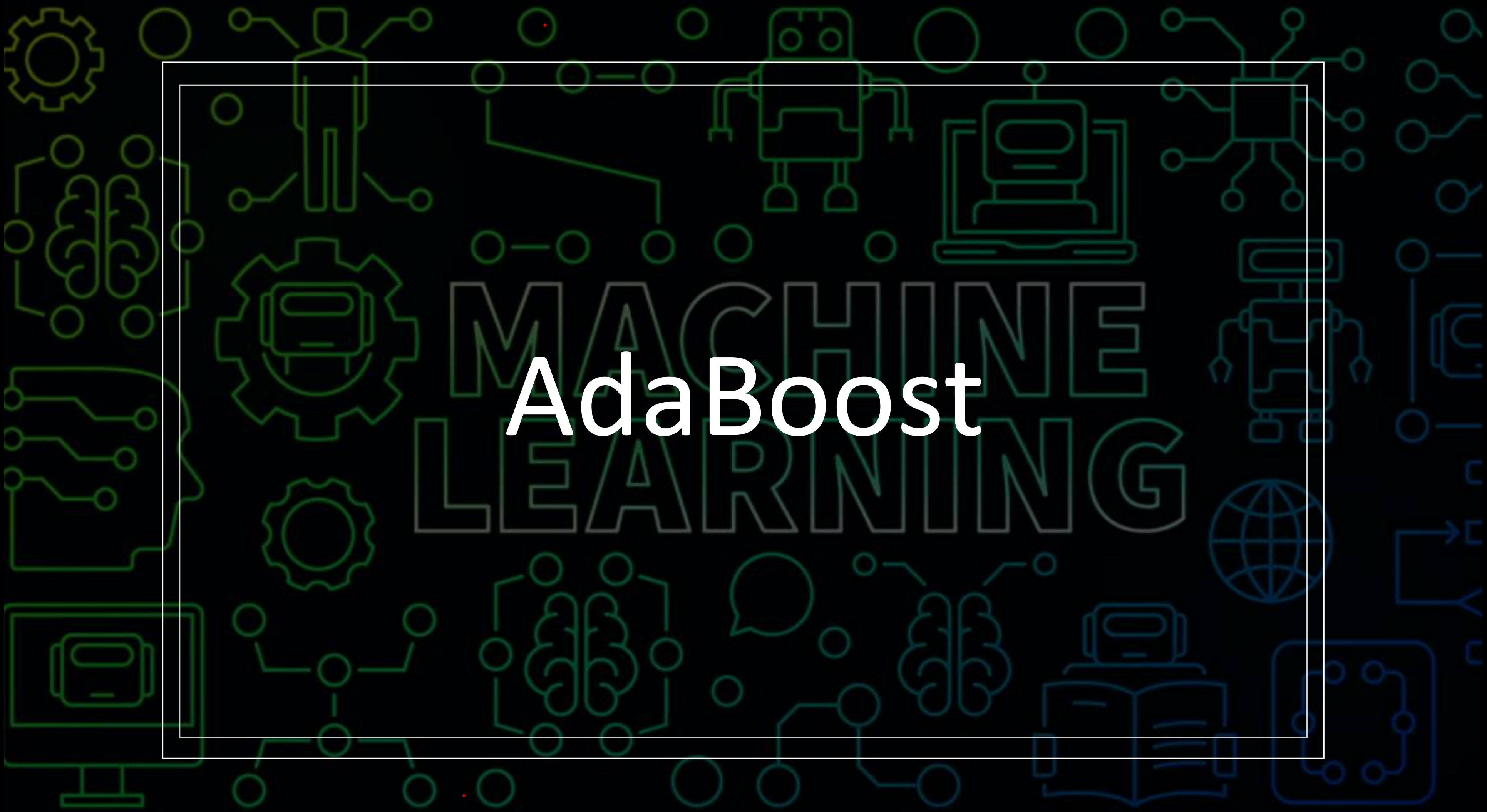
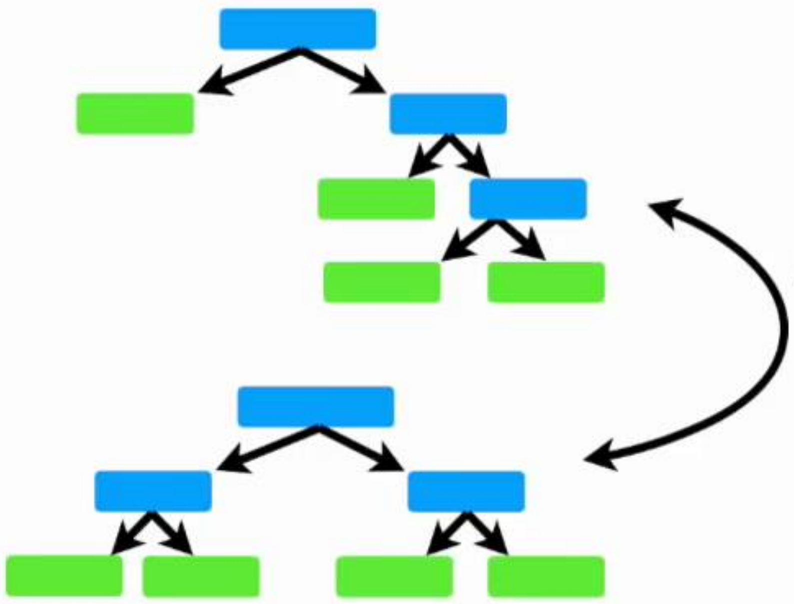
AdaBoost



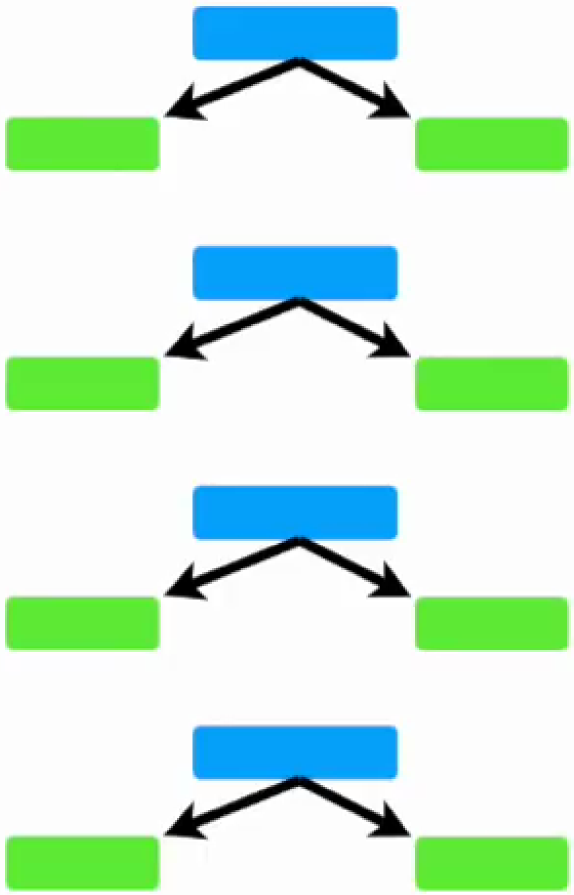
DISCLAIMER

In a **Random Forest**, each time you make a tree, you make a full sized tree.

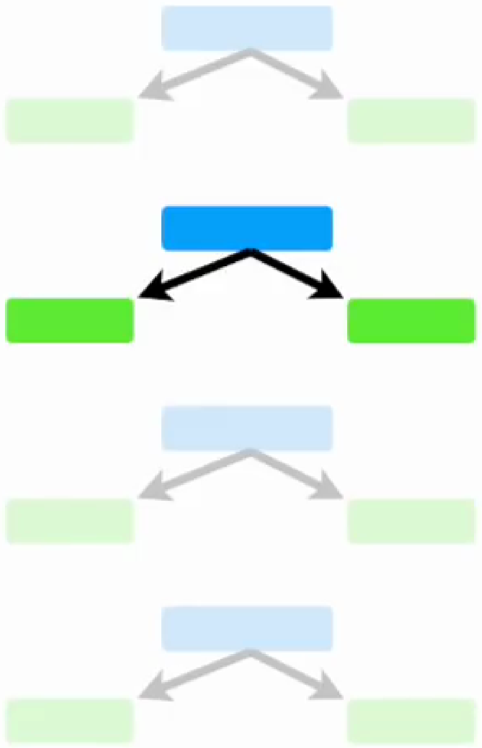


Some trees might be bigger than others, but there is no predetermined maximum depth.

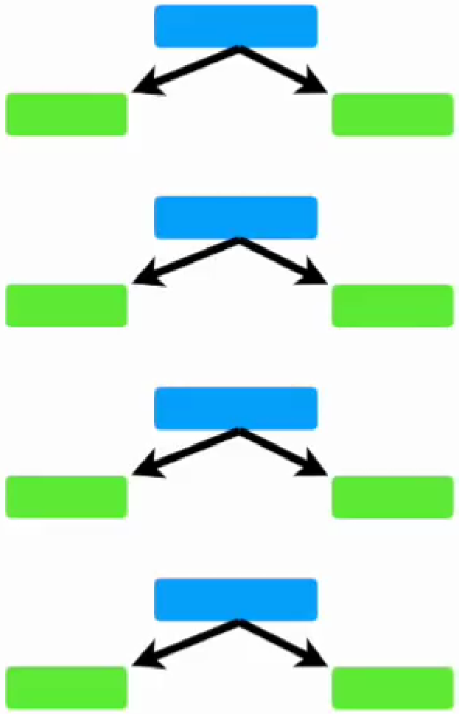
In contrast, in a **Forest of Trees** made with **AdaBoost**, the trees are usually just a **node** and two **leaves**.



A tree with just one node and two leaves is called a ***stump***.

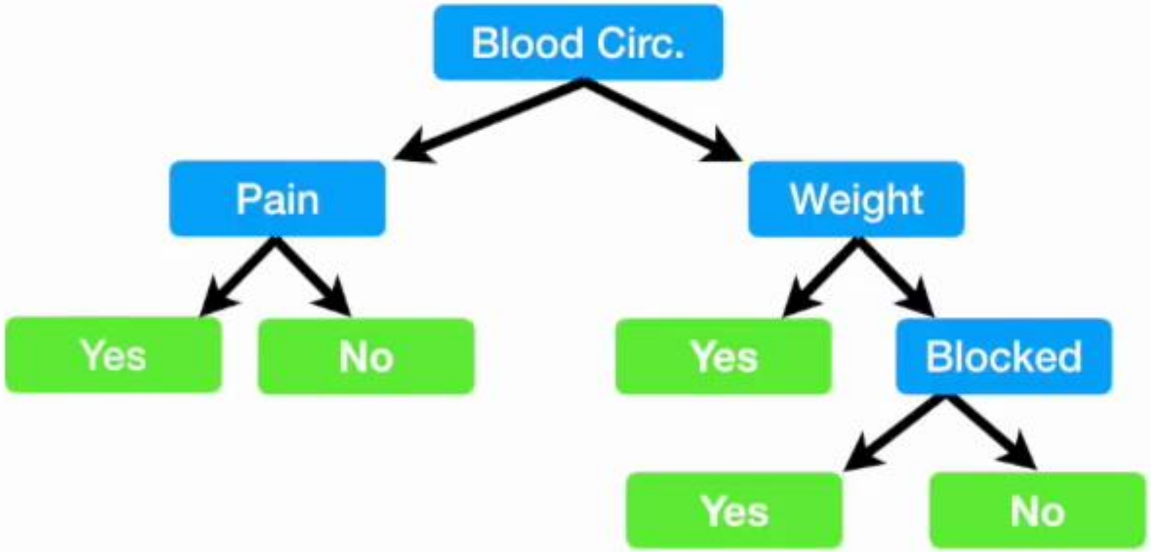


...so this is really a **Forest of Stumps** rather than trees.



...then a full sized **Decision Tree** would take advantage of all **4** variables that we measured (**Chest Pain**, **Blood Circulation**, **Blocked Arteries** and **Weight**) to make a decision...

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
No	No	No	125	No
Yes	Yes	Yes	180	Yes
Yes	Yes	No	210	No
Yes	No	Yes	167	Yes



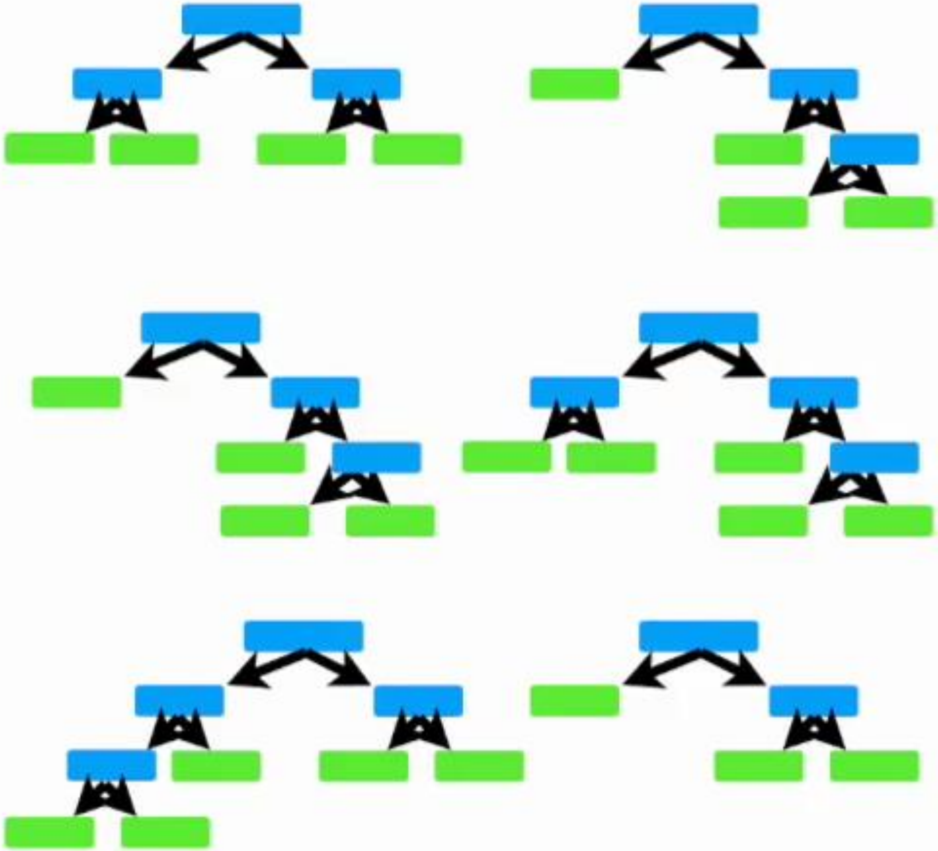
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
No	No	No	125	No
Yes	Yes	Yes	180	Yes
Yes	Yes	No	210	No
Yes	No	Yes	167	Yes

…but a **Stump** can only use one variable to make a decision.

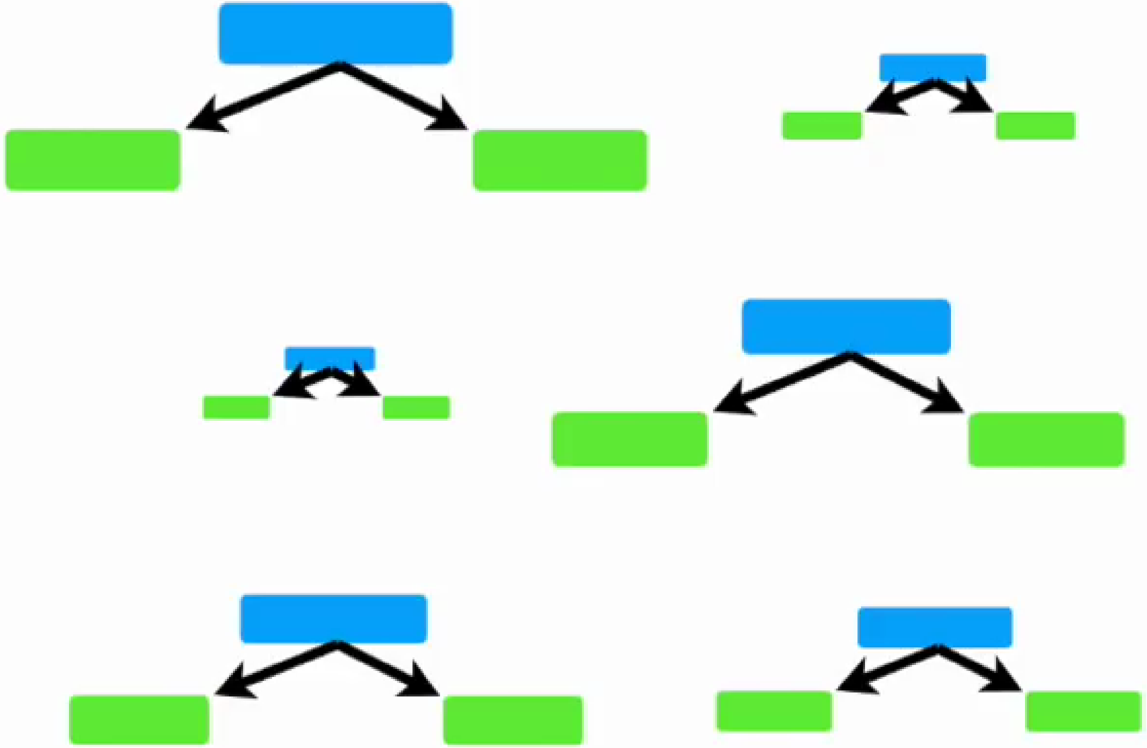
Thus, **Stumps** are technically "weak learners".

However, that's the way **AdaBoost** likes it, and it's one of the reasons why they are so commonly combined.

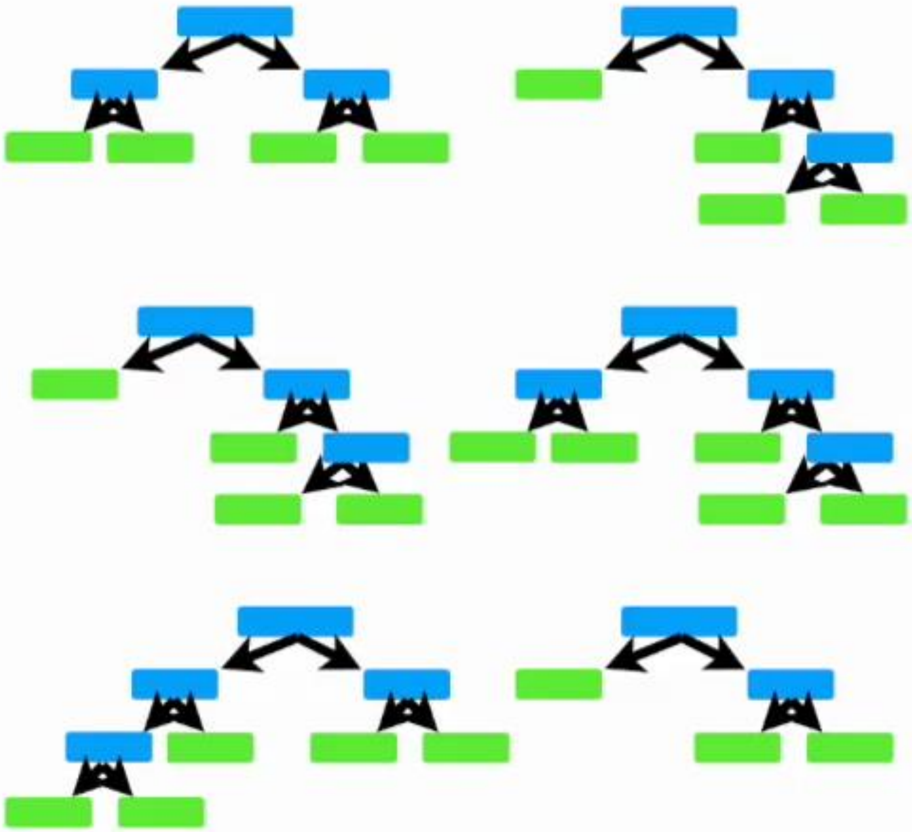
In a **Random Forest**, each tree has an equal vote on the final classification.



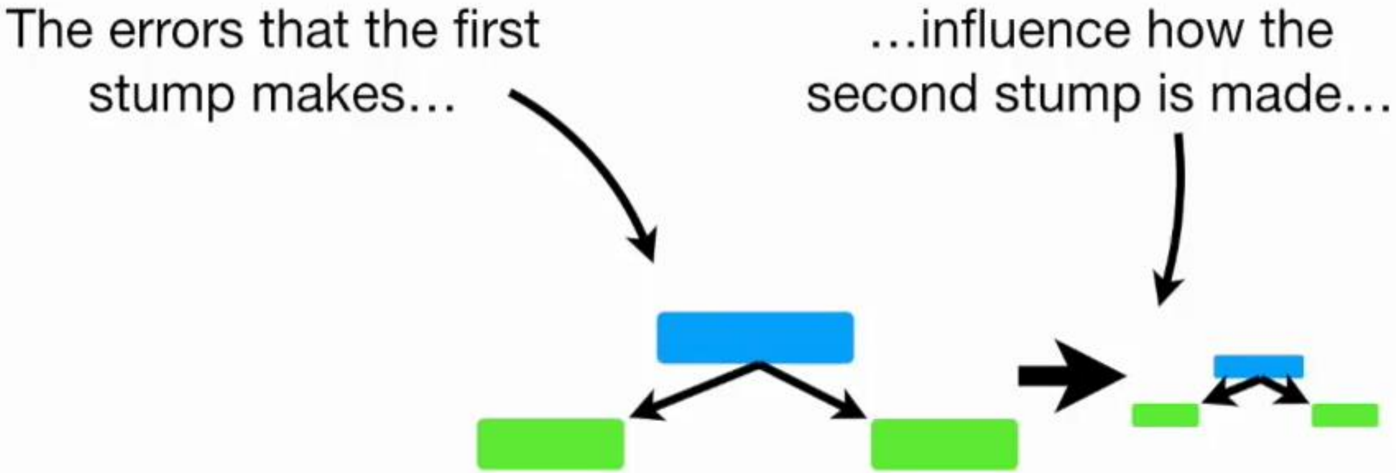
In contrast, in a **Forest of Stumps** made with **AdaBoost**, some stumps get more say in the final classification than others.



Lastly, in a **Random Forest**, each decision tree is made independently of the others.

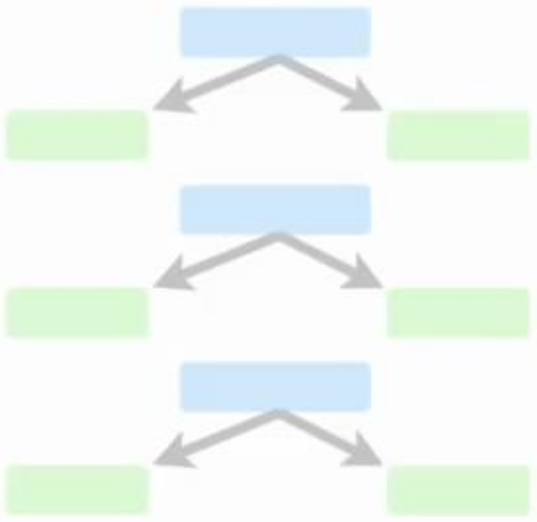


In contrast, in a **Forest of Stumps** made with **AdaBoost**, order is important.

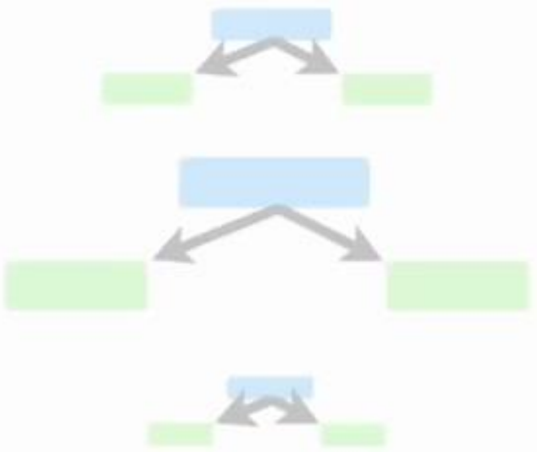


To review, the three ideas behind **AdaBoost** are…

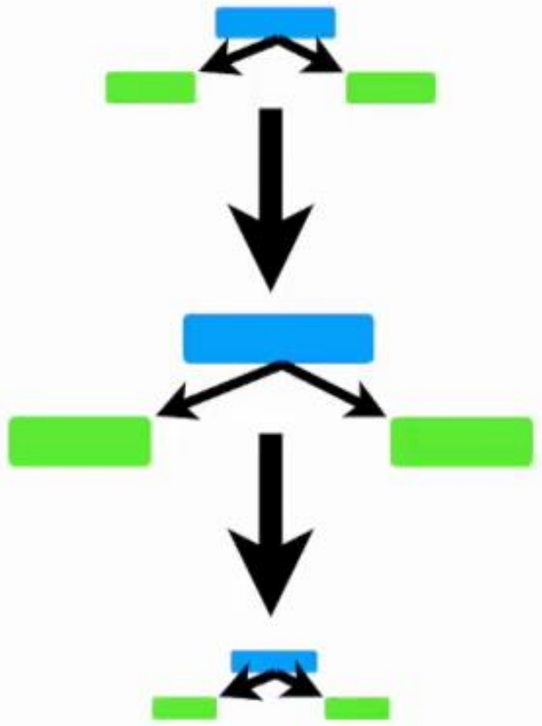
1) **AdaBoost** combines a lot of "weak learners" to make classifications. The weak learners are almost aways **stumps**.



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



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



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

We create a **Forest of Stumps** with **AdaBoost** to predict if a patient has heart disease.

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

We will make these predictions based on a patient's **Chest Pain** and **Blocked Artery** status and their **Weight**.

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

Sample Weight

The first thing we do is give each sample a weight that indicates how important it is to be correctly 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

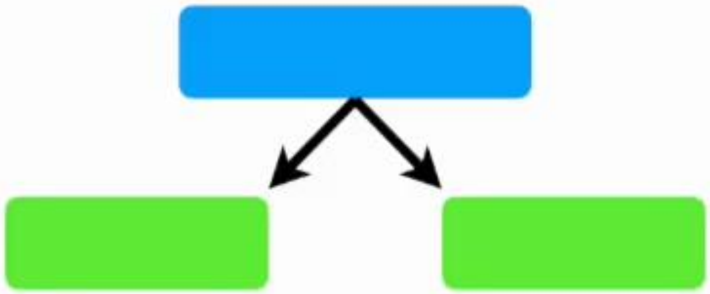
At the start, all samples get the same weight…

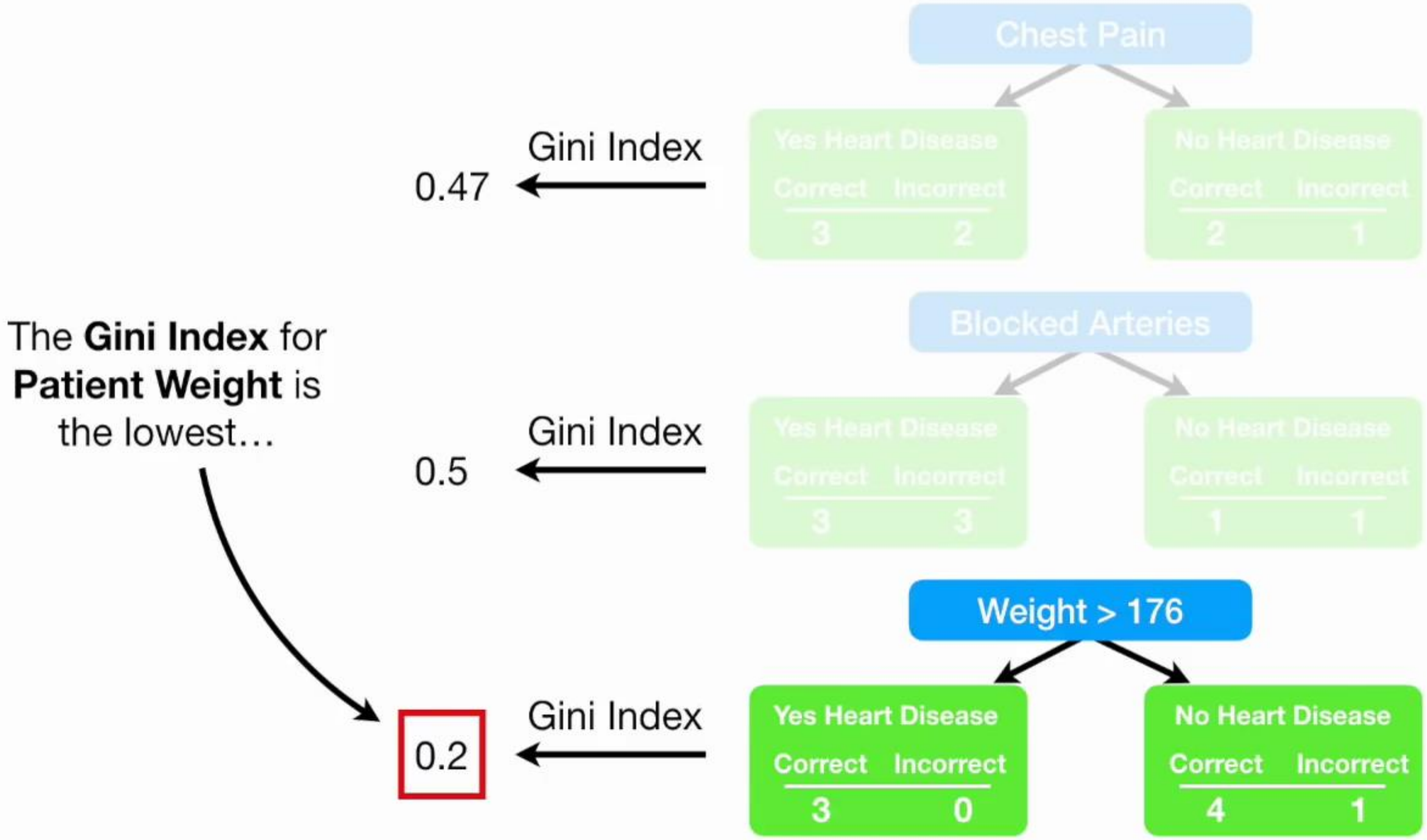
$$\frac{1}{\text{total number of samples}} = \frac{1}{8}$$

However, after we make the first stump, these weights will change in order to guide how the next stump is created.

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 is done finding the variable, **Chest Pain**, **Blocked Arteries** or **Patient Weight**, that does the best job classifying the samples.




Chest Pain
Yes Heart Disease
Correct Incorrect
3 2
No Heart Disease
Correct Incorrect
2 1
Gini Index
0.47
Blocked Arteries
Yes Heart Disease
Correct Incorrect
3 3
No Heart Disease
Correct Incorrect
1 1
Gini Index
0.5
The Gini Index for Patient Weight is the lowest…
Weight > 176
Yes Heart Disease
Correct Incorrect
3 0
No Heart Disease
Correct Incorrect
4 1
Gini Index
0.2

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

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

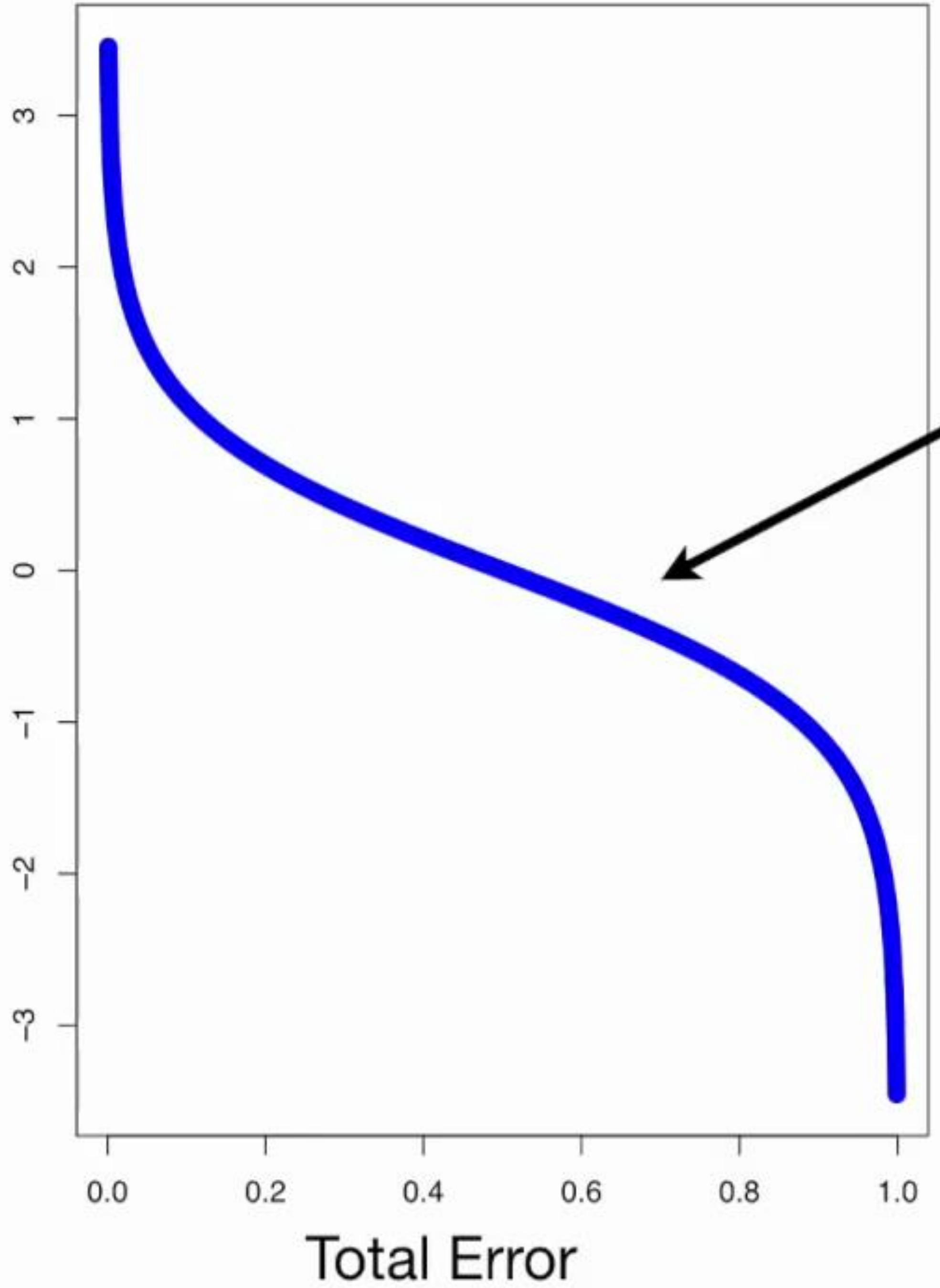
Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

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

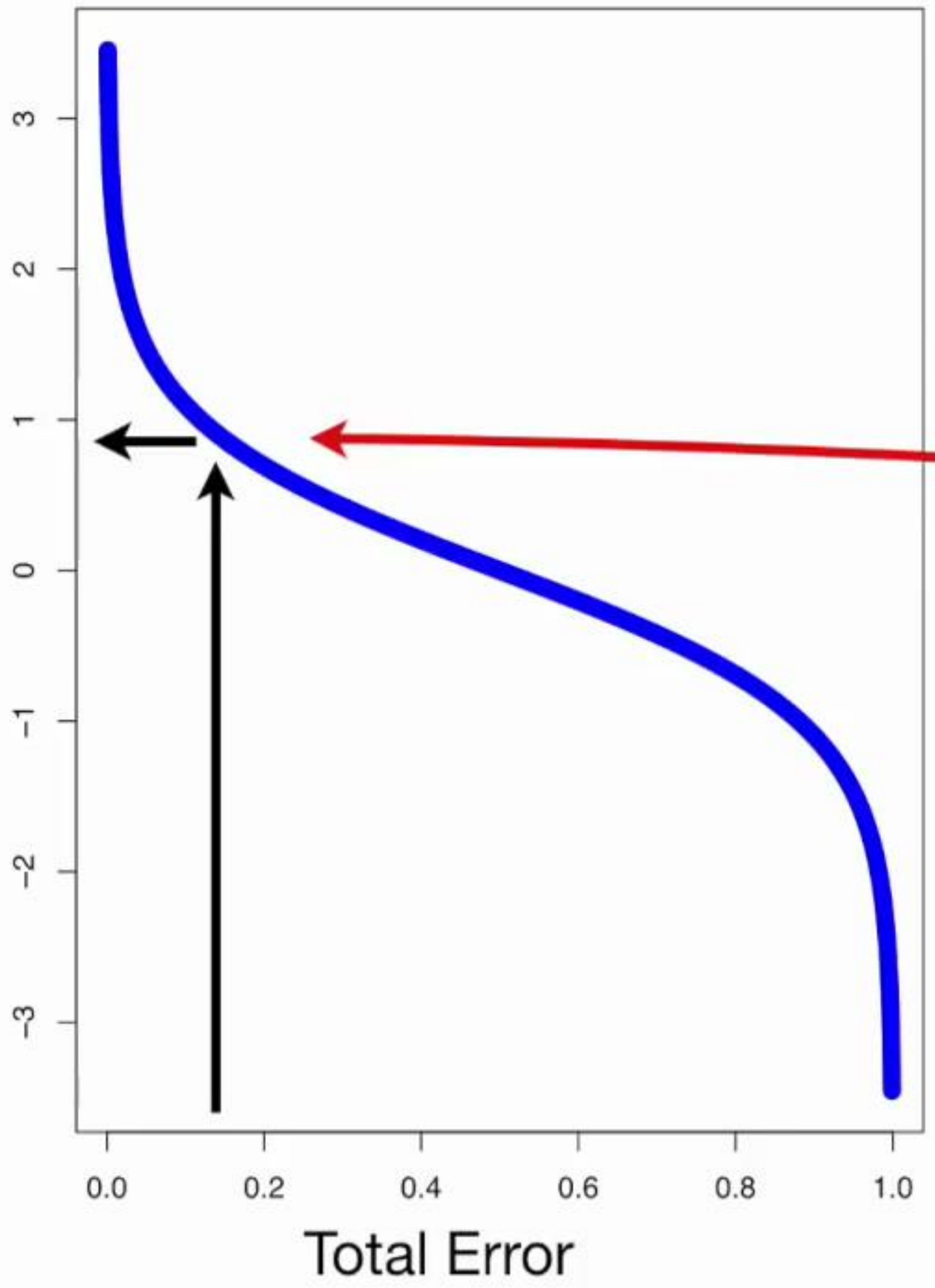
We use the **Total Error** to determine **Amount of Say** this stump has in the final classification with the following formula:

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



The **Blue Line** tells us the **Amount of Say** for **Total Error** values between **0** and **1**.

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



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

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

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**.

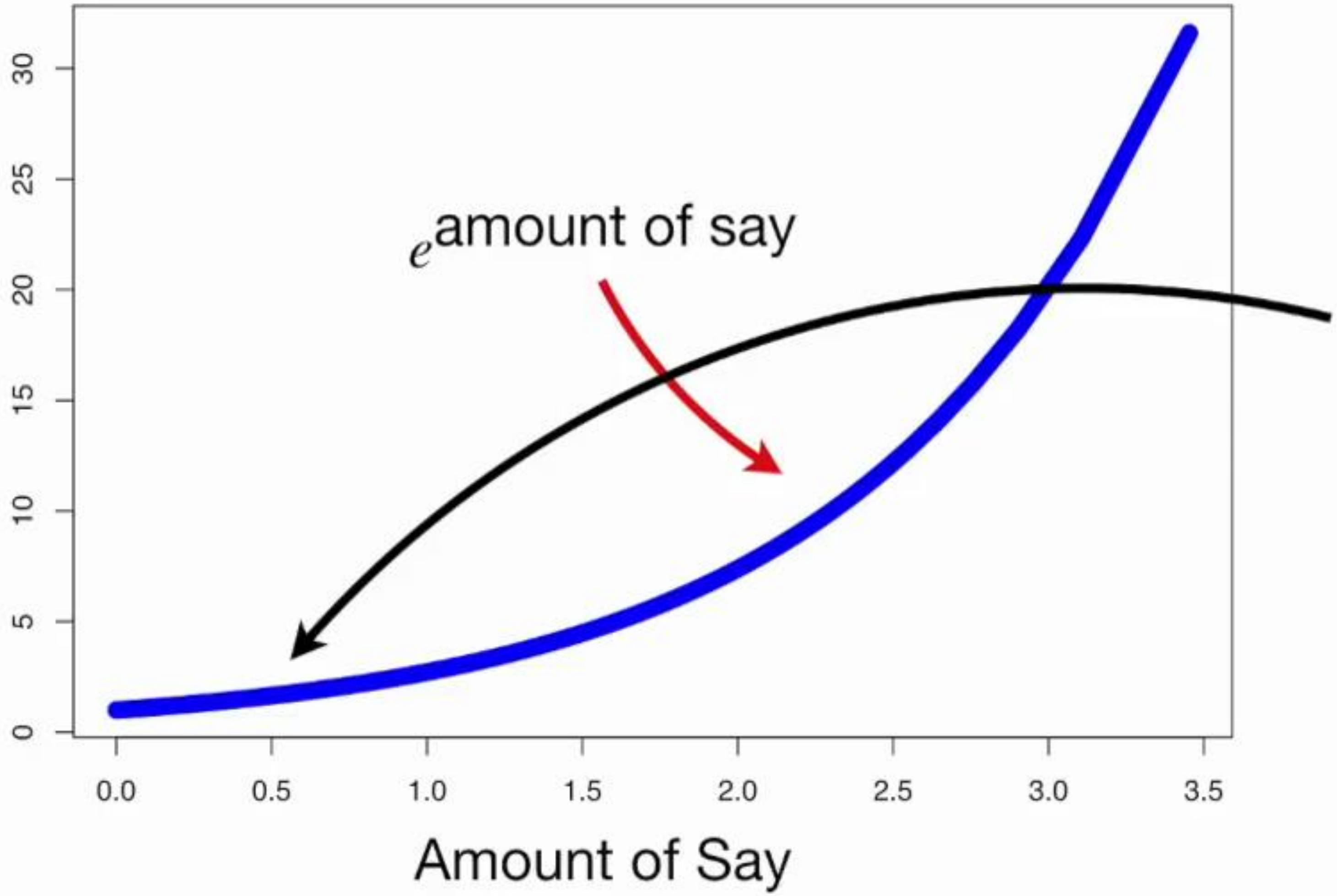
Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

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

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

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

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



...then the previous **Sample Weight** is scaled by a relatively small number.

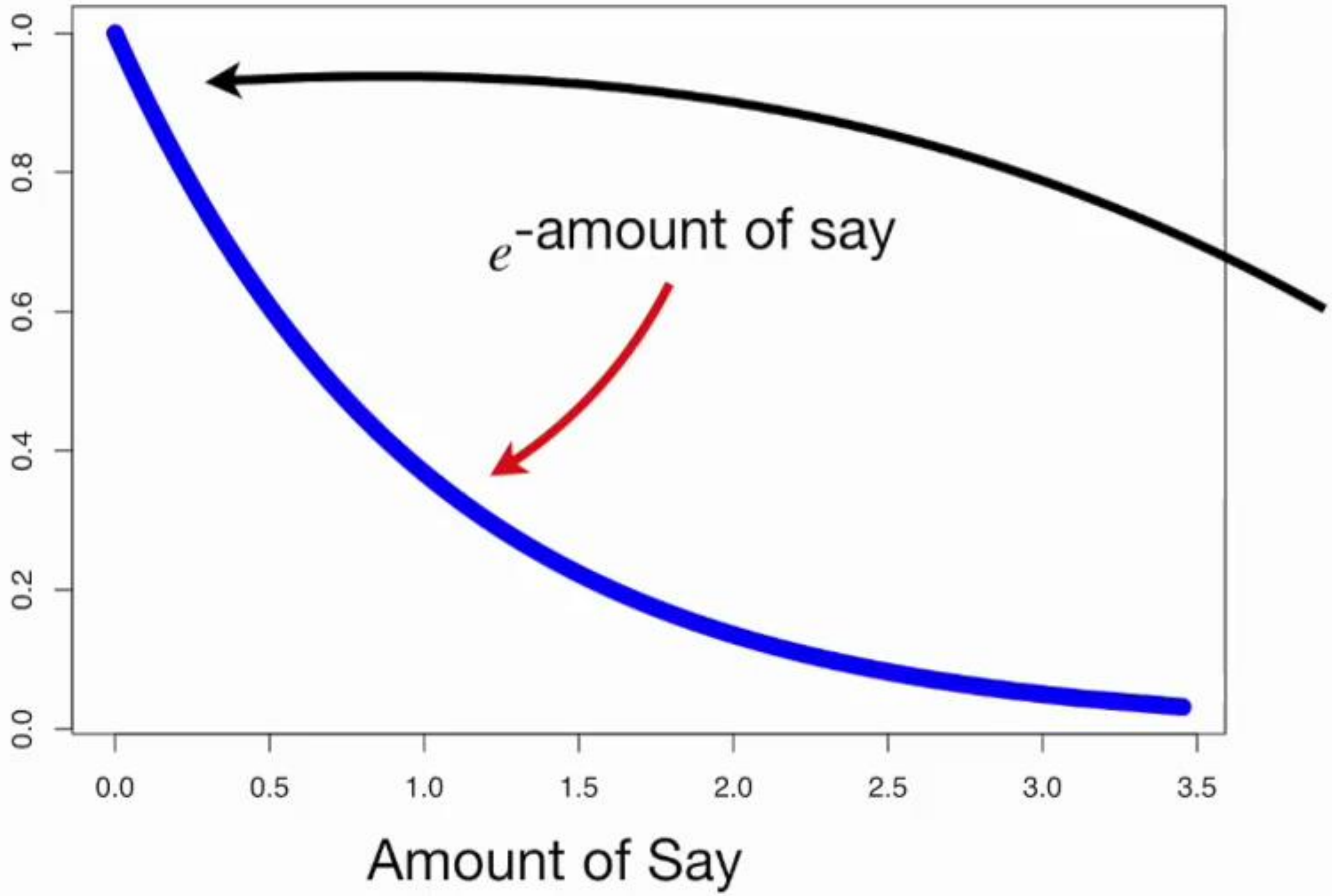
Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

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

The big difference is the *negative* sign in front of **Amount of Say**

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

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



...then we will scale the **Sample Weight** by a value close to **1**.

This means that the **New Sample Weight** will be just a little smaller than the old one.

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

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

Now we need to normalize the **New Sample Weights** so that they will add up to 1.

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

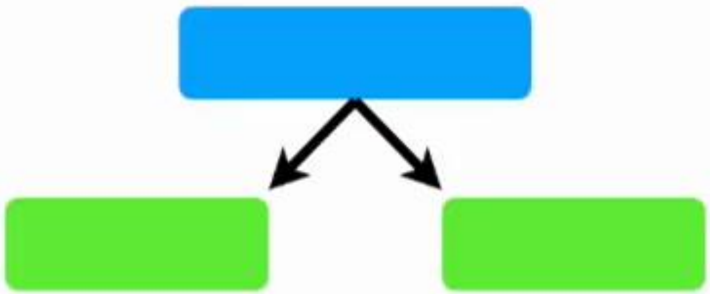
So we divide each **New Sample Weight** by **0.68** to get the normalized values.

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 just transfer the **Normalized Sample Weights** to the **Sample Weights** column, since those are what we will use for the next stump.

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

In theory, we could use the **Sample Weights** to calculate **Weighted Gini Indexes** to determine which variable should split the next stump.



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

Alternatively, instead of using a **Weighted Gini Index**, we can make a new collection of samples that contains duplicate copies of the samples with the largest **Sample Weights**.

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		
Yes	No	168		
Yes	Yes	172		

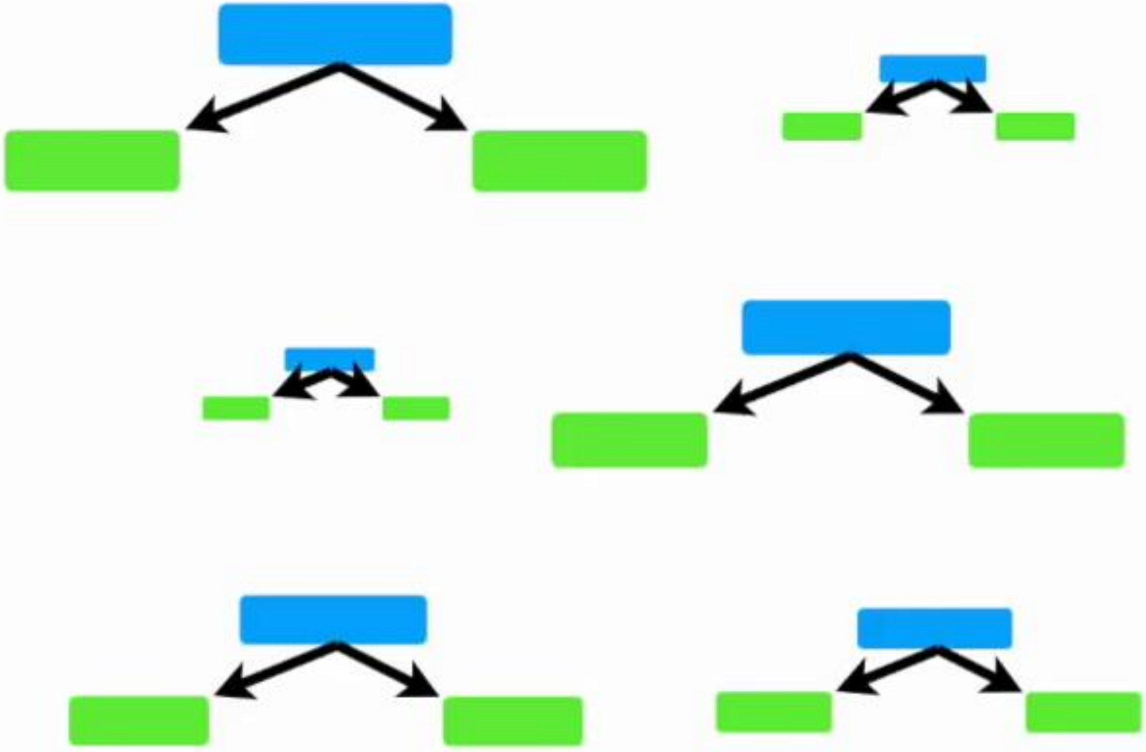
Ultimately, this sample was added to the new collection of samples **4** times, reflecting its larger **Sample Weight**.

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

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.

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



This goes on and on....
Until you train sufficient number of stumps

AdaBoostClassifier in Sklearn

class
sklearn.ensemble.AdaBoostClassifier(base_estimator=None, *, n_estimators=50, learning_rate=1.0, algorithm='SAMME.R', random_state=None)

AdaBoostRegressor in Sklearn

class
sklearn.ensemble.AdaBoostRegressor(base_estimator
=None, *, n_estimators=50, learning_rate=1.0,
loss='linear', random_state=None)[source]

Why Adaboost works?

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