Chapter 8

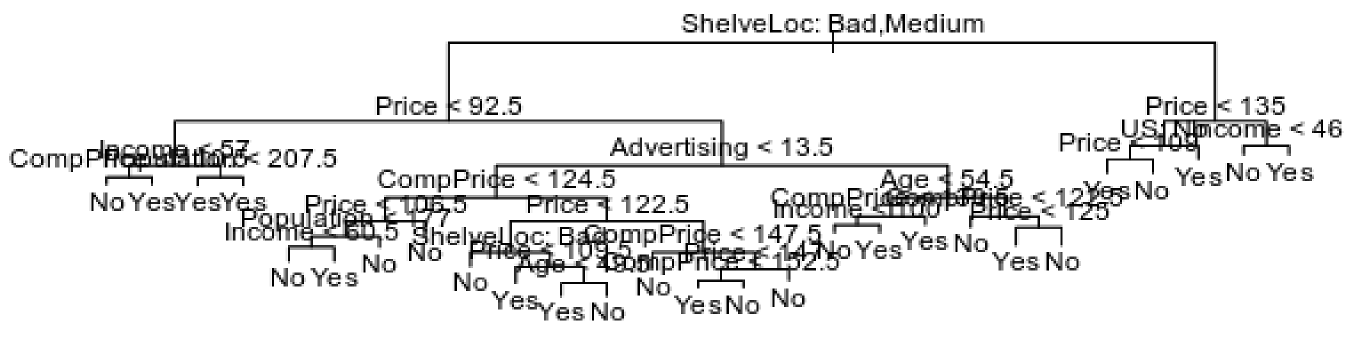
Lab

Fitting Classification Trees

```r
carseats <- as.data.table(ISLR::Carseats)

carseats[, High := as.factor(ifelse(Sales <= 8, "No", "Yes"))]

tree.carseats <- tree(formula = High ~ .-Sales, data = carseats)

summary(tree.carseats)
```

```
Classification tree:
tree(formula = High ~ . - Sales, data = carseats)
Variables actually used in tree construction:
[1] "ShelveLoc"   "Price"       "Income"      "CompPrice"   "Population"
[6] "Advertising" "Age"         "US"
Number of terminal nodes:  27
Residual mean deviance:  0.4575 = 170.7 / 373
Misclassification error rate: 0.09 = 36 / 400
```

```r
plot(tree.carseats)
text(tree.carseats, pretty = 0)
```



```r
set.seed(2)

train <- sample(1:nrow(carseats), 200)

carseats.test <- carseats[-train]
high.test <- carseats[-train]$High

tree.carseats <- tree(High ~.-Sales, data = carseats, subset = train)
tree.pred <- predict(tree.carseats, carseats.test, type = "class")

table(tree.pred, high.test)
```

```
         high.test
tree.pred  No Yes
      No  104  33
      Yes  13  50
```

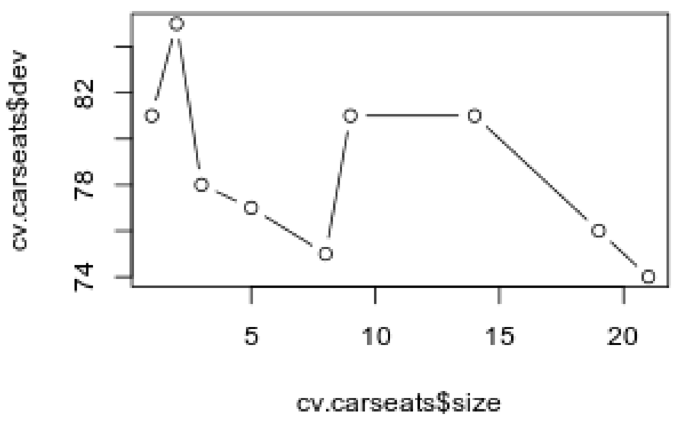
```r
set.seed(3)

cv.carseats <- cv.tree(tree.carseats, FUN = prune.misclass)
names(cv.carseats)
```

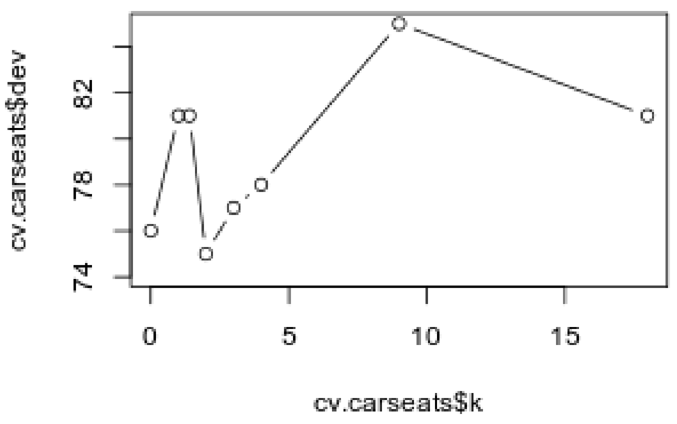
```
[1] "size"   "dev"    "k"      "method"
```

```r
cv.carseats
```

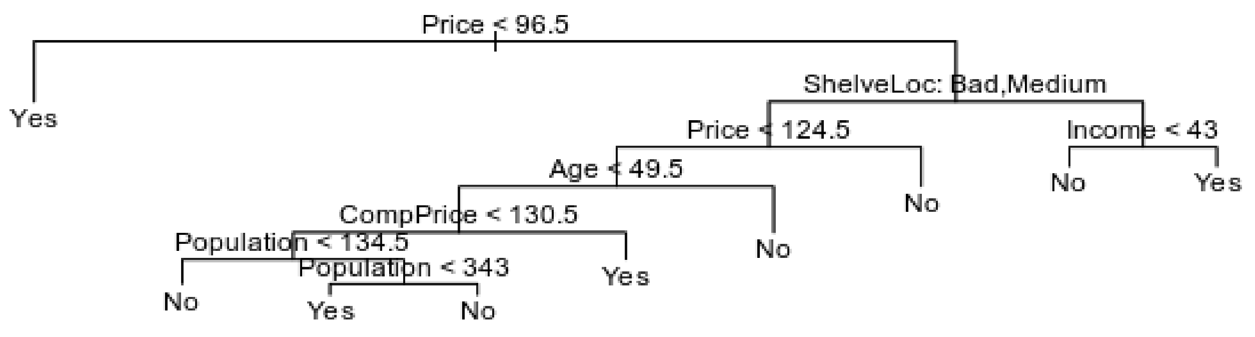
```
$size
[1] 21 19 14  9  8  5  3  2  1

$dev
[1] 74 76 81 81 75 77 78 85 81

$k
[1] -Inf  0.0  1.0  1.4  2.0  3.0  4.0  9.0 18.0

$method
[1] "misclass"

attr(,"class")
[1] "prune"         "tree.sequence"
```

```r
par(mfrow = c(1, 2))
plot(cv.carseats$size, cv.carseats$dev, type = "b")
plot(cv.carseats$k, cv.carseats$dev, type="b")
```





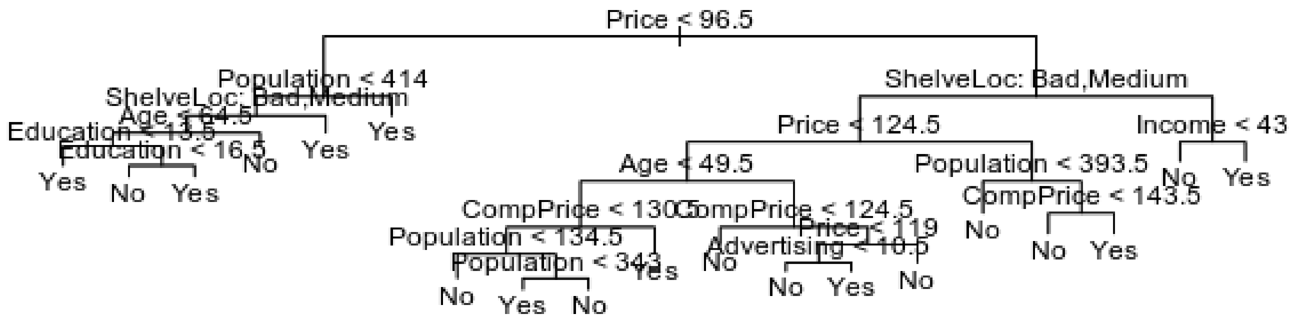
```r
par(mfrow = c(1,1))
prune.carseats <- prune.misclass(tree.carseats, best = 9)
plot(prune.carseats)
text(prune.carseats, pretty = 0)
```



```r
tree.pred <- predict(prune.carseats, carseats.test, type = "class")
table(tree.pred, high.test)
```

```
         high.test
tree.pred No Yes
      No  97  25
      Yes 20  58
```

```r
prune.carseats <- prune.misclass(tree.carseats, best = 15)
plot(prune.carseats)
text(prune.carseats, pretty = 0)
```



```r
tree.pred <- predict(prune.carseats, carseats.test, type = "class")
table(tree.pred, high.test)
```

```
         high.test
tree.pred  No Yes
      No  102  30
      Yes  15  53
```

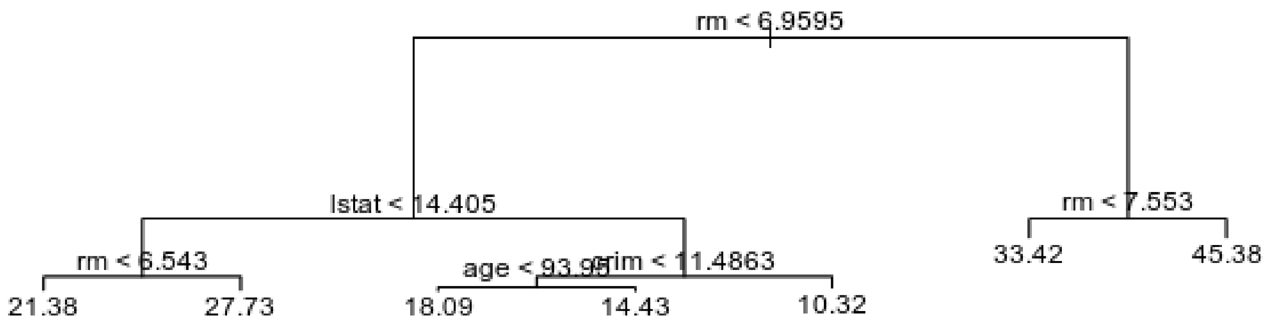
Regression Trees

```r
boston <- as.data.table(Boston)

N <- nrow(boston)

set.seed(1)

train <- sample(1:N, N /2)

tree.boston <- tree(medv ~ ., boston, subset = train)

summary(tree.boston)
```

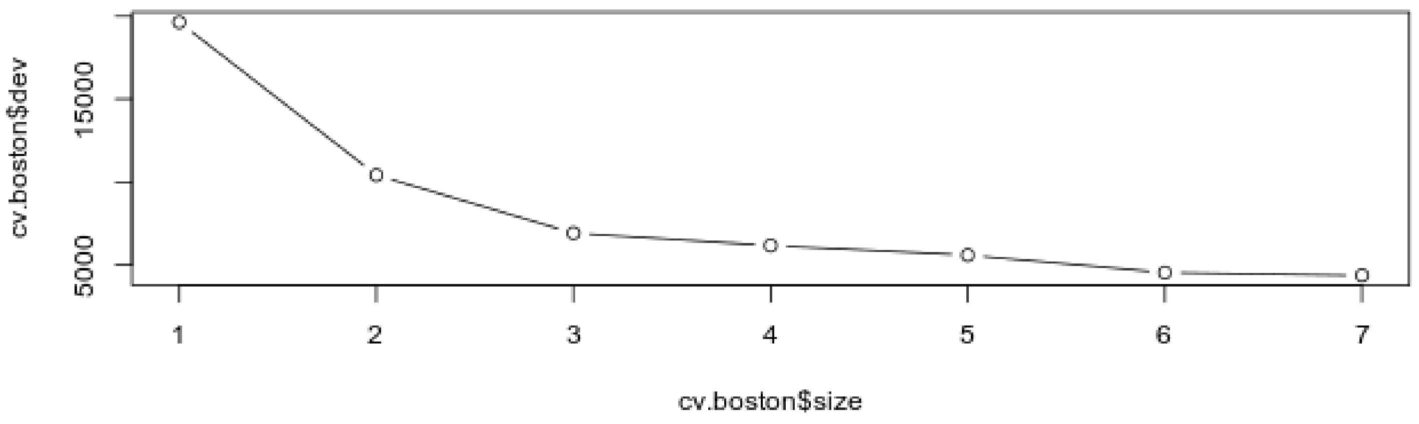
```

Regression tree:
```

```
tree(formula = medv ~ ., data = boston, subset = train)
Variables actually used in tree construction:
[1] "rm"    "lstat" "crim"  "age"
Number of terminal nodes:  7
Residual mean deviance:  10.38 = 2555 / 246
Distribution of residuals:
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
-10.1800  -1.7770  -0.1775   0.0000   1.9230  16.5800
```

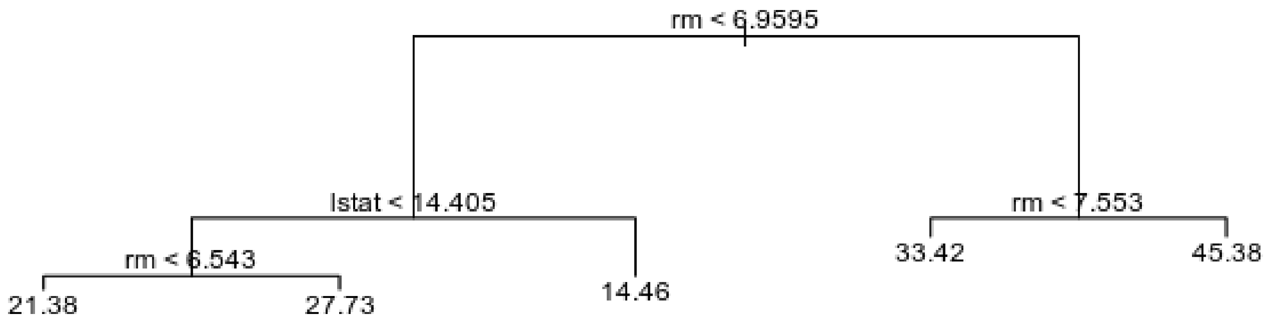
```r
plot(tree.boston)
text(tree.boston, pretty = 0)
```



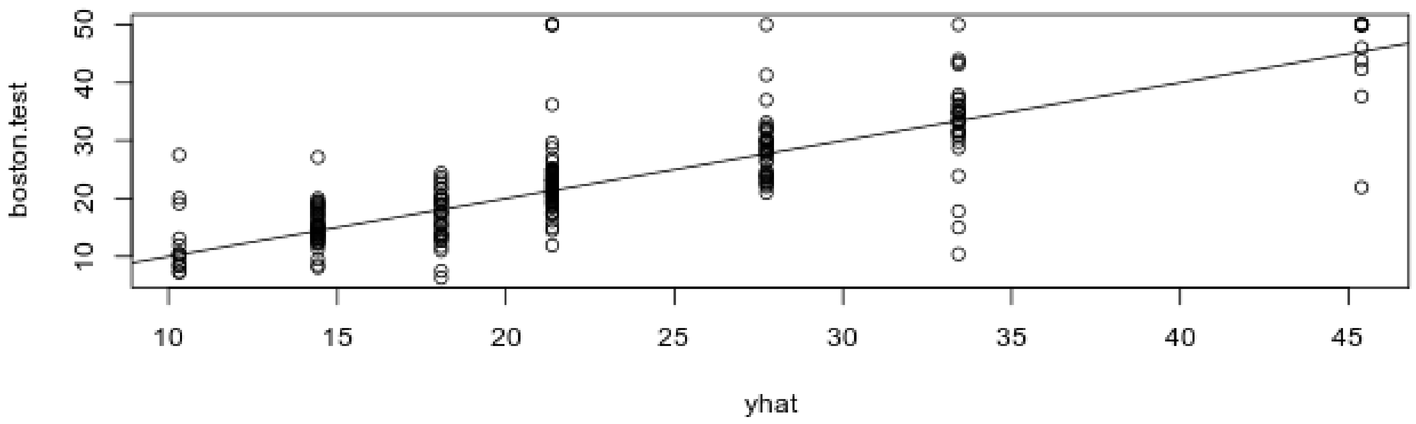
```r
cv.boston <- cv.tree(tree.boston)
plot(cv.boston$size, cv.boston$dev, type = 'b')
```



```r
prune.boston <- prune.tree(tree.boston, best = 5)
plot(prune.boston)
text(prune.boston, pretty = 0)
```



```r
yhat <- predict(tree.boston, newdata = boston[-train,])
boston.test <- boston[-train]$medv

plot(yhat, boston.test)
abline(0, 1)
```



```r
mean((yhat - boston.test)^2)
```

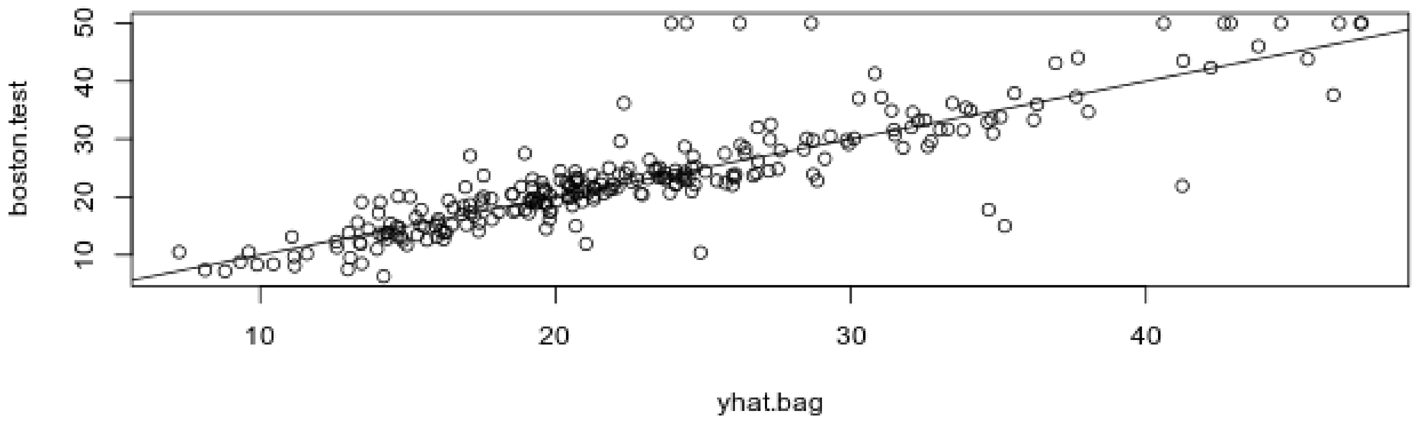
```
[1] 35.28688
```

Bagging and Boosting

```r
set.seed(1)

bag.boston <- randomForest(medv ~ ., data = boston, subset = train, mtry = 13, importance = T)
bag.boston
```

```

Call:
 randomForest(formula = medv ~ ., data = boston, mtry = 13, importance = T,      subset = train
               Type of random forest: regression
                     Number of trees: 500
No. of variables tried at each split: 13

          Mean of squared residuals: 11.39601
                    % Var explained: 85.17
```

```r
yhat.bag <- predict(bag.boston, newdata = boston[-train])
plot(yhat.bag, boston.test)
abline(0, 1)
```



```r
mean((yhat.bag-boston.test)^2)
```

```
[1] 23.59273
```

```r
bag.boston <- randomForest(medv ~ ., data = boston, subset = train, mtry = 13, ntree = 25)
yhat.bag <- predict(bag.boston, newdata = boston[-train,])
mean((yhat.bag - boston.test)^2)
```

```
[1] 23.66716
```

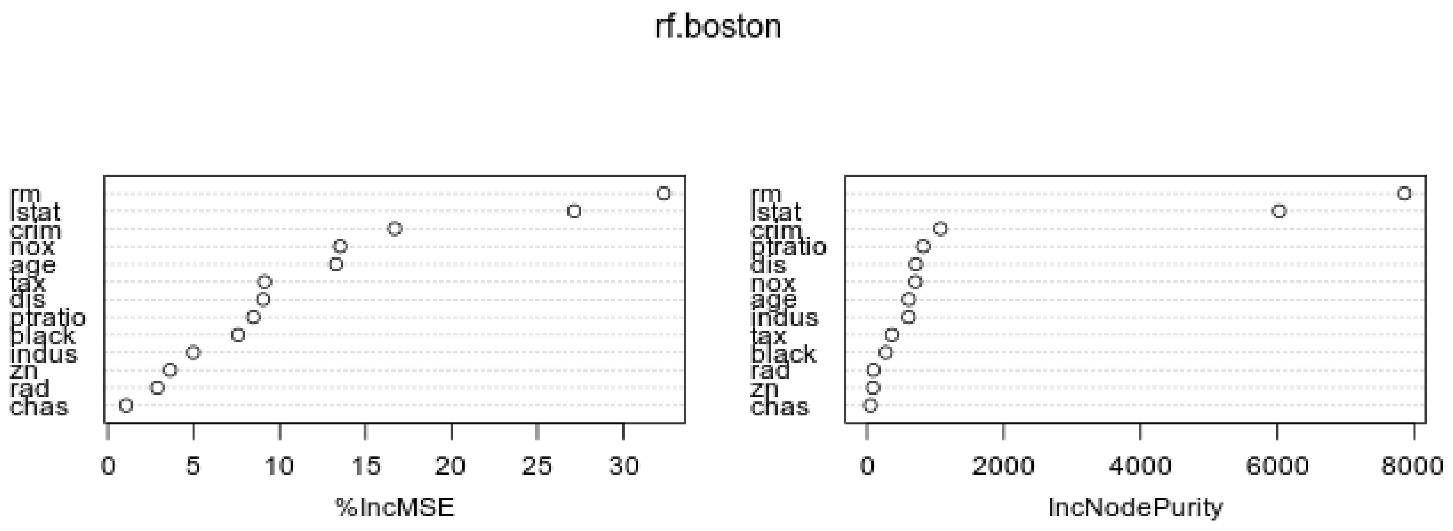
```r
set.seed(1)

rf.boston <- randomForest(medv ~  ., data = boston, subset = train, mtry = 6, importance = T)
yhat.rf <- predict(rf.boston, newdata = boston[-train,])
mean((yhat.rf-boston.test)^2)
```

```
[1] 19.62021
```

```r
importance(rf.boston)
```

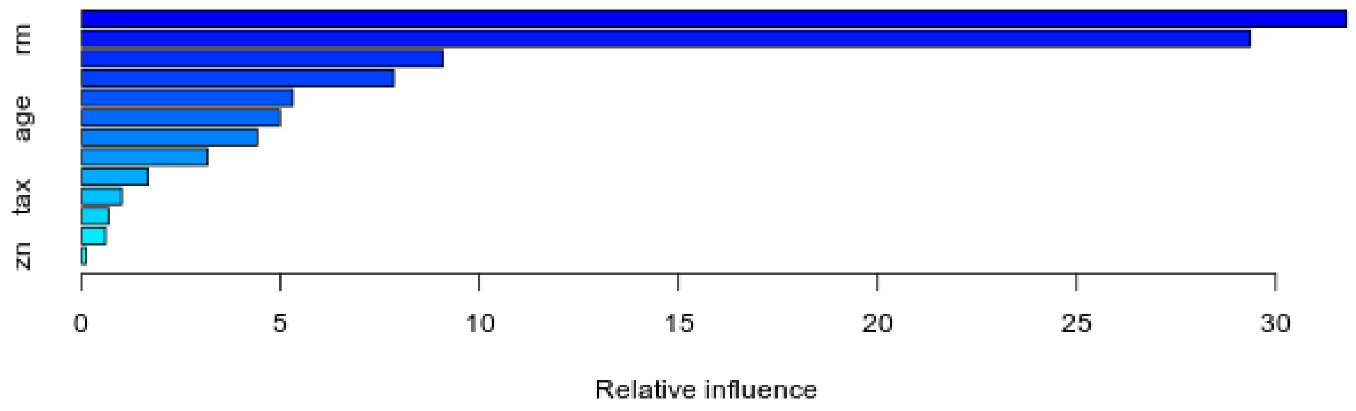
```
          %IncMSE IncNodePurity
crim    16.697017    1076.08786
zn       3.625784      88.35342
indus    4.968621     609.53356
chas     1.061432      52.21793
nox     13.518179     709.87339
rm      32.343305    7857.65451
age     13.272498     612.21424
dis      9.032477     714.94674
rad      2.878434      95.80598
tax      9.118801     364.92479
ptratio  8.467062     823.93341
black    7.579482     275.62272
lstat   27.129817    6027.63740
```

```r
varImpPlot(rf.boston)
```



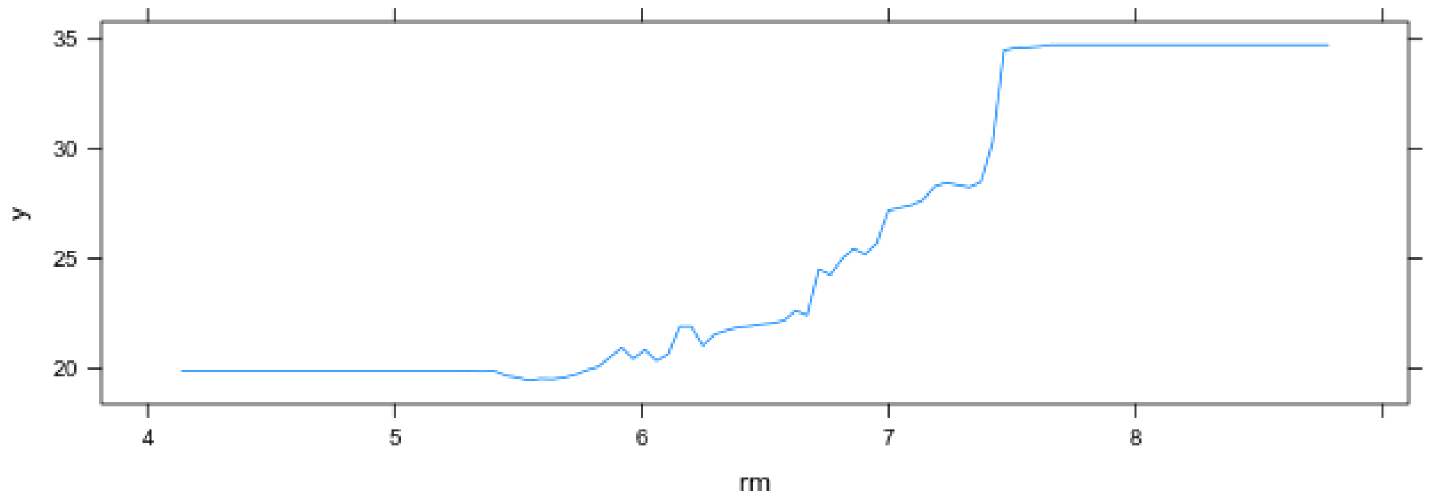
Boosting

```
boost.boston <- gbm(medv ~ ., data = boston[-train,], distribution = "gaussian", n.trees = 5000

summary(boost.boston)
```

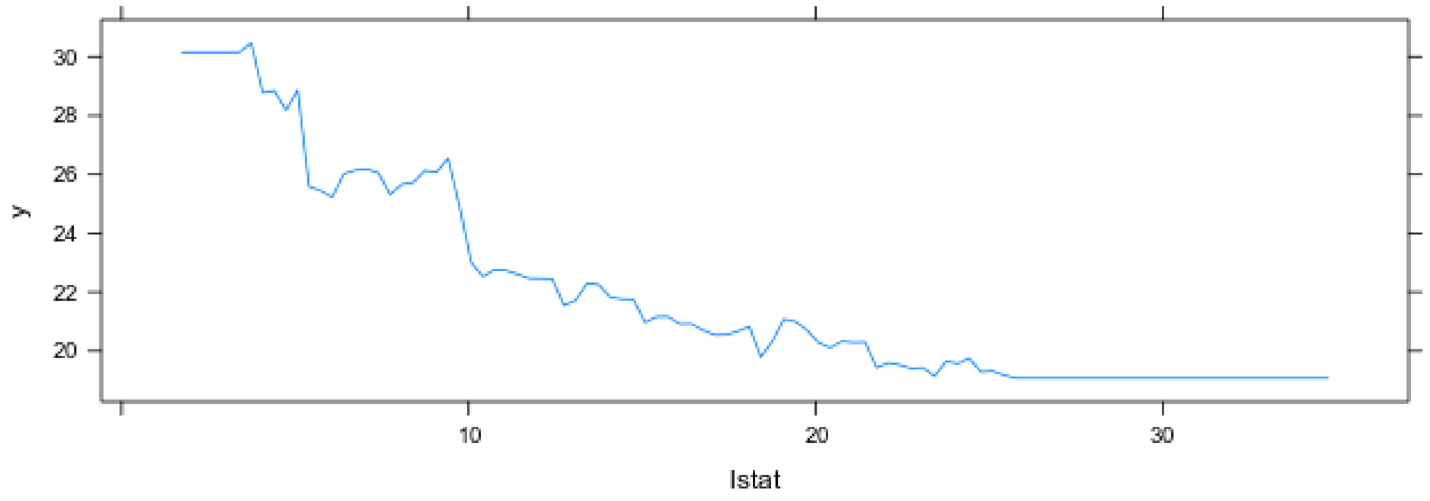


```
            var    rel.inf
lstat     lstat 31.7768815
rm           rm 29.3618406
dis         dis  9.0801247
crim       crim  7.8431133
nox         nox  5.3077691
age         age  4.9799119
black     black  4.4118851
ptratio ptratio  3.1614540
indus     indus  1.6642386
tax         tax  1.0107120
chas       chas  0.6850917
rad         rad  0.6031076
zn           zn  0.1138700
```

```
par(mfrow = c(1, 2))
plot(boost.boston, i = "rm")
```



```r
plot(boost.boston, i = "lstat")
```



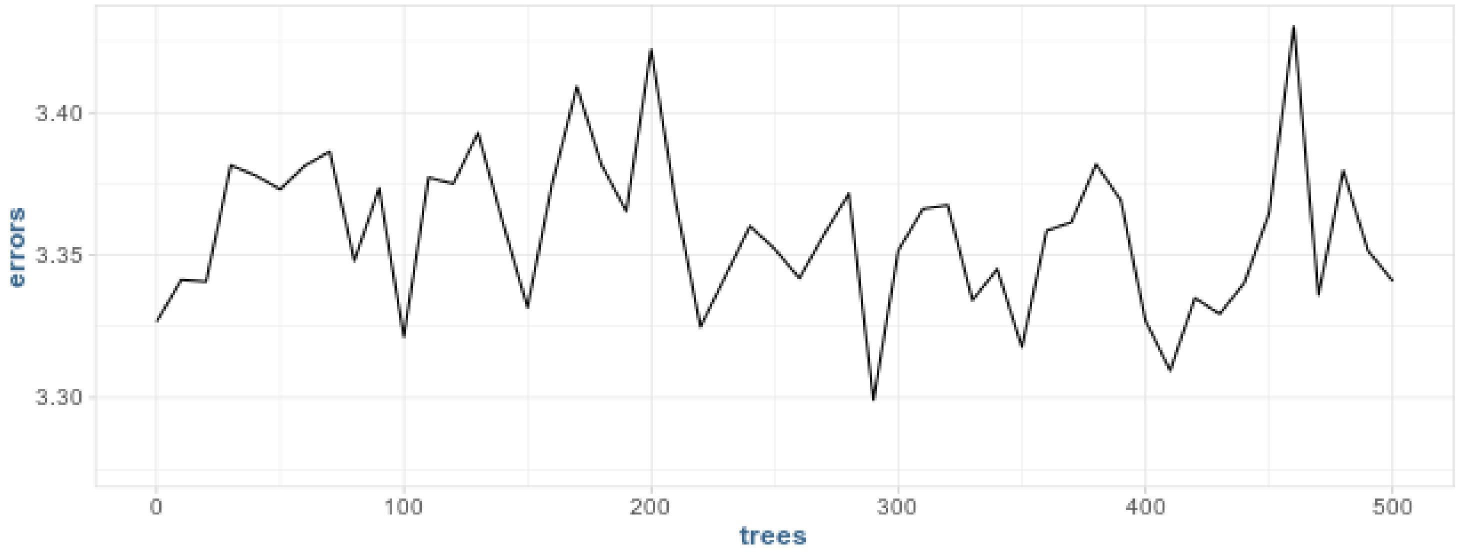
```r
yhat.boost <- predict(boost.boston, newdata = boston[-train,], n.trees = 5000)
mean((yhat.boost - boston.test)^2)
```

```
[1] 2.242007e-06
```

Applied

In the lab, we applied random forests to the *Boston* data using mtry = 6 and using ntree = 25 and ntree = 500. Create a plot displaying the test error resulting from random forests on this data set for a more comprehensive range of values for mtry ntree.

```r
N <- nrow(boston)

train <- sample(1:N, N * .7)

boston.train <- boston[train]
boston.test <- boston[!train]

ntrees <- seq(0, 500, 10)

results <- numeric(length(ntrees))

for(i in 1:length(ntrees))
{
   tree.count <- ntrees[i]

   rf <- randomForest(medv ~ ., data = boston.train, mtry = 6, n.trees = tree.count)

   pred <- predict(rf, newdata = boston.test)

   results[i] <- sqrt(mean((pred - boston.test$medv)^2)) # store the rmse
}

lowest.error <- which.min(results)

rf.results <- data.table(trees = ntrees, errors = results)[, lowest := .I == lowest.error]

ggplot(rf.results, aes(trees, errors, fill = lowest)) +
   geom_line()
```



In the lab, a classification tree was applied to the Carseats data set after converting Sales into a qualitative response variable. Now we will seek to predict Sales using regression trees and related approaches, treating the response as a quantitaive variable.

a.) Split the data into a t training set and a test set.

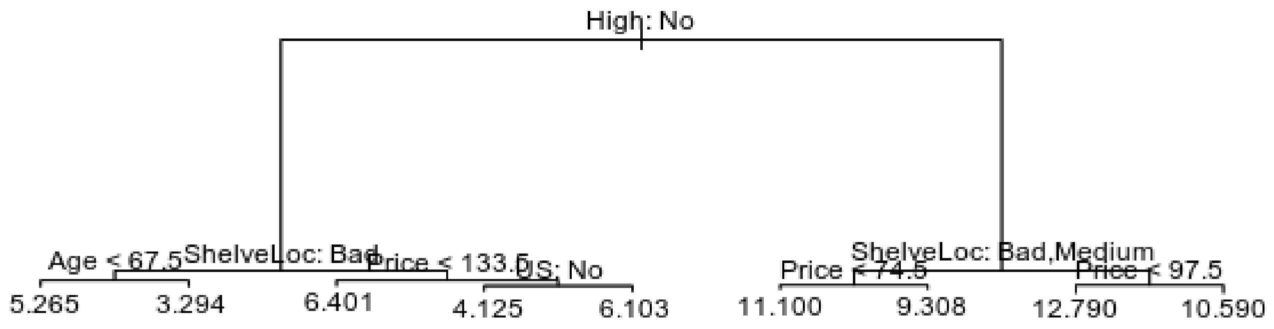
```
N <- nrow(carseats)

index <- sample(1:N, N * .7)

carseats.train <- carseats[index]
carseats.test <- carseats[!index]
```

b.) Fit a regression tree to the training set. Plot the tree, and interpret the results. What test MSE do you obtain?

```
carseat.tree <- tree(Sales ~., data = carseats.train)
pred <- predict(carseat.tree, newdata = carseats.test)
mse <- mean((pred - carseats.test$Sales)^2)

mse
```

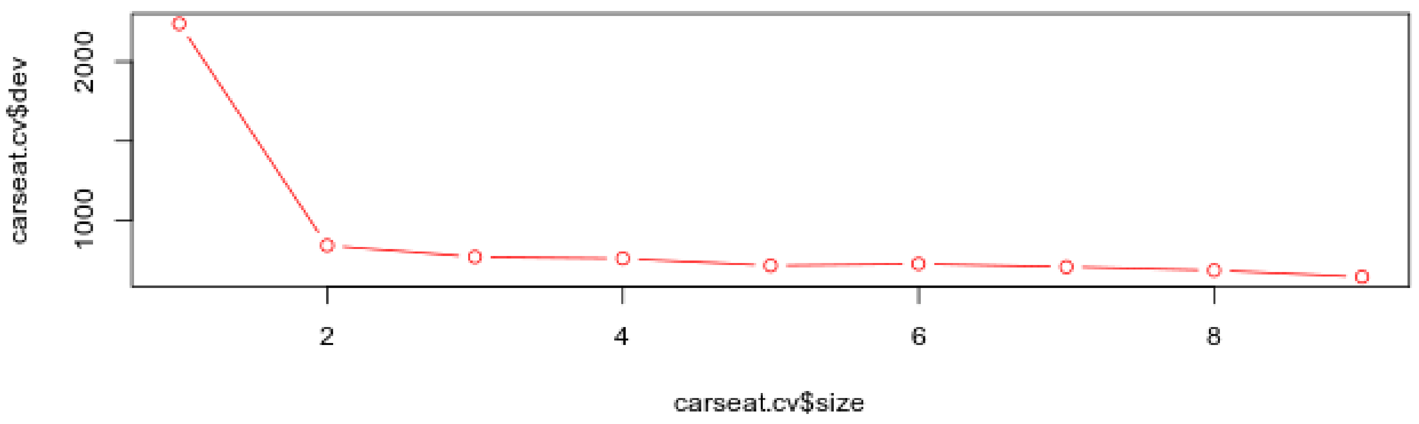
```
[1] 3.004485
```

```
par(mfrow = c(1,1))
plot(carseat.tree)
text(carseat.tree, pretty = 0)
```

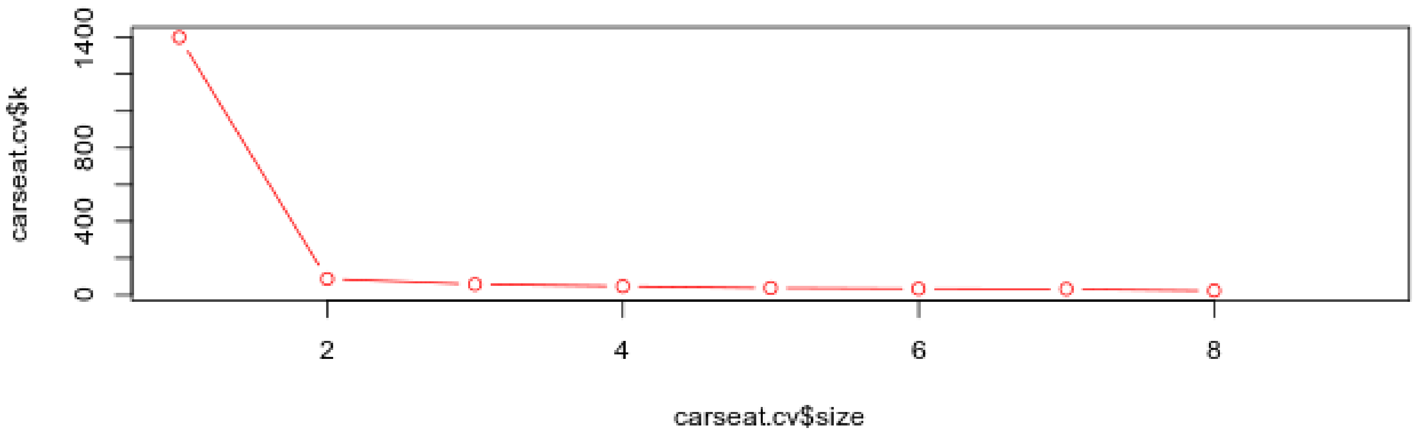


c.) Use cross-validation in order to determine the optimal level of tree complexity. Does pruning the tree improve the test MSE?

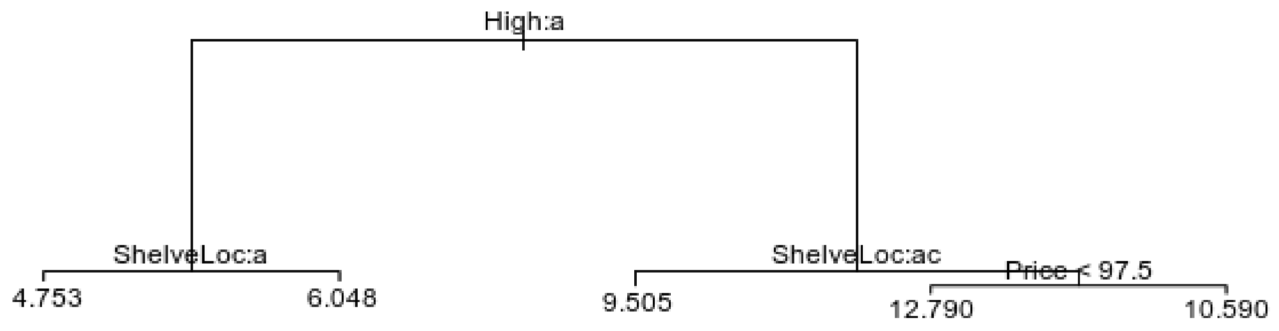
```
carseat.cv <- cv.tree(carseat.tree)

plot(carseat.cv$size, carseat.cv$dev, type = "b", col = "red")
```



```r
plot(carseat.cv$size, carseat.cv$k, type = "b", col = "red")
```



```r
prune.carseats <- prune.tree(carseat.tree, best = 5)

plot(prune.carseats)
text(prune.carseats)
```



d.) Use the bagging approach in order to analyze this data. What test MSE do you obtain? Use the importance() function to determine which variables are most important.

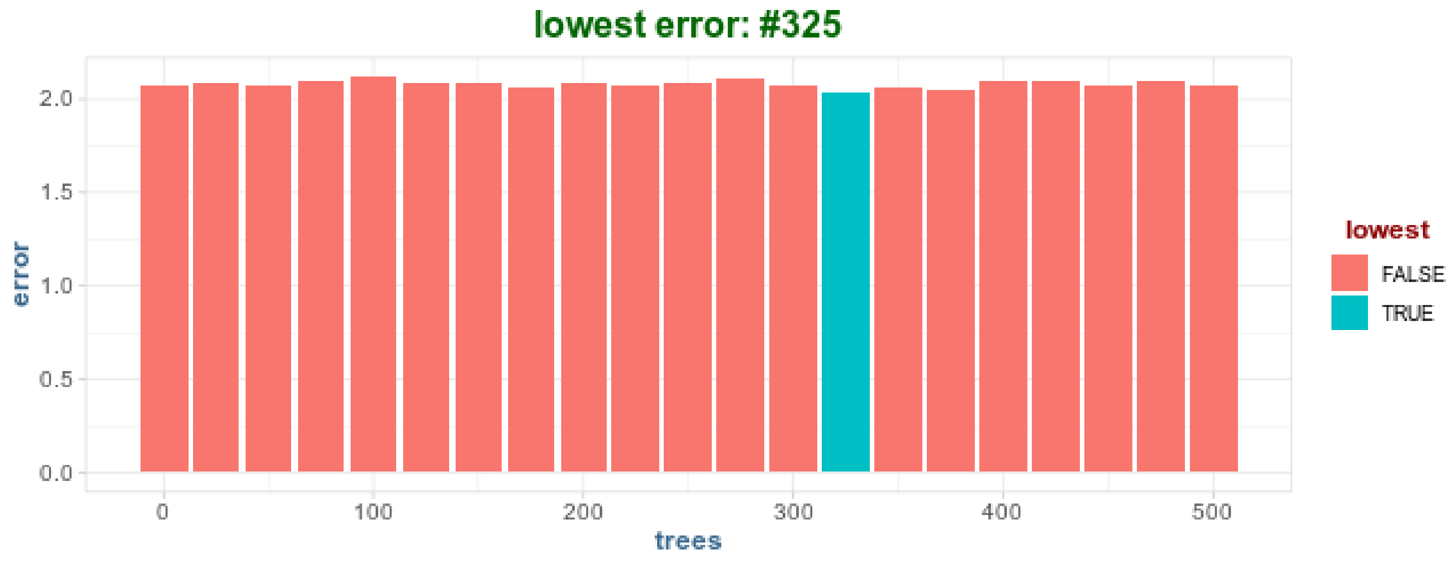
```
p <- ncol(carseats)

ntrees <- seq(0, 500, 25)
rf.error <- numeric(length(ntrees))

for(i in 1:length(ntrees))
{
   carseats.rf <- randomForest(Sales ~ ., data = carseats.train, mtry = p, n.trees = ntrees[i])

   pred <- predict(carseats.rf, newdata = carseats.test)

   rf.error[i] <- mean((pred - carseats.test$Sales)^2)
}
```

```
Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
```

```
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
```

```
range

Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range
```

```
lowest.error <- which.min(rf.error)

results <- data.table(trees = ntrees, error = rf.error)[, lowest := .I == lowest.error]

ggplot(results, aes(trees, error, fill = lowest)) +
   geom_bar(stat = "identity") +
   labs(title = paste0("lowest error: #", ntrees[lowest.error]))
```

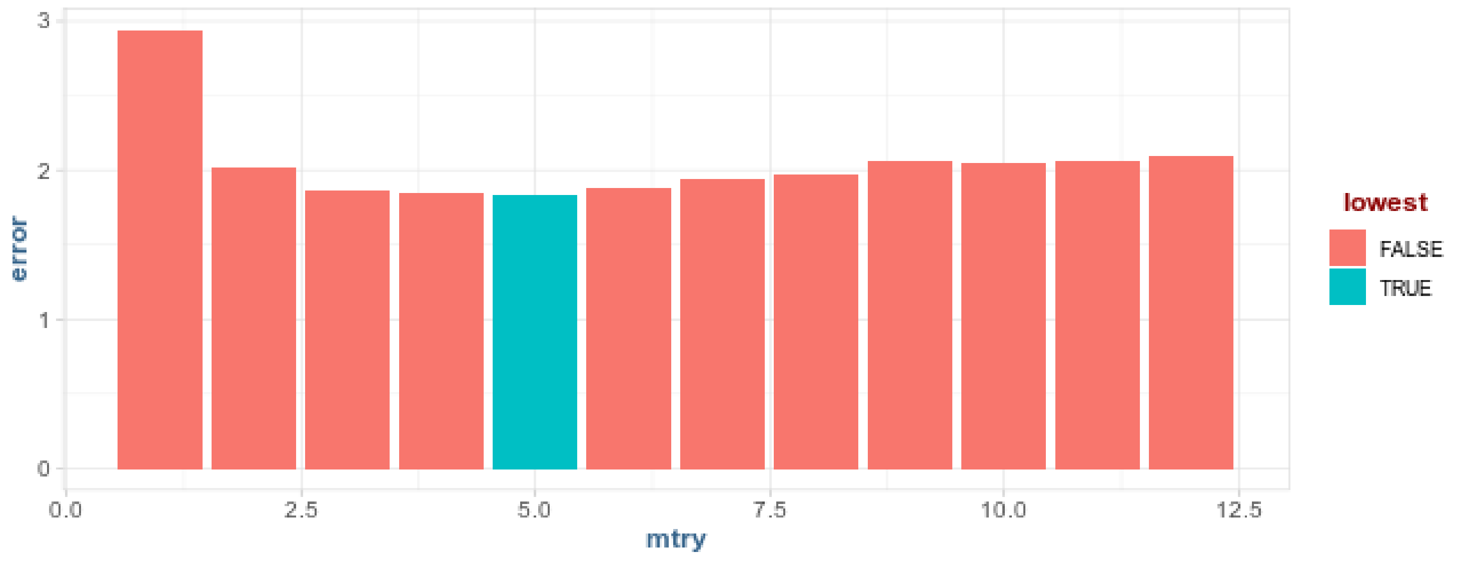


e.) Use random forest to analyize this data. What test MSE do you obtain? Use the importance() fucntion to determine which variables are most important. Describe the effect of m, the number of variables considered at each split, on the error obtained.

```
p <- ncol(carseats)

mtry <- seq(1, p)

rf.error <- numeric(p)

for(i in 1:p)
{
   carseats.rf <- randomForest(Sales ~ ., data = carseats.train, mtry = mtry[i], n.trees = 250)

   pred <- predict(carseats.rf, newdata = carseats.test)

   rf.error[i] <- mean((pred - carseats.test$Sales)^2)
}
```

```
Warning in randomForest.default(m, y, ...): invalid mtry: reset to within valid
range
```

```r
lowest.error <- which.min(rf.error)

results <- data.table(mtry = mtry, error = rf.error, lowest = mtry == lowest.error)

ggplot(results, aes(mtry, error, fill = lowest)) +
   geom_bar(stat = "identity")
```


error
mtry
lowest
FALSE
TRUE