

# Classification and Regression Trees

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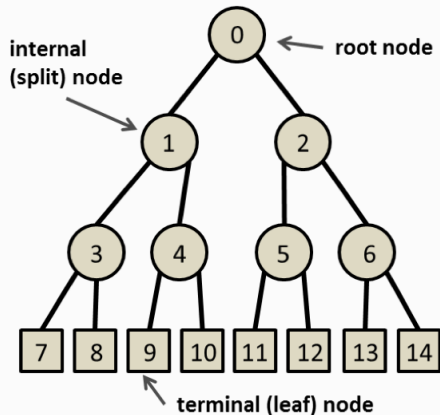
# Contents

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# Trees

# Tree Terminology

## A general tree structure



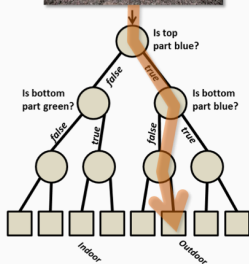
From Criminisi et al. MSR-TR-2011-114, 28 October 2011.

# A Binary Decision Tree

**binary tree:** each node has either 2 children or 0 children



A decision tree

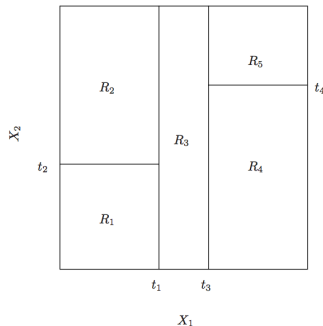
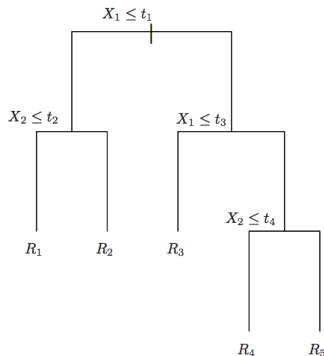


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From Criminisi et al. MSR-TR-2011-114, 28 October 2011.

# Binary Decision Tree on $\mathbf{R}^2$

- Consider a binary tree on  $\{(X_1, X_2) \mid X_1, X_2 \in \mathbf{R}\}$



From *An Introduction to Statistical Learning, with applications in R* (Springer, 2013) with permission from the authors: G. James, D. Witten, T. Hastie and R. Tibshirani.

# Types of Decision Trees

- We'll only consider
  - **binary trees** (vs multiway trees where nodes can have more than 2 children)
  - decisions at each node involve only a single feature (i.e. input coordinate)
  - for continuous variables, splits always of the form

$$x_i \leq t$$

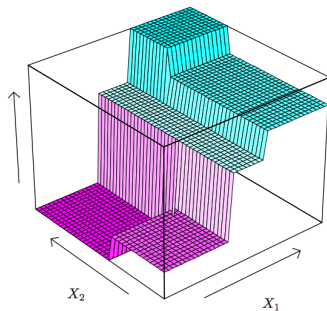
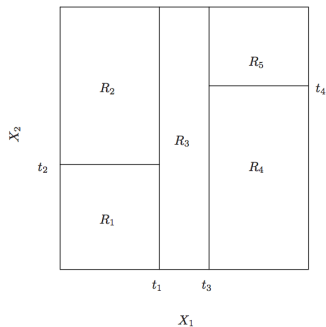
- for discrete variables, partitions values into two groups
- Other types of splitting rules
  - **oblique decision trees** or **binary space partition trees** (BSP trees) have a linear split at each node
  - **sphere trees** – space is partitioned by a sphere of a certain radius around a fixed point

# Regression Trees



# Binary Regression Tree on $\mathbf{R}^2$

- Consider a binary tree on  $\{(X_1, X_2) \mid X_1, X_2 \in \mathbf{R}\}$



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# Fitting a Regression Tree

- The decision tree gives the partition of  $\mathcal{X}$  into regions:

$$\{R_1, \dots, R_M\}.$$

- Recall that a partition is a **disjoint union**, that is:

$$\mathcal{X} = R_1 \cup R_2 \cup \dots \cup R_M$$

and

$$R_i \cap R_j = \emptyset \quad \forall i \neq j$$

# Fitting a Regression Tree

- Given the partition  $\{R_1, \dots, R_M\}$ , final prediction is

$$f(x) = \sum_{m=1}^M c_m 1(x \in R_m)$$

- How to choose  $c_1, \dots, c_M$ ?
- For loss function  $\ell(\hat{y}, y) = (\hat{y} - y)^2$ , best is

$$\hat{c}_m = \text{ave}(y_i \mid x_i \in R_m).$$

# Trees and Overfitting

- If we do enough splitting, every unique  $x$  value will be in its own partition.
- This very likely overfits.
- As usual, we need to control the complexity of our hypothesis space.
- CART (Breiman et al. 1984) uses **number of terminal nodes**.
- Tree depth is also common.

# Complexity of a Tree

- Let  $|T| = M$  denote the number of terminal nodes in  $T$ .
- We will use  $|T|$  to measure the complexity of a tree.
- For any given complexity,
  - we want the tree minimizing square error on training set.
- Finding the optimal binary tree of a given complexity is computationally intractable.
- We proceed with a **greedy algorithm**
  - Means build the tree one node at a time, without any planning ahead.

# Root Node, Continuous Variables

- Let  $x = (x_1, \dots, x_d) \in \mathbf{R}^d$ . ( $d$  features)
- **Splitting variable**  $j \in \{1, \dots, d\}$ .
- **Split point**  $s \in \mathbf{R}$ .
- Partition based on  $j$  and  $s$ :

$$R_1(j, s) = \{x \mid x_j \leq s\}$$

$$R_2(j, s) = \{x \mid x_j > s\}$$

# Root Node, Continuous Variables

- For each splitting variable  $j$  and split point  $s$ ,

$$\hat{c}_1(j, s) = \text{ave}(y_i \mid x_i \in R_1(j, s))$$

$$\hat{c}_2(j, s) = \text{ave}(y_i \mid x_i \in R_2(j, s))$$

- Find  $j, s$  minimizing loss

$$L(j, s) = \sum_{i: x_i \in R_1(j, s)} (y_i - \hat{c}_1(j, s))^2 + \sum_{i: x_i \in R_2(j, s)} (y_i - \hat{c}_2(j, s))^2$$

- How?

# Finding the Split Point

- Consider splitting on the  $j$ 'th feature  $x_j$ .
- If  $x_{j(1)}, \dots, x_{j(n)}$  are the sorted values of the  $j$ 'th feature,
  - we only need to check split points between adjacent values
  - traditionally take split points halfway between adjacent values:

$$s_j \in \left\{ \frac{1}{2} (x_{j(r)} + x_{j(r+1)}) \mid r = 1, \dots, n-1 \right\}.$$

- So only need to check performance of  $n-1$  splits.



## Then Proceed Recursively

- 1 We have determined  $R_1$  and  $R_2$
  - 2 Find best split for points in  $R_1$
  - 3 Find best split for points in  $R_2$
  - 4 Continue...
- When do we stop?

# Complexity Control Strategy

- If the tree is too big, we may overfit.
- If too small, we may miss patterns in the data (underfit).
- Can limit max depth of tree.
- Can require all leaf nodes contain a minimum number of points.
- Can require a node have at least a certain number of data points to split.
- Can do **backward pruning** – the approach of **CART** (Breiman et al 1984):
  - 1 Build a really big tree (e.g. until all regions have  $\leq 5$  points).
  - 2 “**Prune**” the tree back greedily all the way to the root, assessing performance on validation.

# Classification Trees

# Classification Trees

- Consider classification case:  $\mathcal{Y} = \{1, 2, \dots, K\}$ .
- We need to modify
  - criteria for splitting nodes

# Classification Trees

- Let node  $m$  represent region  $R_m$ , with  $N_m$  observations
- Denote proportion of observations in  $R_m$  with class  $k$  by

$$\hat{p}_{mk} = \frac{1}{N_m} \sum_{\{i: x_i \in R_m\}} 1(y_i = k).$$

- **Predicted classification** for node  $m$  is

$$k(m) = \arg \max_k \hat{p}_{mk}.$$

- **Predicted class probability distribution** is  $(\hat{p}_{m1}, \dots, \hat{p}_{mK})$ .

# Misclassification Error

- Consider node  $m$  representing region  $R_m$ , with  $N_m$  observations
- Suppose we predict

$$k(m) = \arg \max_k \hat{p}_{mk}$$

as the class for all inputs in region  $R_m$ .

- What is the misclassification rate on the training data?
- It's just

$$1 - \hat{p}_{mk(m)}.$$

# What loss function to use for node splitting?

- Natural loss function for classification is 0/1 loss.
- Is this tractable for finding the best split? Yes!
- Should we use it? Maybe not!
- If we're only splitting once, then make sense to split using ultimate loss function (say 0/1).
- But we can split nodes repeatedly – don't have to get it right all at once.

# Splitting Example

- Two class problem: 4 observations in each class.
- Split 1: (3,1) and (1,3) [each region has 3 of one class and 1 of other]
- Split 2: (2,4) and (2,0) [one region has 2 of one class and 4 of other, other region pure]
- Misclassification rate for the two splits are same. (2).
- In split 1, we'll want to split each node again, and
  - we'll end up with a leaf node with a single element.
- In split 2, we're already done with the node (2,0).

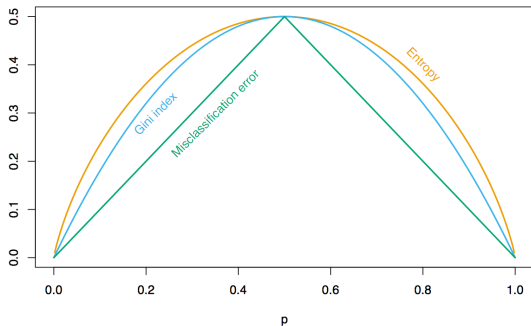


# Splitting Criteria

- Eventually we want **pure** leaf nodes (i.e. as close to a single class as possible).
- We'll find splitting variables and split point minimizing some **node impurity** measure.

# Two-Class Node Impurity Measures

- Consider binary classification
- Let  $p$  be the relative frequency of class 1.
- Here are three node impurity measures as a function of  $p$



HTF Figure 9.3

# Classification Trees: Node Impurity Measures

- Consider leaf node  $m$  representing region  $R_m$ , with  $N_m$  observations
- Three measures  $Q_m(T)$  of **node impurity** for leaf node  $m$ :

- Misclassification error:

$$1 - \hat{p}_{mk(m)}.$$

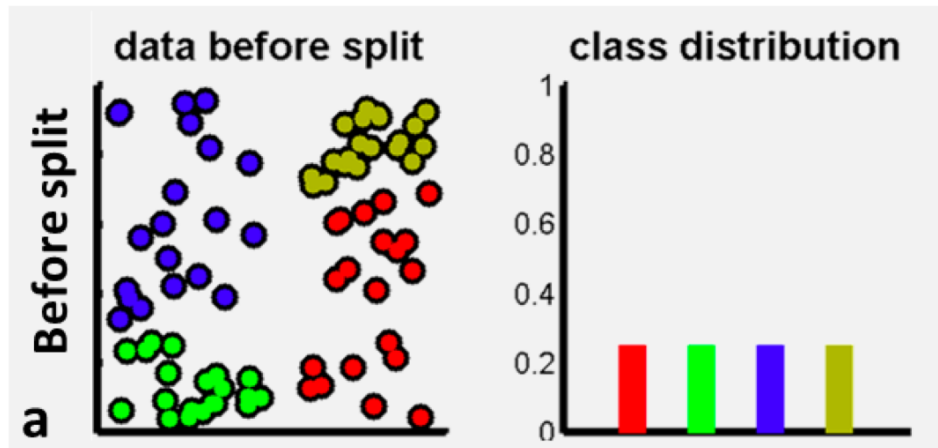
- Gini index:

$$\sum_{k=1}^K \hat{p}_{mk}(1 - \hat{p}_{mk})$$

- Entropy or deviance (equivalent to using information gain):

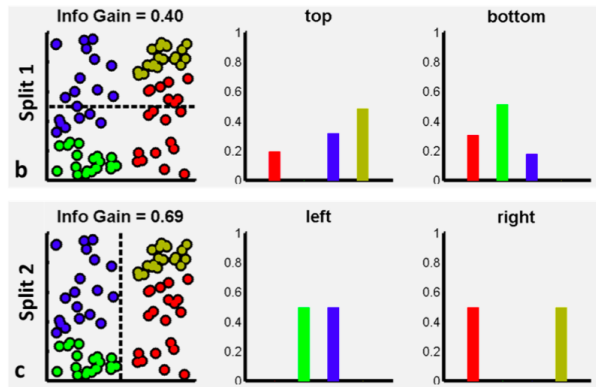
$$-\sum_{k=1}^K \hat{p}_{mk} \log \hat{p}_{mk}.$$

# Class Distributions: Pre-split



From Criminisi et al. MSR-TR-2011-114, 28 October 2011.

# Class Distributions: Split Search



(Maximizing information gain is equivalent to minimizing entropy.)

## Splitting nodes: How exactly do we do this?

- Let  $R_L$  and  $R_R$  be regions corresponding to a potential node split.
- Suppose we have  $N_L$  points in  $R_L$  and  $N_R$  points in  $R_R$ .
- Let  $Q(R_L)$  and  $Q(R_R)$  be the node impurity measures.
- Then find split that minimizes the **weighted average of node impurities**:

$$N_L Q(R_L) + N_R Q(R_R)$$

# Classification Trees: Node Impurity Measures

- For building the tree, Gini and Entropy seem to be more effective.
- They push for more pure nodes, not just misclassification rate
- A good split may not change misclassification rate at all!
- Two class problem: 4 observations in each class.
- Split 1: (3,1) and (1,3) [each region has 3 of one class and 1 of other]
- Split 2: (2,4) and (2,0) [one region has 2 of one class and 4 of other, other region pure]
- Misclassification rate for two splits are same.
- **Gini and entropy split prefer Split 2.**

## Trees in General



- What to do about missing features?
  - Throw out inputs with missing features
  - Impute missing values with feature means
  - If a categorical feature, let “missing” be a new category.
- For trees, we can use **surrogate splits**
  - For every internal node, form a list of surrogate features and split points
  - Goal is to approximate the original split as well as possible
  - Surrogates ordered by how well they approximate the original split.
    - In terms of how many examples are sent in the same direction by each split.

# Categorical Features

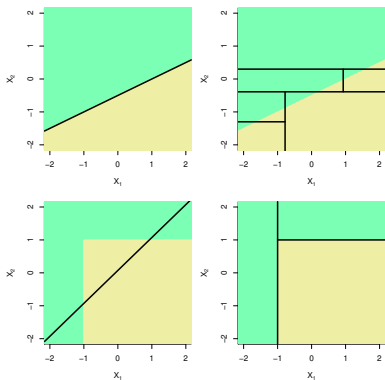
- Suppose we have a categorical feature with  $q$  possible values (unordered).
- We want to find the best split into 2 groups
- There are  $2^{q-1} - 1$  distinct splits.
- Is this tractable? Maybe not in general. But...
- For binary classification  $\mathcal{Y} = \{0, 1\}$ , there is an efficient algorithm.

# Categorical Features in Binary Classification

- Assign each category a number
  - the proportion of class 0 among training examples with that category.
- Then find optimal split as though it were a numeric feature.
- Proved to be equivalent to search over all splits in (Breiman et al. 1984).
- (This trick doesn't work for multiclass – would have to use approximations...)
- Statistical issues with categorical features?
  - If a category has a very large number of categories, we can overfit.
  - Extreme example: Row Number could lead to perfect classification with a single split.

# Trees vs Linear Models

- Trees have to work much harder to capture linear relations.



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- Trees are certainly easy to explain.
- You can show a tree on a slide.
- Small trees seem interpretable.
- For large trees, maybe not so easy.

# Trees for Nonlinear Feature Discovery

- Suppose tree  $T$  gives partition  $R_1, \dots, R_M$ .
- Predictions are

$$f(x) = \sum_{m=1}^M c_m 1(x \in R_m)$$

- Each region  $R_m$  can be viewed as giving a feature function  $x \mapsto 1(x \in R_m)$ .
- Can use these nonlinear features in e.g. lasso regression.

- Trees make no use of **geometry**
  - No inner products or distances
  - called a “nonmetric” method
  - **Feature scale irrelevant**
- Prediction functions are not continuous
  - not so bad for classification
  - may not be desirable for regression

## Appendix: Tree Pruning

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# Stopping Conditions for Building the Big Tree

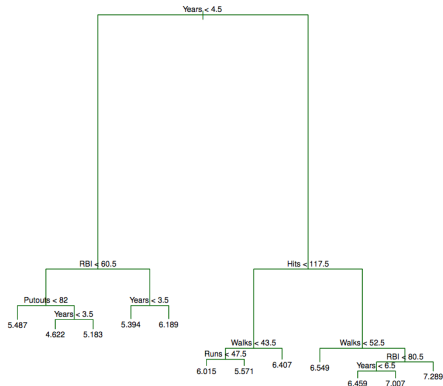
- First step is to build the “big tree”.
- Keep splitting nodes until every node either has
  - Zero error OR
  - Node has  $C$  or fewer examples (typically  $C = 5$  or  $C = 1$ ) OR
  - All inputs in node are identical (and thus we cannot split more)

# Pruning the Tree

- Consider an internal node  $n$ .
- To prune the subtree rooted at  $n$ 
  - eliminate all descendants of  $n$
  - $n$  becomes a terminal node

# Tree Pruning

- Full Tree  $T_0$



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# Tree Pruning

- Subtree  $T \subset T_0$



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# Empirical Risk and Tree Complexity

- Suppose we want to prune a big tree  $T_0$ .
- Let  $\hat{R}(T)$  be the empirical risk of  $T$  (i.e. square error on training)
- Clearly, for any subtree  $T \subset T_0$ ,  $\hat{R}(T) \geq \hat{R}(T_0)$ .
- Let  $|T|$  be the number of terminal nodes in  $T$ .
- $|T|$  is our measure of complexity for a tree.

# Cost Complexity (or Weakest Link) Pruning

## Definitions

The **cost complexity criterion** with parameter  $\alpha$  is

$$C_{\alpha}(T) = \hat{R}(T) + \alpha|T|$$

- Trades off between empirical risk and complexity of tree.
- Cost complexity pruning:
  - For each  $\alpha$ , find the subtree  $T \subset T_0$  minimizing  $C_{\alpha}(T)$  (on training data).
  - Use cross validation to find the right choice of  $\alpha$ .

# Do we need to search over all subtrees?

- The **cost complexity criterion** with parameter  $\alpha$  is

$$C_\alpha(T) = \hat{R}(T) + \alpha|T|$$

- $C_\alpha(T)$  has familiar regularized ERM form, but
- Cannot just differentiate w.r.t. parameters of a tree  $T$ .
- To minimize  $C_\alpha(T)$  over subtrees  $T \subset T_0$ ,
  - seems like we need to evaluate exponentially many<sup>1</sup> subtrees  $T \subset T_0$ .
  - (In particular, we can include or exclude any subset of internal nodes that are parents of leaf nodes.)
- Amazingly, we only need to try  $N_{\text{Int}}$ , where  $N_{\text{Int}}$  is the number of internal nodes of  $T_0$ .

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<sup>1</sup>See [On subtrees of trees](#).

# Cost Complexity Greedy Pruning Algorithm

- Find a proper<sup>2</sup> subtree  $T_1 \subset T_0$  that minimizes  $\hat{R}(T_1) - \hat{R}(T_0)$ .
  - Can get  $T_1$  by removing a single pair of leaf nodes, and their internal node parent becomes a leaf node.
  - This  $T_1$  will have 1 fewer internal node than  $T_0$ . (And 1 fewer leaf node.)
- Then find proper subtree  $T_2 \subset T_1$  that minimizes  $\hat{R}(T_2) - \hat{R}(T_1)$ .
- Repeat until we have removed all internal nodes are left with just a single node (a leaf node).
- If  $N_{\text{Int}}$  is the number of internal nodes of  $T_0$ , then we end up with a nested sequence of trees:

$$\mathcal{T} = \{T_0 \supset T_1 \supset T_2 \supset \cdots \supset T_{|N_{\text{Int}}|}\}$$

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<sup>2</sup>  $T_1$  is a proper subtree of  $T_0$  if tree  $T_1 \subset T_0$  and  $T_1 \neq T_0$ .



# Greedy Pruning is Sufficient

- Cost complexity pruning algorithm gives us a set of nested trees:

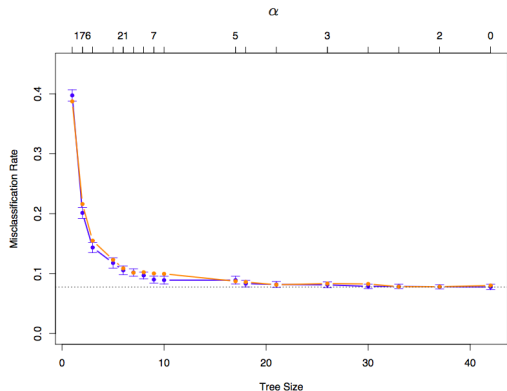
$$\mathcal{T} = \{T_0 \supset T_1 \supset T_2 \supset \cdots \supset T_{|N_{\text{Int}}|}\}$$

- Breiman et al. (1984) proved that this is all you need. That is:

$$\left\{ \arg \min_{T \in \mathcal{T}} C_\alpha(T) \mid \alpha \geq 0 \right\} \subset \mathcal{T}$$

- Only need to evaluate  $N_{\text{Int}}$  trees.

## Regularization Path for Trees on SPAM dataset (HTF Figure 9.4)



For each  $\alpha$ , we find optimal tree  $T_\alpha$  on training set. Corresponding tree size  $|T_\alpha|$  is shown on bottom. Blue curves gives error rate estimates from cross-validation (tree-size in each fold may be different from  $|T_\alpha|$ ). Orange curve is test error.