Boosting

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Boosting

Boosting builds lots of smaller trees. Unlike random forests, each new tree in boosting tries to patch up the deficiencies of the current ensemble.

```
library(gbm)

## Warning: package 'gbm' was built under R version 3.3.3

## Loading required package: survival

## Loading required package: lattice

## Loading required package: splines

## Loading required package: parallel

## Loaded gbm 2.1.3

library(ISLR)

## Warning: package 'ISLR' was built under R version 3.3.3

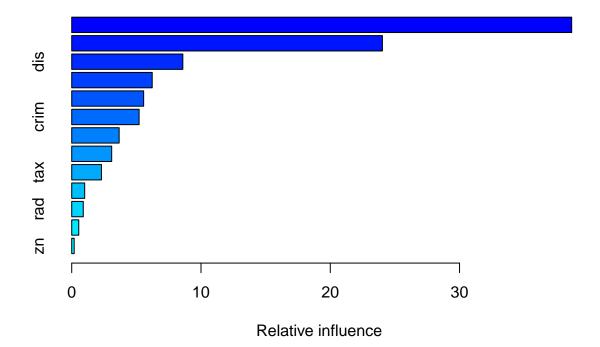
library(MASS)

## Warning: package 'MASS' was built under R version 3.3.3

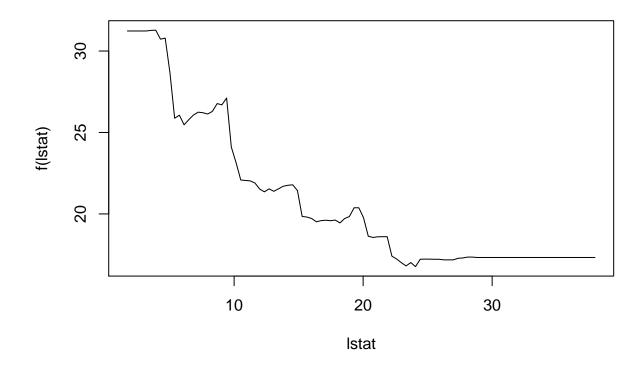
#View(Boston)

train=sample(1:nrow(Boston),300)

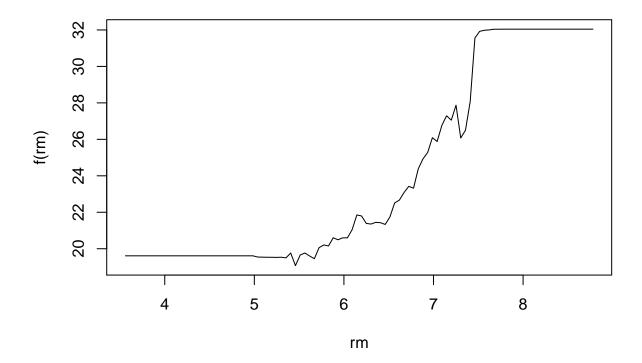
boost.boston=gbm(medv~.,data=Boston[train,],distribution="gaussian",n.trees=10000,shrinkage=0.01,intera summary(boost.boston)
```



```
##
               var
                      rel.inf
## lstat
            1stat 38.6743820
               rm 24.0341064
## rm
## dis
              dis 8.5945754
## nox
                    6.2267140
              nox
              age 5.5646177
## age
              crim 5.2125267
## crim
## black
            black 3.6692445
## ptratio ptratio
                   3.0925433
## tax
              tax 2.2994252
## indus
             indus 1.0031019
## rad
                    0.8944638
              rad
## chas
              chas
                    0.5448754
## zn
                zn 0.1894238
plot(boost.boston,i="lstat")
```



plot(boost.boston,i="rm")



Lets make a prediction on the test set. With boosting, the number of trees is a tuning parameter, and if we have too many we can overfit. So we should use cross-validation to select the number of trees. We will leave this as an exercise. Instead, we will compute the test error as a function of the number of trees, and make a plot.

test.err=double(13)

```
n.trees=seq(from=100,to=10000,by=100)
predmat=predict(boost.boston,newdata=Boston[-train,],n.trees=n.trees)
dim(predmat)

## [1] 206 100
berr=with(Boston[-train,],apply( (predmat-medv)^2,2,mean))
plot(n.trees,berr,pch=19,ylab="Mean Squared Error", xlab="# Trees",main="Boosting Test Error")
abline(h=min(test.err),col="red")
```

Boosting Test Error

