TreeBasedRegression

November 4, 2019

1 Tree-based regression

Tree-based regression makes predictions on a target variable y by developing rules that divide our X data set (called our feature space) into regions. Given a vector of covariates x_i^* , a TBR model looks at the training observations, picks those observations that are simialr, and averages the corresponding y values. A TBR model does this by partitioning the training observations through a series of rules. TBR models are non-linear.

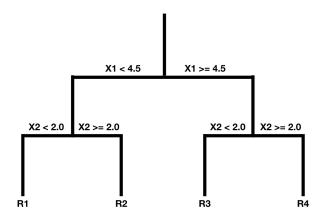
As an example, a TBR model could specify the following rules: (i) if $x_1 < 4.5$ and $x_2 < 2.0$ then y falls in region 1, (ii) if $x_1 < 4.5$ and $x_2 < 2.0$ then y < 4.5 and $x_2 < 2.0$ then $x_2 < 2.0$ then y < 4.5 and $x_3 < 4.5$ and $x_4 < 4.5$ and $x_4 < 4.5$ and $x_5 < 4.5$ and x_5

 \geq

 \geq 2.0\$ then y falls in region 2,if x_{1} \geq 4.5\$ and $x_{2} <$ 2.0 then y falls in region 3, and if x_{1} \geq 4.5\$ and x_{2}

2.0\$ then y falls in region 4.

And the above rule can be represented as a tree.



You start at the top (root) of the tree with your x covariates. Work your way down the tree, and every time you come to a split, take the path that corresponds to your x data. For example, if my x data was x = [2,5] I would move to the left at the first split because $x_1 = 2 < 4.5$. I would continue down the left side of the tree until the next split. At the next split I would move right because $x_2 = 5 > 2.0$ and the prediction my tree would make is the average of all y values in region 2.

There is a simple idea behind trees and rule-based regression methods. Observations that have similar characteristics can be predicted with a simpler model that explains P(Y|X). Rather than try to model P(Y|X) directly, which could have complicated nonlinearities, model a small portion of $P(Y|X^*)$ that has a simpler structure. By taking a simple average of y values we are assuming that, in any given small region of feature space, the y values can be predicted to be a simple average.

Rather than a tree or textual rules, we can graphically understand how the tree above splits our data. First, we can load the ISLR package that includes the Hitters dataset.

```
[1]: require(ISLR) print(head(Hitters))
```

Loading required package: ISLR

	AtBat	${\tt Hits}$	${\tt HmRun}$	Runs	RBI	Walks	Years	${\tt CAtBat}$	\mathtt{CHits}	${\tt CHmRun}$
-Andy Allanson	293	66	1	30	29	14	1	293	66	1
-Alan Ashby	315	81	7	24	38	39	14	3449	835	69
-Alvin Davis	479	130	18	66	72	76	3	1624	457	63
-Andre Dawson	496	141	20	65	78	37	11	5628	1575	225
-Andres Galarraga	321	87	10	39	42	30	2	396	101	12
-Alfredo Griffin	594	169	4	74	51	35	11	4408	1133	19
	CRuns	CRBI	CWalks	Leag	gue I	Divisio	n Put(Outs Ass	sists E	Errors

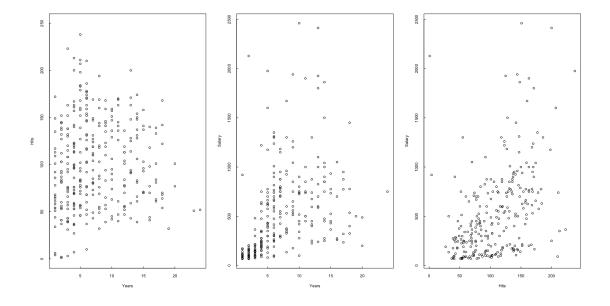
-Andy Allanson	30	29	14	Α	E	446	33	20
-Alan Ashby	321	414	375	N	W	632	43	10
-Alvin Davis	224	266	263	Α	W	880	82	14
-Andre Dawson	828	838	354	N	E	200	11	3
-Andres Galarraga	48	46	33	N	E	805	40	4
-Alfredo Griffin	501	336	194	Α	W	282	421	25
	Salary	NewL	eague					
-Andy Allanson	NA		Α					
-Alan Ashby	475.0		N					
-Alvin Davis	480.0		Α					
-Andre Dawson	500.0		N					
-Andres Galarraga	91.5		N					
-Alfredo Griffin	750.0		A					

For this example, I'm using the number of years the baseball is active and the number of hits they have as my *X* data. I will try and predict baseball player's salary, my target (*y*) variable.

```
[6]: x1 = Hitters$Years
x2 = Hitters$Hits
y = Hitters$Salary
```

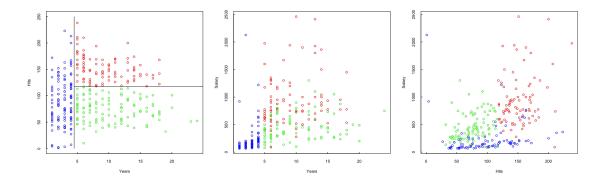
First I will plot my x1 and x2 data.

```
[12]: options(repr.plot.width=15,repr.plot.height=8)
    par(mfrow=c(1,3))
    plot(x1,x2, ylim=c(0,250),ylab='Hits' ,xlab='Years',tck=0.01)
    plot(x1,y ,ylab='Salary',xlab='Years',tck=0.01)
    plot(x2,y ,ylab='Salary',xlab='Hits',tck=0.01)
```



The relationship between salary, and hits and years appears non-linear. A linear model could be difficult to fit, and accurately predict salary. Assume instead we created a tree (like the above example) with two rules. The first rule partitions the data into Years less than or greater than or equal 4.5. The second rule then partitions the data by the average number of hits a player has as greater than or equal, or less than 117.5.

```
[25]: options(repr.plot.width=15,repr.plot.height=5)
      par(mfrow=c(1,3))
      color = rep(0,length(x1))
      for (i in 1:length(x1)){
          singleX1 = x1[i]
          singleX2 = x2[i]
          if (singleX1 < 4.5){
             color[i] = "blue"
          else if (singleX1 >= 4.5 \& singleX2 < 117.5){
             color[i] = "green"
          }
          else if (singleX1 >= 4.5 \& singleX2 >= 117.5){
             color[i] = "red"
          }
      }
      plot(x1,x2,col=color, ylim=c(0,250),ylab='Hits',xlab='Years',tck=0.01)
      lines(rep(4.5,2),c(0,250))
      lines(c(4.5,25), rep(117.5,2))
      plot(x1,y,col=color ,ylab='Salary',xlab='Years',tck=0.01)
      plot(x2,y,col=color ,ylab='Salary',xlab='Hits',tck=0.01)
```



The feature space (left) is partitioned into three regions. These regions correspond to predictions of salary.

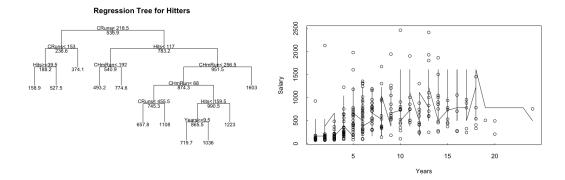
This tree is relatively simple. More complicated trees can be built from these same two *X* variables

```
[46]: library(rpart)
    fit <- rpart(Salary~Hits+Years+CHmRun+CRuns+Errors, method="anova", data=Hitters)

par(mfrow=c(1,2))
plot(fit, uniform=TRUE,
    main="Regression Tree for Hitters ")
    text(fit, use.n=FALSE, all=TRUE, cex=0.8)

X = Hitters[,c("Hits","Years","CHmRun","CRuns","Errors")]
X = X[order(Hitters$Years),]
    predictions = predict(fit,X)

plot(x1,y,xlab='Years',ylab="Salary",tck=0.01)
lines(X$Years,predictions)</pre>
```



On the left, a tree is made by splitting the feature space over and over into finer and finer sets of observations. Within each region the *y* values are averaged and considered the predictions for all observations in that region.

On the right, the predictions are plotted over the data "Years" by "Salary". The constant, and jagged looking, appearance of the predictions is because of this "constant within region" approach to prediction.

1.1 Prediction by splitting the feature space

To make it clear, Trees split our feature space (X data) into J different regions. Given x_{new} , a prediction is made by finding the region x_{new} belongs to and averaging all the training example y values that fall into that same region. The same prediction is made for **all** observations that fall into that region.

1.2 How to find the splits

To find a tree that makes the "best" predictions, we need to define what best means. For this class, by best we mean the tree that minimizes

$$SSE(\hat{y}_{R_j}) = \sum_{j=1}^{J} \sum_{x_i \in R_j} (y_i - \hat{y}_{R_j})^2$$

or the sum square errors. The Sum square errors is a function of j different variables, one prediction for each region (R_j) . An exhaustive approach to finding the best set of \hat{y}_{R_j} that minimize the SSE would consider every possible tree. But this means we would need to compute the SSE for every possible combination of every possible cut point for all variable in our feature space. This type of computation isn't feasible in a reasonable amount of time.

Instead, we will take a top-down approach called recursive binary splitting. Recursive binary splitting examines, for all variables X_k and corresponding cut points, the single X variable and cut point that minimizes the SSE. The above equation reduces to

$$SSE_{RBS}(\hat{y}_{R_1}, \hat{y}_{R_2}) = \sum_{x_i \in R_1} (y_i - \hat{y}_{R_1})^2 + \sum_{x_i \in R_2} (y_i - \hat{y}_{R_2})^2$$

where \hat{y}_{R_1} and \hat{y}_{R_2} correspond to the two regions generated by picking a single covariate X_j and a single cut point $X_j < s$ that minimize the SSE. This SSE_{RBS} set j equal to 2 in the more general SSE equation above.

The process is repeated, except now we find the best covariate and cutpoint that minimizes SSE_{RBS} inside R_1 and inside R_2 .

```
[]: library(rpart)
fit <- rpart(Salary~Hits+Years, method="anova", data=Hitters)

plot(fit, uniform=TRUE,
    main="Regression Tree for Hitters ")
text(fit, use.n=TRUE, all=TRUE, cex=.8)</pre>
```