

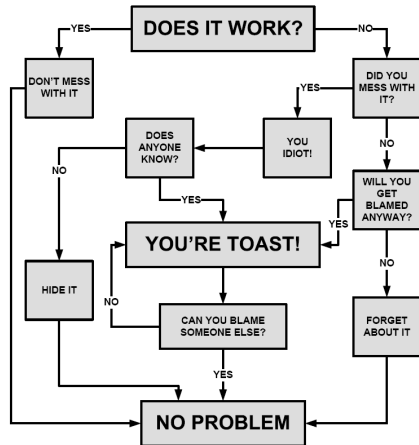
Data, Environment and Society:

Lecture 19: Classification and regression trees

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GSI: Salma Elmallah

November 5, 2019

Problem Solving Flowchart



Today's objectives

- Wrap up regression trees
 - ▶ How to choose with cross validation
- Classification trees
 - ▶ Same as regression, just different loss functions
- Boosting, bagging and random forests

Reading

- Today: ISLR Ch. 8.1 - 8.2
- Next time:
 - ▶ ISLR 9.1-9.3 (Support Vector Machines)
 - ▶ Badger (NYT article on algorithm discrimination)

Announcements

- Guest lecture – Elinor Benami, author of one of the first papers we read this semester.
- Exam review 11/14 in class, 11/18 in lab.
- Exam 11/19

Last time: 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^{th} step, choose the single best possible split from among the n regions, resulting in $n + 1$ regions to take to the next step.

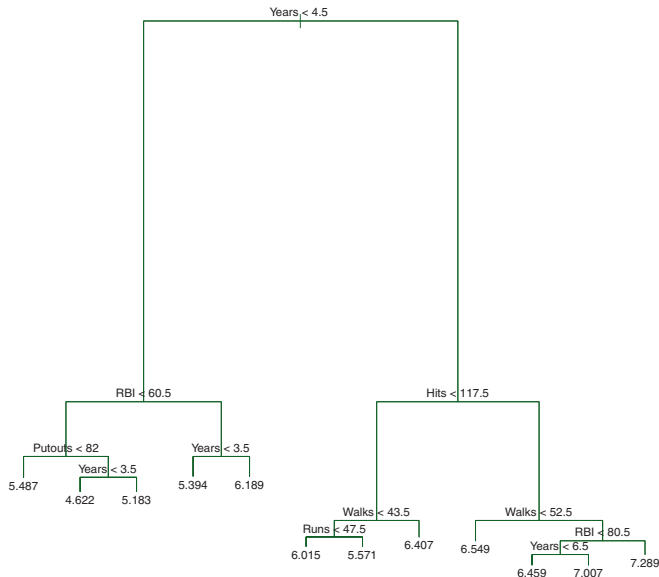
Repeat this process until you reach a stopping criterion – typically a maximum number of observations in each region. (For example all regions have no more than 5 observations.)

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.

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).



Choosing the final tree, **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.)

Choosing the final tree, **Step 2:** Tune up your α

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

For a given α , *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 α grows you'll choose successively smaller trees.

Quick quiz

For a given α , *one* of the T_i will minimize :

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

Fill in the blank: As α increases, bias goes ____ and variance goes ____.

Quick quiz

For a given α , *one* of the T_i will minimize :

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

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

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

The (cross validation) process

- ➊ Split your data into K folds.
- ➋ 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 α .
 - d. Record the test MSE for each value of α .
- ➌ Average the test MSE across all folds *for each value of α* ,
- ➍ Choose the α that gives the lowest cross validated error,
- ➎ Build your final model with the chosen α with *all the data*.

Why use α ?

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

That is, is α just overly complicating things?

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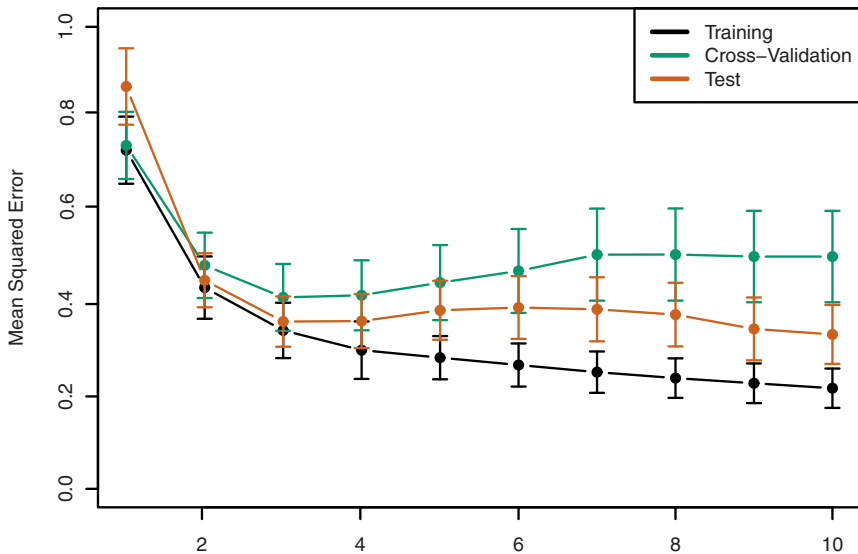
Why didn't we just evaluate cross validated error for each tree size?

That is, is α just overly complicating things?

Ans: Sometimes it might. But it may be that across different folds we'd choose different subtrees. α 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 α . Argh!

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.

Example: Test scores and pollution

Environmental Pollution 230 (2017) 730–740



Contents lists available at ScienceDirect

Environmental Pollution

journal homepage: www.elsevier.com/locate/envpol



Using machine learning to identify air pollution exposure profiles associated with early cognitive skills among U.S. children[☆]



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Does pollution change cognitive ability?

Stingone et al point out that few studies have looked at the effects of multiple pollutants at once

Key data:

- Kindergarten math scores from National Center of Education Statistics Early Childhood Longitudinal Study. Randomly selected children.
- Census tract estimates of 104 toxic pollutants from U.S. Environmental Protection Agency's National Air Toxics Assessment (NATA)
- Other confounders including mother age, marital status, hhld income, etc. (Used in second stage *after* tree building.)

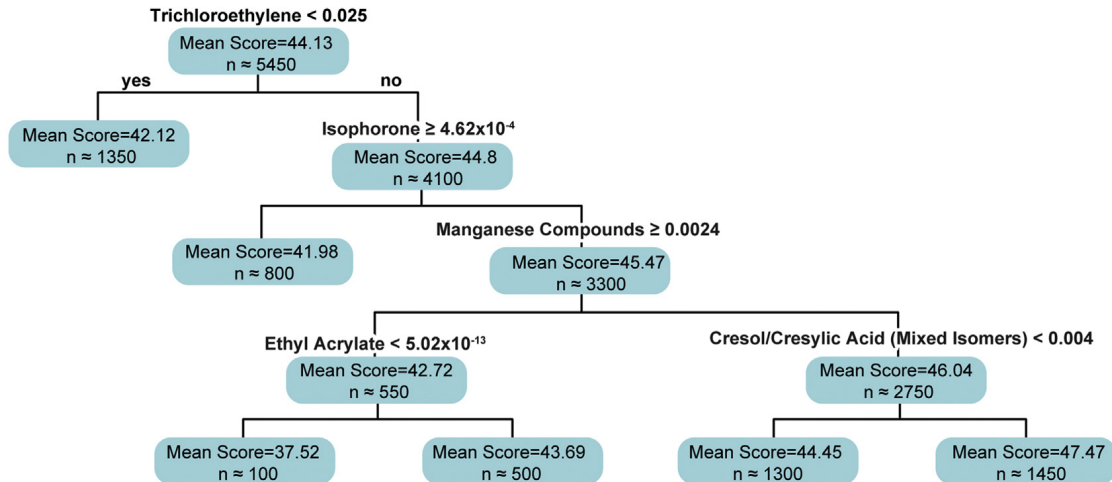
Stingone *et al* two step approach

- ① Build trees for test score outcome based on pollutant exposure (what we'll focus on here)
- ② Run basic multiple linear regression *within* each leaf to identify the effect of pollutants on test scores. (We won't cover this part.)

Why trees? Stingone *et al*'s justification

- Easy interpretability in terms of understandable trees and/or rules,
- Ability to identify non-linear relationships between the features (exposures) and the outcome (math scores),
- Possibility of identifying interactions among the features (exposures),
- Making no/minimal assumptions about data distributions,
- Tolerance to missing values and outliers in the data,

Example result



Constructed with 10-fold cross-validation. Also used additional random partitioning – stay tuned.

A trick that *Stingone et al* used

They note that Trees are:

- Prone to overfitting the (training) data,
- Sensitive to small perturbations in the data and/or model/algorithm parameters

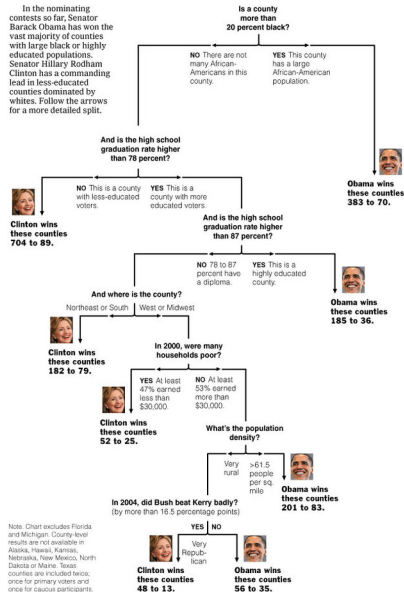
Their approach to manage this is to build a lot of different trees using random partitions of the data.

Their approach is a little unconventional (for reasons they don't provide).

Instead, we'll soon talk about formal strategies to deal with this sensitivity – boosting, bagging and random forests.

Classification trees (Covered 11/8, not 11/6)

Decision Tree: The Obama-Clinton Divide



What's a classification tree?

As you might imagine, it's just like a regression tree, but we use it to predict a categorical or qualitative variable.

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What's a classification tree?

As you might imagine, it's just like a regression tree, but we use it to predict a categorical or qualitative variable.

Rather than setting the prediction equal to the mean, the prediction is:

the most commonly occurring class within the partition.

However we still use recursive binary splitting and cost-complexity pruning

Though the *criteria* for splitting and pruning will have to change

What's the error?

The typical error, $\text{RSS} = \sum_{i=1}^N (y_i - \hat{y}_i)^2$ won't work.

Alternatives? Let's start by defining

p_{mk} = fraction of observations belonging to class k in region m .

Then a simple measure is:

Classification error rate = how many training observations don't fall into the assigned class.

Within-region this is simply:

$$E_m = 1 - \max_k (\hat{p}_{mk})$$

The trouble with Classification Error

Suppose you have a two-class problem with 400 observations in each class. Consider two possible splits (S1 and S2):

S1: $R_1 : (100, 300), R_2 : (300, 100) \Rightarrow$ weighted error $E_{S1} = 0.25$

S2: $R_1 : (200, 400), R_2 : (200, 0) \Rightarrow$ weighted error $E_{S2} = 0.25$

Can you make a case for one of these being preferable to the other?

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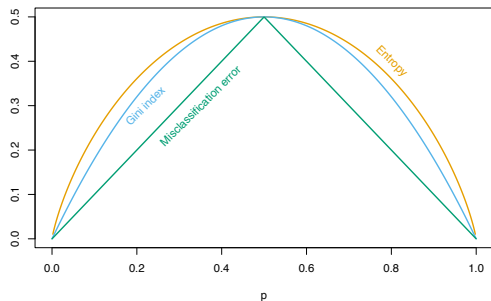
S2: $R_1 : (200, 400), R_2 : (200, 0) \Rightarrow$ weighted error $E_{S2} = 0.25$

Can you make a case for one of these being preferable to the other?

S2 has a “pure” split, meaning there are *no* errors in one of the splits. You won't need to split this region any further.

Alternative errors

Remember, p_{mk} = fraction of observations in class k in region m .



(Measures for two-class classification; p is the proportion in class 2. Cross-entropy scaled to pass through (0.5, 0.5).)

$$E_m = 1 - \max_k(\hat{p}_{mk})$$

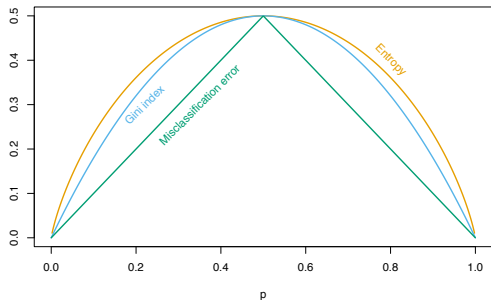
$$G_m = \sum_{k=1}^K \hat{p}_{mk}(1 - \hat{p}_{mk}) \quad \text{"Gini"}$$

$$D_m = - \sum_{k=1}^K \hat{p}_{mk} \log \hat{p}_{mk} \quad \text{"Entropy"}$$

G and D have two advantages:

- 1 Differentiable everywhere – good for optimization
- 2 Score better for “pure” splits

Why do Gini and Entropy score pure splits better?

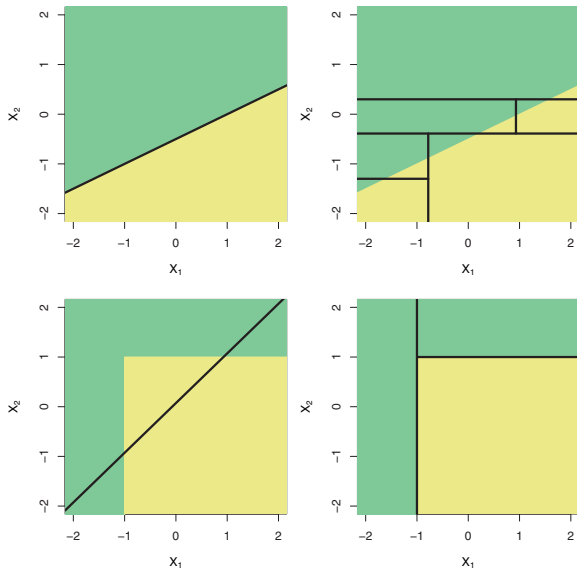


- Misclassification indifferent between
 - 1 two regions with $p = 0.0$ and $p = 0.4$ or
 - 2 two regions with $p = 0.2$ and $p = 0.2$.
- ...but Gini and cross entropy would clearly prefer the first option.

Which error rate to use?

- Since they are more “sensitive” to pure splits, it’s better to use either Gini or cross-entropy when *growing* the tree.
- Any of the three measures can be used for cost-complexity pruning. Common practice is to use the misclassification rate.
 - ▶ That’s because prediction is usually the final goal, and misclassification measures ability to do that.

When are trees better than linear models?



Reminder: advantages and disadvantages

Advantages

- Easy to explain and non-experts can understand the results.
- They're more like human decision-making. Doctors like them.
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Disadvantages

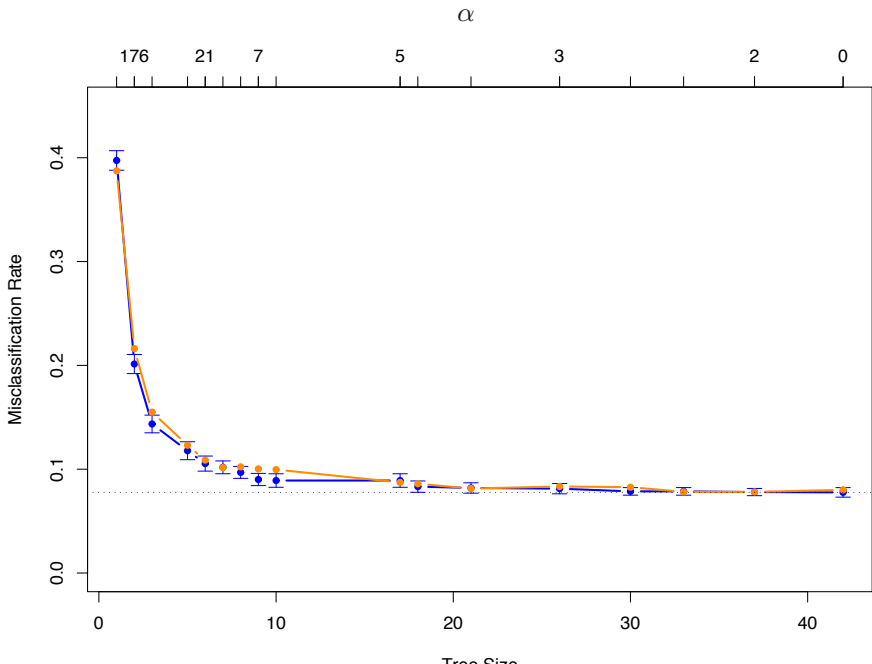
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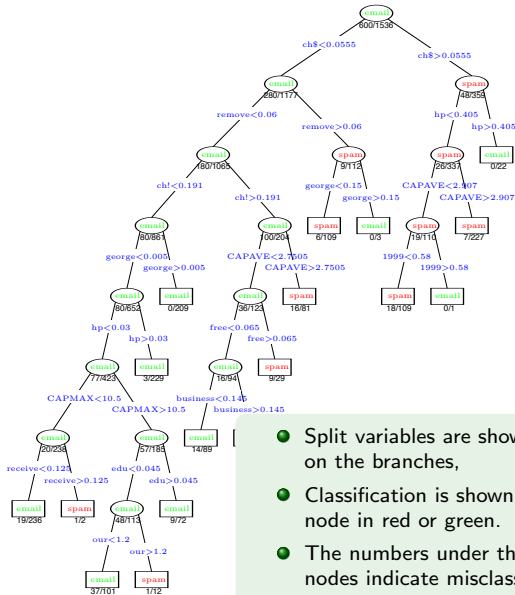
Supplemental Slides

A spam example

Email data set, donated by George Forman from HP. 4601 messages.

- 48 quantitative predictors: the percentage of words in the email that match a given word. Examples include business, address, internet, free, and george. (These could be customized for individual users.)
- 6 quantitative predictors: the percentage of characters in the email that match a given character. The characters are ch;, ch(, ch[, ch!, ch\$, and ch#.
- The average length of uninterrupted sequences of capital letters: CAPAVE.
- The length of the longest uninterrupted sequence of capital letters: CAPMAX.
- The sum of the length of uninterrupted sequences of capital letters: CAPTOT.





- Split variables are shown in blue on the branches,
- Classification is shown in every node in red or green.
- The numbers under the terminal nodes indicate misclassification rates on the test data.

Figure from ESLII

A zoom in

