# Big Data Computing

Master's Degree in Computer Science 2022-2023

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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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- Other 2 measures are preferable: Gini Index and Entropy

# Node Impurity: Gini Index

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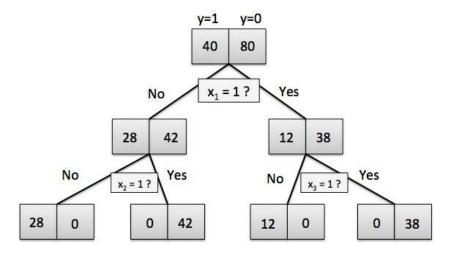
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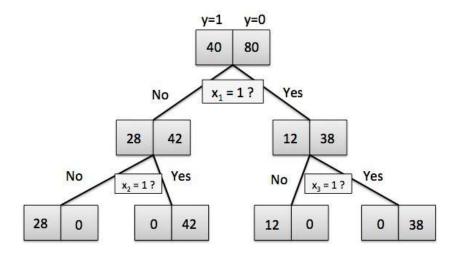
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- It ranges between [0, +infinity]
- Like Gini, a small value of entropy is obtained whenever all the proportions are either close to 1 or to 0
- In practice, both entropy and Gini can be used to grow a tree

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



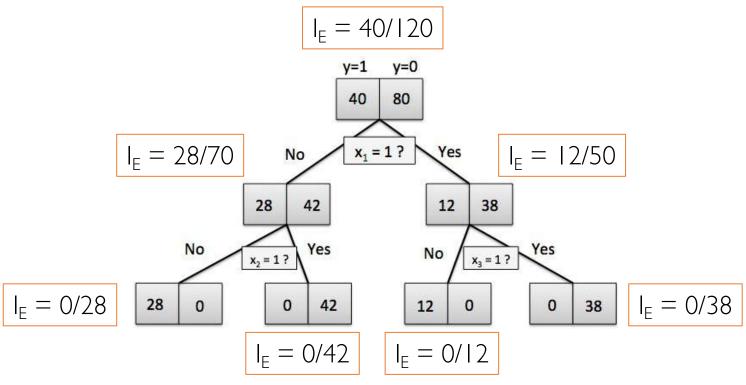
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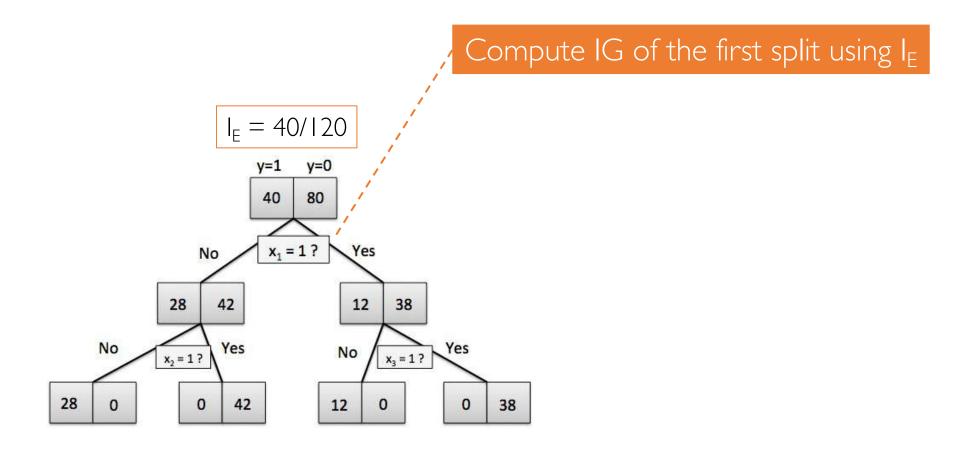
#### Question

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

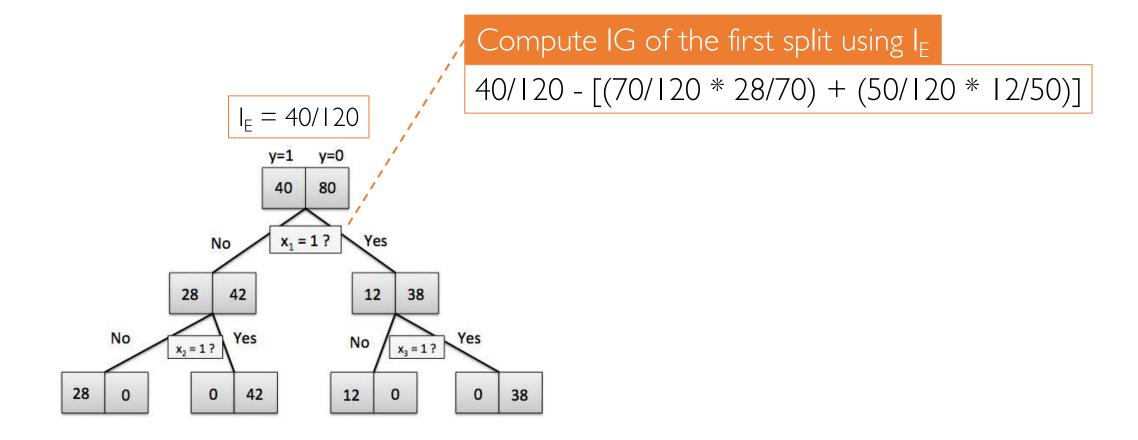
Node impurity using I<sub>E</sub>



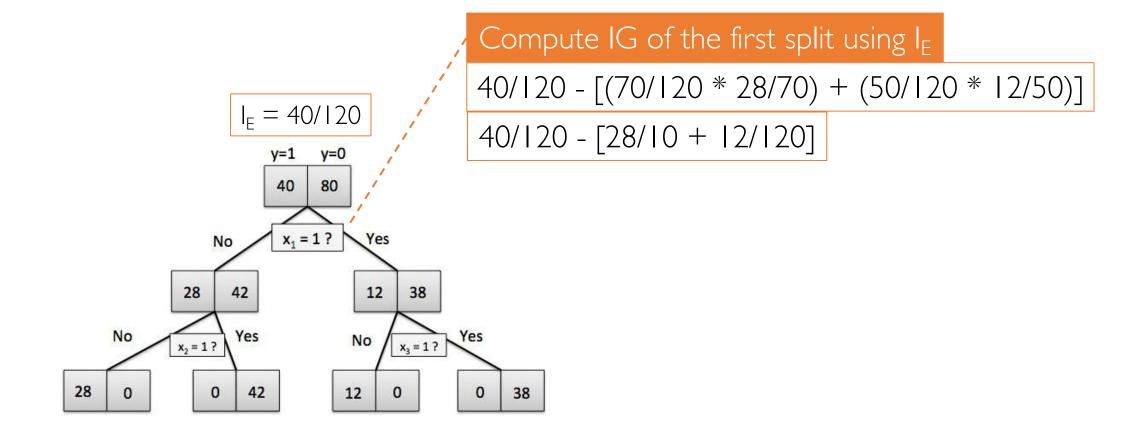
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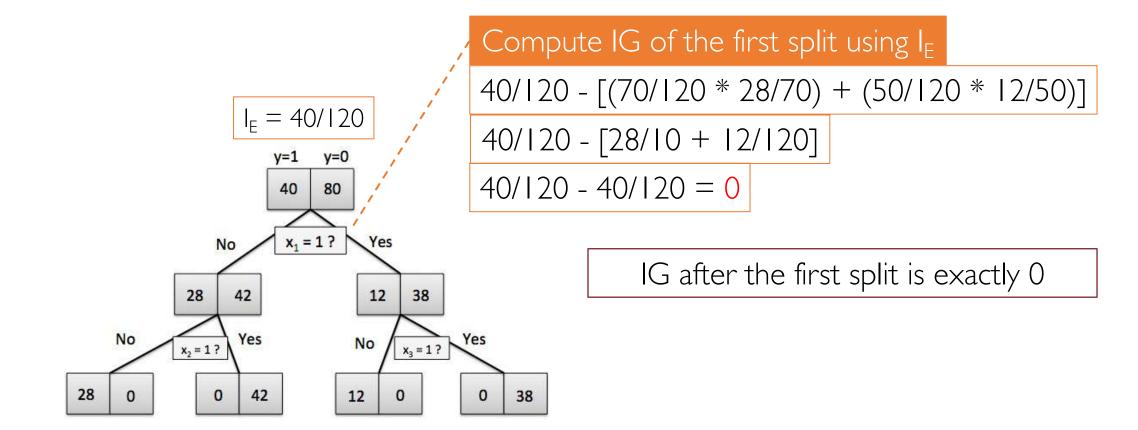
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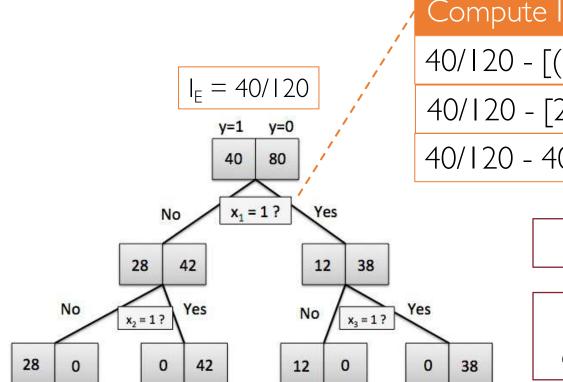
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#### Compute IG of the first split using I<sub>F</sub>

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

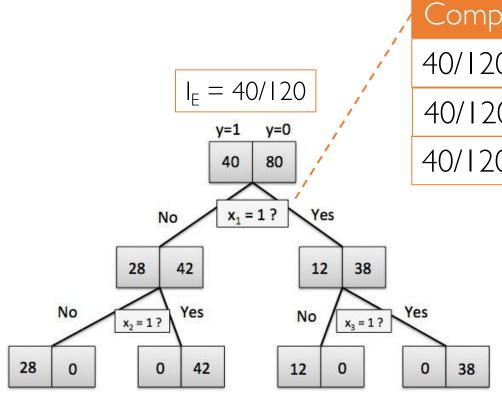
40/120 - [28/10 + 12/120]

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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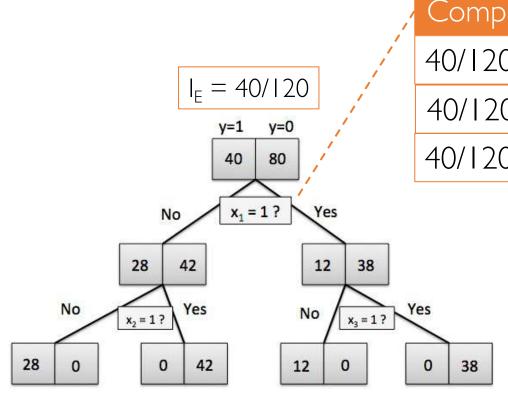
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Splitting root gives no IG improvement in terms of I<sub>E</sub>

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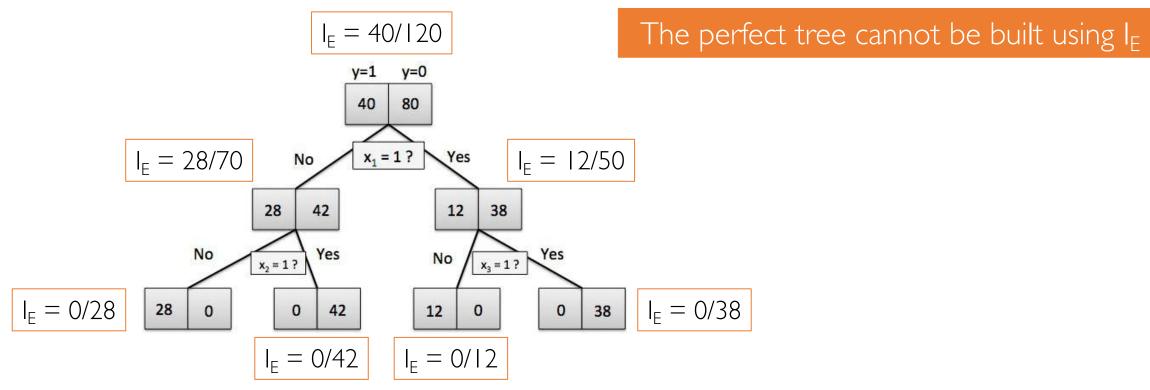
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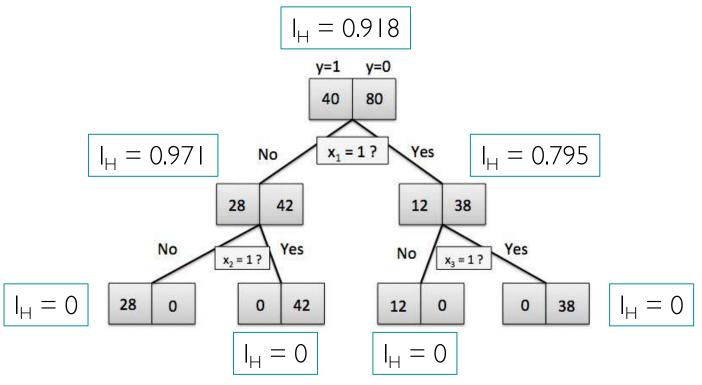
The tree learning algorithm would stop at this point

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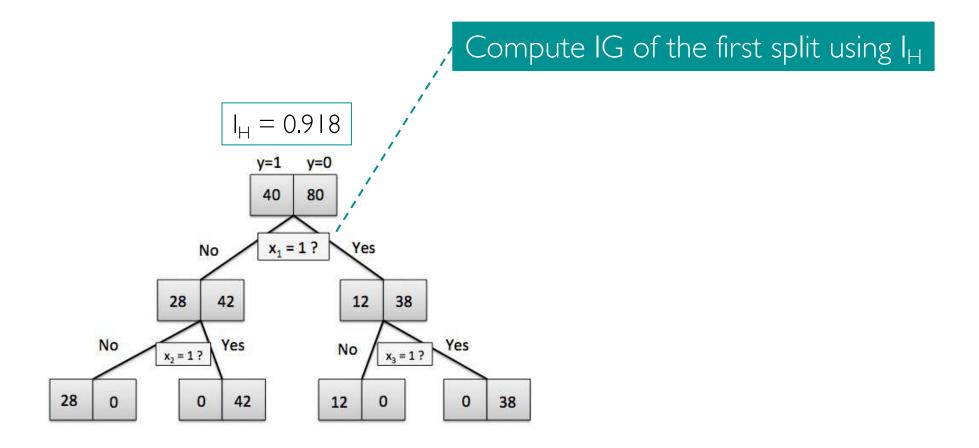


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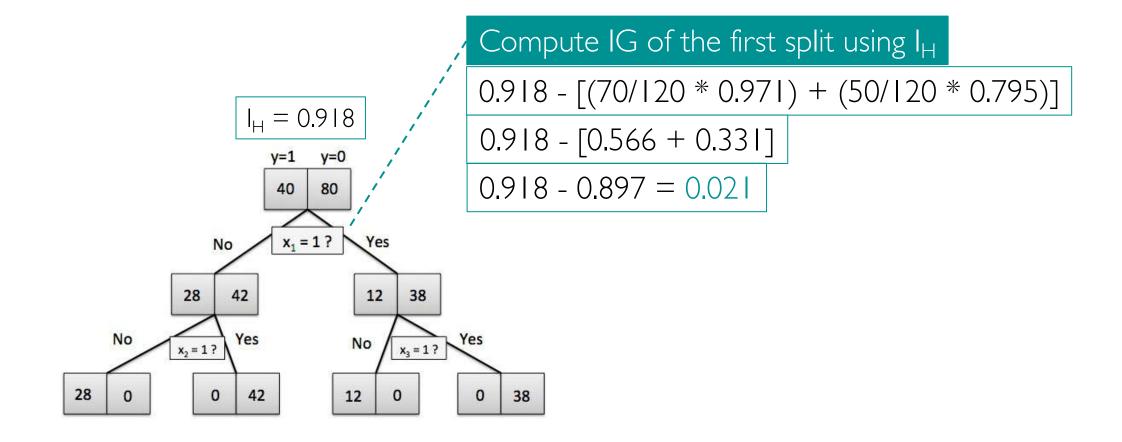
Node impurity using I<sub>H</sub>



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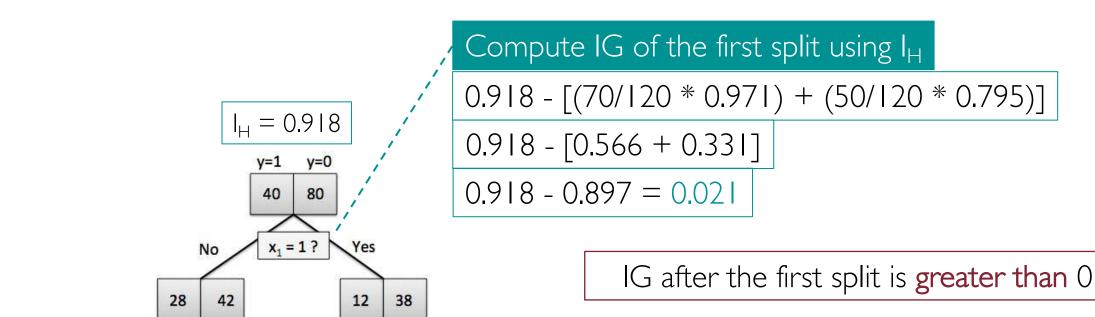


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No

12

Yes

42

 $x_2 = 1$ ?

No

28

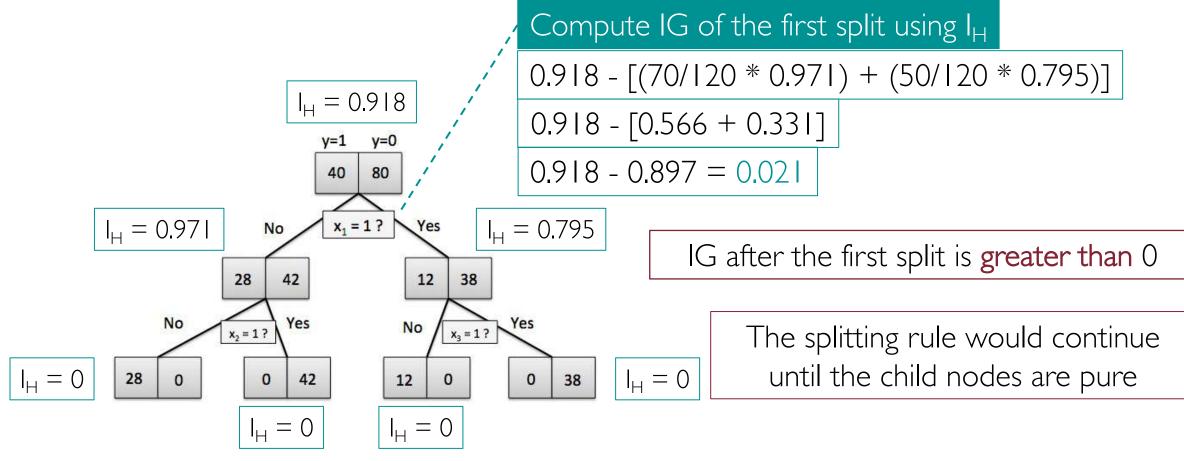
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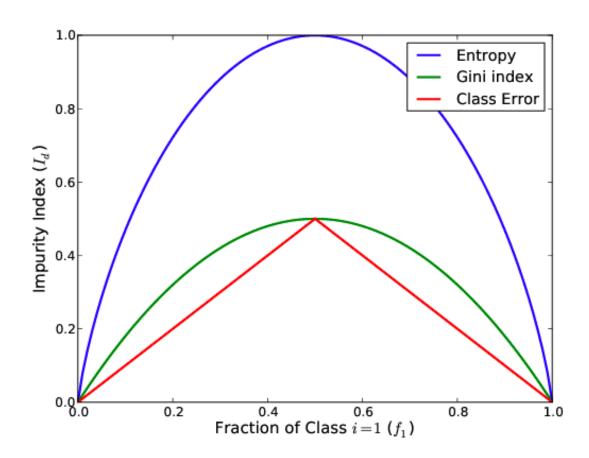
Yes

x<sub>3</sub> = 1?

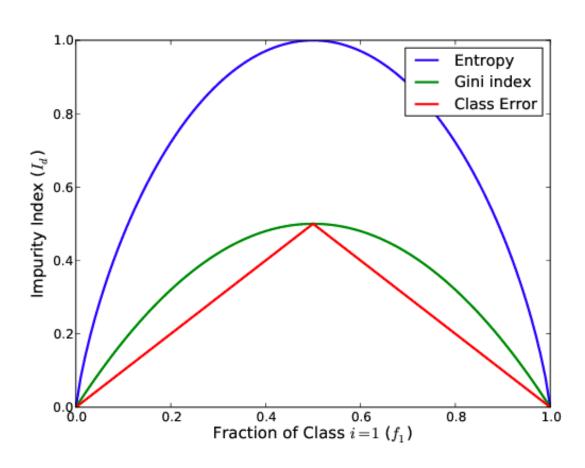
0



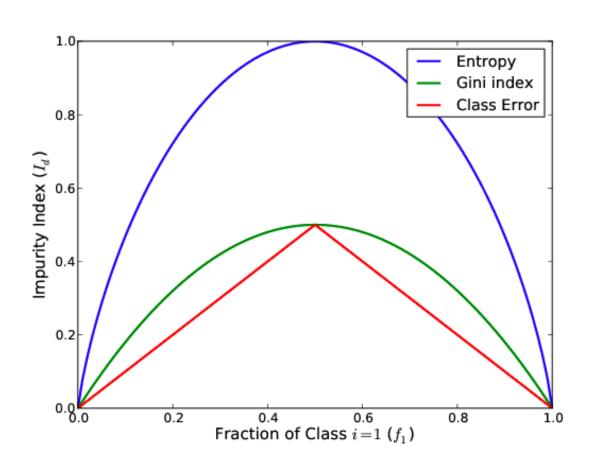
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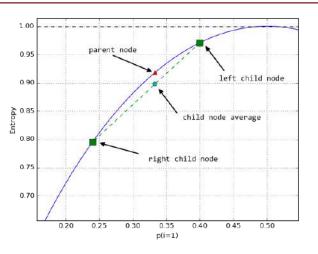
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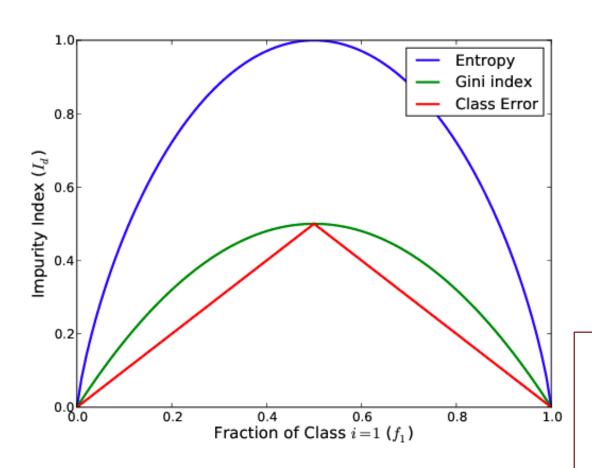


Gini and Entropy are "smoother" than classification error

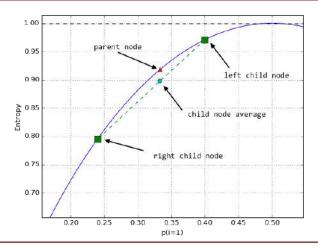


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If the parent's entropy sits between children's entropy, it will always be larger than the weighted averaged children's entropy due to its "bell shape"

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- 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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Since each  $x_i$  takes on a binary value (K=2), H ranges in [0, 1], in general it 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**

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

Learned hypothesis is constant within a region

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#### Which one is better?

If there is a strong linear relationship between input and output

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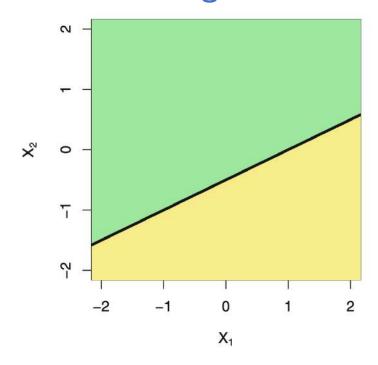
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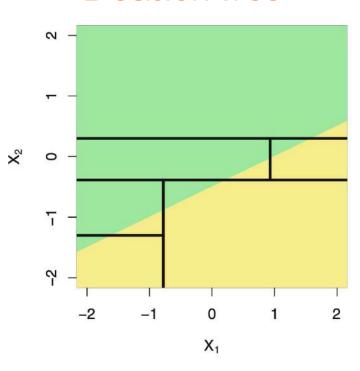
If there is a highly non-linear relationship between input and output

## Linear Models vs. Decision Trees: Example

#### Linear Regression

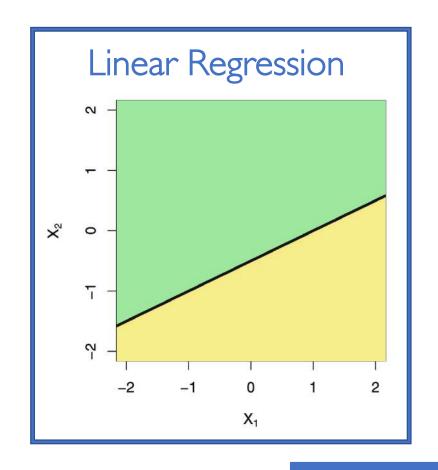


#### **Decision Tree**

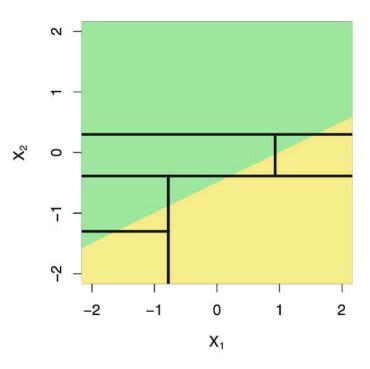


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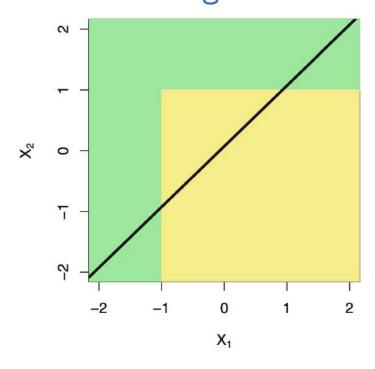




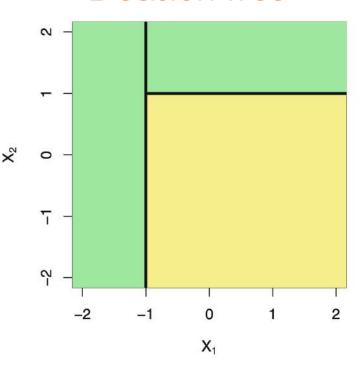
Nice linear decision boundary

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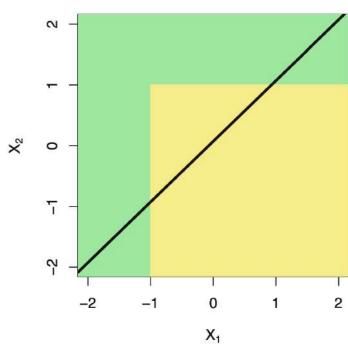


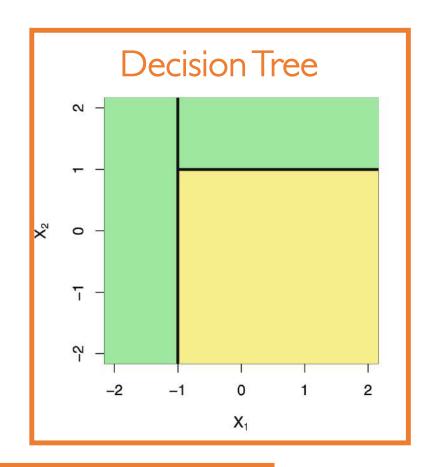
#### **Decision Tree**



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Non-linear decision boundary

- Greedy tree growing strategy may lead to:
  - Overfitting  $\rightarrow$  if we keep splitting as long as there is an information gain

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How do we determine such a subtree?

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- A better strategy is to grow a very large tree T<sub>0</sub>, and then prune it back in order to obtain a subtree

#### How do we determine such a subtree?

Intuitively, by selecting the subtree with the smalles test error!

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

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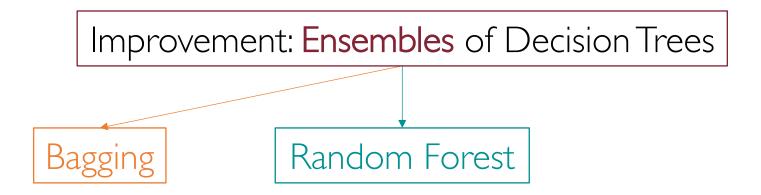
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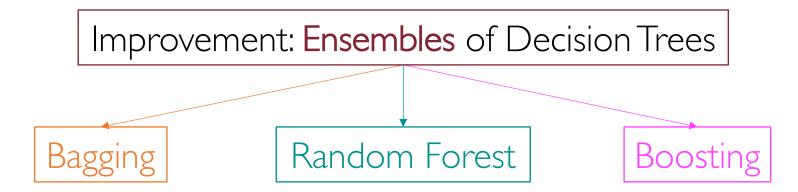
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- If we randomly split a training set in two halves and fit a decision tree on each, chances are we end up with 2 very different trees
- Low-variance approaches, instead, are less sensitive to different training sets
- Bootstrap aggregation (Bagging)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

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### Bagging: Variable Importance

- The improved prediction accuracy of bagging trees comes at the expense of the interpretability of a single tree
- 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
- But for each individual tree, every time it comes to splitting a node only a random sample of k < n features is considered
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Lower variance reduction

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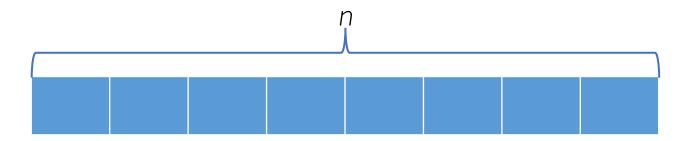
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- As with bagging, random forests will not overfit if we increase B

## 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?

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It might be easier to compute the following:

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It might be easier to compute the following:

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

$$1 - \left[ \underbrace{\frac{n-1}{n} * \frac{n-2}{n-1} * \dots * \frac{n-(k-1)}{n-(k-2)} * \frac{n-k}{n-(k-1)}}_{k \text{ times}} \right] =$$

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

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

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$$egin{pmatrix} (n{-}1) & extit{f} ext{ is alrea} \ k{-}1 \end{pmatrix}$$

f is already chosen: we need to count the subsets of size k-1 of n-1 elements

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

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

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- Again, general approach that can be applied to many statistical learning methods for regression or classification
- In bagging, each tree is built on a bootstrap data set, independent of the other trees
- Boosting works in a similar way, except that the trees are grown sequentially using information from previously grown trees
- Boosting does not involve bootstrap sampling; instead each tree is fit on a modified version of the original data set

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# Boosting

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# Boosting

- 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  $\lambda$  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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  - The number d of splits in each tree, which controls the complexity of the boosted ensemble (often d = 1 works well, in which case each tree is a stump)
- Tuning done via validation or cross-validation

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- Learning the optimal DT is NP-Complete: Recursive Binary Splitting algorithm is an effective greedy heuristic
- DTs tend to overfit and have a low prediction accuracy
- Pruning and Ensembling techniques overcome both issues