

# Trees and random forests

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Hicham Janati · *INSEA* · [hjanati@insea.ac.ma](mailto:hjanati@insea.ac.ma)

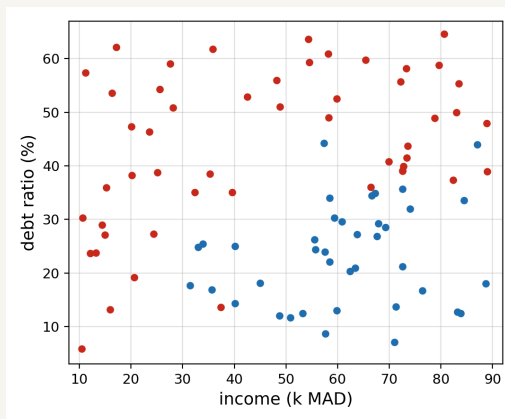
# Decision trees

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# Predicting default

A bank wants to predict a future **loan default** (when a client does not reimburse) from two features.

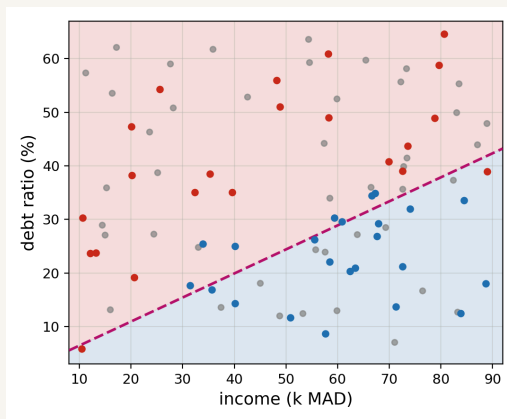
| income<br>(kDh) | debt<br>(%) | default |
|-----------------|-------------|---------|
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| 33              | 25          | 0       |
| 58              | 49          | 1       |
| 72              | 56          | 1       |
| ⋮               | ⋮           | ⋮       |
| 62              | 29          | ?       |



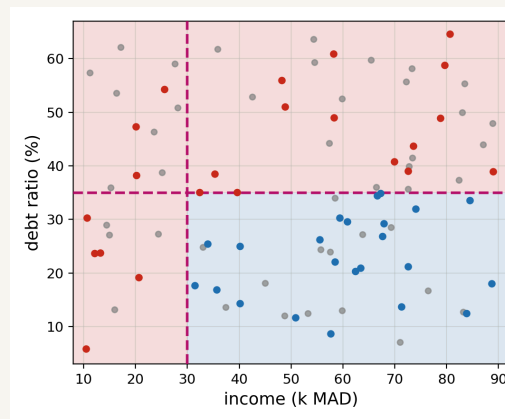
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linear model: train **20%**, test **16%**



best function: train **0%**, test **9%**

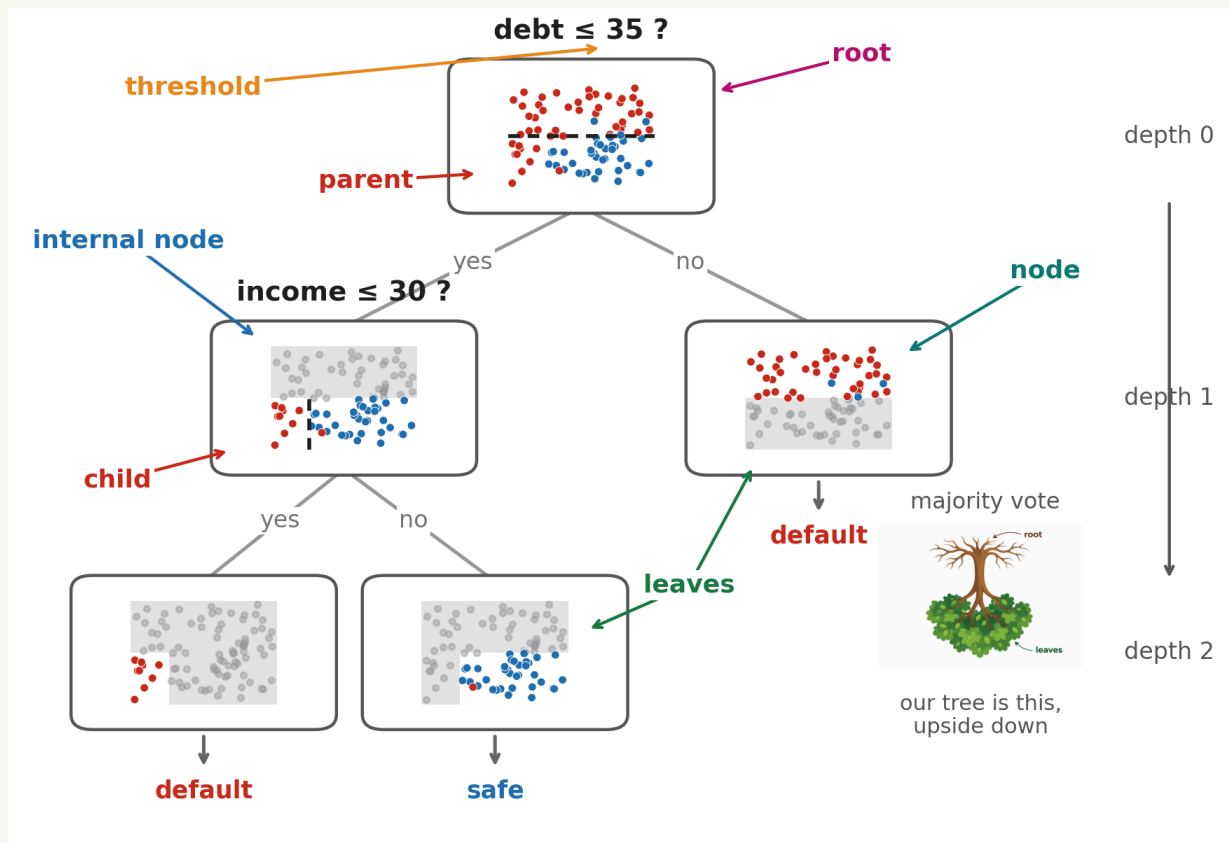
How can we define such a function ?

$$f(x) = 1 \Leftrightarrow \text{income} \leq 30 \text{ or } \text{debt} \geq 35$$

$$x_1 \leq 30 \text{ or } x_2 \geq 35$$

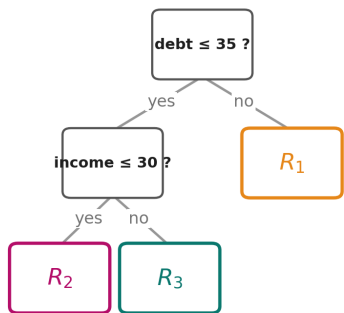
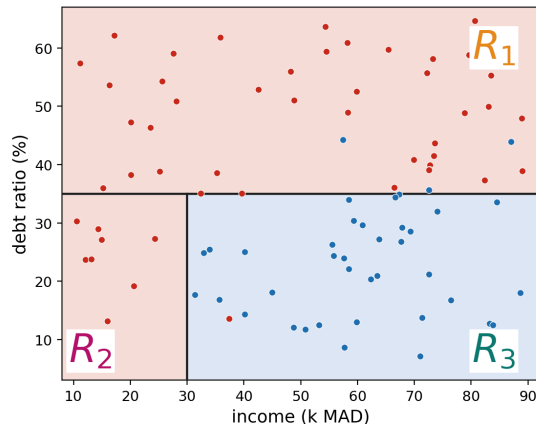
By thresholding the feature space: **a decision tree.**

# Visualizing a classification tree

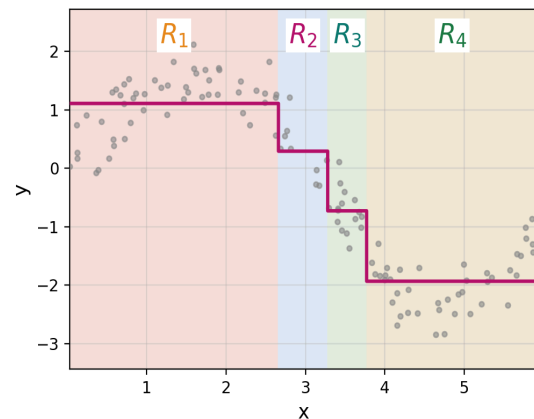


# Decision trees: piecewise-constant functions

A decision tree carves the space into a **partition of regions**: its **leaves**.



Classification



Regression

On each region  $R_j$ : what is the value of  $f$  ?

**Classification:** the region's majority class.

**Regression:** the region's average,  $\mathbf{x} \in R_j \Rightarrow f(\mathbf{x}) = \bar{y}_{R_j}$

# The best regression tree, formally

What is the **best regression tree** for a partition of  $J$  regions ?

$$\min_{R_1, \dots, R_J} \sum_{j=1}^J \sum_{i: \mathbf{x}_i \in R_j} (y_i - \bar{y}_{R_j})^2$$

The unknown is the **partition itself**, combinatorially many candidates. NP-hard problem.

*Greedy optimization (Algorithme glouton):*

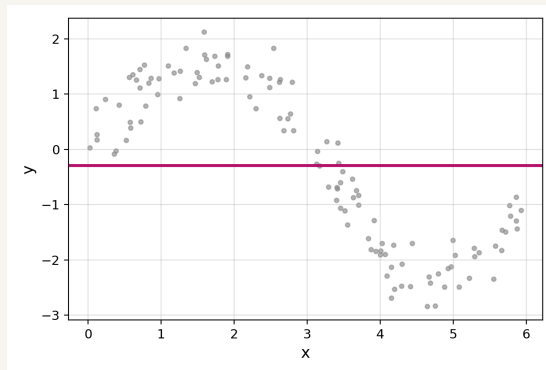
0. Start with root node =  $\mathbb{R}^d$
1. find the best split at the *current* node
2. apply it to get two **children** nodes
3. repeat steps 1 and 2 on each child node



# CART algorithm

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What about **regression**: data  $(\mathbf{x}_i, y_i)$  with  $y_i \in \mathbb{R}$ . What does a **tree**  $f$  look like ?



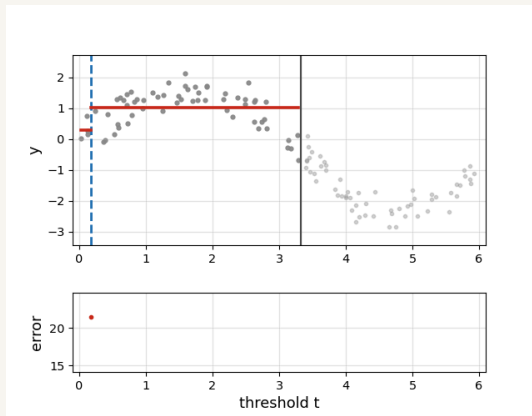
Start simple: fix **depth = 0**: no split allowed. What is the *best* possible tree ?

A **constant** ! One leaf, predicting the global average  $\bar{y}$

**Depth 1**: one split allowed. We only have one variable  $x$ . **Where** do we cut it ?

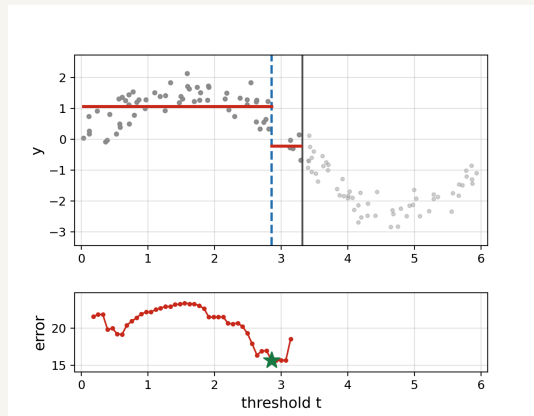


# Recurse: left, then right

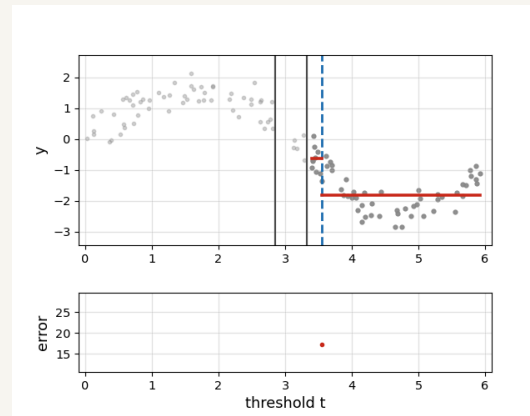


the same sweep, **inside the left** region

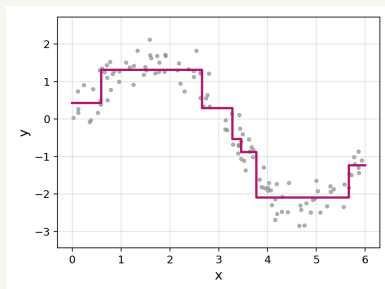
# Recurse: left, then right



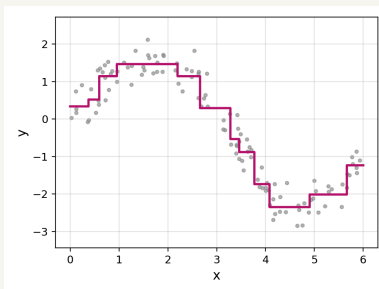
the same sweep, **inside the left** region



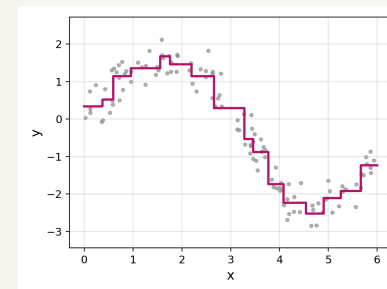
then **inside the right**



... and again: **depth 3**



**depth 5**

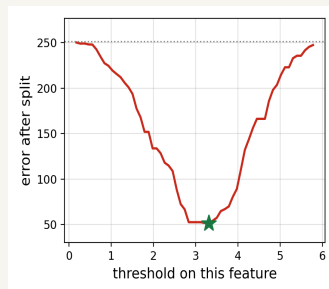


**depth 10**

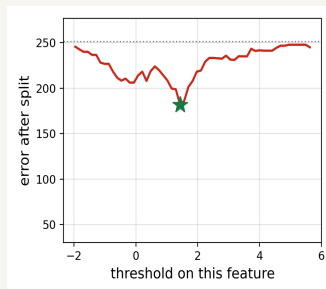
That was one variable. With  $d$  features: **which one** gets the cut ?

CART is *greedy*: THE BEST ONE in terms of **decreasing prediction error**.

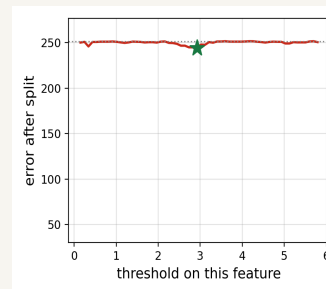
So we need to  
try to split  
**every single**  
feature:



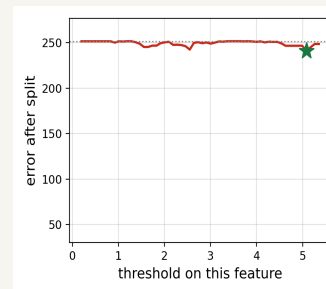
feature 1



feature 2



feature 3

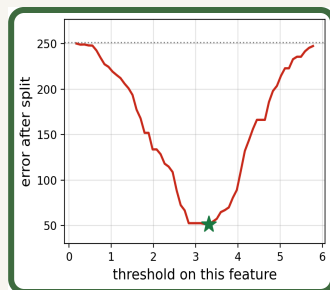


feature 4

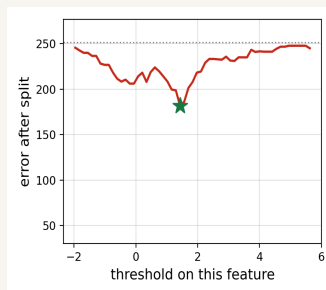
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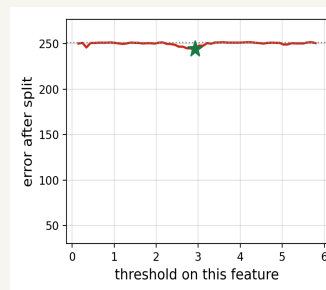
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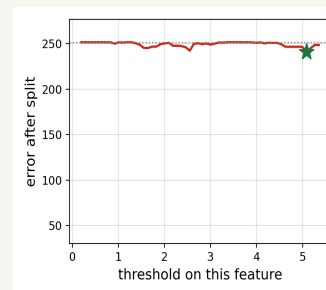
feature 1



feature 2



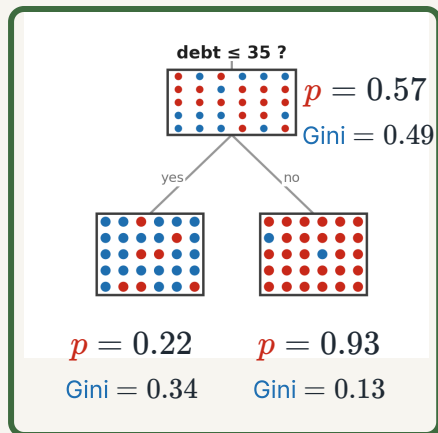
feature 3



feature 4

Find the best **threshold** for every **feature**, select the (feature, threshold) pair with the **largest gain**.

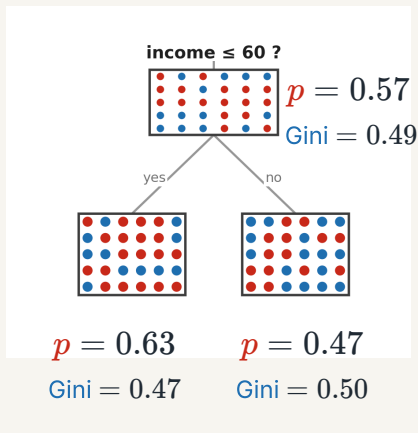
Back to classification: the **same parent node**, two candidate cut:



split A

average Gini  $\approx 0.24$

$$\Delta \text{Gini} = -0.25$$



split B

average Gini  $\approx 0.48$

$$\Delta \text{Gini} = -0.01$$

Which split is better ?

**Split A:** its children are *cleaner*.

How can we define a score for *cleanliness* ?

$p$  = the frequency of class 1 in a leaf node

$$\mathbb{P}(y_1 \neq y_2) = 2p(1 - p)$$

*Gini Impurity*

If we draw samples at random  $\mathbb{P}(y_1 \neq y_2)$  must be low.

The same greedy recursion runs both classification and regression trees:

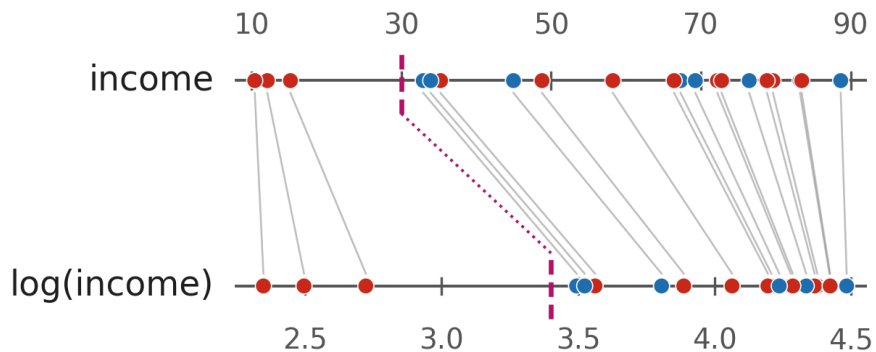
|               | regression                                                                     | classification               |
|---------------|--------------------------------------------------------------------------------|------------------------------|
| split score   | children's squared error                                                       | children's Gini $2p(1-p)$    |
| leaf output   | the leaf's average $\bar{y}$                                                   | majority class / proportions |
| the recursion | scan every (feature, threshold), keep the largest gain, repeat on the children |                              |

CART algorithm: *Classification And Regression Trees* (1984)

# Trees in practice

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# Rescaling a feature ?



the split income  $\leq 30$

Chapter 5 standardized the columns before any penalty. What happens to a **tree** if we use  $\log(\text{income})$  instead ?

the split  $\log(\text{income}) \leq 3.40$ : the **same clients** on each side

$x_j \leq t \iff \varphi(x_j) \leq \varphi(t)$  for any strictly increasing  $\varphi$  (log, z-score, min-max)

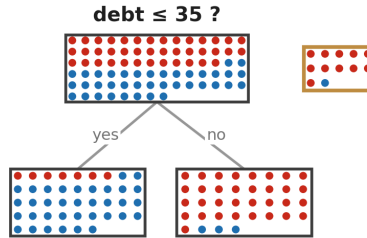
Same order, same splits, **same tree**: a tree needs no standardization.

# Missing values ?

Some clients left their **debt** blank. The root asks  $\text{debt} \leq 35$ : where do **they** go ?

| income (kDh) | debt (%) | default |
|--------------|----------|---------|
| 80           | 59       | 1       |
| 33           | 25       | 0       |
| 58           | ?        | 1       |
| 72           | ?        | 1       |
| ⋮            | ⋮        | ⋮       |

- debt missing: 12 of 90 clients

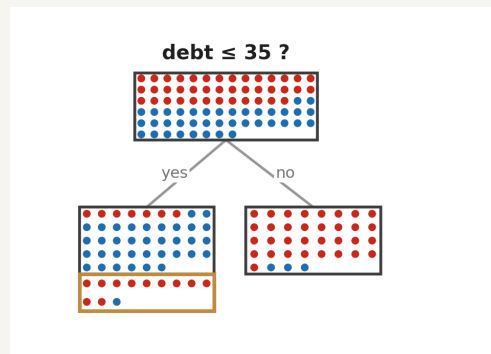


# Missing values ?

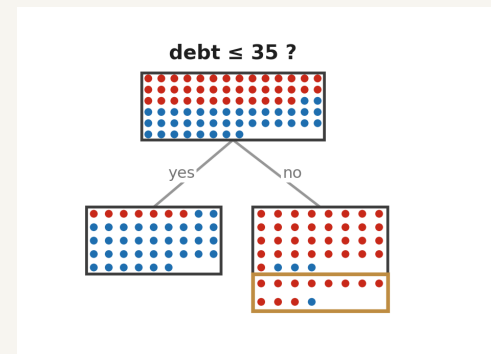
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■ debt missing: 12 of 90 clients



missing → **left**: average Gini **0.33**

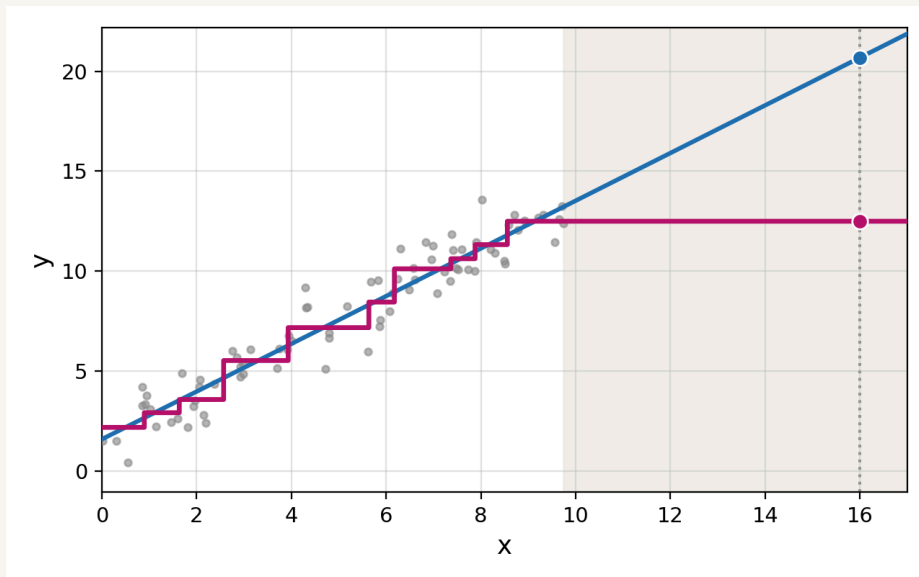


missing → **right**: average Gini **0.21**

The lower-loss side becomes the split's **default direction**, stored with it: a new client with a missing debt follows it.

No imputation: scikit-learn trees and random forests accept **NaN** directly, and boosting libraries do the same.

# Extrapolation ?



training data up to  $x = 9.7$ ; the shaded region holds **no data**

A new point at  $x = 16$  (dotted line):  
what do a **line** and a **tree** predict ?

**line**: 20.7, it follows the trend

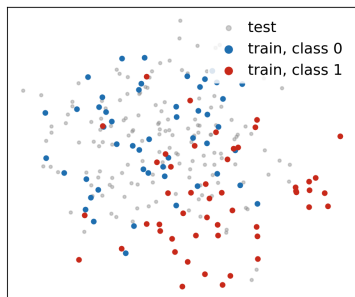
**tree**: 12.5, exactly its value at  $x = 9.7$

Past the last training value, a tree **freezes** at its boundary leaf's constant; a line keeps moving.

# Complexity of a decision tree

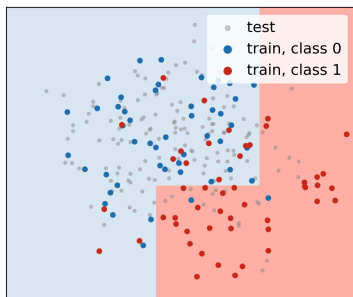
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Can a tree overfit ?



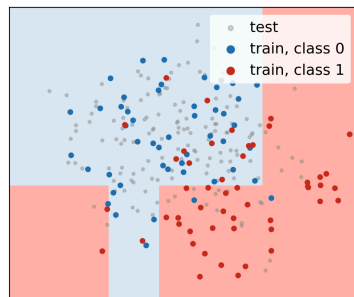
the data

train / test error



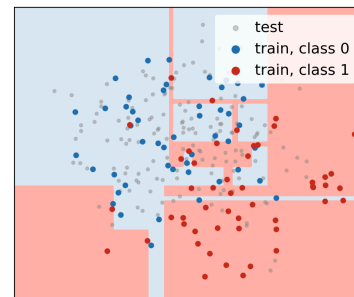
depth 2

0.17 / 0.23



depth 3

0.15 / 0.24



depth 10

0.01 / 0.28

What happens if when we increase depth further ?

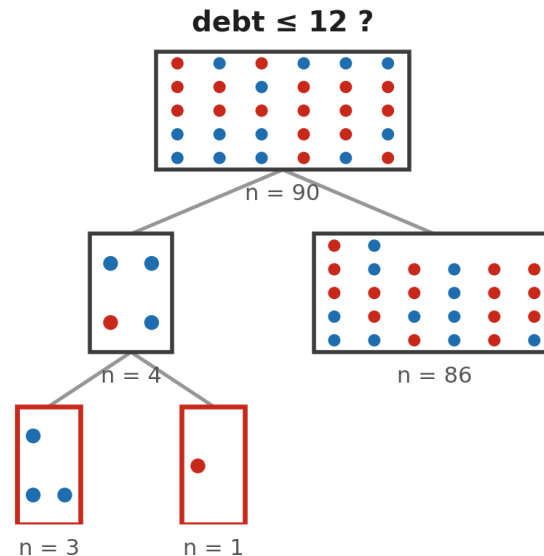
We keep splitting until **all leaves** are pure !

# Depth is not enough

So we should **restrict max depth** to avoid overfitting.

What about **this** depth-2 tree ?

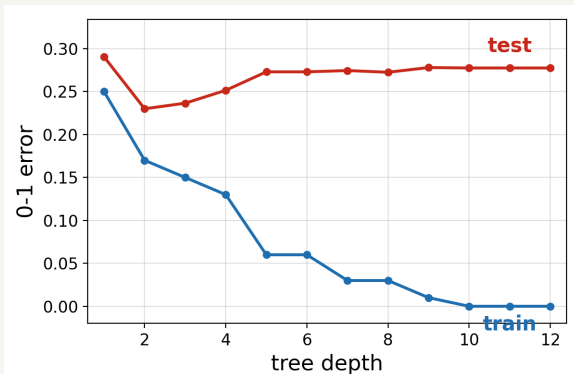
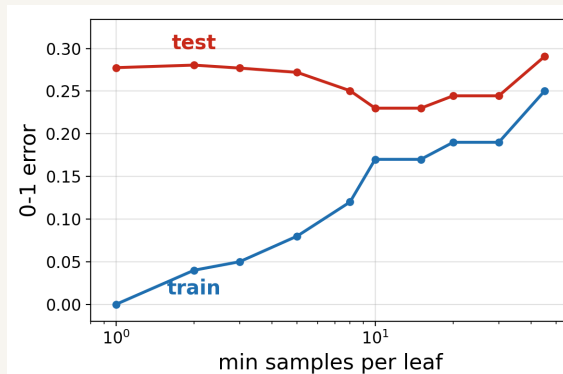
We need to avoid having very small leaves.



Another hyperparameter to restrict the possible splits: *minimum samples per leaf*

# U-curve

What happens to the **train error** when we increase each hyperparameter ?



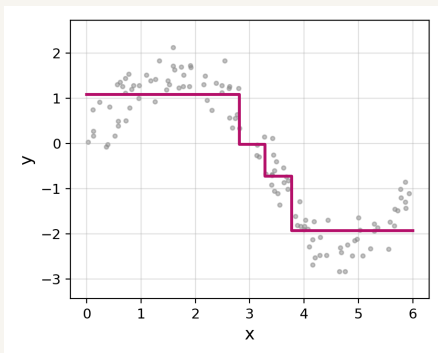
And the **test error** ?

These are (two of) the main hyperparameters of a Decision Tree

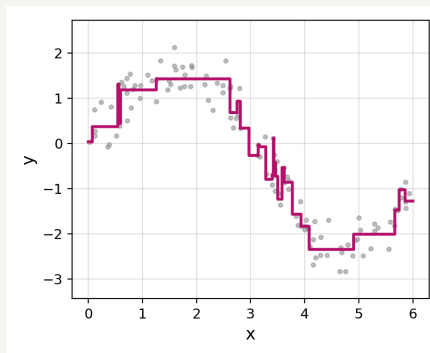
Chosen exactly as in chapter 5: a **grid, cross-validation**.

# Trees have high variance

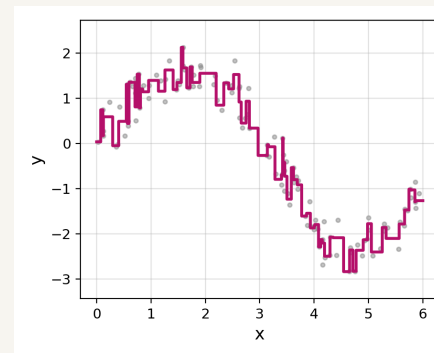
To fit anything interesting, a tree must be **deep**. What is the price ?



depth 2: train 0.23, test 0.29



depth 5: train 0.07, test 0.17



depth 12: train 0.03, test 0.22

The **useful** trees are the deep ones, and deep trees **overfit**: they have **high variance**.

# Bagging and random forests

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# Bagging: the idea

We want to **reduce the variance**. How do we reduce the variance of a random variable ?

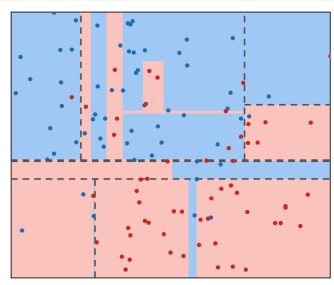
**Average** different estimates;  $\mathbb{V}(\bar{X}) = \sigma^2/n$ . But average **what** ? We only have **one** dataset, one tree.

Chapter 4's **bootstrap**: resample the rows **with replacement**, fit one tree per replica.

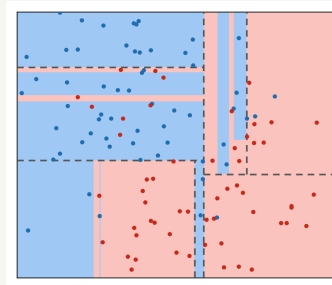
original row indices: 1 2 3 4 5 6



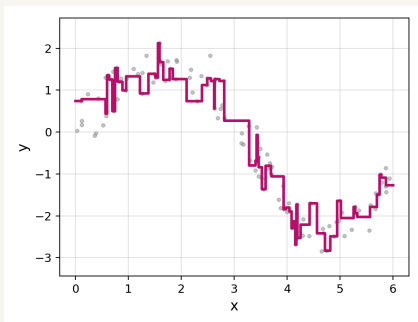
Bootstrap sample: 2 **2** 5 1 6 4  
→ tree  $T_1$



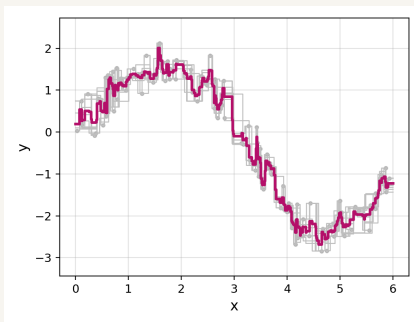
Bootstrap sample: 3 6 **6** 2 4 1  
→ tree  $T_2$



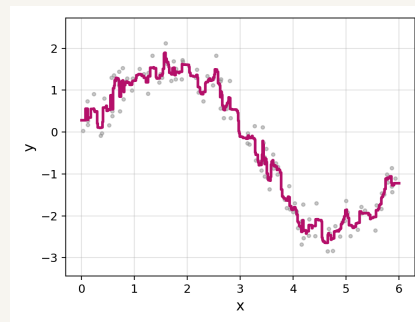
Draw  $n$  rows with replacement, fit one **deep** tree; repeat  $B$  times; **average** the  $B$  predictions.



one bootstrap tree ( $B = 1$ )



$B = 12$  trees (gray) and their **average**



the average of  $B = 200$  trees

Even with  $B = 200$ , the variance is still high, why could that be?

Consider  $B$  different trees  $T_1, \dots, T_B$  with variance  $\sigma^2$  and pairwise correlation  $\rho$ . How much variance did averaging remove ?

$$\mathbb{V}\left(\frac{1}{B} \sum_{b=1}^B T_b\right) = ?$$

# Random forests: decorrelate

Consider  $B$  different trees  $T_1, \dots, T_B$  with variance  $\sigma^2$  and pairwise correlation  $\rho$ . How much variance did averaging remove ?

$$\mathbb{V}\left(\frac{1}{B} \sum_{b=1}^B T_b\right) = \rho \sigma^2 + \frac{1 - \rho}{B} \sigma^2$$



If the **correlation**  $\rho$  is high, the variance never dies even if  $B \rightarrow +\infty$  !

How do we make the trees **uncorrelated** ?

**Don't give them the same features:** for every split consider only a **random subset** of the features !

# The forest, one tree at a time

At **every split**, each node draws a fresh random subset of  $m = 2$  of the  $d = 4$  features.

**data** (n rows, features  $x_1, x_2, x_3, x_4$ )  $\rightarrow$  three bootstraps, three trees grown **in parallel**

bootstrap 1  $\rightarrow T_1$

menu  $\{x_1, x_3\}$  : split on  $x_3$

$\{x_2, x_4\}$

$\{x_1, x_4\}$

bootstrap 2  $\rightarrow T_2$

menu  $\{x_2, x_4\}$  : split on  $x_2$

$\{x_1, x_3\}$

$\{x_1, x_2\}$

bootstrap 3  $\rightarrow T_3$

menu  $\{x_1, x_4\}$  : split on  $x_4$

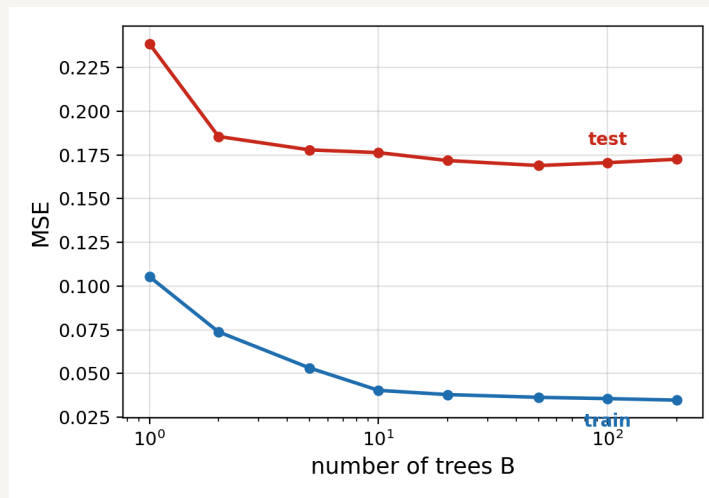
$\{x_3, x_4\}$

$\{x_2, x_3\}$

different random subsets  $\rightarrow$  **different splits**  $\rightarrow$  decorrelated trees

then **average**:  $\hat{F}_B(\mathbf{x}) = \frac{1}{B} \sum_{b=1}^B T_b(\mathbf{x})$ . That is a **random forest**.

What should be the effect of a large  $B$  on the test error ?



The error falls and **flattens**.  $B$  is not a complexity dial; more trees reduce overfitting.

# What to remember

|                 | decision tree                       | bagging                                              | random forest                                         |
|-----------------|-------------------------------------|------------------------------------------------------|-------------------------------------------------------|
| <b>what</b>     | one deep tree, axis-aligned regions | average of <b>B</b> trees, one per bootstrap replica | bagging + a <b>random feature menu</b> at every split |
| <b>fights</b>   | bias: any partition, no assumption  | the <b>variance</b> of a single tree                 | the <b>correlation</b> $\rho$ left between trees      |
| <b>dials</b>    | max depth, min samples per leaf     | B: not a complexity dial                             | + m features per split                                |
| <b>overfits</b> | depth (the U-curve)                 | not in B                                             | not in B                                              |

A deep tree has **low bias** and **high variance**. Averaging removes the variance **without** paying bias; decorrelating removes what averaging alone cannot: the floor  $\rho\sigma^2$ .

The out-of-bag error, variable importance, and the **other** way to combine trees (boosting): **chapter 7** of the lecture notes.

# Contents

1. Decision trees
2. CART algorithm
3. Trees in practice
4. Complexity of a decision tree
5. Bagging and random forests