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

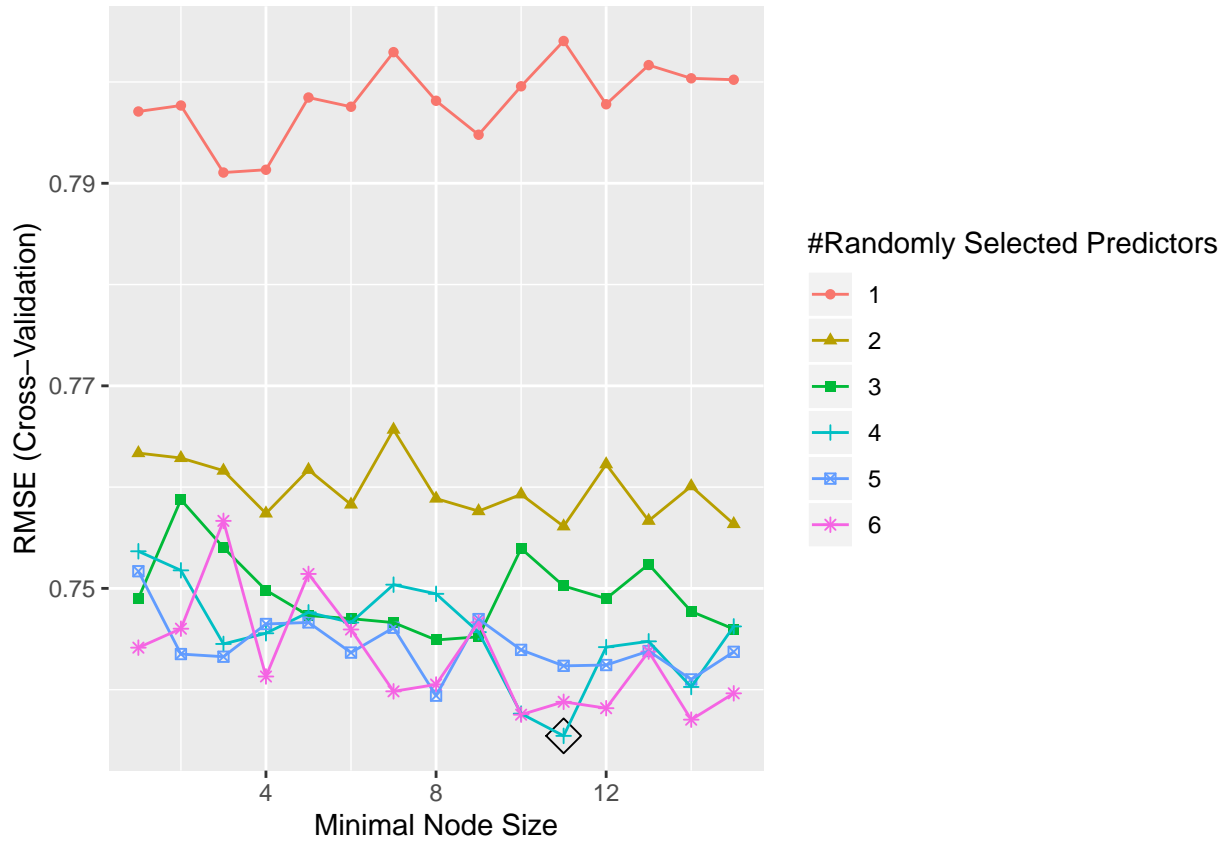
```

bagging.grid <- expand.grid(mtry = 1:6,
                           splitrule = "variance",
                           min.node.size = 1:15)

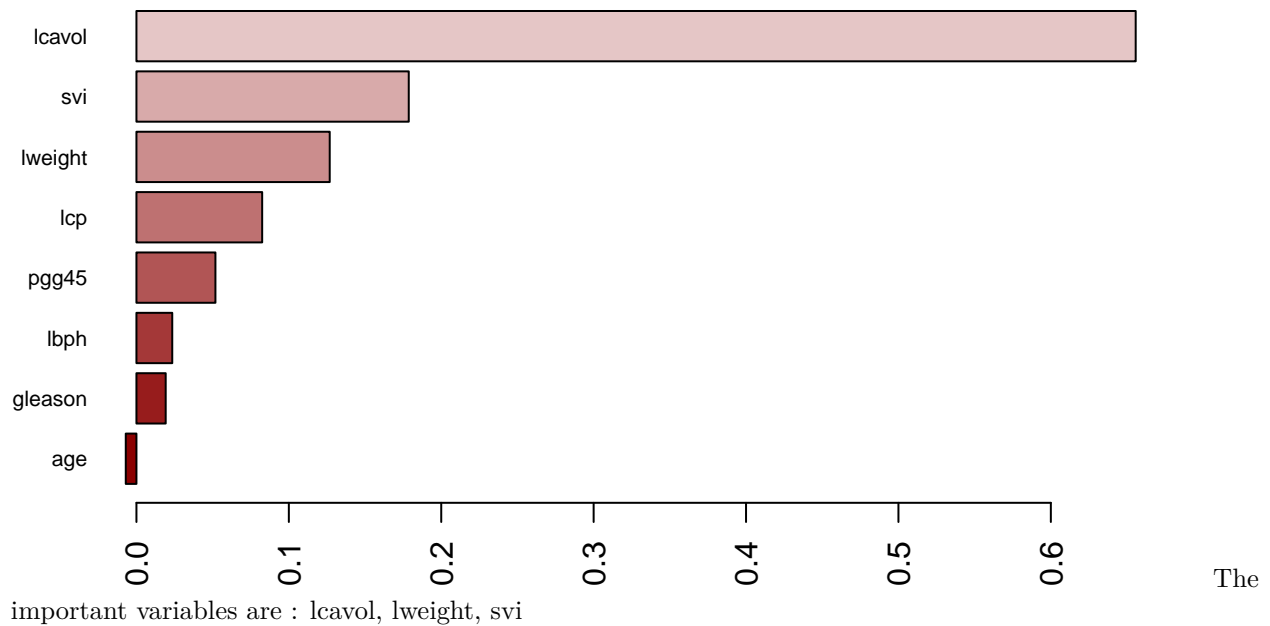
set.seed(1)
bagging <- train(lpsa~., Prostate,
                 method = "ranger",
                 tuneGrid = bagging.grid,
                 trControl = ctrl,
                 importance = "permutation")

ggplot(bagging, highlight = TRUE)

```



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



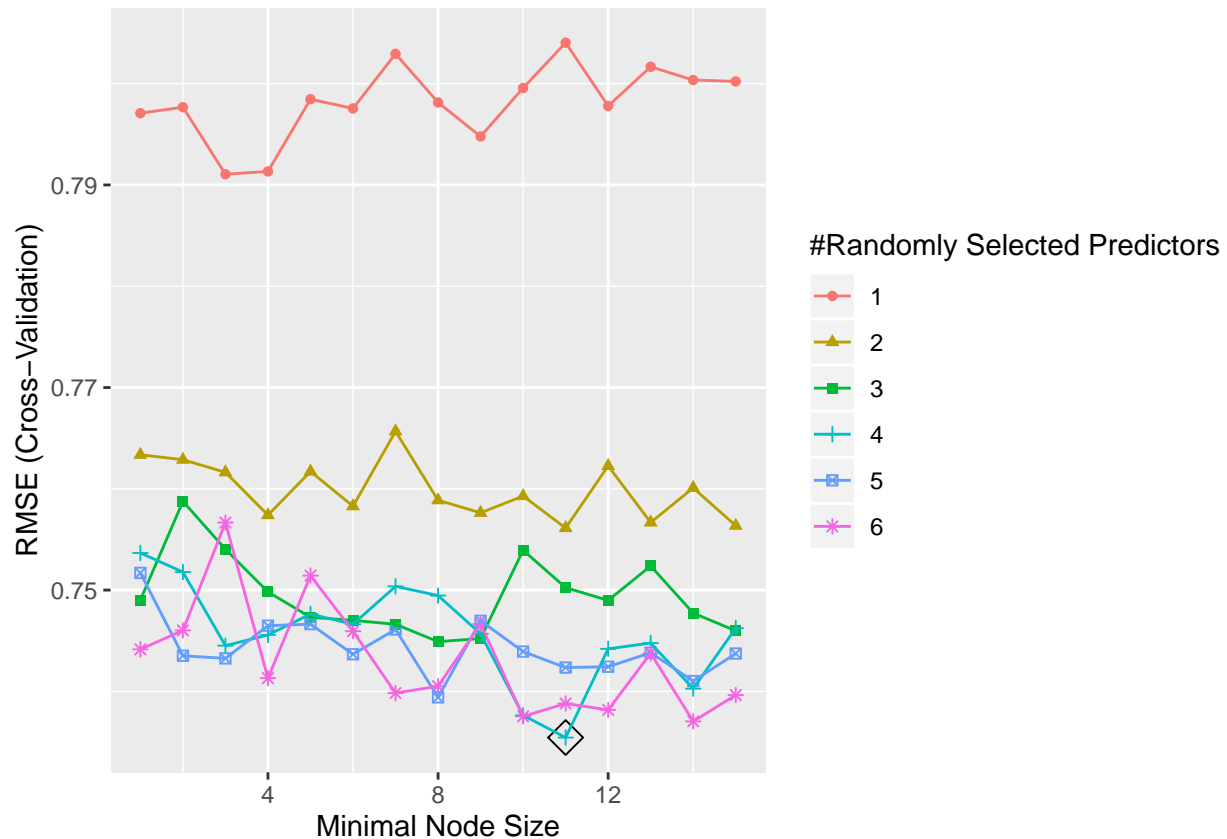
(d) Perform random forests and report the variable importance.

```

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)

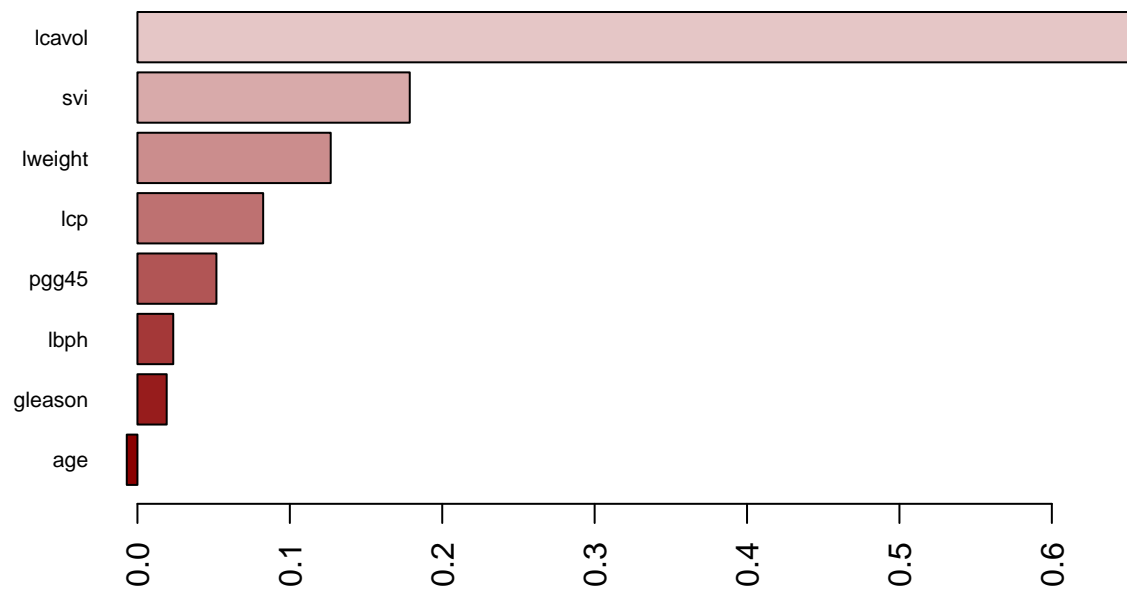
```



```

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))

```

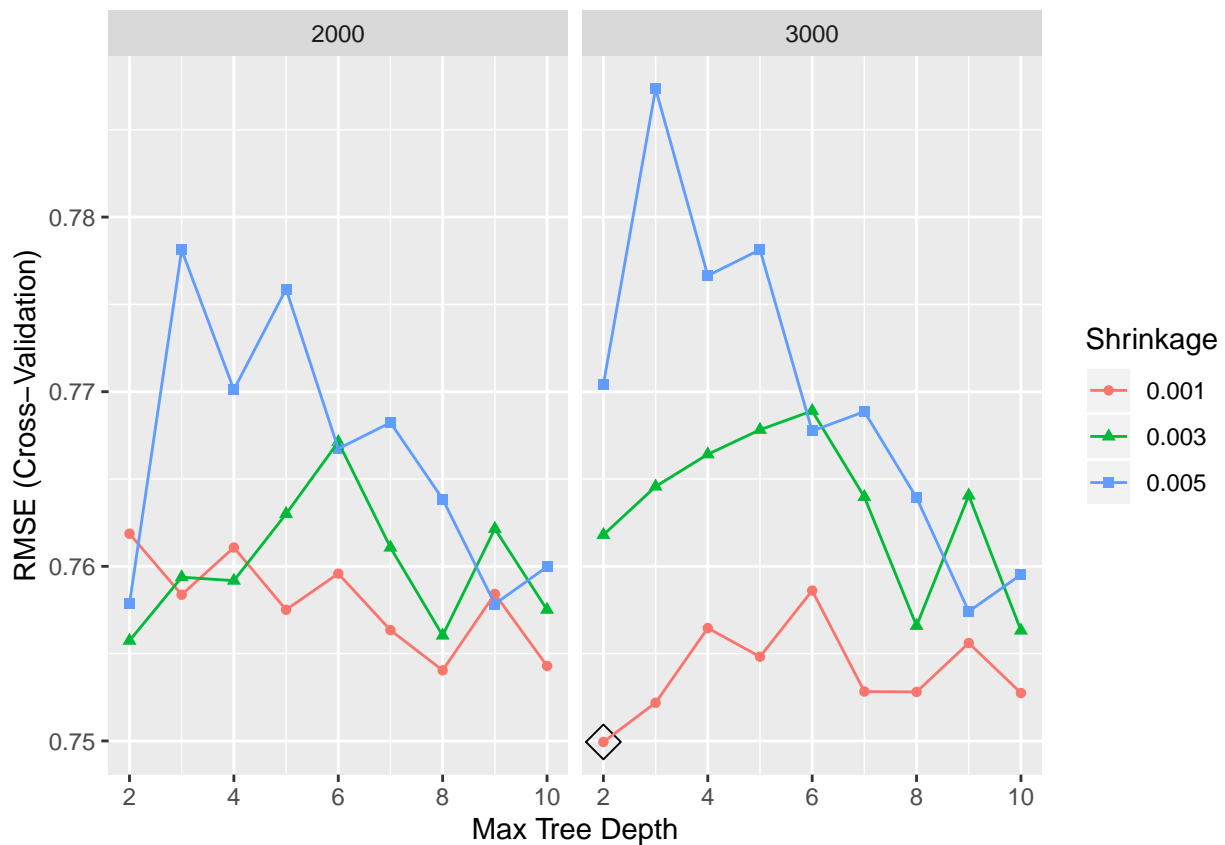


(e) Perform boosting and report the variable importance.

```
gbm.grid <- expand.grid(n.trees = c(2000,3000),
                      interaction.depth = 2:10,
                      shrinkage = c(0.001,0.003,0.005),
                      n.minobsinnode = 1)

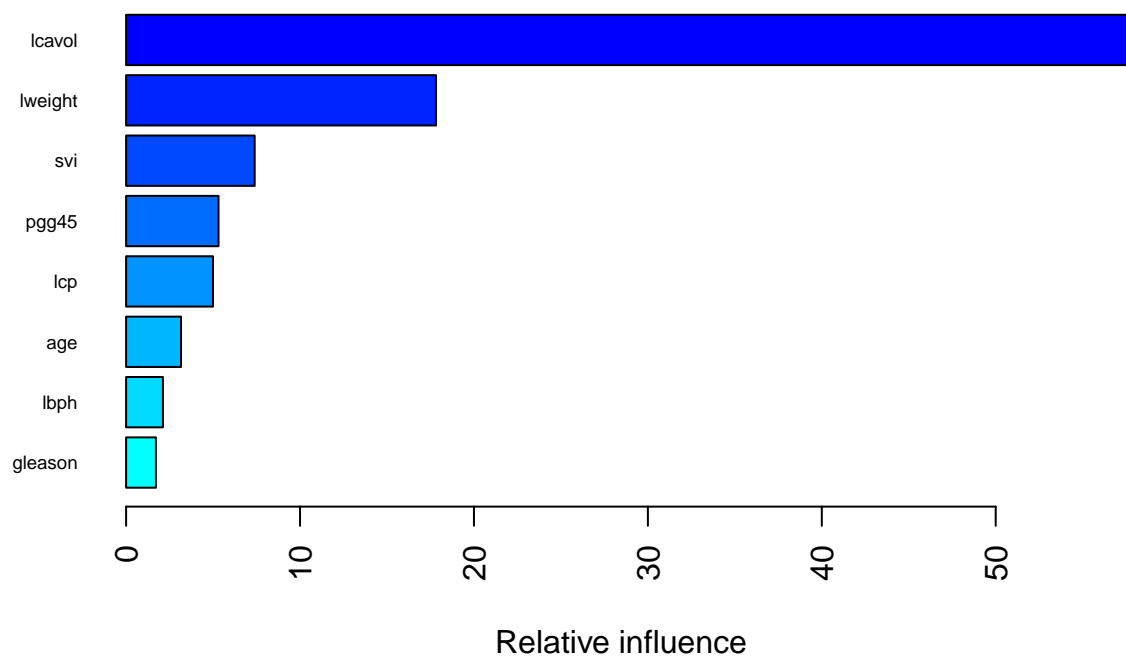
set.seed(1)
gbm.fit <- train(lpsa~., Prostate,
                method = "gbm",
                tuneGrid = gbm.grid,
                trControl = ctrl,
                verbose = FALSE)

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
```

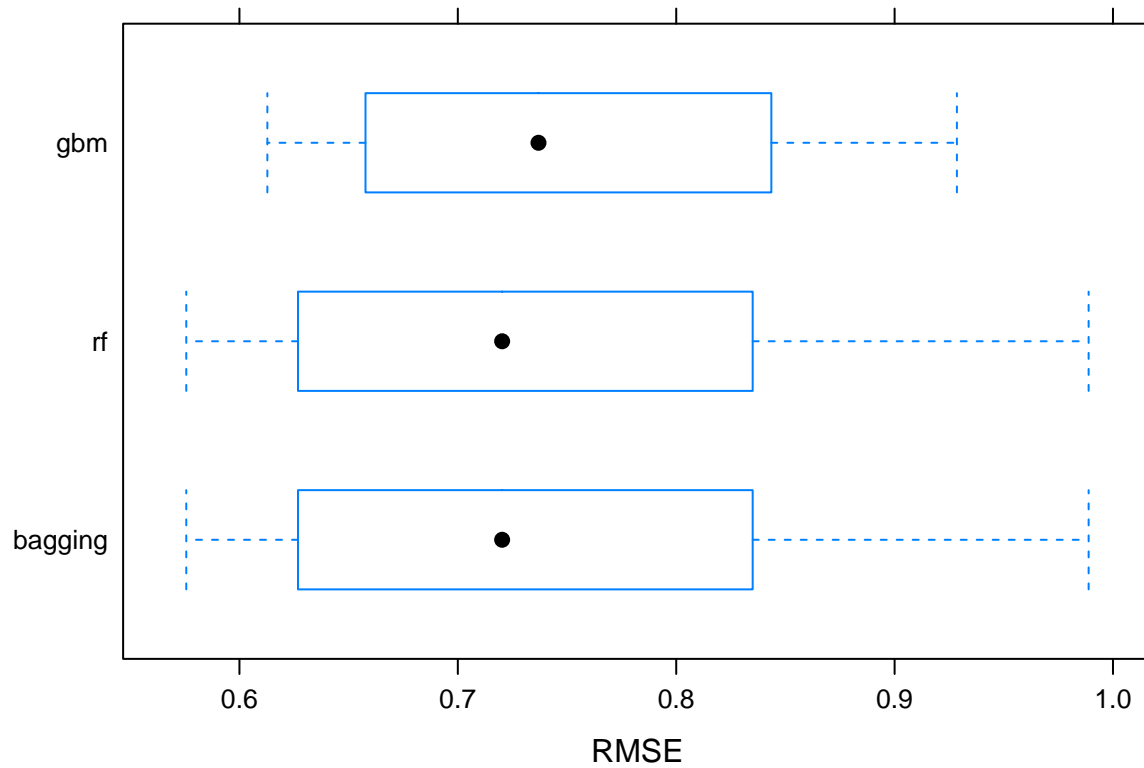
(f) Which of the above models will you select to predict PSA level? Explain.

```
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
```

```
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")
```

- (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?