Big Data Computing

Master's Degree in Computer Science 2021-2022

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Recap from Last Lecture

- Decision Trees (DTs) highly **expressive** yet **interpretable** models both for regression and classification
- Learning the optimal DT is NP-Complete: Recursive Binary Splitting algorithm is an effective greedy training heuristic
- Regression Trees:
 - Use Residual Sum of Squares (RSS) as splitting criterion
 - At inference time, predictions are the mean of the leaf observations

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- Very similar to a regression tree
- Used to predict a categorical response rather than a numerical one
- Tree building is still based on Recursive Binary Splitting algorithm but RSS cannot be used as a criterion for splitting nodes
- A natural alternative to RSS minimization is to minimize the "impurity"
- The predicted label of a test instance is the most frequent label (mode) of the instances belonging to the region where it falls

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- We would like to grow a tree whose nodes are as purest as possible
- Several different measures to represent this notion of node "impurity":
 - Classification Error Rate
 - Gini Index
 - Entropy
- It is often convenient to refer to the information gain of a split

Subset of training instances falling into region R
$$\mathcal{D}_R = \mathcal{D} \cap R = \{ (\mathbf{x}_i, y_i) \in \mathcal{D} \mid \mathbf{x}_i \in R \}$$

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impurity of a region $I(\mathcal{D}_R)$

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$$IG(\mathcal{D}_{R}, f, s) = \underbrace{I(\mathcal{D}_{R})}_{\text{parent node's impurity}} - \underbrace{\left[\frac{|\mathcal{D}_{R_{\text{left}}(f, s)}|}{|\mathcal{D}_{R}|}I(\mathcal{D}_{R_{\text{left}}(f, s)}) + \frac{|\mathcal{D}_{R_{\text{right}}(f, s)}|}{|\mathcal{D}_{R}|}I(\mathcal{D}_{R_{\text{right}}(f, s)})\right]}_{\text{parent node's impurity}}$$

children nodes' impurity

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- Although this is the most intuitive notion of impurity we will see how this may not be a great choice
- Other 2 measures are preferable: Gini Index and Entropy

Node Impurity: Gini Index

• Measures the variance across the K classes

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- A small value of Gini is obtained whenever all the proportions are either close to 1 or to 0
- A small value indicates that a node contains predominantly observations from a single class

• Alternative, yet similar to Gini

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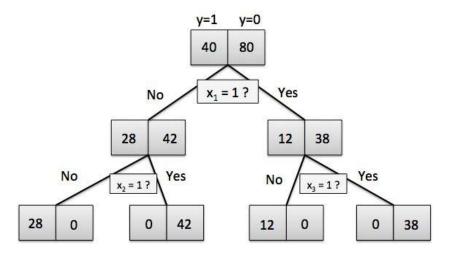
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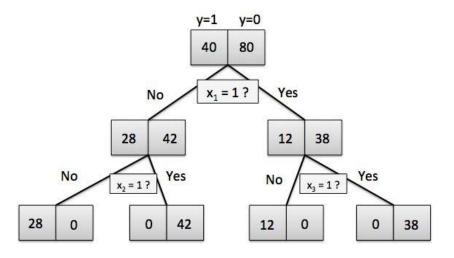
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- It ranges between [0, +infinity]
- Like Gini, a small value of entropy is obtained whenever all the proportions are either close to 1 or to 0
- In practice, both entropy and Gini can be used to grow a tree

Consider this decision tree which perfectly separates positive (y=1) from negative (y=0) samples using 3 splits on 3 binary features x_1, x_2, x_3



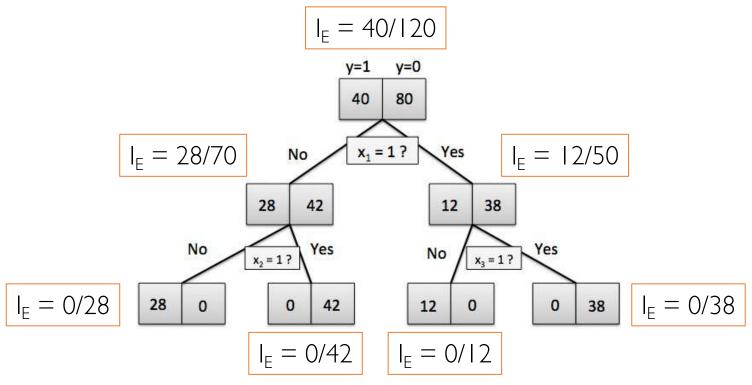
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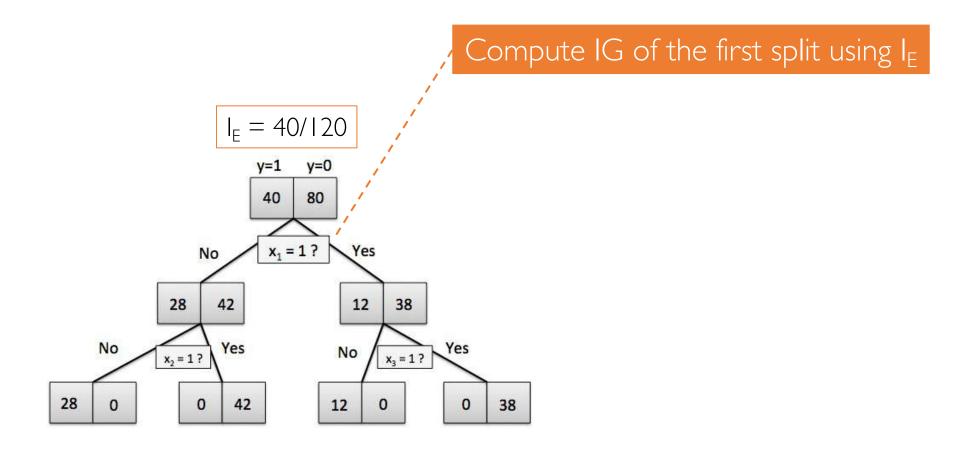
Question

Would we be able to learn the tree above using classification error rate as splitting criterion?

Node impurity using I_E



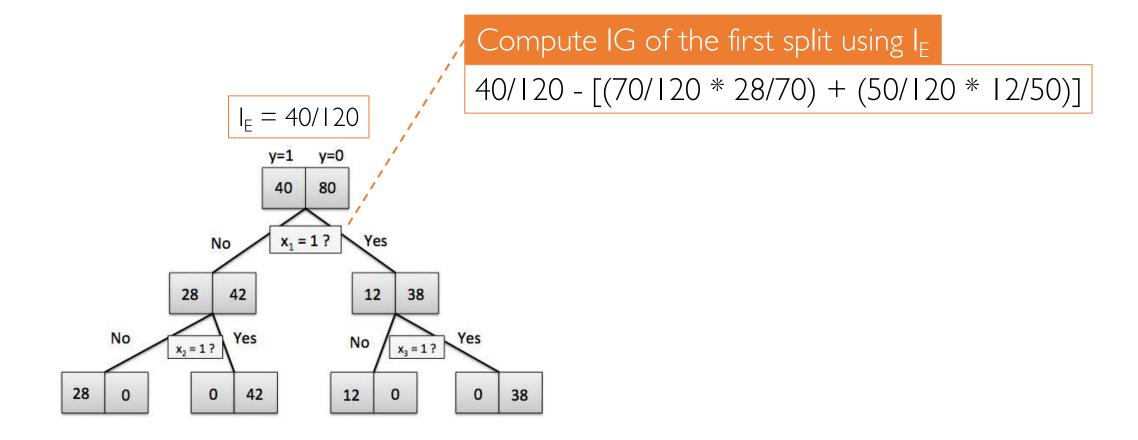
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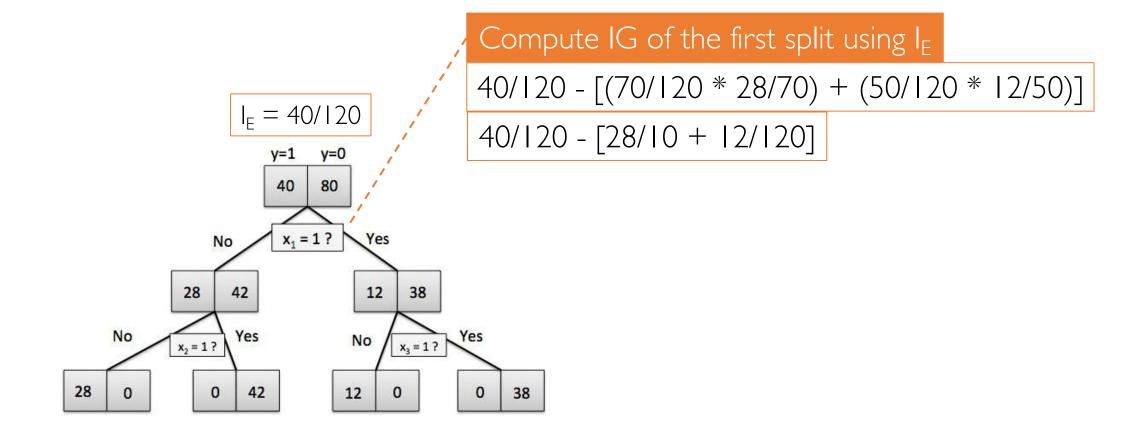
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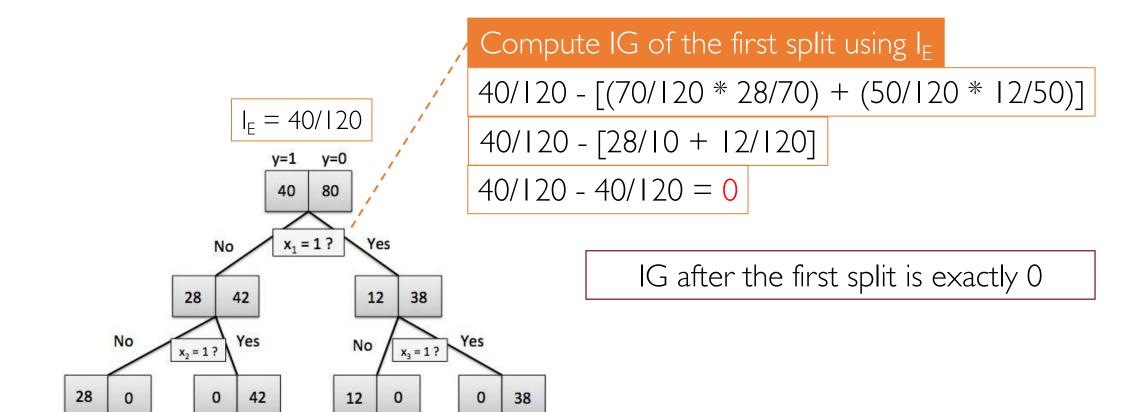


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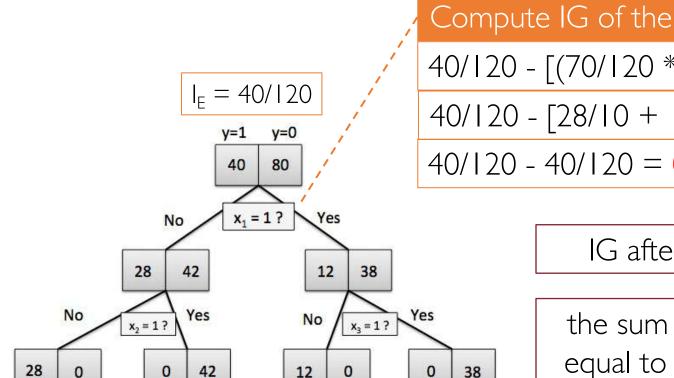


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Compute IG of the first split using I_F

40/120 - [(70/120 * 28/70) + (50/120 * 12/50)]

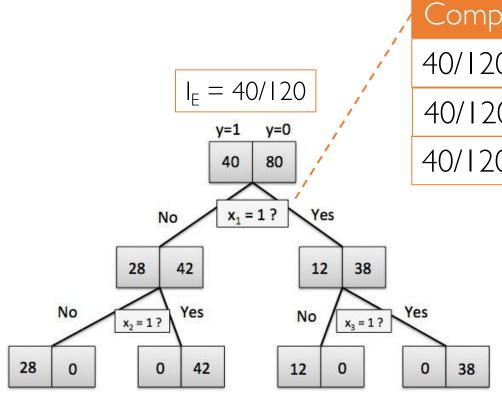
40/120 - [28/10 + 12/120]

40/120 - 40/120 = 0

IG after the first split is exactly 0

the sum of I_F of the 2 child nodes is equal to that of the parent (40/120)

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Compute IG of the first split using I_E

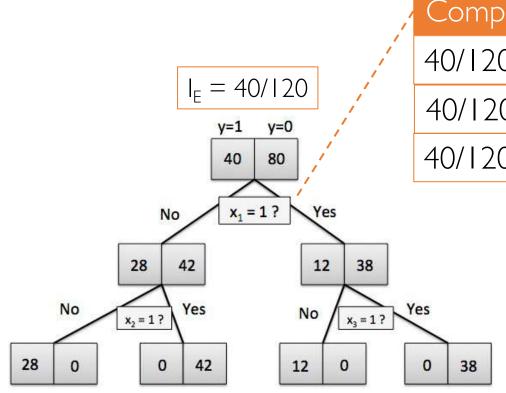
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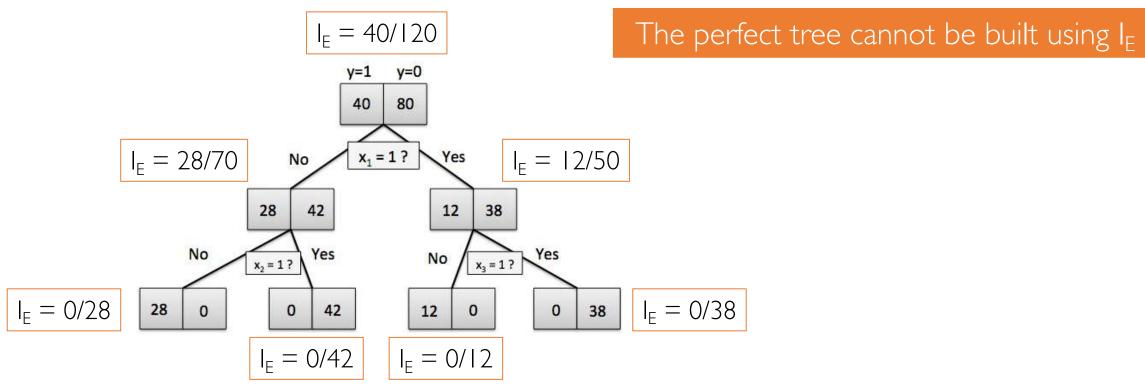
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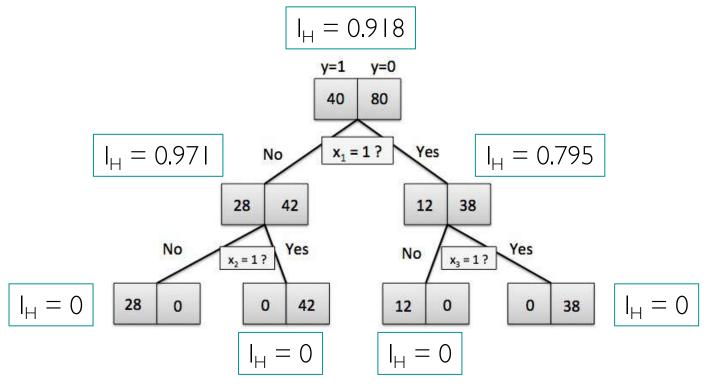
The tree learning algorithm would stop at this point

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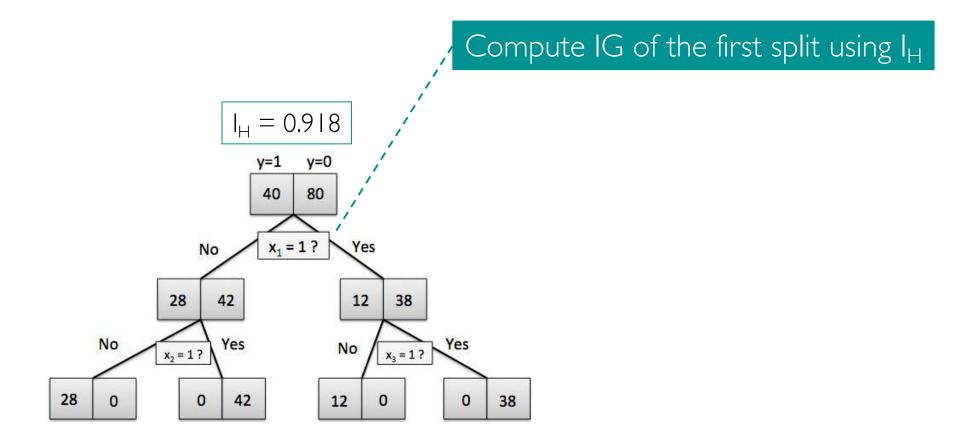


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Node impurity using I_H

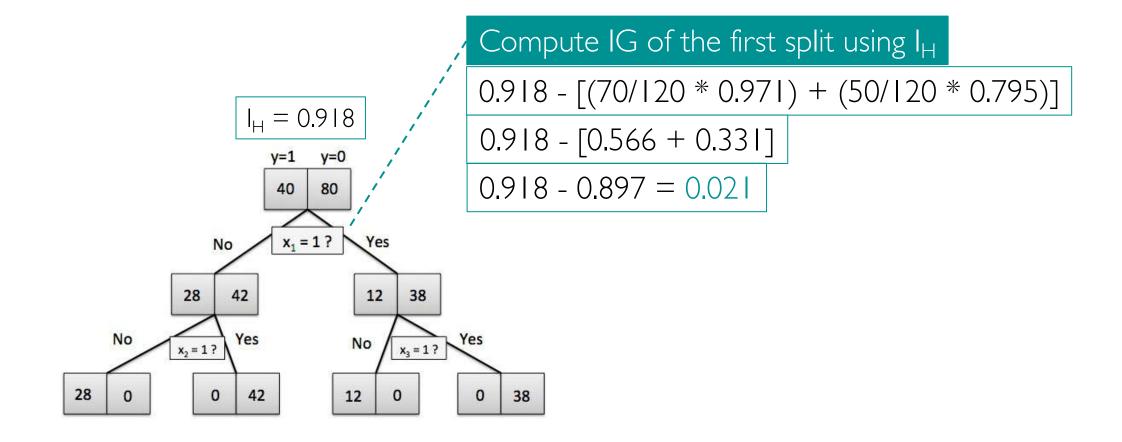


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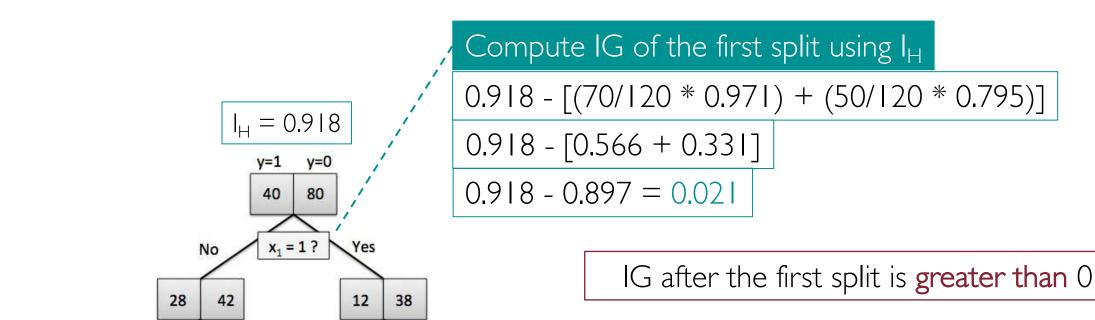
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No

12

Yes

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 $x_2 = 1$?

No

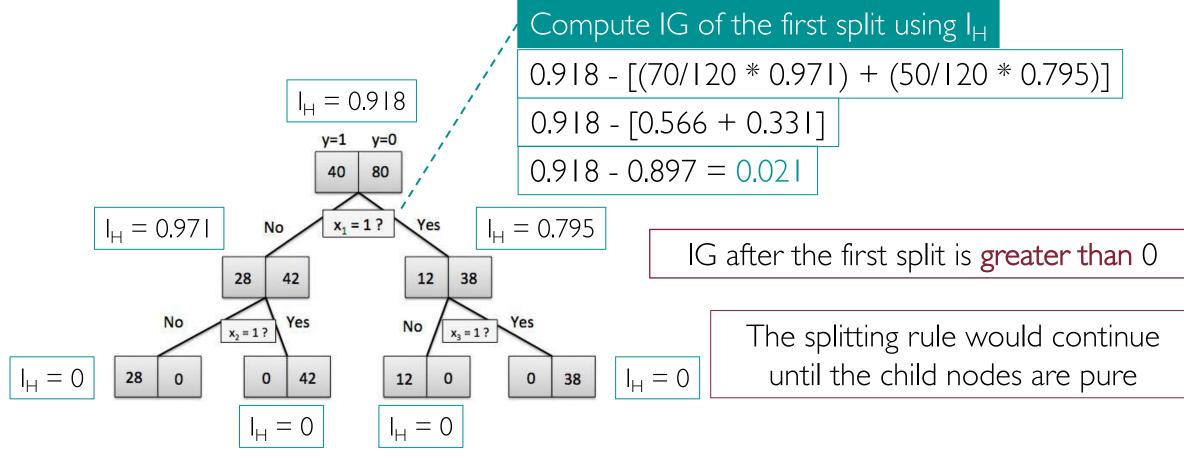
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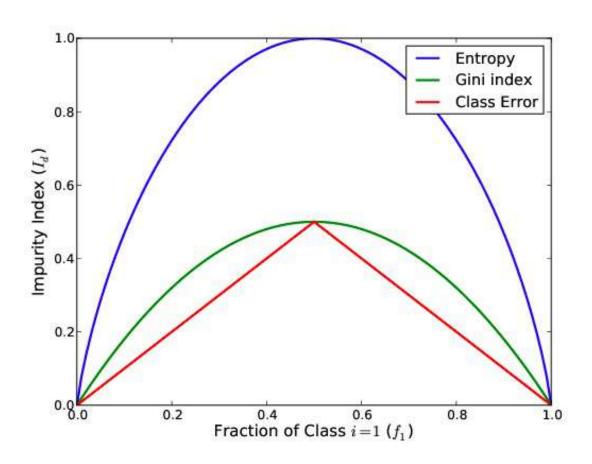
Yes

x₃ = 1?

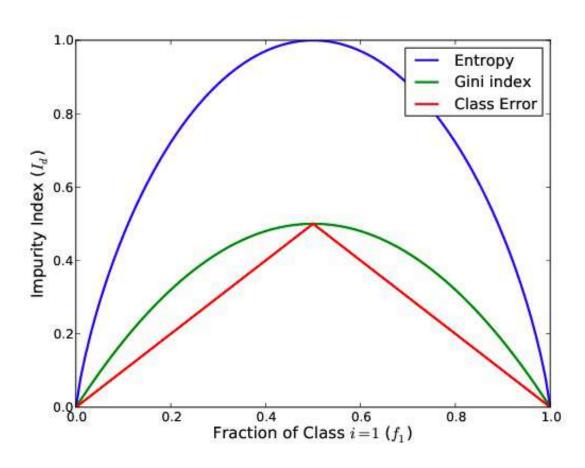
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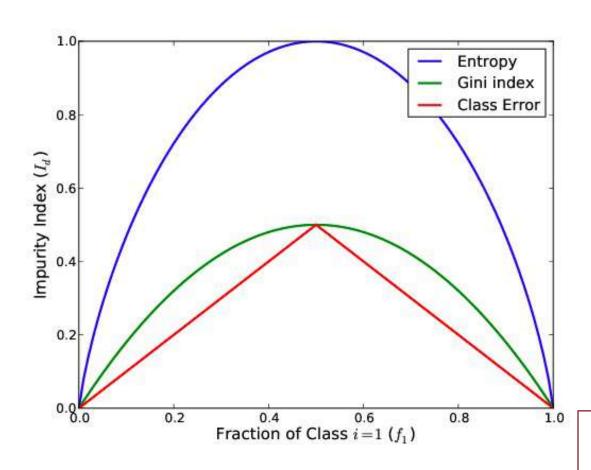
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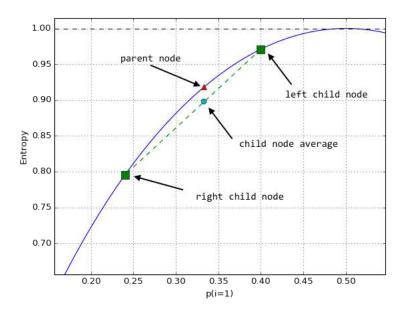
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Gini and Entropy are "smoother" than classification error



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Entropy is always larger than the weighted averaged entropy due to its "bell shape"

• Suppose we have $x_1, ..., x_N$ N items

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- Suppose we have $x_1, ..., x_N$ N items
- Each item is labelled either as positive (y=1) or negative (y=0)
- Let N⁺ (N⁻) be the number of positive (negative) elements
- We define the ratio $p = N^+/N$ and $q = N^-/N$
- The entropy is defined as:

$$H = -\left[p\log_2(p) + q\log_2(q)\right] = -\frac{N^+}{N}\log_2\left(\frac{N^+}{N}\right) - \frac{N^-}{N}\log_2\left(\frac{N^-}{N}\right)$$

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Only because each x_i takes on a binary value, in general H ranges in [0, +infinity]

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 Splitting can't do worst!

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Linear Models

$$h_{\boldsymbol{\theta}}(\mathbf{x}) = \theta_0 + \sum_{i=1}^n \theta_i x_i$$

Decision Trees

$$h(\mathbf{x}) = \sum_{j=1}^{J} c_j \cdot \mathbf{1}_{R_j}(\mathbf{x})$$

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Learned hypothesis is constant within a region

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If there is a strong linear relationship between input and output

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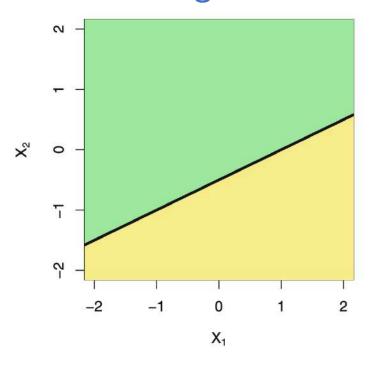
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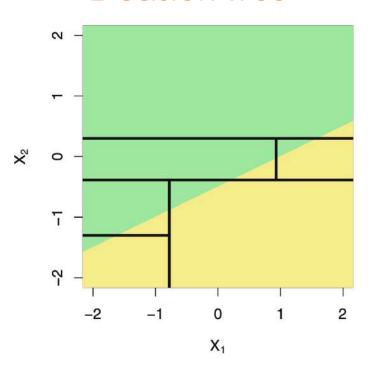
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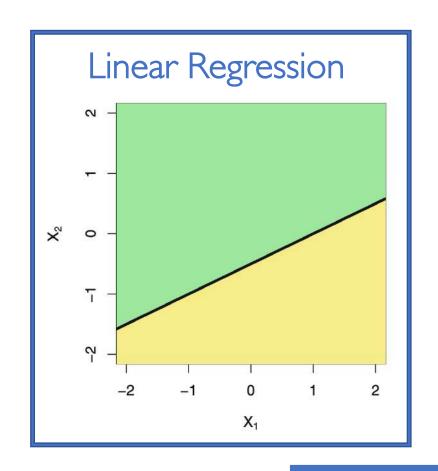
If there is a highly non-linear relationship between input and output

Linear Regression

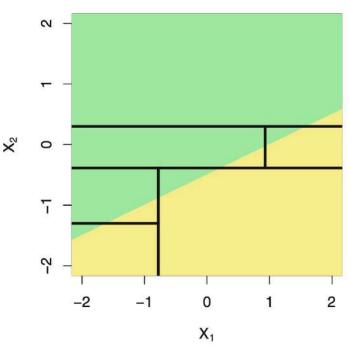


Decision Tree



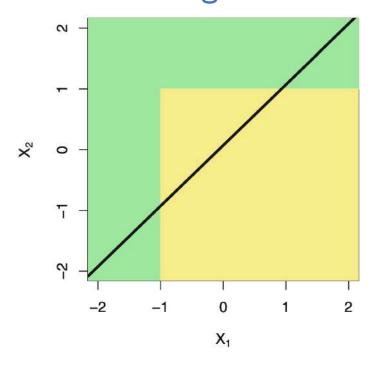




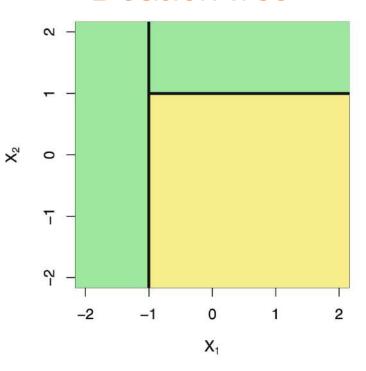


Nice linear decision boundary

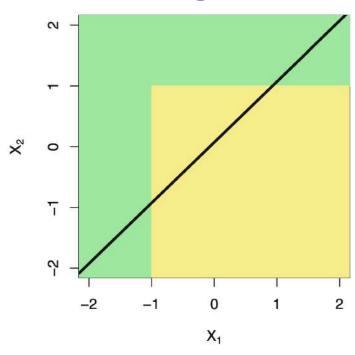
Linear Regression

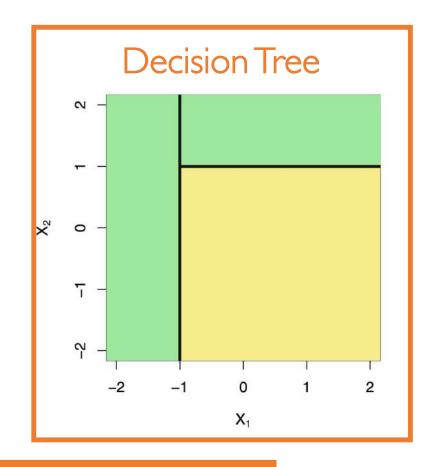


Decision Tree









Non-linear decision boundary

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How do we determine such a subtree?

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Cost Complexity Pruning (a.k.a. Weakest Link Pruning)

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 $j{=}1 \ i{:} \ \mathbf{x}_i{\in}R_j$ • |T| indicates the number of terminal nodes of the tree T

- Rather than considering every possible subtree, we consider a sequence of trees indexed by a non-negative tuning parameter α
- For each value of α there is a subtree $T \subset T_0$ so as to minimize:

$$\sum_{j=1}^{|T|} \sum_{i: \mathbf{x}_i \in R_j} (y_i - \hat{y}_{R_j})^2 + \alpha |T|$$

- $j{=}1 \ i{:} \ \mathbf{x}_i{\in}R_j$ |T| indicates the number of terminal nodes of the tree T
- R_i is the subset of feature space corresponding to the j-th leaf

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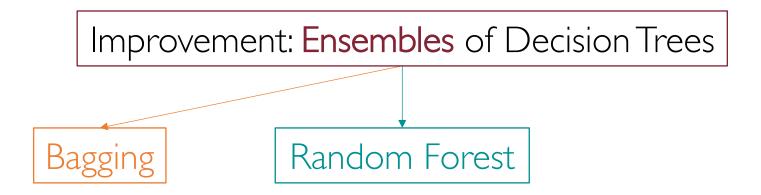
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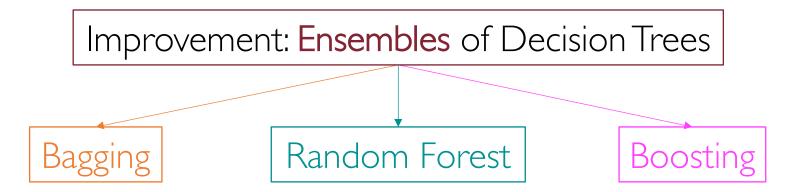
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- If we randomly split a training set in two halves and fit a decision tree on each, chances are we end up with 2 very different trees
- Low-variance approaches, instead, are less sensitive to different training sets
- Bootstrap aggregation (Bagging) is a general-purpose method to lower the variance of a statistical learning method

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Bootstrap

Taking repeated samples from the same training set

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$$h_{\text{bagging}}(\mathbf{x}) = \frac{1}{B} \sum_{b=1}^{B} h^{b*}(\mathbf{x})$$

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- It can be used in combination with any model
- When used with classification trees the final prediction is typically obtained via majority voting
 - The overall prediction is just the most common across the B models

Bagging: Variable Importance

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- Still, one can obtain an overall summary of the importance of each feature using RSS (regression) or Gini index/Entropy (classification)
- Add up the total RSS/Gini index reduction obtained splitting on a certain feature and take the average over all the B trees

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- As in bagging, there will be B decision trees learned on bootstrapped samples of the original training set
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- This may sound crazy, but it has a clever rationale

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Lower variance reduction

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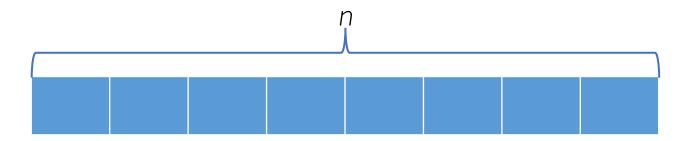
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- As with bagging, random forests will not overfit if we increase B

Why k/n?



Randomly choose k features out of n, each with uniform probability p = 1/n

What is the probability that the highly predictive feature f is contained in the k-sized random sample?

Why k/n? – Approach I.a.

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Why k/n? — Approach 1.b.

It might be easier to compute the following:

 $1 - P(f \text{ is } \mathbf{NOT} \text{ extracted as } 1 \text{st } \mathbf{AND} f \text{ is } \mathbf{NOT} \text{ extracted as } 2 \text{nd } \mathbf{AND} \dots \mathbf{AND} f \text{ is } \mathbf{NOT} \text{ extracted as } k \text{-th})$

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$$1 - \frac{n-k}{n} = \frac{k}{n}$$

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 $\binom{n}{k}$ Combinations of k out of n elements "n choose k"

$$= \frac{\frac{(n-1)!}{(k-1)!(n-1-(k-1))!}}{\frac{n!}{k!(n-k)!}} = \frac{(n-1)!}{(k-1)!(n-k)!} * \frac{k!(n-k)!}{n!} = \frac{k}{n}$$

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- Unlike fitting a single large decision tree to the data, potentially leading to overfitting, the boosting approach instead learns slowly
- Consider boosting regression trees:
 - I. Fit the tree to the current residuals rather than the actual response Y
 - 2. Add this new decision tree into the fitted function so as to update the residuals
 - 3. Each of these trees can be rather small, with just a few terminal nodes, determined by a model's hyperparameter (d)
 - 4. The shrinkage parameter λ slows the process down even further, allowing more and different shaped trees to attack the residuals

Boosting: Algorithm

Algorithm 8.2 Boosting for Regression Trees

- 1. Set $\hat{f}(x) = 0$ and $r_i = y_i$ for all i in the training set.
- 2. For b = 1, 2, ..., B, repeat:
 - (a) Fit a tree \hat{f}^b with d splits (d+1) terminal nodes) to the training data (X, r).
 - (b) Update \hat{f} by adding in a shrunken version of the new tree:

$$\hat{f}(x) \leftarrow \hat{f}(x) + \lambda \hat{f}^b(x). \tag{8.10}$$

(c) Update the residuals,

$$r_i \leftarrow r_i - \lambda \hat{f}^b(x_i). \tag{8.11}$$

3. Output the boosted model,

$$\hat{f}(x) = \sum_{b=1}^{B} \lambda \hat{f}^b(x).$$
 (8.12)

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- Tuning done via validation or cross-validation

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- DTs tend to overfit and have a low prediction accuracy
- Pruning and Ensembling techniques overcome both issues