
Lesson #20
Ensemble Learning II

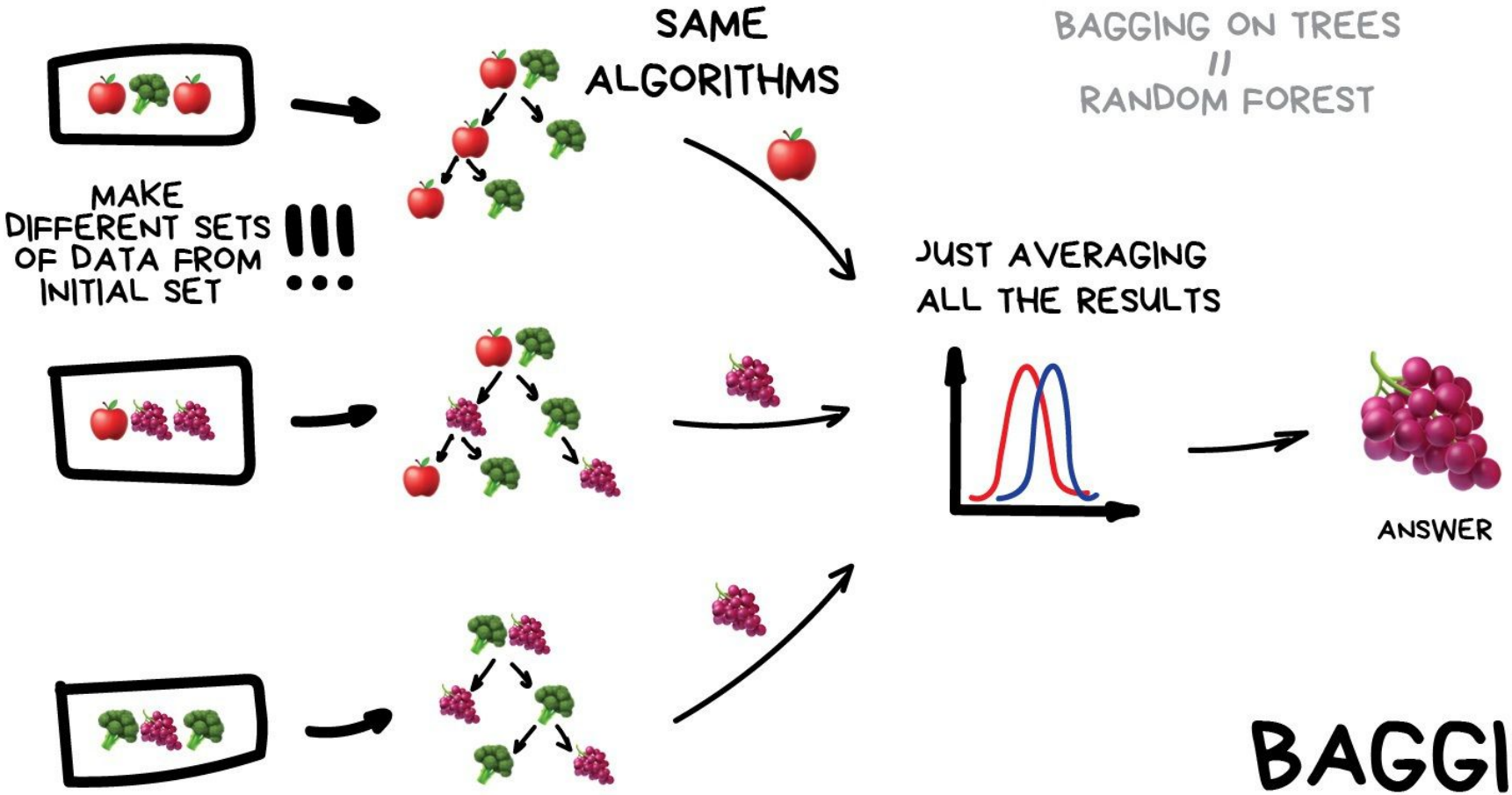
notas

- Ensembles (cont.)
- Boosting
  - Adaboost
  - Gradient Boost
  - XGBoost

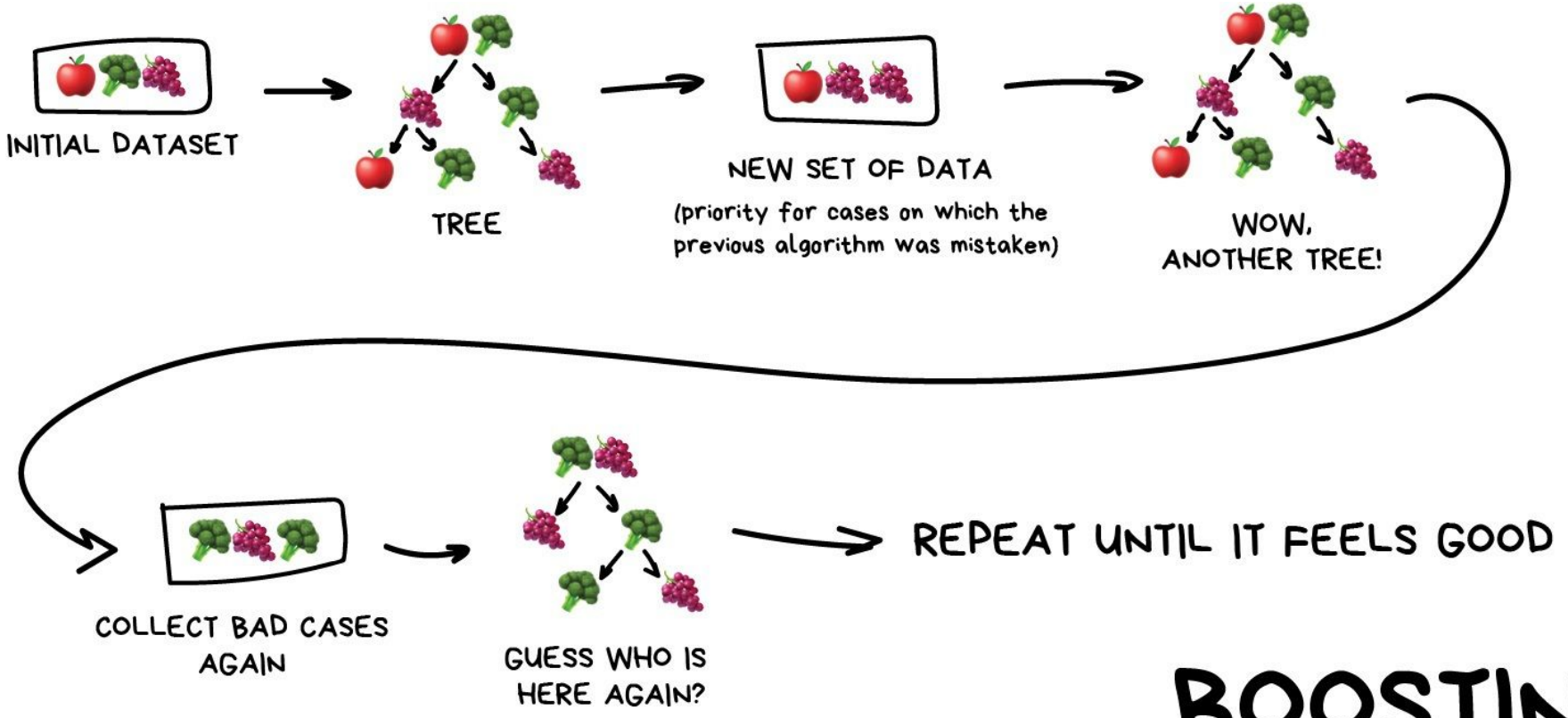
notas

ENSEMBLE METHODS

BAGGING & PASTING
BOOSTING
STACKING


SAME
ALGORITHMS
BAGGING ON TREES
=
RANDOM FOREST
MAKE
DIFFERENT SETS
OF DATA FROM
INITIAL SET
!!!
JUST AVERAGING
ALL THE RESULTS
ANSWER
BAGGING

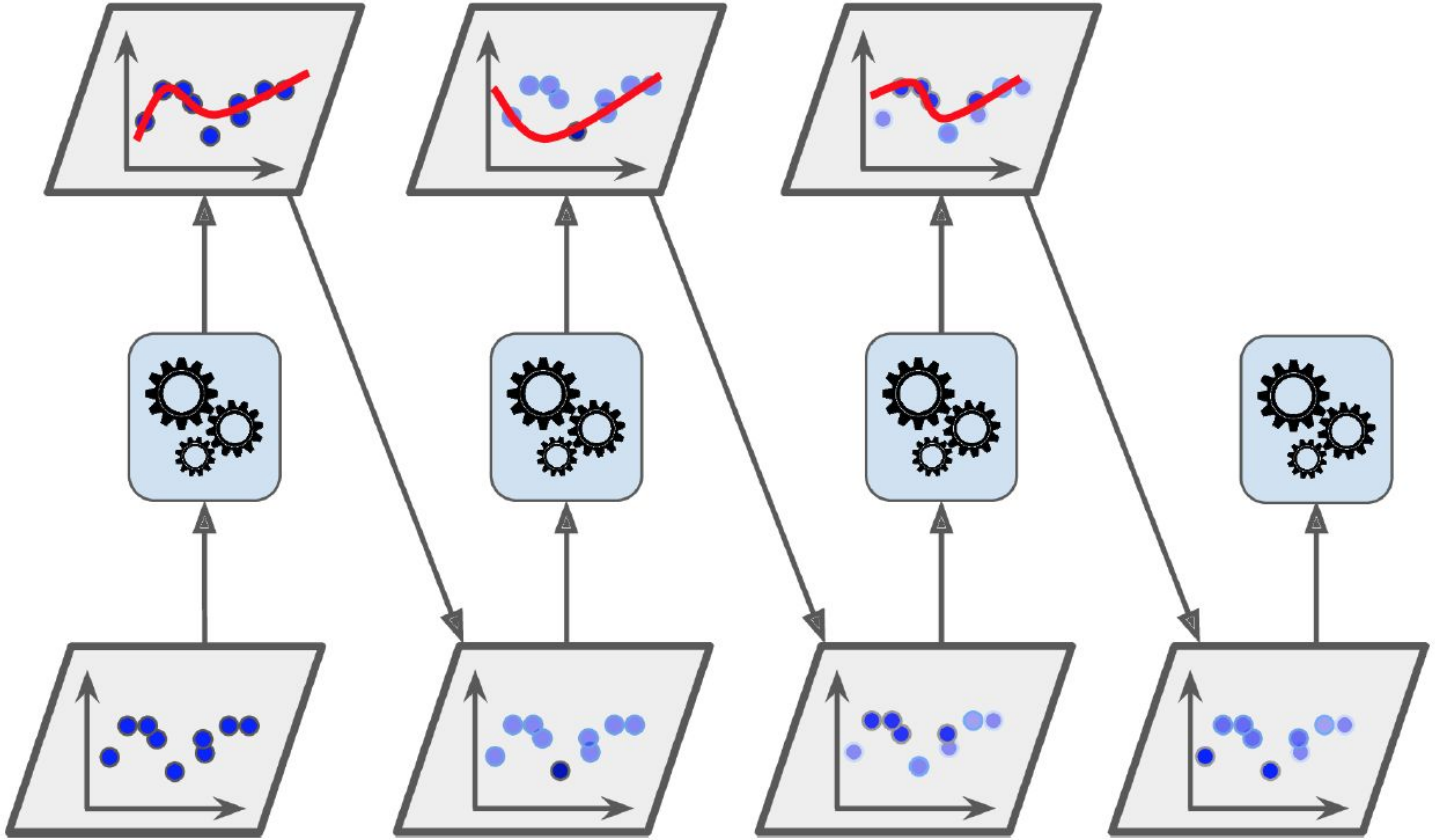
```
# Random Forest using BaggingClassifier
bag_clf = BaggingClassifier(DecisionTreeClassifier(max_features="auto",
                                                   max_leaf_nodes=16,
                                                   random_state=42),
                            n_estimators=500,
                            max_samples=1.0,
                            bootstrap=True,
                            random_state=42)

# Random Forest using RandomForestClassifier
rnd_clf = RandomForestClassifier(n_estimators=500,
                                 max_leaf_nodes=16,
                                 random_state=42)
```

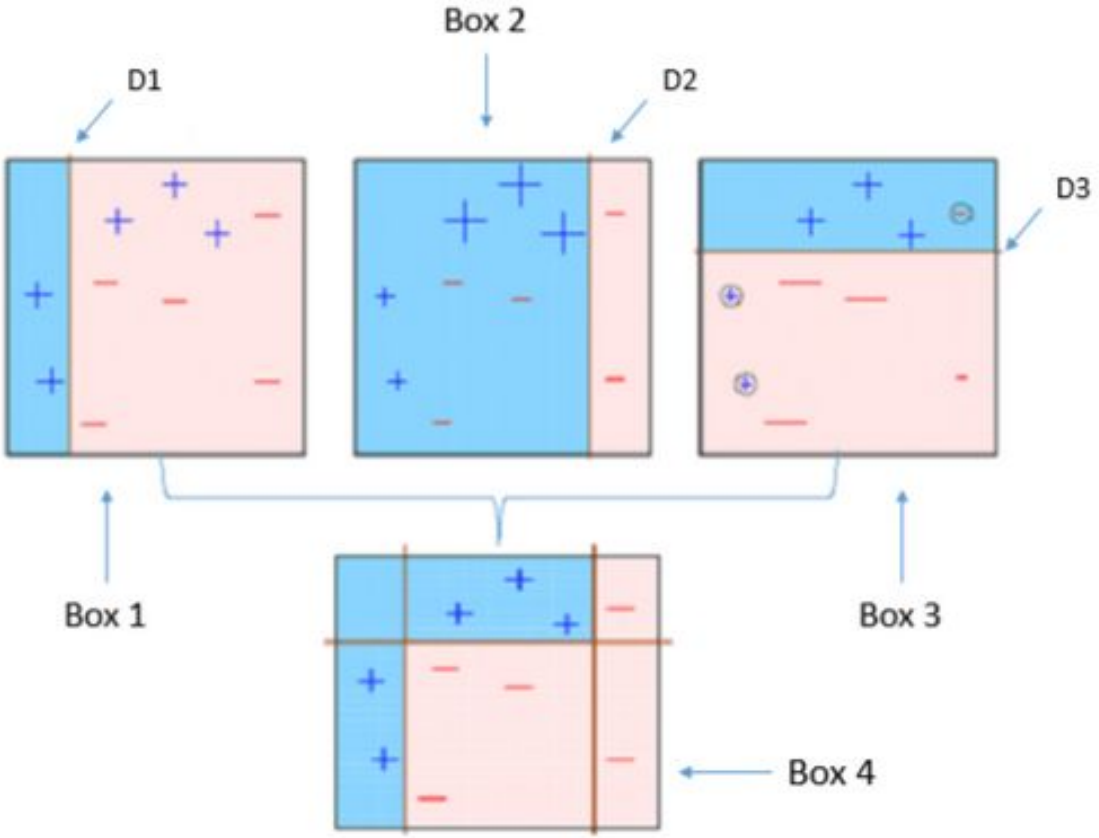

INITIAL DATASET
TREE
NEW SET OF DATA
(priority for cases on which the previous algorithm was mistaken)
WOW, ANOTHER TREE!
REPEAT UNTIL IT FEELS GOOD
GUESS WHO IS HERE AGAIN?
COLLECT BAD CASES AGAIN

BOOSTING

Adaptive Boosting (AdaBoosting)

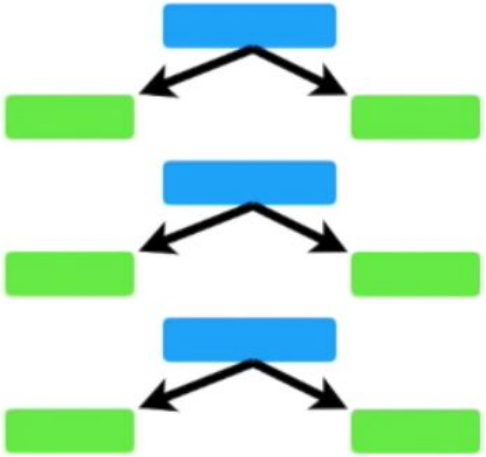
AdaBoost sequential training with instance weight updates





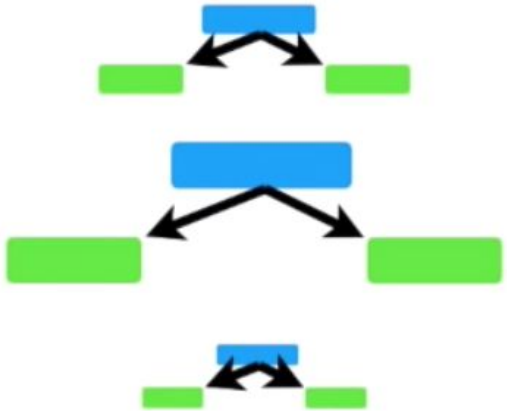
Efficiency of the algorithm is highly affected by outliers

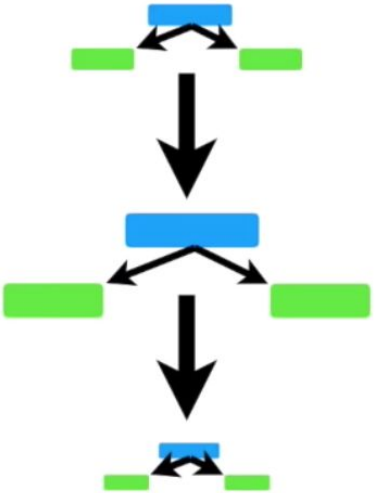
1. AdaBoost combines a lot of "weak learners" to make classifications. The weak learners are almost always **stumps**



3. Each **stump** is made by taking the previous stump's mistake into account

2. Some **stumps** get more say in the classification than others





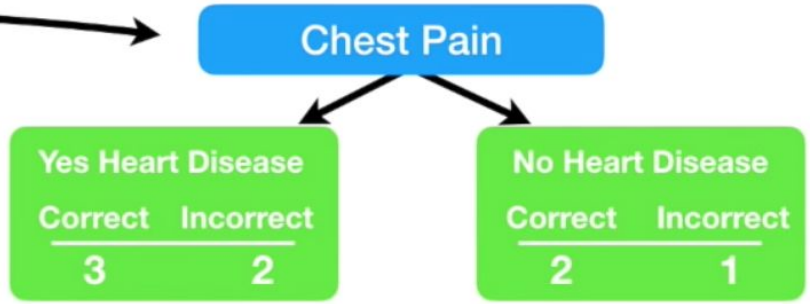
Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

At the start, all samples get the same weight…

$$\frac{1}{\text{total number of samples}} = \frac{1}{8}$$

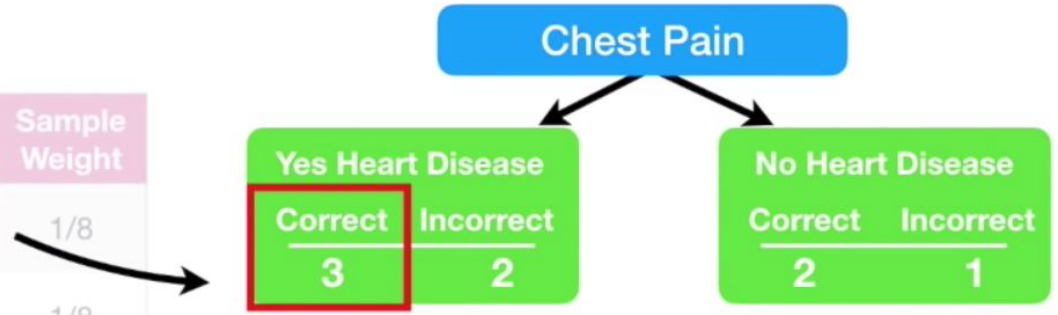
…and that makes the samples all equally important.

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8



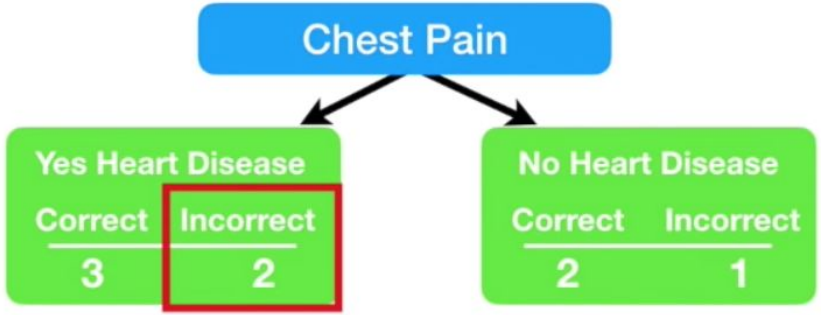
We start by seeing how well **Chest Pain** classifies the samples.

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8



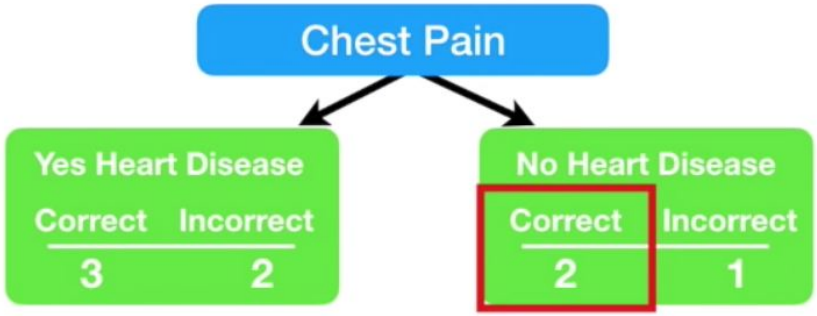
Of the 5 samples with **Chest Pain**, 3 were *correctly* classified as having **Heart Disease**…

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8



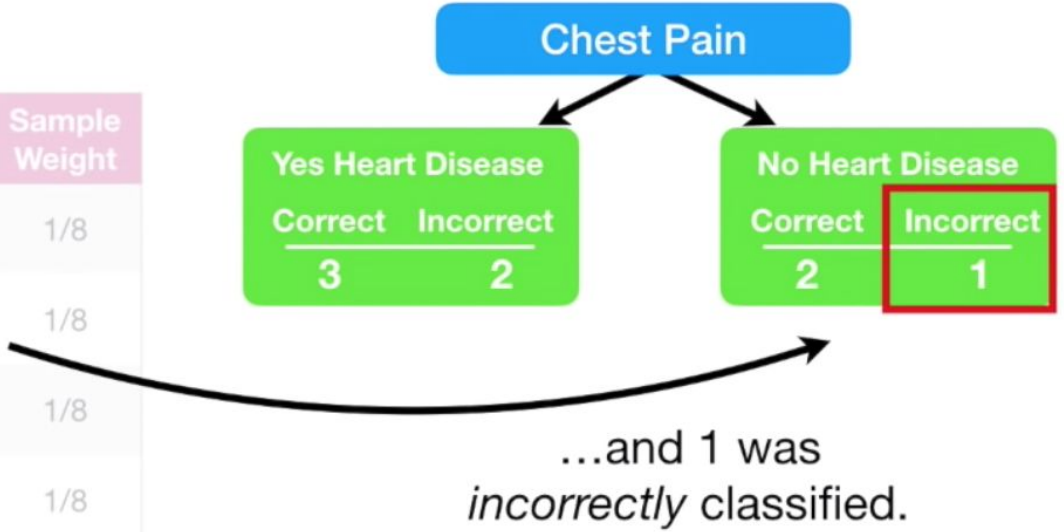
…and 2 were *incorrectly* classified.

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

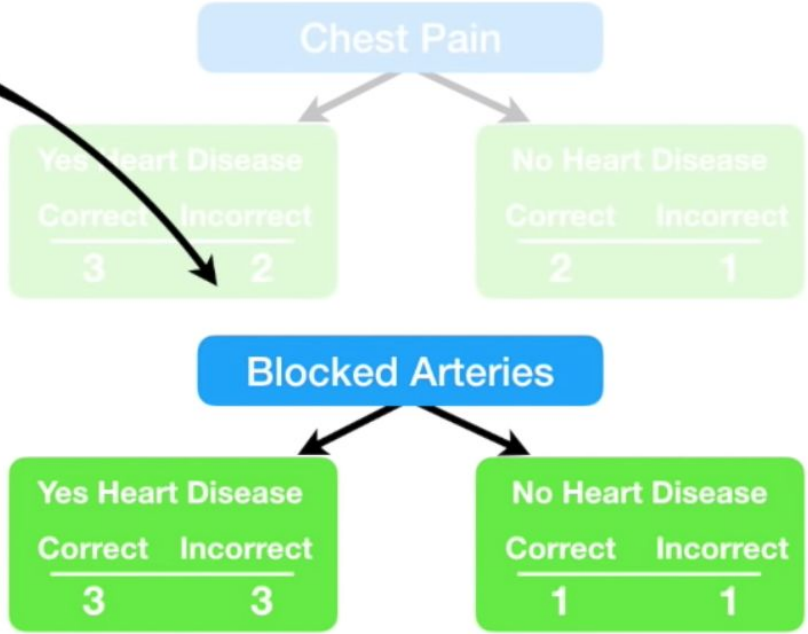


Of the 3 samples *without* **Chest Pain**, 2 were *correctly* classified as *not* having **Heart Disease**…

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8



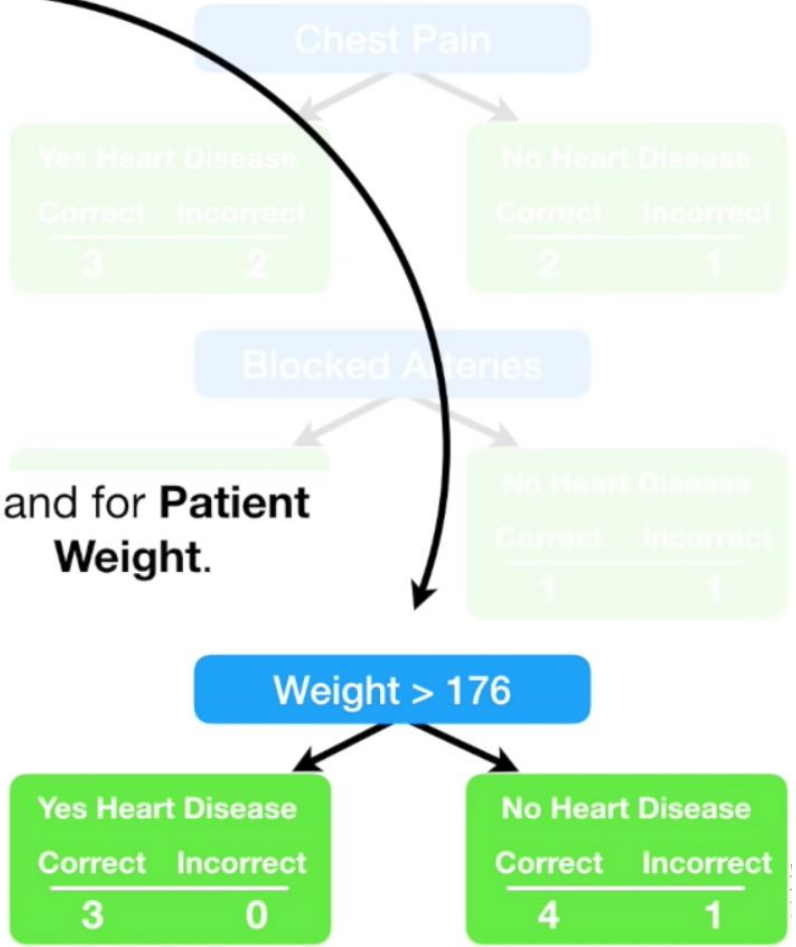
Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8



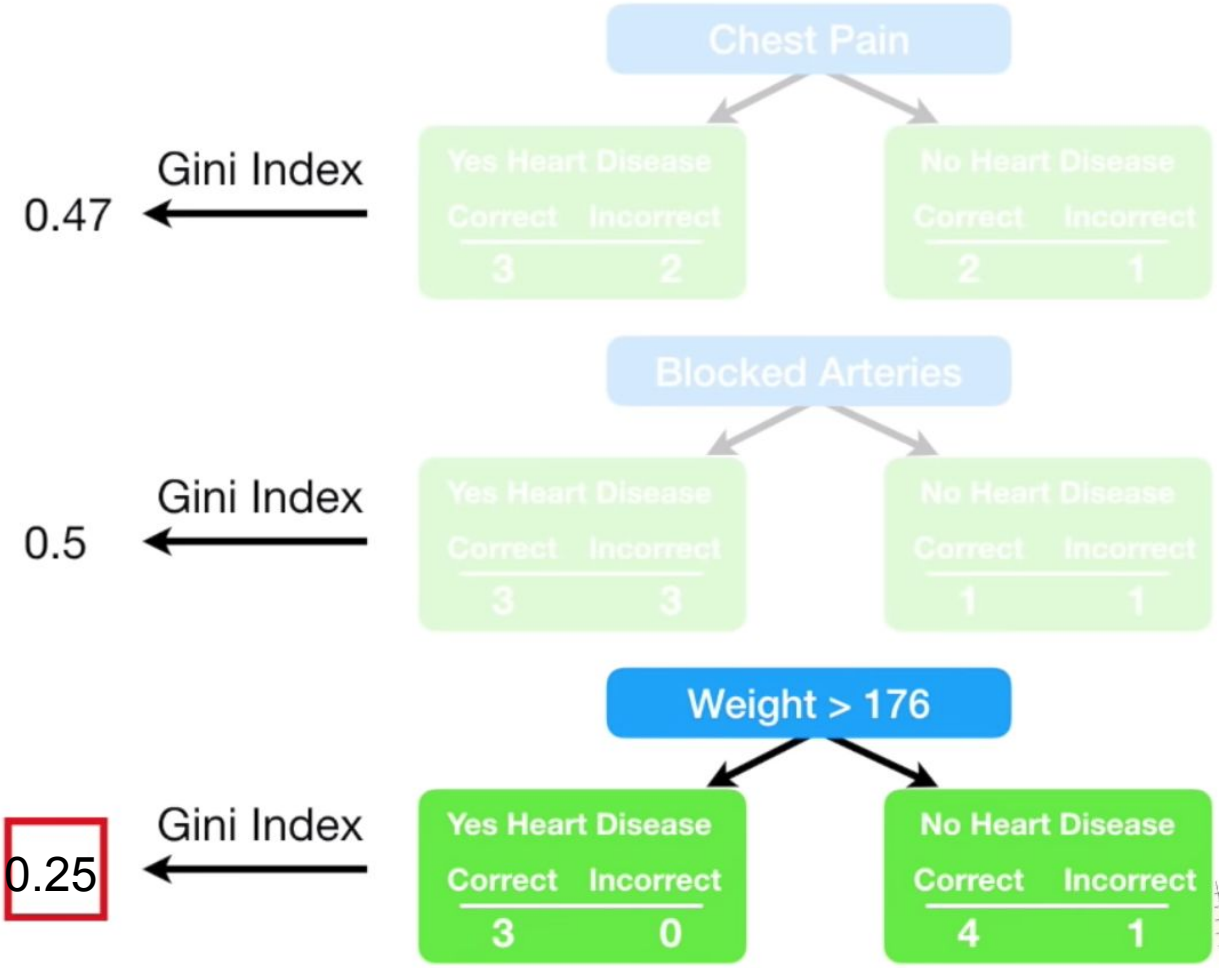
Now we do the same thing for **Blocked Arteries**…

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

…and for **Patient Weight.**

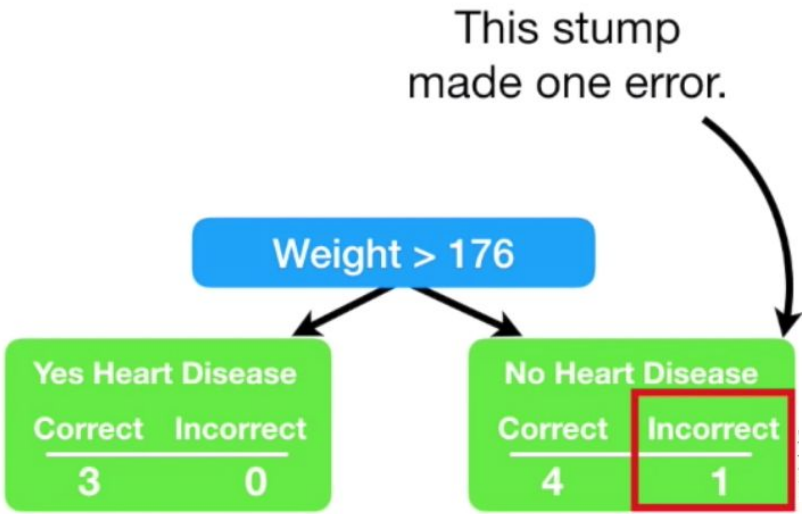


$$Gini(x) = 1 - \sum_{i=1}^{c} P(x_i)^2$$



…so this will be the first stump in the forest.

Now we need to determine how much say this stump will have in the final classification.


This stump
made one error.
Weight > 176
Yes Heart Disease
Correct
Incorrect
3
0
No Heart Disease
Correct
Incorrect
4
1

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

This patient, who weighs less than 176, *has* heart disease, but the stump says they do not.

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

The **Total Error** for a stump is the sum of the weights associated with the *incorrectly* classified samples.

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

Thus, in this case, the **Total Error** is **1/8**.

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

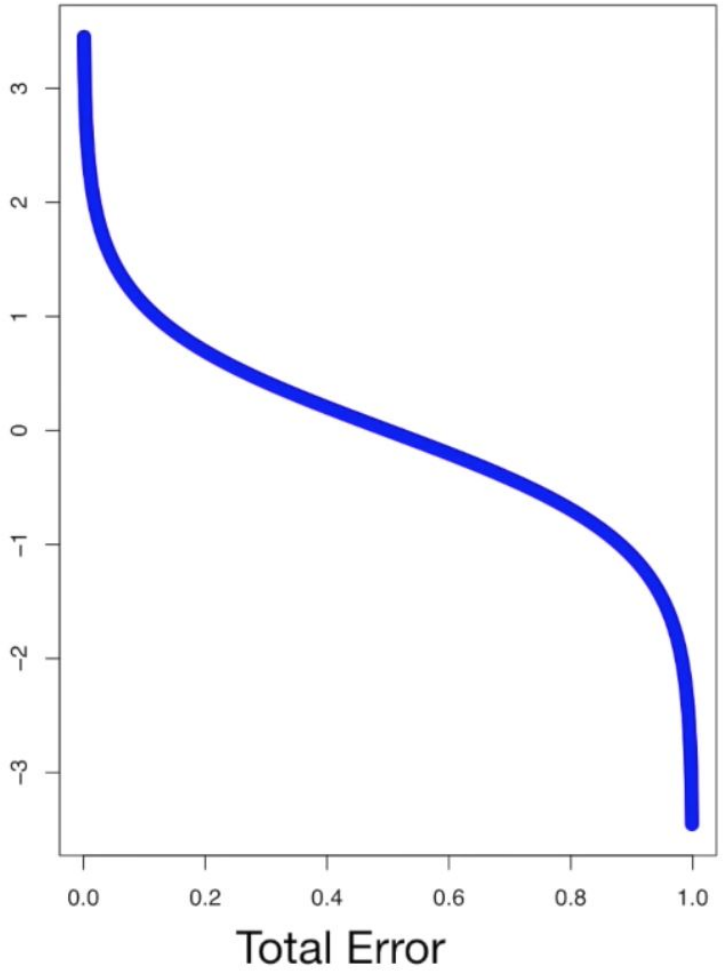
NOTE: Because all of the **Sample Weights** add up to **1**, **Total Error** will always be between **0**, for a perfect stump, and **1**, for a horrible stump.

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

We use the **Total Error** to determine **Amount of Say** this stump has in the final classification with the following formula:

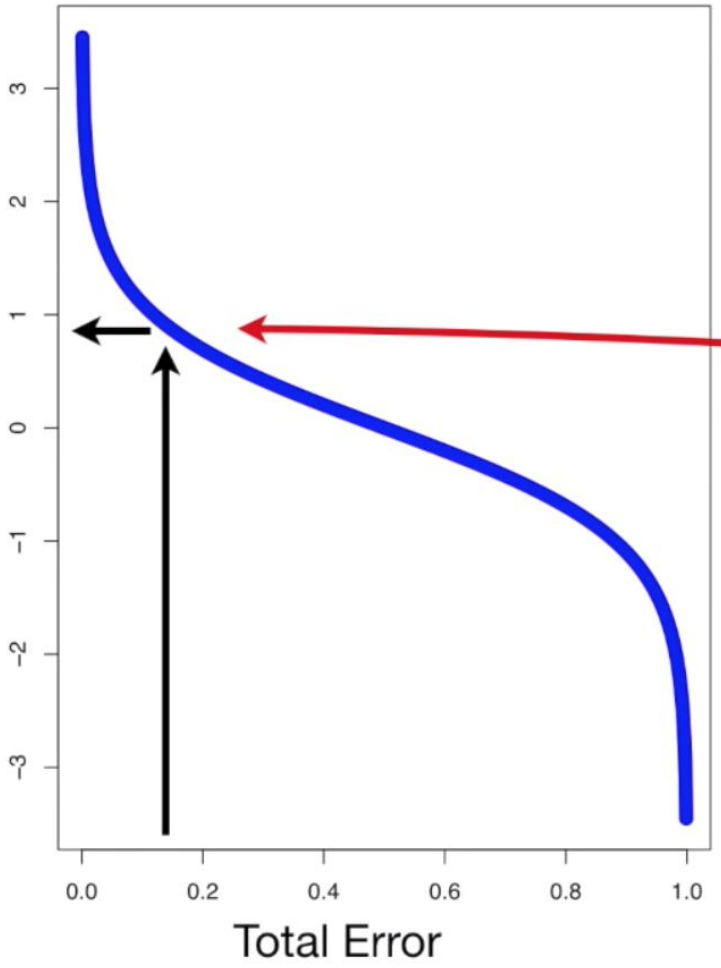
$$\text{Amount of Say} = \frac{1}{2}\log\left(\frac{1 - \text{Total Error}}{\text{Total Error}}\right)$$

Learning Rate



We can draw a graph of the **Amount of Say** by plugging in a bunch of numbers between **0** and **1** for **Total Error**.

$$\text{Amount of Say} = \frac{1}{2}\log\left(\frac{1 - \text{Total Error}}{\text{Total Error}}\right)$$



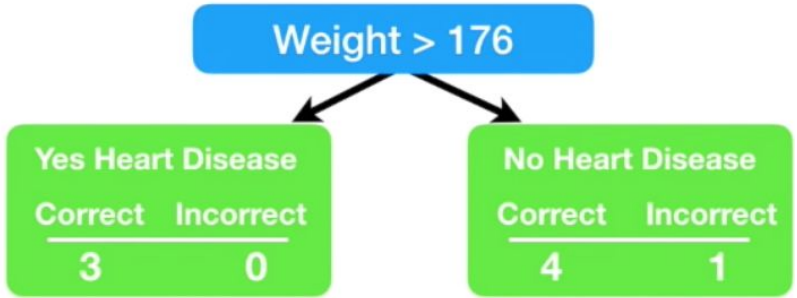
…and the **Amount of Say** that this stump has on the final classification is **0.97**.

$$\text{Amount of Say} = \frac{1}{2}\log(7) = 0.97$$

Now we need to learn how to modify the weights so that the next stump will take the errors that the current stump made into account.

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

When we created this stump, all of the **Sample Weights** were the same…



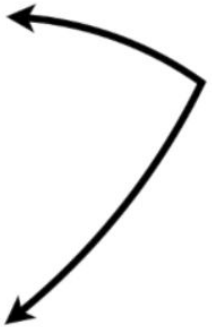
Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

…and that meant we did not emphasize the importance of correctly classifying any particular sample…

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

…we will emphasize the need for the next stump to correctly classify it by increasing its **Sample Weight**…

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

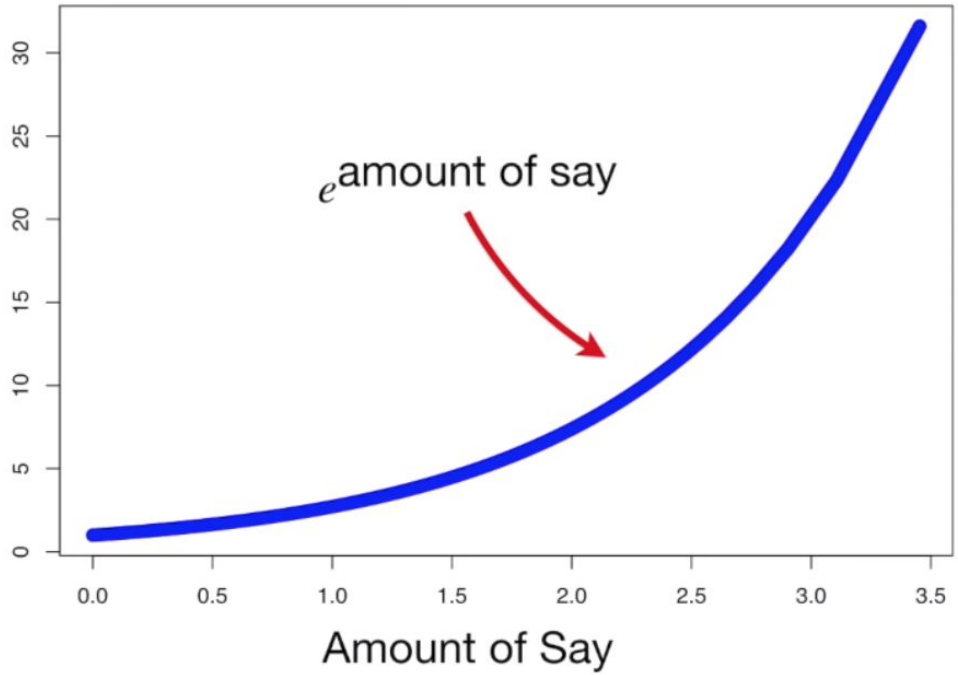


…and decreasing all of the other **Sample Weights**.

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

$$\text{New Sample Weight} = \text{sample weight} \times e^{\text{amount of say}}$$

This is the formula we will use to *increase* the **Sample Weight** for the sample that was *incorrectly* classified.



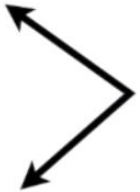
$$\text{New Sample Weight} = \text{sample weight} \times e^{\text{amount of say}}$$

$$= \frac{1}{8} e^{\text{amount of say}}$$

$$= \frac{1}{8} e^{0.97} = \frac{1}{8} \times 2.64 = 0.33$$

That means the new **Sample Weight** is **0.33**, which is *more* than the old one (**1/8** = **0.125**).

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8



Now we need to *decrease* the **Sample Weights** for all of the *correctly* classified samples.

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

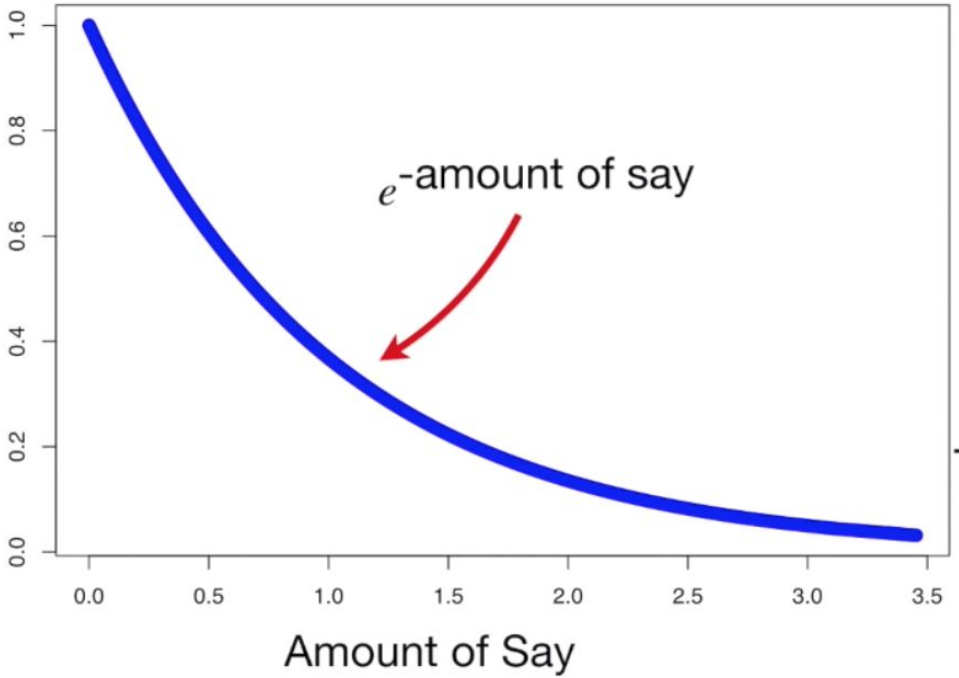
$$\text{New Sample Weight} = \text{sample weight} \times e^{\text{-amount of say}}$$

This is the formula we will use to *decrease* the **Sample Weights**.

$$\text{New Sample Weight} = \text{sample weight} \times e^{\text{-amount of say}}$$

$$= \frac{1}{8} e^{\text{-amount of say}}$$

$$= \frac{1}{8} e^{-0.97} = \frac{1}{8} \times 0.38 = 0.05$$



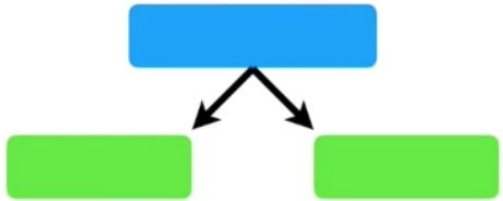
The new **Sample Weight** is **0.05**, which is *less* than the old one (**1/8** = **0.125**).

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight	New Weight	Norm. Weight
Yes	Yes	205	Yes	1/8	0.05	0.07
No	Yes	180	Yes	1/8	0.05	0.07
Yes	No	210	Yes	1/8	0.05	0.07
Yes	Yes	167	Yes	1/8	0.33	0.49
No	Yes	156	No	1/8	0.05	0.07
No	Yes	125	No	1/8	0.05	0.07
Yes	No	168	No	1/8	0.05	0.07
Yes	Yes	172	No	1/8	0.05	0.07

So we divide each **New Sample Weight** by **0.68** to get the normalized values.

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	0.07
No	Yes	180	Yes	0.07
Yes	No	210	Yes	0.07
Yes	Yes	167	Yes	0.49
No	Yes	156	No	0.07
No	Yes	125	No	0.07
Yes	No	168	No	0.07
Yes	Yes	172	No	0.07

Now we can use the modified **Sample Weights** to make the second **stump** in the forest.



Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	0.07
No	Yes	180	Yes	0.07
Yes	No	210	Yes	
Yes	Yes	167	Yes	
No	Yes	156	No	
No	Yes	125	No	0.07
Yes	No	168	No	0.07
Yes	Yes	172	No	0.07

So we start by making a new, but empty, dataset that is the same size as the original…

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	0.07
No	Yes	180	Yes	0.07
Yes	No	210	Yes	0.07
Yes	Yes	167	Yes	0.49
No	Yes	156	No	0.07
No	Yes	125	No	0.07
Yes	No	168	No	0.07
Yes	Yes	172	No	0.07

…and we see where that number falls when we use the **Sample Weights** like a distribution.

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	0.07
No	Yes	180	Yes	0.07
Yes	No	210	Yes	0.07
Yes	Yes	167	Yes	0.49
No	Yes	156	No	0.07
No	Yes	125	No	0.07
Yes	No	168	No	0.07
Yes	Yes	172	No	0.07

If the number is between **0** and **0.07**, then we would put this sample into the new collection of samples…

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	0.07
No	Yes	180	Yes	0.07
Yes	No	210	Yes	0.07
Yes	Yes	167	Yes	0.49
No	Yes	156	No	0.07
No	Yes	125	No	0.07
Yes	No	168	No	0.07
Yes	Yes	172	No	0.07

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease

…and if the number is between **0.07** and **0.14** (**0.07** + **0.07** = **0.14**), then we would put this sample into the new collection of samples…

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	0.07
No	Yes	180	Yes	0.07
Yes	No	210	Yes	0.07
Yes	Yes	167	Yes	0.49
No	Yes	156	No	0.07
No	Yes	125	No	0.07
Yes	No	168	No	0.07
Yes	Yes	172	No	0.07

…and if the number is between **0.14** and **0.21** (**0.14** + **0.07** = **0.21**), then we would put this sample into the new collection of samples…

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	0.07
No	Yes	180	Yes	0.07
Yes	No	210	Yes	0.07
Yes	Yes	167	Yes	0.49
No	Yes	156	No	0.07
No	Yes	125	No	0.07
Yes	No	168	No	0.07
Yes	Yes	172	No	0.07

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease

…and if the number is between **0.21** and **0.70** (**0.21** + **0.49** = **0.70**), then we would put this sample into the new collection of samples…

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	0.07
No	Yes	180	Yes	0.07
Yes	No	210	Yes	0.07
Yes	Yes	167	Yes	0.49
No	Yes	156	No	0.07
No	Yes	125	No	0.07
Yes	No	168	No	0.07
Yes	Yes	172	No	0.07

For example, imagine the first number I picked was **0.72**...

...then I would put this sample into my new collection of samples...

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	0.07
No	Yes	180	Yes	0.07
Yes	No	210	Yes	0.07
Yes	Yes	167	Yes	0.49
No	Yes	156	No	0.07
No	Yes	125	No	0.07
Yes	No	168	No	0.07
Yes	Yes	172	No	0.07

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease
No	Yes	156	No

Then I pick another random number and get **0.42**…

…and I would put this sample into my new collection of samples…

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	0.07
No	Yes	180	Yes	0.07
Yes	No	210	Yes	0.07
Yes	Yes	167	Yes	0.49
No	Yes	156	No	0.07
No	Yes	125	No	0.07
Yes	No	168	No	0.07
Yes	Yes	172	No	0.07

…and I would put this sample into my new collection of samples…

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease
No	Yes	156	No
Yes	Yes	167	Yes

Then I pick **0.83**…

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	0.07
No	Yes	180	Yes	0.07
Yes	No	210	Yes	0.07
Yes	Yes	167	Yes	0.49
No	Yes	156	No	0.07
No	Yes	125	No	0.07
Yes	No	168	No	0.07
Yes	Yes	172	No	0.07

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease
No	Yes	156	No
Yes	Yes	167	Yes
No	Yes	125	No

Then I pick **0.51**…

…and I would put this sample into my new collection of samples…

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	0.07
No	Yes	180	Yes	0.07
Yes	No	210	Yes	0.07
Yes	Yes	167	Yes	.49
No	Yes	156	No	0.07
No	Yes	125	No	0.07
Yes	No	168	No	0.07
Yes	Yes	172	No	0.07

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease
No	Yes	156	No
Yes	Yes	167	Yes
No	Yes	125	No
Yes	Yes	167	Yes

NOTE: This is the second time that we have added this particular sample to the new collection of samples.

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	0.07
No	Yes	180	Yes	0.07
Yes				
Yes				
No				
No	Yes	125	No	0.07
Yes	No	168	No	0.07
Yes	Yes	172	No	0.07

We then continue to pick random numbers and add samples to the new collection until we the new collection is the same size as the original.

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease
No	Yes	156	No
Yes	Yes	167	Yes
No	Yes	125	No
Yes	Yes	167	Yes
Yes	Yes	167	Yes
Yes	Yes	172	No
Yes	Yes	205	Yes
Yes	Yes	167	Yes

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	0.07
No	Yes	180	Yes	0.07
Yes	No	210	Yes	0.07
Yes	Yes	167	Yes	0.49
No	Yes	156	No	0.07
No	Yes	125	No	0.07
Yes	No	168	Yes	0.07
Yes	Yes	172	No	0.07

Ultimately, this sample was added to the new collection of samples **4** times, reflecting its larger **Sample Weight**.

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease
No	Yes	156	No
Yes	Yes	167	Yes
No	Yes	125	No
Yes	Yes	167	Yes
Yes	Yes	167	Yes
Yes	Yes	172	No
Yes	Yes	205	Yes
Yes	Yes	167	Yes

Now we get rid of the original samples…

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease
No	Yes	156	No
Yes	Yes	167	Yes
No	Yes	125	No
Yes	Yes	167	Yes
Yes	Yes	167	Yes
Yes	Yes	172	No
Yes	Yes	205	Yes
Yes	Yes	167	Yes

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease
No	Yes	156	No
Yes	Yes	167	Yes
No	Yes	125	No
Yes	Yes	167	Yes
Yes	Yes	167	Yes
Yes	Yes	172	No
Yes	Yes	205	Yes
Yes	Yes	167	Yes

…and use the new collection of samples.

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease
No	Yes	156	No
Yes	Yes	167	Yes
No	Yes	125	No
Yes	Yes	167	Yes
Yes	Yes	167	Yes
Yes	Yes	172	No
Yes	Yes	205	Yes
Yes	Yes	167	Yes

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
No	Yes	156	No	1/8
Yes	Yes	167	Yes	1/8
No	Yes	125	No	1/8
Yes	Yes	167	Yes	1/8
Yes	Yes	167	Yes	1/8
Yes	Yes	172	No	1/8
Yes	Yes	205	Yes	1/8
Yes	Yes	167	Yes	1/8

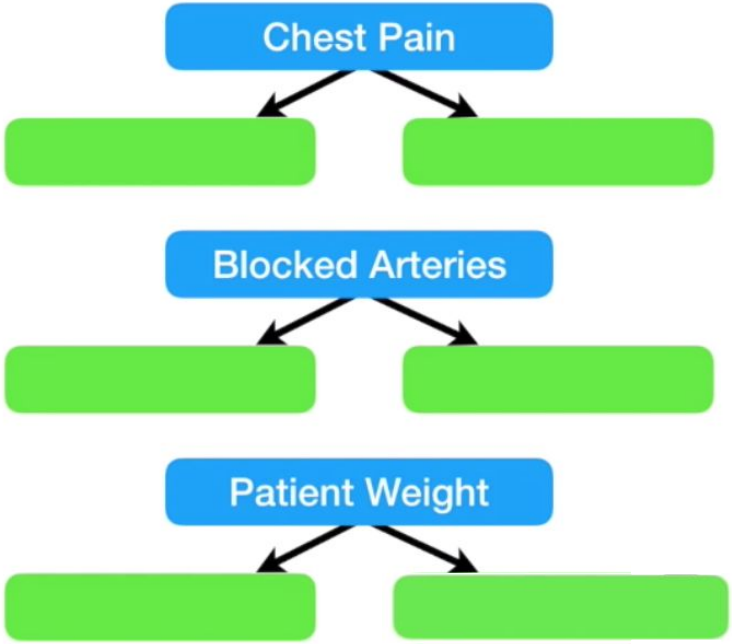
Lastly, we give all the samples equal **Sample Weights**, just like before.

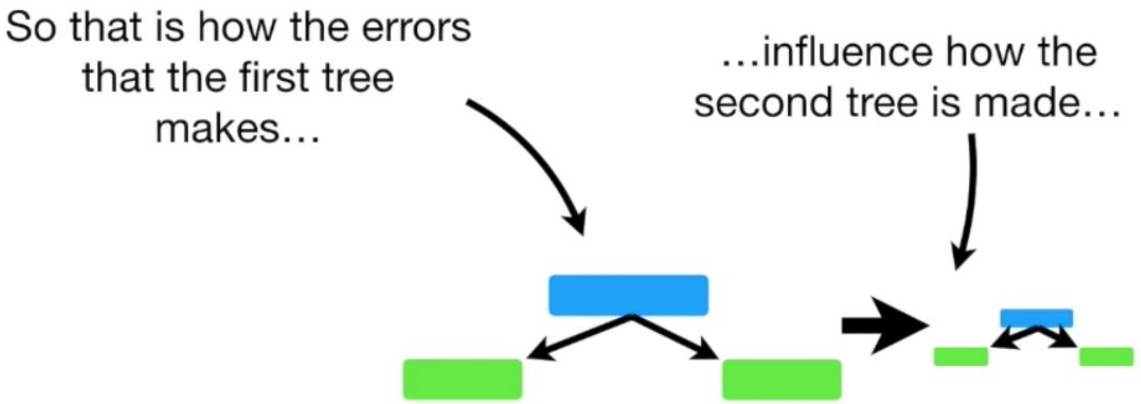
Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
No	Yes	156	No	1/8
Yes	Yes	167	Yes	1/8
No	Yes	125	No	1/8
Yes	Yes	167	Yes	1/8
Yes	Yes	167	Yes	1/8
Yes	Yes	172	No	1/8
Yes	Yes	205	Yes	1/8
Yes	Yes	167	Yes	1/8

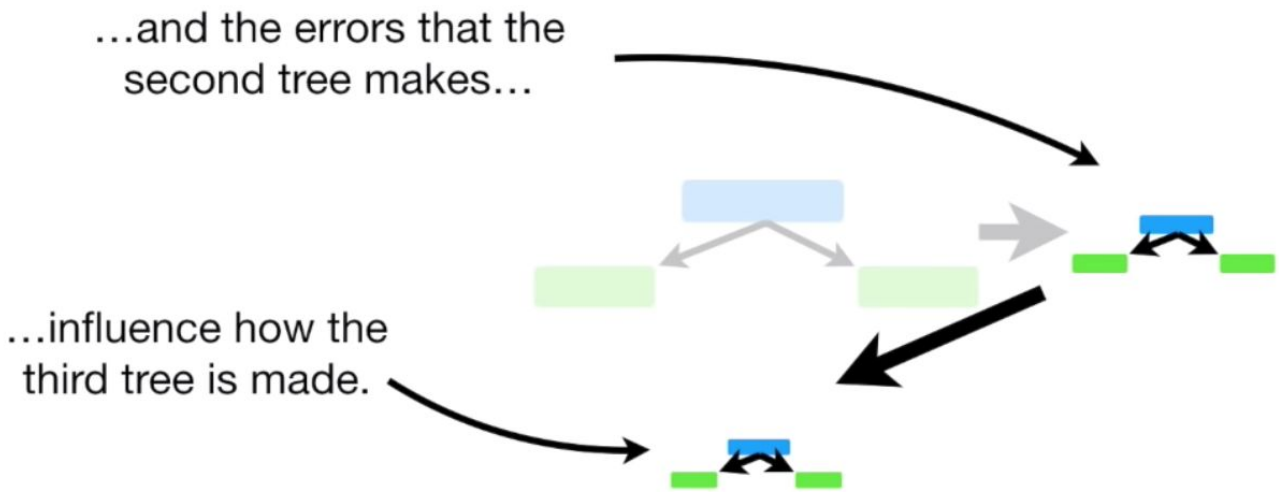
Because these samples are all the same, they will be treated as a block, creating a large penalty for being misclassified.

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
No	Yes	156	No	1/8
Yes	Yes	167	Yes	1/8
No	Yes	125	No	1/8
Yes	Yes	167	Yes	1/8
Yes	Yes	167	Yes	1/8
Yes	Yes	172	No	1/8
Yes	Yes	205	Yes	1/8
Yes	Yes	167	Yes	1/8

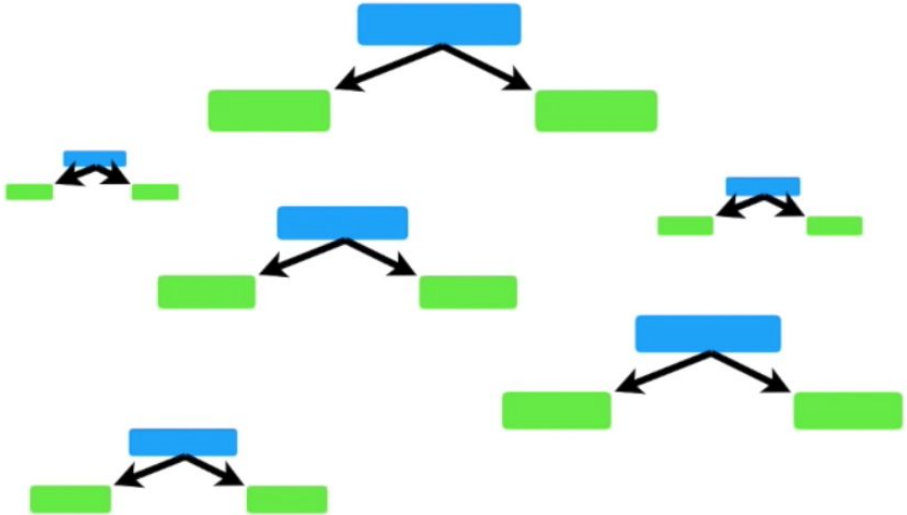
Now we go back to the beginning and try to find the stump that does the best job classifying the new collection of samples.



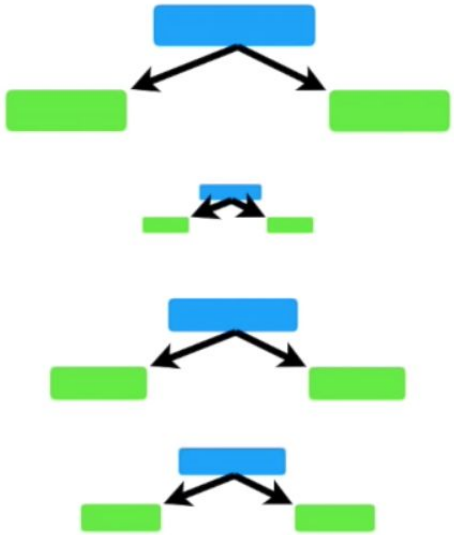

So that is how the errors that the first tree makes…
…influence how the second tree is made…

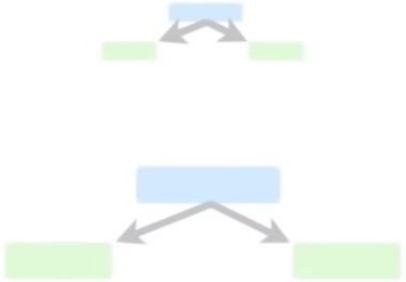

…and the errors that the second tree makes…
…influence how the third tree is made.

Now we need to talk about how a forest of stumps created by **AdaBoost** makes classifications…

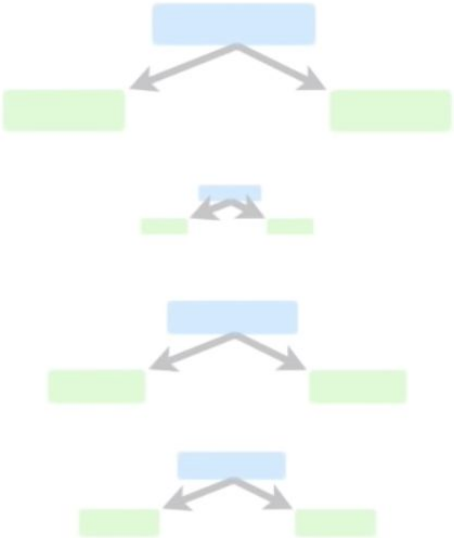


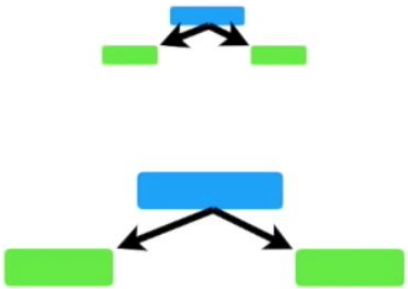
Imagine that these stumps classified a patient as **Has Heart Disease**…





…and these stumps classified the patient as **Does Not Have Heart Disease**.





Ultimately, the patient is classified as **Has Heart Disease** because this is the larger sum.

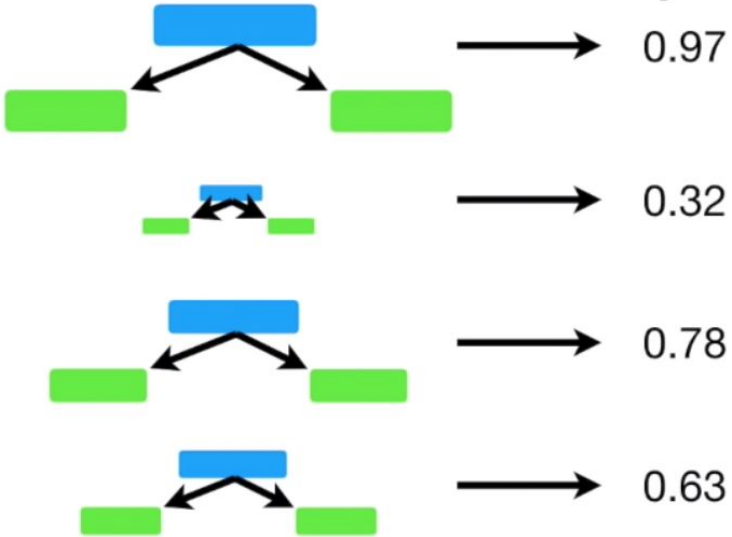
Has Heart Disease

Total = 2.7

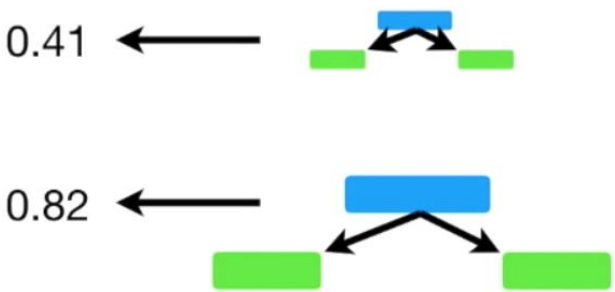
Total = 1.23

Does Not Have Heart Disease

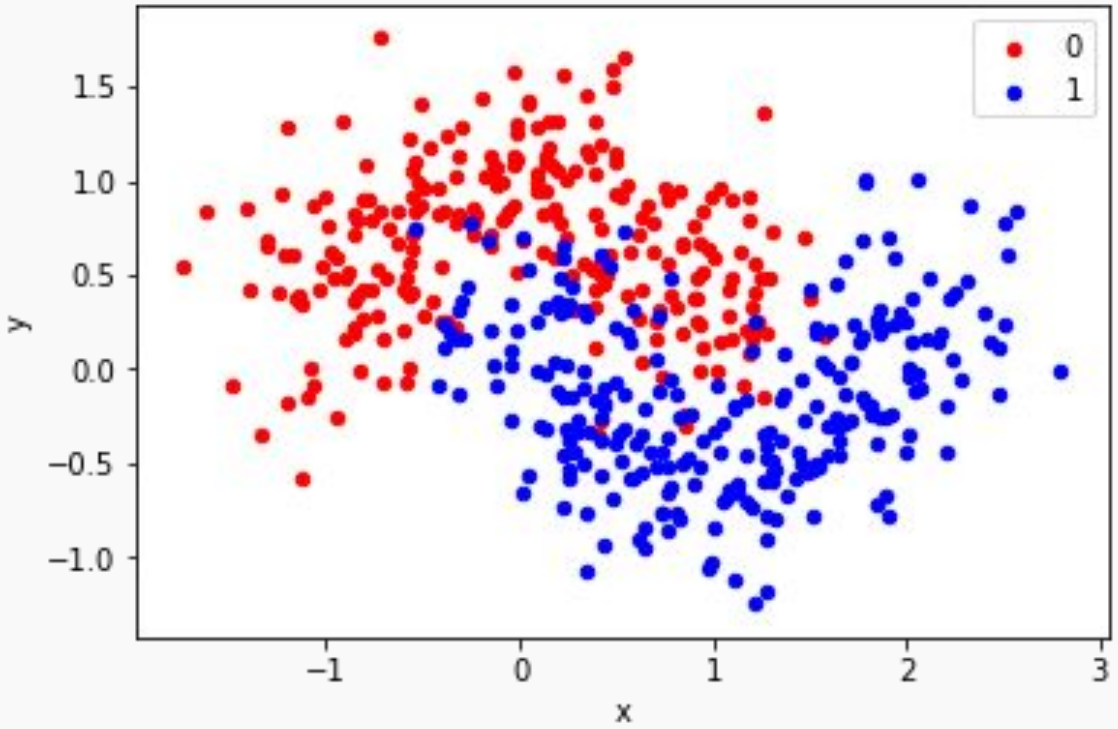
Amount of Say



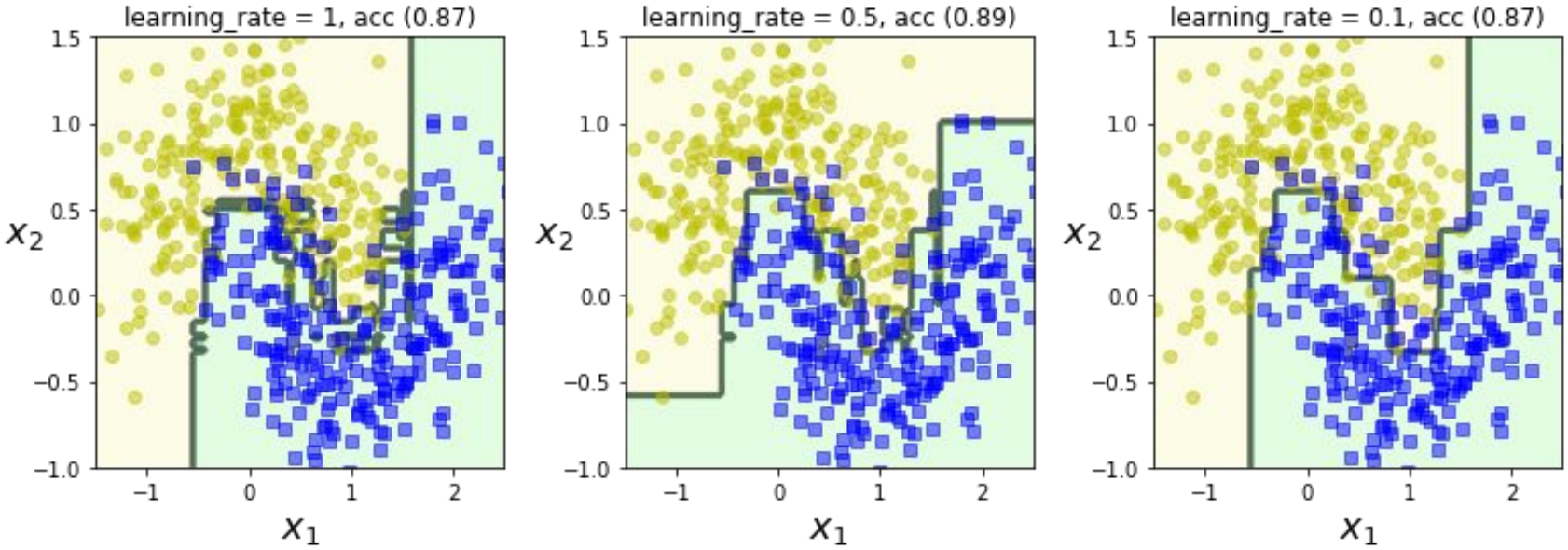
Amount of Say



Estudo de Caso



```
ada_clf = AdaBoostClassifier(DecisionTreeClassifier(max_depth=1),
                             n_estimators=200,
                             algorithm="SAMME.R",
                             learning_rate=learning_rate,
                             random_state=42)
```



Gradient Boosting

Greedy Function Approximation: A Gradient Boosting Machine

Jerome H. Friedman*
IMS 1999 Reitz Lecture

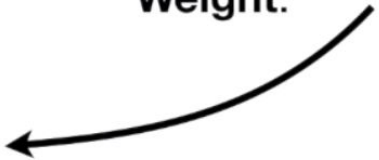
February 24,1999 (modified March 15, 2000, April 19, 2001)

Abstract

Function estimation/approximation is viewed from the perspective of numerical optimization in function space, rather than parameter space. A connection is made between stagewise additive expansions and steepest–descent minimization. A general gradient–descent "boosting" paradigm is developed for additive expansions based on any fitting criterion. Specific algorithms are presented for least–squares, least–absolute–deviation, and Huber–M loss functions for regression, and multi–class logistic likelihood for classification. Special enhancements are derived for the particular case where the individual additive components are regression trees, and tools for interpreting such "TreeBoost" models are presented. Gradient boosting of regression trees produces competitive, highly robust, interpretable procedures for both regression and classification, especially appropriate for mining less than clean data. Connections between this approach and the boosting methods of Freund and Shapire 1996, and Friedman, Hastie, and Tibshirani 2000 are discussed.

1 Function estimation

…let's see how the most common **Gradient Boost** configuration would use this **Training Data** to **Predict Weight**.



Height (m)	Favorite Color	Gender	Weight (kg)
1.6	Blue	Male	88
1.6	Green	Female	76
1.5	Blue	Female	56
1.8	Red	Male	73
1.5	Green	Male	77
1.4	Blue	Female	57

Average Weight

71.2

The first thing we do is calculate the average **Weight.**

Height (m)	Favorite Color	Gender	Weight (kg)
1.6	Blue	Male	88
1.6	Green	Female	76
1.5	Blue	Female	56
1.8	Red	Male	73
1.5	Green	Male	77
1.4	Blue	Female	57

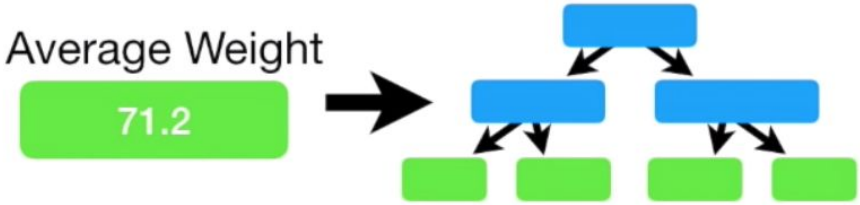
Average Weight

71.2

Height (m)	Favorite Color	Gender	Weight (kg)
1.6	Blue	Male	88
1.6	Green	Female	76
1.5	Blue	Female	56
1.8	Red	Male	73
1.5	Green	Male	77
1.4	Blue	Female	57

In other words, if we stopped right now, we would predict that everyone **Weighed 71.2** kg.

However, **Gradient Boost** doesn't stop here.

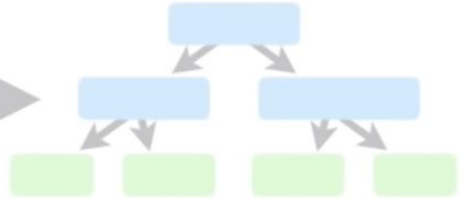


Height (m)	Favorite Color	Gender	Weight (kg)
1.6	Blue	Male	88
1.6	Green	Female	76
1.5	Blue	Female	56
1.8	Red	Male	73
1.5	Green	Male	77
1.4	Blue	Female	57

The next thing we do is build a tree based on the errors from the first tree.

Average Weight

71.2



Height (m)	Favorite Color	Gender	Weight (kg)
1.6	Blue	Male	88
1.6	Green	Female	76
1.5	Blue	Female	56
1.8	Red	Male	73
1.5	Green	Male	77
1.4	Blue	Female	57

The errors that the previous tree made are the differences between the **Observed Weights** and the **Predicted Weight**, **71.2**.

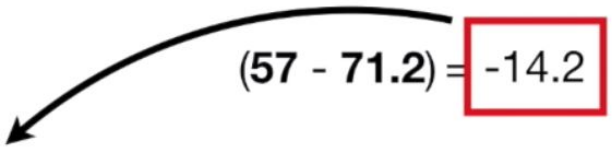
(Observed Weight - Predicted Weight)

Average Weight

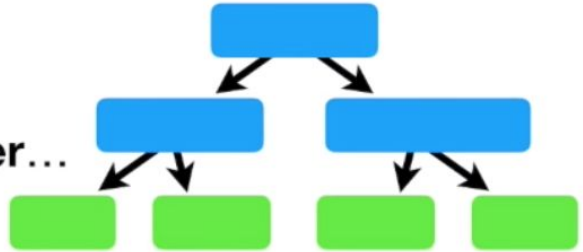
71.2

Height (m)	Favorite Color	Gender	Weight (kg)	Residual
1.6	Blue	Male	88	16.8
1.6	Green	Female	76	4.8
1.5	Blue	Female	56	-15.2
1.8	Red	Male	73	1.8
1.5	Green	Male	77	5.8
1.4	Blue	Female	57	-14.2

Now do the same thing for the remaining **Weights**…



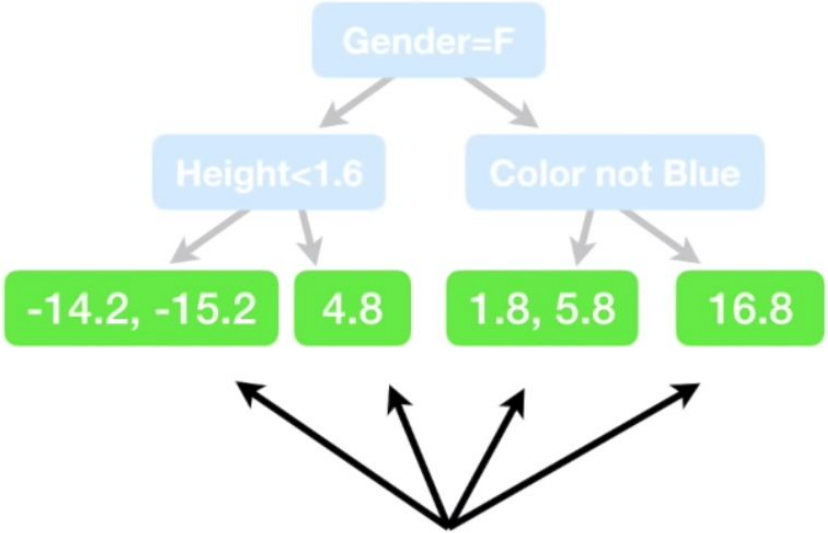
Now we will build a **Tree**, using **Height**, **Favorite Color** and **Gender**…



Height (m)	Favorite Color	Gender	Weight (kg)	Residual
1.6	Blue	Male	88	16.8
1.6	Green	Female	76	4.8
1.5	Blue	Female	56	-15.2
1.8	Red	Male	73	1.8
1.5	Green	Male	77	5.8
1.4	Blue	Female	57	-14.2

…to **Predict** the **Residuals**.

Height (m)	Favorite Color	Gender	Residual
1.6	Blue	Male	16.8
1.6	Green	Female	4.8
1.5	Blue	Female	-15.2
1.8	Red	Male	1.8
1.5	Green	Male	5.8
1.4	Blue	Female	-14.2



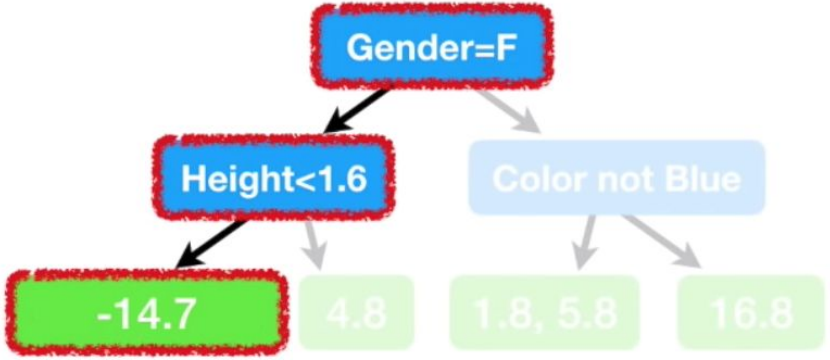
Remember, in this example we are only allowing up to four leaves…

…but when using a larger dataset, it is common to allow anywhere from **8** to **32**.

Height (m)	Favorite Color	Gender	Weight (kg)	Residual
1.6	Blue	Male	88	16.8
1.6	Green	Female	76	4.8
1.5	Blue	Female	58	-15.2
1.8	Red	Male	73	1.8
1.5	Green	Male	77	5.8
1.4	Blue	Female	57	-14.2

As a result, these two rows of data go to the same leaf.

Height (m)	Favorite Color	Gender	Weight (kg)	Residual
1.6	Blue	Male	88	16.8
1.6	Green	Female	76	4.8
1.5	Blue	Female	56	-15.2
1.8	Red	Male	73	1.8
1.5	Green	Male	77	5.8
1.4	Blue	Female	57	-14.2



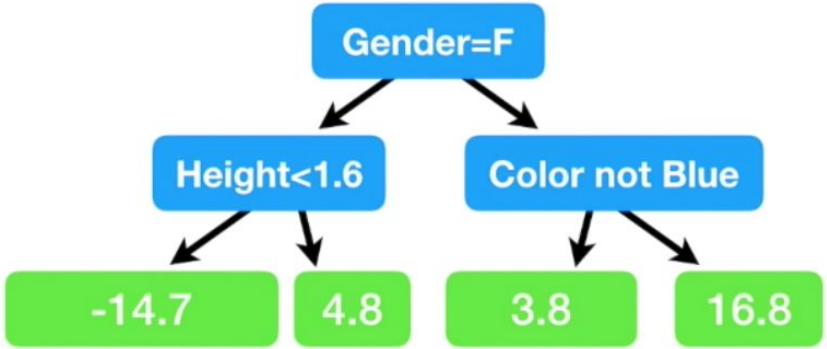
So we replace these residuals with their average.

$$\frac{(-14.2 + -15.2)}{2} = -14.7$$

Average Weight

71.2

+



Height (m)	Favorite Color	Gender	Weight (kg)
1.6	Blue	Male	88

…to make a new **Prediction** of an individual's **Weight** from the **Training Data**.

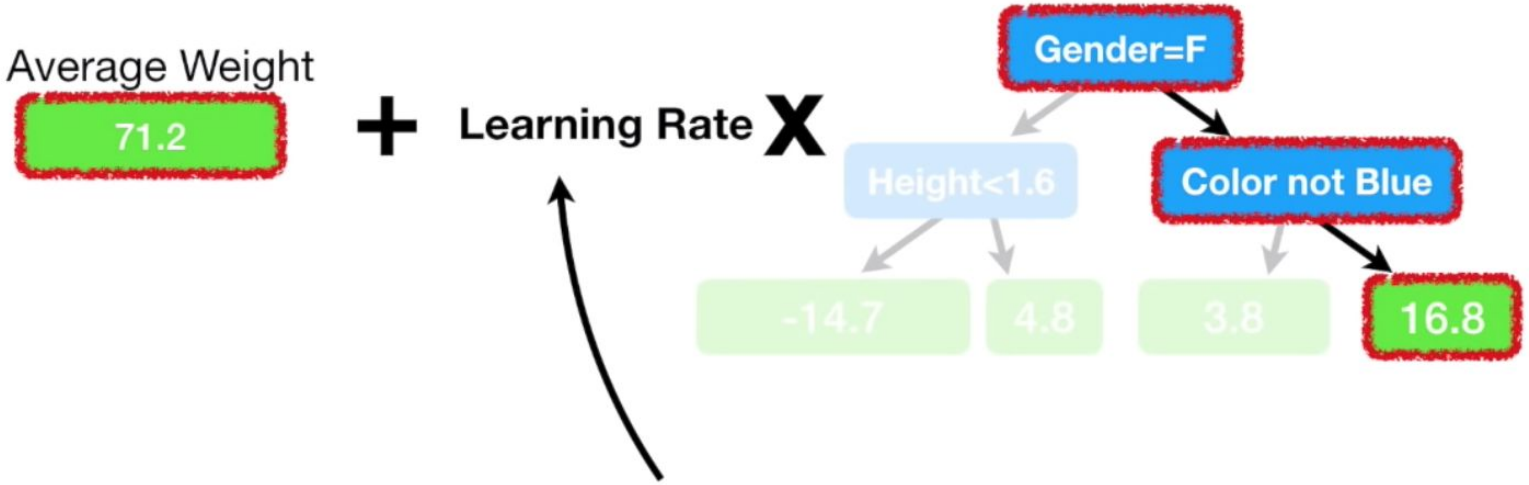
Predicted Weight = 71.2 + 16.8 = 88

Height (m)	Favorite Color	Gender	Weight (kg)
1.6	Blue	Male	88

Is this awesome???

No. The model fits the **Training Data** too well.

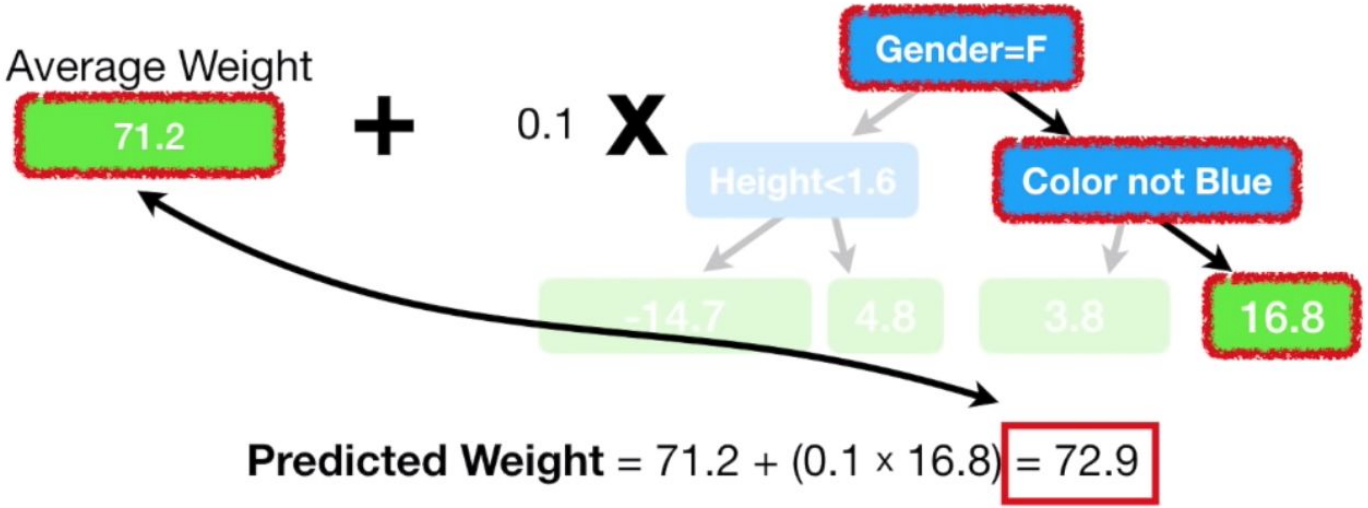
In other words, we have low **Bias**, but probably very high **Variance**.



Height (m)	Favorite Color	Gender	Weight (kg)
1.6	Blue	Male	88

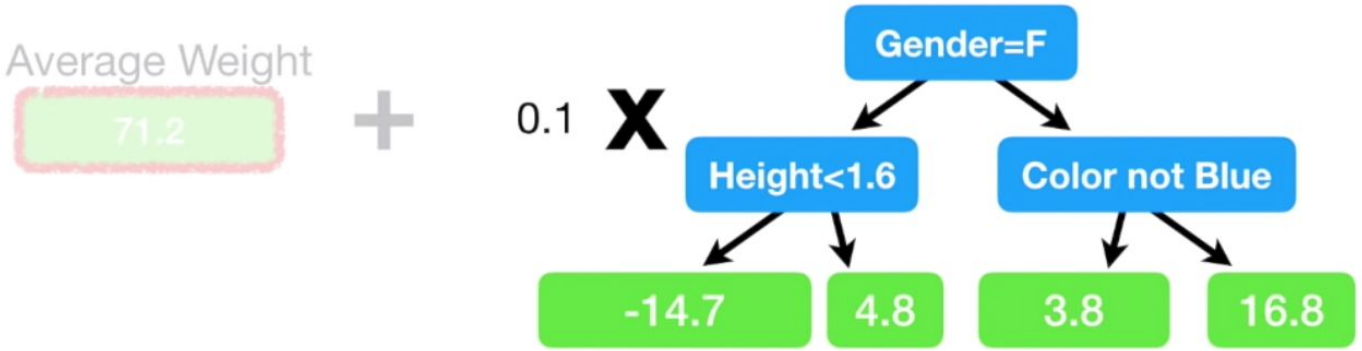
Gradient Boost deals with this problem by using a **Learning Rate** to scale the contribution from the new tree.

The **Learning Rate** is a value between **0** and **1**.

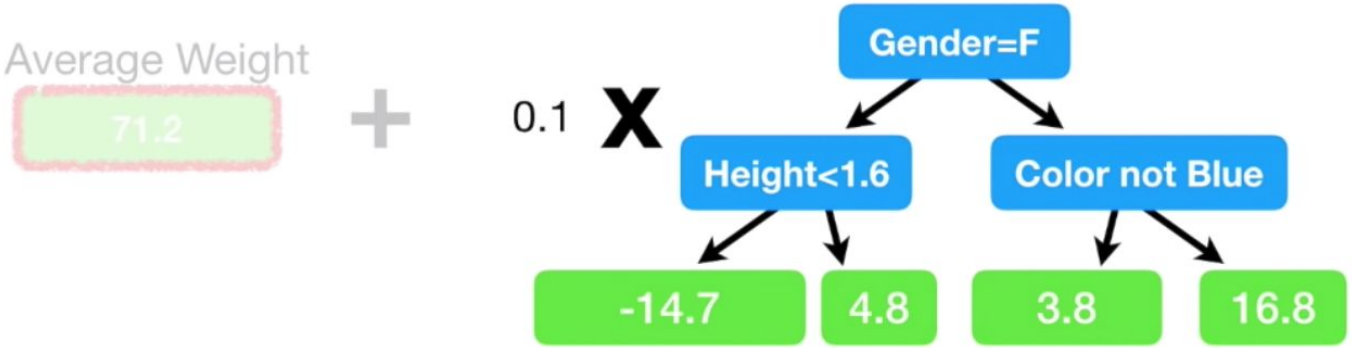


Height (m)	Favorite Color	Gender	Weight (kg)
1.6	Blue	Male	88

…but it's a little bit better than the **Prediction** made with just the original leaf, which predicted that all samples would weigh **71.2**.



According to the dude that invented **Gradient Boost**, Jerome Friedman, empirical evidence shows that taking lots of small steps in the right direction results in better **Predictions** with a **Testing Dataset**, i.e. lower **Variance**.



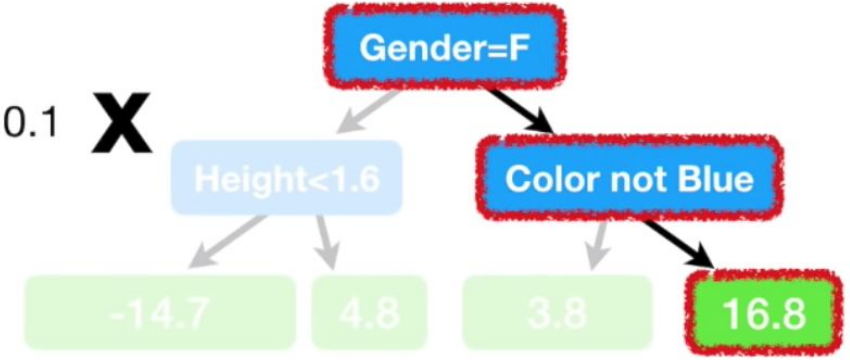
So let's build another tree so we can take another small step in the right direction.

Average Weight

71.2

+

0.1 X



Height (m)	Favorite Color	Gender	Weight (kg)	Residual
1.6	Blue	Male	88	
1.6	Green	Female	76	
1.5	Blue	Female	56	
1.8	Red	Male	73	
1.5	Green	Male	77	
1.4	Blue	Female	57	

Residual = (**88** - (71.2 + 0.1 × 16.8))

= 15.1

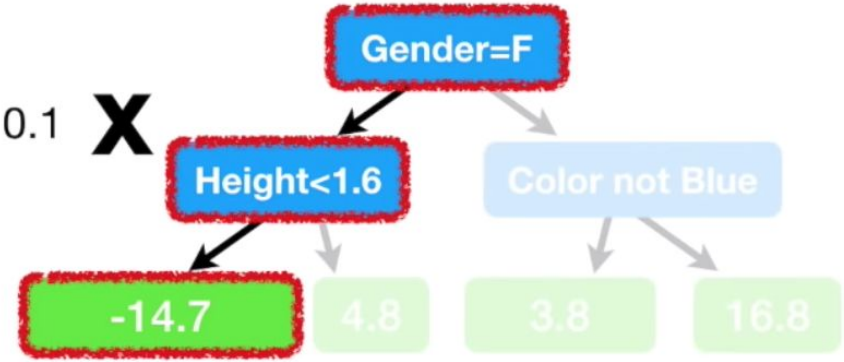
…and we save that in the column for **Pseudo Residuals**.

Average Weight

71.2

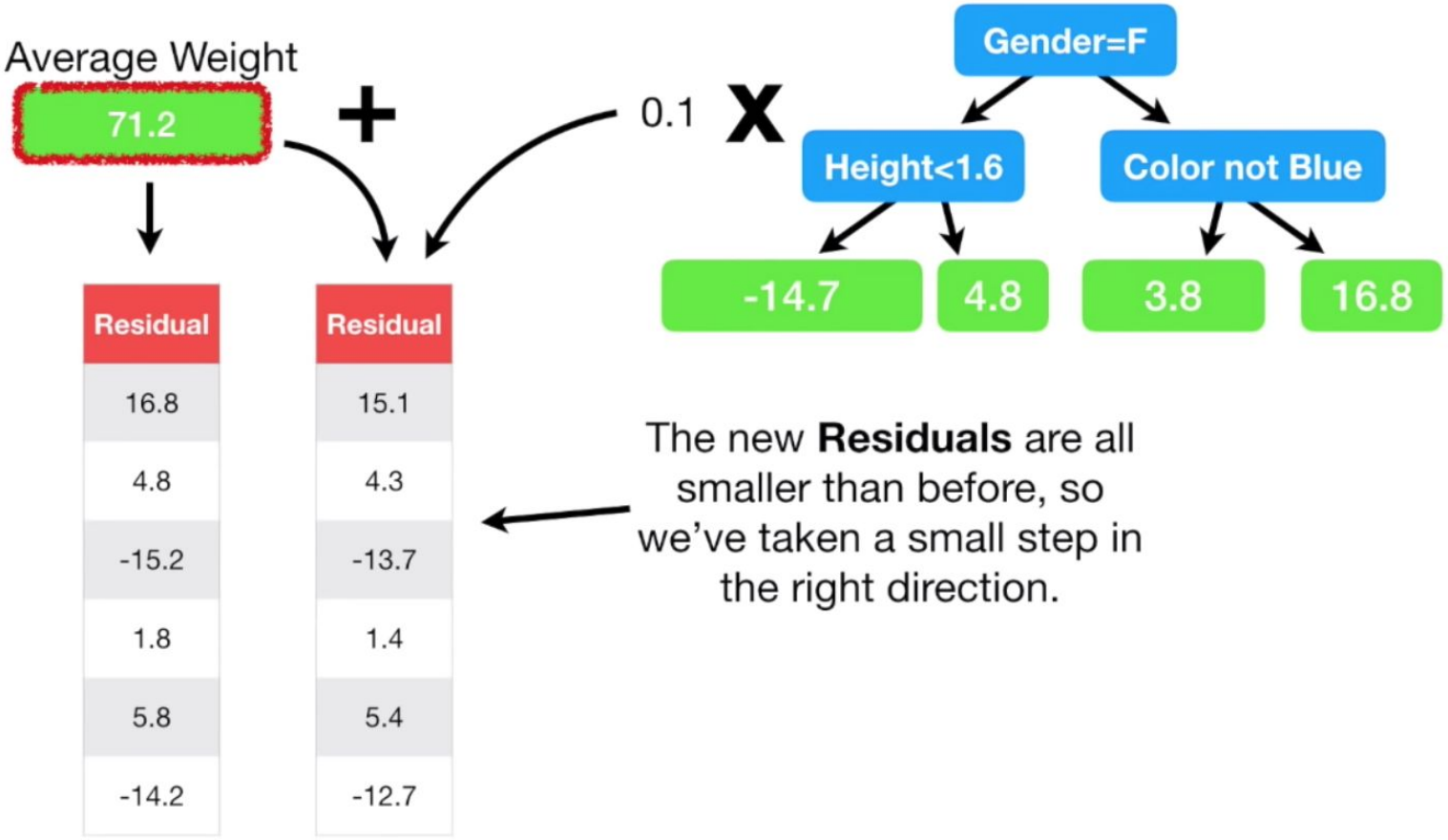
+

0.1 X

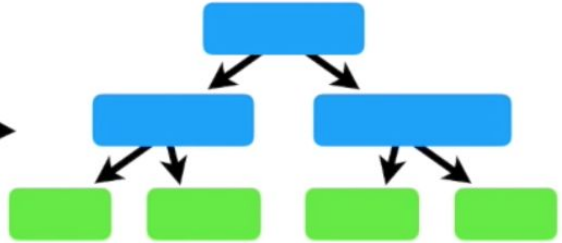


Height (m)	Favorite Color	Gender	Weight (kg)	Residual
1.6	Blue	Male	88	15.1
1.6	Green	Female	76	4.3
1.5	Blue	Female	56	-13.7
1.8	Red	Male	73	1.4
1.5	Green	Male	77	5.4
1.4	Blue	Female	57	-12.7

Residual = (Observed - Predicted)

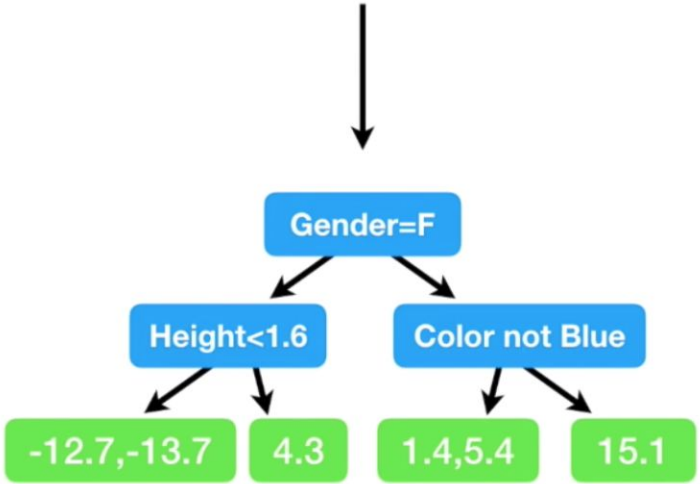

Average Weight
71.2
+
0.1
X
Gender=F
Height<1.6
Color not Blue
-14.7
4.8
3.8
16.8
Residual
16.8
4.8
-15.2
1.8
5.8
-14.2
Residual
15.1
4.3
-13.7
1.4
5.4
-12.7
The new **Residuals** are all smaller than before, so we've taken a small step in the right direction.

Now let's build a new tree to predict the new **Residuals**.



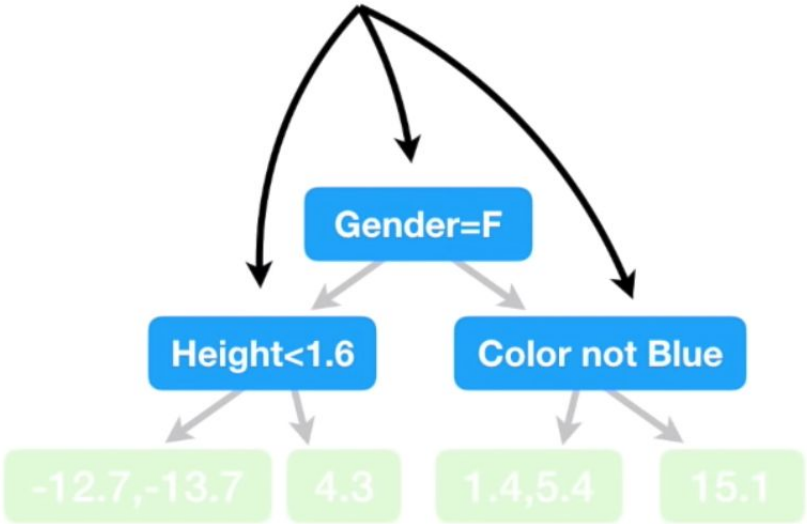
Height (m)	Favorite Color	Gender	Weight (kg)	Residual
1.6	Blue	Male	88	15.1
1.6	Green	Female	76	4.3
1.5	Blue	Female	56	-13.7
1.8	Red	Male	73	1.4
1.5	Green	Male	77	5.4
1.4	Blue	Female	57	-12.7

And here's the new tree!

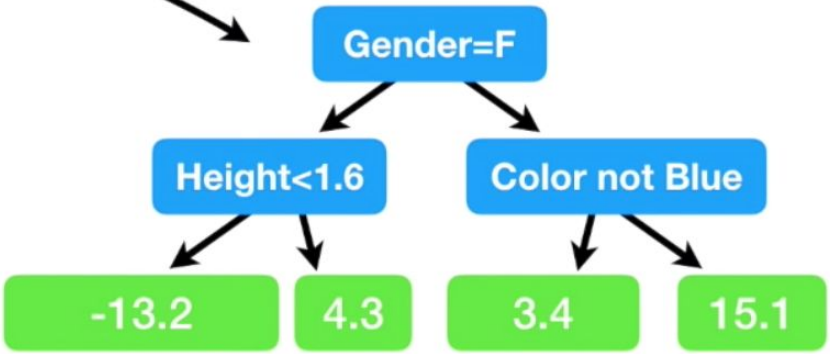


Height (m)	Favorite Color	Gender	Weight (kg)	Residual
1.6	Blue	Male	88	15.1
1.6	Green	Female	76	4.3
1.5	Blue	Female	56	-13.7
1.8	Red	Male	73	1.4
1.5	Green	Male	77	5.4
1.4	Blue	Female	57	-12.7

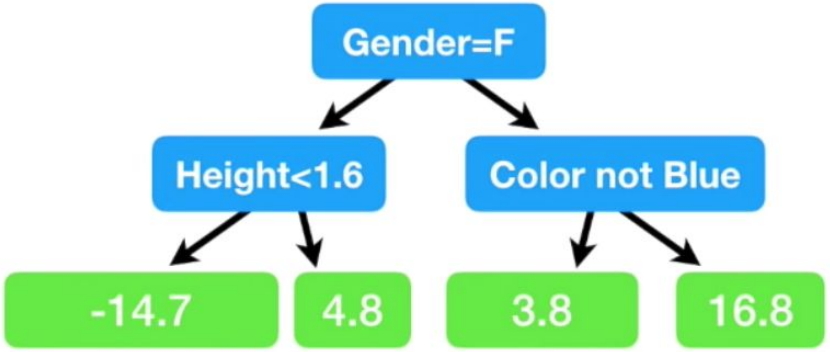
NOTE: In this simple example the branches are the same as before. However, in practice, the trees can be different each time.



Now we combine the new **Tree**



Now we combine the new **Tree** with the previous **Tree**



Average Weight

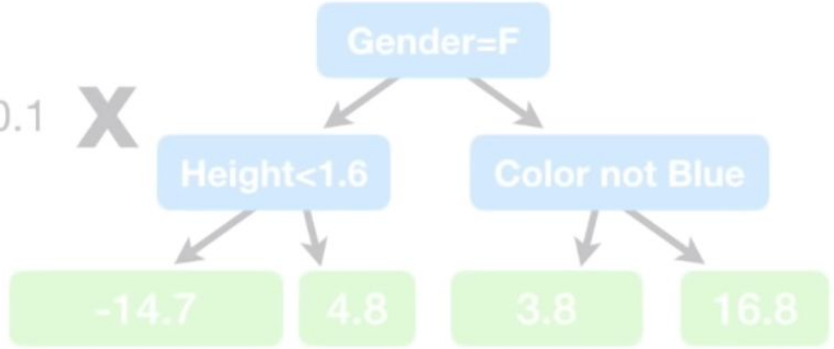
71.2

Now we combine the new **Tree** with the previous **Tree** and the initial **Leaf.**

Average Weight

71.2

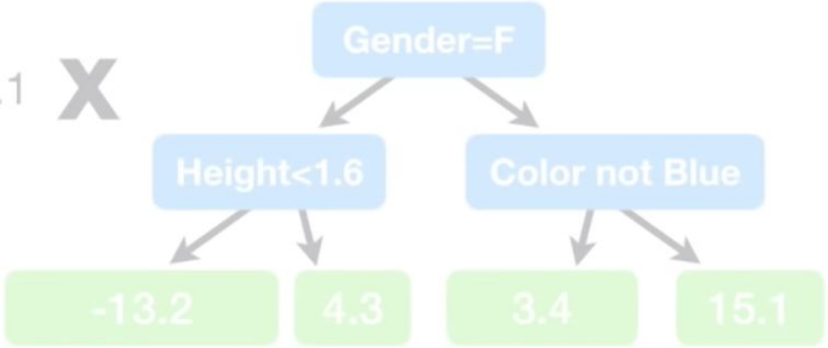
+ 0.1 X



Now we're ready to make a new **Prediction** from the **Training Data**.

Height (m)	Favorite Color	Gender	Weight (kg)
1.6	Blue	Male	88

+ 0.1 X

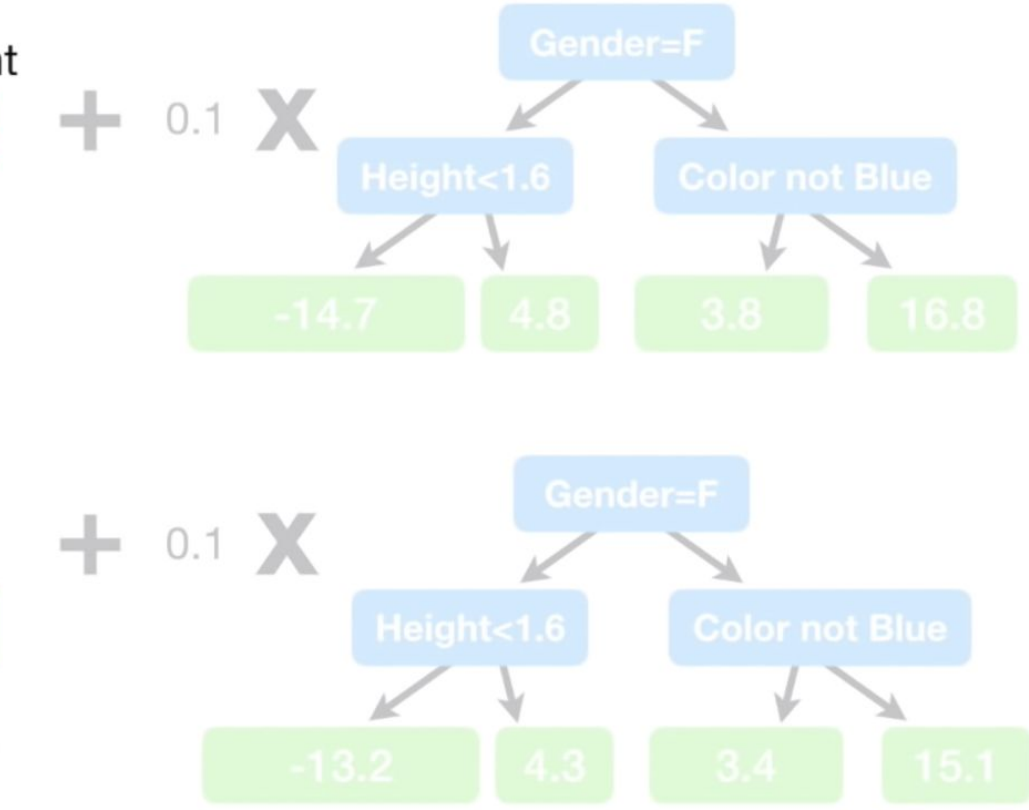


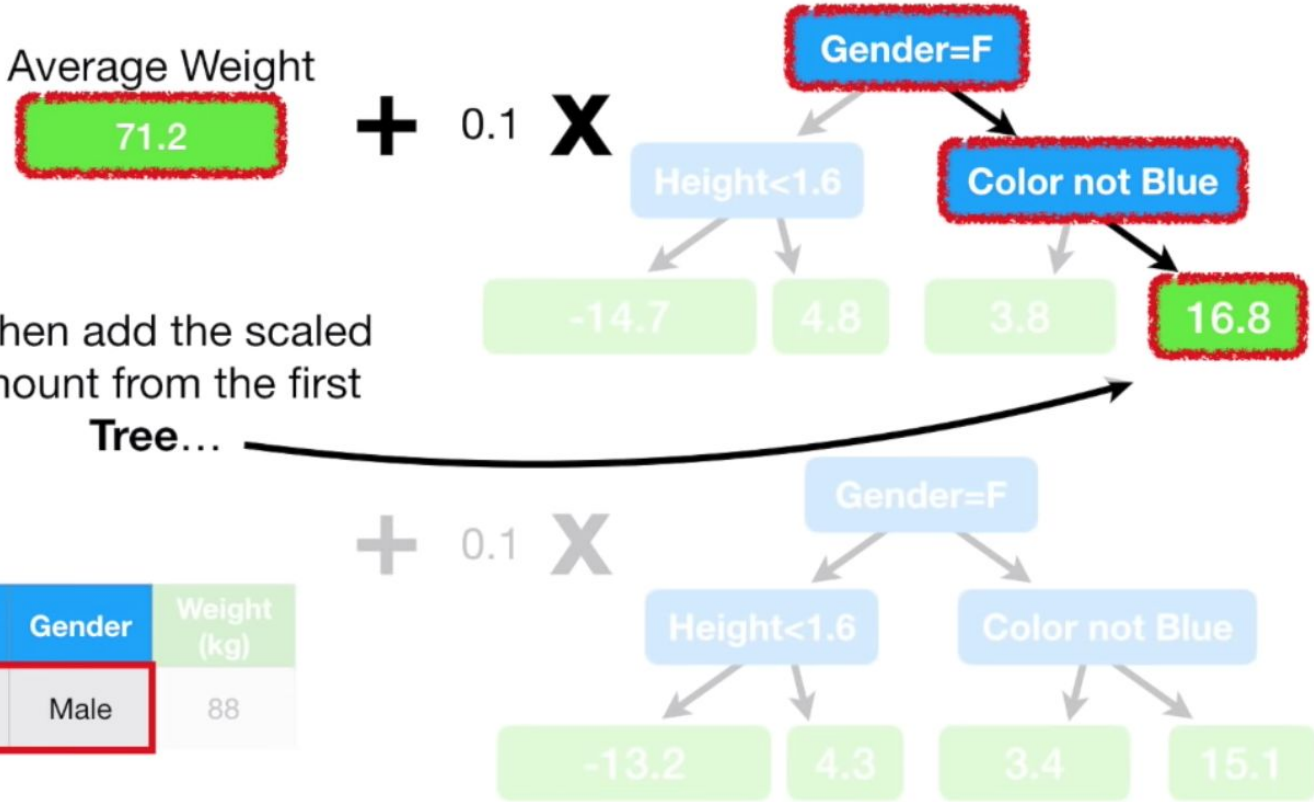
Average Weight

71.2

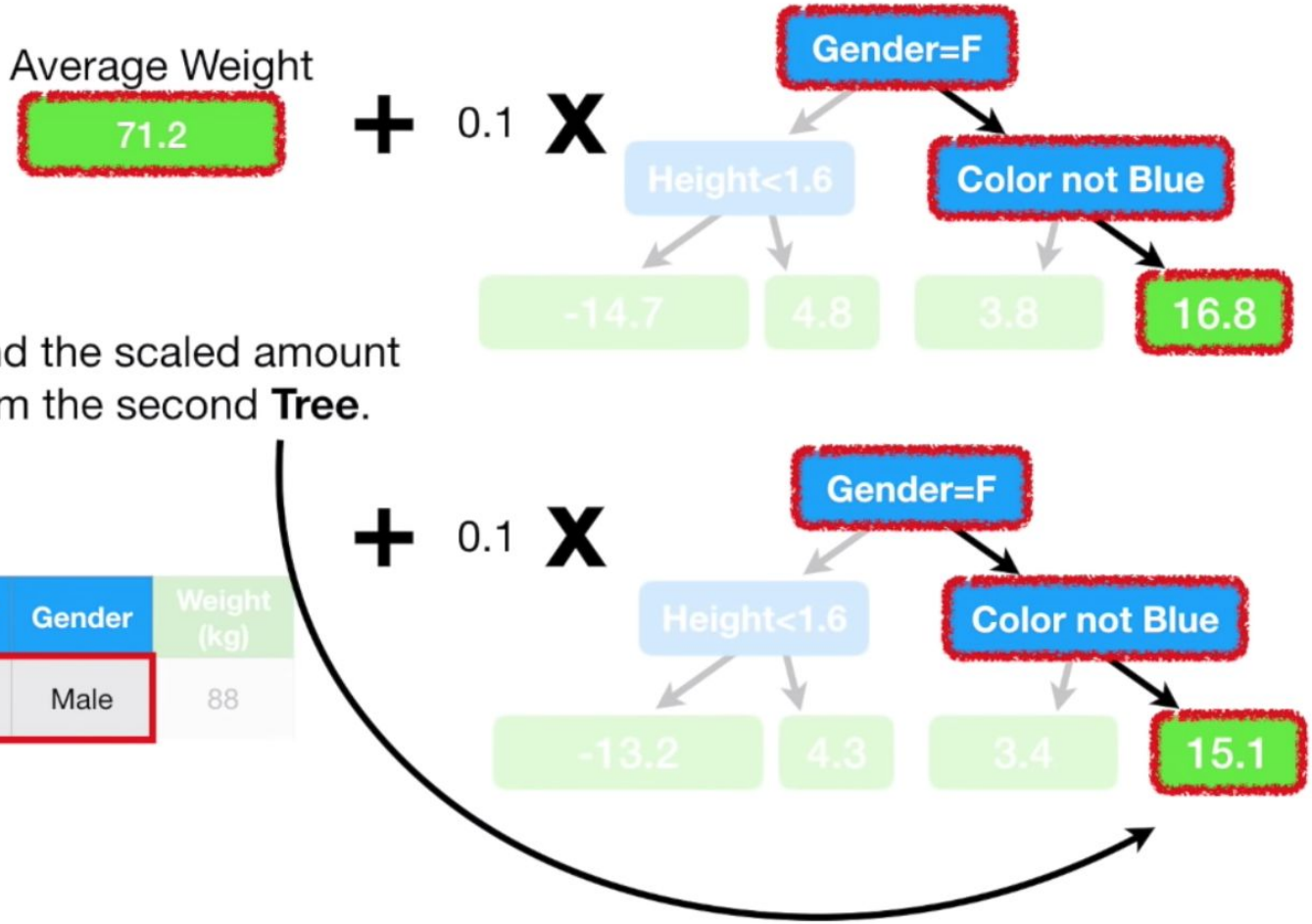
Just like before, we start with the initial **Prediction**…

Height (m)	Favorite Color	Gender	Weight (kg)
1.6	Blue	Male	88





Height (m)	Favorite Color	Gender	Weight (kg)
1.6	Blue	Male	88



Height (m)	Favorite Color	Gender	Weight (kg)
1.6	Blue	Male	88

Average Weight

71.2

+ 0.1 X

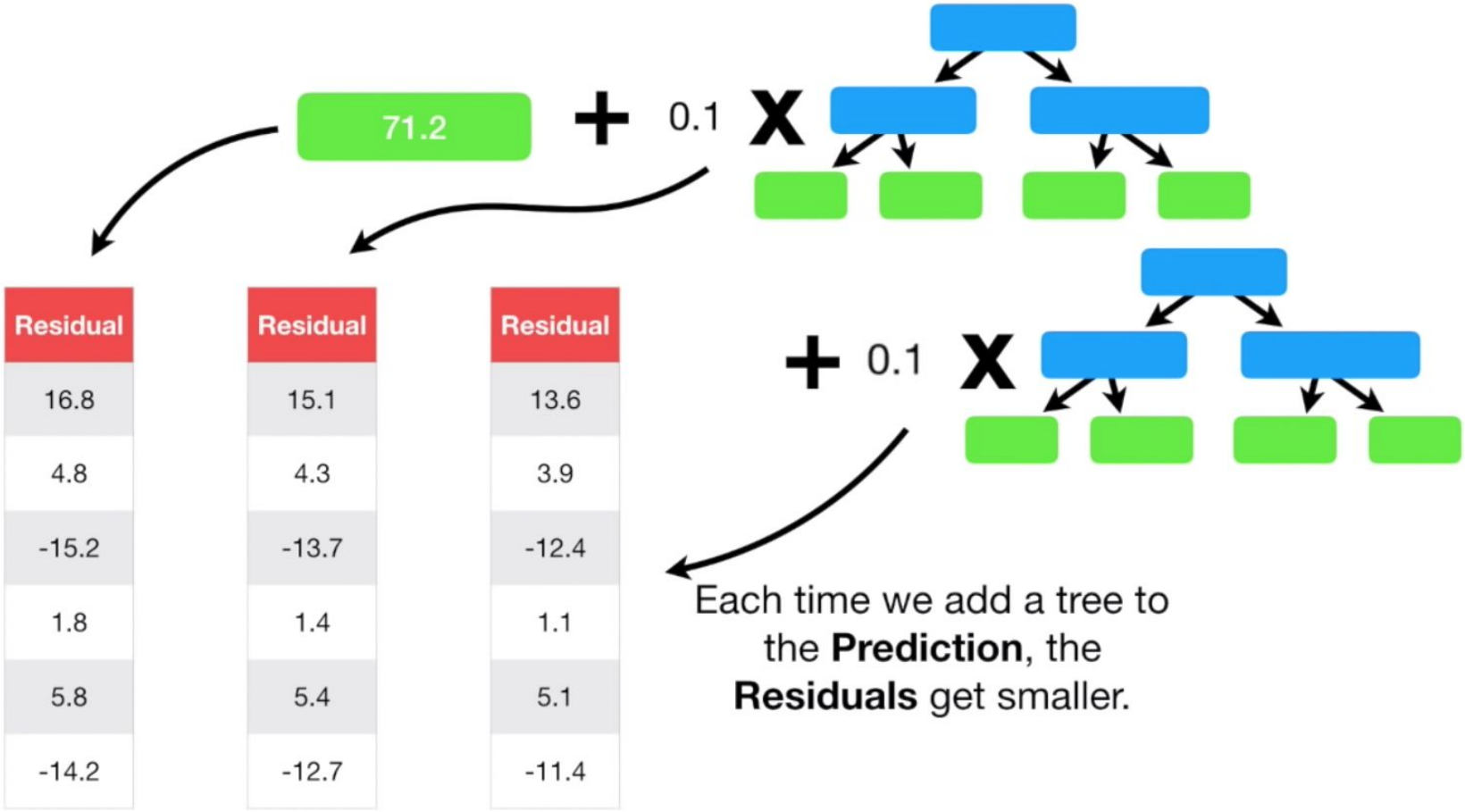
Which is another small step closer to the **Observed Weight**.

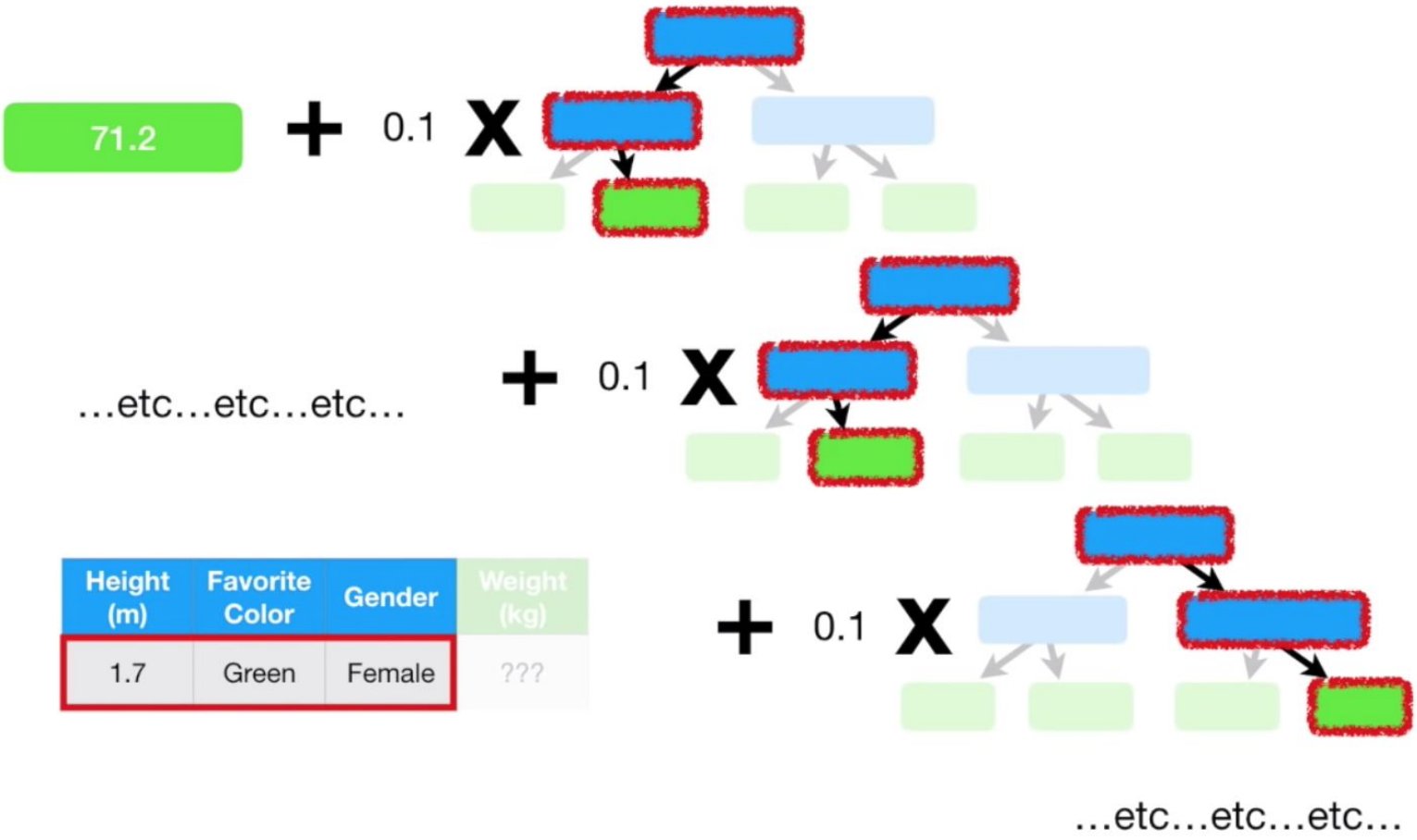
$$71.2 + (0.1 \times 16.8) + (0.1 \times 15.1)$$

$$= 74.4$$

+ 0.1 X

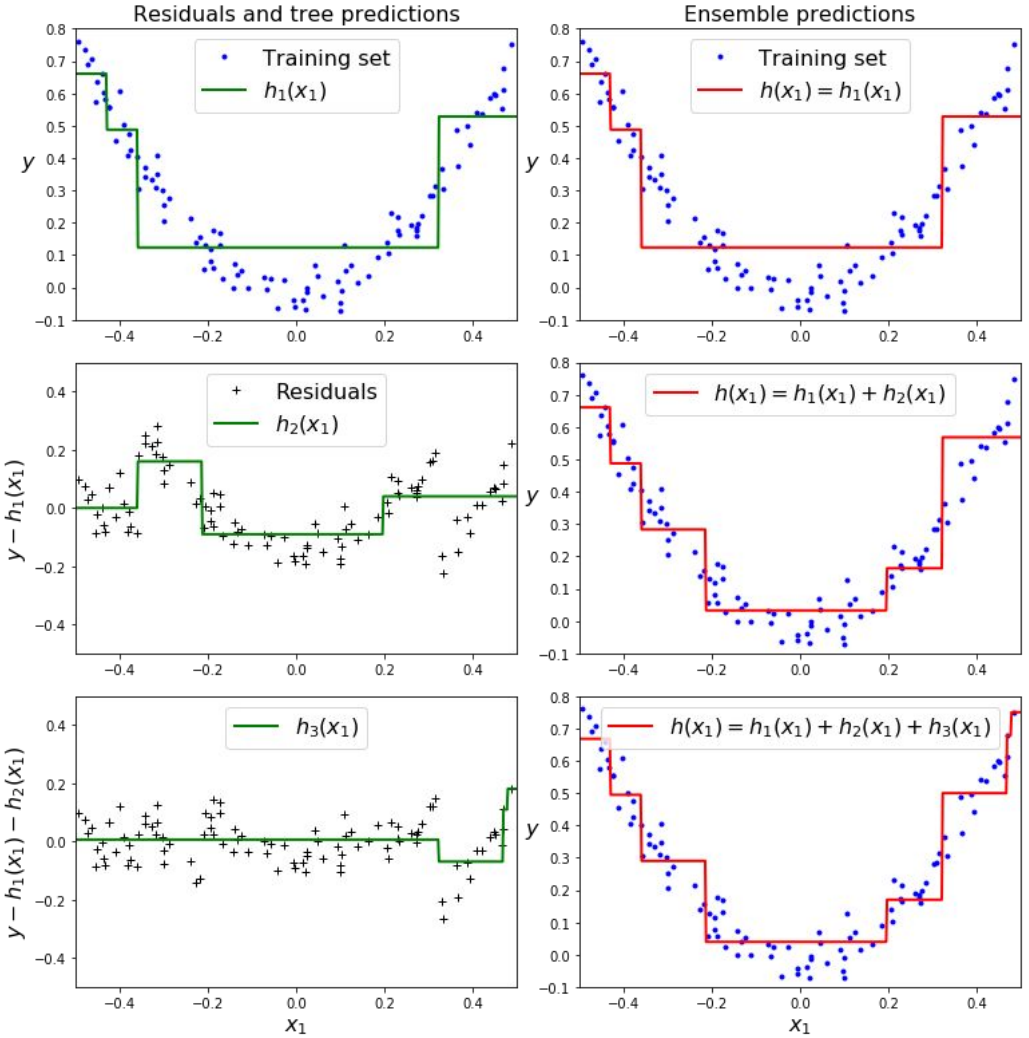
Height (m)	Favorite Color	Gender	Weight (kg)
1.6	Blue	Male	88


71.2
+ 0.1 X
+ 0.1 X
Residual
16.8
4.8
-15.2
1.8
5.8
-14.2
Residual
15.1
4.3
-13.7
1.4
5.4
-12.7
Residual
13.6
3.9
-12.4
1.1
5.1
-11.4
Each time we add a tree to the **Prediction**, the **Residuals** get smaller.

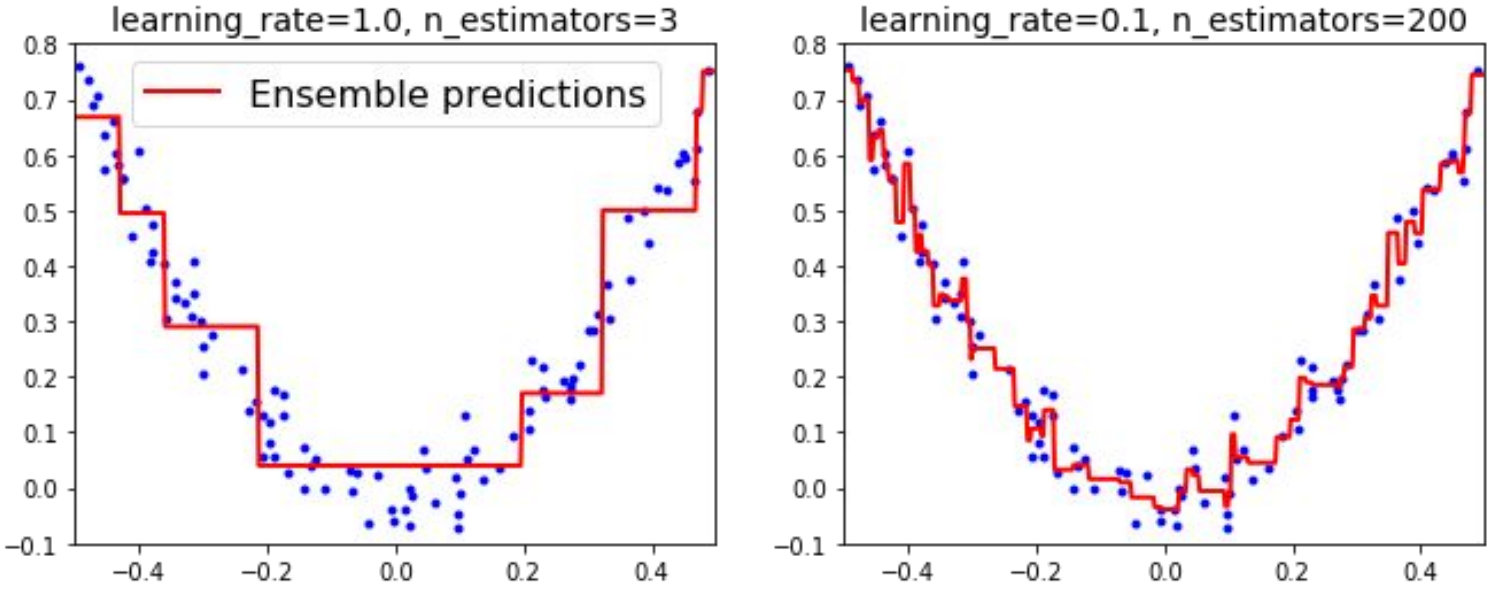


Height (m)	Favorite Color	Gender	Weight (kg)
1.7	Green	Female	???

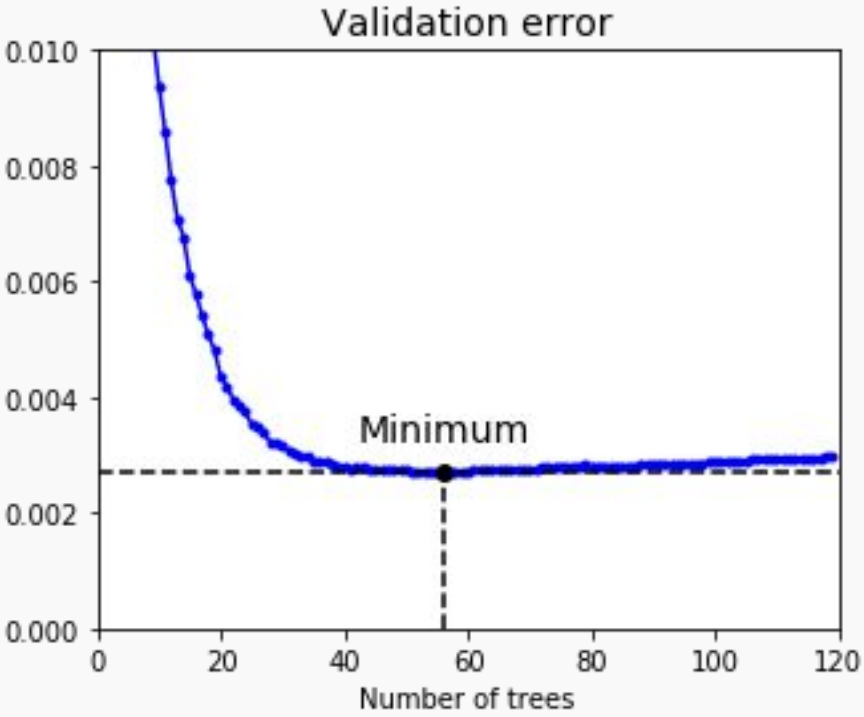
```
np.random.seed(42)
X = np.random.rand(100, 1) - 0.5
y = 3*X[:, 0]**2 + 0.05 * np.random.randn(100)

# create a simple DecisionTreeRegressor
tree_reg1 = DecisionTreeRegressor(max_depth=2, random_state=42)
tree_reg1.fit(X, y)


# now train a second DecisionTreeRegressor
# on the residual errors made by the first predictor
y2 = y - tree_reg1.predict(X)
tree_reg2 = DecisionTreeRegressor(max_depth=2, random_state=42)
tree_reg2.fit(X, y2)

# then we train a third regressor on the residual errors
# made by the second predictor
y3 = y2 - tree_reg2.predict(X)
tree_reg3 = DecisionTreeRegressor(max_depth=2, random_state=42)
tree_reg3.fit(X, y3)
```

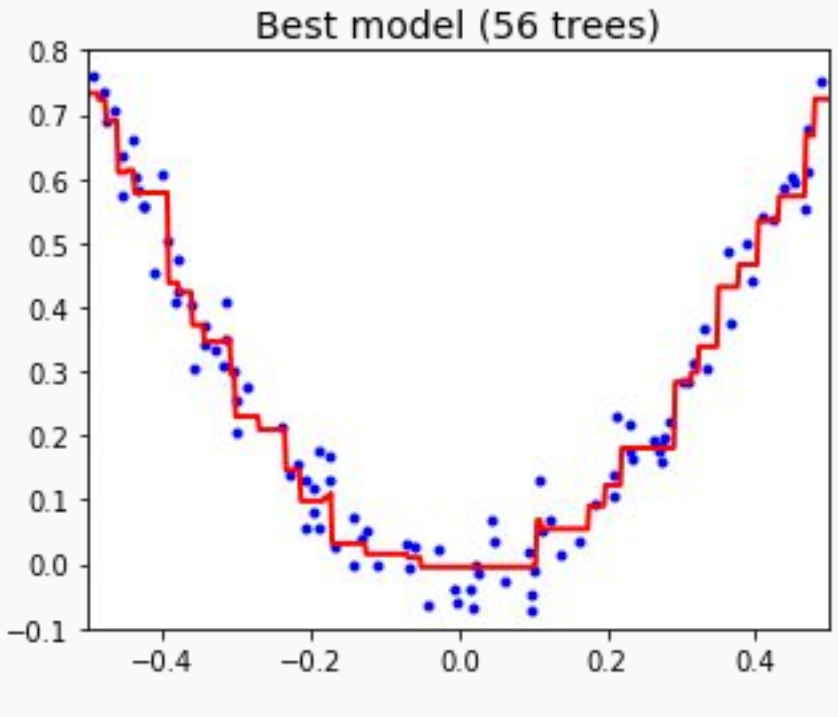

Residuals and tree predictions
Ensemble predictions
Training set
$h_1(x_1)$
$h(x_1) = h_1(x_1)$
Residuals
$h_2(x_1)$
$h(x_1) = h_1(x_1) + h_2(x_1)$
$h_3(x_1)$
$h(x_1) = h_1(x_1) + h_2(x_1) + h_3(x_1)$
y
$y - h_1(x_1)$
$y - h_1(x_1) - h_2(x_1)$
x_1

```
gbrt = GradientBoostingRegressor(max_depth=2,
                                 n_estimators=3,
                                 learning_rate=1.0,
                                 random_state=42)
```



Early Stopping





Improvements to Basic Gradient Boosting (best practices)

1. Tree Constraints
   a. the advice is to keep adding trees until no further improvement is observed.
   b. tree depth, deeper trees are more complex trees and shorter trees are preferred.
   c. generally, better results are seen with 4-8 levels.
2. Shrinkage
   a. decreasing the value of the learning rate increases the best value for the number of trees.
   b. it is common to have small values for learning rate in the range of 0.1 to 0.3, as well as values less than 0.1.
3. Random Sampling (Stochastic Gradient Boosting)
   a. at each iteration a subsample of the training data is drawn at random
   b. generally, aggressive sub-sampling such as selecting only 50% of the data has shown to be beneficial.
4. Penalized Gradient Boosting (L1, L2)

dmlc

XGBoost

https://xgboost.ai

XGBoost: A Scalable Tree Boosting System

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ABSTRACT

Tree boosting is a highly effective and widely used machine learning method. In this paper, we describe a scalable end-to-end tree boosting system called XGBoost, which is used widely by data scientists to achieve state-of-the-art results on many machine learning challenges. We propose a novel sparsity-aware algorithm for sparse data and weighted quantile sketch for approximate tree learning. More importantly, we provide insights on cache access patterns, data compression and sharding to build a scalable tree boosting system. By combining these insights, XGBoost scales beyond billions of examples using far fewer resources than existing systems.

Keywords

Large-scale Machine Learning

1. INTRODUCTION

Machine learning and data-driven approaches are becoming very important in many areas. Smart spam classifiers protect our email by learning from massive amounts of spam data and user feedback; advertising systems learn to match the right ads with the right context; fraud detection systems protect banks from malicious attackers; anomaly event detection systems help experimental physicists to find events that lead to new physics. There are two important factors that drive these successful applications: usage of effective

problems. Besides being used as a stand-alone predictor, it is also incorporated into real-world production pipelines for ad click through rate prediction [15]. Finally, it is the de-facto choice of ensemble method and is used in challenges such as the Netflix prize [3].

In this paper, we describe XGBoost, a scalable machine learning system for tree boosting. The system is available as an open source package[2]. The impact of the system has been widely recognized in a number of machine learning and data mining challenges. Take the challenges hosted by the machine learning competition site Kaggle for example. Among the 29 challenge winning solutions [3] published at Kaggle's blog during 2015, 17 solutions used XGBoost. Among these solutions, eight solely used XGBoost to train the model, while most others combined XGBoost with neural nets in ensembles. For comparison, the second most popular method, deep neural nets, was used in 11 solutions. The success of the system was also witnessed in KDDCup 2015, where XGBoost was used by every winning team in the top-10. Moreover, the winning teams reported that ensemble methods outperform a well-configured XGBoost by only a small amount [1].

These results demonstrate that our system gives state-of-the-art results on a wide range of problems. Examples of the problems in these winning solutions include: store sales prediction; high energy physics event classification; web text classification; customer behavior prediction; motion detection; ad click through rate prediction; malware classification;

Why use XGBoost?

- Execution Speed
- Model Performance
- Good Documentation


XGBoost
Gradient Boosting > Random Forest > Bagging > Single Trees

szilard / benchm-ml

A minimal benchmark for scalability, speed and accuracy of commonly used open source implementations (R packages, Python scikit-learn, H2O, xgboost, Spark MLlib etc.) of the top machine learning algorithms for binary classification (random forests, gradient boosted trees, deep neural networks etc.).

machine-learning data-science r python gradient-boosting-machine random-forest deep-learning xgboost h2o spark

522 commits 1 branch 0 releases 9 contributors MIT

Branch: master New pull request Create new file Upload files Find File Clone or download

szilard fix typo — Latest commit 941dfd4 on Aug 19

0-init	Removes .Rhistory from archive.	3 years ago
1-linear	spark 2.0	3 years ago
2-rf	fix h2o v3 new importFile API	3 years ago
3-boosting	lightGBM	3 years ago
4-DL	theano	3 years ago
x1-data-higgs	DL	3 years ago
z-other-tools	doc	2 years ago
.gitignore	spark logistic accuracy	4 years ago
LICENSE.txt	Update LICENSE.txt	5 months ago
README.md	fix typo	last month

szilard / GBM-perf

Performance of various open source GBM implementations

machine-learning gradient-boosting-machine gbm h2oai xgboost lightgbm benchmark

287 commits 1 branch 0 releases 2 contributors MIT

Branch: master New pull request Create new file Upload files Find File Clone or download

szilard spark xgb — Latest commit 6e5f8e1 on May 24

analysis	spark	4 months ago
cpu	add catboost	5 months ago
gpu	GPU lightgbm crash	5 months ago
v1-keep-old-before_docker	archive v1 before docker	2 years ago
wip-testing	spark xgb	4 months ago
.gitignore	lightgbm GPU	2 years ago
GBM-perf.Rproj	Rstudio	2 years ago
LICENSE	add licence (MIT)	5 months ago
README.md	reorg	4 months ago
comparison_table.png	nicer	5 months ago
poll.png	poll final	5 months ago
results.txt	cleanup results file	5 months ago

Machine Learning Challenge Winning Solutions

XGBoost is extensively used by machine learning practitioners to create state of art data science solutions, this is a list of machine learning winning solutions with XGBoost. Please send pull requests if you find ones that are missing here.

- Maksims Volkovs, Guangwei Yu and Tomi Poutanen, 1st place of the 2017 ACM RecSys challenge. Link to paper.
- Vlad Sandulescu, Mihai Chiru, 1st place of the KDD Cup 2016 competition. Link to the arxiv paper.
- Marios Michailidis, Mathias Müller and HJ van Veen, 1st place of the Dato Truely Native? competition. Link to the Kaggle interview.
- Vlad Mironov, Alexander Guschin, 1st place of the CERN LHCb experiment Flavour of Physics competition. Link to the Kaggle interview.
- Josef Slavicek, 3rd place of the CERN LHCb experiment Flavour of Physics competition. Link to the Kaggle interview.
- Mario Filho, Josef Feigl, Lucas, Gilberto, 1st place of the Caterpillar Tube Pricing competition. Link to the Kaggle interview.
- Qingchen Wang, 1st place of the Liberty Mutual Property Inspection. Link to the Kaggle interview.
- Chenglong Chen, 1st place of the Crowdflower Search Results Relevance. Link to the winning solution.
- Alexandre Barachant (“Cat”) and Rafał Cycoń (“Dog”), 1st place of the Grasp-and-Lift EEG Detection. Link to the Kaggle interview.
- Halla Yang, 2nd place of the Recruit Coupon Purchase Prediction Challenge. Link to the Kaggle interview.
- Owen Zhang, 1st place of the Avito Context Ad Clicks competition. Link to the Kaggle interview.
- Keiichi Kuroyanagi, 2nd place of the Airbnb New User Bookings. Link to the Kaggle interview.
- Marios Michailidis, Mathias Müller and Ning Situ, 1st place Homesite Quote Conversion. Link to the Kaggle interview.

https://github.com/dmlc/xgboost/tree/master/demo

https://xgboost.readthedocs.io/en/latest/index.html

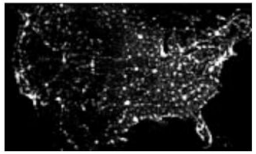
XGBoost Documentation

XGBoost is an optimized distributed gradient boosting library designed to be highly **efficient**, **flexible** and **portable**. It implements machine learning algorithms under the Gradient Boosting framework. XGBoost provides a parallel tree boosting (also known as GBDT, GBM) that solve many data science problems in a fast and accurate way. The same code runs on major distributed environment (Hadoop, SGE, MPI) and can solve problems beyond billions of examples.

Contents

Adult Data Set

Download: Data Folder, Data Set Description



Abstract: Predict whether income exceeds $50K/yr based on census data. Also known as "Census Income" dataset.

Data Set Characteristics:	Multivariate	**Number of Instances:**	48842	**Area:**	Social
Attribute Characteristics:	Categorical, Integer	**Number of Attributes:**	14	**Date Donated**	1996-05-01
Associated Tasks:	Classification	**Missing Values?**	Yes	**Number of Web Hits:**	1592237

Source:

Donor:

Ronny Kohavi and Barry Becker
Data Mining and Visualization
Silicon Graphics.
e-mail: ronnyk '@' live.com for questions.

Data Set Information:

Extraction was done by Barry Becker from the 1994 Census database. A set of reasonably clean records was extracted using the following conditions: ((AAGE>16) && (AGI>100) && (AFNLWGT>1)&& (HRSWK>0))

Prediction task is to determine whether a person makes over 50K a year.

Lesson #20 - XGBoost

```
0.8737908797789037
[[4659  286]
 [ 536 1032]]
              precision    recall  f1-score   support

           0       0.90      0.94      0.92      4945
           1       0.78      0.66      0.72      1568

    accuracy                           0.87      6513
   macro avg       0.84      0.80      0.82      6513
weighted avg       0.87      0.87      0.87      6513
```

Lesson #19 - RandomForest

```
0.8662674650698603
[[4728  217]
 [ 654  914]]
              precision    recall  f1-score   support

           0       0.88      0.96      0.92      4945
           1       0.81      0.58      0.68      1568

    accuracy                           0.87      6513
   macro avg       0.84      0.77      0.80      6513
weighted avg       0.86      0.87      0.86      6513
```

Lesson #17 - Decision Tree

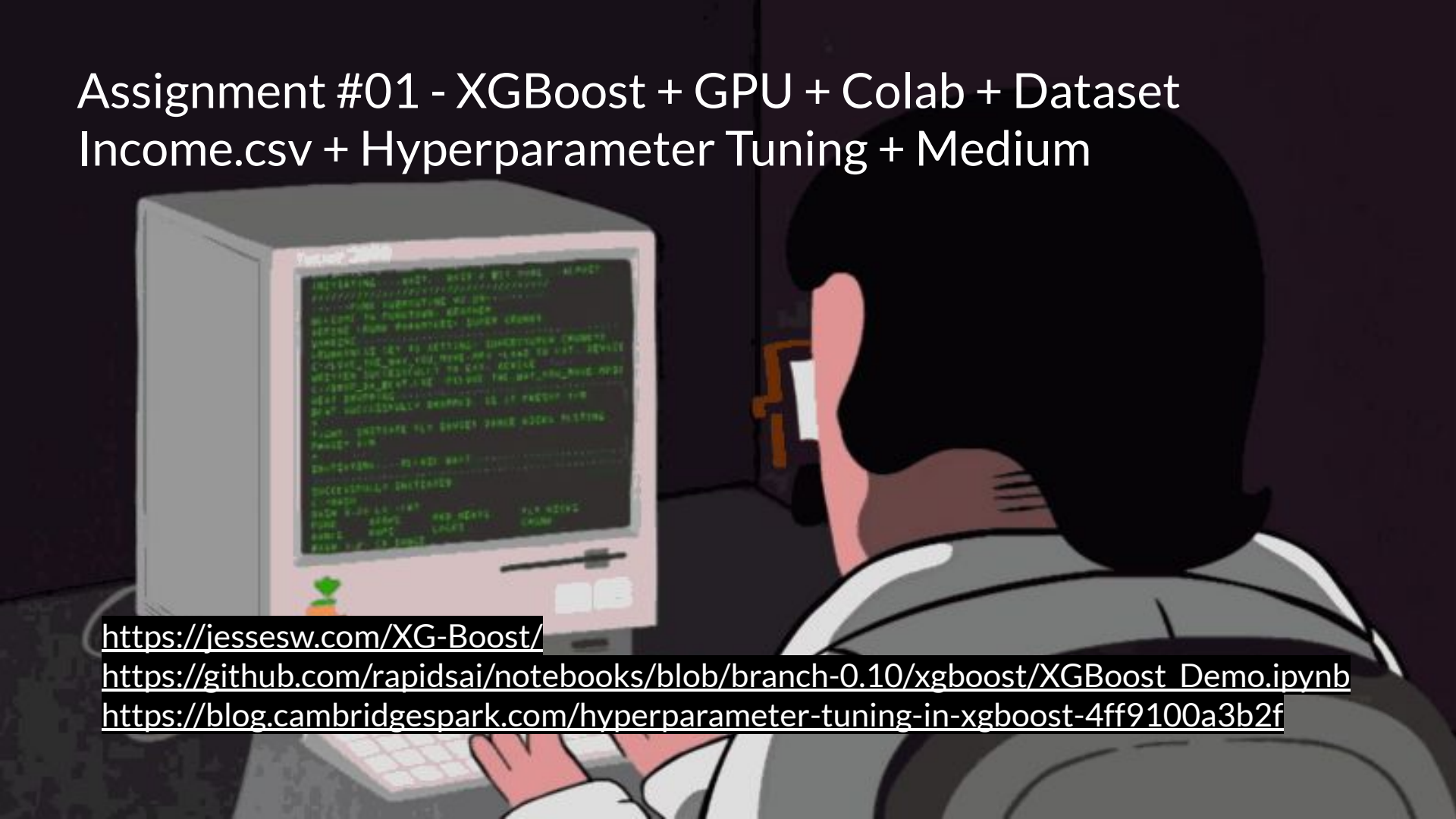
```
0.8191309688315677
[[4342  603]
 [ 575  993]]
              precision    recall  f1-score   support

           0       0.88      0.88      0.88      4945
           1       0.62      0.63      0.63      1568

    accuracy                           0.82      6513
   macro avg       0.75      0.76      0.75      6513
weighted avg       0.82      0.82      0.82      6513
```

Lesson #20 - Hyperparameter Tuning (Sklearn Wrapper)
Section 1.3.3

Assignment #01 - XGBoost + GPU + Colab + Dataset Income.csv + Hyperparameter Tuning + Medium



https://jessesw.com/XG-Boost/
https://github.com/rapidsai/notebooks/blob/branch-0.10/xgboost/XGBoost_Demo.ipynb
https://blog.cambridgespark.com/hyperparameter-tuning-in-xgboost-4ff9100a3b2f

Assignment #02