Decision Trees for Regression

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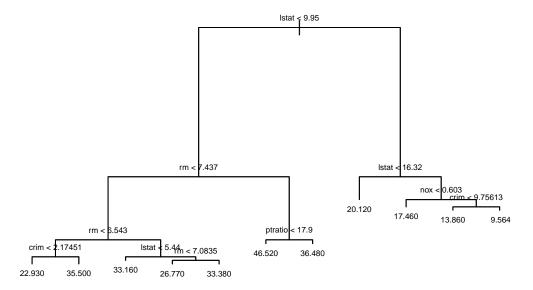
Try linear regression on Boston

We get a correlation of 0.8 and a rmse of 5.36. So, the median home value was off by about \$5,360.

```
library(tree)
library(MASS)
names (Boston)
  [1] "crim"
                  "zn"
                            "indus"
                                       "chas"
                                                 "nox"
                                                           "rm"
                                                                      "age"
                  "rad"
                                                           "lstat"
  [8] "dis"
                            "tax"
                                       "ptratio" "black"
                                                                      "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
                                     30
                                             Max
## -15.2049 -2.5360 -0.6665
                                1.8159
                                        26.6255
##
## Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)
                32.411618
                            5.713098
                                        5.673 2.74e-08 ***
## crim
                -0.110754
                            0.033940 -3.263 0.001199 **
## zn
                 0.045643
                            0.014616
                                        3.123 0.001925 **
                            0.066244
                                      -0.328 0.742828
## indus
                -0.021751
## chas
                 2.878843
                            0.925365
                                        3.111 0.002001 **
## nox
                                      -4.151 4.06e-05 ***
               -17.056324
                            4.108702
                 4.263719
                            0.469918
                                        9.073 < 2e-16 ***
                            0.014672 -0.985 0.325241
                -0.014451
## age
## dis
                -1.485880
                            0.217730
                                      -6.824 3.39e-11 ***
## rad
                            0.071664
                                       3.849 0.000139 ***
                 0.275831
                -0.012435
                            0.004041 -3.077 0.002235 **
## tax
                -0.892542
                            0.144594
                                      -6.173 1.68e-09 ***
## ptratio
                 0.009214
                            0.002961
                                        3.111 0.001999 **
## black
## 1stat
                -0.405280
                            0.056926 -7.119 5.25e-12 ***
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 4.618 on 390 degrees of freedom
## Multiple R-squared: 0.7589, Adjusted R-squared: 0.7509
## F-statistic: 94.43 on 13 and 390 DF, p-value: < 2.2e-16
```

```
pred <- predict(lm1, newdata=test)</pre>
cor_lm <- cor(pred, test$medv)</pre>
print(paste("cor = ", cor_lm))
## [1] "cor = 0.804577519382442"
rmse_lm <- sqrt(mean((pred-test$medv)^2))</pre>
print(paste("rmse = ", rmse_lm))
## [1] "rmse = 5.3663515302298"
Using tree
Correlation was 0.88 and rmse was 4.19. The tree performed better than the linear regression model.
tree1 <- tree(medv~., data=train)</pre>
summary(tree1)
##
## Regression tree:
## tree(formula = medv ~ ., data = train)
## Variables actually used in tree construction:
## [1] "lstat"
                 "rm"
                            "crim"
                                       "ptratio" "nox"
## Number of terminal nodes: 11
## Residual mean deviance: 12.91 = 5073 / 393
## Distribution of residuals:
##
        Min.
              1st Qu.
                           Median
                                        Mean
                                               3rd Qu.
                                                             Max.
## -14.58000 -1.98500 -0.06153
                                     0.00000
                                               1.79600 16.84000
pred <- predict(tree1, newdata=test)</pre>
cor_tree <- cor(pred, test$medv)</pre>
print(paste('correlation:', cor_tree))
## [1] "correlation: 0.88477699936987"
rmse_tree <- sqrt(mean((pred-test$medv)^2))</pre>
print(paste('rmse:', rmse_tree))
## [1] "rmse: 4.1984948374158"
plot(tree1)
```

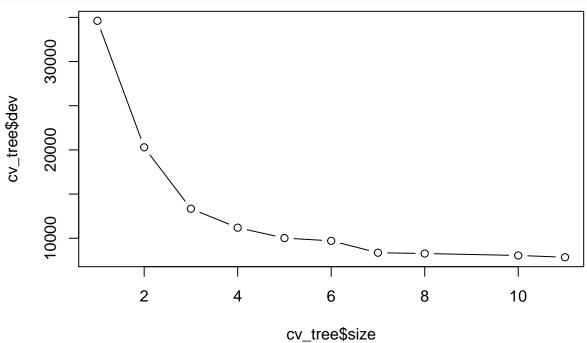
text(tree1, cex=0.5, pretty=0)



cross validation

The plot shows the deviance for various tree sizes. The full tree with 11 terminal (leaf) nodes has the smallest deviance, but it might overfit the data. At the other extreme, a tree with one node has the highest deviance. A happy medium is somewhere in the bend of the curve.

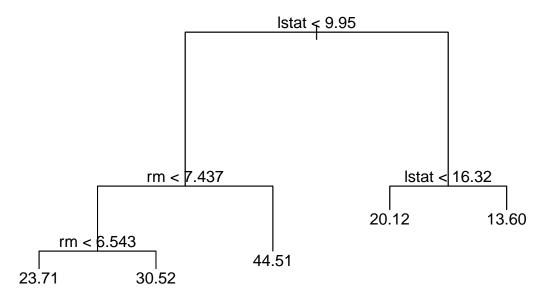
```
cv_tree <- cv.tree(tree1)
plot(cv_tree$size, cv_tree$dev, type='b')</pre>
```



prune the tree

The tree is pruned to 5 terminal nodes, and then plotted.

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



test on the pruned tree

The correlation and rmse are not as good as the unpruned tree but still slightly better than the linear regression model. 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_pruned <- cor(pred_pruned, test$medv)
rmse_pruned <- sqrt(mean((pred_pruned-test$medv)^2))
print(paste("cor of pruned tree = ", cor_pruned))
## [1] "cor of pruned tree = 0.814280213110326"
print(paste("rmse of pruned tree = ", rmse_pruned))
## [1] "rmse of pruned tree = 5.27185392365713"</pre>
```

Random Forest

The importance=TRUE argument tells the algorithm to consider the importance of predictors.

```
library(randomForest)
## randomForest 4.6-14
## Type rfNews() to see new features/changes/bug fixes.
set.seed(1234)
rf <- randomForest(medv~., data=train, importance=TRUE)</pre>
rf
##
## 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: 10.66999
                        % Var explained: 87.5
##
```

predict on the random forest

[1] "rmse: 3.49118767038579"

The random forest model got improved results over any of the previous models in this notebook.

```
pred_rf <- predict(rf, newdata=test)</pre>
cor_rf <- cor(pred_rf, test$medv)</pre>
print(paste('corr:', cor_rf))
## [1] "corr: 0.931673264971012"
rmse_rf <- sqrt(mean((pred_rf-test$medv)^2))</pre>
print(paste('rmse:', rmse_rf))
## [1] "rmse: 3.43580269934469"
bagging
Setting mtry to the number of predictors, p, will result in bagging
bag <- randomForest(medv~., data=train, mtry=13)</pre>
bag
##
## Call:
    randomForest(formula = medv ~ ., data = train, mtry = 13)
##
                   Type of random forest: regression
##
                          Number of trees: 500
## No. of variables tried at each split: 13
##
              Mean of squared residuals: 9.849697
##
##
                         % Var explained: 88.46
predict
Our results for bagging were slightly lower than for the random forest.
pred_bag <- predict(bag, newdata=test)</pre>
cor_bag <- cor(pred_bag, test$medv)</pre>
print(paste('corr:', cor_bag))
## [1] "corr: 0.924091397871912"
rmse_bag <- sqrt(mean((pred_bag-test$medv)^2))</pre>
print(paste('rmse:', rmse_bag))
```