An R Markdown document converted from Lab 8

Lab 8:

- Decision Tree
- Random Forest

```
library(tree)
```

```
library(repr)
options(repr.plot.width=12, repr.plot.height=6)
```

Classification Tree

- Use the `Carseats` dataset
- Transform a continuous variable `Sales` to a binary variable.

```
library(ISLR2)
attach(Carseats)
```

```
High <- factor(ifelse(Sales <= 8, "No", "Yes"))
```

```
Carseats <- data.frame(Carseats, High)
```

Use `tree` function to fit a classification tree to predict `High` using all variables but `Sales`.

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

```
head(Carseats)
```

```
##   Sales CompPrice Income Advertising Population Price ShelveLoc Age Education
## 1  9.50       138     73          11        276   120       Bad  42        17
## 2 11.22       111     48          16        260    83      Good  65        10
## 3 10.06       113     35          10        269    80    Medium  59        12
## 4  7.40       117    100           4        466    97    Medium  55        14
## 5  4.15       141     64           3        340   128       Bad  38        13
## 6 10.81       124    113          13        501    72       Bad  78        16
##   Urban  US High
## 1   Yes Yes  Yes
## 2   Yes Yes  Yes
## 3   Yes Yes  Yes
## 4   Yes Yes   No
## 5   Yes  No   No
## 6    No Yes  Yes
```

```
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
```

The deviance is given by

$$-2\sum_m\sum_k n_{mk}\log\hat{p}_{mk}$$

where n_{mk} is the number of observations in the mth terminal node that belong to the kth class and $\hat{p}_{mk}$ represents the proportion of training observations in the m-th region that are from the kth class.

It is closely related to the entropy

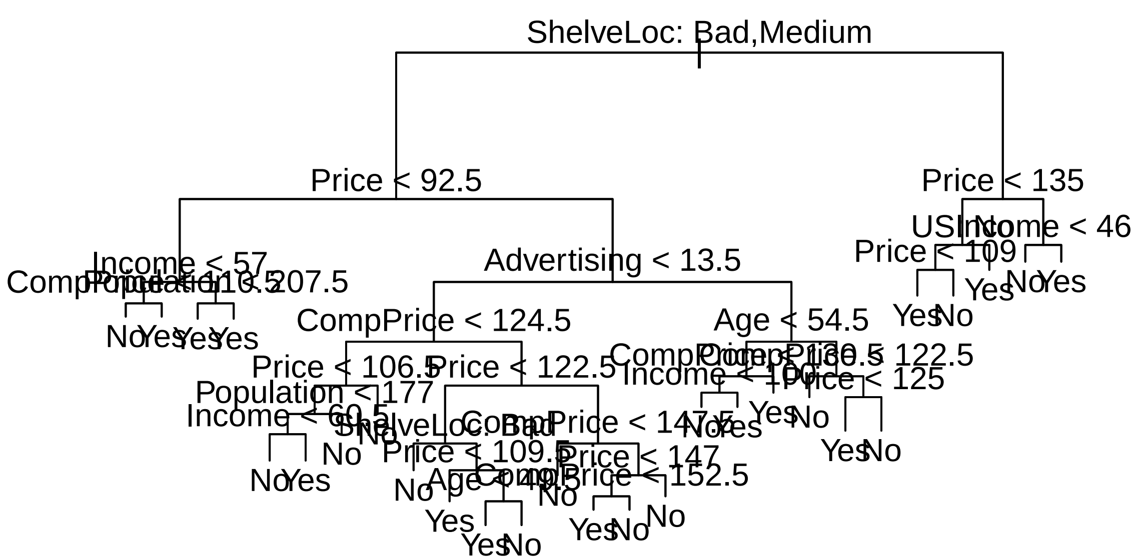
$$-\sum_m\sum_k \hat{p}_{mk}\log\hat{p}_{mk}$$

A small deviance indicates a tree provide a good fit to the training data.

The *residual mean deviance* is simply the deviance divided by $n-|T_0|$ and in this case $400-27=373$.

We can also plot a tree with `plot` function.

```
plot(tree.carseats)
text(tree.carseats, pretty = 0) # pretty means that to include the category names for any qualitative v
```



Seems like that the most important variable is shelving location, as the first branch differentiates `Good` locations from `Bad` and `Medium`.

It turns out that the left branch corresponds to the split being true. So the left branch is for `Bad` and `Medium`, while the right branc his for `Good`.

```
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 ) *
```

Now estimate test error

```r
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)

# We specify type = class to instruct R to return the actual class prediction.
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
(104 + 50) / 200
```

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

Use `cv.tree` to perform cross validation

Cost complexity pruning is used in order to select a sequence of trees for consideration

- Estimating the cross-validation error for every possible subtree would be computationally imposibble, given that there are so many possible subtrees
- We start with a very big tree T_0, then we consider a sequence of tees indexed by a nonnegative tuning parameter α.
- For each value of α, there corresponds to a subtree $T \subset T_0$ such that

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

  is as small as possible.
- $|T|$ is the number of terminal nodes, R_m is the rectangel for the m-th terminal node, $\hat{y}_{R_m}$ is the predicted response for R_m.

- As we increase α from 0, branches get pruned from the tree in a nested and predictable fasion, so obtaining the whole sequence of subtrees as a function of α is easy.
- Then we can use cross validation to select among this sequence of trees. ### We use argument `FUN = prune.misclass` in order to indicate that we want to use classification error as the metric to guide the cross-validation and pruning process ### The default for `cv.tree` is deviance.

```
set.seed(7)
cv.carseats <- cv.tree(tree.carseats, FUN=prune.misclass)
names(cv.carseats)
```

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

`Size` stands for the number of terminal nodes and `k` is the cost-complexity parameter (corresponds to α

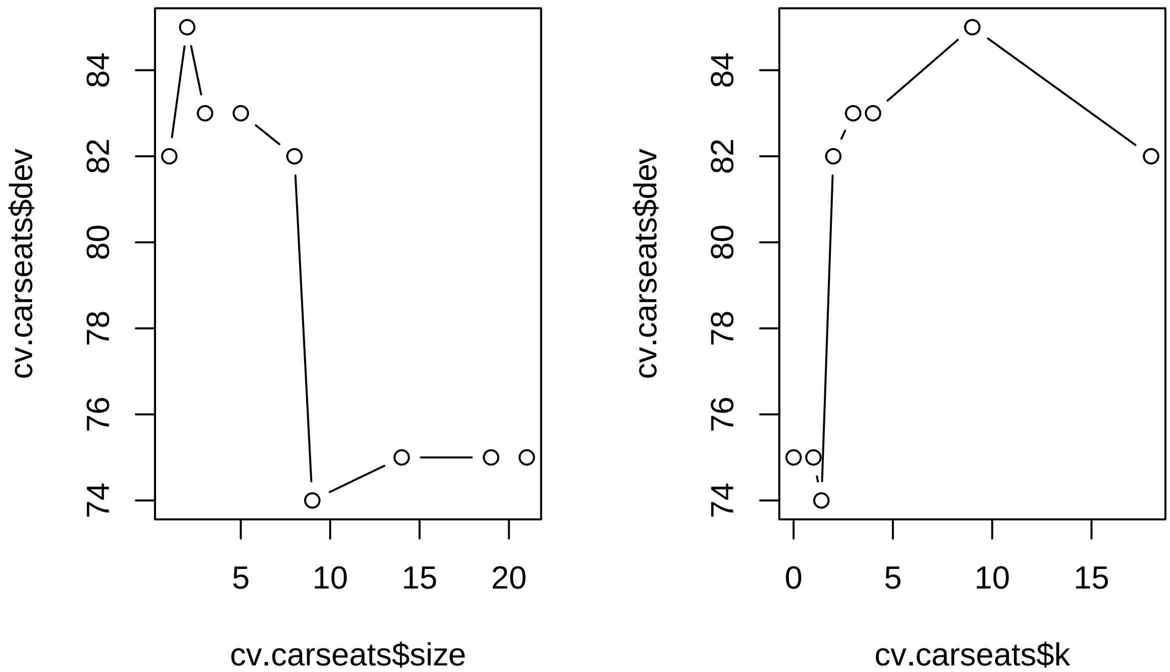
```
cv.carseats
```

```
## $size
## [1] 21 19 14  9  8  5  3  2  1
##
## $dev
## [1] 75 75 75 74 82 83 83 85 82
##
## $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"
```

`Dev` actually means the misclassification errors

We should then select the tree with 9 terminal nodes

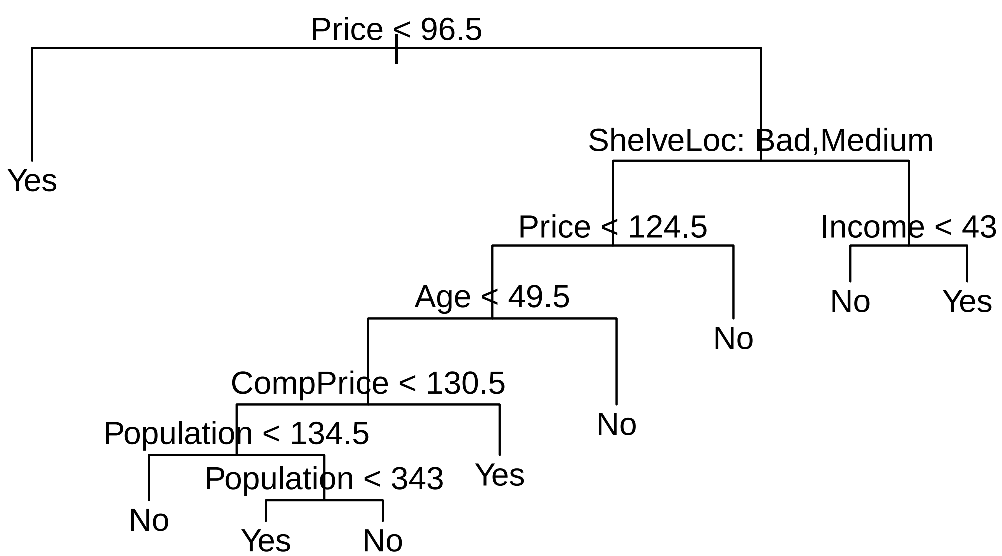
```
par(mfrow = c(1, 2))
plot(cv.carseats$size, cv.carseats$dev, type="b")
plot(cv.carseats$k, cv.carseats$dev, type="b")
```



Use `prune.misclass` function to prune the tree to obtain the nine-node tree

```
prune.carseats <- prune.misclass(tree.carseats, best=9)
```

```
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  97  25
##       Yes 20  58
```

```r
(97 + 58) / 200
```

```
## [1] 0.775
```

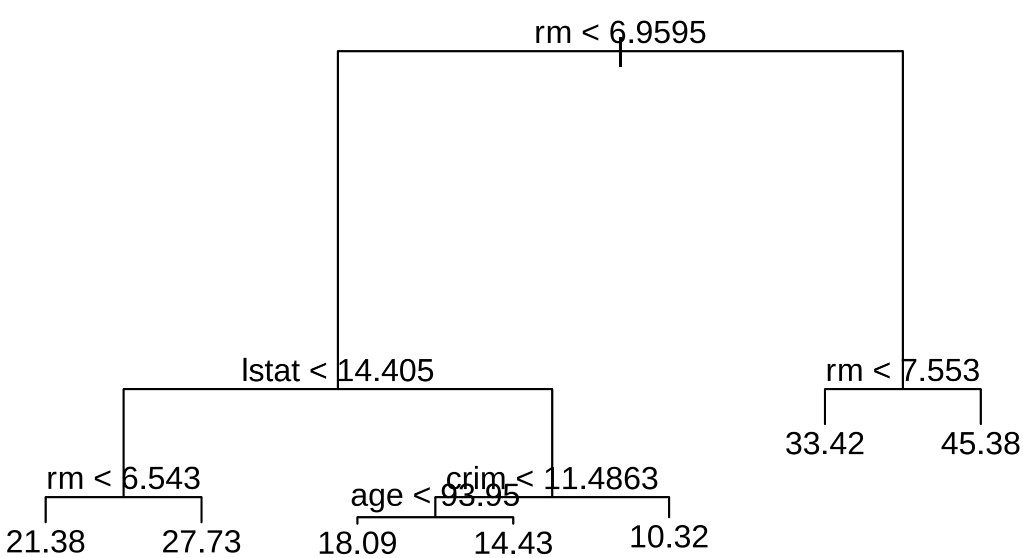
Regression Tree

Now use `Boston` dataset

```r
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] "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)
```

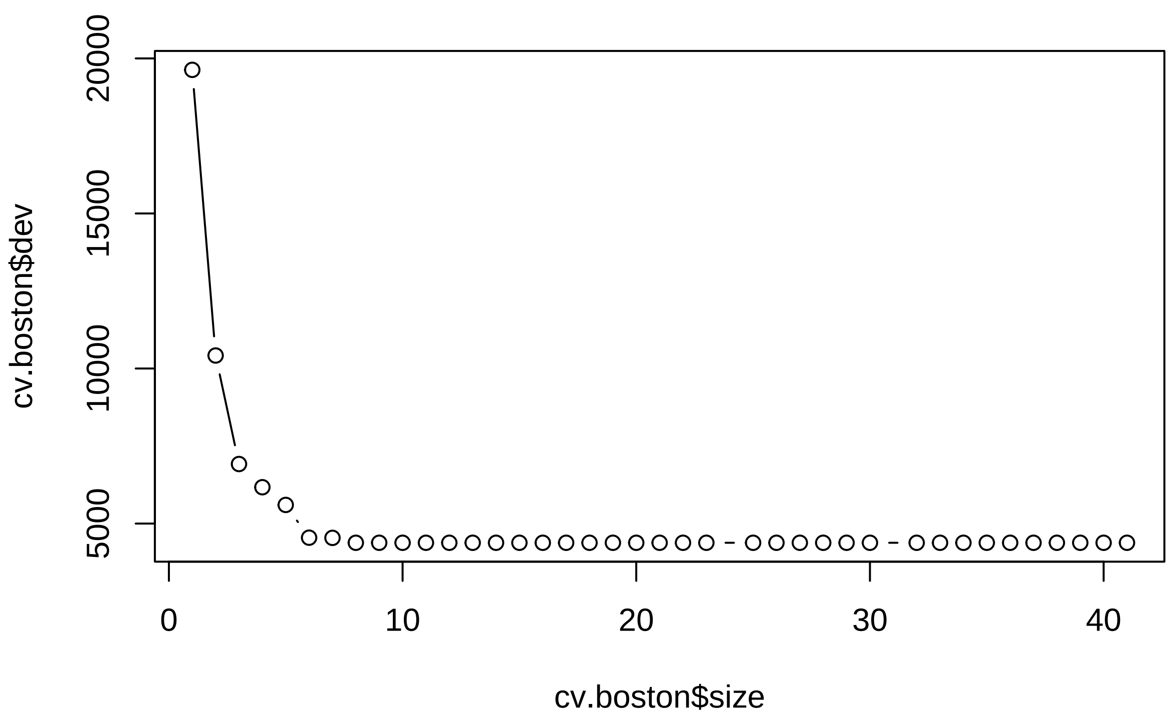


```
tree.boston <- tree(medv ~ ., Boston, subset = train, control = tree.control(nobs = length(train), minde
```

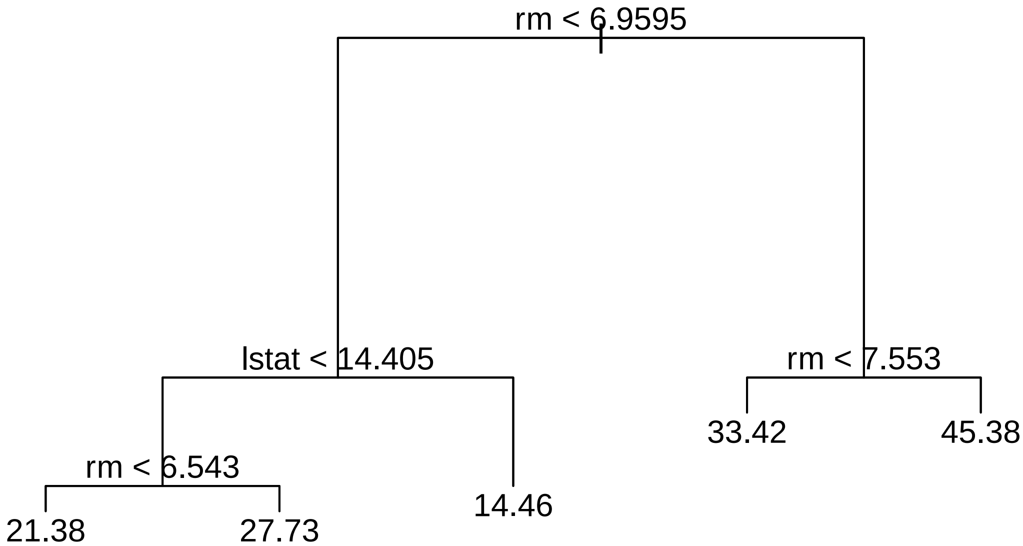
```
summary(tree.boston)
```

```
##
## Regression tree:
## tree(formula = medv ~ ., data = Boston, subset = train, control = tree.control(nobs = length(train),
##     mindev = 0))
## Variables actually used in tree construction:
## [1] "rm"      "lstat"   "indus"   "age"     "nox"     "dis"     "ptratio"
## [8] "tax"     "crim"
## Number of terminal nodes:  41
## Residual mean deviance:  5.542 = 1175 / 212
## Distribution of residuals:
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  -8.140  -1.200   0.000   0.000   1.087  12.860
```

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

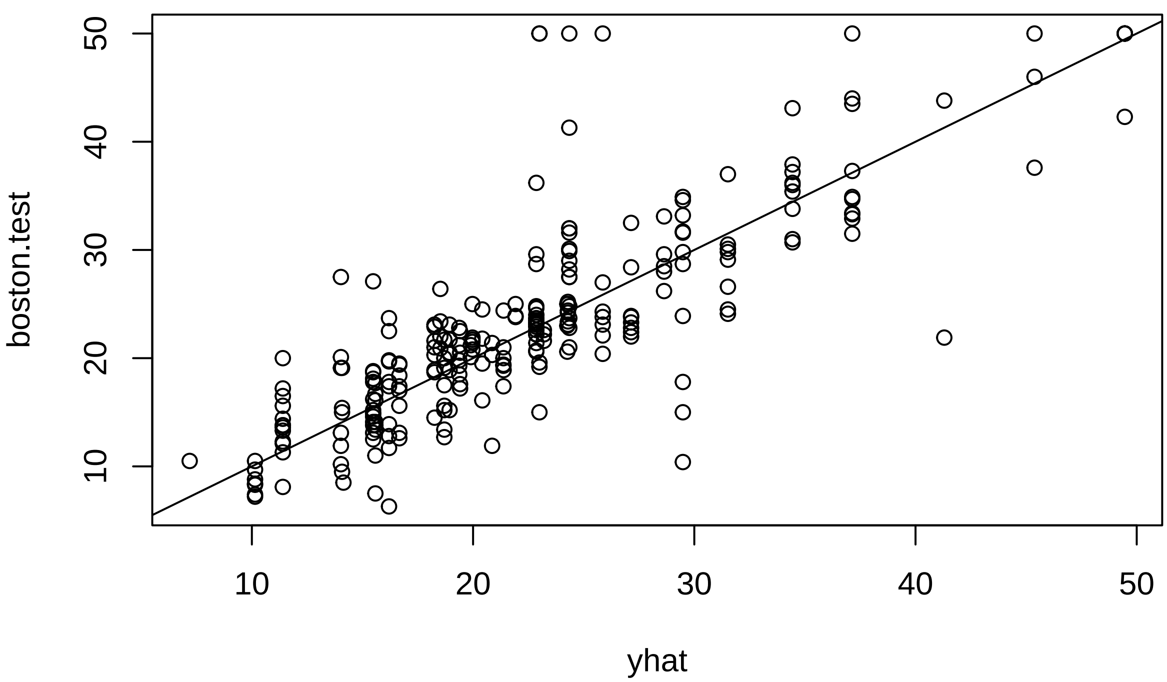



```
prune.boston <- prune.tree(tree.boston, best = 5)
plot(prune.boston)
text(prune.boston, pretty = 0)
```




```
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] 30.19368
```

Bagging and Random Forests

```
library(randomForest)
```

```
## randomForest 4.7-1
```

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

Recal that bagging is simply a special case of a random forest with $m = p$. Therefore, `randomForest` can be used to perform both random forests and bagging.

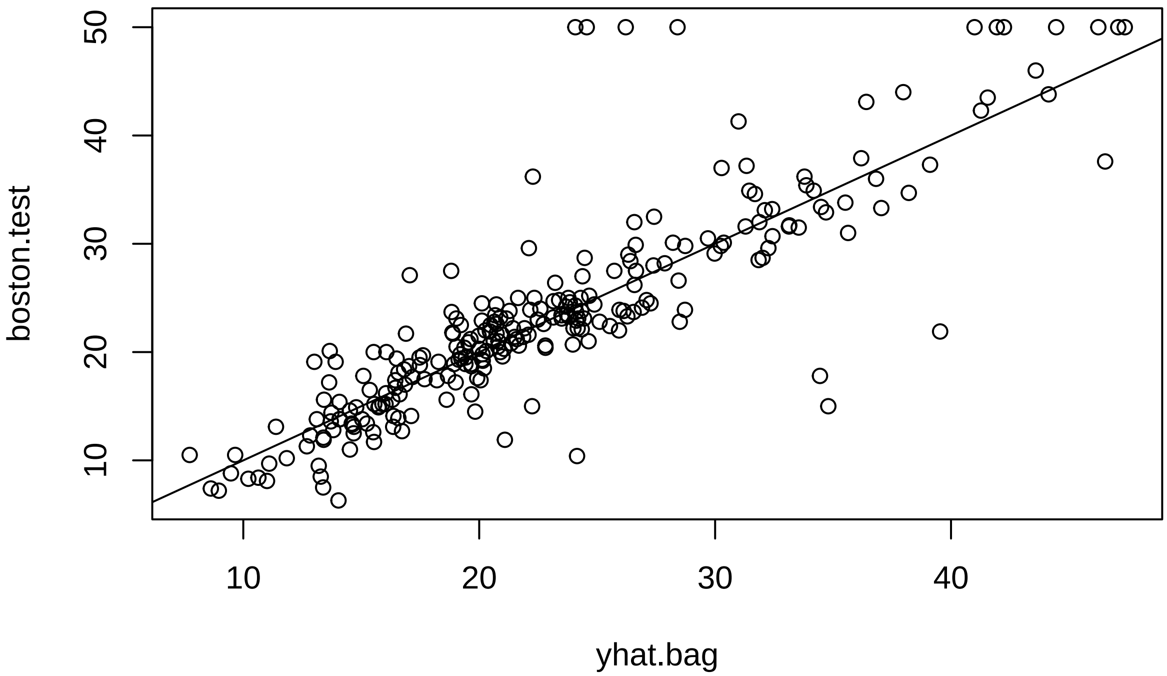
```
set.seed(1)
bag.boston <- randomForest(medv ~., data = Boston,
                           subset=train, mtry=12, importance = TRUE)
```

```
bag.boston
```

```
##
## Call:
##  randomForest(formula = medv ~ ., data = Boston, mtry = 12, importance = TRUE,      subset = train)
##                Type of random forest: regression
##                      Number of trees: 500
## No. of variables tried at each split: 12
##
##           Mean of squared residuals: 11.40162
##                     % Var explained: 85.17
```

```
yhat.bag <- predict(bag.boston, newdata = Boston[-train, ])
```

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




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

```
## [1] 23.41916
```

```
bag.boston <- randomForest(medv ~ ., data = Boston,
                           subset = train, mtry=12, ntree=25)
yhat.bag <- predict(bag.boston, newdata = Boston[-train, ])
mean((yhat.bag - boston.test)^2)
```

```
## [1] 25.75055
```

For random forest, we will specify a smaller `mtry` argument. The default is for regression trees, we set $m = p/3$ and for classification trees, we set $m = \sqrt{p}$.

```
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] 20.06644
```

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

```
##           %IncMSE IncNodePurity
## crim    19.435587    1070.42307
```

```
## zn        3.091630      82.19257
## indus     6.140529     590.09536
## chas      1.370310      36.70356
## nox      13.263466     859.97091
## rm       35.094741    8270.33906
## age      15.144821     634.31220
## dis       9.163776     684.87953
## rad       4.793720      83.18719
## tax       4.410714     292.20949
## ptratio   8.612780     902.20190
## lstat    28.725343    5813.04833
```

First column is based on the mean decrease of accuracy in predictions on the out-of-bag samples when a given variable is permuted.

The second column is a measure of the total decrease in node impurity that results from splits over that variable, averaged over all trees.

For regression trees, node impurity is measured by the training RSS, and for classification, node impurity is measured by the deviance.

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