# MATH 567: Mathematical Techniques in Data Science

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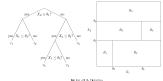
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#### Decision trees

#### Tree-based methods:

- · Partition the feature space into a set of rectangles.
- Fit a simple model (e.g. a constant) in each rectangle.
- Conceptually simple vet powerful.



Tanner, 2013, Figure 1

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## Example: spam data

in person.

### Decision trees

## Advantages:

- Often mimics human decision-making process (e.g. doctor examining patient).
- Very easy to explain and interpret.
- Can handle both regression and classification problems.

#### Disadvantage:

- Basic implementation is generally not competitive compared to other methods.
- However, by aggregating many decision trees and using other variants, one can improve the performance significantly.
- Such techniques lead to state of the art models.
- However, in doing so, one loses the easy interpretability of decision trees.

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#### Binary decision trees

To simplify, we will only consider binary decision trees.



Top Left: Not binary. Top Right: binary. Bottom Left: Tree corresponding to Top Right partition, Bottom Right: Prediction surface,

How to grow a decision tree?

#### Regression tree:

• Data:  $y \in \mathbb{R}^n$ ,  $X \in \mathbb{R}^{n \times p}$ .

• Each observation:  $(u_i, x_i) \in \mathbb{R}^{p+1}$ , i = 1, ..., n,

Suppose we have a partition of  $\mathbb{R}^p$  into M regions  $R_1, \dots, R_m$ .

We predict the response using a constant on each  $R_i$ :

$$f(x) = \sum_{i=1}^{m} c_i \cdot \mathbf{1}_{x \in R_i}$$
.

In order to minimize  $\sum_{i=1}^{n} (y_i - f(x_i))^2$ , one needs to choose:  $\hat{c}_i = \text{ave}(u_i : x_i \in R_i),$ 

$$c_i = \text{ave}(y_j : x_j \in R_i)$$

How do we determine the regions  $R_i$ , i.e., how do we "grow" the tree?

- We need to decide:
- Which variable to solit.
- Where to solit that variable.

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## Growing a tree

- Finding a (globally) optimal tree is generally computationally info scible
- · We use a greedy algorithm.
- Consider a splitting variable  $i \in \{1, ..., p\}$  and splitting point
- $s \in \mathbb{R}$ . Define the two half-planes:

 $R_1(i, s) := \{x \in \mathbb{R}^p : x_i \le s\}, R_2(i, s) := \{x \in \mathbb{R}^p : x_i > s\},$ 

We choose 
$$j,s$$
 to minimize 
$$\min_{j,s} \left[ \min_{c_1 \in \mathbb{R}} \sum_{x_i \in R_1(j,s)} (y_i - c_1)^2 + \min_{c_2 \in \mathbb{R}} \sum_{x_i \in R_2(j,s)} (y_i - c_2)^2 \right].$$

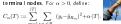
- The determination of the splitting point s can be done very a nickly
- Hence, determining the best pair (j, s) is feasible.

Repeat the same process to each block.

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## Stopping rules and pruning

- · Generally, the process is stopped for a given region when there are less than 5 observations in that region.
- Problem with previous methodology:
- Likely to overfit the data.
- Can lead to poor prediction error.
- Pruning the tree. Strategy: Grow a large tree (overfits), and the prune it (better).
- Weakest link pruning:
- (a.k.a cost complexity pruning) Let  $T \subset T_0$  be a **subtree** of  $T_0$  with |T|
- terminal nodes. For  $\alpha > 0$ , define:





Pick a subtree minimizing  $C_{\alpha}(T)$ .

### Pruning (cont.)

Pick a subtree  $T \subset T_0$  minimizing:

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

(Here,  $\hat{y}_{R_m}$  =average response for observations in  $R_m$ .)

- α is a tuning parameter.
- Trade-off between fit of the model, and tree complexity.
- Choose α using cross-validation.

Once  $\alpha$  has been chosen by CV, use whole dataset to find the tree corresponding to that value.

Classification trees

- . So far, we discussed regression trees (continuous output).
- We can easily modify the methodology to predict a categorical output.
- We only need to modify our splitting and pruning criteria. For continuous variables, we picked a constant in each box  $R_i$  to minimize the sum of squares in that region

$$\min_{c \in \mathbb{R}} \sum_{x, c \in R} (y_i - c)^2.$$

As a result, we choose:

$$\hat{c}_i = \frac{1}{N_i} \sum_{x_k \in R_i} y_k,$$

where  $N_i$  denotes the number of observations in  $R_i$ .

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## Classification trees (cont.)

Similarly, when the output is categorical, we can count the proportion of class k observations in node i:

$$\hat{p}_{ik} = \frac{1}{N_i} \sum_{i} \mathbf{1}_{y_i \in R_i}$$
.

We then classify the observations in node i using a majority vote:

$$k(i) := \operatorname{argmax} \hat{p}_{ik}$$
.

Different measures are commonly used to determine how good a given partition is (and how to split a given partition):

- $\bullet$  Misclassification error:  $\frac{1}{N_i} \sum_{x_l \in R_i} \mathbf{1}_{y_l \neq k(i)} = 1 \hat{p}_{i,k(i)}$
- **9** Gini index:  $\sum_{k \neq k'} \hat{p}_{ik} \hat{p}_{ik'} = \sum_{k=1}^{K} \hat{p}_{ik} (1 \hat{p}_{ik})$ .
- ② Cross-entropy (or deviance):  $-\sum_{k=1}^K \hat{p}_{ik} \log \hat{p}_{ik}$ .

## Classification trees (cont.)

With two classes and a proportion of 0 observations in the second class, we have (exercise):

 $\begin{array}{lll} \text{Measure} & \text{Value} \\ \\ \text{Misclassification error} & 1 - \max(p, 1-p) \\ \text{Gini index} & 2p(1-p) \\ \text{Cross-entropy} & -p\log p - (1-p)\log(1-p) \end{array}$ 



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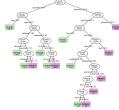
## Case study: Pima Indians Diabetes (Izenman, 2013)

- Pima Indian (nativa American) population lives near Phoenix, Arizona.
- The diversion of the water and the introduction of non-native diet had devastating effects on the health of the people. They have the lighest prevalence of type 2 diabetes in the world, much more than is observed in other U.S. populations. They have been the subject of intensive study of libetes.
- Patients listed in the dataset are females at least 21 years old of Pima Indian heritage.
- 8 input variables (e.g. number of times pregnant, body mass index, plasma glucose concentration, etc.).

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#### Case study (cont.)



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