```
# boosting.r
RNGkind(sample.kind = 'Rounding')
## Warning in RNGkind(sample.kind = "Rounding"): non-uniform 'Rounding' sampler
## used
library(MASS)
                   # Boston dataset
library(gbm)
                   # gbm()
## Loaded gbm 2.1.5
dim(Boston)
## [1] 506 14
# response is medu
# p=13 predictors
n = nrow(Boston)
set.seed(1)
train = sample(1:n,n/2) # 253 train rows
# boosted regression trees
set.seed(1)
boost1=gbm(medv~.,data=Boston[train,],distribution="gaussian",
           n.trees=5000,interaction.depth=4)
boost1
## gbm(formula = medv ~ ., distribution = "gaussian", data = Boston[train,
       ], n.trees = 5000, interaction.depth = 4)
## A gradient boosted model with gaussian loss function.
## 5000 iterations were performed.
## There were 13 predictors of which 13 had non-zero influence.
# for categorical response use distribution="bernoulli"
# depth of each tree limited to 4 splits
# 5000 trees (default is 100 trees)
# interaction.depth is d
names (boost1)
## [1] "initF"
                            "fit"
                                                 "train.error"
## [4] "valid.error"
                            "oobag.improve"
                                                 "trees"
## [7] "c.splits"
                            "bag.fraction"
                                                 "distribution"
## [10] "interaction.depth" "n.minobsinnode"
                                                 "num.classes"
                                                 "train.fraction"
## [13] "n.trees"
                            "nTrain"
## [16] "response.name"
                            "shrinkage"
                                                 "var.levels"
                                                 "var.type"
## [19] "var.monotone"
                            "var.names"
## [22] "verbose"
                            "data"
                                                 "Terms"
## [25] "cv.folds"
                            "call"
                                                 "m"
# lambda -default value
boost1$shrinkage
```

importance of predictors summary(boost1);

```
##
                    rel.inf
             var
## lstat lstat 37.0661275
           rm 25.3533123
dis 11.7903016
crim 8.0388750
## rm
## dis
## crim
## black black 4.2531659
## nox
            nox 3.5058570
            age 3.4868724
## age
## ptratio ptratio 2.2500385
## indus indus 1.7725070
## tax
            tax 1.1836592
## chas
           chas 0.7441319
## rad
            rad 0.4274311
## zn
             zn 0.1277206
grid()
```

