# Decision Trees for Regression

Karen Mazidi

# Try linear regression on Boston

We get a correlation of 0.9 and a rmse of 4.35.

```
library(tree)
library (MASS)
names (Boston)
   [1] "crim"
                  "zn"
                            "indus"
                                       "chas"
                                                 "nox"
                                                           "rm"
                                                                      "age"
   [8] "dis"
                  "rad"
                             "tax"
                                       "ptratio" "black"
                                                           "lstat"
                                                                      "medv"
# divide into train and test
set.seed(1234)
i <- sample(nrow(Boston), 0.8*nrow(Boston), replace = FALSE)
train <- Boston[i,]</pre>
test <- Boston[-i,]</pre>
lm1 <- lm(medv~., data=train)</pre>
summary(lm1)
##
## Call:
## lm(formula = medv ~ ., data = train)
##
## Residuals:
##
      Min
                1Q Median
                                3Q
                                       Max
## -13.537 -2.913 -0.546
                             1.848
                                    24.915
##
## Coefficients:
##
                 Estimate Std. Error t value Pr(>|t|)
## (Intercept) 44.900577
                            6.016980
                                       7.462 5.59e-13 ***
                            0.049892 -1.704 0.08924 .
## crim
                -0.085000
                 0.047219
                                               0.00307 **
## zn
                            0.015849
                                       2.979
## indus
                 0.038249
                            0.070942
                                       0.539 0.59008
                                       2.818 0.00507 **
## chas
                 2.724575
                            0.966685
## nox
               -19.139048
                           4.382515 -4.367 1.62e-05 ***
                                      6.145 1.98e-09 ***
## rm
                 2.949428
                            0.479982
## age
                -0.007757
                            0.015670 -0.495 0.62087
## dis
                -1.558391
                            0.224867 -6.930 1.75e-11 ***
                                       3.952 9.21e-05 ***
## rad
                0.302988
                            0.076673
                -0.012284
                            0.004206 -2.920 0.00370 **
## tax
## ptratio
                -1.008491
                            0.152951
                                      -6.594 1.40e-10 ***
                            0.003345
                 0.008717
                                       2.606 0.00951 **
## black
## lstat
                -0.555420
                            0.056482 -9.834 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 4.884 on 390 degrees of freedom
## Multiple R-squared: 0.7203, Adjusted R-squared: 0.711
## F-statistic: 77.28 on 13 and 390 DF, p-value: < 2.2e-16
```

```
pred <- predict(lm1, newdata=test)
cor(pred, test$medv)

## [1] 0.900081

rmse_lm <- sqrt(mean((pred-test$medv)^2))</pre>
```

## Using tree

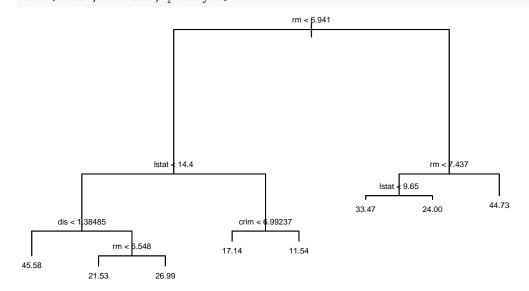
## [1] 0.8913526

Correlation was 0.8433 and rmse was 5.14.

```
tree1 <- tree(medv~., data=train)
summary(tree1)</pre>
```

```
##
## Regression tree:
## tree(formula = medv ~ ., data = train)
## Variables actually used in tree construction:
## [1] "rm"
              "lstat" "dis"
                             "crim"
## Number of terminal nodes: 8
## Residual mean deviance: 13.36 = 5292 / 396
## Distribution of residuals:
      Min. 1st Qu. Median
##
                              Mean 3rd Qu.
                                              Max.
## -22.830 -2.031 0.212
                             0.000
                                     2.265 14.670
pred <- predict(tree1, newdata=test)</pre>
cor(pred, test$medv)
```

```
rmse_tree <- sqrt(mean((pred-test$medv)^2))
plot(tree1)
text(tree1, cex=0.5, pretty=0)</pre>
```



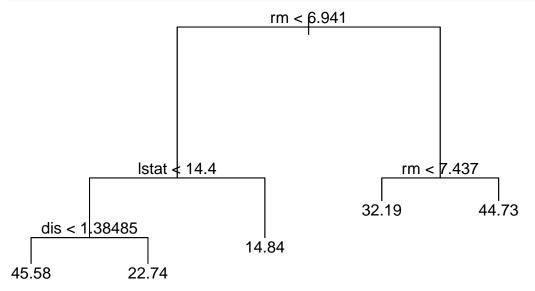
# cross validation

```
cv_tree <- cv.tree(tree1)
plot(cv_tree$size, cv_tree$dev, type='b')</pre>
```



# prune the tree

```
tree_pruned <- prune.tree(tree1, best=5)
plot(tree_pruned)
text(tree_pruned, pretty=0)</pre>
```



#### test on the pruned tree

The cor is now 0.845, very slightly above the unpruned tree but still lower than linear regression. The rmse is 5.18, very similar to the unpruned tree but higher than linear regression.

In this case pruning did not improve results on the test data but the tree is simpler and easier to interpret.

```
pred_pruned <- predict(tree_pruned, newdata=test)
cor(pred_pruned, test$medv)

## [1] 0.8456787

rmse_pruned <- sqrt(mean((pred_pruned-test$medv)^2))</pre>
```

### bagging

The importance=TRUE argument tells the algorithm to consider the importance of predictors. This effectively is the same as bagging.

```
library(randomForest)
## randomForest 4.6-12
## Type rfNews() to see new features/changes/bug fixes.
set.seed(1234)
tree_bagged <- randomForest(medv~., data=train, importance=TRUE)</pre>
tree_bagged
##
## Call:
    randomForest(formula = medv ~ ., data = train, importance = TRUE)
##
##
                  Type of random forest: regression
                        Number of trees: 500
##
## No. of variables tried at each split: 4
##
             Mean of squared residuals: 10.84628
##
##
                       % Var explained: 86.83
```

# predict on the bagged tree

Now the correlation is much higher than even linear regression and the rmse is almost half.

```
pred_bag <- predict(tree_bagged, newdata=test)
cor(pred_bag, test$medv)

## [1] 0.9619739

rmse_bag <- sqrt(mean((pred_bag-test$medv)^2))</pre>
```

## random forest

Removing argument importance=TRUE will result in a random forest.

```
tree_forest <- randomForest(medv~., data=train)
tree_forest</pre>
```

```
##
## Call:
   randomForest(formula = medv ~ ., data = train)
##
##
                   Type of random forest: regression
                         Number of trees: 500
##
## No. of variables tried at each split: 4
##
##
             Mean of squared residuals: 10.73234
##
                        % Var explained: 86.97
predict
Our results for the random forest were slightly lower than for the bagging.
pred_forest <- predict(tree_forest, newdata=test)</pre>
cor(pred_forest, test$medv)
## [1] 0.9607446
rmse_rforest <- sqrt(mean((pred_forest-test$medv)^2))</pre>
```