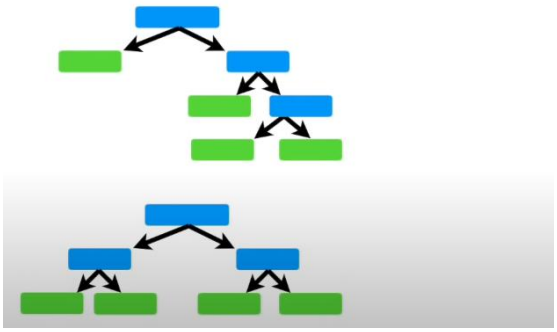
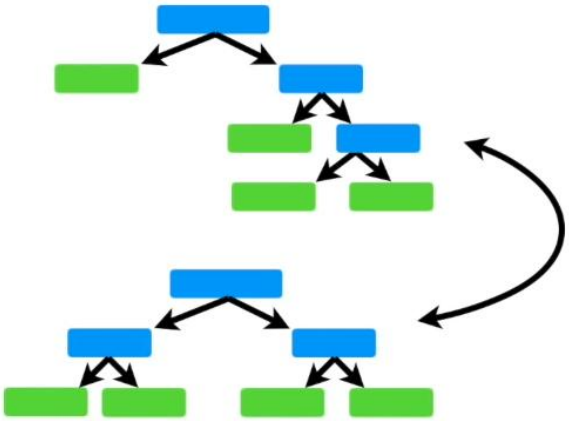
So let's start by using **Decision Trees** and **Random Forests** to explain the three main concepts behind **AdaBoost**!

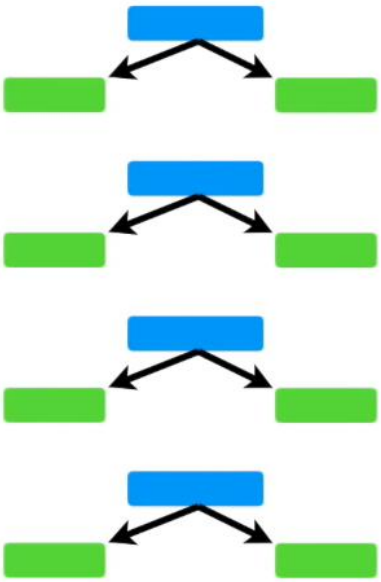
In a **Random Forest**, each time you make a tree, you make a full sized tree.



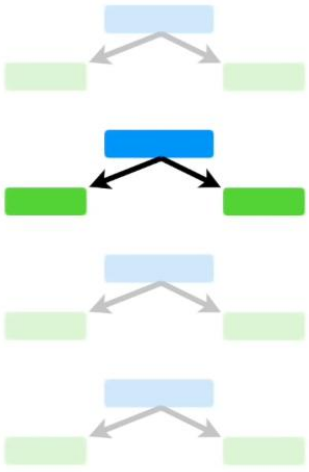


Some trees might be bigger than others, but there is no predetermined maximum depth.

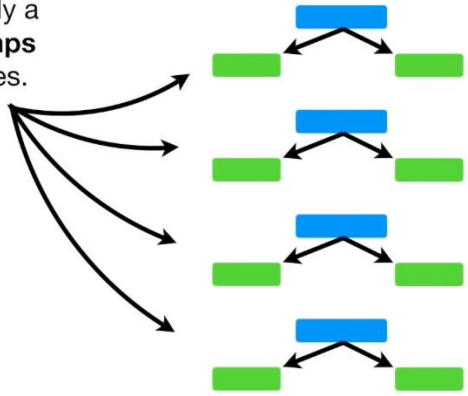
In contrast, in a **Forest of Trees** made with **AdaBoost**, the trees are usually just a **node** and two **leaves**.



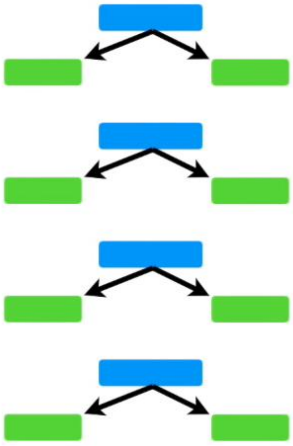
A tree with just one node and two leaves is called a ***stump***.



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



Stumps are not great at making accurate classifications.

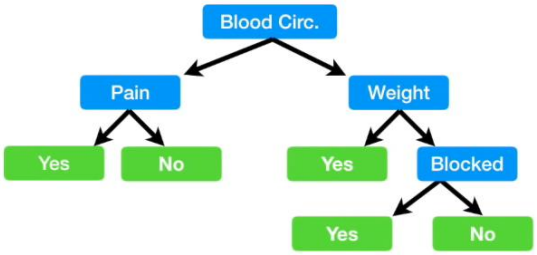


For example, if we were using this data to determine if someone had heart disease or not…

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

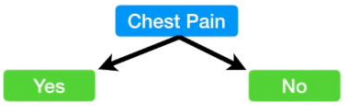
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
No	No	No	125	No
Yes	Yes	Yes	180	Yes
Yes	Yes	No	210	No
Yes	No	Yes	167	Yes

…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

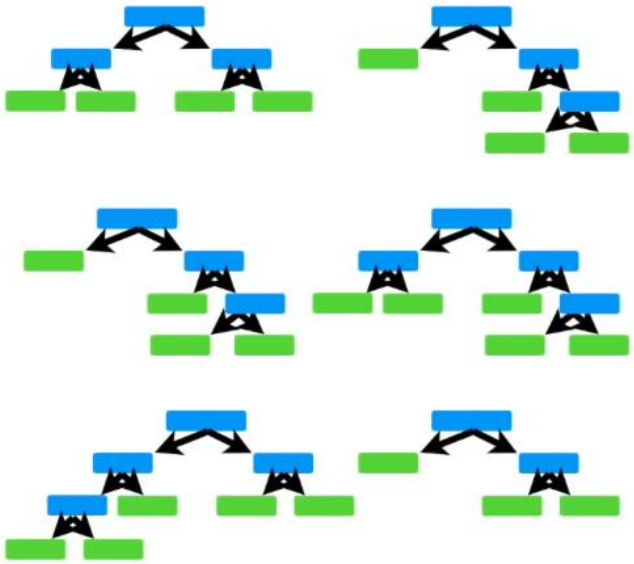
…but a **Stump** can only use one variable to make a decision.



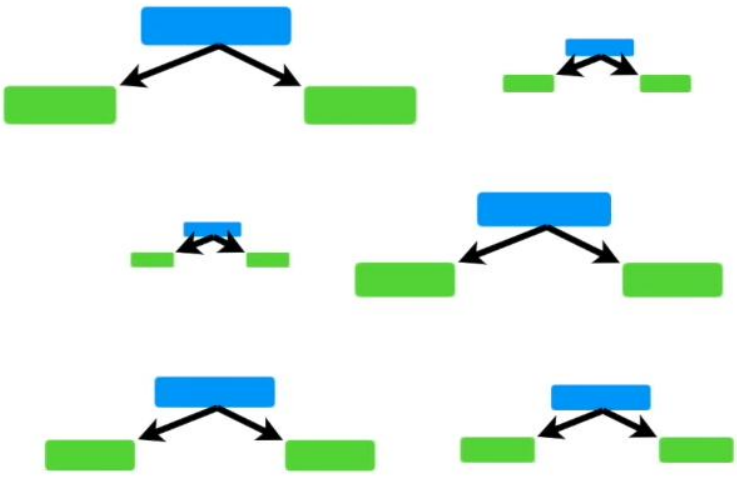
Thus, **Stumps** are technically "weak learners".

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.

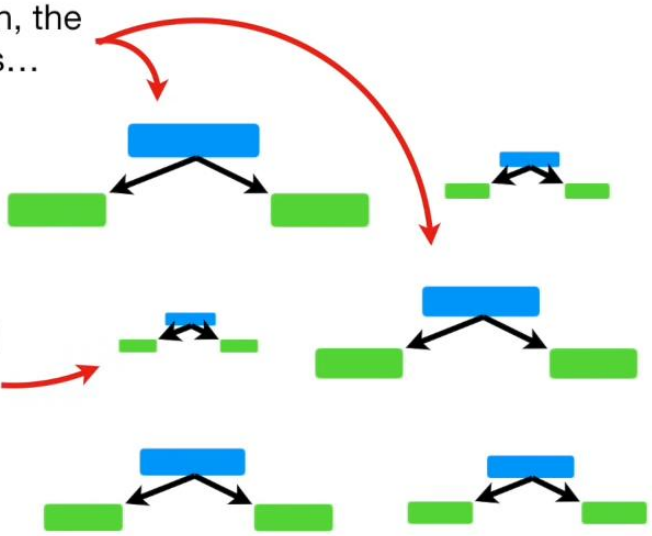


In contrast, in a **Forest of Stumps** made with **AdaBoost**, some stumps get more say in the final classification than others.

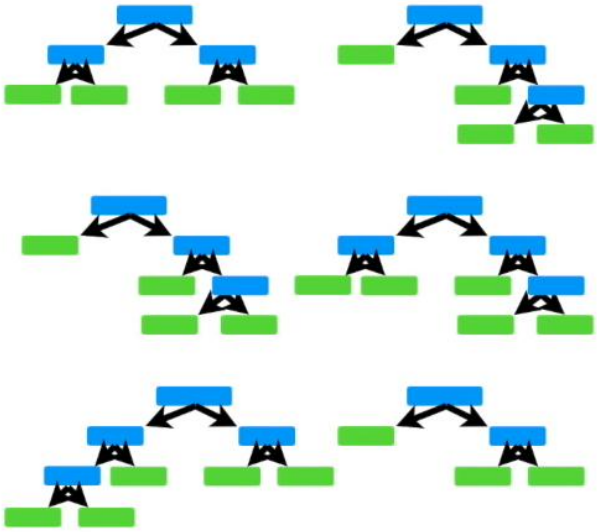


In this illustration, the larger stumps…

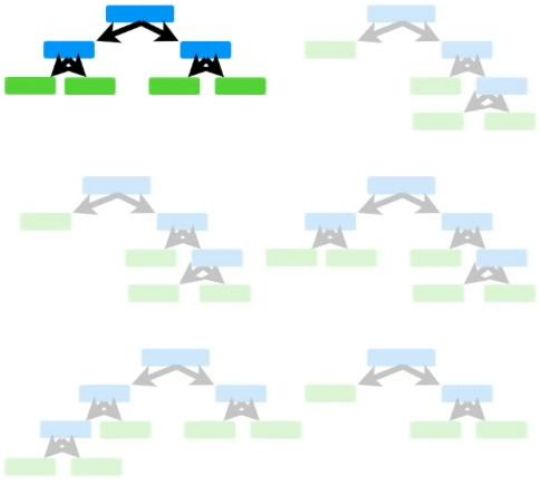
…get more say in the final classification than the smaller stumps.



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



In other words, it doesn't matter if this tree was made first…



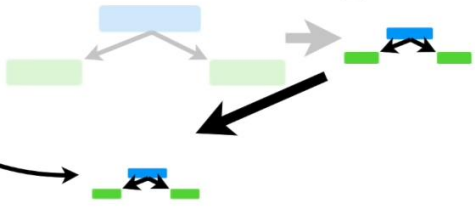
In contrast, in a **Forest of Stumps** made with **AdaBoost**, order is important.

The errors that the first stump makes…

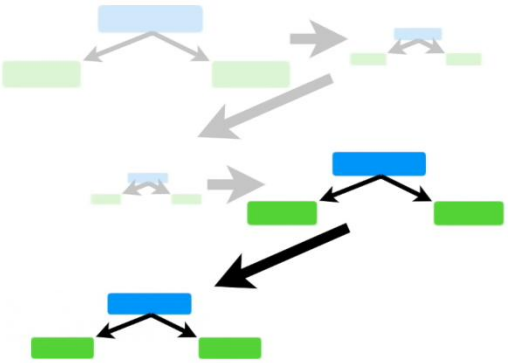
…influence how the second stump is made…

…and the errors that the second stump makes…

…influence how the third stump is made.

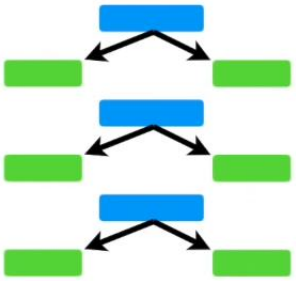


etc. etc. etc.



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**.



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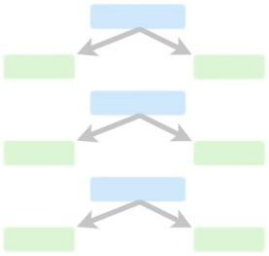
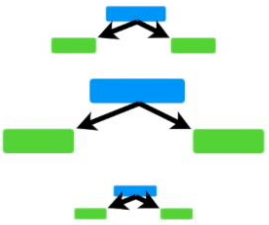


2) Some **stumps** get more say in the classification than others.



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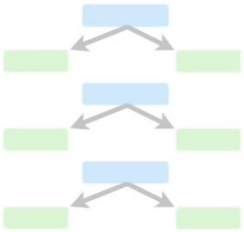

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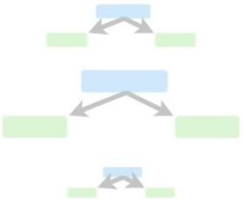
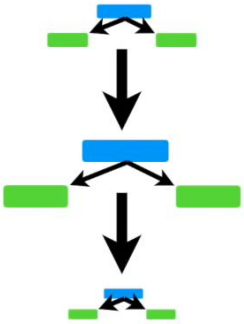


3) Each **stump** is made by taking the previous **stump's** mistakes into account.



Now let's dive into the nitty gritty detail of how to create a **Forest of Stumps** using **AdaBoost**.

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	Sample Weight
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	

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…

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

…and that makes the samples all equally important.

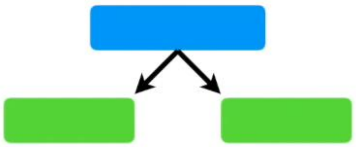
Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

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

In other words, we'll talk more about the **Sample Weights** later!

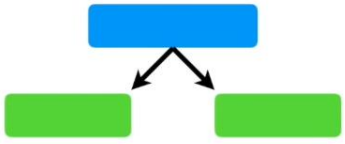
Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

Now we need to make the first **stump** in the forest.



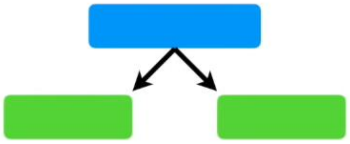
Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

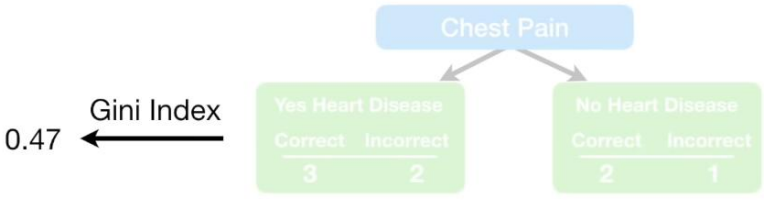
This is done finding the variable, **Chest Pain**, **Blocked Arteries** or **Patient Weight**, that does the best job classifying the samples.



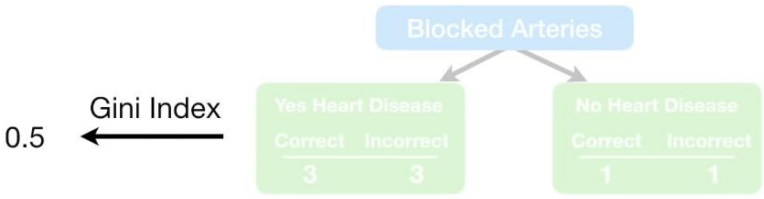
Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

NOTE: Because all of the weights are the same, we can ignore them right now.





Gini Index
0.47



Gini Index
0.5

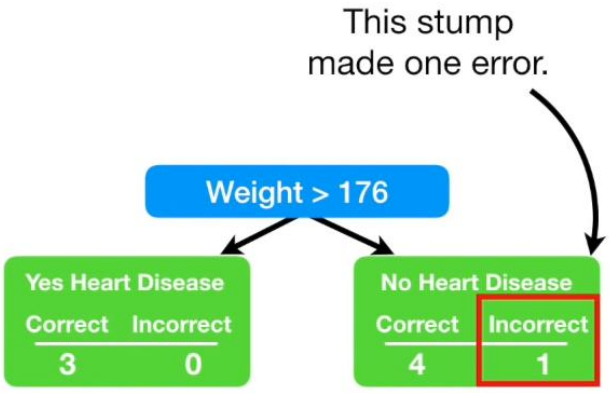
The **Gini Index** for **Patient Weight** is the lowest…

Gini Index
0.2

…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.

We determine how much say a stump has in the final classification based on how well it classified the samples.



Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
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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

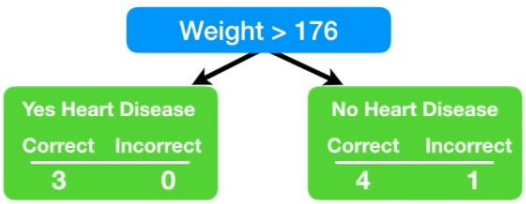
This patient, who weighs less than 176, *has* heart disease, but the stump says they do not.

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**.



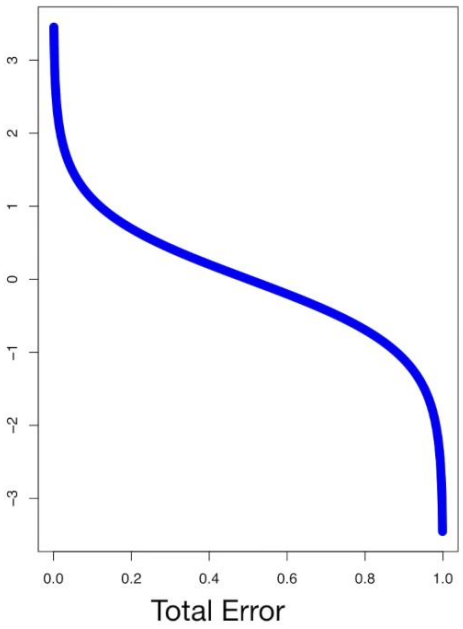
Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	1/8
No	Yes	180	Yes	1/8
Yes	No	210	Yes	1/8
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

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:

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



NOTE: If **Total Error** is **1** or **0**, then this equation will freak out.

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

In practice a small error term is added to prevent this from happening.

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

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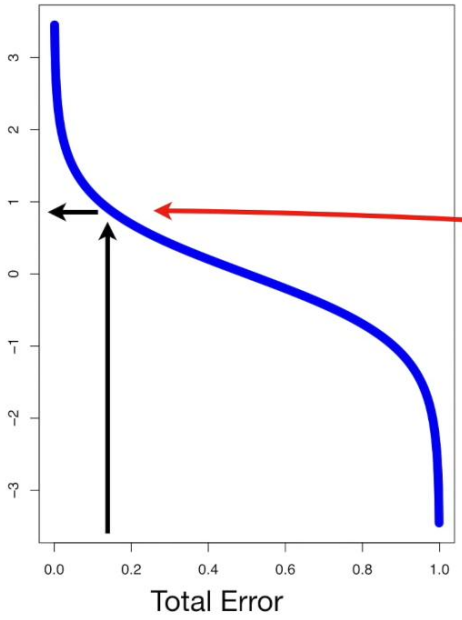
Yes	Yes	167	Yes	1/8
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

With **Patient Weight > 176**, the **Total Error** is **1/8**, so we just plug and chug…

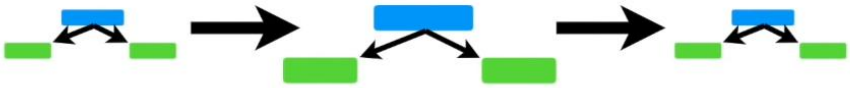
$$\text{Amount of Say} = \frac{1}{2}\log\left(\frac{1 - \text{Total Error}}{\text{Total Error}}\right)$$



…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.



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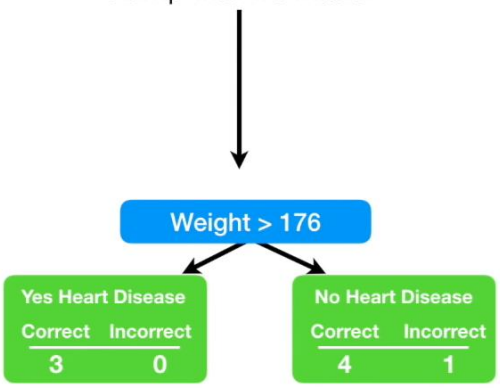
No	Yes	156	No	1/8
No	Yes	125	No	1/8
Yes	No	168	No	1/8
Yes	Yes	172	No	1/8

Let's go back to the first stump that we made.



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

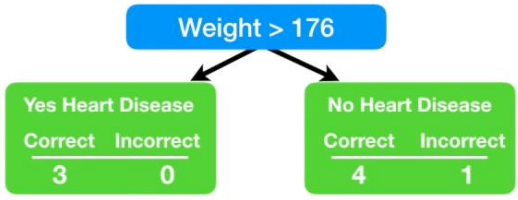
…but since this stump *incorrectly* classified this sample…

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

Let's start by increasing the **Sample Weight** for the *incorrectly* classified 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

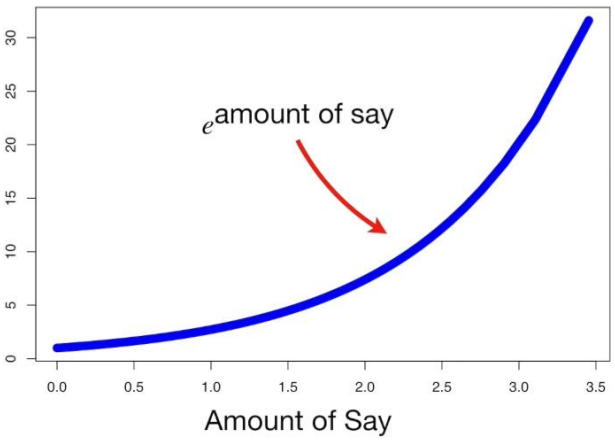
$$\text{New Sample Weight} = \text{sample weight} \times e^{\text{amount of say}}$$

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

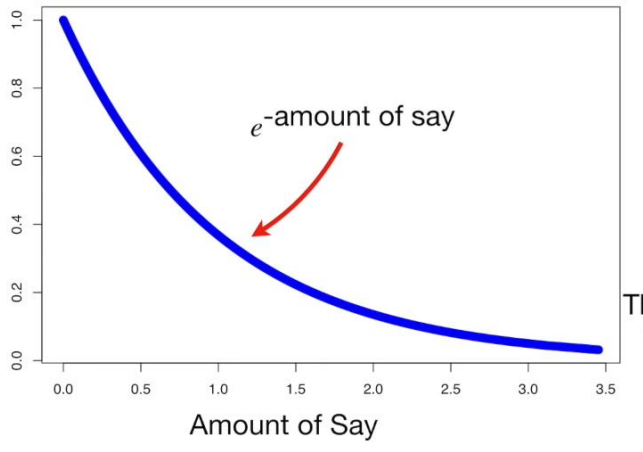
$$\text{New Sample Weight} = \text{sample weight} \times e^{\text{-amount of say}}$$

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
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
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

Right now, if you add up the **New Sample Weights**, you get **0.68**.

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	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

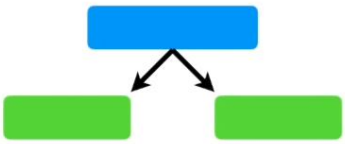
Now, when we add up the **New Sample Weights**, we get **1** (plus or minus a little rounding error).

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.

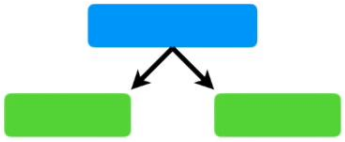
Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	0.07
No	Yes	180	Yes	0.07
Yes	No	210	Yes	0.07
Yes	Yes	167	Yes	0.49
No	Yes	156	No	0.07
No	Yes	125	No	0.07
Yes	No	168	No	0.07
Yes	Yes	172	No	0.07

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



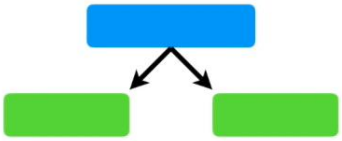
Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
Yes	Yes	205	Yes	0.07
No	Yes	180	Yes	0.07
Yes	No	210	Yes	0.07
Yes	Yes	167	Yes	0.49
No	Yes	156	No	0.07
No	Yes	125	No	0.07
Yes	No	168	No	0.07
Yes	Yes	172	No	0.07

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

The **Weighted Gini Index** would put more emphasis on correctly classifying this sample (the one that was misclassified by the last stump), since this sample has the largest **Sample Weight**.



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

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

Then we pick a random number between 0 and 1…

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

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease

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	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

Chest Pain	Blocked Arteries	Patient Weight	Heart Disease

…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	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 **0.21** 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

Multinomial Distribution

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

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	No	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	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

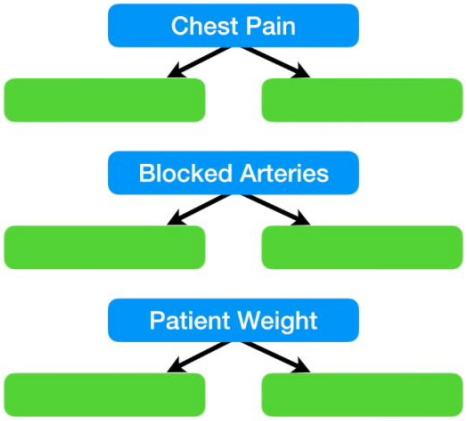
However, that doesn't mean the next stump will not emphasize the need to correctly classify these samples.

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.

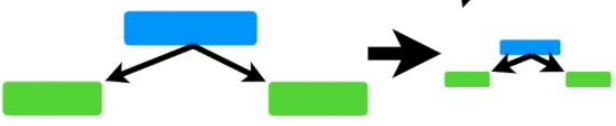
Chest Pain	Blocked Arteries	Patient Weight	Heart Disease	Sample Weight
No	Yes	156	No	1/8
Yes	Yes	167	Yes	1/8
No	Yes	125	No	1/8
Yes	Yes	167	Yes	1/8
Yes	Yes	167	Yes	1/8
Yes	Yes	172	No	1/8
Yes	Yes	205	Yes	1/8
Yes	Yes	167	Yes	1/8

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



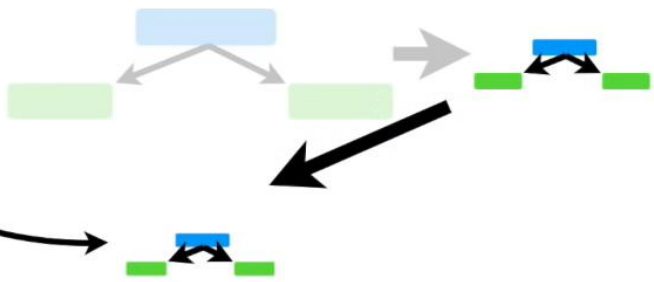
So that is how the errors that the first tree makes…

…influence how the second tree is made…

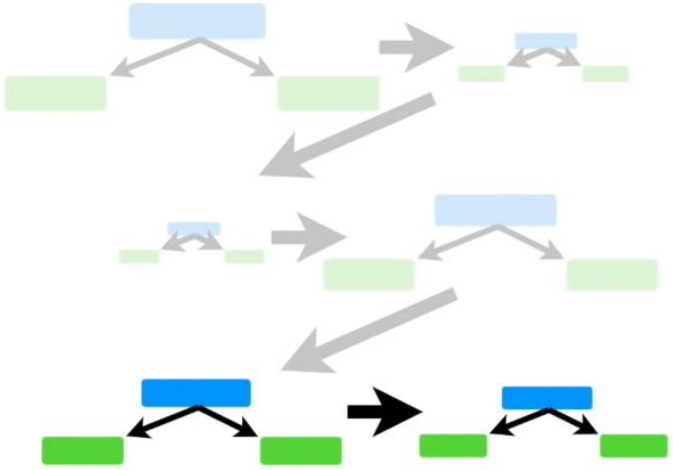


…and the errors that the second tree makes…

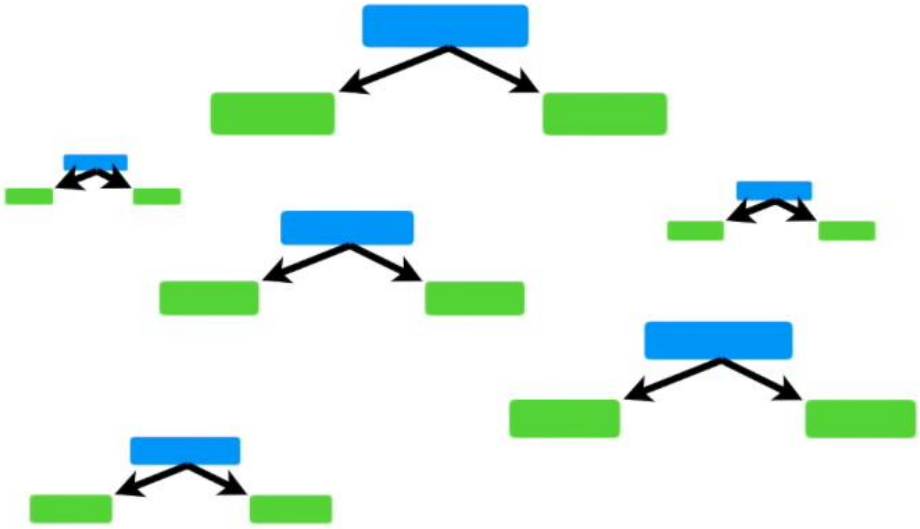
…influence how the third tree is made.



etc. etc. etc.

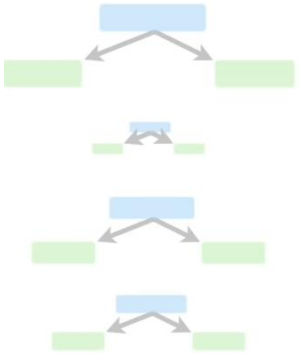


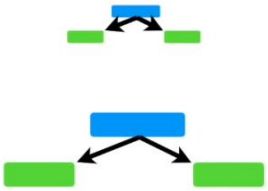
Now we need to talk about how a forest of stumps created by **AdaBoost** makes classifications…



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

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





These are the **Amounts of Say** for these stumps…

Has Heart Disease

Amount of Say

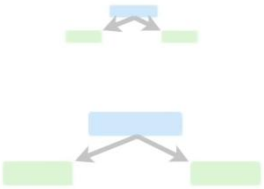
0.97

0.32

0.78

0.63

Does Not Have Heart Disease



…and these are the **Amounts of Say** for these stumps…

Has Heart Disease

Amount of Say

0.97

0.32

0.78

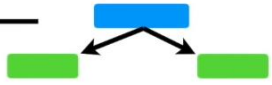
0.63

Does Not Have Heart Disease

Amount of Say

0.41

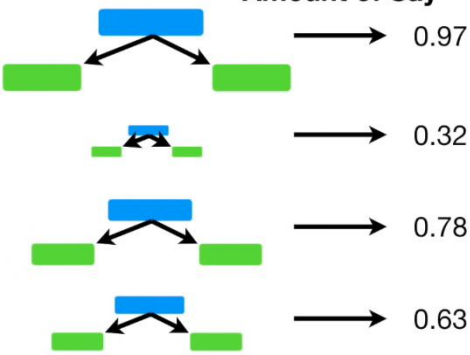
0.82



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

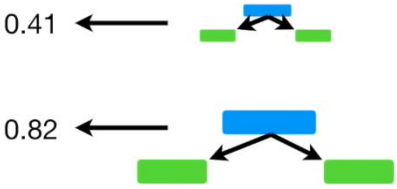
Has Heart Disease **Total = 2.7**

Amount of Say



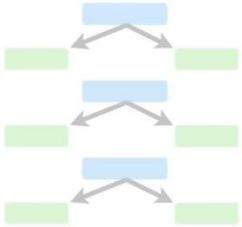
Total = 1.23 Does Not Have Heart Disease

Amount of Say

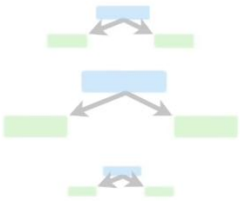


To review, the three ideas behind **AdaBoost** are…

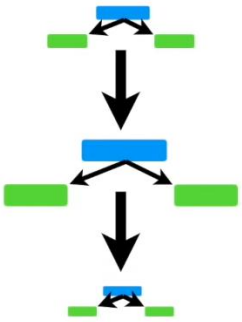
1) **AdaBoost** combines a lot of "weak learners" to make classifications. The weak learners are almost aways **stumps**.



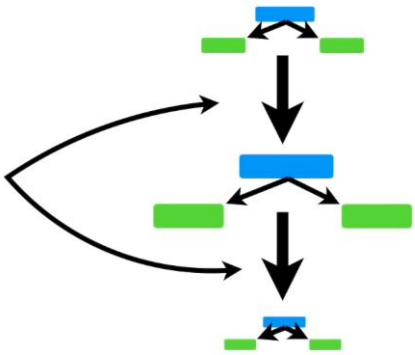
2) Some **stumps** get more say in the classification than others.



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



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



If we have a **Weighted Gini Function**, then we use it with the **Sample Weights**, otherwise we use the **Sample Weights** to make a new dataset that reflects those weights.