Trees

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1. Trees

Tree based methods are a major player in data-mining.

Good:

- flexible fitters, capture non-linearity and interactions.
- do not have to think about scale of x variables.
- handles categorical and numeric y and x very nicely.
- fast.
- interpretable (when small).

Bad:

Not the best in out-of-sample predictive performance
(*but not bad!!*).

But,

If we **bag** or **boost** trees, we can get the best off-the-shelf prediction available.

Bagging and Boosting are *ensemble methods* that combine the fit from many (hundreds, thousands) of tree models to get an overall predictor.

2. Regression Trees

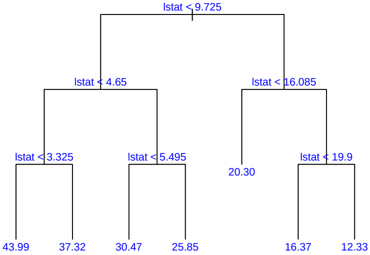
Let's look at a simple 1-dimensional example so that we can see what is going on.

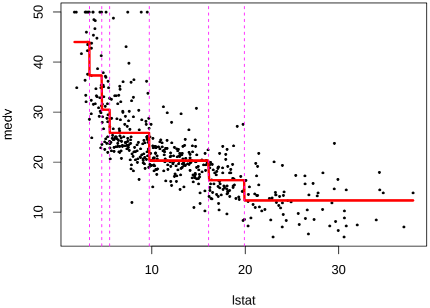
We'll use the Boston housing data and relate x=lstat to y=medval.

At left is the *tree* fit to the data.

At each *interior node* there is a decision rule of the form $\{x < c\}$. If $x < c$ you go left, otherwise you go right.

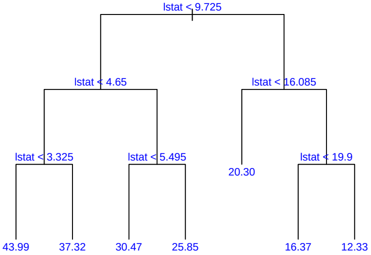
Each observation is sent down the tree until it hits a bottom node or *leaf* of the tree.

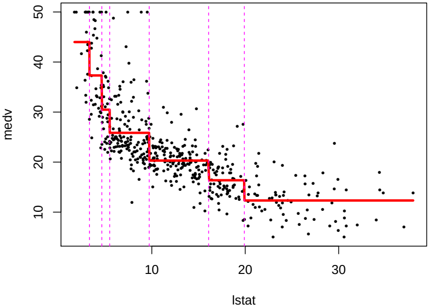




The set of bottom nodes gives us a partition of the predictor (x) space into disjoint regions. At right, the vertical lines display the partition. With just one x, this is just a set of intervals.

Within each region (interval) we compute the average of the y values for the subset of training data in the region. This gives us the step function which is our $\hat{f}$. The $\bar{y}$ values are also printed at the bottom nodes (left plot).





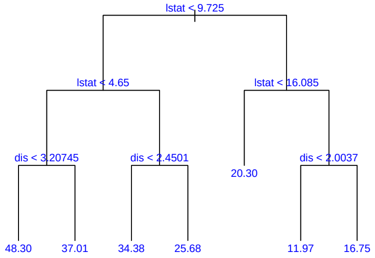
To predict, we just use our step function estimate of $f(x)$.

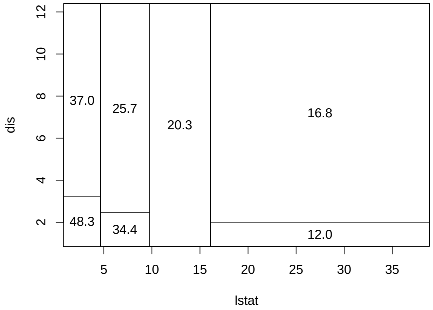
Equivalently, we drop x down the tree until it lands in a leaf and then predict the average of the y values for the training observations in the same leaf.

A Tree with Two Explanatory Variables

Here is a tree with $x = (x_1, x_2) =$ (lstat,dis) and y=medv.

Now the decision rules can use either of the two x's.





At right is the *partition* of the x space corresponding to the set of bottom nodes (leaves).

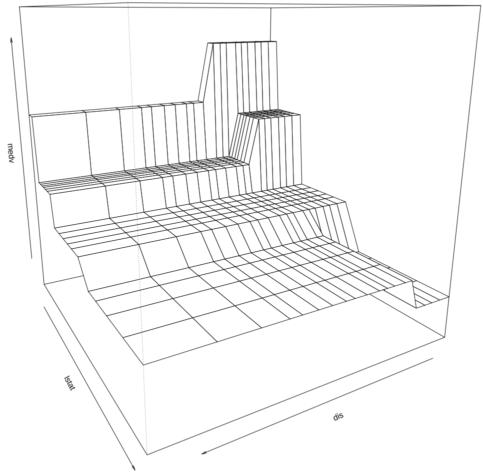
The average y for training observations assigned to a region is printed in each region and at the bottom nodes.

This is the regression function given by the tree.

It is a step function which can seem dumb, but it delivers non-linearity *and* interactions in a simple way and works with a lot of variables.

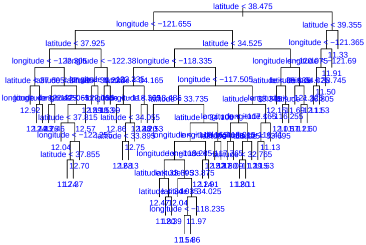
Notice the interaction.

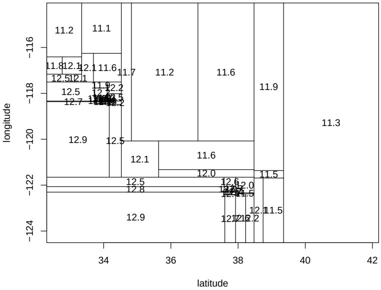
The effect of `dis` depends on `lstat`!!



The California Housing Data

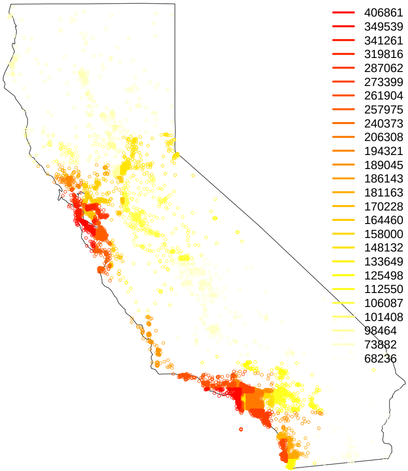
Here is a tree with 50 bottom nodes fit to the California Housing data using only `longitude` and `latitude`.





Don't extrapolate into the ocean!

Here is a view of the fit using the map of the state.
(units are dollars, the logMedVal was exponentiated for the labels).



In R:

```
#------------------------------------------------
#load tree package (and MASS), attach Boston data
library(tree)
library(MASS)
#data(Boston) #don't need this
attach(Boston)

#------------------------------------------------
#fit a tree to boston data just using lstat.
#first get a big tree using a small value of mindev
temp = tree(medv~lstat,data=Boston,mindev=.0001)
cat("first big tree size: \n")
print(length(unique(temp$where)))
#if the tree is too small, make mindev smaller!!

#------------------------------------------------
#then prune it down to one with 7 leaves
boston.tree=prune.tree(temp,best=7)
cat("pruned tree size: \n")
print(length(unique(boston.tree$where)))
```

```
#-----------------------------------------------
#plot the tree
plot(boston.tree,type="uniform")
text(boston.tree,col="blue",label=c("yval"),cex=.8)

#-----------------------------------------------
#plot data with fit
#get fit
boston.fit = predict(boston.tree) #get training fitted values
#plot fit
plot(lstat,medv,cex=.5,pch=16) #plot data
oo=order(lstat)
lines(lstat[oo],boston.fit[oo],col="red",lwd=3) #step function fit

#-----------------------------------------------
#predict at lstat = 15 and 25.
preddf = data.frame(lstat=c(15,25))
yhat = predict(boston.tree,preddf)
points(preddf$lstat,yhat,col="blue",pch="*",cex=3)
```

Let's fit the tree using `lstat` and `dis`.

```
#--------------------------------------------------
df2=Boston[,c(8,13,14)] #pick off dis,lstat,medv
print(names(df2))

#--------------------------------------------------
#big tree
temp = tree(medv~.,df2,mindev=.0001)
cat("first big tree size: \n")
print(length(unique(temp$where)))

#--------------------------------------------------
#then prune it down to one with 7 leaves
boston.tree=prune.tree(temp,best=7)
cat("pruned tree size: \n")
print(length(unique(boston.tree$where)))

#--------------------------------------------------
# plot tree and partition in x.
par(mfrow=c(1,2))
#plot tree
plot(boston.tree,type="u")
text(boston.tree,col="blue",label=c("yval"),cex=.8)
#plot 2-dimesional partition in (x1,x2) = (lstat,dis)
partition.tree(boston.tree)
```

```
#-----------------------------------------------
#let's compare in-sample fits from our two trees with each other and y
boston.fit2 = predict(boston.tree)
fmat = cbind(medv,boston.fit,boston.fit2)
colnames(fmat)=c("y=medv","treel","treeld")
pairs(fmat)
print(cor(fmat))

#-----------------------------------------------
#predict at lstat = 15 and 25 and dis = 2 both times
preddf=data.frame(lstat=c(15,25),dis=c(2,2))
yhat2 = predict(boston.tree,preddf)
cat("predictions are:\n")
print(yhat2)
```

Lets try p = 4 with nox, rm, ptratio, and lstat.

```
#--------------------------------------------------
df4=Boston[,c(5,6,11,13,14)] #pick off variables
print(names(df4))
temp = tree(medv~.,df4,mindev=.0001)
cat("first big tree size: \n")
print(length(unique(temp$where)))

#--------------------------------------------------
#then prune it down to one with 15 leaves (picked 15 arbitrarily)
boston.tree4=prune.tree(temp,best=15)
cat("pruned tree size: \n")
print(length(unique(boston.tree4$where)))

#--------------------------------------------------
#plot tree
par(mfrow=c(1,1))
plot(boston.tree4,type="u")
text(boston.tree4,col="blue",label=c("yval"),cex=.8)

#--------------------------------------------------
#compare fits
fmat4=cbind(fmat,predict(boston.tree4))
colnames(fmat4)[4]="tree4"
pairs(fmat4)
print(cor(fmat4))
```

3. Classification Trees

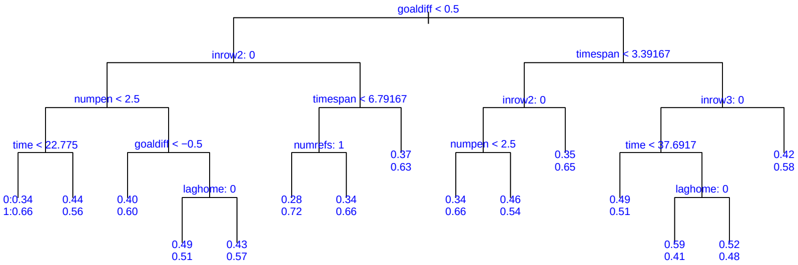
Let's do a tree for a classification problem.

We'll use the hockey penalty data.

The response is whether or not the next penalty is on the other team and x is a bunch of stuff about the game situation (the score ...).

In addition, this time some of our predictors (features, x's) are categorical.

Here is the tree:



- Each bottom node gives the fraction of training data in the two outcome categories. Think of it as $\hat{p}$ for the kind of x associated with that bottom node.

- The form of the decision rule can't be $x < c$ for categorical variables.
  We pick a subset of the levels to go left. `inrow2:0` means all the observations with `inrow2` in the category labeled 0 go left.

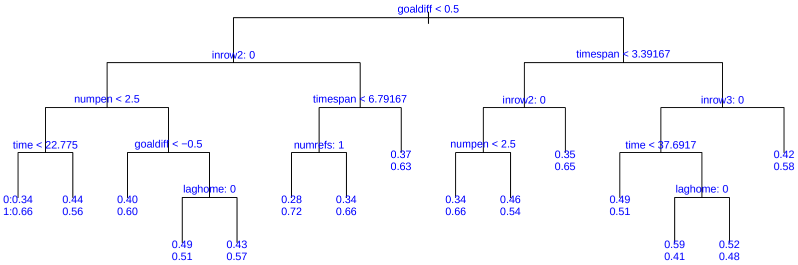
There is a lot of fit!!!

if:

- if you are not winning
- you had the last two penalties
- it has not been long since the last call
- and there is only 1 referee

then:

there is a 72% chance the next call will be on the other team.



Whilst there is another game situation where the chance the next call is on the other team is only 41%.

4. Trees: A Summary

Trees:

- Trees use recursive binary splits to partition the predictor space.
- Each binary split consists of a decision rule which sends x left or right.
- For numeric x_i, the decision rule is of the form if $x_i < c$.
- For categorical x_i, the rule lists the set of categories sent left.
- The set of bottom nodes (or leaves) give a partition of the x space.
- To predict, we drop an out-of-sample x down the tree until it lands in a bottom node.
- For numeric y, we predict the average y value for the training data that ended up in the bottom node.
- For categorical y we use the category proportions for the training data that ended up in the bottom node.

Good:

- Handles categorical/numeric x and y nicely.
- Don't have to think about the scale of x's !!!
- Computationally fast ("scales").
- Small trees are interpretable.
- Variable selection.

Bad:

- Step function is crude, does not give the best predictive performance.
- Hard to assess uncertainly.
- Big trees are not interpretable.