Random Forest: building and evaluating random forest

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Decision trees

- Decision tree are easy:
  - to build
  - to use
  - to interpret

- But in practice… Decision trees are not that awesome.

- ***"Trees have one aspect that prevents them from being the ideal tool for predictive learning, namely inaccuracy."*** (The elements of statistical learning)

- In other words, they work great with the data used to create them, but they are not flexible when it comes to classifying new samples.

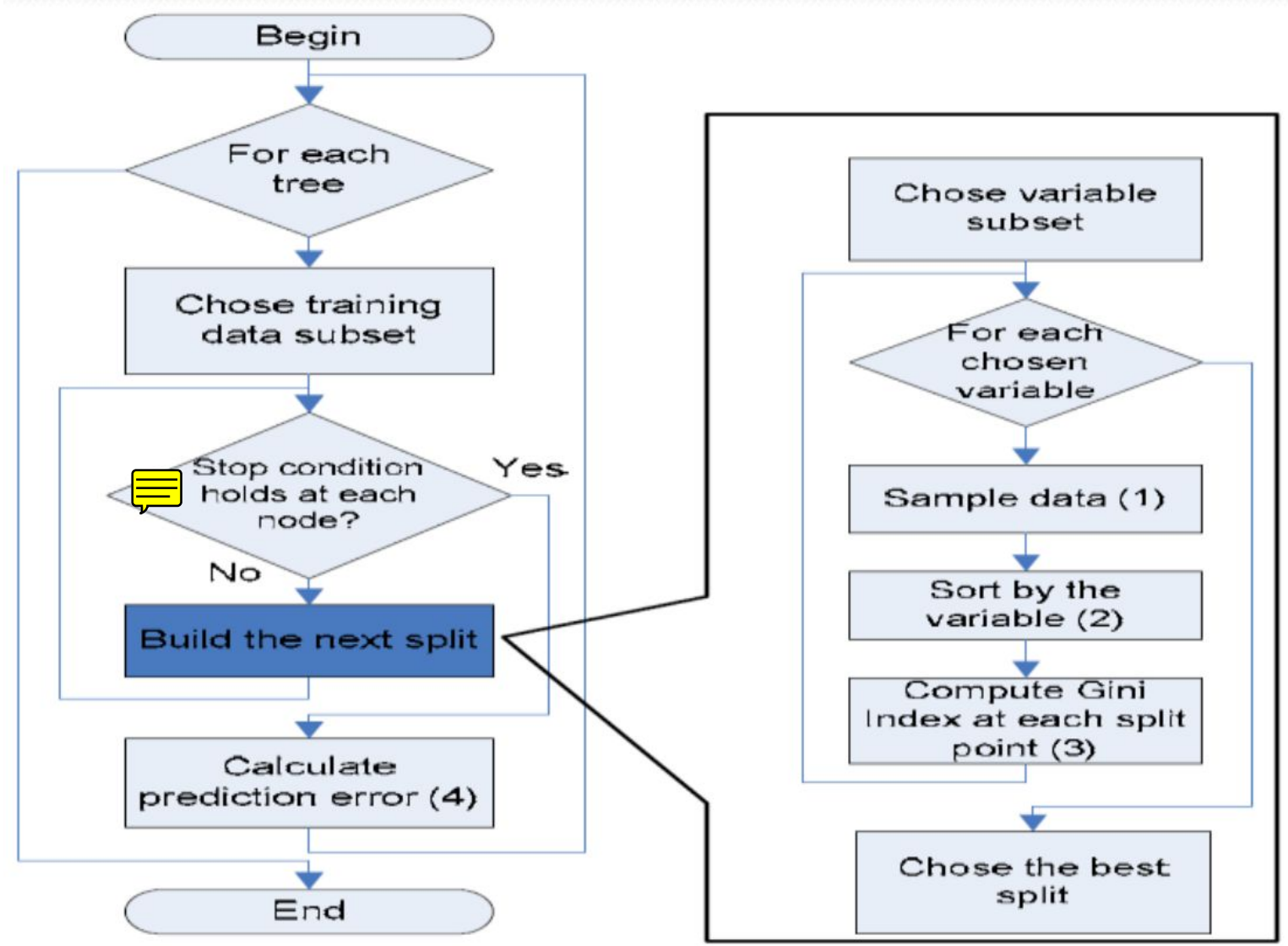
What is Random Forest?

- An ensemble classifier using **many decision tree models**.
- Can be used for classification or Regression.
- Random Forest combine the simplicity of decision trees with flexibility resulting in a vast **improvement in accuracy.**

Random Forest: the Algorithm

- Let the number of examples be N, and the number of features in the classifier be M.
- Choose a training set for this tree by choosing N times with replacement from all N available training cases.
  - Use the rest of the cases to estimate the error of the tree, by predicting their classes.
- For each node of the tree, randomly choose m features on which to base the decision at that node.
  - m should be much less than M
  - Calculate the best split based on these m variables in the training set.

The Algorithm (flow chart)



Operation of Random Forest

1. A **random seed** is chosen which pulls out at random a collection of **samples from the training dataset** while maintaining the class distribution.

2. With this selected data set, a **random set of features** from the original data set is chosen based on user defined values. All the input variables are not considered because of *enormous computation* and high chances of *over fitting*.

3. In a dataset where M is the total number of input attributes in the dataset, only m attributes are chosen at random for each tree where **m< M**.

Operation of Random Forest

4. The attributes from this set create **the best possible split using the gini index** to develop a decision tree model. The process repeats for each of the branches until the termination condition stating that leaves are the nodes that are too small to split.

Pro and Cons

- Random forests constitute one of the most robust and effective machine learning algorithms for many problems.

- Advantages of the Random Forest:
  - It produces a highly accurate classifier and learning is fast
  - It runs efficiently on large data bases.
  - It can handle thousands of input variables without variable deletion.
  - It computes proximities between pairs of cases that can be used in clustering, locating outliers or (by scaling) give interesting views of the data.

- Random forests remain however:
  - hard to analyze theoretically
  - non-trivial to interpret
  - difficult to implement properly.

Example of Random Forest

Original Dataset

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

Imagine that these 4 samples are the entire dataset that we are going to build a tree from…

… I know it's crazy small, but just pretend for now.

Original Dataset

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

Bootstrapped Dataset

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease

To create a bootstrapped dataset that is the same size as the original, we just randomly select samples from the original dataset.

The important detail is that we're allowed to pick the same sample more than once.

Original Dataset

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

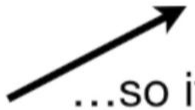
This is the first sample that we randomly select…

Bootstrapped Dataset

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease

Original Dataset

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



…so it's the first sample in our bootstrapped dataset.

Bootstrapped Dataset

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	Yes	Yes	180	Yes

Original Dataset

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

This is the second randomly selected sample from the original dataset…

Bootstrapped Dataset

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	Yes	Yes	180	Yes

Original Dataset

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

Bootstrapped Dataset

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

…so it's the second sample in our bootstrapped dataset.

Original Dataset

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

Here's the third randomly selected sample…

Bootstrapped Dataset

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

Original Dataset

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

…so here it is in the bootstrapped dataset.

Bootstrapped Dataset

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

Original Dataset

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

Here's the fourth randomly selected sample (**Note**: it's the same as the third)…

Bootstrapped Dataset

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

Original Dataset

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

Bootstrapped Dataset

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

…and here it is.

Bam!!! We've created a bootstrapped dataset!!!

Original Dataset

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

Bootstrapped Dataset

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

Step 2: Create a decision tree using the bootstrapped dataset, but only use a random subset of variables (or columns) at each step.

In this example, we will only consider 2 variables (columns) at each step.

NOTE: We'll talk more about how to determine the optimal number of variables to consider later…

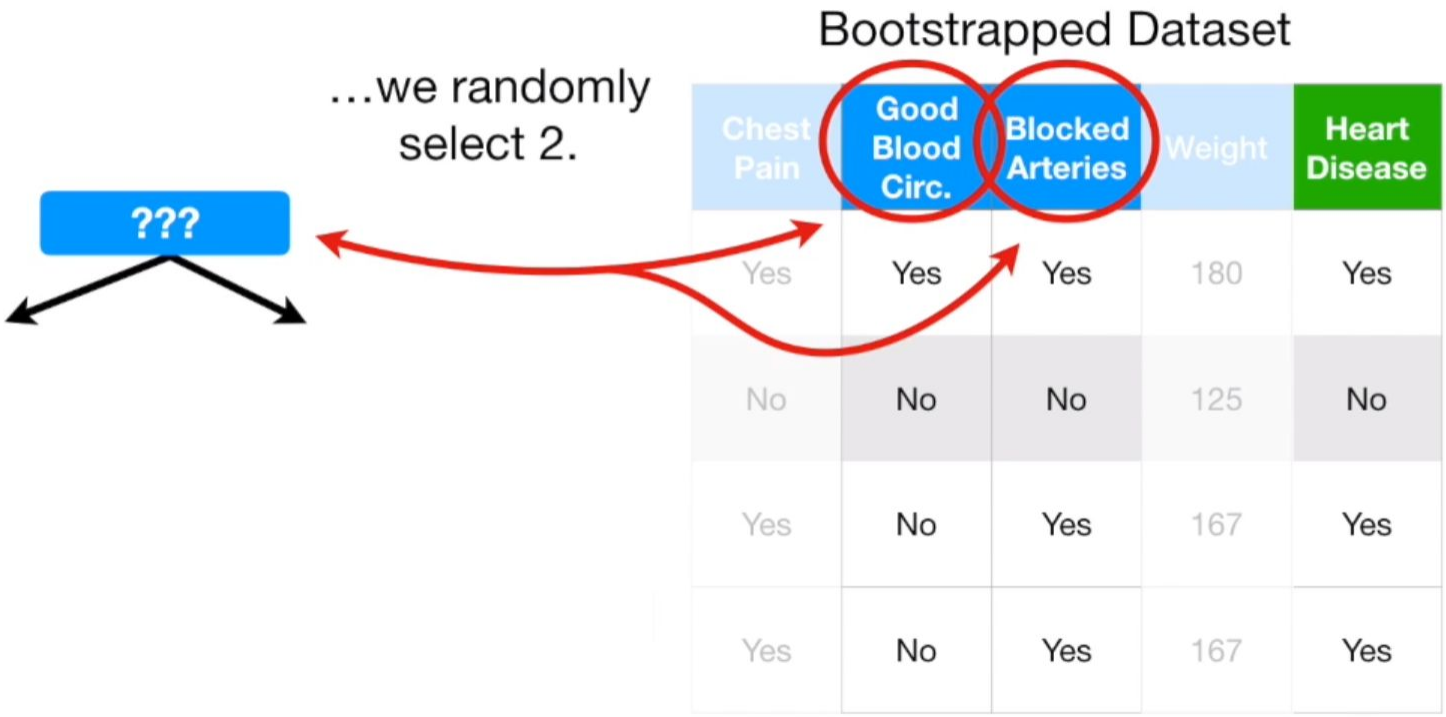
Bootstrapped Dataset

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

Thus, instead of considering all 4 variables to figure out how to split the root node…

Bootstrapped Dataset

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


Bootstrapped Dataset
…we randomly select 2.
???
Chest Pain
Good Blood Circ.
Blocked Arteries
Weight
Heart Disease
Yes
Yes
Yes
180
Yes
No
No
No
125
No
Yes
No
Yes
167
Yes
Yes
No
Yes
167
Yes

Bootstrapped Dataset

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

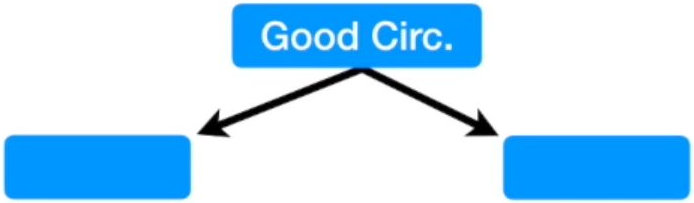
In this case, we randomly selected **Good Blood Circulation** and **Blocked Arteries** as candidates for the root node.

Just for the sake of the example, assume that **Good Blood Circulation** did the best job separating the samples.

Bootstrapped Dataset

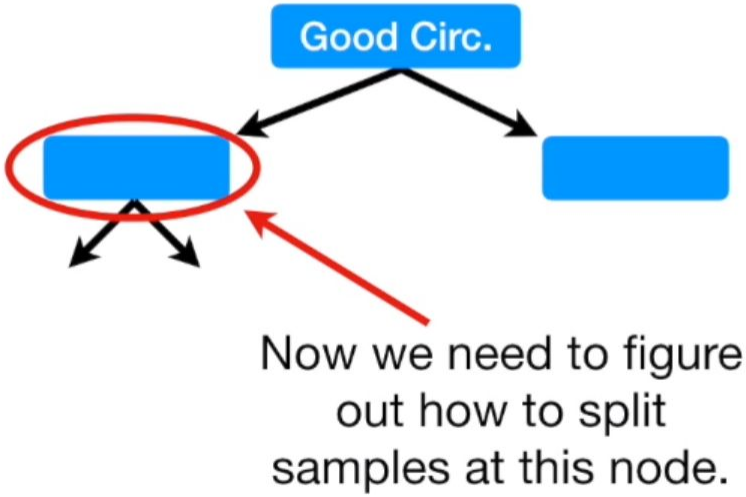
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	Yes	Yes	180	Yes
No	No	No	125	No
Yes	No	Yes	167	Yes
Yes	No	Yes	167	Yes

Since we used **Good Blood Circulation**, I'm going to grey it out so that we focus on the remaining variables.



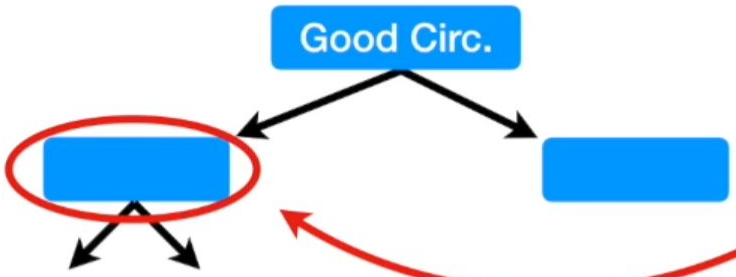
Bootstrapped Dataset

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



Bootstrapped Dataset

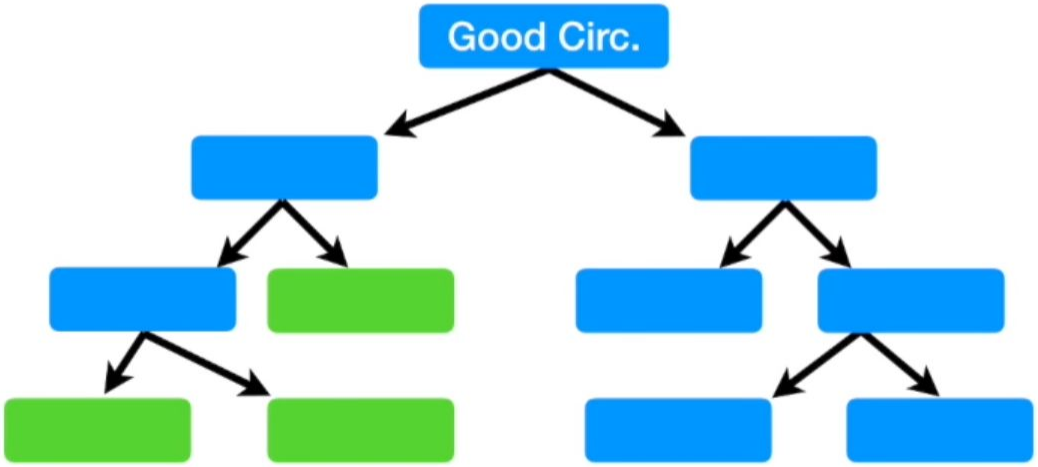
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	Yes	Yes	180	Yes
No	No	No	125	No
Yes	No	Yes	167	Yes
Yes	No	Yes	167	Yes



Just like for the root, we randomly select 2 variables as candidates, instead of all 3 remaining columns.

Bootstrapped Dataset

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



Bootstrapped Dataset

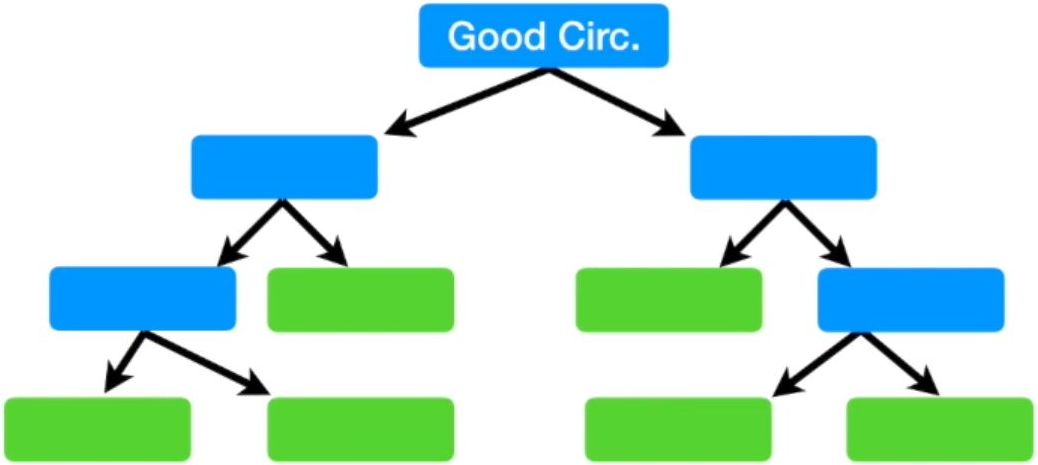
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	Yes	Yes	180	Yes
Yes	No	Yes	167	Yes
Yes	No	Yes	167	Yes
Yes	No	Yes	167	Yes

And we just build the tree as usual, but only considering a random subset of variables at each step.

We built a tree…

1) Using a bootstrapped dataset

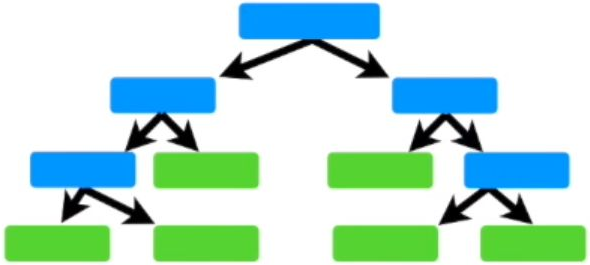
2) Only considering a random a subset of variables at each step.



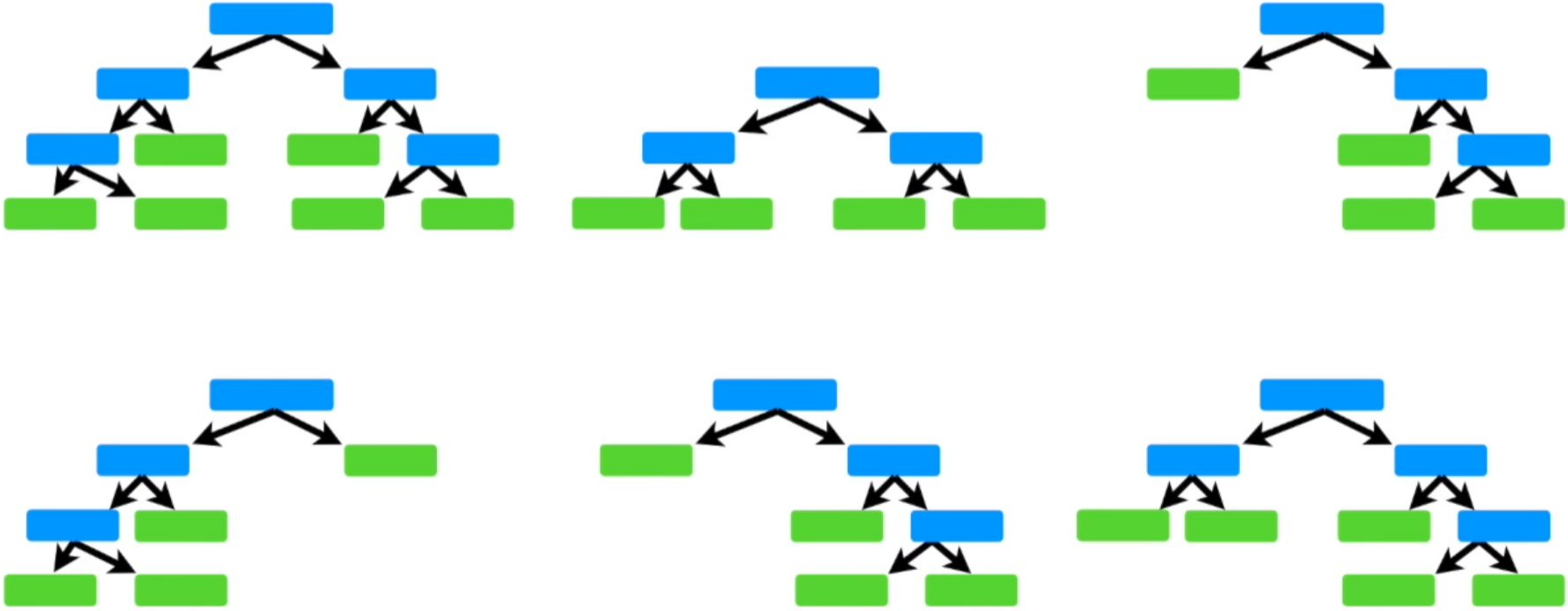
Bootstrapped Dataset

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

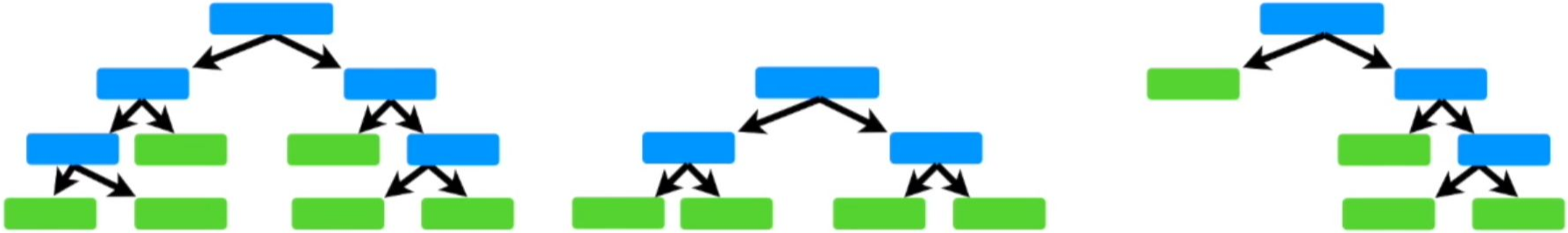
Here’s the tree we just made…



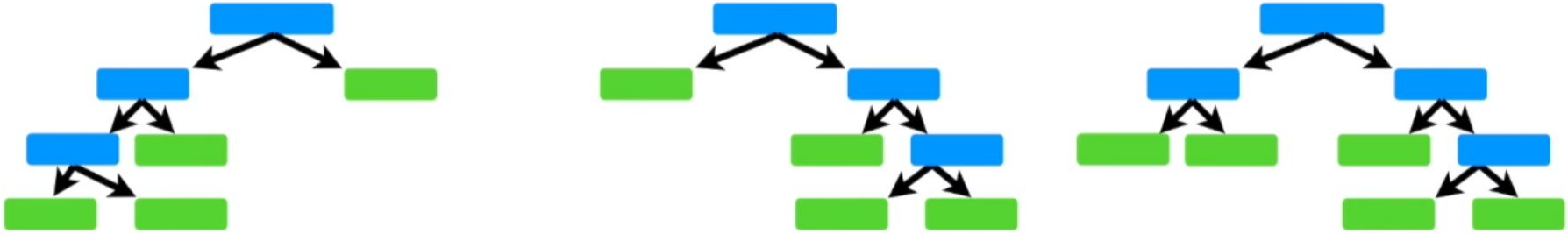
Now go back to Step 1 and repeat: Make a new bootstrapped dataset and build a tree considering a subset of variables at each step.



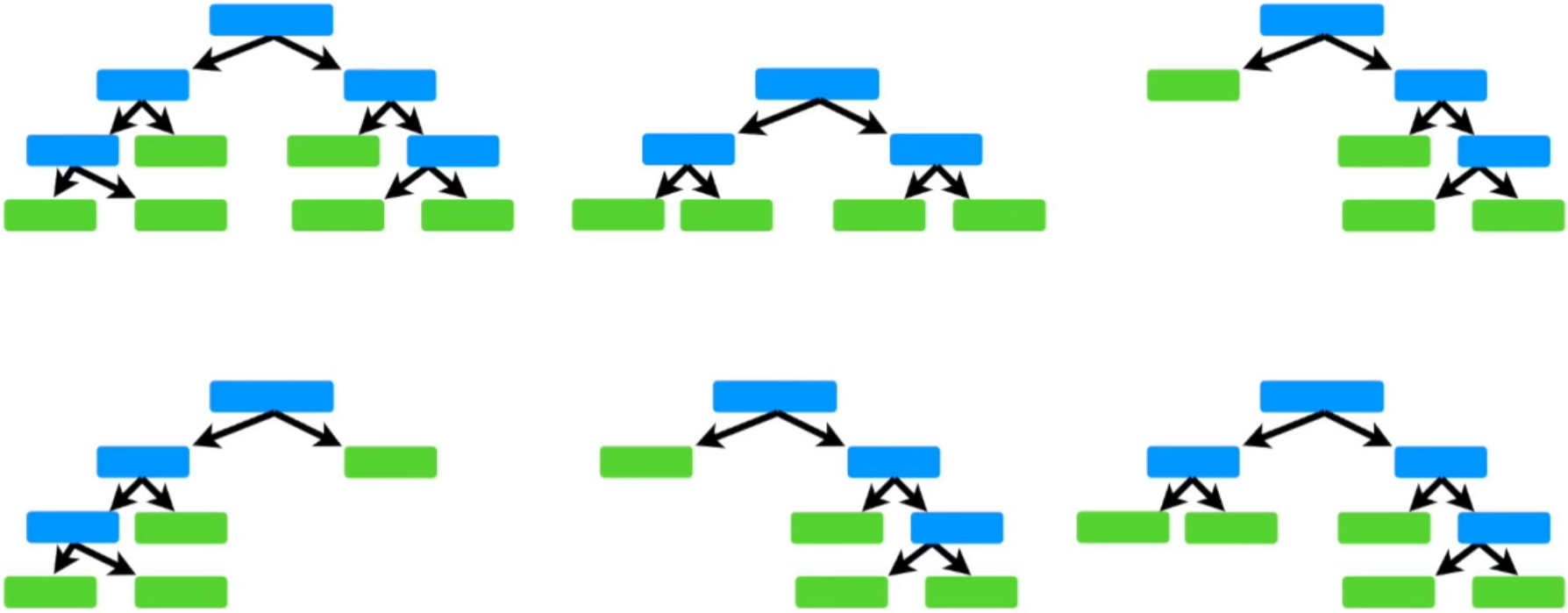
Using a bootstrapped sample and considering only a subset of the variables at each step results in a wide variety of trees.



The variety is what makes random forests more effective than individual decision trees.



Sweet!!! Now that we've created a random forest, how do we use it?



Well, first we get a new patient…

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	No	168	

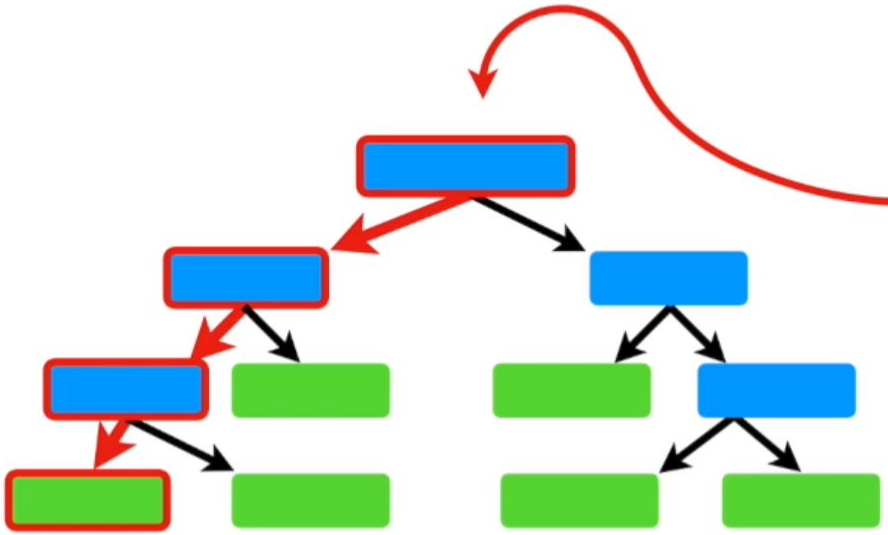
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	No	168	

…we've got all the measurements…

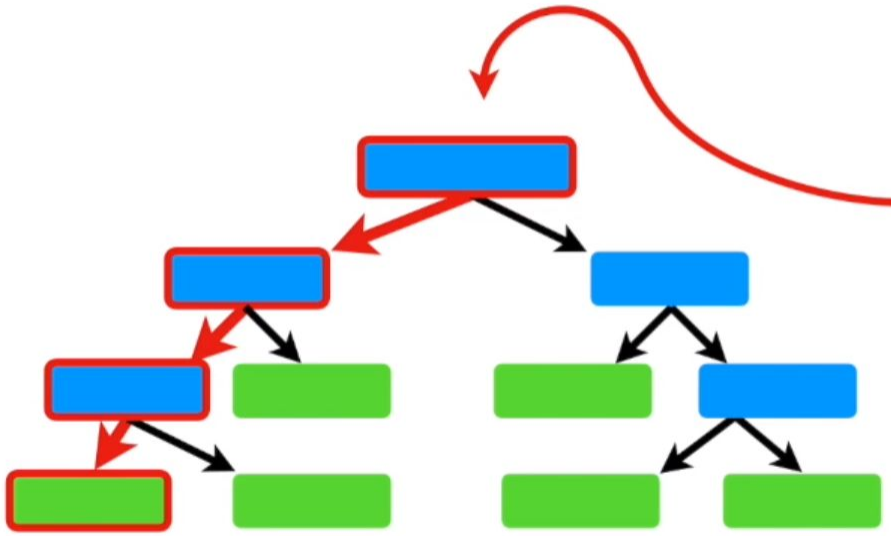
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	No	168	

…and now we want to know if they have heart disease or not.

So we take the data and run it down the first tree that we made…

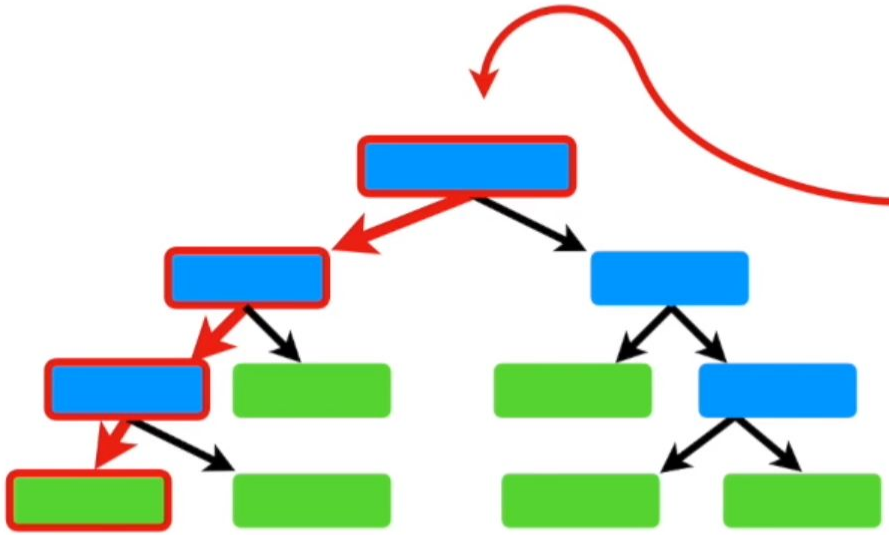


Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	No	168	



Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	No	168	

The first tree says
"Yes"…



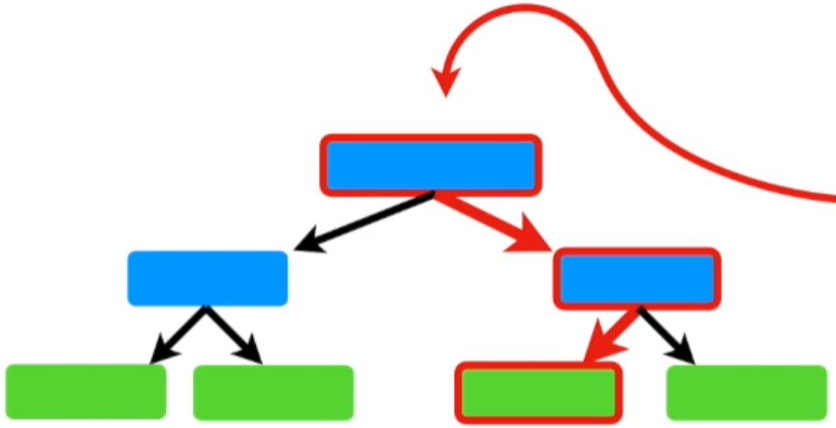
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	No	168	

Heart Disease	
Yes	No
1	0

The first tree says "Yes"…

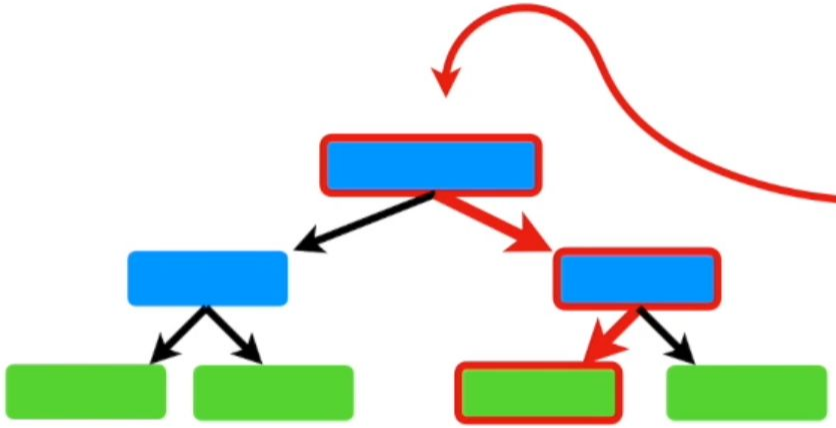
…and we keep track of that here.

Now we run the data down the second tree that we made…



Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	No	168	

Heart Disease	
Yes	No
1	0



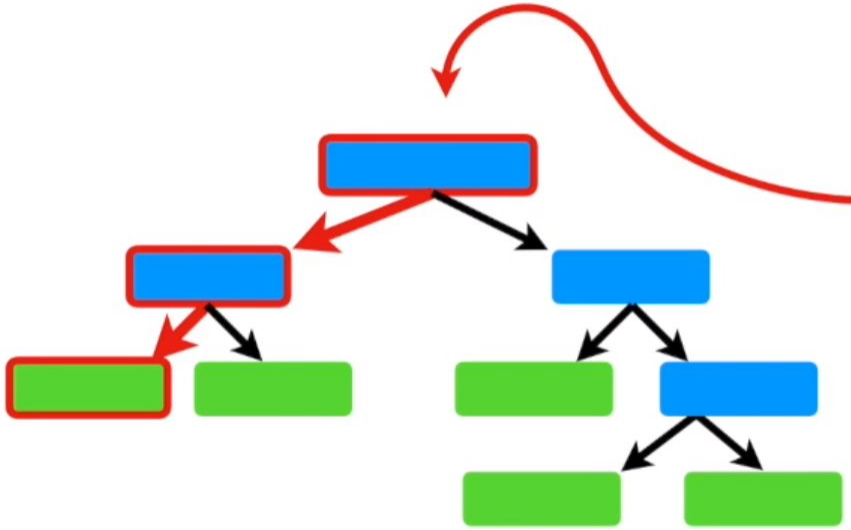
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	No	168	

The second tree also says “Yes”…

Heart Disease	
Yes	No
2	0

…and we keep track of that here.

Then we repeat for all the trees that we made…



Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	No	168	

Heart Disease	
Yes	No
5	1

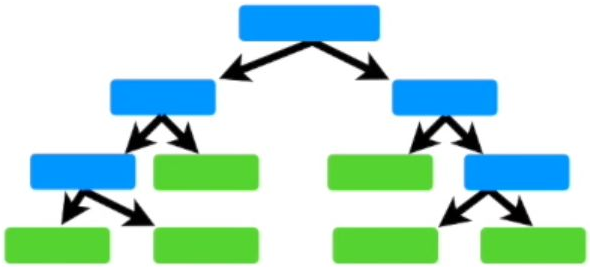
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	No	168	

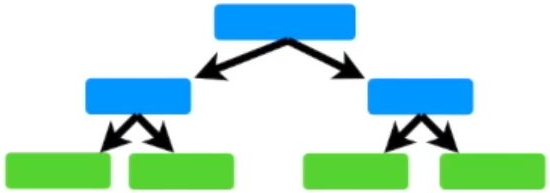
After running the data down all of the trees in the random forest, we see which option received more votes.

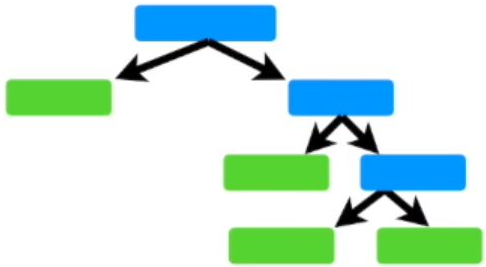
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	No	168	**YES**

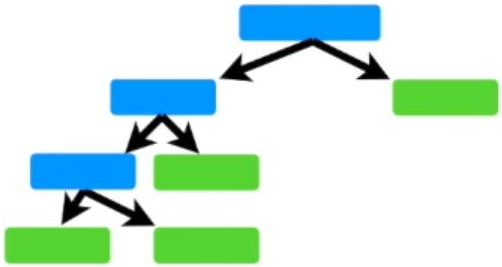
In this case, "**Yes**" received the most votes, so we will conclude that this patient has heart disease.

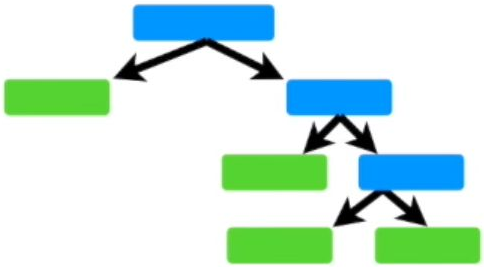
How do we know if it's any good?

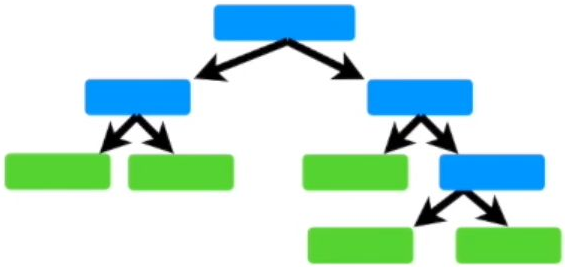












Remember when we created the bootstrapped dataset?

Original Dataset

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

Bootstrapped Dataset

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

We allowed duplicate entries in the bootstrapped dataset…

Original Dataset

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

Bootstrapped Dataset

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

As a result, this entry was not included in the bootstrapped dataset.

Original Dataset

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

Bootstrapped Dataset

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

Typically, about 1/3 of the original data does not end up in the bootstrapped dataset.

Original Dataset

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

Bootstrapped Dataset

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

Here is the entry that didn't end up in the bootstrapped dataset..

Original Dataset

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
Yes	Yes	No	210	No

Original Dataset

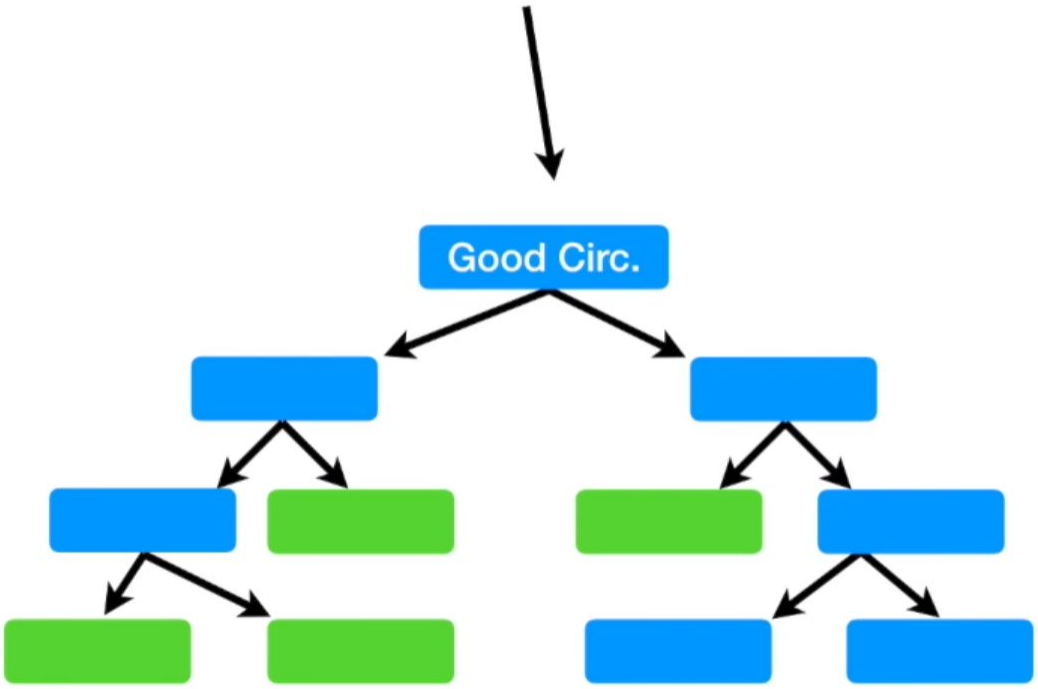
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
No	No	No	125	No
Yes	Yes	Yes	180	Yes
Yes	Yes	No	210	No
Yes	No	Yes	167	Yes

This is called the
"**Out-Of-Bag Dataset**"

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

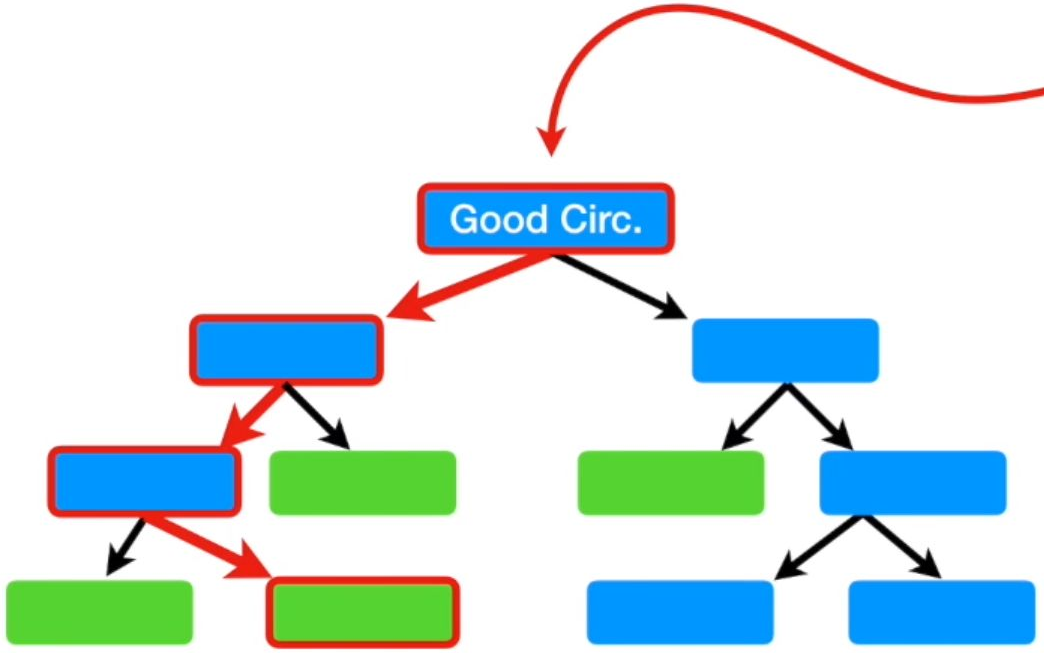
(If it were up to me, I would have named it the "**Out-Of-Boot Dataset**", since it's the entries that didn't make it into the bootstrap dataset.)

Since the Out-Of-Bag data was not used to create this tree…

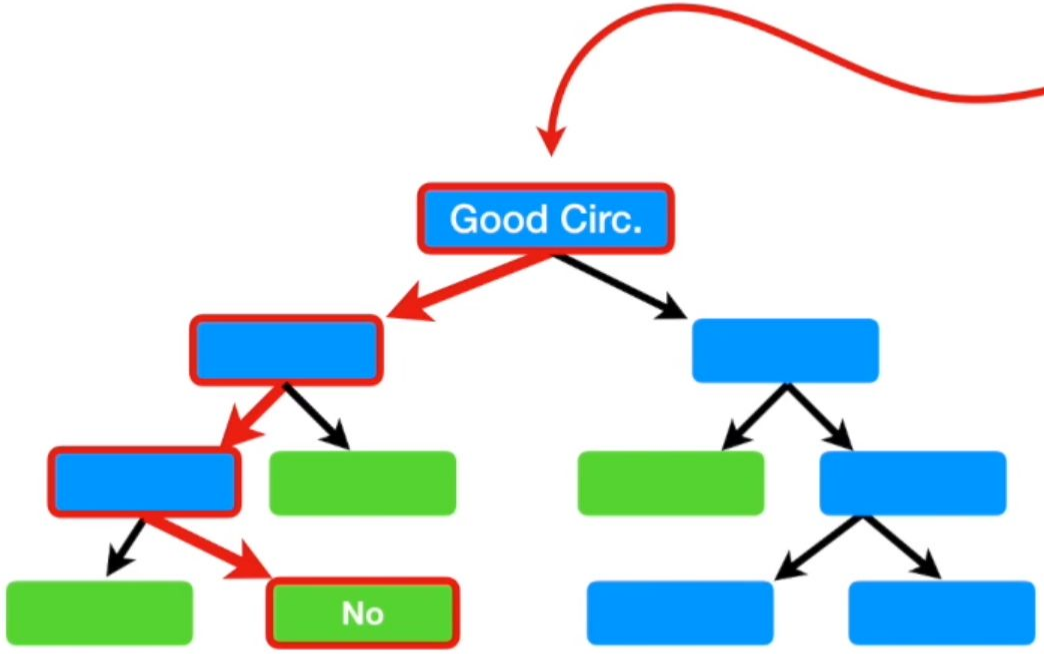


Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	Yes	No	210	No

…we can run it through and see if it correctly classifies the sample as "No Heart Disease"

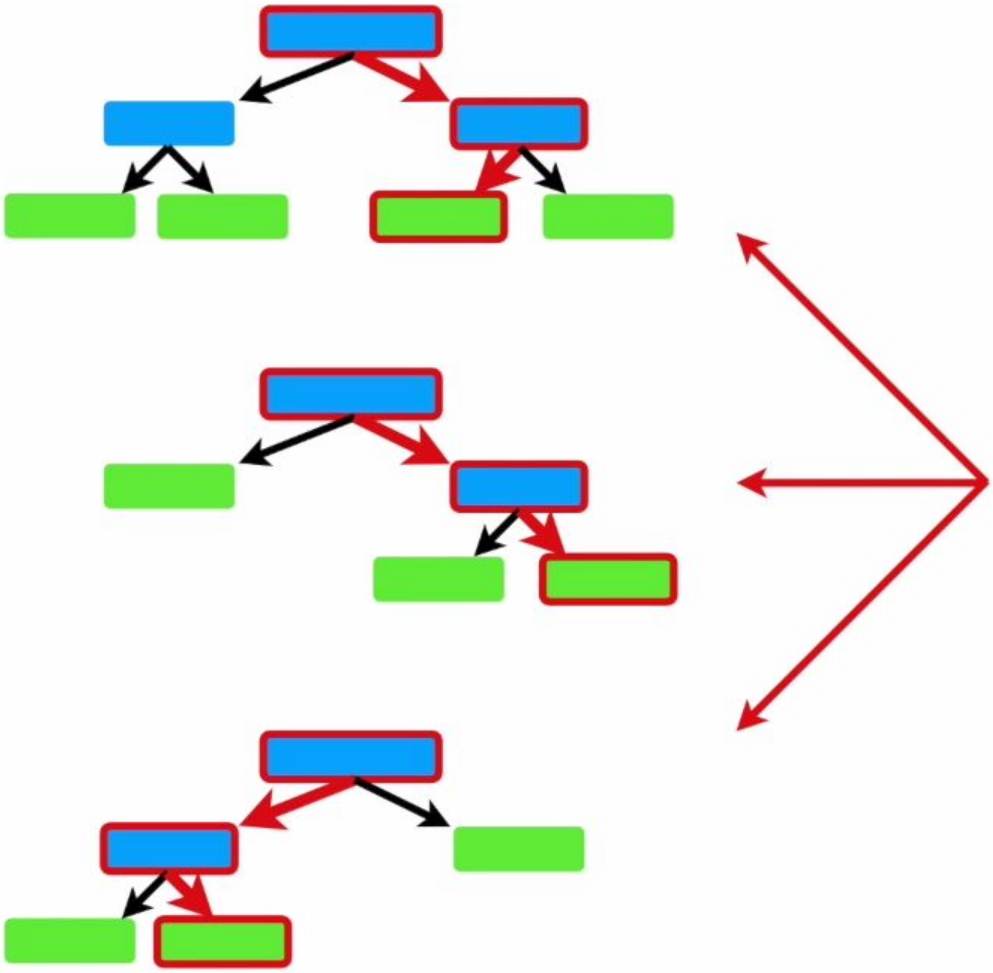


Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	Yes	No	210	No



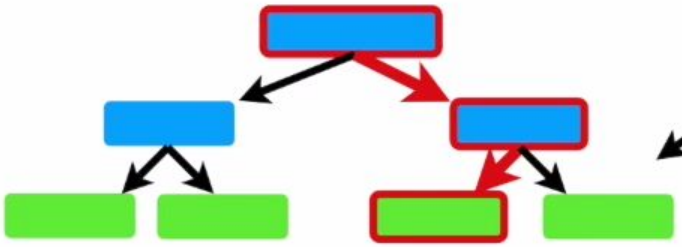
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	Yes	No	210	No

In this case, the tree correctly labels the Out-of-Bag sample "**No**".

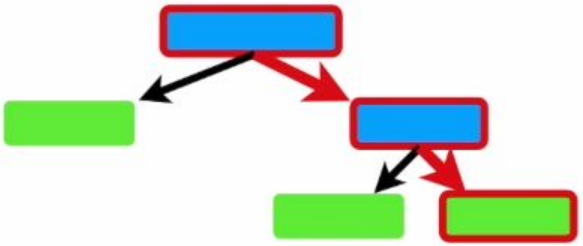


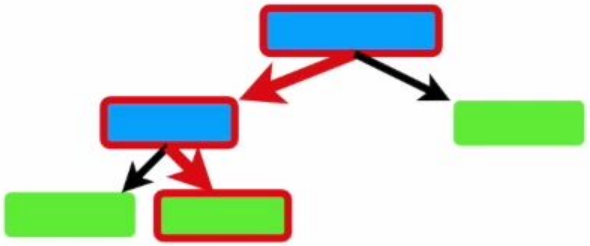
Then we run this Out-Of-Bag sample through all of the other trees that were built without it…

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

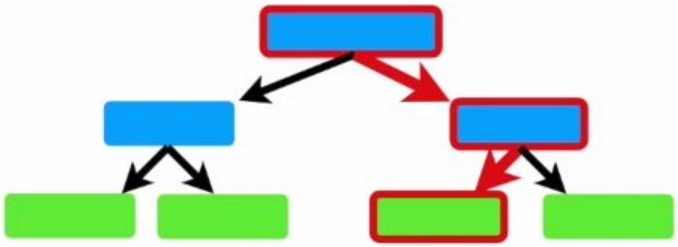


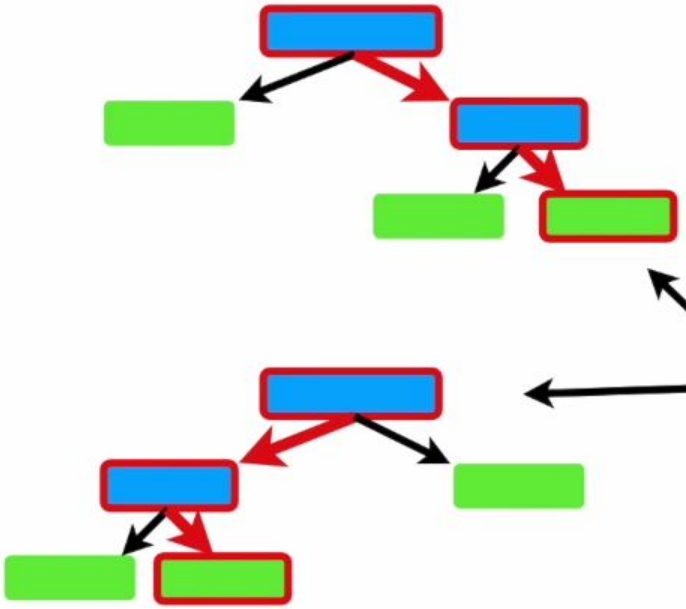
This tree incorrectly labeled the Out-of-Bag sample "**Yes**".





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





These trees correctly labeled the Out-of-Bag sample "**No**".

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

Classification of the Out-Of-Bag sample	
Yes	No
1	3

Since the label with the most votes wins, it is the label that we assign this Out-of-Bag sample.

In this case, the Out-of-Bag sample is correctly labeled by the Random Forest.

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

Classification of the Out-Of-Bag sample	
Yes	No
1	3

We then do the same thing for all of the other Out-Of-Bag samples for all of the trees.

Classification of the Out-Of-Bag sample	
Yes	No
1	3

Classification of the Out-Of-Bag sample	
Yes	No
4	0

Classification of the Out-Of-Bag sample	
Yes	No
3	1

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
No	No	No	125	No

This Out-of-Bag sample was *incorrectly* labeled…

Classification of the Out-Of-Bag sample	
Yes	No
1	3

Classification of the Out-Of-Bag sample	
Yes	No
4	0

Classification of the Out-Of-Bag sample	
Yes	No
3	1

etc… etc… etc…

Ultimately, we can measure how accurate our random forest is by the proportion of Out-Of-Bag samples that were correctly classified by the Random Forest.

The proportion of Out-Of-Bag samples that were *incorrectly* classified is the "**Out-Of-Bag Error**"

OK, we now know how to:

1) Build a Random Forest

2) Use a Random Forest

3) Estimate the accuracy of a Random Forest.

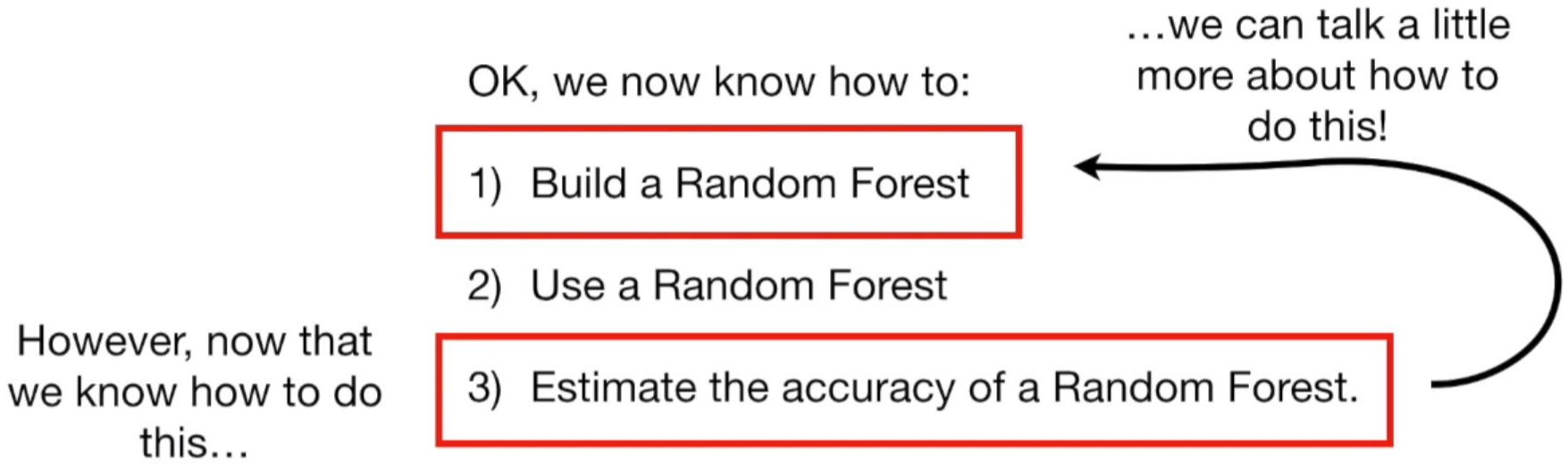
However, now that we know how to do this…

OK, we now know how to:

1) Build a Random Forest

2) Use a Random Forest

3) Estimate the accuracy of a Random Forest.


…we can talk a little more about how to do this!
OK, we now know how to:
1) Build a Random Forest
2) Use a Random Forest
However, now that we know how to do this…
3) Estimate the accuracy of a Random Forest.

Now we can compare the Out-Of-Bag error for a random forest built using only 2 variables per step…

Bootstrapped Dataset

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

…to random forest built using 3 variables per step…

Bootstrapped Dataset

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

…to random forest built using 3 variables per step…

…and we test a bunch of different settings and choose the most accurate random forest.

Bootstrapped Dataset

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

In other words…

…change the number of variables used per step…

1) Build a Random Forest

2) Estimate the accuracy of a Random Forest.

Do this for a bunch of times and then choose the one that is most accurate.

In other words…

…change the number of variables used per step…

1) Build a Random Forest

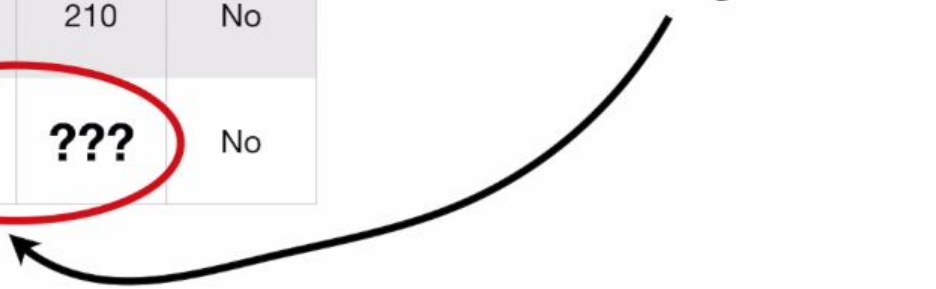
2) Estimate the accuracy of a Random Forest.

Typically, we start by using the root square of the number of variables and then try a few settings above and below that value.

Random Forest: Missing Data and sample clustering

Original Dataset

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	???	???	No

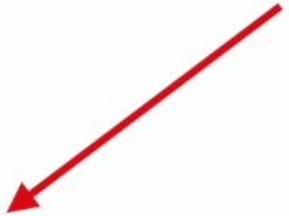


Original Dataset

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	???	???	No

Random Forests consider 2 types of missing data…

1) Missing data in the original dataset used to create the random forest.



Random Forests consider 2 types of missing data…

1) Missing data in the original dataset used to create the random forest.

2) Missing data in a new sample that you want to categorize.

Original Dataset

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	???	???	No

New Sample

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
No	No	No	???	

Original Dataset

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	???	???	No

Random Forests consider 2 types of missing data…

1) Missing data in the original dataset used to create the random forest.

We'll start with this one…

So we want to create a random forest from this data…

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	Yes	**???**	**???**	No

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	Yes	???	???	No

However, we don't know if this patient has blocked arteries or their weight.

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	Yes	???	???	No

The general idea for dealing with missing data in this context is to make an initial guess that could be bad, then gradually refine the guess until it is (hopefully) a good guess.

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	Yes	???	???	No

So the initial (possibly bad) guess for the blocked arteries value is just the most common value for “Blocked Arteries”.

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	Yes	???	???	No

"**No**" is the most common value for Blocked arteries - it occurs in 2 out of 3 samples.

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	Yes	**No**	???	No

← So "**No**" is our initial guess.

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	Yes	**No**	**???**	No

Since weight is numeric, our initial guess will be the median value.

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	Yes	No	180	No

In this case, the median value is 180

Filled-in Missing Values

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	Yes	**No**	**180**	No

Here's our new dataset with the filled in missing values…

Filled-in Missing Values

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	Yes	**No**	**180**	No

Now we want to refine these guesses.

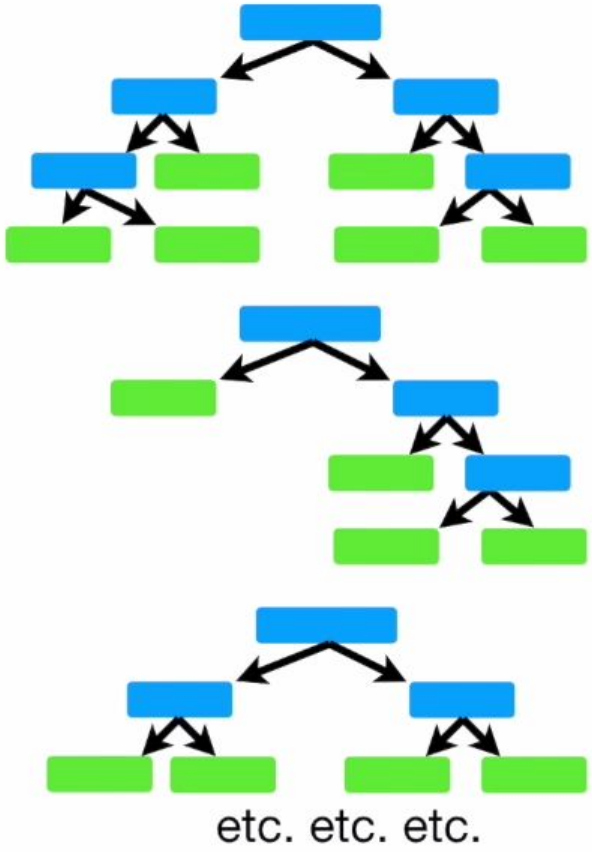
We do this by first determining which samples are similar to the one with missing data.

So let's talk about how to determine similarity…

Filled-in Missing Values

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	Yes	**No**	**180**	No

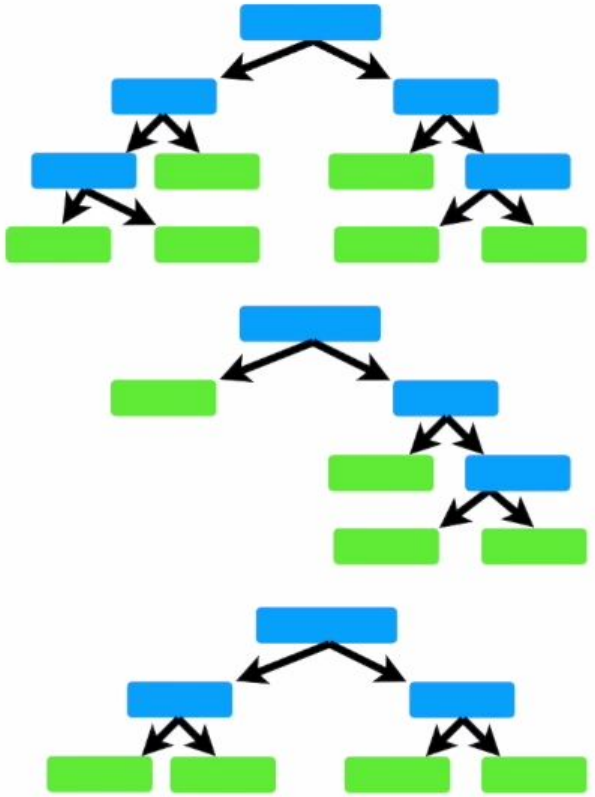
Step 1: Build a random forest…



Filled-in Missing Values

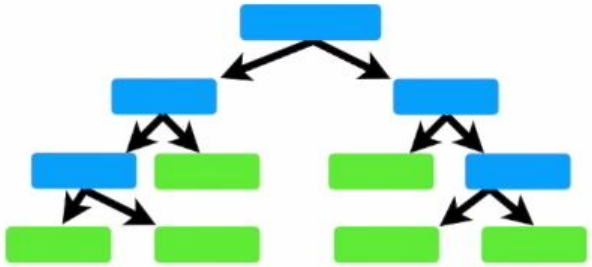
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
No	No	No	125	No
Yes	Yes	Yes	180	Yes
Yes	Yes	No	210	No
Yes	Yes	**No**	**180**	No

Step 2: Run all of the data down all of the trees.



Filled-in Missing Values

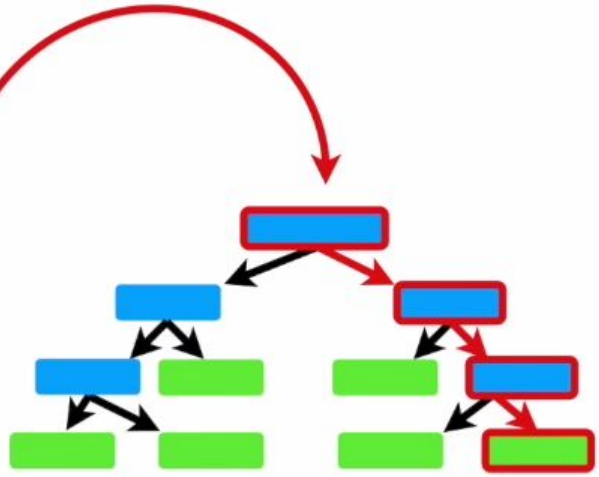
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
No	No	No	125	No
Yes	Yes	Yes	180	Yes
Yes	Yes	No	210	No
Yes	Yes	**No**	**180**	No



We'll start by running all of the data down the first tree.

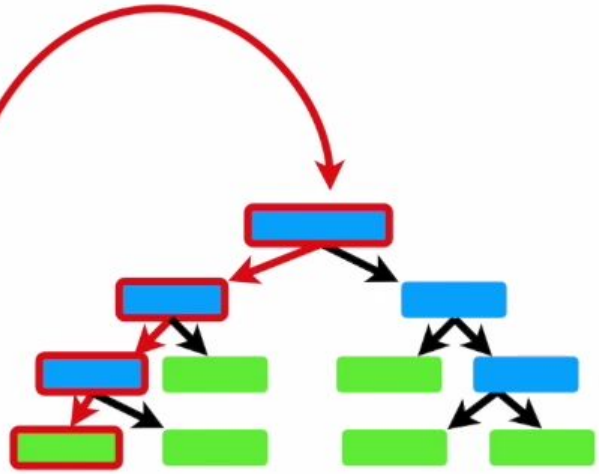
Filled-in Missing Values

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	Yes	**No**	**180**	No



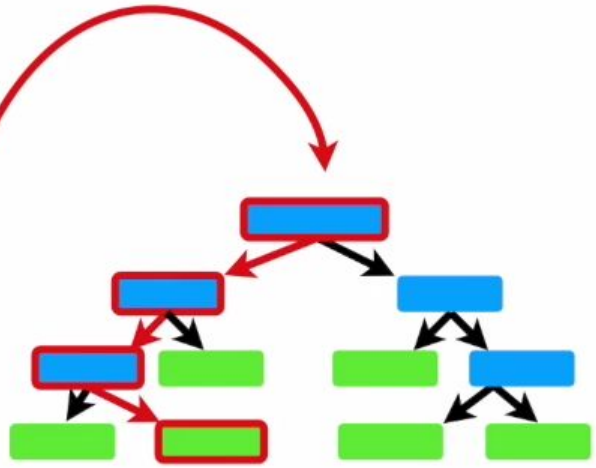
Filled-in Missing Values

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	Yes	**No**	**180**	No



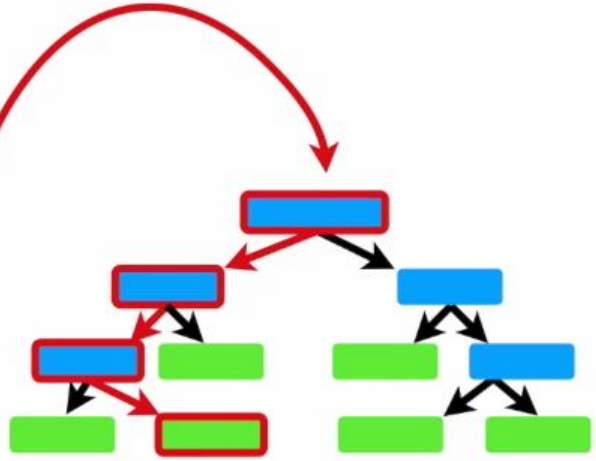
Filled-in Missing Values

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	Yes	**No**	**180**	No



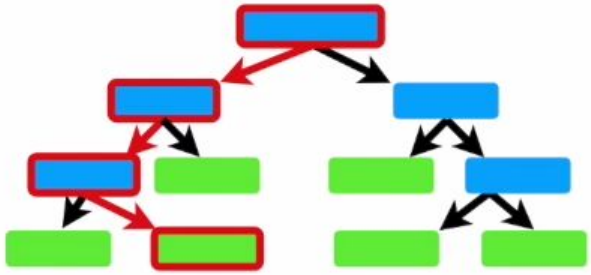
Filled-in Missing Values

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	Yes	**No**	**180**	No



Filled-in Missing Values

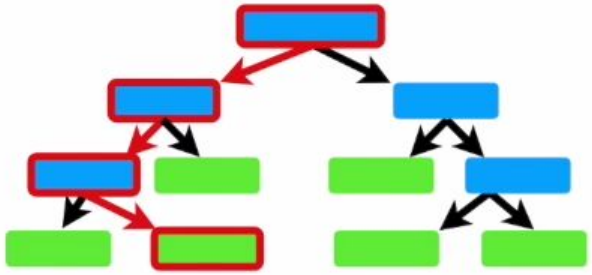
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
No	No	No	125	No
Yes	Yes	Yes	180	Yes
Yes	Yes	No	210	No
Yes	Yes	**No**	**180**	No



Notice that Sample 3 and Sample 4 both ended up at the same leaf node.

Filled-in Missing Values

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	Yes	**No**	**180**	No



That means they are similar.

Filled-in Missing Values

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	Yes	**No**	**180**	No

We keep track of similar samples using a "Proximity Matrix"

	1	2	3	4
1				
2				
3				
4				

Filled-in Missing Values

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	Yes	**No**	**180**	No

The proximity matrix has a row for each sample..

	1	2	3	4
1				
2				
3				
4				

Filled-in Missing Values

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	Yes	**No**	**180**	No

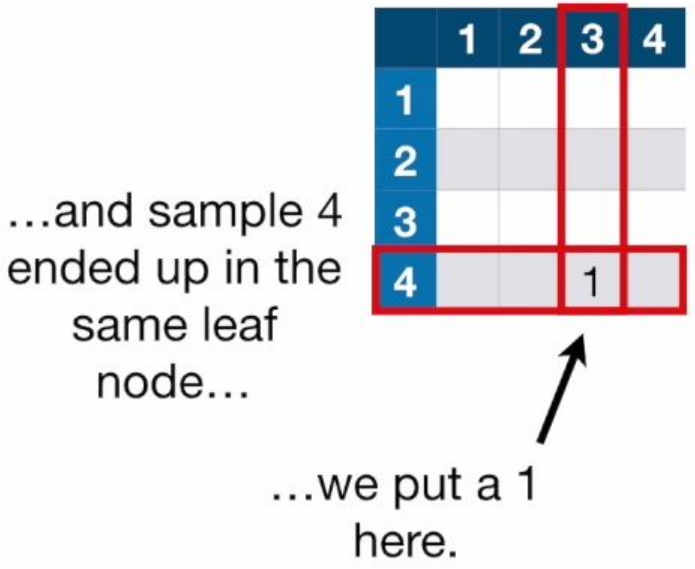
…and it has a column for each sample.

	1	2	3	4
1				
2				
3				
4				

Filled-in Missing Values

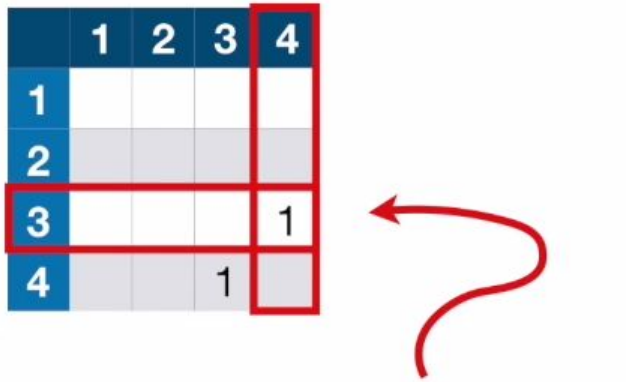
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
No	No	No	125	No
Yes	Yes	Yes	180	Yes
Yes	Yes	No	210	No
Yes	Yes	**No**	**180**	No

Because sample 3…



Filled-in Missing Values

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	Yes	**No**	**180**	No



We also put a 1 here, since this position also represents samples 3 and 4.

Filled-in Missing Values

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	Yes	**No**	**180**	No

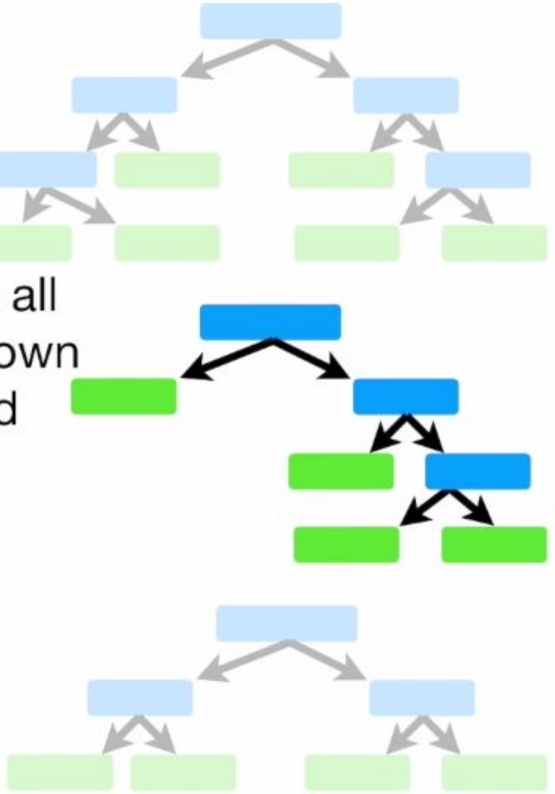
Because no other pair of samples ended in the same leaf node, our proximity matrix looks like this after running the samples down the first tree.

	1	2	3	4
1				
2				
3				1
4			1	

Filled-in Missing Values

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	Yes	**No**	**180**	No

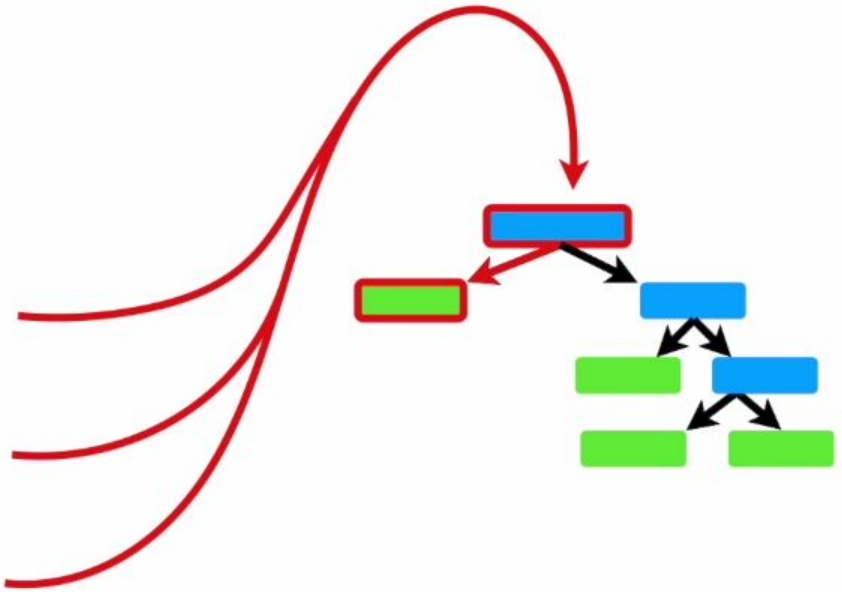
Now we run all of the data down the second tree…



Filled-in Missing Values

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	Yes	**No**	**180**	No

NOTE: Samples 2, 3 and 4 all ended up in the same leaf node.



Filled-in Missing Values

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	Yes	**No**	**180**	No

This is what the proximity matrix looked like after running the data down the first tree…

	1	2	3	4
1				
2				
3				1
4			1	

Filled-in Missing Values

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	Yes	**No**	**180**	No

…after the second tree, we add 1 to any pair of samples that ended up in the same leaf node.

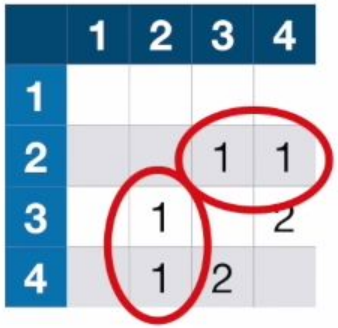
	1	2	3	4
1				
2			1	1
3		1		2
4		1	2	

Samples 3 and 4 ended up in the same node together again…

Filled-in Missing Values

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	Yes	**No**	**180**	No

…after the second tree, we add 1 to any pair of samples that ended up in the same leaf node.



Sample 2 also ended up in that same node.

Filled-in Missing Values

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	Yes	**No**	**180**	No

Ultimately, we run the data down all the trees and the proximity matrix fills in.

	1	2	3	4
1		2	1	1
2	2		1	1
3	1	1		8
4	1	1	8	

Filled-in Missing Values

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	Yes	**No**	**180**	No

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

Then we divide each proximity value by the total number of trees. In this example, assume we had 10 trees.

Filled-in Missing Values

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	Yes	???	???	No

Now we use the proximity values for sample 4 to make better guesses about the missing data.

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

Filled-in Missing Values

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	Yes	???	???	No

For Blocked Arteries, we calculate the weighted frequency of "Yes" and "No, using proximity values as the weights.

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

Filled-in Missing Values

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	Yes	???	???	No

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

Filled-in Missing Values

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	Yes	???	???	No

Yes = 1/3

No = 2/3

The frequency of “No”.

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

Filled-in Missing Values

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	Yes	**???**	???	No

The weighted frequency for **"Yes"** is…

$$\text{Yes} = \frac{1}{3} \times \text{The weight for "Yes"}$$

Yes = 1/3

No = 2/3

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

The weight for "Yes" =

$$\frac{\text{Proximity of "Yes"}}{\text{All Proximities}}$$

Filled-in Missing Values

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	Yes	**???**	???	No

The weighted frequency for **"Yes"** is…

Yes = $\frac{1}{3}$ x The weight for **"Yes"**

Yes = 1/3

No = 2/3

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

The weight for "Yes" = 0.1

The proximity value for Sample 2 (the only one with "Yes")

Filled-in Missing Values

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	Yes	**???**	???	No

The weighted frequency for **"Yes"** is…

$$\text{Yes} = \frac{1}{3} \times 0.1$$

Yes = 1/3

No = 2/3

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

The weight for "Yes" =

$$\frac{0.1}{0.1 + 0.1 + 0.8} = \frac{0.1}{1} = 0.1$$

Filled-in Missing Values

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	Yes	???	???	No

The weighted frequency for **"Yes"** is…

Yes = $\frac{1}{3}$ x 0.1 = 0.03

The weighted frequency for "**Yes**".

Yes = 1/3

No = 2/3

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

Filled-in Missing Values

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	Yes	**???**	???	No

The weighted frequency for **"No"** is…

Yes = $\frac{1}{3}$ x 0.1 = 0.03

No = $\frac{2}{3}$ x 0.9 =

Yes = 1/3

No = 2/3

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

The weight for "No" = $\frac{0.1 + 0.8}{0.1 + 0.1 + 0.8} = \frac{0.9}{1} = 0.9$

Filled-in Missing Values

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	Yes	???	???	No

The weighted frequency for **"No"** is…

Yes = 1/3

No = 2/3

$$\text{Yes} = \frac{1}{3} \times 0.1 = 0.03$$

$$\text{No} = \frac{2}{3} \times 0.9 = 0.6$$

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

Filled-in Missing Values

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	Yes	**NO**	???	No

The weighted frequency for **"No"** is…

Yes = 1/3

No = 2/3

$$\text{Yes} = \frac{1}{3} \times 0.1 = 0.03$$

$$\text{No} = \frac{2}{3} \times 0.9 = 0.6$$

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

"No" has a way higher weighted frequency, so we'll go with it.

Filled-in Missing Values

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	Yes	NO	???	No

For weight, we use the proximities to calculate a weighted average.

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

Weighted average = 125 x Sample 1's weighted average weight…

Filled-in Missing Values

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	Yes	NO	???	No

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

Weighted average = 125 x Sample 1's weighted average weight…

0.1

The proximity for Sample 1

Filled-in Missing Values

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	Yes	NO	???	No

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

Weighted average = 125 x $\frac{\text{Sample 1's weighted average weight...}}{0.1 + 0.1 + 0.8}$

Divided by the sum of the proximities.

Filled-in Missing Values

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	Yes	NO	???	No

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

Weighted average = 125 x 0.1

$$\frac{0.1}{0.1 + 0.1 + 0.8} = \frac{0.1}{1} = 0.1$$

Filled-in Missing Values

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	Yes	NO	???	No

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

Weighted average = (125 x 0.1) + (180 x 0.1) + (210 x 0.8)

= 198.5

Filled-in Missing Values

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	Yes	NO	???	No

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

Weighted average = (125 x 0.1) + (180 x 0.1) + (210 x 0.8)

= 198.5

Filled-in Missing Values

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	Yes	**NO**	**198.5**	No

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

The weighted average weight!

Filled-in Missing Values

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	Yes	**NO**	**198.5**	No

Now that we've revised our guesses a little bit, we do the whole thing over again…

We build a random forest, run the data through the trees, recalculate the proximities and recalculate the missing values.

We do this 6 or 7 times until the missing values converge (i.e. no longer change each time we recalculate).

Let me show you something super cool
we can do with the proximity matrix!!!

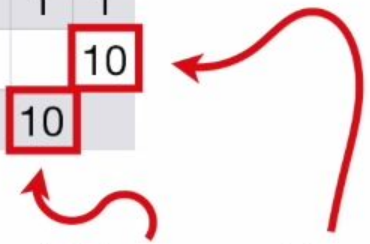
	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		0.8
4	0.1	0.1	0.8	

This is the proximity matrix before we divided each value by 10, the number of trees in the pretend random forest.

	1	2	3	4
1		2	1	1
2	2		1	1
3	1	1		8
4	1	1	8	

Just for the sake of easy math, imagine if Samples 3 and 4 ended up in the same leaf node in all 10 trees.

	1	2	3	4
1		2	1	1
2	2		1	1
3	1	1		10
4	1	1	10	



Now we have 10 here and here…

After dividing by 10 (the number of trees in the forest), we see that the largest number in the proximity matrix is 1.

	1	2	3	4
1		2	1	1
2	2		1	1
3	1	1		10
4	1	1	10	

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		1
4	0.1	0.1	1	

1 in the proximity matrix means the samples are as close as close can be.

	1	2	3	4
1		2	1	1
2	2		1	1
3	1	1		10
4	1	1	10	

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		1
4	0.1	0.1	1	

	1	2	3	4
1		2	1	1
2	2		1	1
3	1	1		10
4	1	1	10	

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		1
4	0.1	0.1	1	

That means…
1 - the proximity values
= ???

	1	2	3	4
1		0.8	0.9	0.9
2	0.8		0.9	0.9
3	0.9	0.9		0
4	0.9	0.9	0	

	1	2	3	4
1		2	1	1
2	2		1	1
3	1	1		10
4	1	1	10	

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		1
4	0.1	0.1	1	

That means…
1 - the proximity values
= distance

	1	2	3	4
1		0.8	0.9	0.9
2	0.8		0.9	0.9
3	0.9	0.9		0
4	0.9	0.9	0	

	1	2	3	4
1		2	1	1
2	2		1	1
3	1	1		10
4	1	1	10	

	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		1
4	0.1	0.1	1	

That means…
1 - the proximity values
= distance

	1	2	3	4
1		0.8	0.9	0.9
2	0.8		0.9	0.9
3	0.9	0.9		0
4	0.9	0.9	0	

Close as can be = no distance between.

	1	2	3	4
1		2	1	1
2	2		1	1
3	1	1		10
4	1	1	10	

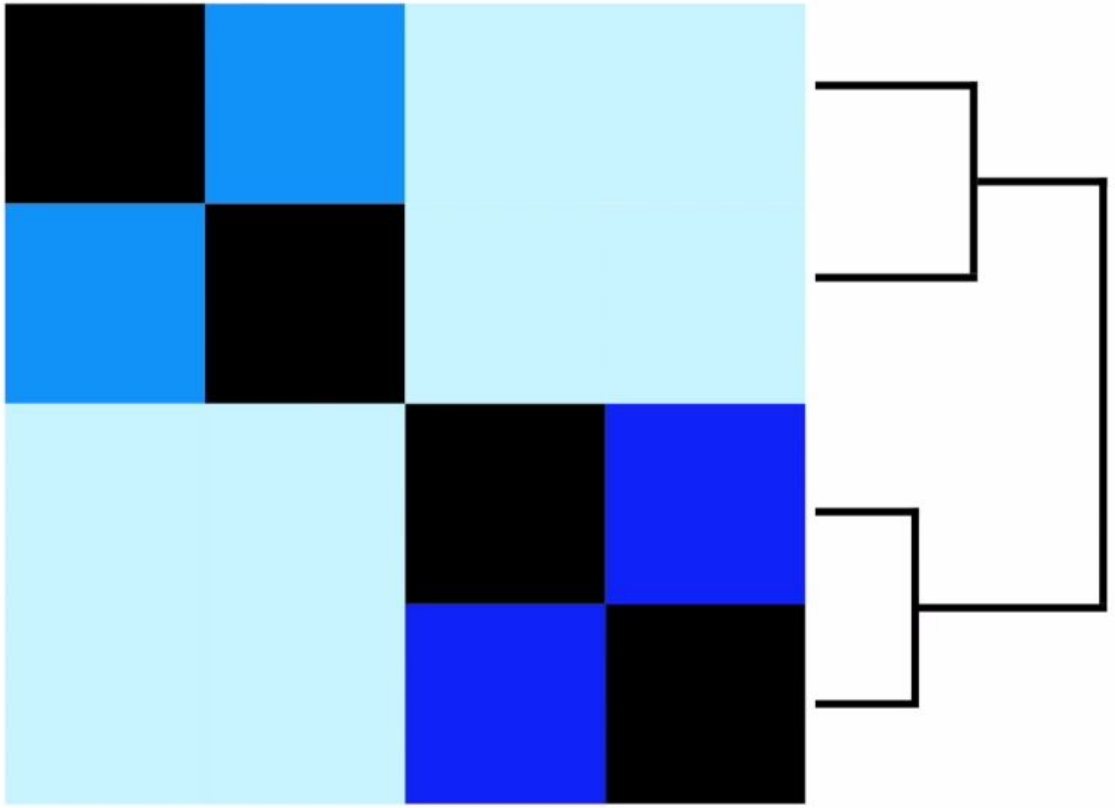
	1	2	3	4
1		0.2	0.1	0.1
2	0.2		0.1	0.1
3	0.1	0.1		1
4	0.1	0.1	1	

That means…
1 - the proximity values
= distance

	1	2	3	4
1		0.8	0.9	0.9
2	0.8		0.9	0.9
3	0.9	0.9		0
4	0.9	0.9	0	

Not close = far away

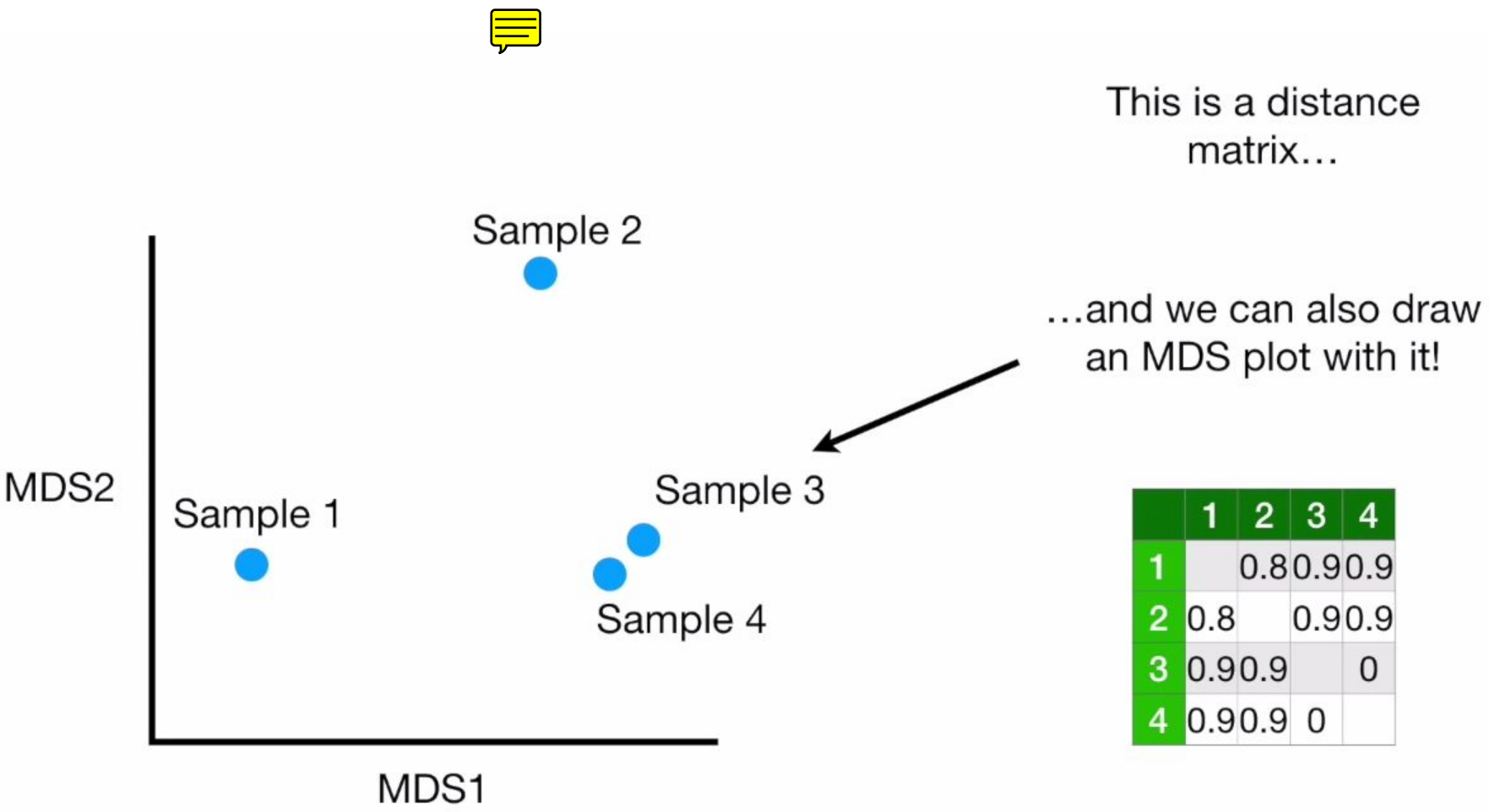
Sample 1 Sample 2 Sample 3 Sample 4



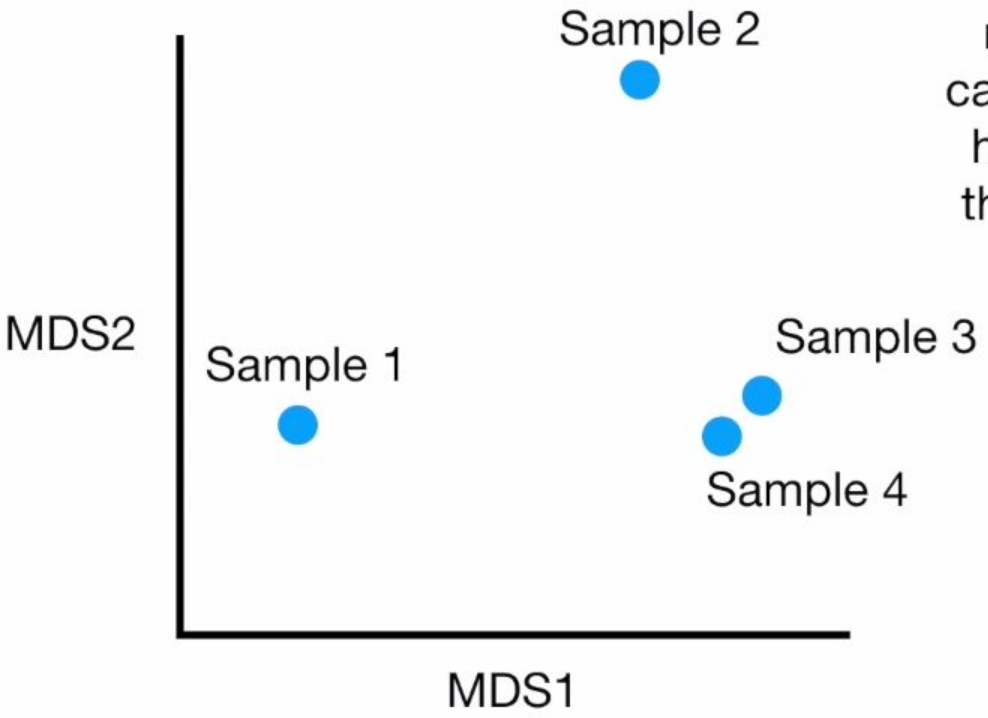
This is a distance matrix…

…and that means we can draw a heatmap with it!!!

	1	2	3	4
1		0.8	0.9	0.9
2	0.8		0.9	0.9
3	0.9	0.9		0
4	0.9	0.9	0	



	1	2	3	4
1		0.8	0.9	0.9
2	0.8		0.9	0.9
3	0.9	0.9		0
4	0.9	0.9	0	



This is super cool because it means that no matter what the data are (ranks, multiple choice, numeric, etc)… if we can use it to make a tree, we can draw a heatmap or an MDS plot to show how the samples are related to each other!!!

	1	2	3	4
1		0.8	0.9	0.9
2	0.8		0.9	0.9
3	0.9	0.9		0
4	0.9	0.9	0	

Back to the missing data

At long last, we'll talk about the second method!

Random Forests consider 2 types of missing data…

1) Missing data in the original dataset used to create the random forest.

2) Missing data in a new sample that you want to categorize.

New Sample

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
No	No	No	???	

Imagine we had already built a Random Forest with existing data and wanted to classify this new patient.

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	???	168	

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	???	168	

So we want to know if they have heart disease or not…

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	???	168	

…but we don't know if they have blocked arteries…

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	???	168	

…so we need to make a guess about Blocked Arteries so we can run the patient down all the trees in the forest.

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	???	168	YES

The first thing we do is create two copies of the data, one that has heart disease…

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	???	168	NO

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	???	168	YES

…and one that doesn't have heart disease.

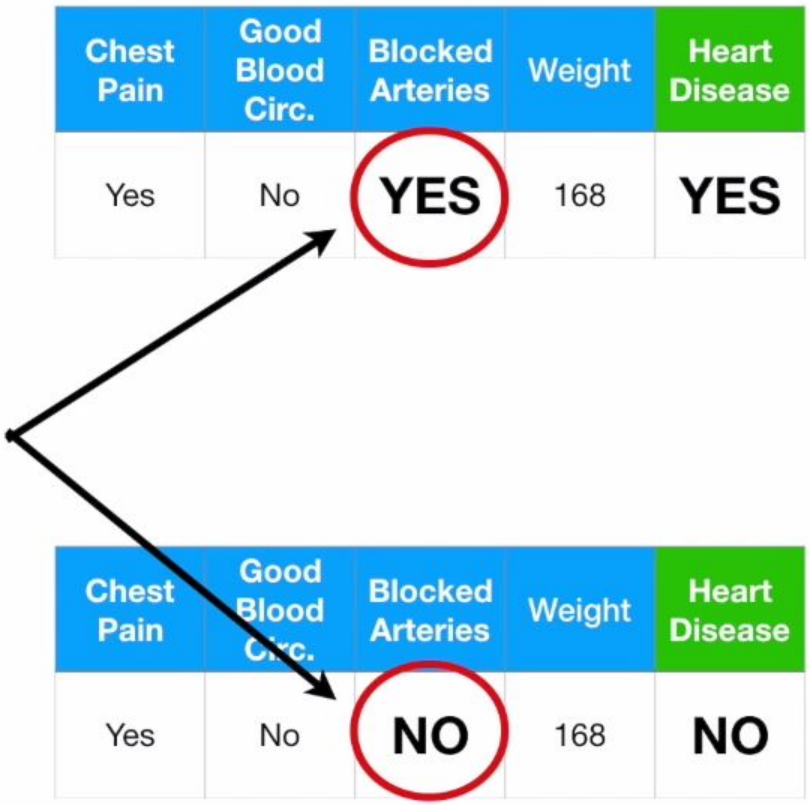
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	???	168	NO

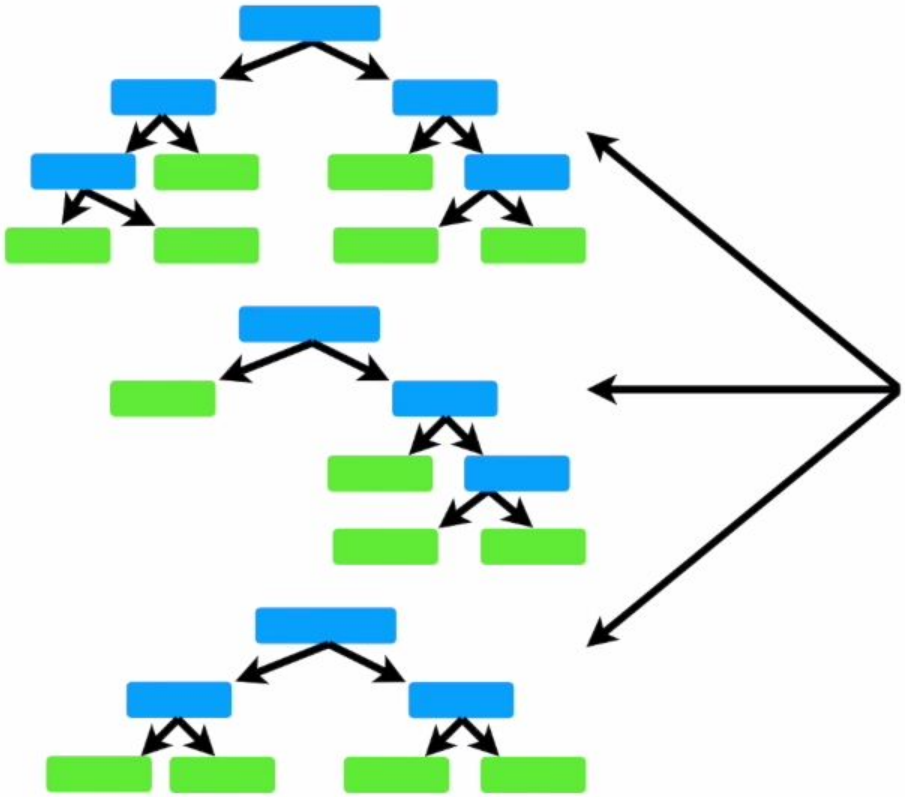
Then we use the iterative method we just talked about to make a good guess about the missing values.

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	???	168	YES

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	???	168	NO

Then we use the iterative method we just talked about to make a good guess about the missing values.

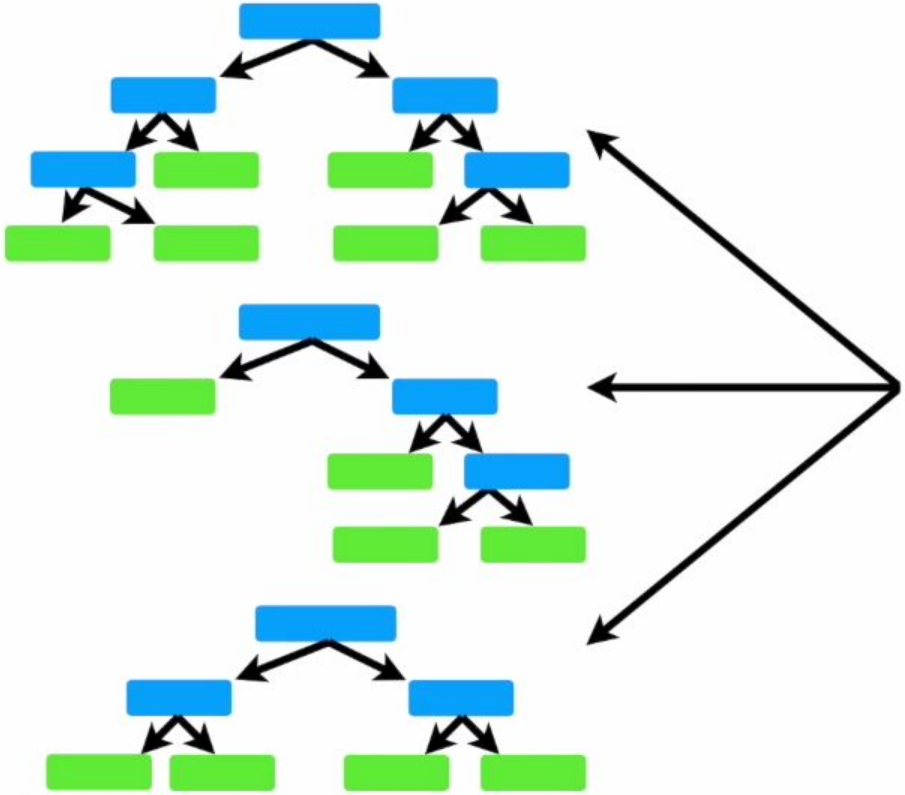




Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	YES	168	YES

Then we run the two samples down the trees in the forest…

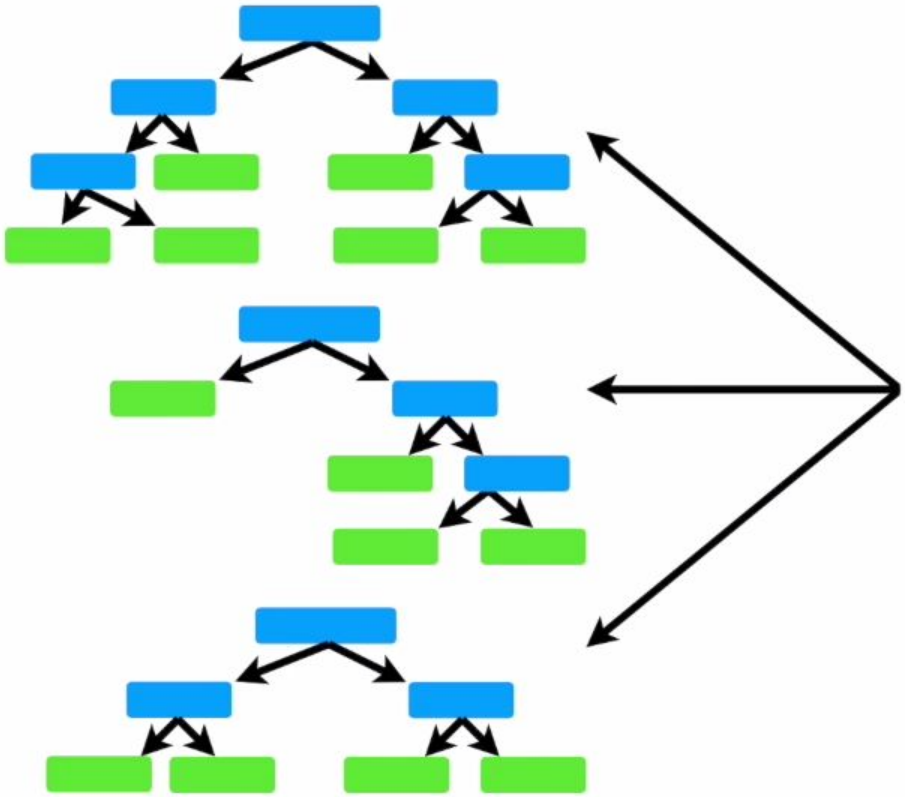
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	NO	168	NO



Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	YES	168	YES

…and we see which of the two is correctly labeled by the random forest the most times.

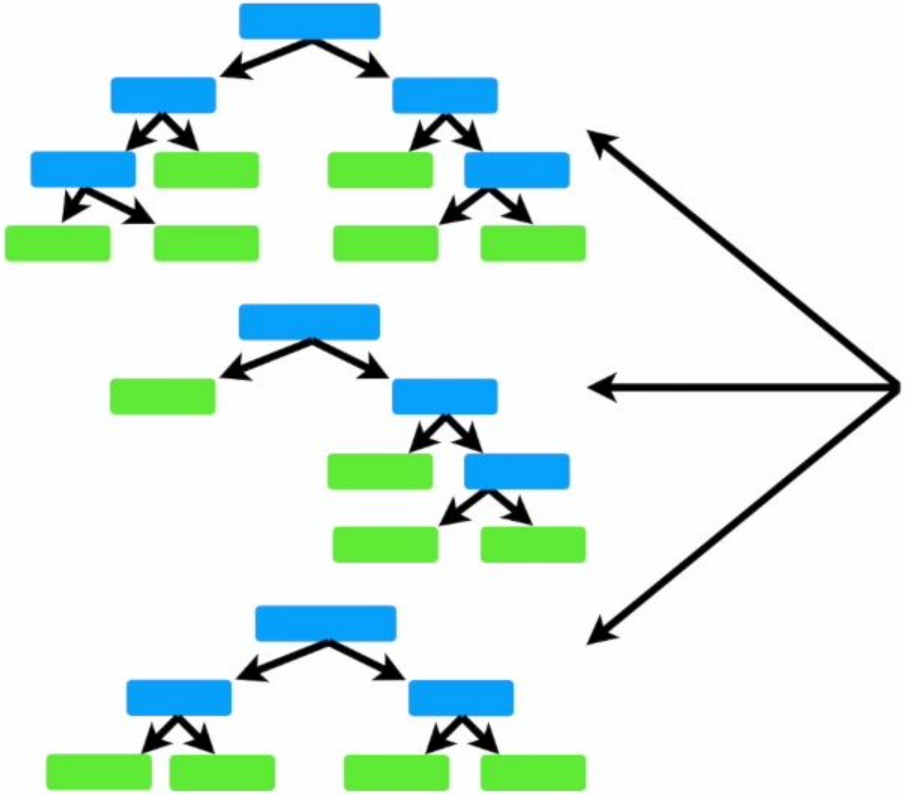
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	NO	168	NO



Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	YES	168	YES

Then we run the two samples down the trees in the forest…

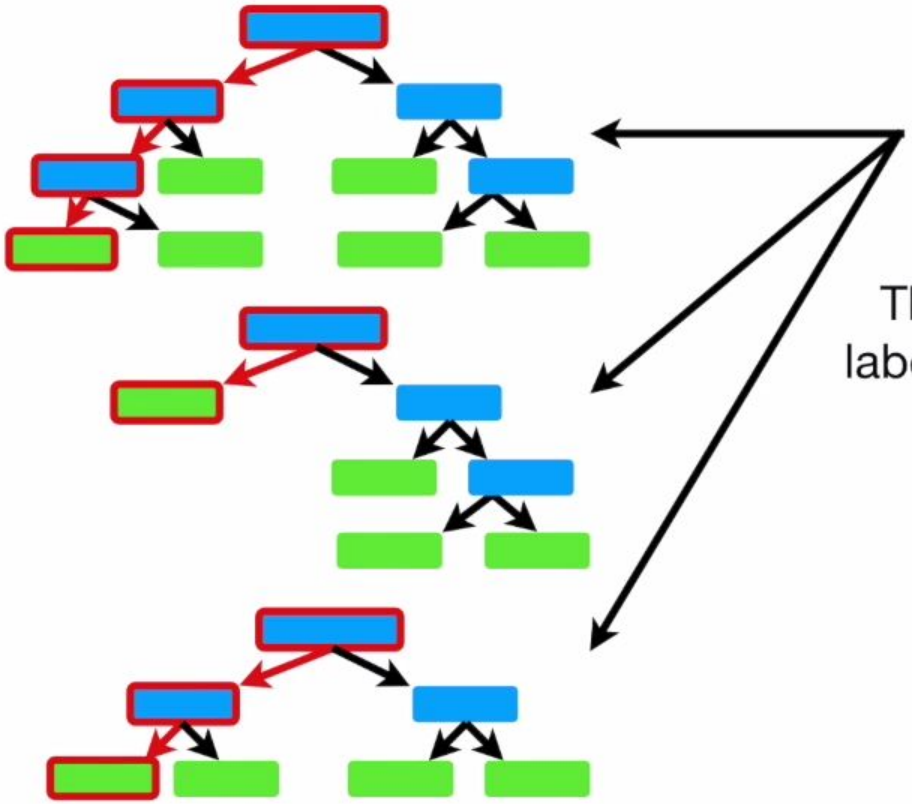
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	NO	168	NO



Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	YES	168	YES

…and we see which of the two is correctly labeled by the random forest the most times.

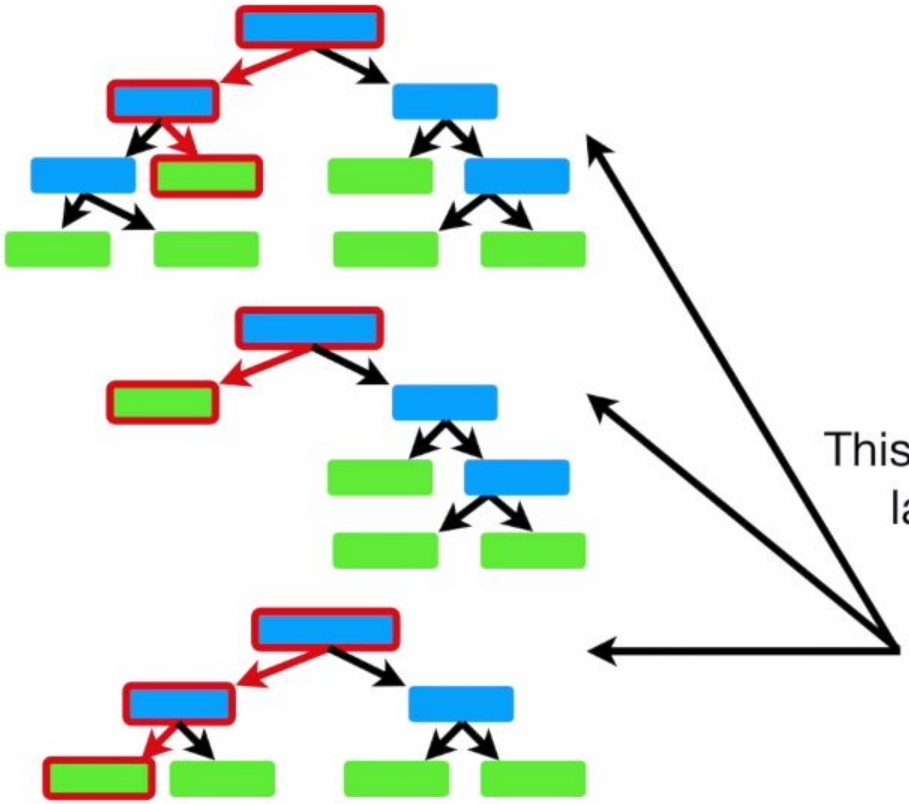
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	NO	168	NO



Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	**YES**	168	**YES**

This option was correctly labeled "**Yes**" in all 3 trees…

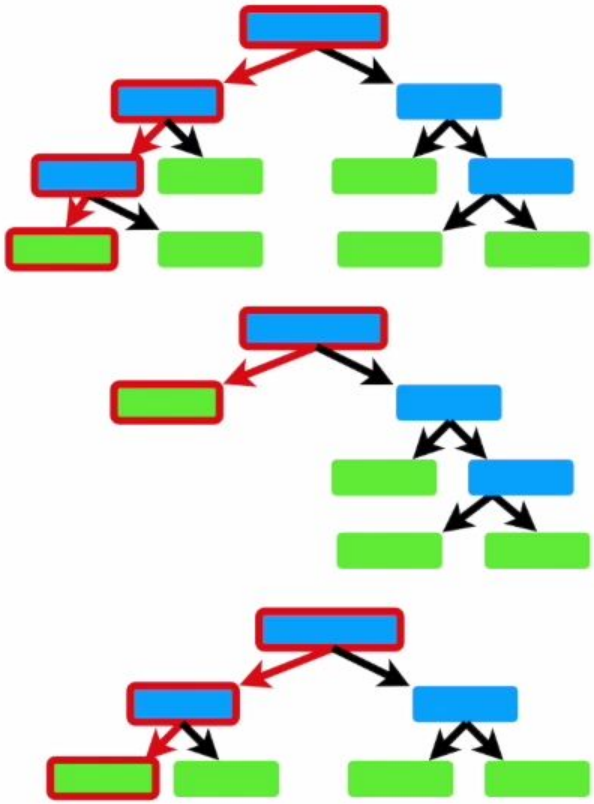
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	**NO**	168	**NO**



Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	**YES**	168	**YES**

This option was only correctly labeled "**No**" in 1 tree…

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	**NO**	168	**NO**



Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	**YES**	168	**YES**

This option wins because it was correctly labeled more than the other option.

Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	**NO**	168	**NO**

The end