Stats 415 Lab 10

April Cho

3/22/2018

Today's objectives

1. Learn how to implement a classification tree and regression tree.
2. Learn how to implement bagging and random forests.
3. Learn how to implement boosting

Decision Trees

1) Fitting Classification Trees

The 'tree' library is used to construct classification and regression trees.

```
library(tree)
```

We first use classification trees to analyze the Carseats data set. In these data, Sales is a continuous variable, and so we begin by recoding it as a binary variable. We use the ifelse() function to create a variable, called High, which takes on a value of Yes if the Sales variable exceeds 8, and takes on a value of No otherwise.

```
library(ISLR)
```

```
## Warning: package 'ISLR' was built under R version 3.2.5
```

```
attach(Carseats)
High=ifelse(Sales<=8,"No","Yes")
```

Finally, we use the data.frame() function to merge High with the rest of the Carseats data.

```
Carseats=data.frame(Carseats,High)
```

We now use the tree() function to fit a classification tree in order to predict High using all variables but Sales. The syntax of the tree() function is quite similar to that of the lm() function.

```
tree.carseats=tree(High~.-Sales,Carseats)
```

The summary() function lists the variables that are used as internal nodes in the tree, the number of terminal nodes, and the (training) error rate.

```
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
```

just training

Question: What is the training error rate from the classification tree? What does a deviance indicate about the model fit?

For classification trees, the deviance reported in the output of summary() is given by

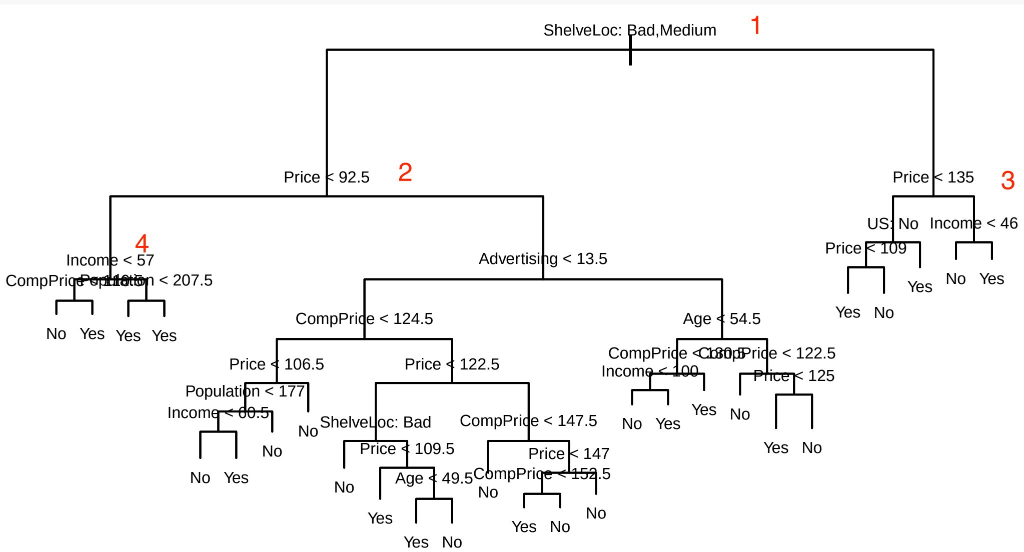
$$-2\sum_m \sum_k n_{mk} \log \widehat{p_{mk}}$$

where n_{mk} is the number of observations in the mth terminal node that belong to the kth class. A small deviance indicates a tree that provides a good fit to the (training) data. The residual mean deviance reported is simply the deviance divided by $n - |T_0|$, which in this case is $400 - 27 = 373$.

Visualization

One of the most attractive properties of trees is that they can be graphically displayed. We use the plot() function to display the tree structure, and the text() function to display the node labels. The argument pretty=0 instructs R to include the category names for any qualitative predictors, rather than simply displaying a letter for each category.

```r
plot(tree.carseats)
text(tree.carseats,pretty=0,cex=0.5)
```



Question: What appears to be the most important indicator of Sales from the plot above?

Since the first branch differentiates Good locations from Bad and Medium locations, the most important indicator of Sales appears to be shelving location!

If we just type the name of the tree object, R prints output corresponding to each branch of the tree. R displays the split criterion (e.g. Price<92.5), the number of observations in that branch, the deviance, the overall prediction for the branch (Yes or No), and the fraction of observations in that branch that take on values of Yes and No. Branches that lead to terminal nodes are indicated using asterisks.

```
tree.carseats
```

```
## node), split, n, deviance, yval, (yprob)
##       * denotes terminal node
##
##   1) root 400 541.500 No ( 0.59000 0.41000 )
##     2) ShelveLoc: Bad,Medium 315 390.600 No ( 0.68889 0.31111 )
##       4) Price < 92.5 46  56.530 Yes ( 0.30435 0.69565 )
##         8) Income < 57 10  12.220 No ( 0.70000 0.30000 )
##          16) CompPrice < 110.5 5   0.000 No ( 1.00000 0.00000 ) *
##          17) CompPrice > 110.5 5   6.730 Yes ( 0.40000 0.60000 ) *
##         9) Income > 57 36  35.470 Yes ( 0.19444 0.80556 )
##          18) Population < 207.5 16  21.170 Yes ( 0.37500 0.62500 ) *
##          19) Population > 207.5 20   7.941 Yes ( 0.05000 0.95000 ) *
##       5) Price > 92.5 269 299.800 No ( 0.75465 0.24535 )
##        10) Advertising < 13.5 224 213.200 No ( 0.81696 0.18304 )
##          20) CompPrice < 124.5 96  44.890 No ( 0.93750 0.06250 )
##            40) Price < 106.5 38  33.150 No ( 0.84211 0.15789 )
##              80) Population < 177 12  16.300 No ( 0.58333 0.41667 )
##               160) Income < 60.5 6   0.000 No ( 1.00000 0.00000 ) *
##               161) Income > 60.5 6   5.407 Yes ( 0.16667 0.83333 ) *
##              81) Population > 177 26   8.477 No ( 0.96154 0.03846 ) *
##            41) Price > 106.5 58   0.000 No ( 1.00000 0.00000 ) *
##          21) CompPrice > 124.5 128 150.200 No ( 0.72656 0.27344 )
##            42) Price < 122.5 51  70.680 Yes ( 0.49020 0.50980 )
##              84) ShelveLoc: Bad 11   6.702 No ( 0.90909 0.09091 ) *
##              85) ShelveLoc: Medium 40  52.930 Yes ( 0.37500 0.62500 )
##               170) Price < 109.5 16   7.481 Yes ( 0.06250 0.93750 ) *
##               171) Price > 109.5 24  32.600 No ( 0.58333 0.41667 )
##                 342) Age < 49.5 13  16.050 Yes ( 0.30769 0.69231 ) *
##                 343) Age > 49.5 11   6.702 No ( 0.90909 0.09091 ) *
##            43) Price > 122.5 77  55.540 No ( 0.88312 0.11688 )
##              86) CompPrice < 147.5 58  17.400 No ( 0.96552 0.03448 ) *
##              87) CompPrice > 147.5 19  25.010 No ( 0.63158 0.36842 )
##               174) Price < 147 12  16.300 Yes ( 0.41667 0.58333 )
##                 348) CompPrice < 152.5 7   5.742 Yes ( 0.14286 0.85714 ) *
##                 349) CompPrice > 152.5 5   5.004 No ( 0.80000 0.20000 ) *
##               175) Price > 147 7   0.000 No ( 1.00000 0.00000 ) *
##        11) Advertising > 13.5 45  61.830 Yes ( 0.44444 0.55556 )
##          22) Age < 54.5 25  25.020 Yes ( 0.20000 0.80000 )
##            44) CompPrice < 130.5 14  18.250 Yes ( 0.35714 0.64286 )
##              88) Income < 100 9  12.370 No ( 0.55556 0.44444 ) *
##              89) Income > 100 5   0.000 Yes ( 0.00000 1.00000 ) *
##            45) CompPrice > 130.5 11   0.000 Yes ( 0.00000 1.00000 ) *
##          23) Age > 54.5 20  22.490 No ( 0.75000 0.25000 )
##            46) CompPrice < 122.5 10   0.000 No ( 1.00000 0.00000 ) *
##            47) CompPrice > 122.5 10  13.860 No ( 0.50000 0.50000 )
##              94) Price < 125 5   0.000 Yes ( 0.00000 1.00000 ) *
```

```
##             95) Price > 125 5   0.000 No ( 1.00000 0.00000 ) *
##     3) ShelveLoc: Good 85  90.330 Yes ( 0.22353 0.77647 )
##       6) Price < 135 68  49.260 Yes ( 0.11765 0.88235 )
##        12) US: No 17  22.070 Yes ( 0.35294 0.64706 )
##          24) Price < 109 8   0.000 Yes ( 0.00000 1.00000 ) *
##          25) Price > 109 9  11.460 No ( 0.66667 0.33333 ) *
##        13) US: Yes 51  16.880 Yes ( 0.03922 0.96078 ) *
##       7) Price > 135 17  22.070 No ( 0.64706 0.35294 )
##        14) Income < 46 6   0.000 No ( 1.00000 0.00000 ) *
##        15) Income > 46 11  15.160 Yes ( 0.45455 0.54545 ) *
```

Evaluation of the tree

In order to properly evaluate the performance of a classification tree on these data, we must estimate the test error rather than simply computing the training error. We split the observations into a training set and a test set, build the tree using the training set, and evaluate its performance on the test data. The predict() function can be used for this purpose. In the case of a classification tree, the argument type="class" instructs R to return the actual class prediction. This approach leads to correct predictions for around 71.5% of the locations in the test data set.

```
set.seed(2)
train=sample(1:nrow(Carseats), 200)
Carseats.test=Carseats[-train,]
High.test=High[-train]
tree.carseats=tree(High~.-Sales,Carseats,subset=train)
tree.pred=predict(tree.carseats,Carseats.test,type="class")
table(tree.pred,High.test)
```

```
##          High.test
## tree.pred No Yes
##       No  86  27
##       Yes 30  57
```

```
(86+57)/200
```

```
## [1] 0.715
```

Pruning the tree

Next, we consider whether pruning the tree might lead to improved results. The function cv.tree() performs cross-validation in order to determine the optimal level of tree complexity; cost complexity pruning is used in order to select a sequence of trees for consideration. We use the argument FUN=prune.misclass in order to indicate that we want the classification error rate to guide the cross-validation and pruning process, rather than the default for the cv.tree() function, which is deviance. The cv.tree() function reports the number of terminal nodes of each tree considered (size) as well as the corresponding error rate and the value of the cost-complexity parameter used (k, which corresponds to in below formula).

$$\sum_{m=1}^{|T|} \sum_{i:x_i \in R_m} (y_i - \widehat{y_{R_m}})^2 + \alpha|T|$$

```
set.seed(3)
cv.carseats=cv.tree(tree.carseats,FUN=prune.misclass)
names(cv.carseats)
```

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

```
cv.carseats
```

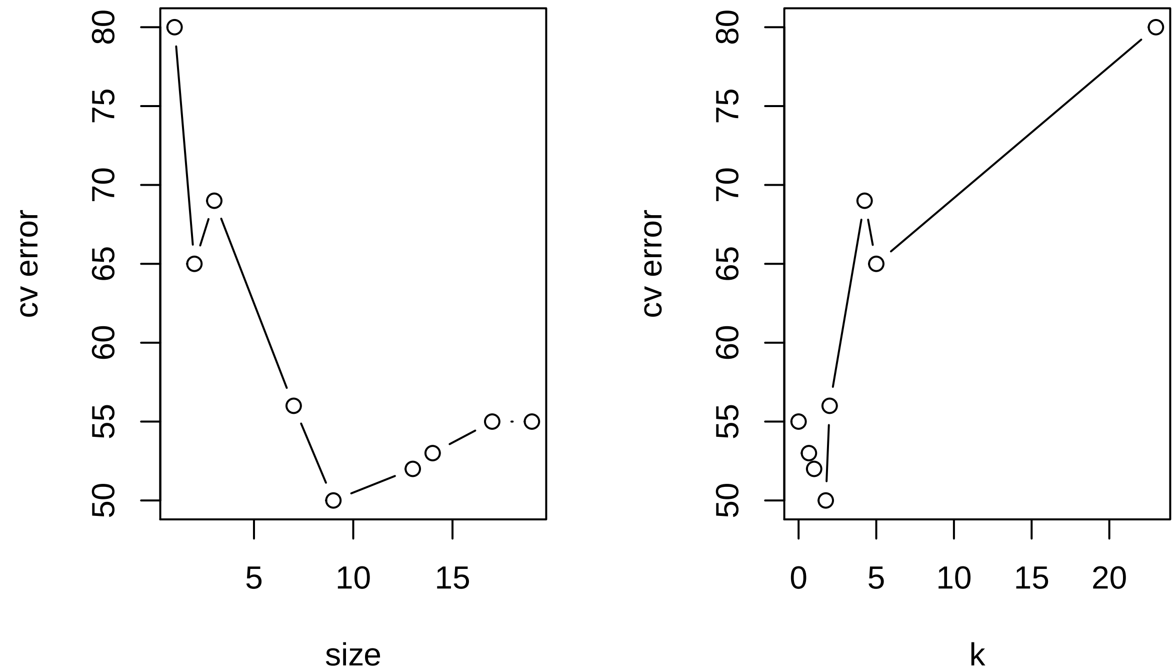
```
## $size
## [1] 19 17 14 13  9  7  3  2  1
```
optimized size is 9
```
##
## $dev
## [1] 55 55 53 52 50 56 69 65 80
##
## $k
## [1]       -Inf  0.0000000  0.6666667  1.0000000  1.7500000  2.0000000
## [7]  4.2500000  5.0000000 23.0000000
##
## $method
## [1] "misclass"
##
## attr(,"class")
## [1] "prune"         "tree.sequence"
```

Note that, despite the name, dev corresponds to the cross-validation error rate in this instance.

Question: What is the number of terminal nodes associated with the lowest cross-validation error rate? What is the value of that lowest cross-validation error?

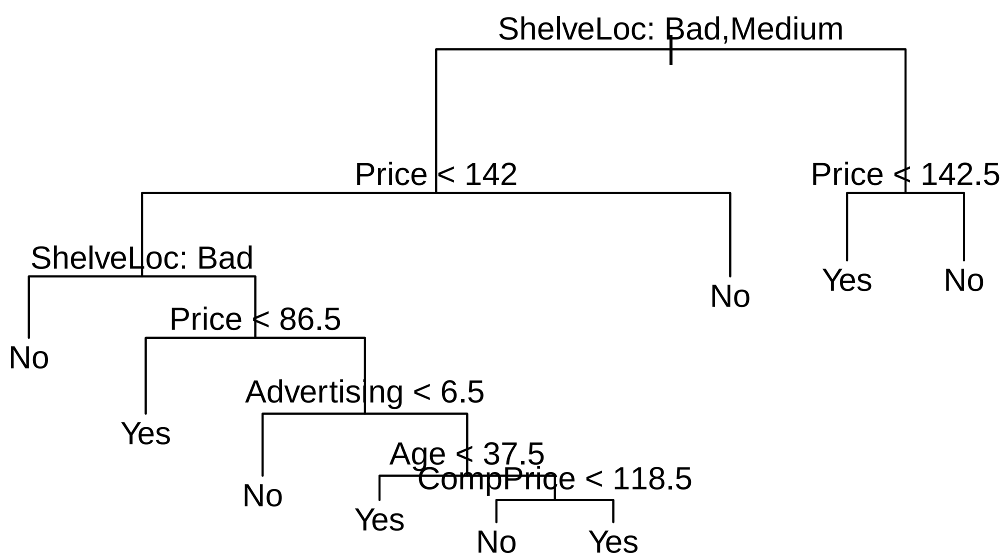
We plot the error rate as a function of both size and k.

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



We now apply the prune.misclass() function in order to prune the tree to obtain the nine-node tree.

```r
prune.carseats=prune.misclass(tree.carseats,best=9)
plot(prune.carseats)
text(prune.carseats,pretty=0)
```



How well does this pruned tree perform on the test data set? Once again, we apply the predict() function.

```r
tree.pred=predict(prune.carseats,Carseats.test,type="class")
table(tree.pred,High.test)
```

```
##          High.test
## tree.pred No  Yes
##       No  94   24
##       Yes 22   60
```

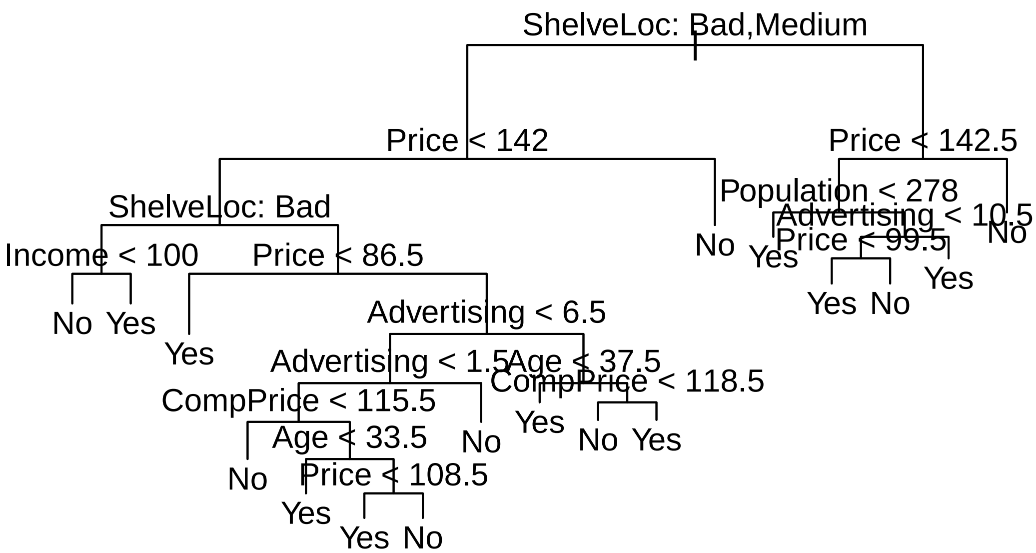
```
(94+60)/200
```

```
## [1] 0.77
```

Now 77% of the test observations are correctly classified, so not only has the pruning process produced a more interpretable tree, but it has also improved the classification accuracy.

If we increase the value of the argument `best`, we obtain a larger pruned tree with lower classification accuracy:

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




```
tree.pred=predict(prune.carseats,Carseats.test,type="class")
table(tree.pred,High.test)
```

```
##          High.test
## tree.pred No Yes
##       No  86  22
##       Yes 30  62
```

```
(86+62)/200
```

```
## [1] 0.74
```

2) Fitting Regression Trees

Here we fit a regression tree to the Boston data set. First, we create a training set, and fit the tree to the training data.

```
library(MASS)
```

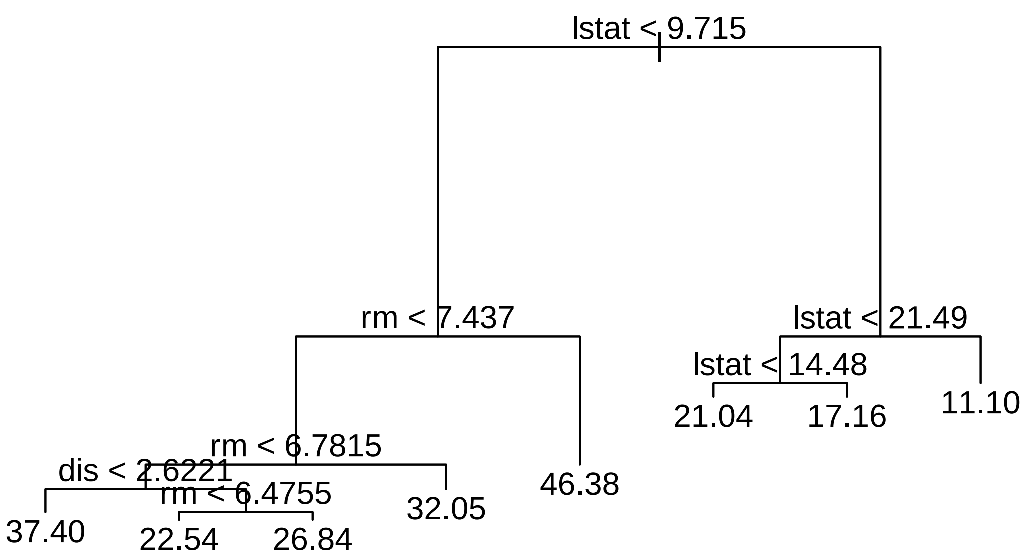
```
## Warning: package 'MASS' was built under R version 3.2.5
```

```
set.seed(1)
train = sample(1:nrow(Boston), nrow(Boston)/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] "lstat" "rm"    "dis"
## Number of terminal nodes:  8
## Residual mean deviance:  12.65 = 3099 / 245
## Distribution of residuals:
##      Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
## -14.10000  -2.04200  -0.05357   0.00000   1.96000  12.60000
```

Notice that the output of summary() indicates that only three of the variables have been used in constructing the tree. In the context of a regression tree, the deviance is simply the sum of squared errors for the tree. We now plot the tree.

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



The variable lstat measures the percentage of individuals with lower socioeconomic status. The tree indicates that lower values of lstat correspond to more expensive houses. The tree predicts a median house price of $46,400 for larger homes in suburbs in which residents have high socioeconomic status (rm>=7.437 and lstat<9.715).

Pruning the regression tree

Now we use the cv.tree() function to see whether pruning the tree will improve performance.

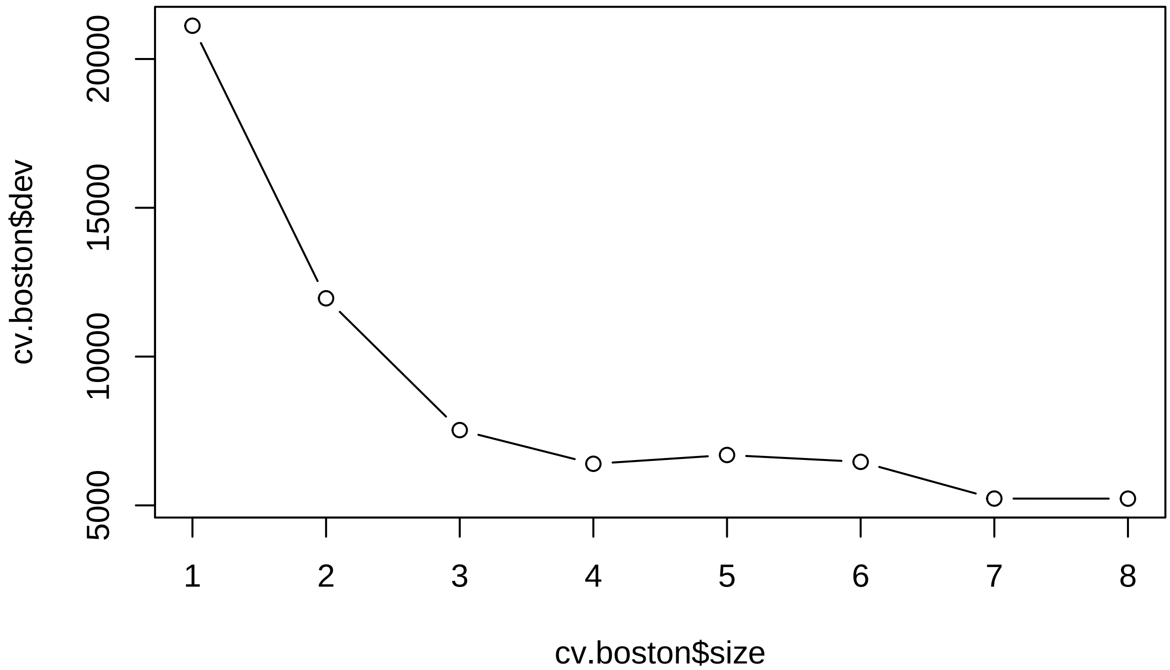
```
cv.boston=cv.tree(tree.boston)
cv.boston
```

```
## $size
## [1] 8 7 6 5 4 3 2 1
##
## $dev
## [1]  5226.322  5228.360  6462.626  6692.615  6397.438  7529.846 11958.691
## [8] 21118.139
##
## $k
```

7 and 8 are all reasonable choice

```
## [1]      -Inf  255.6581  451.9272  768.5087  818.8885 1559.1264 4276.5803
## [8] 9665.3582
##
## $method
## [1] "deviance"
##
## attr(,"class")
## [1] "prune"         "tree.sequence"
```

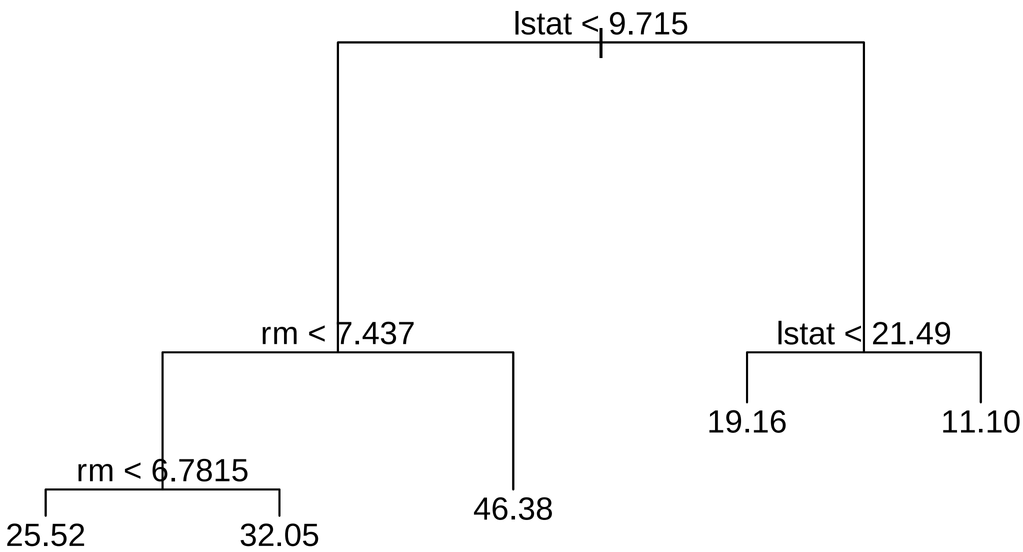
```
plot(cv.boston$size,cv.boston$dev,type='b')
```



Question: What number of terminal nodes would you choose based on the cross-validation result?

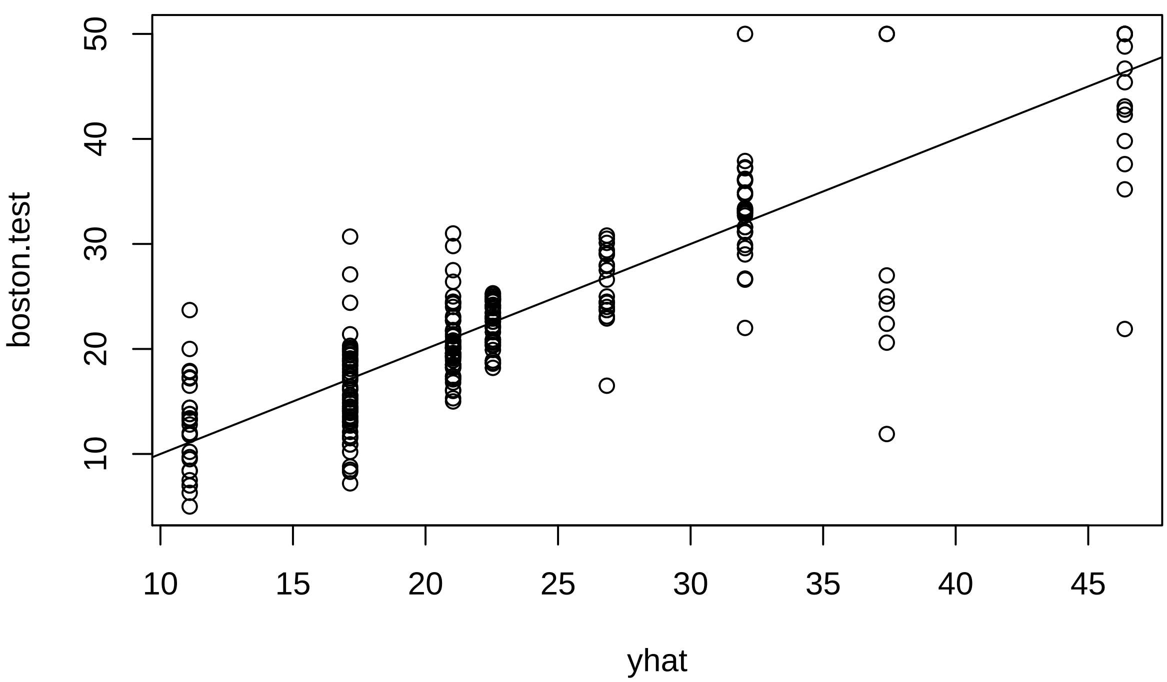
In this case, the most complex tree is selected by cross-validation. However, if we wish to prune the tree, we could do so as follows, using the prune.tree() function:

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



In keeping with the cross-validation results, we use the unpruned tree to make predictions on the test set.

```
yhat=predict(tree.boston,newdata=Boston[-train,])
boston.test=Boston[-train,"medv"]
plot(yhat,boston.test)
abline(0,1)
```




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

```
## [1] 25.04559
```

In other words, the test set MSE associated with the regression tree is 25.05.

Question: What does this MSE impy about the prediction? How do you interpret the test MSE? Does large test MSE mean bad prediction? (Think about the huge test MSEs you got in hw6!)

The square root of the MSE is around 5.005, indicating that this model leads to test predictions that are within around $5,005 of the true median home value for the suburb.

3) Bagging and Random Forests

Here we apply bagging and random forests to the Boston data, using the randomForest package in R. The exact results obtained in this section may depend on the version of R and the version of the randomForest package installed on your computer. Recall that bagging is simply a special case of a random forest with m = p. Therefore, the randomForest() function can be used to perform both random forests and bagging. We perform bagging as follows:

```r
library(randomForest)
```

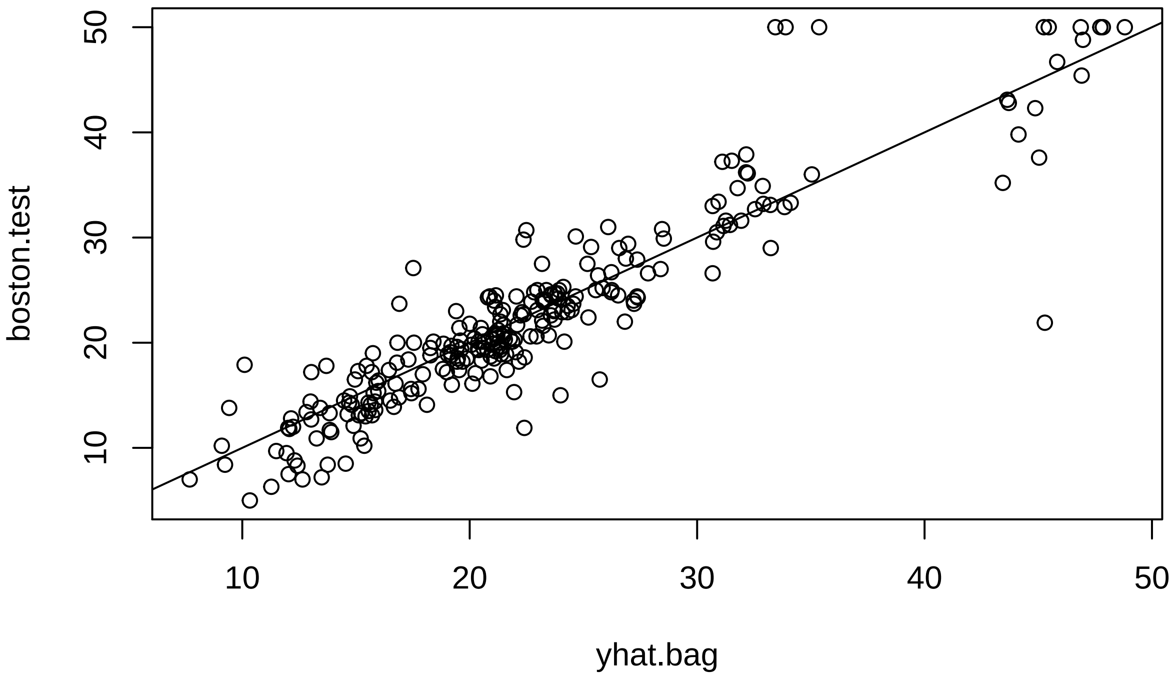
```
## randomForest 4.6-12

## Type rfNews() to see new features/changes/bug fixes.
```

```r
set.seed(1)
bag.boston=randomForest(medv~.,data=Boston,subset=train,mtry=13,importance=TRUE)
bag.boston
```

```
##
## Call:
##  randomForest(formula = medv ~ ., data = Boston, mtry = 13, importance = TRUE,      subset = train)
##                Type of random forest: regression
##                      Number of trees: 500
## No. of variables tried at each split: 13
##
##           Mean of squared residuals: 11.02509
##                     % Var explained: 86.65
```

The argument mtry=13 indicates that all 13 predictors should be considered for each split of the tree. In other words, that bagging should be done. How well does this bagged model perform on the test set?

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




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

```
## [1] 13.47349
```

The test setMSE associated with the bagged regression tree is 13.16, almost half that obtained using an optimally-pruned single tree. We could change the number of trees grown by randomForest() using the ntree argument:

```
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] 13.43068
```

Growing a random forest proceeds in exactly the same way, except that we use a smaller value of the mtry argument. By default, randomForest() uses $p/3$ variables when building a random forest of regression trees, and $\sqrt{p}$ variables when building a random forest of classification trees. Here we use mtry = 6.

```
set.seed(1)
rf.boston=randomForest(medv~.,data=Boston,subset=train,mtry=6,importance=TRUE)
yhat.rf = predict(rf.boston,newdata=Boston[-train,])
mean((yhat.rf-boston.test)^2)
```

```
## [1] 11.48022
```

The test set MSE is 11.31; this indicates that random forests yielded an improvement over bagging in this case.

Using the importance() function, we can view the importance of each variable.

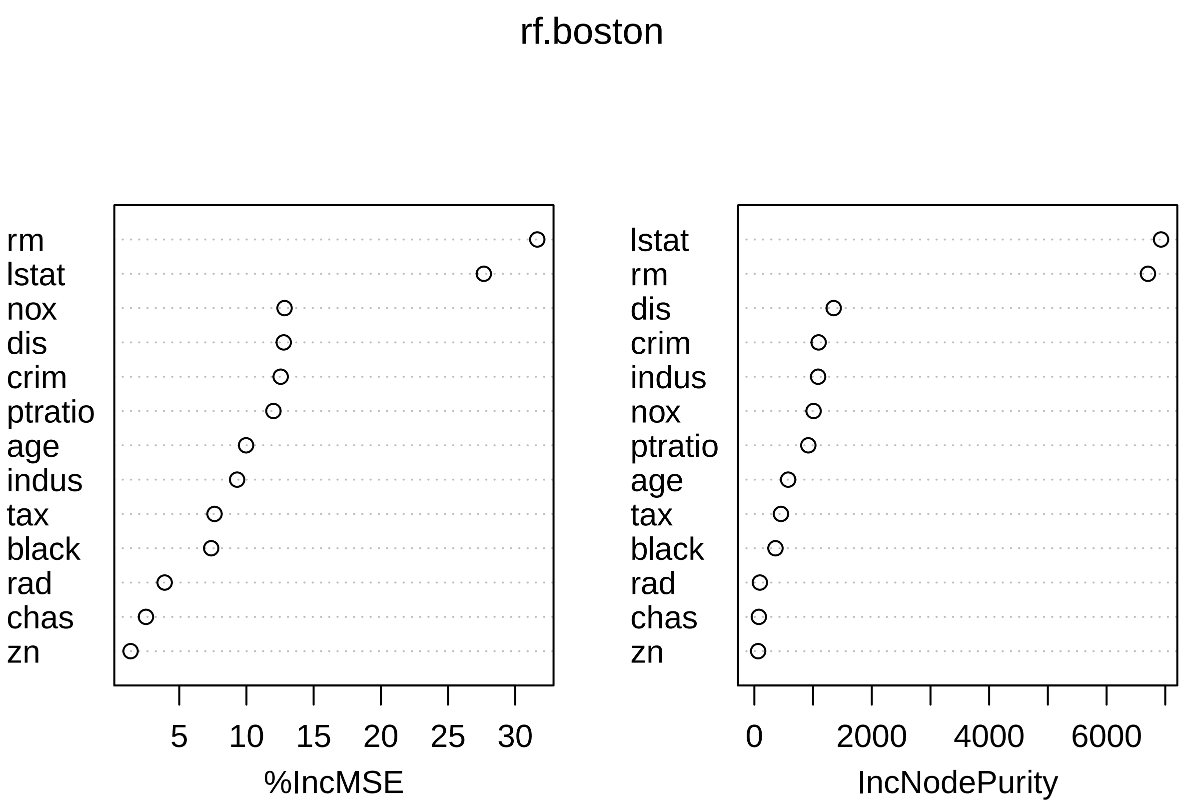
```
importance(rf.boston)
```

```
##          %IncMSE IncNodePurity
## crim    12.547772    1094.65382
## zn       1.375489      64.40060
## indus    9.304258    1086.09103
## chas     2.518766      76.36804
```

```
## nox      12.835614    1008.73703
## rm       31.646147    6705.02638
## age       9.970243     575.13702
## dis      12.774430    1351.01978
## rad       3.911852      93.78200
## tax       7.624043     453.19472
## ptratio 12.008194     919.06760
## black     7.376024     358.96935
## lstat    27.666896    6927.98475
```

Two measures of variable importance are reported. The former is based upon the mean decrease of accuracy in predictions on the out of bag samples when a given variable is excluded from the model. The latter is a measure of the total decrease in node impurity that results from splits over that variable, averaged over all trees. In the case of regression trees, the node impurity is measured by the training RSS, and for classification trees by the deviance. Plots of these importance measures can be produced using the varImpPlot() function.

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



The results indicate that across all of the trees considered in the random forest, the wealth level of the community (lstat) and the house size (rm) are by far the two most important variables.

4) Boosting

Here we use the gbm package, and within it the gbm() function, to fit boosted regression trees to the Boston data set. We run gbm() with the option distribution="gaussian" since this is a regression problem; if it were a binary classification problem, we would use distribution="bernoulli". The argument n.trees=5000 indicates that we want 5000 trees, and the option interaction.depth=4 limits the depth of each tree.

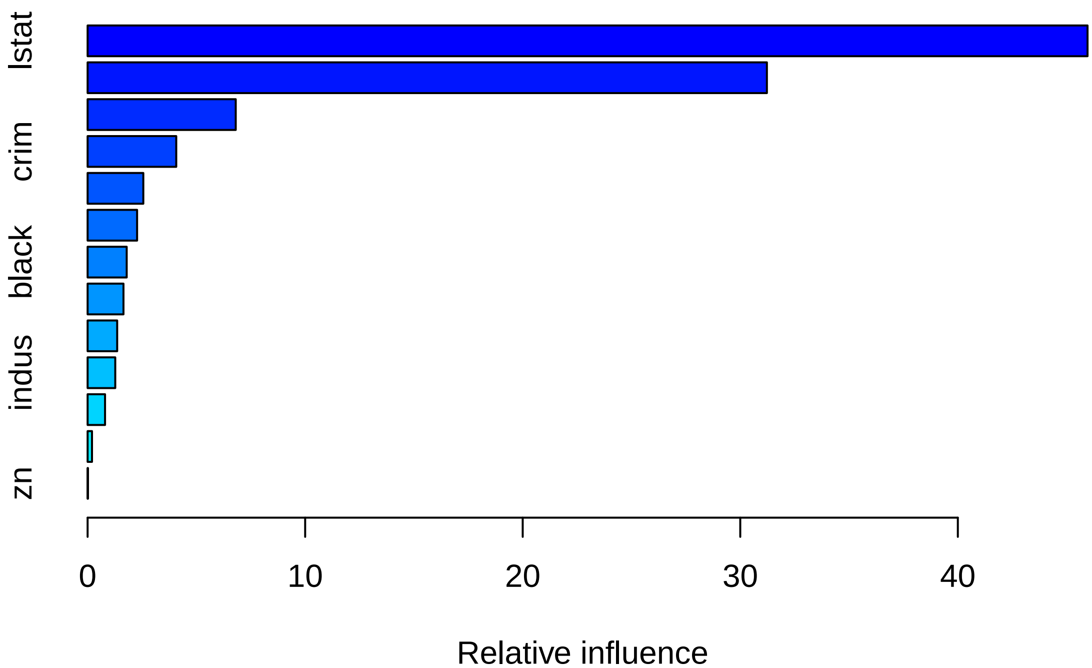
```r
library(gbm)
```

```
## Warning: package 'gbm' was built under R version 3.2.5

## Loading required package: survival

## Loading required package: lattice

## Warning: package 'lattice' was built under R version 3.2.5

## Loading required package: splines

## Loading required package: parallel

## Loaded gbm 2.1.3
```

```r
set.seed(1)
boost.boston=gbm(medv~.,data=Boston[train,],distribution="gaussian",n.trees=5000,interaction.depth=4)
```

The summary() function produces a relative influence plot and also outputs the relative influence statistics.

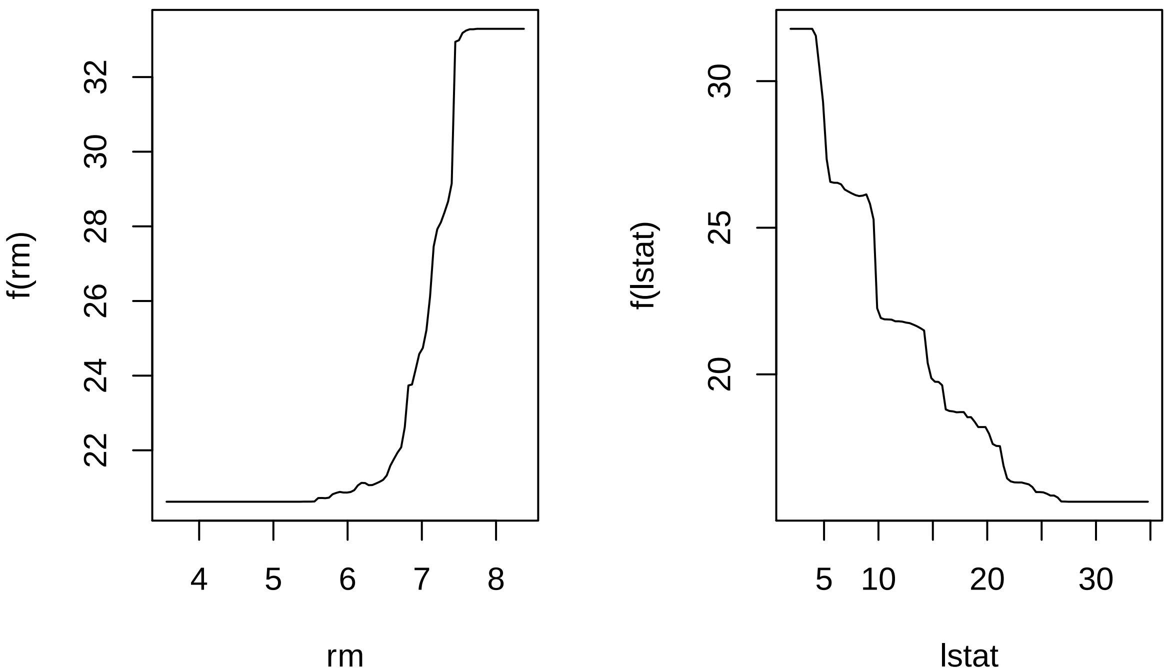
```r
summary(boost.boston)
```




```
##             var    rel.inf
## lstat     lstat 45.9627334
## rm           rm 31.2238187
## dis         dis  6.8087398
## crim       crim  4.0743784
## nox         nox  2.5605001
## ptratio ptratio  2.2748652
## black     black  1.7971159
## age         age  1.6488532
## tax         tax  1.3595005
## indus     indus  1.2705924
## chas       chas  0.8014323
## rad         rad  0.2026619
## zn           zn  0.0148083
```

We see that lstat and rm are by far the most important variables. We can also produce partial dependence plots for these two variables. These plots illustrate the marginal effect of the selected variables on the response after integrating out the other variables. In this case, as we might expect, median house prices are increasing with rm and decreasing with lstat.

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



We now use the boosted model to predict medv on the test set:

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

```
## [1] 11.84434
```

The test MSE obtained is 11.8; similar to the test MSE for random forests and superior to that for bagging. If we want to, we can perform boosting with a different value of the shrinkage parameter λ. The default value is 0.001, but this is easily modified. Here we take $\lambda = 0.2$.

```
boost.boston=gbm(medv~.,data=Boston[train,],distribution="gaussian",n.trees=5000,interaction.depth=4,sh
yhat.boost=predict(boost.boston,newdata=Boston[-train,],n.trees=5000)
mean((yhat.boost-boston.test)^2)
```

```
## [1] 11.51109
```

In this case, using $\lambda = 0.2$ leads to a slightly lower test MSE than $\lambda = 0.001$.