Boosting and Random Forests

ACM

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In this example we'll use some data on the number of carseats sold at 400 different stores.

```
library(printr)
library(randomForest)
library(tidyverse)
library(MASS)
library(gbm)
library(tree)
library(ISLR)
library(rpart)
```

Random Forests

```
?Carseats
```

```
Sales of Child Car Seats

Description:

     A simulated data set containing sales of child car seats at 400
     different stores.

Usage:

     Carseats
```

```
Carseats <- Carseats %>% mutate(High = factor(1*I(Sales > 8)) )
head(Carseats)
```

Sales	CompPrice	Income	Advertising	Population	Price	ShelveLoc	Age	Education	Urban	US	High
9.50	138	73	11	276	120	Bad	42	17	Yes	Yes	1
11.22	111	48	16	260	83	Good	65	10	Yes	Yes	1
10.06	113	35	10	269	80	Medium	59	12	Yes	Yes	1
7.40	117	100	4	466	97	Medium	55	14	Yes	Yes	0
4.15	141	64	3	340	128	Bad	38	13	Yes	No	0
10.81	124	113	13	501	72	Bad	78	16	No	Yes	1

```
?randomForest
```

```
Classification and Regression with Random Forest

Description:
```

'randomForest' implements Breiman's random forest algorithm (based on Breiman and Cutler's original Fortran code) for classification and regression. It can also be used in unsupervised mode for assessing proximities among data points.

Usage:

```
     ## S3 method for class 'formula'
     randomForest(formula, data=NULL, ..., subset, na.action=na.fail)
     ## Default S3 method:
     randomForest(x, y=NULL,  xtest=NULL, ytest=NULL, ntree=500,
                  mtry=if (!is.null(y) && !is.factor(y))
                  max(floor(ncol(x)/3), 1) else floor(sqrt(ncol(x))),
                  replace=TRUE, classwt=NULL, cutoff, strata,
                  sampsize = if (replace) nrow(x) else ceiling(.632*nrow(x)),
                  nodesize = if (!is.null(y) && !is.factor(y)) 5 else 1,
                  maxnodes = NULL,
                  importance=FALSE, localImp=FALSE, nPerm=1,
                  proximity, oob.prox=proximity,
                  norm.votes=TRUE, do.trace=FALSE,
                  keep.forest=!is.null(y) && is.null(xtest), corr.bias=FALSE,
                  keep.inbag=FALSE, ...)
     ## S3 method for class 'randomForest'
     print(x, ...)
```

Arguments:

```
    data: an optional data frame containing the variables in the model.
          By default the variables are taken from the environment which
          'randomForest' is called from.

  subset: an index vector indicating which rows should be used.  (NOTE:
          If given, this argument must be named.)

na.action: A function to specify the action to be taken if NAs are
          found.  (NOTE: If given, this argument must be named.)

x, formula: a data frame or a matrix of predictors, or a formula
          describing the model to be fitted (for the 'print' method, an
          'randomForest' object).

       y: A response vector.  If a factor, classification is assumed,
          otherwise regression is assumed.  If omitted, 'randomForest'
          will run in unsupervised mode.

   xtest: a data frame or matrix (like 'x') containing predictors for
          the test set.

   ytest: response for the test set.

   ntree: Number of trees to grow.  This should not be set to too small
          a number, to ensure that every input row gets predicted at
          least a few times.
    mtry: Number of variables randomly sampled as candidates at each
          split.  Note that the default values are different for
          classification (sqrt(p) where p is number of variables in
          'x') and regression (p/3)

 replace: Should sampling of cases be done with or without replacement?

 classwt: Priors of the classes.  Need not add up to one.  Ignored for
          regression.

  cutoff: (Classification only) A vector of length equal to number of
          classes.  The `winning' class for an observation is the one
          with the maximum ratio of proportion of votes to cutoff.
          Default is 1/k where k is the number of classes (i.e.,
          majority vote wins).

  strata: A (factor) variable that is used for stratified sampling.

sampsize: Size(s) of sample to draw.  For classification, if sampsize
          is a vector of the length the number of strata, then sampling
          is stratified by strata, and the elements of sampsize
          indicate the numbers to be drawn from the strata.

nodesize: Minimum size of terminal nodes.  Setting this number larger
          causes smaller trees to be grown (and thus take less time).
          Note that the default values are different for classification
          (1) and regression (5).

maxnodes: Maximum number of terminal nodes trees in the forest can
          have.  If not given, trees are grown to the maximum possible
          (subject to limits by 'nodesize').  If set larger than
          maximum possible, a warning is issued.

importance: Should importance of predictors be assessed?

localImp: Should casewise importance measure be computed?  (Setting
          this to 'TRUE' will override 'importance'.)

   nPerm: Number of times the OOB data are permuted per tree for
          assessing variable importance.  Number larger than 1 gives
          slightly more stable estimate, but not very effective.
          Currently only implemented for regression.

proximity: Should proximity measure among the rows be calculated?

oob.prox: Should proximity be calculated only on ``out-of-bag'' data?

norm.votes: If 'TRUE' (default), the final result of votes are
          expressed as fractions.  If 'FALSE', raw vote counts are
          returned (useful for combining results from different runs).
          Ignored for regression.

do.trace: If set to 'TRUE', give a more verbose output as
```

```
          'randomForest' is run.  If set to some integer, then running
          output is printed for every 'do.trace' trees.

keep.forest: If set to 'FALSE', the forest will not be retained in the
          output object.  If 'xtest' is given, defaults to 'FALSE'.

corr.bias: perform bias correction for regression?  Note: Experimental.
          Use at your own risk.

keep.inbag: Should an 'n' by 'ntree' matrix be returned that keeps
          track of which samples are ``in-bag'' in which trees (but not
          how many times, if sampling with replacement)

     ...: optional parameters to be passed to the low level function
          'randomForest.default'.
```

```r
set.seed(2)
train=sample(1:nrow(Carseats), 267)

num_vars <- 1:10
tst.loss <- NULL
for(m in num_vars){
  set.seed(2)
  RF_Carseats=randomForest(High~.-Sales, data =
                            Carseats,subset=train,ntree=1000,mtry=m)
  yhat.bag = predict(RF_Carseats,newdata=Carseats[-train,])
  tst.loss <- c(tst.loss,mean(yhat.bag==Carseats$High[-train]))
}
data.frame(num_vars,tst.loss)
```

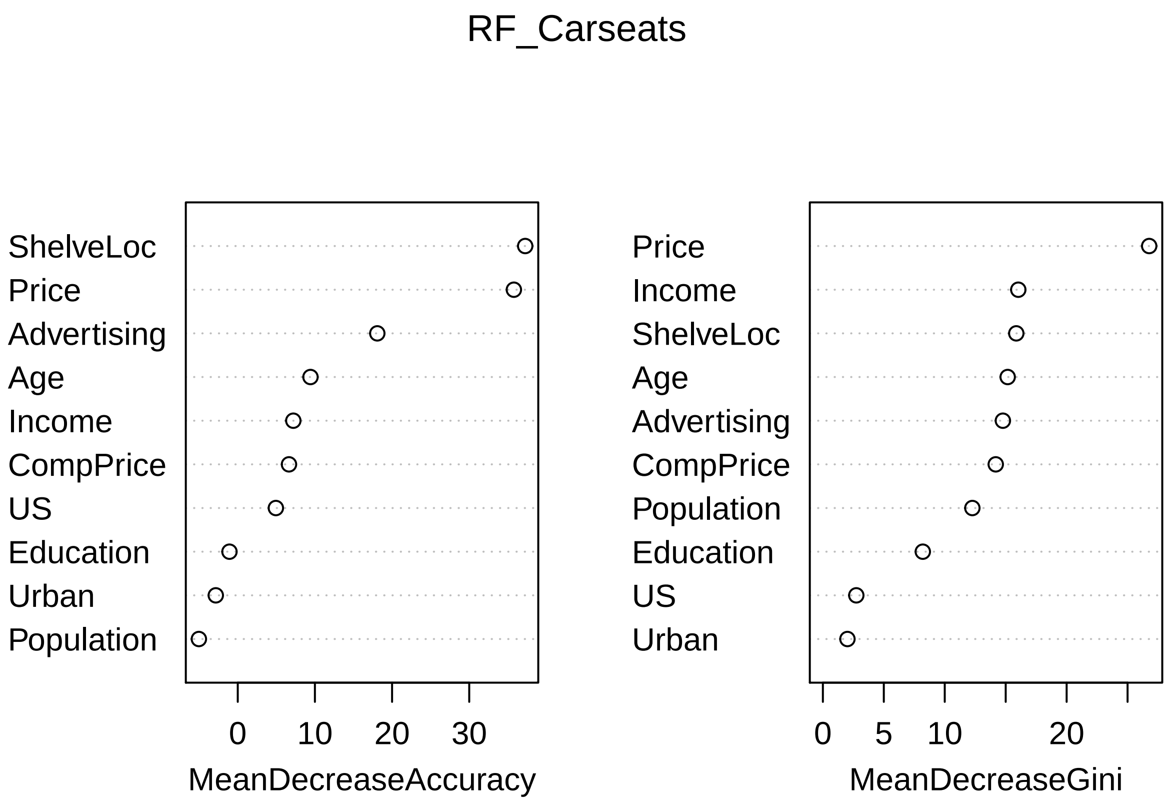
num_vars	tst.loss
1	0.8421053
2	0.8270677
3	0.8421053
4	0.8345865
5	0.8496241
6	0.8646617
7	0.8571429
8	0.8571429
9	0.8796992
10	0.8872180

```r
M <- num_vars[which.min(tst.loss)]

RF_Carseats=randomForest(High~.-Sales,data=Carseats,subset=train,
                         ntree = 1000, mtry=M, importance=TRUE)

importance(RF_Carseats)
```

	0	1	MeanDecreaseAccuracy	MeanDecreaseGini
CompPrice	5.9860144	3.056744	6.640112	14.183728
Income	4.5176511	6.281224	7.200431	16.032777
Advertising	11.0294448	14.988769	18.085826	14.768819

	0	1	MeanDecreaseAccuracy	MeanDecreaseGini
Population	-2.4329274	-4.892453	-5.038674	12.263879
Price	28.1697563	25.842802	35.785353	26.774985
ShelveLoc	29.6632045	29.063534	37.256053	15.868877
Age	6.6661633	7.154780	9.425158	15.163227
Education	0.0413564	-1.593005	-1.073007	8.198613
Urban	-1.1242089	-3.067516	-2.846262	2.015437
US	2.8817603	3.602869	4.941539	2.742976

```
varImpPlot(RF_Carseats)
```



Fitting Regression Trees

Here we'll fit regression trees to the Boston housing dataset.

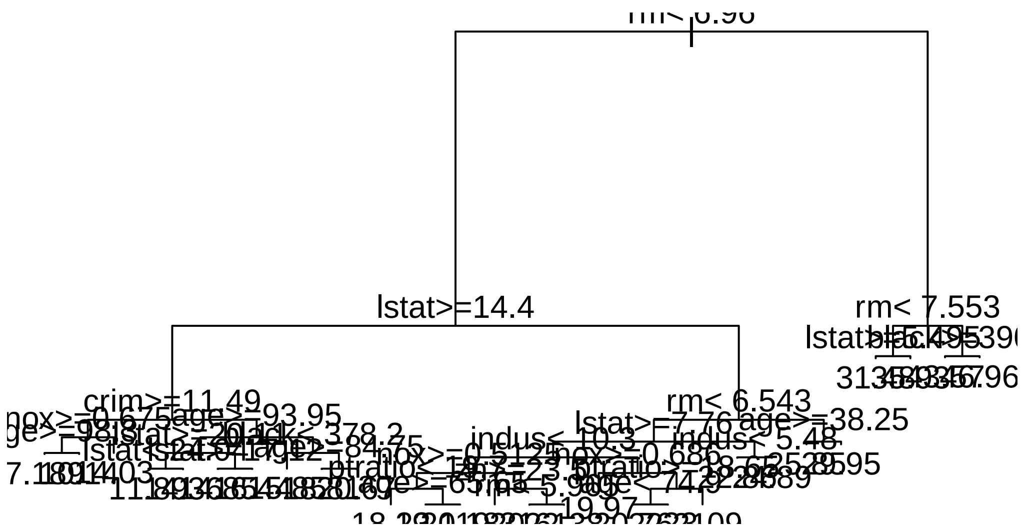
```
?Boston
```

```
Housing Values in Suburbs of Boston

Description:

     The 'Boston' data frame has 506 rows and 14 columns.

Usage:

     Boston
```

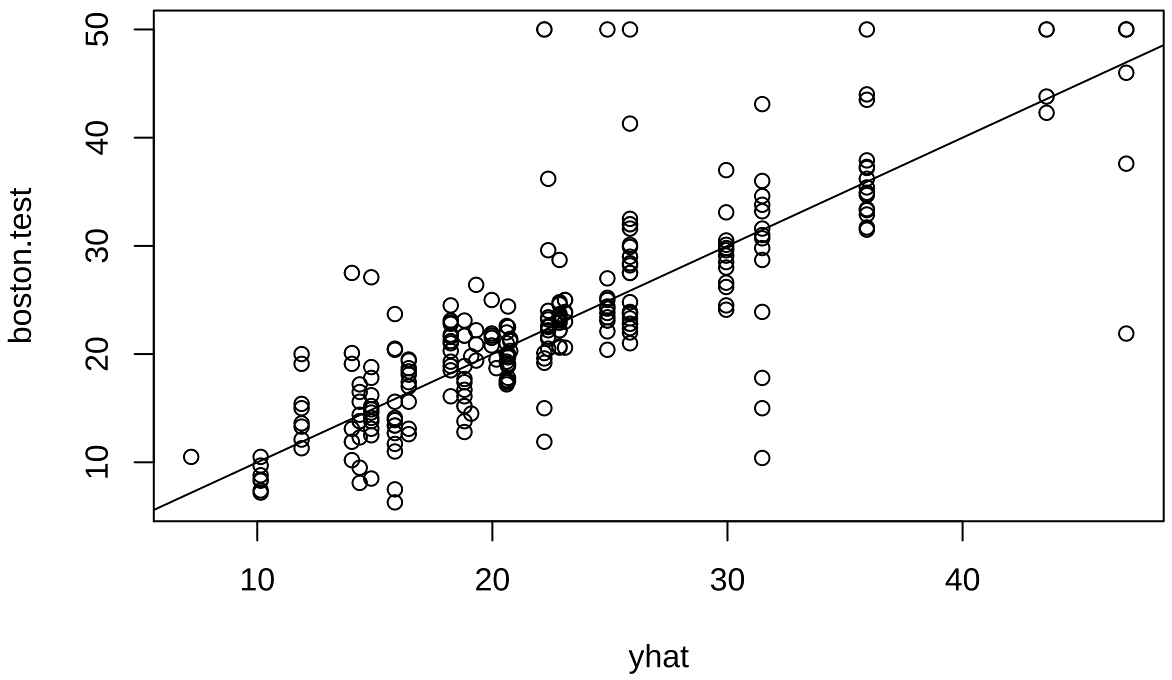
```r
set.seed(1)
train = sample(1:nrow(Boston), nrow(Boston)/2)

tree.boston <- rpart(medv~., data = Boston[train,], method="anova",
                 control = list(cp = 0,xval=10, minsplit = 0))
printcp(tree.boston)
```

```
Regression tree:
rpart(formula = medv ~ ., data = Boston[train, ], method = "anova",
    control = list(cp = 0, xval = 10, minsplit = 0))

Variables actually used in tree construction:
[1] age     black   crim    indus   lstat   nox     ptratio rm      zn

Root node error: 19448/253 = 76.869

n= 253

           CP nsplit rel error  xerror     xstd
1  0.55145333      0  1.000000 1.00246 0.126271
2  0.17610053      1  0.448547 0.48456 0.042763
3  0.05689532      2  0.272446 0.30320 0.030609
4  0.04093613      3  0.215551 0.27604 0.029893
5  0.03276814      4  0.174615 0.23875 0.028484
6  0.01048773      5  0.141847 0.21692 0.027290
7  0.00985230      6  0.131359 0.21760 0.027319
8  0.00817667      7  0.121507 0.21208 0.027800
9  0.00588100      8  0.113330 0.19448 0.025474
10 0.00512910      9  0.107449 0.18930 0.025913
11 0.00401073     10  0.102320 0.19029 0.026063
12 0.00224451     11  0.098309 0.19649 0.028806
13 0.00220749     12  0.096065 0.20285 0.028590
14 0.00219850     13  0.093857 0.20084 0.028143
15 0.00202124     14  0.091659 0.20094 0.028155
16 0.00197575     15  0.089637 0.20092 0.028214
17 0.00172550     16  0.087662 0.19970 0.028200
18 0.00112897     17  0.085936 0.19861 0.028171
19 0.00109924     18  0.084807 0.19841 0.028167
20 0.00101740     19  0.083708 0.19775 0.028115
21 0.00096903     20  0.082690 0.20045 0.028145
22 0.00082276     21  0.081721 0.19985 0.028141
23 0.00074870     22  0.080899 0.20096 0.028145
24 0.00055812     23  0.080150 0.20248 0.028171
25 0.00053719     24  0.079592 0.20440 0.028255
26 0.00049705     25  0.079055 0.20435 0.028256
27 0.00023769     26  0.078558 0.20507 0.028271
28 0.00000000     27  0.078320 0.20424 0.028223
```

```r
plot(tree.boston)
text(tree.boston,pretty=1)
```



```r
tree.boston.cp <- as.data.frame(tree.boston$cptable)
cp <- tree.boston.cp$CP[which.min(tree.boston.cp$xerror)][1]
prune.boston=prune(tree.boston,cp=cp)

yhat=predict(tree.boston,newdata=Boston[-train,])
boston.test=Boston[-train,"medv"]
plot(yhat,boston.test)
abline(0,1)
```



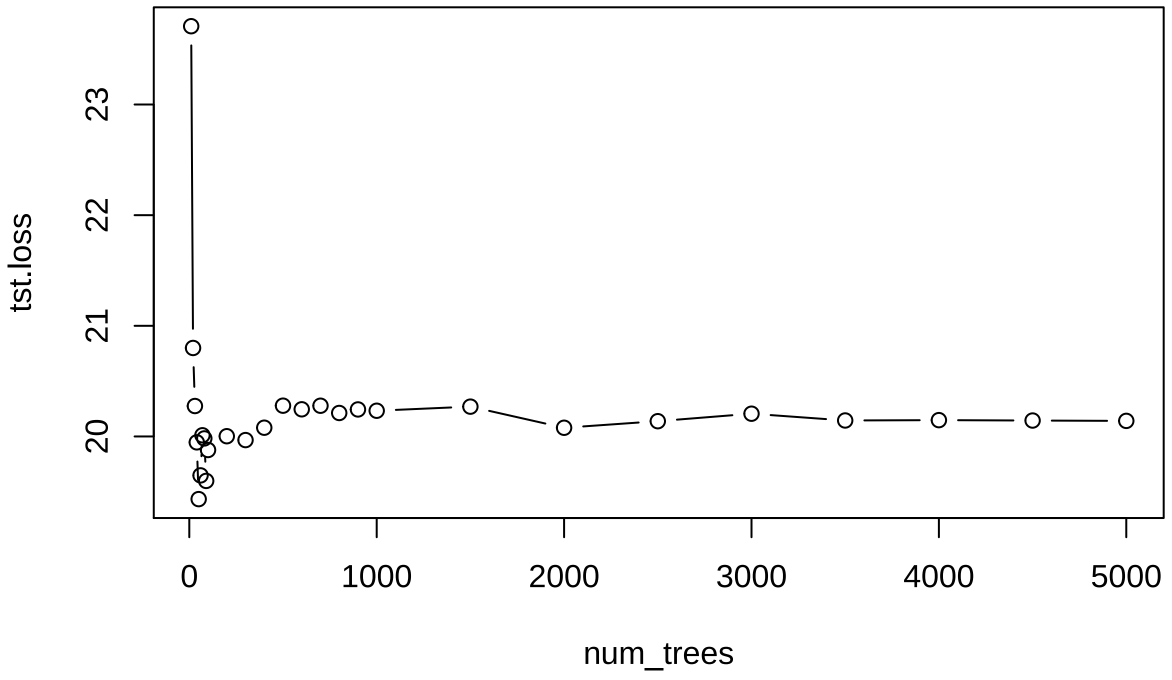
```r
mean((yhat-boston.test)^2)
```

```
[1] 31.70559
```

```r
num_vars <- 1:10
tst.loss <- NULL
for(m in num_vars){
set.seed(1)
bag.boston=randomForest(medv~.,data=Boston, subset = train,
                        mtry = m, ntree = 1000)
yhat.bag = predict(bag.boston,newdata=Boston[-train,])
tst.loss <- c(tst.loss,mean((yhat.bag-Boston$medv[-train])^2))
}
data.frame(num_vars,tst.loss)
```

num_vars	tst.loss
1	25.84646
2	19.57372
3	18.58931
4	18.72469
5	19.03545
6	19.37815
7	20.23230
8	20.77523
9	21.37730
10	22.16682

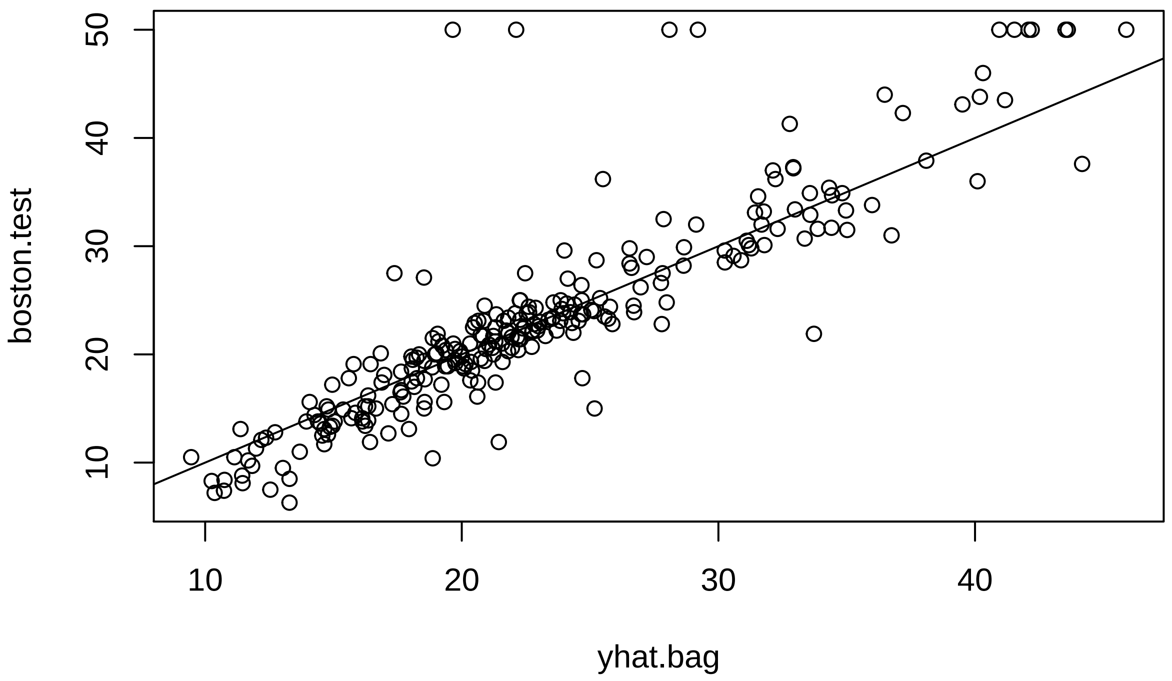
```
M <- num_vars[ which.min(tst.loss)]

num_trees <- c(seq(10,90,10), seq(100,1000,100), seq(1500, 5000, 500))
tst.loss <- NULL
for(m in num_trees){
set.seed(1)
bag.boston=randomForest(medv~.,data=Boston,subset=train,mtry=7,ntree=m)
yhat.bag = predict(bag.boston,newdata=Boston[-train,])
tst.loss <- c(tst.loss,mean((yhat.bag-Boston$medv[-train])^2))
}
plot(num_trees,tst.loss,type = "b")
```



```
T <- num_trees[ which.min(tst.loss)]


set.seed(1)
bag.boston=randomForest(medv~.,data=Boston,subset=train,
                        mtry=M, ntree=T, importance=TRUE)
bag.boston
```

```
Call:
 randomForest(formula = medv ~ ., data = Boston, mtry = M, ntree = T,      importance = TRUE, subset = 
               Type of random forest: regression
                     Number of trees: 50
No. of variables tried at each split: 3

          Mean of squared residuals: 11.91747
                    % Var explained: 84.5
```

```
yhat.bag = predict(bag.boston,newdata=Boston[-train,])
plot(yhat.bag, boston.test)
abline(0,1)
```



```
mean((yhat.bag-Boston$medv[-train])^2)
```

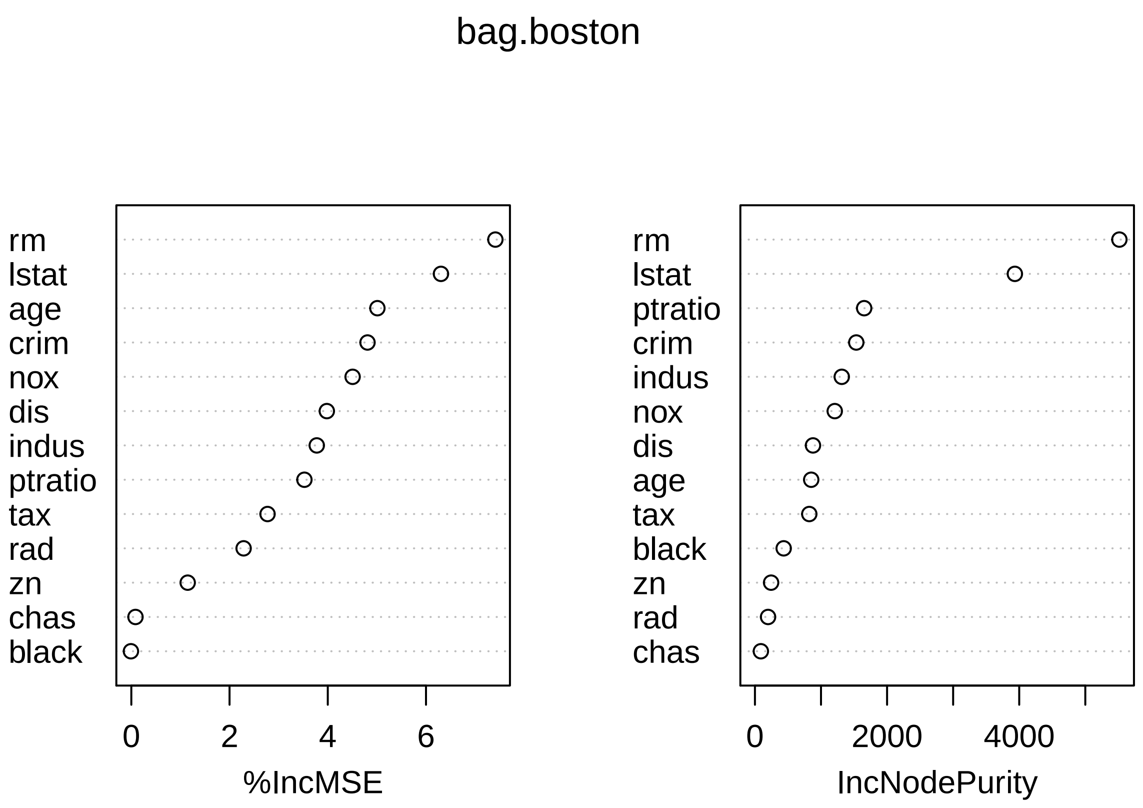
```
[1] 19.87878
```

```
importance(bag.boston)
```

	%IncMSE	IncNodePurity
crim	4.8090615	1533.67818
zn	1.1476379	244.71330
indus	3.7756917	1314.17840
chas	0.0845674	89.61804
nox	4.5055961	1208.35732

	%IncMSE	IncNodePurity
rm	7.4123996	5516.08528
age	5.0102894	851.67309
dis	3.9807567	878.43951
rad	2.2865442	198.88599
tax	2.7738072	822.75109
ptratio	3.5242156	1653.30955
black	-0.0083146	435.18696
lstat	6.3044846	3934.15080

```
varImpPlot(bag.boston)
```



Now let's take a look at some other RF's with different tuning parameters

```
bag.boston=randomForest(medv~.,data=Boston,subset=train,mtry=13,ntree=1000)
yhat.bag = predict(bag.boston,newdata=Boston[-train,])
mean((yhat.bag-Boston$medv[-train])^2)
```

```
## [1] 23.57299
```

Boosting

```
?gbm
```

```
Generalized Boosted Regression Modeling (GBM)

Description:
```

Fits generalized boosted regression models. For technical details, see the vignette: 'utils::browseVignettes("gbm")'.

Usage:

```
     gbm(
       formula = formula(data),
       distribution = "bernoulli",
       data = list(),
       weights,
       var.monotone = NULL,
       n.trees = 100,
       interaction.depth = 1,
       n.minobsinnode = 10,
       shrinkage = 0.1,
       bag.fraction = 0.5,
       train.fraction = 1,
       cv.folds = 0,
       keep.data = TRUE,
       verbose = FALSE,
       class.stratify.cv = NULL,
       n.cores = NULL
     )
```

Arguments:

formula: A symbolic description of the model to be fit. The formula may include an offset term (e.g. y~offset(n)+x). If 'keep.data = FALSE' in the initial call to 'gbm' then it is the user's responsibility to resupply the offset to 'gbm.more'.

distribution: Either a character string specifying the name of the distribution to use or a list with a component 'name' specifying the distribution and any additional parameters needed. If not specified, 'gbm' will try to guess: if the response has only 2 unique values, bernoulli is assumed; otherwise, if the response is a factor, multinomial is assumed; otherwise, if the response has class '"Surv"', coxph is assumed; otherwise, gaussian is assumed.

Currently available options are '"gaussian"' (squared error), '"laplace"' (absolute loss), '"tdist"' (t-distribution loss), '"bernoulli"' (logistic regression for 0-1 outcomes), '"huberized"' (huberized hinge loss for 0-1 outcomes), classes), '"adaboost"' (the AdaBoost exponential loss for 0-1 outcomes), '"poisson"' (count outcomes), '"coxph"' (right censored observations), '"quantile"', or '"pairwise"' (ranking measure using the LambdaMart algorithm).

If quantile regression is specified, 'distribution' must be a list of the form 'list(name = "quantile", alpha = 0.25)' where 'alpha' is the quantile to estimate. The current

version's quantile regression method does not handle
non-constant weights and will stop.

If '"tdist"' is specified, the default degrees of freedom is
4 and this can be controlled by specifying 'distribution =
list(name = "tdist", df = DF)' where 'DF' is your chosen
degrees of freedom.

If "pairwise" regression is specified, 'distribution' must be
a list of the form
'list(name="pairwise",group=...,metric=...,max.rank=...)'
('metric' and 'max.rank' are optional, see below). 'group' is
a character vector with the column names of 'data' that
jointly indicate the group an instance belongs to (typically
a query in Information Retrieval applications). For training,
only pairs of instances from the same group and with
different target labels can be considered. 'metric' is the IR
measure to use, one of

list("conc") Fraction of concordant pairs; for binary labels,
    this is equivalent to the Area under the ROC Curve

: Fraction of concordant pairs; for binary labels, this is
    equivalent to the Area under the ROC Curve

list("mrr") Mean reciprocal rank of the highest-ranked
    positive instance

: Mean reciprocal rank of the highest-ranked positive
    instance

list("map") Mean average precision, a generalization of 'mrr'
    to multiple positive instances

: Mean average precision, a generalization of 'mrr' to
    multiple positive instances

list("ndcg:") Normalized discounted cumulative gain. The
    score is the weighted sum (DCG) of the user-supplied
    target values, weighted by log(rank+1), and normalized to
    the maximum achievable value. This is the default if the
    user did not specify a metric.

'ndcg' and 'conc' allow arbitrary target values, while binary
targets 0,1 are expected for 'map' and 'mrr'. For 'ndcg' and
'mrr', a cut-off can be chosen using a positive integer
parameter 'max.rank'. If left unspecified, all ranks are
taken into account.

Note that splitting of instances into training and validation
sets follows group boundaries and therefore only approximates
the specified 'train.fraction' ratio (the same applies to
cross-validation folds). Internally, queries are randomly
shuffled before training, to avoid bias.

```
          Weights can be used in conjunction with pairwise metrics,
          however it is assumed that they are constant for instances
          from the same group.

          For details and background on the algorithm, see e.g. Burges
          (2010).

    data: an optional data frame containing the variables in the model.
          By default the variables are taken from
          'environment(formula)', typically the environment from which
          'gbm' is called. If 'keep.data=TRUE' in the initial call to
          'gbm' then 'gbm' stores a copy with the object. If
          'keep.data=FALSE' then subsequent calls to 'gbm.more' must
          resupply the same dataset. It becomes the user's
          responsibility to resupply the same data at this point.

 weights: an optional vector of weights to be used in the fitting
          process. Must be positive but do not need to be normalized.
          If 'keep.data=FALSE' in the initial call to 'gbm' then it is
          the user's responsibility to resupply the weights to
          'gbm.more'.

var.monotone: an optional vector, the same length as the number of
          predictors, indicating which variables have a monotone
          increasing (+1), decreasing (-1), or arbitrary (0)
          relationship with the outcome.

 n.trees: Integer specifying the total number of trees to fit. This is
          equivalent to the number of iterations and the number of
          basis functions in the additive expansion. Default is 100.

interaction.depth: Integer specifying the maximum depth of each tree
          (i.e., the highest level of variable interactions allowed). A
          value of 1 implies an additive model, a value of 2 implies a
          model with up to 2-way interactions, etc. Default is 1.

n.minobsinnode: Integer specifying the minimum number of observations
          in the terminal nodes of the trees. Note that this is the
          actual number of observations, not the total weight.

shrinkage: a shrinkage parameter applied to each tree in the expansion.
          Also known as the learning rate or step-size reduction; 0.001
          to 0.1 usually work, but a smaller learning rate typically
          requires more trees. Default is 0.1.

bag.fraction: the fraction of the training set observations randomly
          selected to propose the next tree in the expansion. This
          introduces randomnesses into the model fit. If 'bag.fraction'
          < 1 then running the same model twice will result in similar
          but different fits. 'gbm' uses the R random number generator
          so 'set.seed' can ensure that the model can be reconstructed.
          Preferably, the user can save the returned 'gbm.object' using
          'save'. Default is 0.5.
```

train.fraction: The first 'train.fraction * nrows(data)' observations are used to fit the 'gbm' and the remainder are used for computing out-of-sample estimates of the loss function.

cv.folds: Number of cross-validation folds to perform. If 'cv.folds'>1 then 'gbm', in addition to the usual fit, will perform a cross-validation, calculate an estimate of generalization error returned in 'cv.error'.

keep.data: a logical variable indicating whether to keep the data and an index of the data stored with the object. Keeping the data and index makes subsequent calls to 'gbm.more' faster at the cost of storing an extra copy of the dataset.

verbose: Logical indicating whether or not to print out progress and performance indicators ('TRUE'). If this option is left unspecified for 'gbm.more', then it uses 'verbose' from 'object'. Default is 'FALSE'.

class.stratify.cv: Logical indicating whether or not the cross-validation should be stratified by class. Defaults to 'TRUE' for 'distribution = "multinomial"' and is only implemented for '"multinomial"' and '"bernoulli"'. The purpose of stratifying the cross-validation is to help avoiding situations in which training sets do not contain all classes.

n.cores: The number of CPU cores to use. The cross-validation loop will attempt to send different CV folds off to different cores. If 'n.cores' is not specified by the user, it is guessed using the 'detectCores' function in the 'parallel' package. Note that the documentation for 'detectCores' makes clear that it is not failsafe and could return a spurious number of available cores.

Details:

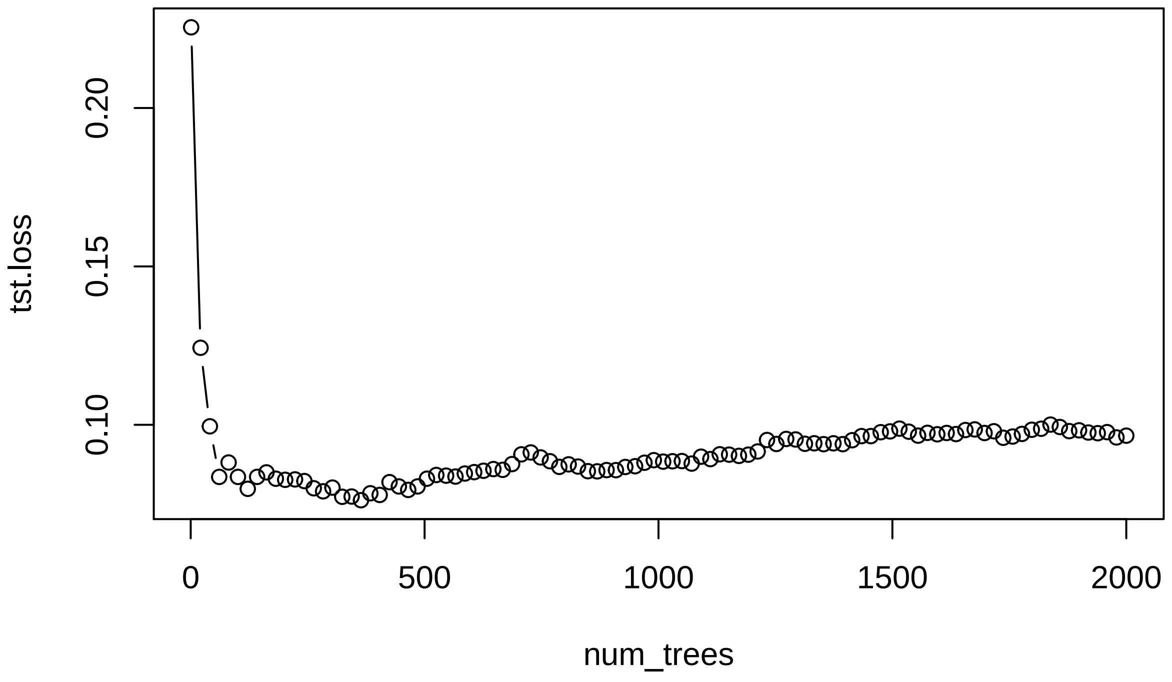
'gbm.fit' provides the link between R and the C++ gbm engine. 'gbm' is a front-end to 'gbm.fit' that uses the familiar R modeling formulas. However, 'model.frame' is very slow if there are many predictor variables. For power-users with many variables use 'gbm.fit'. For general practice 'gbm' is preferable.

This package implements the generalized boosted modeling framework. Boosting is the process of iteratively adding basis functions in a greedy fashion so that each additional basis function further reduces the selected loss function. This implementation closely follows Friedman's Gradient Boosting Machine (Friedman, 2001).

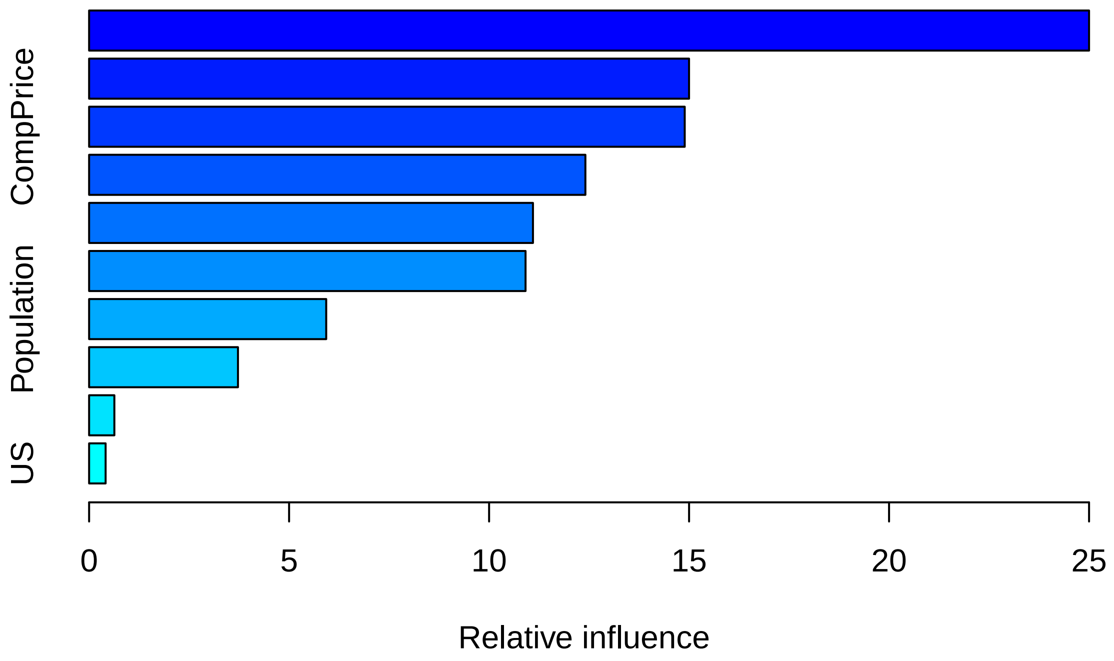
In addition to many of the features documented in the Gradient Boosting Machine, 'gbm' offers additional features including the out-of-bag estimator for the optimal number of iterations, the

```
ability to store and manipulate the resulting 'gbm' object, and a
variety of other loss functions that had not previously had
associated boosting algorithms, including the Cox partial
likelihood for censored data, the poisson likelihood for count
outcomes, and a gradient boosting implementation to minimize the
AdaBoost exponential loss function.
```

```r
set.seed(2)
train=sample(1:nrow(Carseats), 267)
set.seed(1)

Carseats <- Carseats %>% mutate(High = 1*I(Sales > 8) )
num_trees <- floor(seq(1,2000,length.out = 100))
tst.loss <- NULL
boost.carseats=gbm(High~.-Sales,data=Carseats[train,], distribution = "bernoulli",
                   n.trees = 10000, interaction.depth = 4)
for(m in num_trees){
yhat.bag = predict(boost.carseats, newdata=Carseats[-train,],
                   n.trees = m, type = "response")
tst.loss <- c(tst.loss,mean((yhat.bag-Carseats$High[-train])^2))
}
plot(num_trees,tst.loss,type = "b")
```

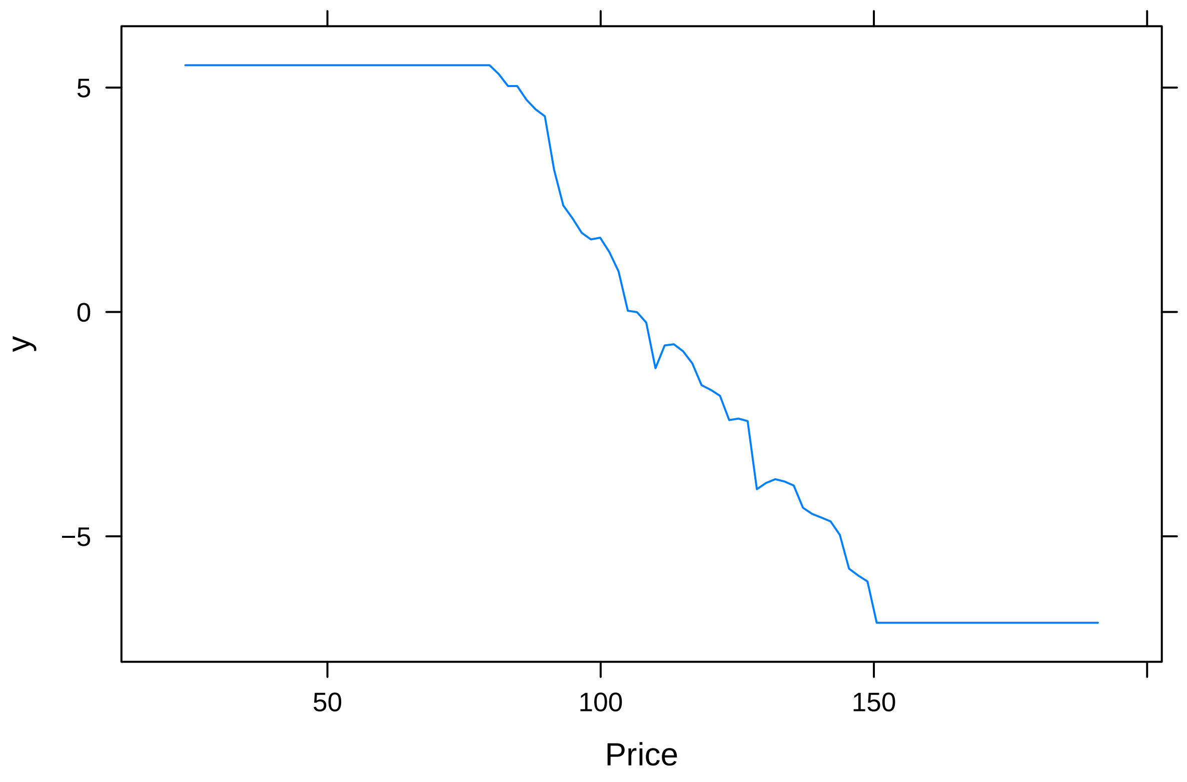


```r
M <- num_trees[which.min(tst.loss)]

boost.carseats=gbm(High ~.-Sales, data = Carseats[train,],
                   distribution = "bernoulli", n.trees=M,
                   interaction.depth=4)
summary(boost.carseats)
```

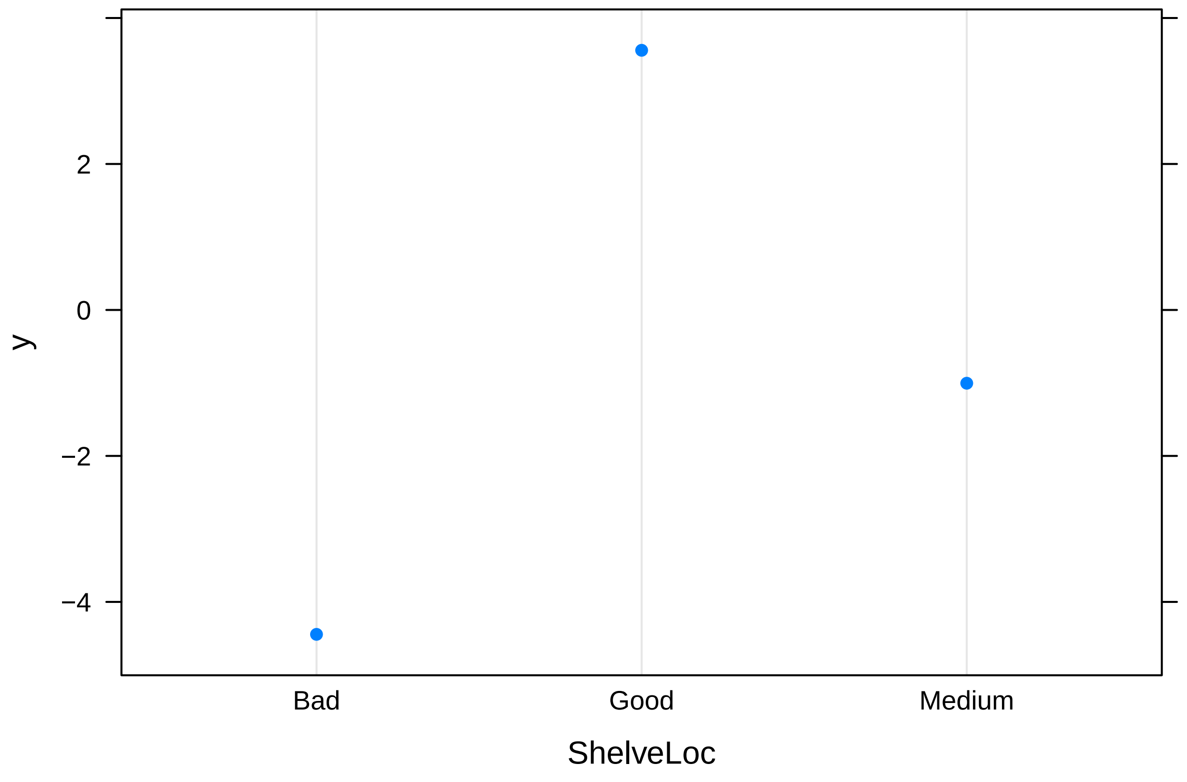


	var	rel.inf
Price	Price	25.0002044
ShelveLoc	ShelveLoc	14.9993402
CompPrice	CompPrice	14.8914526
Income	Income	12.4078644
Age	Age	11.0967828
Advertising	Advertising	10.9114654
Population	Population	5.9276064
Education	Education	3.7214651
Urban	Urban	0.6312512
US	US	0.4125676

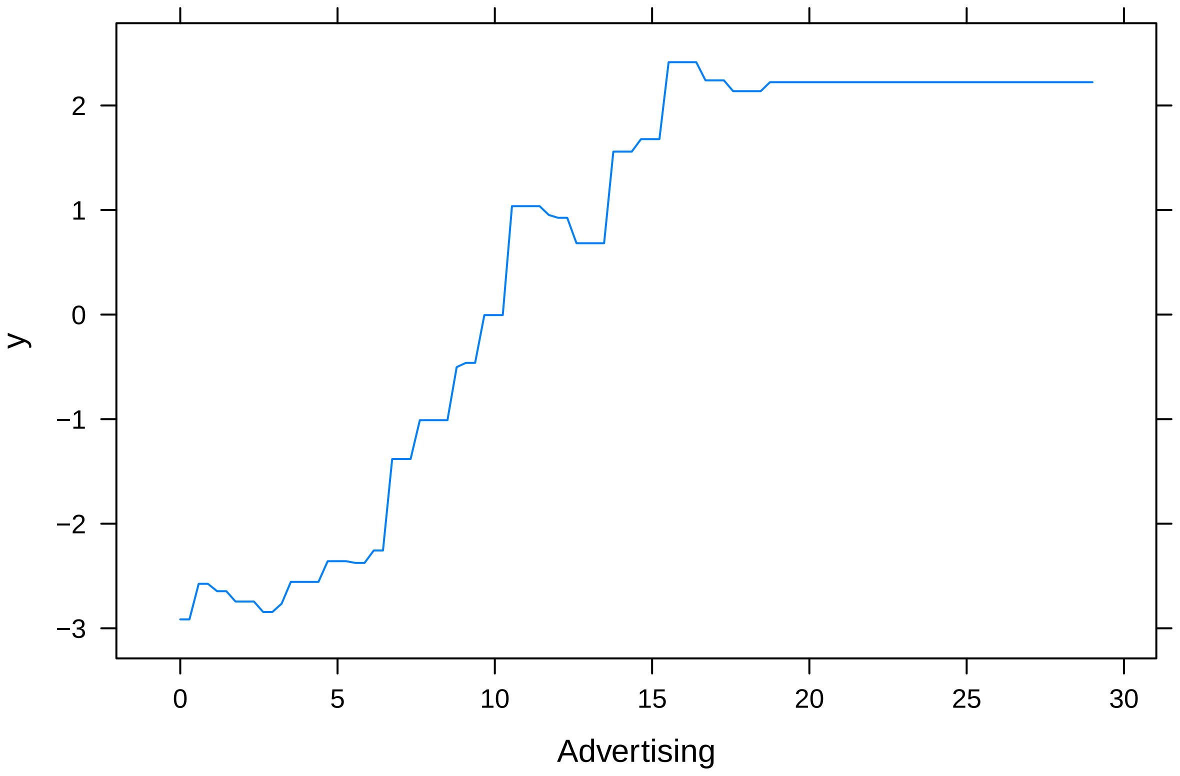
```r
par(mfrow=c(2,2))
plot(boost.carseats,i="Price")
```



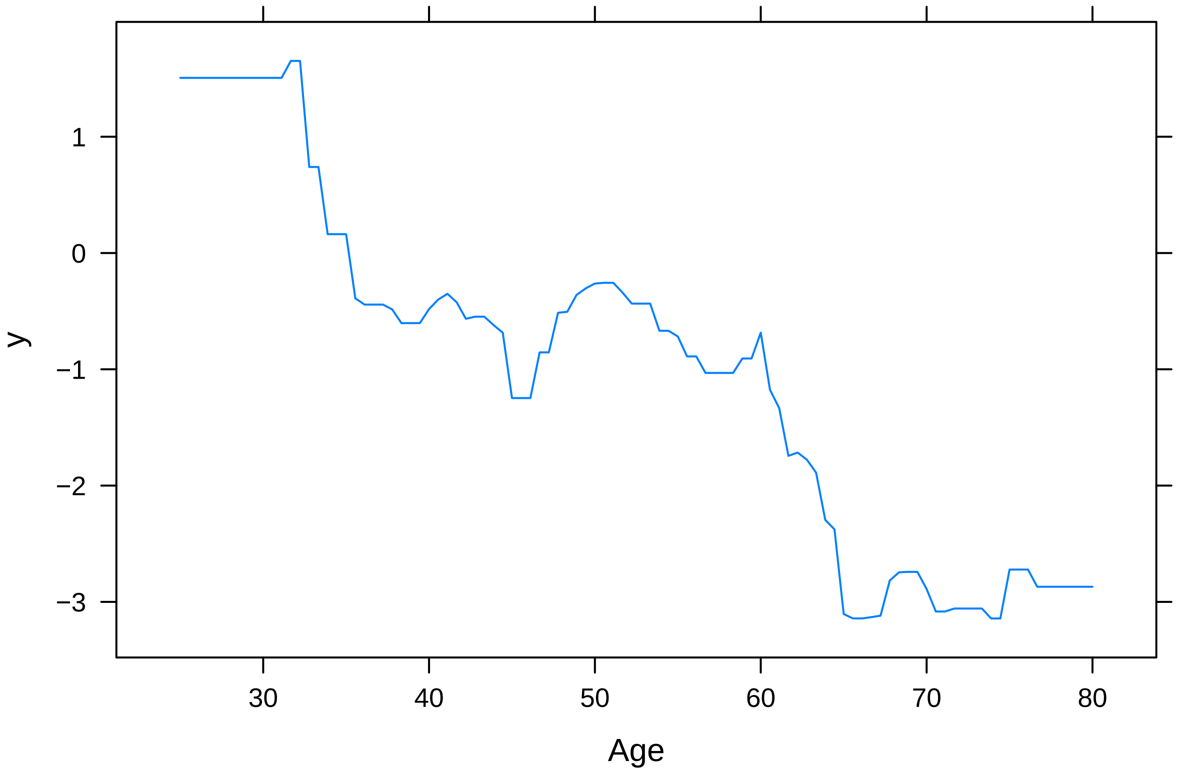
```
plot(boost.carseats,i="ShelveLoc")
```



```
plot(boost.carseats,i="Advertising")
```



```
plot(boost.carseats,i="Age")
```



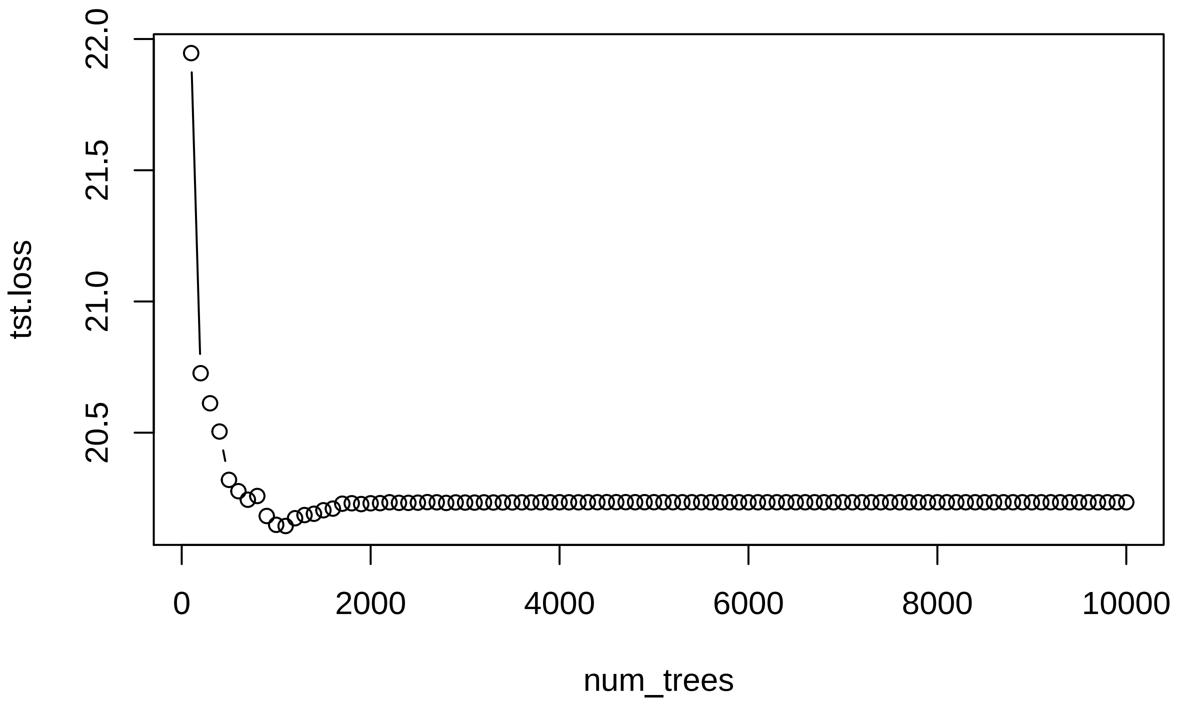
```
yhat.boost=predict( boost.carseats, newdata=Carseats[-train,],
                    n.trees = M, type = "response")
mean((yhat.boost-Carseats$High[-train])^2)
```

```
## [1] 0.08926975
```

```
boost.carseats=gbm(High~.-Sales, data = Carseats[train,], distribution="bernoulli",
                   n.trees = 5000, interaction.depth = 4, shrinkage = 0.2, verbose=F)
yhat.boost=predict( boost.carseats, newdata = Carseats[-train,], n.trees = M,
                    type = "response")
mean((yhat.boost-Carseats$High[-train])^2)
```

```
## [1] 0.09672414
```

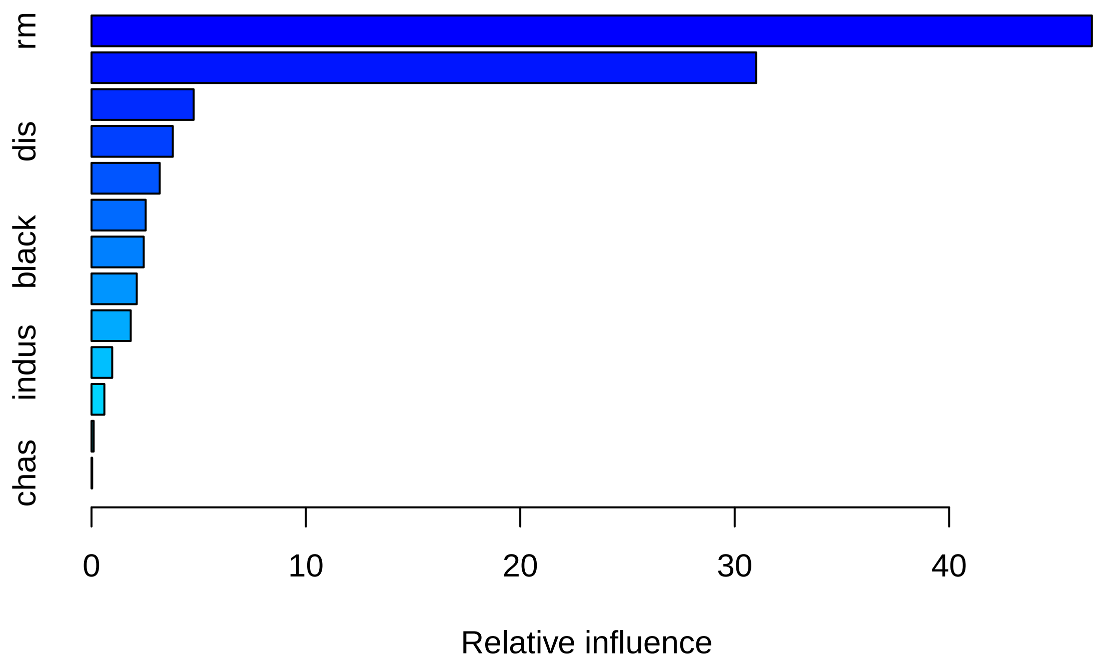
```
set.seed(1)
train = sample(1:nrow(Boston), nrow(Boston)/2)
set.seed(1)

num_trees <- floor(seq(100,10000,length.out = 100))
tst.loss <- NULL
boost.boston=gbm( medv~., data=Boston[train,], distribution="gaussian",
                  n.trees=max(num_trees), interaction.depth=5)
for(m in num_trees){
yhat.bag = predict(boost.boston,newdata=Boston[-train,],n.trees = m,
                   type = "response")
tst.loss <- c(tst.loss,mean((yhat.bag-Boston$medv[-train])^2))
}
plot(num_trees,tst.loss,type = "b")
```



```
M <- num_trees[which.min(tst.loss)]
M
```

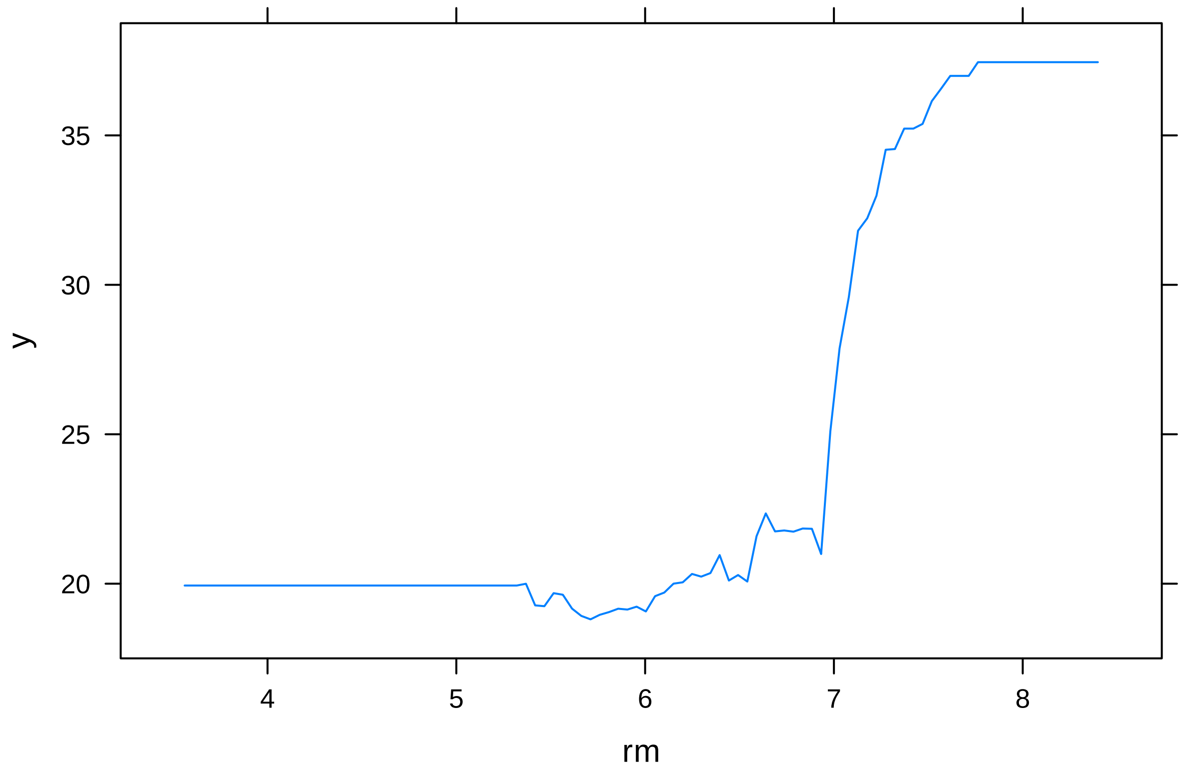
```
## [1] 1100
```

```
boost.boston=gbm(medv~., data=Boston[train,], distribution="gaussian",
                 n.trees=M, interaction.depth=5)
summary(boost.boston)
```

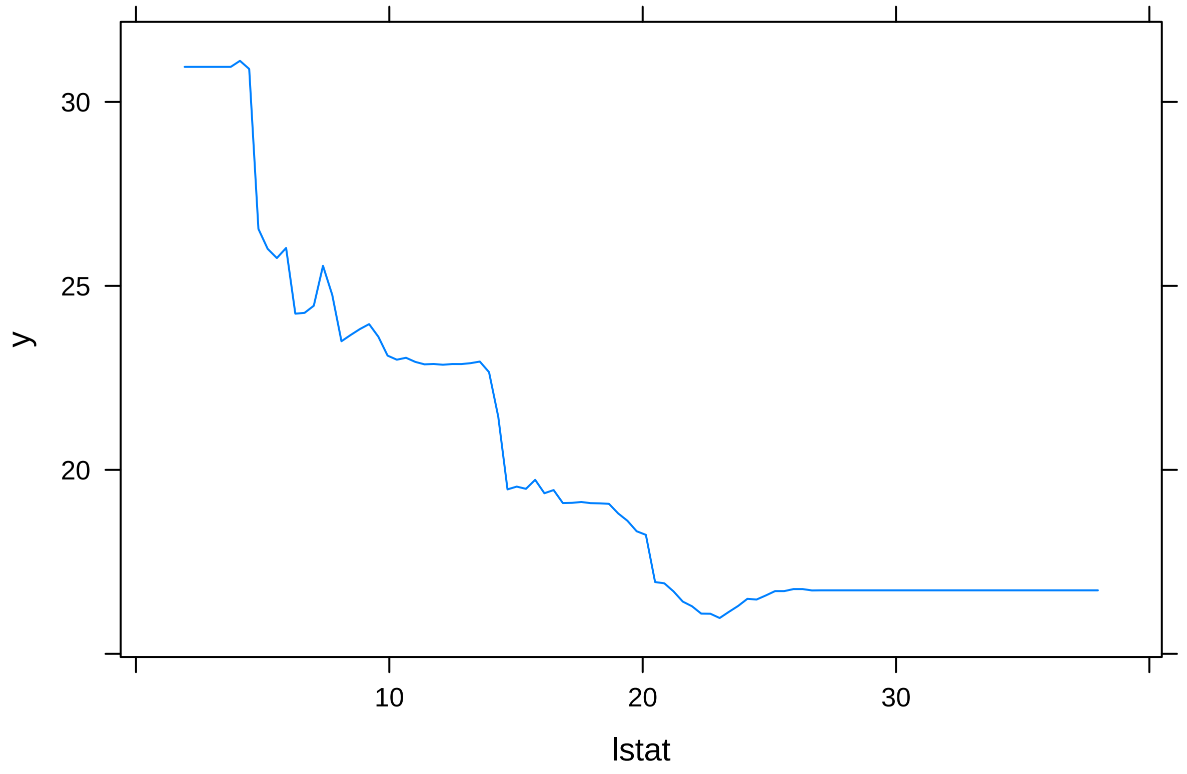


	var	rel.inf
rm	rm	46.6601217
lstat	lstat	31.0014372
crim	crim	4.7628832
dis	dis	3.7922972
nox	nox	3.1805425
age	age	2.5260908
black	black	2.4348971
ptratio	ptratio	2.1110133
tax	tax	1.8287830
indus	indus	0.9675263
rad	rad	0.6007242
zn	zn	0.1004767
chas	chas	0.0332068

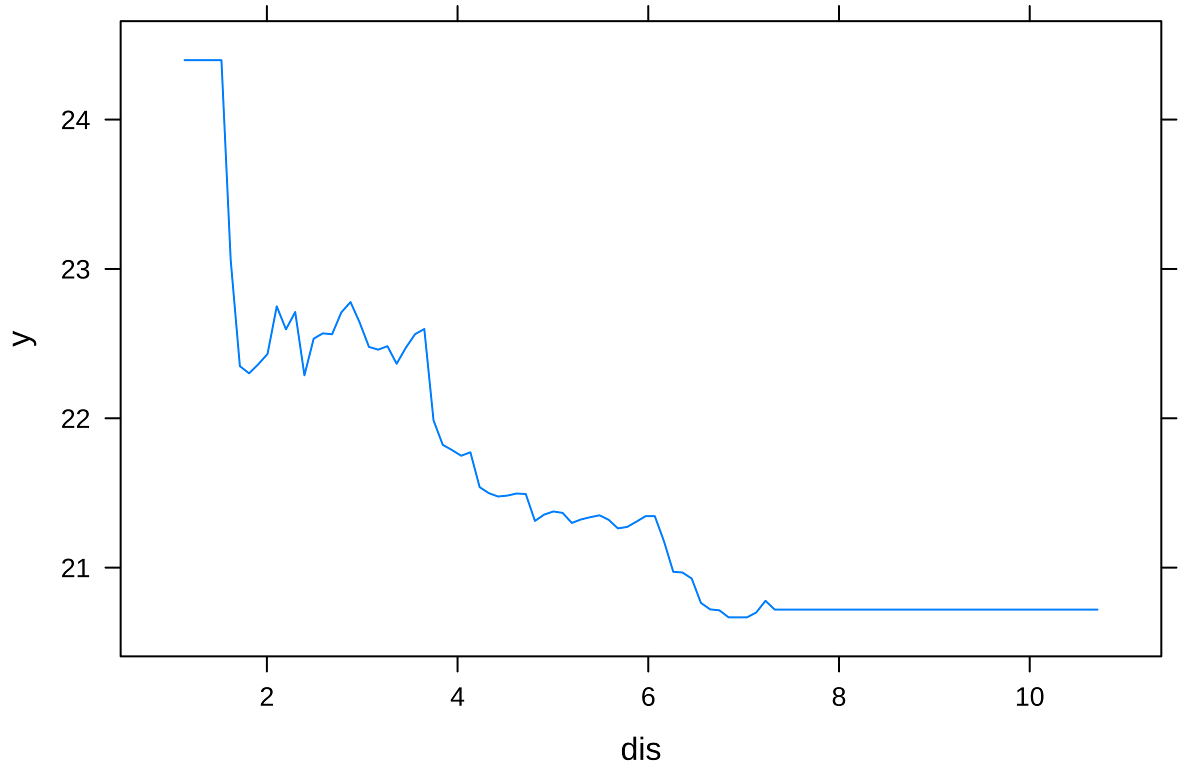
```r
par(mfrow=c(2,2))
plot(boost.boston,i="rm")
```



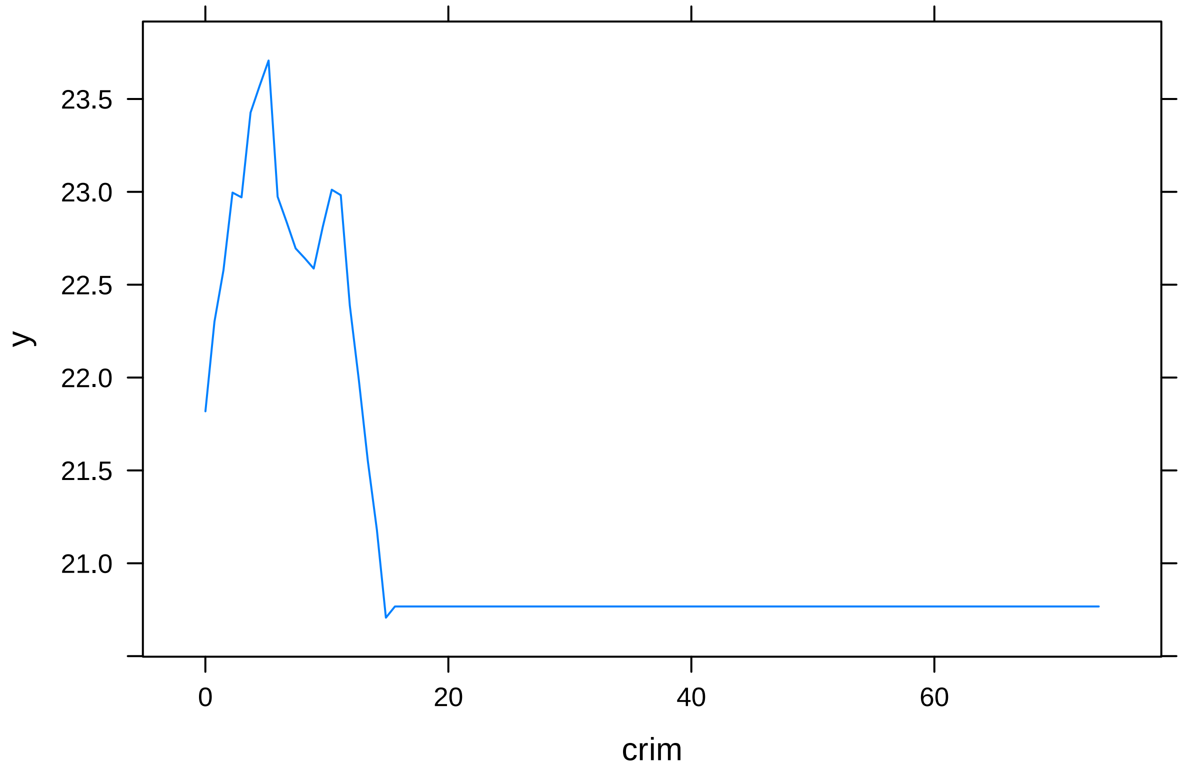
```
plot(boost.boston,i="lstat")
```



```
plot(boost.boston,i="dis")
```



```
plot(boost.boston,i="crim")
```



```
yhat.boost=predict(boost.boston,newdata=Boston[-train,], n.trees = M,
                   type = "response")
mean((yhat.boost-boston.test)^2)
```

```
## [1] 19.19356
```

```
boost.boston=gbm(medv~.,data=Boston[train,], distribution="gaussian",
                 n.trees=M, interaction.depth=5, shrinkage=0.2, verbose=F)
yhat.boost=predict(boost.boston,newdata=Boston[-train,],n.trees=M,type = "response")
mean((yhat.boost-boston.test)^2)
```

```
## [1] 19.69013
```