

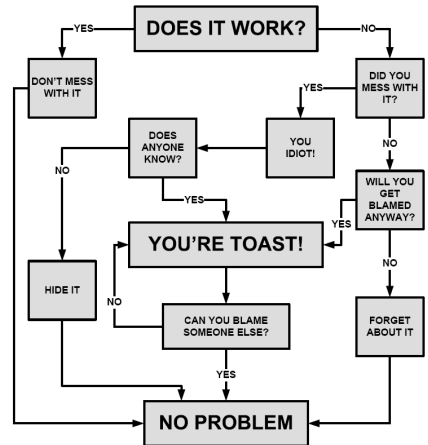
# Data, Environment and Society:

## Lecture 16: Regression trees

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GSI: Salma Elmallah

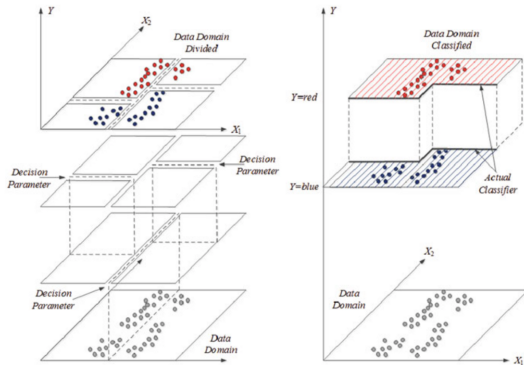
October 24, 2019

### Problem Solving Flowchart



# Objectives

- Introduction to regression trees
  - ▶ Terminology
  - ▶ How they are built
  - ▶ How to choose with cross validation
- Next week, we'll discuss classification trees
  - ▶ Same as regression, just different loss functions



(medium.com)

## Terminology we'll cover...

- Terminal node
- Internal node
- Branches
- Leaves
- Binary splits
- Recursive binary splitting  $\leftrightarrow$  Top-down greedy
- Cost complexity pruning

## Basic idea for regression trees

All we are doing is “splitting” the observations into regions in the predictor space, and averaging the response variable within each region.

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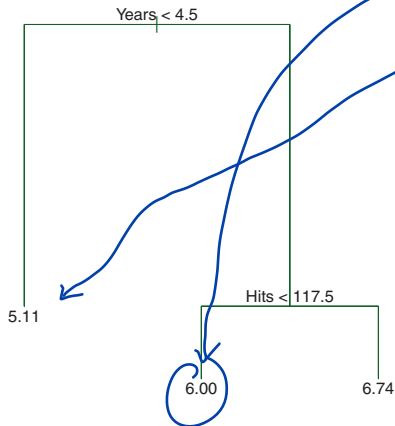
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Big decision in regression trees: *What are the regions we should use?*

## Example, from the textbook



“Hitters” data from ISLR.

263 major league players stats.

Here, this tree is “splitting” on two variables – years in league and number of hits

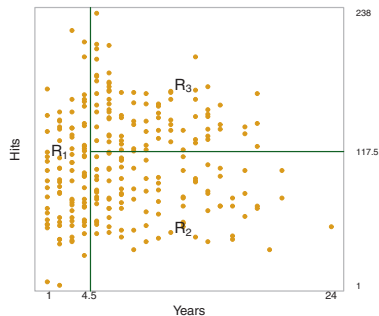
The numbers at the ends are the average (log-transformed) average salaries for players

## Example, from the textbook, ctd

$$R_1 = \{X | \text{years} < 4.5\}$$

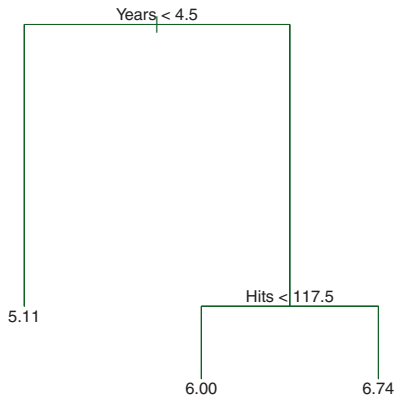
$$R_2 = \{X | \text{years} \geq 4.5, \text{hits} < 117.5\}$$

$$R_3 = \{X | \text{years} \geq 4.5, \text{hits} \geq 117.5\}$$





# Terminology

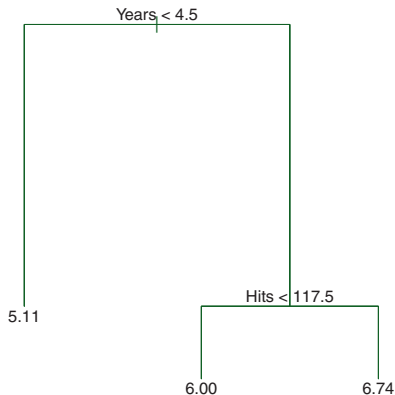


Each region  $R_i$  is a *terminal node*

Each numeric value at which a split happens is an *internal node*

Segments connecting nodes (terminal or internal) are...

# Terminology

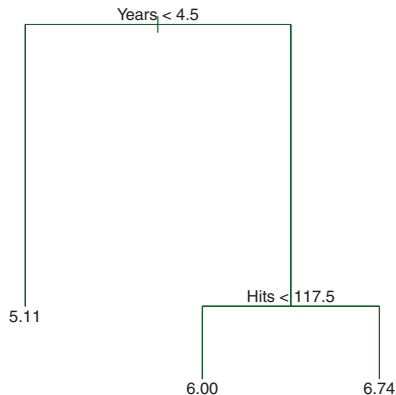


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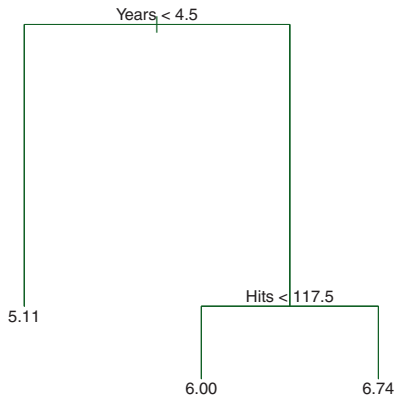
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## Terminology so far...

- Terminal node
- Internal node
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## Regression trees – basic approach

- ① Divide the **predictor** space into non-overlapping regions
  - ▶ This distinguishes the method from KNN regression
- ② Within each region, the prediction is just the average of the **response variable** from training data.
  - ▶ This is similar to KNN regression

## Regression trees – basic approach

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Two Basic Questions:

- 1 Where should I put the internal nodes?
- 2 How many regions should there be?

The answers are, as it turns out, really simple.

## Where to put the internal nodes?

First, for simplicity, the nodes are structured to make rectangles in the a 2-D predictor space (or hyper-rectangles in higher dimensions).



## How do I split regions?

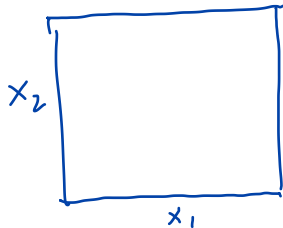
Let

- $j$  index predictor variables
- $s$  denote the location of the split within the region
  - ▶ (With  $n$  observations we have to consider at most  $n - 1$  split points; the numeric value of the split is the mid-way point between two adjacent observations.)

Then all splits can be described as:

$$R_1(j, s) = \{X | X_j < s\} \text{ and } R_2(j, s) = \{X | X_j \geq s\}$$

But where should the splits be?



Then we partition any region by choosing  $j$  and  $s$  as follows:

$$\{j, s\} = \arg \min_{j \in J, s \in X_j} \sum_{i: x_i \in R_1(j, s)} (y_i - \hat{y}_{R_1})^2 + \sum_{i: x_i \in R_2(j, s)} (y_i - \hat{y}_{R_2})^2$$

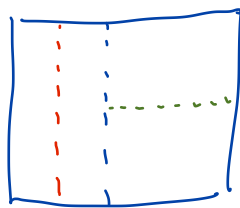
where  $\hat{y}_{R_k}$  is the mean of all response variables in region  $k$ .

It would be tedious to identify  $j$  and  $s$  by hand, but it's actually very quick computationally. (Remember, there are only  $n - 1$  possible splits for each predictor.)

Ok, we've split one predictor in two. Now what?

Next choose the single best split from among *all* possible splits of the two new regions. **Now we'll have three regions.**

In general, on the  $n^{\text{th}}$  step, choose the single best split from among the  $n$  regions, resulting in  $n + 1$  regions to take to the next step.



## Repeating the splits

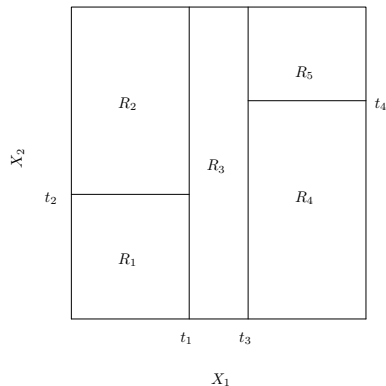
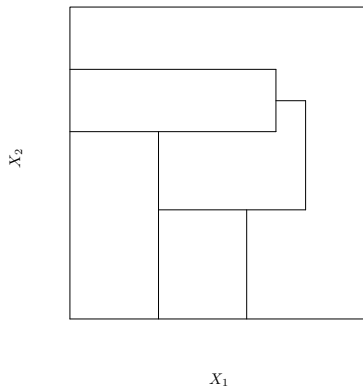
On each step, we're choosing the single best possible split from among the  $n$  regions, resulting in  $n + 1$  regions to take to the next step.

Repeat this process until you reach a stopping criterion – typically a maximum number of observations in each region. (For example all regions have no more than 5 observations.)

**Call the resulting tree  $T_0$ .**

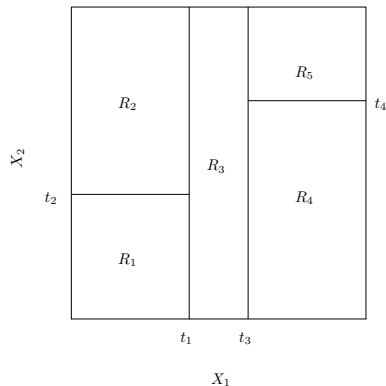
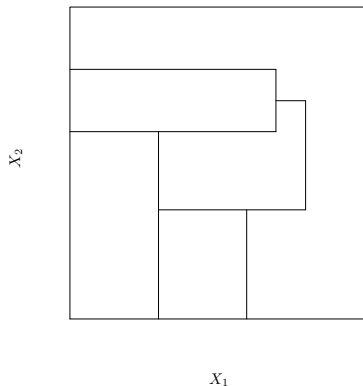
**We call this approach “greedy”** because when we do the first partition we're not thinking ahead to future partitions to evaluate it.

One of these doesn't belong...



Q: Which picture results from successively splitting the regions into values greater or less than predictor values?

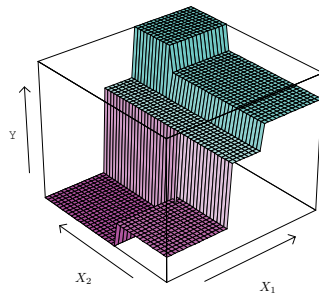
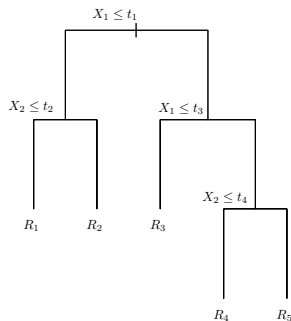
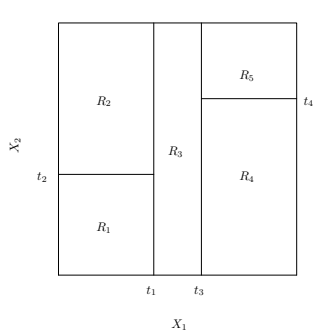
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Q: Which picture results from successively splitting the regions into values greater or less than predictor values?

A: The right one. The left one is not possible with simple splitting.

## A five region example... with two dimensional predictor space



## What do we call it?

The process of splitting regions over and over is called...

**“recursive binary splitting”**

You can also call it a **“top-down greedy”** approach.

Because it's “greedy” we can't be sure that the splits we're getting are the best possible splits.



## Why binary?

In other words, why not multiway splits?

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In general multiway splits fragment the data too quickly, leaving insufficient data at the next level down

Since we do the binary splitting recursively, we get the same flexibility as a multiway split, since a region can be split a second time later.

## Terminology so far...

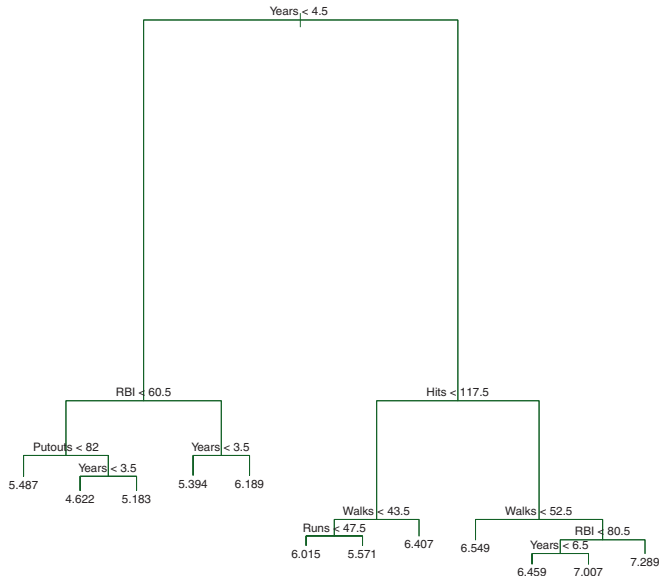
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## Example $T_0$

Remember,  $T_0$  is the biggest tree we build. We get there by recursively splitting until we meet a threshold (often a maximum number of observations per terminal node).



## When will we test?

All the steps above involve model *building*. We have yet to evaluate different models against one another. First let's build the candidate models, then we can evaluate.

## Step 1: “cost complexity pruning”

We'll test models that are **subtrees** of  $T_0$ . (trees that are the same as  $T_0$  except they are missing some internal nodes and branches).

We identify subtrees using **cost-complexity pruning** a.k.a. weakest link pruning:

- To get the first subtree, evaluate model performance for all subtrees with one leaf removed from  $T_0$ . Choose the best one, call it  $T_1$ .
  - ▶  $R^2$  works for measuring performance
  - ▶ ...but not for categorical variables, stay tuned!
- Then evaluate performance for all models with one leaf removed from  $T_1$ . Choose the best, call it  $T_2$ . And so on.

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(Smart researchers have shown that this “greedy” approach is an optimal *pruning* strategy. But recursive binary splitting is not always optimal for growth.)



## Step 2: Tune up your $\alpha$

Take your set of subtrees,  $T_0$  through  $T_{N-2}$ . Call  $|T|$  the number of terminal nodes in the tree.

For a given  $\alpha$ , *one* of the  $T_i$  will minimize :

$$\sum_{m=1}^{|T|} \sum_{x_i \in R_m} (y_i - \hat{y}_{R_m})^2 + \alpha |T|$$

- $\alpha = 0$  will choose  $T_0$ , the biggest tree.
- As  $\alpha$  grows you'll choose successively smaller trees.

## Quick quiz

For a given  $\alpha$ , *one* of the  $T_i$  will minimize :

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Fill in the blank: As  $\alpha$  increases, bias goes \_\_\_\_ and variance goes \_\_\_\_.

## Quick quiz

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Fill in the blank: As  $\alpha$  increases, bias goes **up** and variance goes **down**. Bigger  $\alpha$  means fewer leaves, which means more bias but less variance.

Though it seems unnecessary to define  $\alpha$  (why not just evaluate all subtrees?), we'll see it's useful for cross validation.

# The (cross validation) process

- ❶ Split your data into  $K$  folds.
- ❷ Repeat this process for each fold: Withhold the fold and for remaining training data:
  - a. Grow a large tree via recursive binary splitting. “Large” means each leaf has some pre-specified maximum number of observations (e.g. 5)
  - b. Then “prune” the tree via cost complexity pruning to get a sequence of subtrees.
  - c. Choose the tree in the sequence that minimizes  $\sum_{m=1}^{|T|} \sum_{x_i \in R_m} (y_i - \hat{y}_{R_m})^2 + \alpha |T|$  for each of a range of values of  $\alpha$ .
  - d. Record the test MSE for each value of  $\alpha$ .
- ❸ Average the test MSE across all folds *for each value of  $\alpha$* ,
- ❹ Choose the  $\alpha$  that gives the lowest cross validated error,
- ❺ Build your final model with the chosen  $\alpha$  with *all the data*.

## Why use $\alpha$ ?

Why didn't we just evaluate cross validated error for each tree size?

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Ans: Sometimes it might. But it may be that across different folds we'd choose different subtrees.  $\alpha$  provides a better representation of the bias-variance tradeoff across folds.

But: out of convenience the book *displays* results in terms of tree size rather than  $\alpha$ . Argh!

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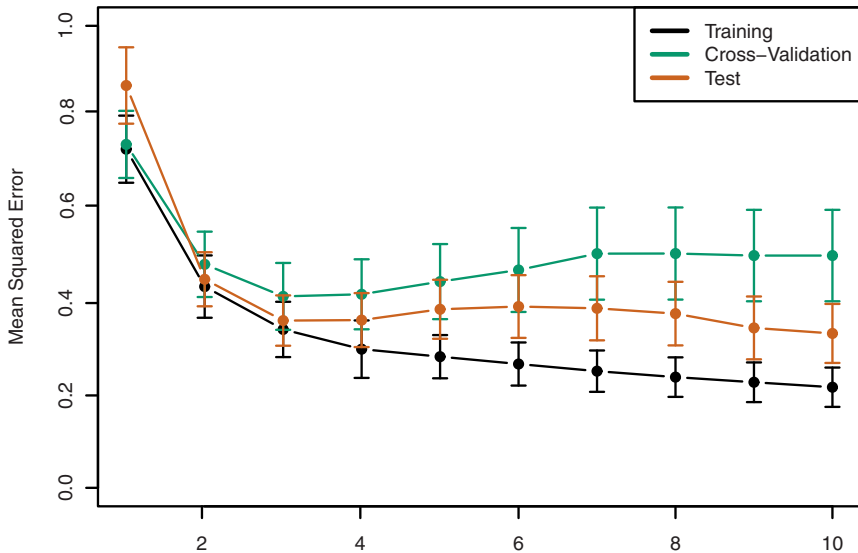
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- Cross validation to choose best  $\alpha$



## Results on Hitters data



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How about some disadvantages?

- As described, they don't usually provide the same predictive power that the other tools we've studied can.
- They can be pretty sensitive to small changes in the data.
- Recursive binary splitting may generate a suboptimal tree (like forward / backward model selection). Things later in the chapter address this.