Machine Learning Basis

Random Forests

05/01/2020

傳統統計方法最常被用來解決的問題

- **Group difference (比較: 不同組群的組別差異)**

-- diseased vs. healthy control subjects

(group factor: disease)

-- elder vs. younger subjects

(group factor: age)

… etc.

- **Correlation (相關性, 自變數”independent variable”與應變數”dependent variable”之間的關係式)**

--身高= a*體重+b

-- blood T1 = 1817 − 8.2*age − 37.4*sex (sex: male=1, female=0)

… etc.

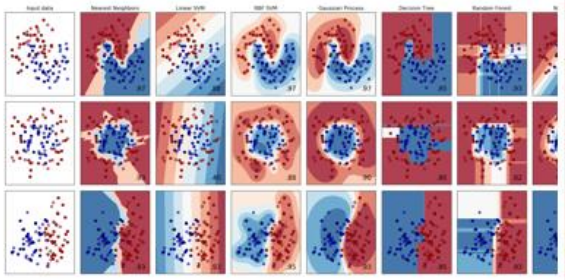
Machine Learning

- 監督式學習（Supervised learning）
  - 分類（Classification）
    Group difference
  - 迴歸（Regression）
    Correlation/ Group difference
- 非監督式學習（Unsupervised learning）
  - 分群（Clustering）
    Group difference

Classification

Identifying which category an object belongs to.

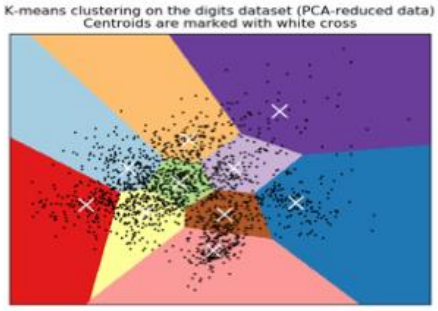
Applications: Spam detection, image recognition.
Algorithms: SVM, nearest neighbors, random forest, and more...



Clustering

Automatic grouping of similar objects into sets.

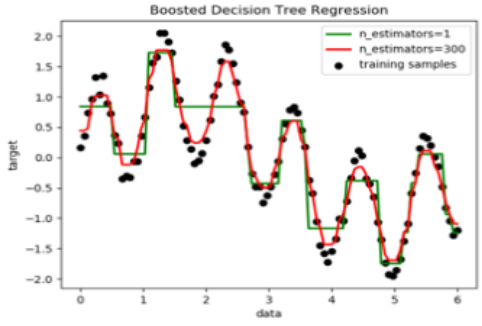
Applications: Customer segmentation, Grouping experiment outcomes
Algorithms: k-Means, spectral clustering, mean-shift, and more...



Regression

Predicting a continuous-valued attribute associated with an object.

Applications: Drug response, Stock prices.
Algorithms: SVR, nearest neighbors, random forest, and more...



https://scikit-learn.org/stable/index.html

Machine Learning Algorithms
常見的演算法

- Random forest (Heather)
- SVM (support vector machine, 支撐向量機) (CK)
- k-nearest neighbors (Charles)
- k-means (Danny)
- Regression

-- linear regression, multiple regression, logistic regression (姝儀+郁慈)

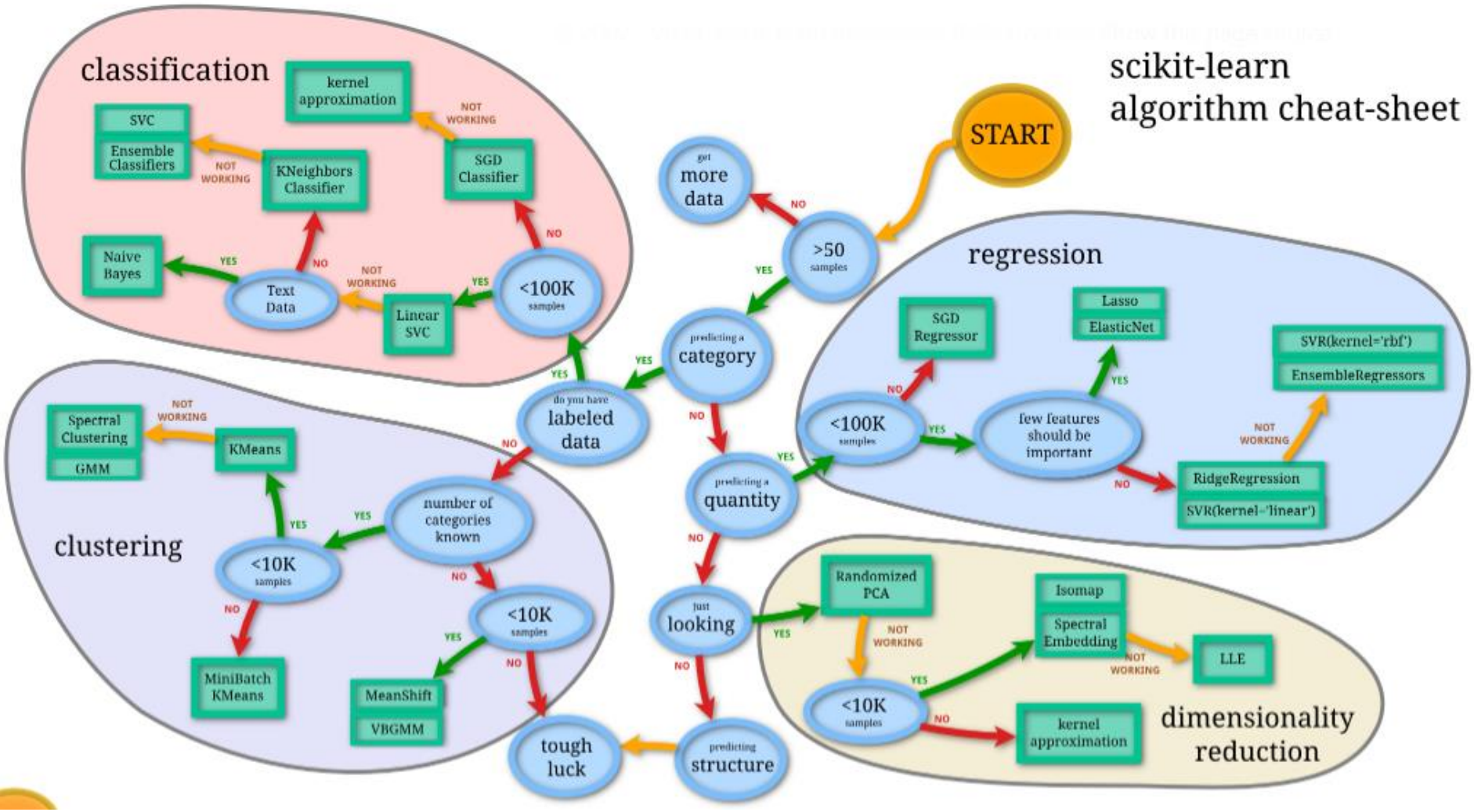
-- PCA (Principal Component Analysis, 主成分分析) (Larry)

- CNN (Convolutional Neural Network)
- AdaBoost
- Gradient Boosting
- Naive Bayes
- LDA
- QDA
- RBMs
- …

Requirements for your presentations in leading the Discussion

- PPT files
- References for everyone

Machine Learning Map

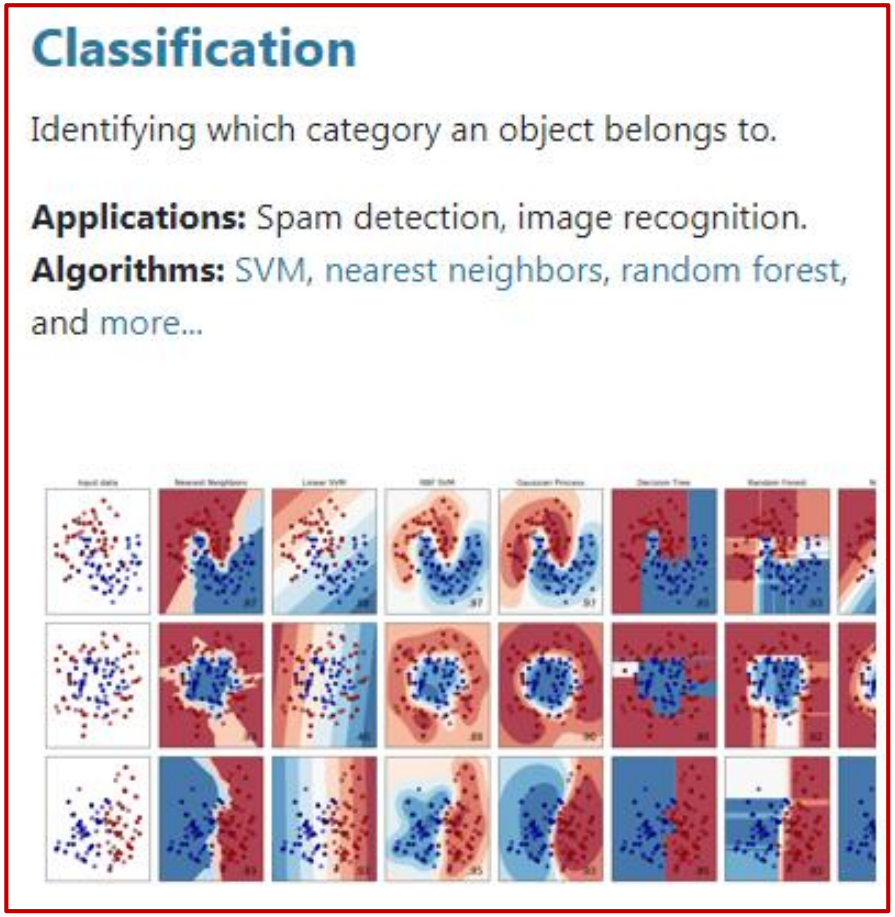


https://scikit-learn.org/stable/tutorial/machine_learning_map/

Machine Learning Algorithms in Classification

Classifiers

- SVM (Support Vector Machine)
- k-nearest neighbors
- Random Forest
- AdaBoost Classifier
- Gradient Boosting
- Naive Bayes
- LDA
- QDA
- RBMs
- Logistic Regression
- RBM + Logistic Regression Classifier
- CNN (Convolutional Neural Network)
- …



https://martin-thoma.com/comparing-classifiers/

Machine Learning Algorithms in Regression

Regression algorithms

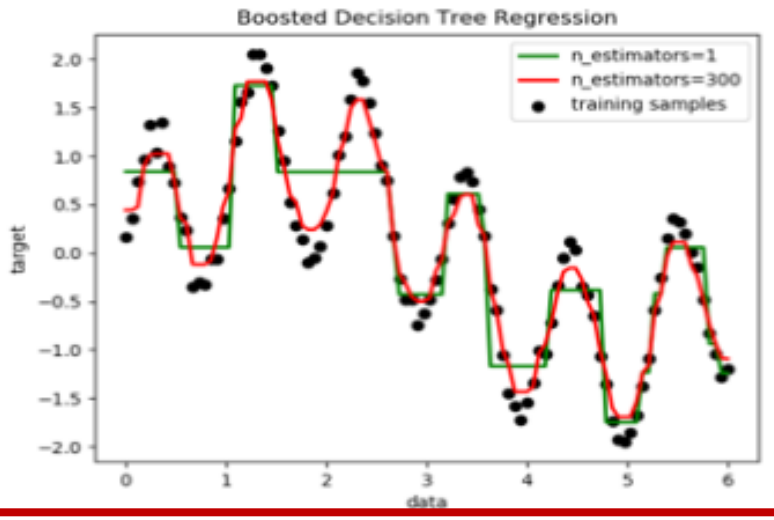
- SVM (Support Vector Machine)
- k-nearest neighbors
- Random Forest
- SVR
- LASSO
- RBMs
- Logistic Regression
- RBM + Logistic Regression Classifier
- CNN (Convolutional Neural Network)
- …

Regression

Predicting a continuous-valued attribute associated with an object.

Applications: Drug response, Stock prices.

Algorithms: SVR, nearest neighbors, random forest, and more...



https://scikit-learn.org/stable/index.html

Machine Learning Algorithms in Clustering

Clustering methods

- K-means (FCM)
- Affinity propagation
- Mean-shift
- Spectral clustering
- Ward hierarchical clustering
- Agglomerative clustering
- DBSCAN
- OPTICS
- Gaussian mixtures
- Birch

MRI 常用: imaging segmentation

Clustering

Automatic grouping of similar objects into sets.

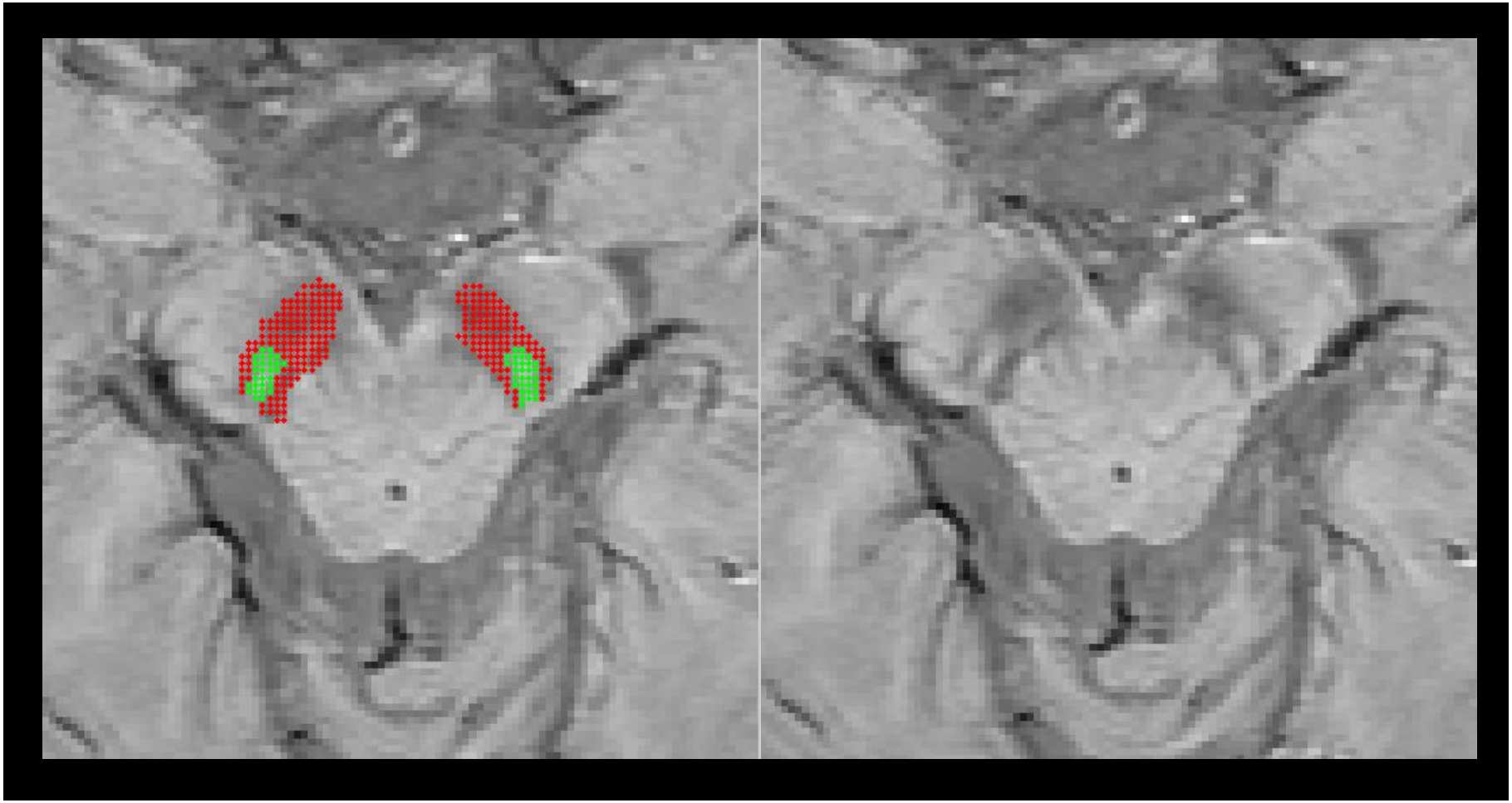
Applications: Customer segmentation, Grouping experiment outcomes

Algorithms: k-Means, spectral clustering, mean-shift, and more...

https://scikit-learn.org/stable/modules/clustering.html#clustering

https://scikit-learn.org/stable/index.html

FCM (fuzzy-cluster mean) in Nigrosome-1 segmentation



Random Forests Algorithm

Random Forests Algorithm

Main references

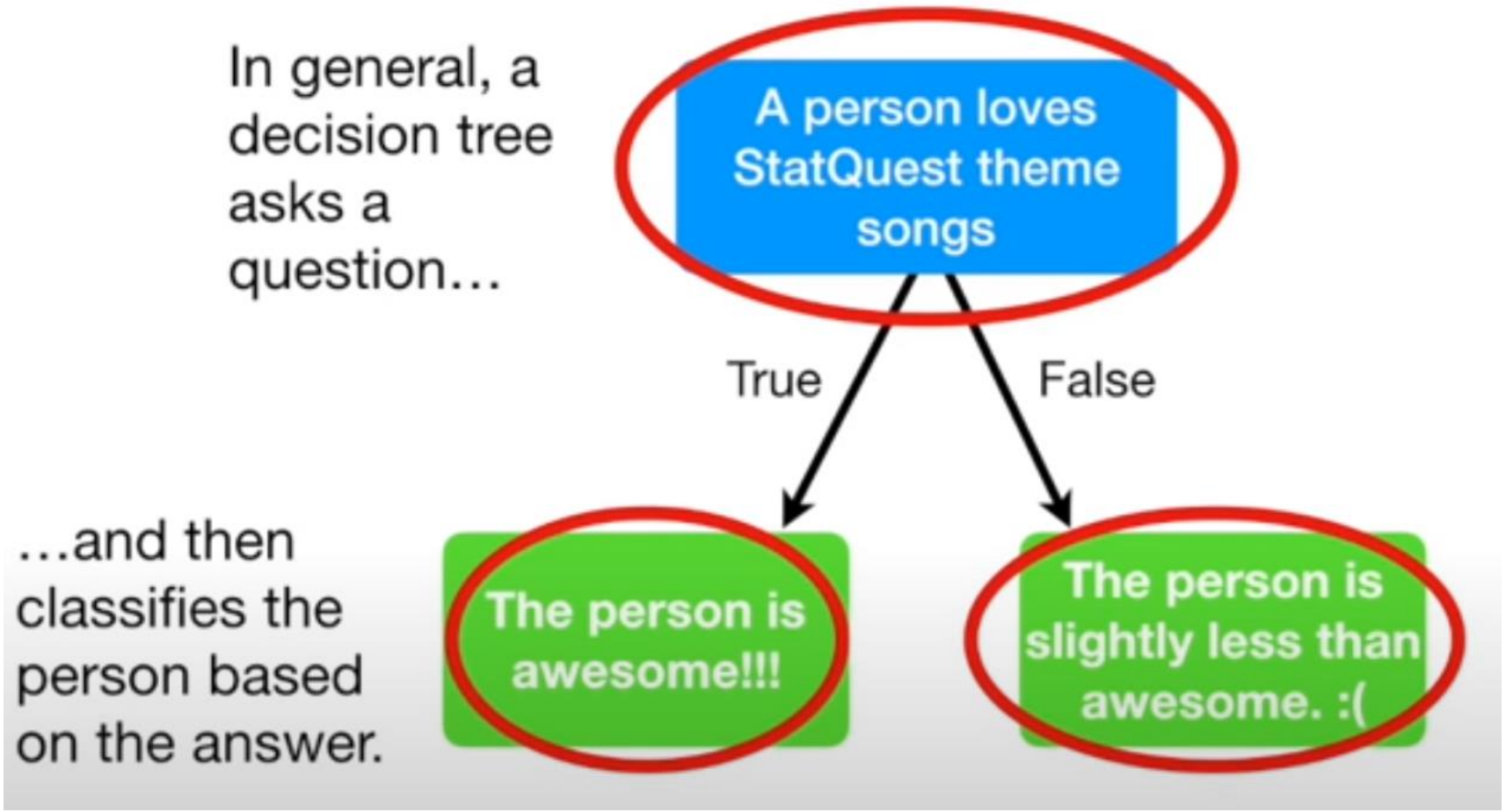
https://www.youtube.com/watch?v=7VeUPuFGJHk

https://www.youtube.com/watch?v=J4Wdy0Wc_xQ

Outline

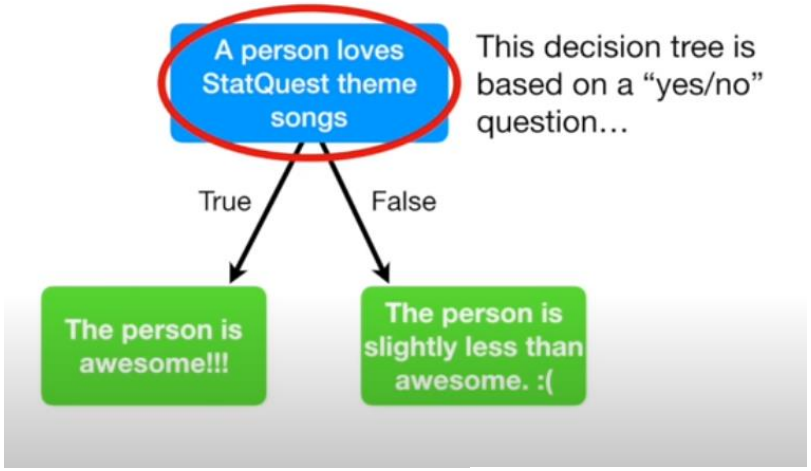
- Decision trees
- Random Forests
  - Classification
  - Regression
- Performance Scores
- Examples:
  - *Magnetic resonance perfusion image features uncover an angiogenic subgroup of glioblastoma patients with poor survival and better response to antiangiogenic treatment (Liu et al., Neuro-Oncology 2016)*
  - *Prediction of Core Signaling Pathway by Using Diffusion- and Perfusion-based MRI Radiomics and Next-generation Sequencing in Isocitrate Dehydrogenase Wild-type Glioblastoma (Park et al., Radiology 2020)*

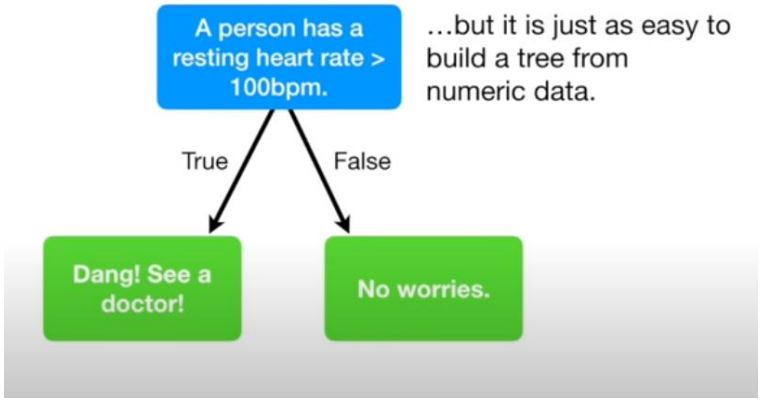
Decision trees:
ask a question, then classifies the answer

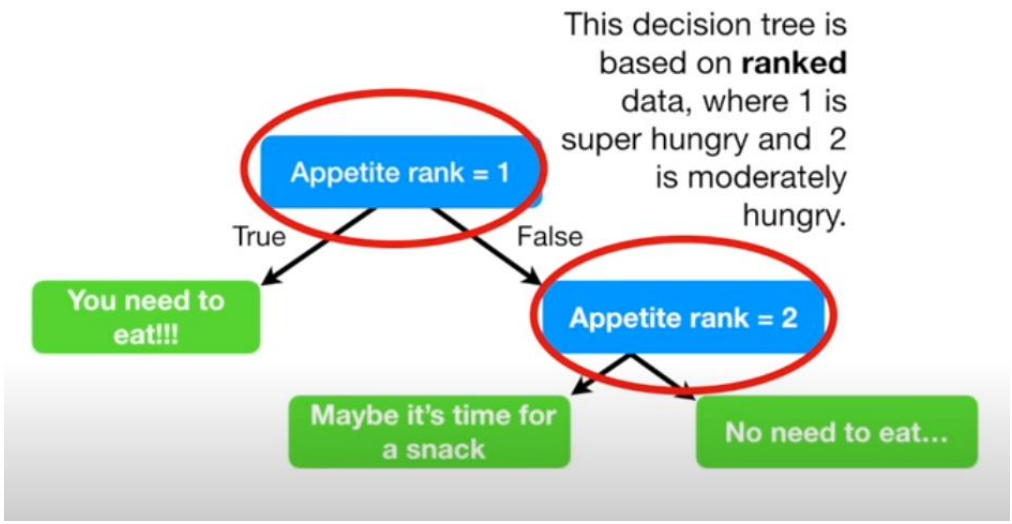


https://www.youtube.com/watch?v=7VeUPuFGJHk

Decision trees: types of questions

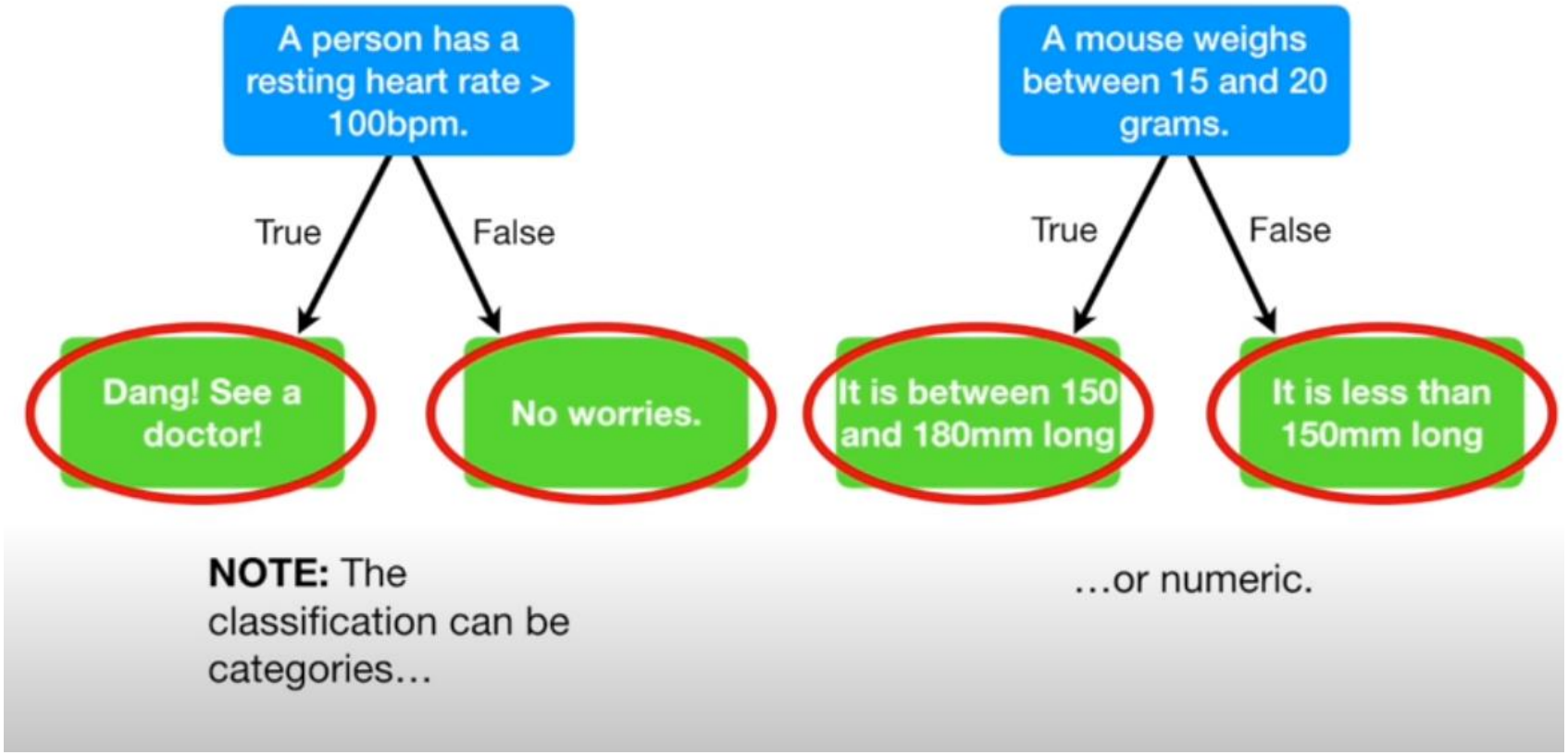






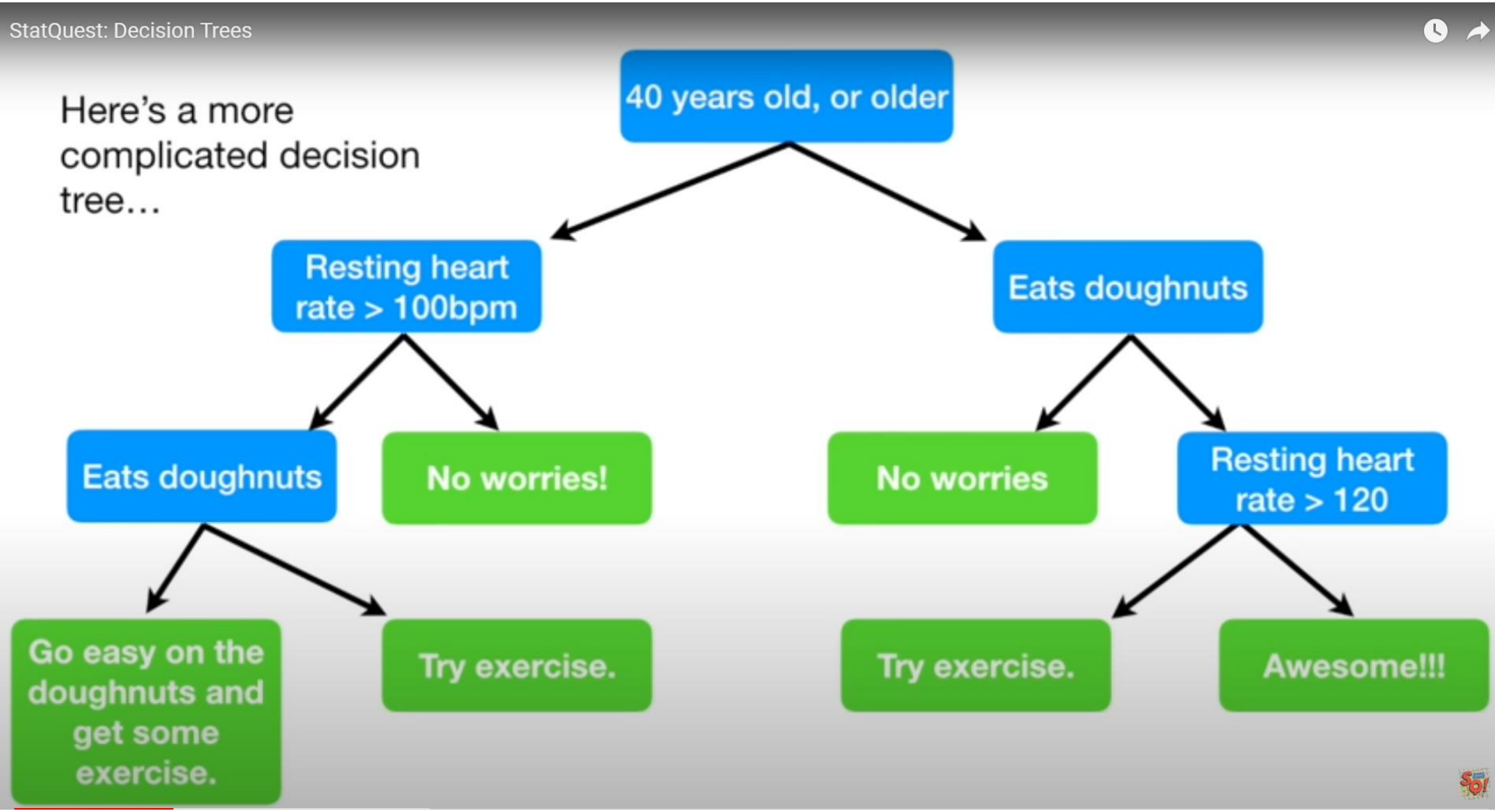
https://www.youtube.com/watch?v=7VeUPuFGJHk

Decision trees: types of answers



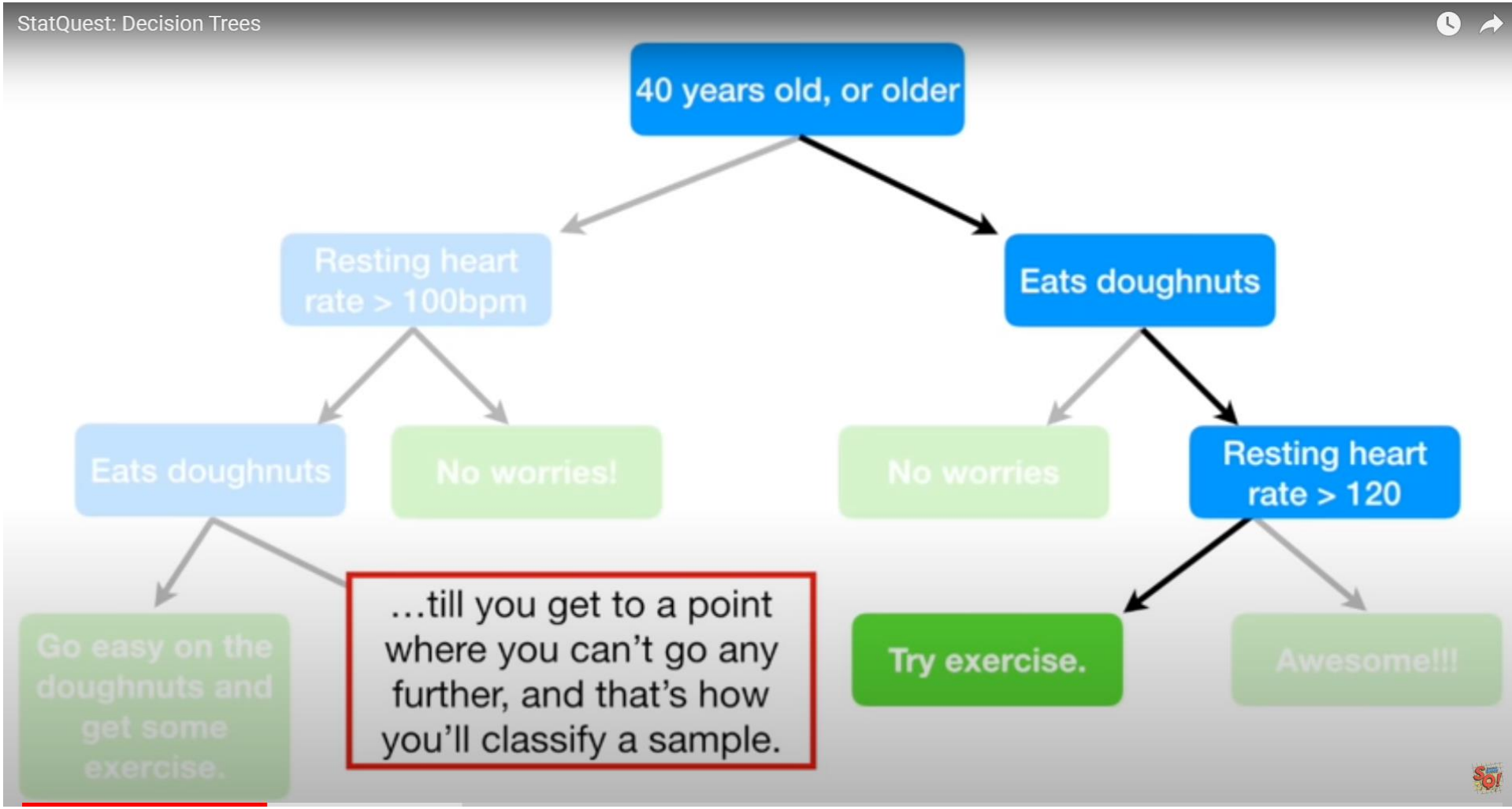
https://www.youtube.com/watch?v=7VeUPuFGJHk

A more complicated decision tree…



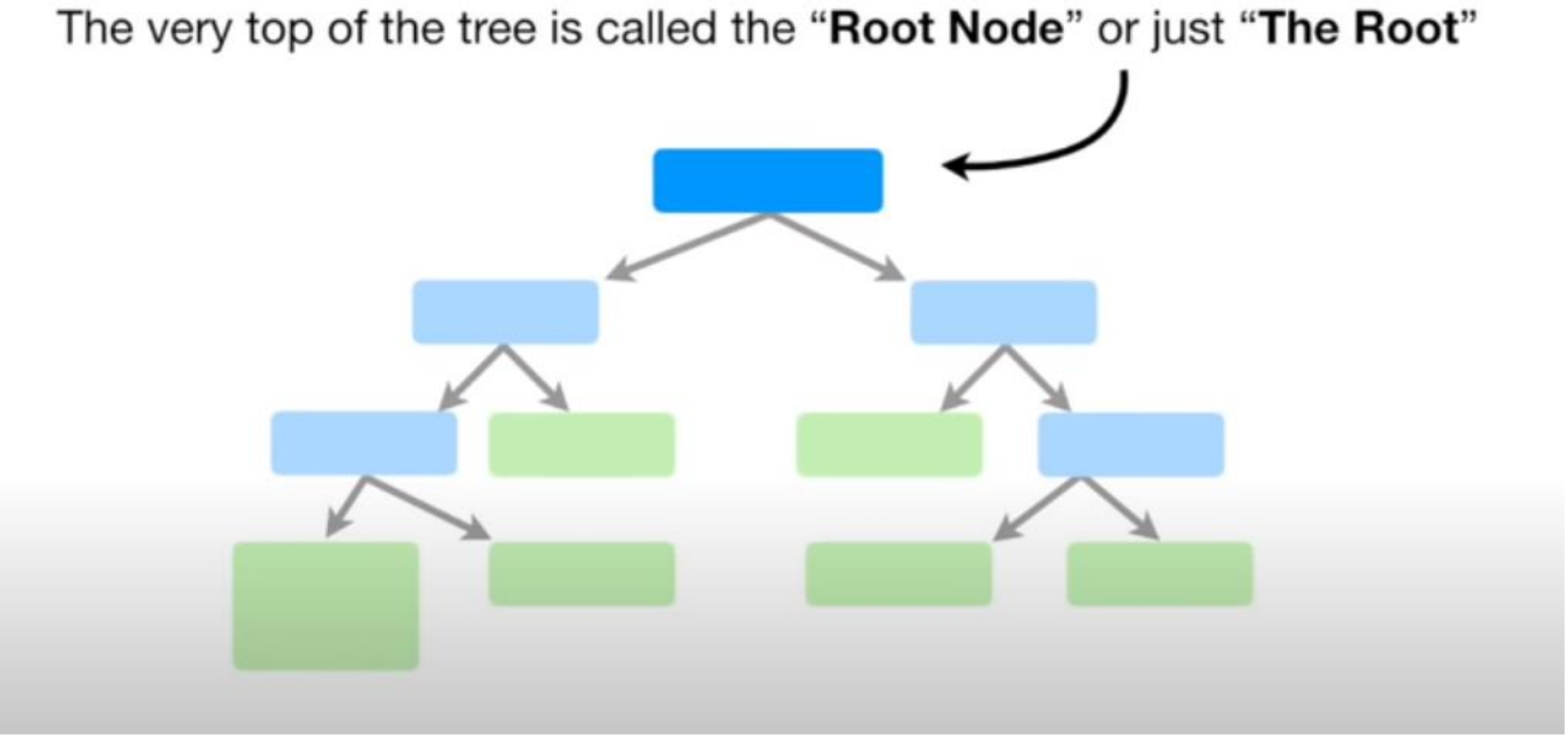
https://www.youtube.com/watch?v=7VeUPuFGJHk

Decision trees



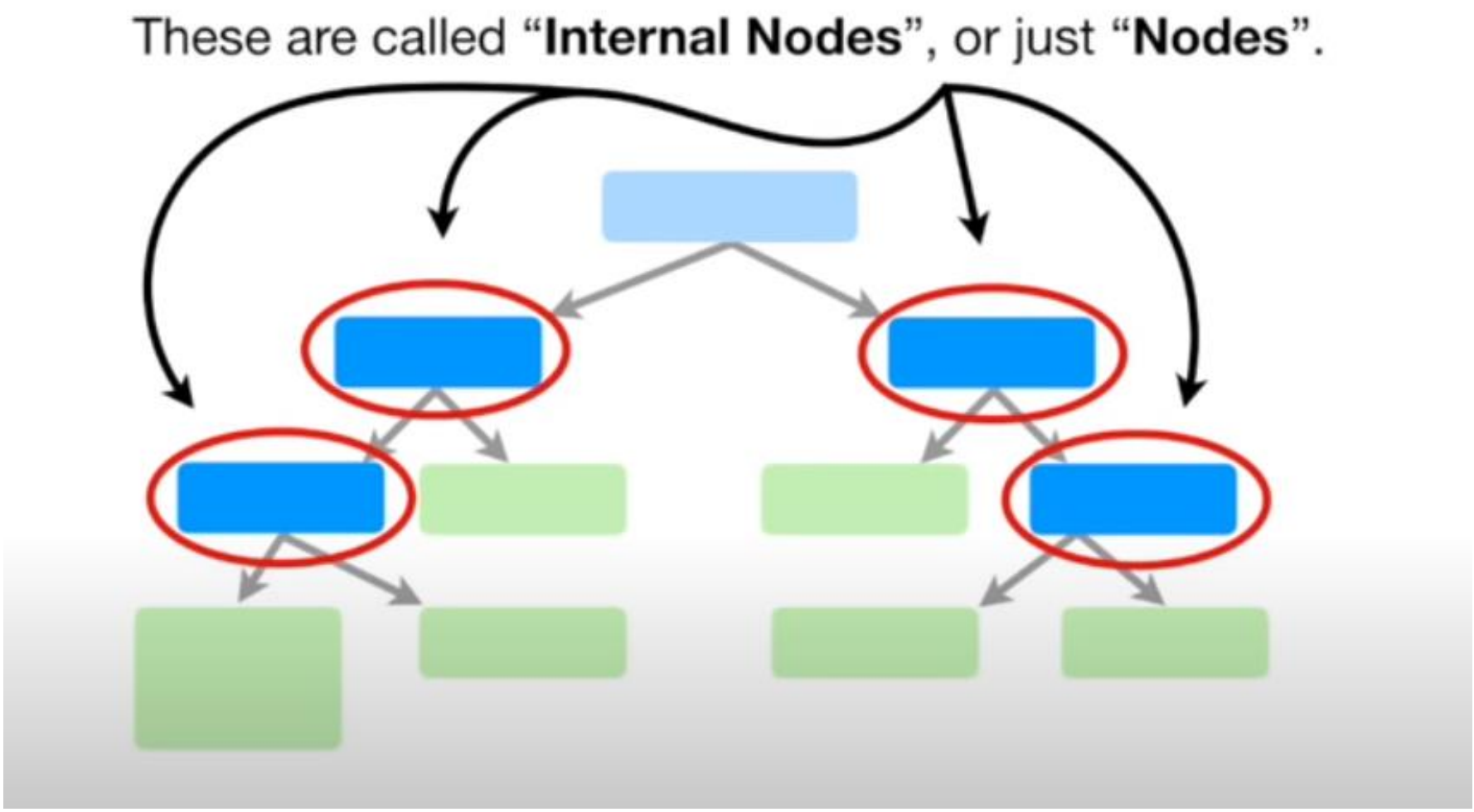
https://www.youtube.com/watch?v=7VeUPuFGJHk

Decision trees: Root Node (The Root)



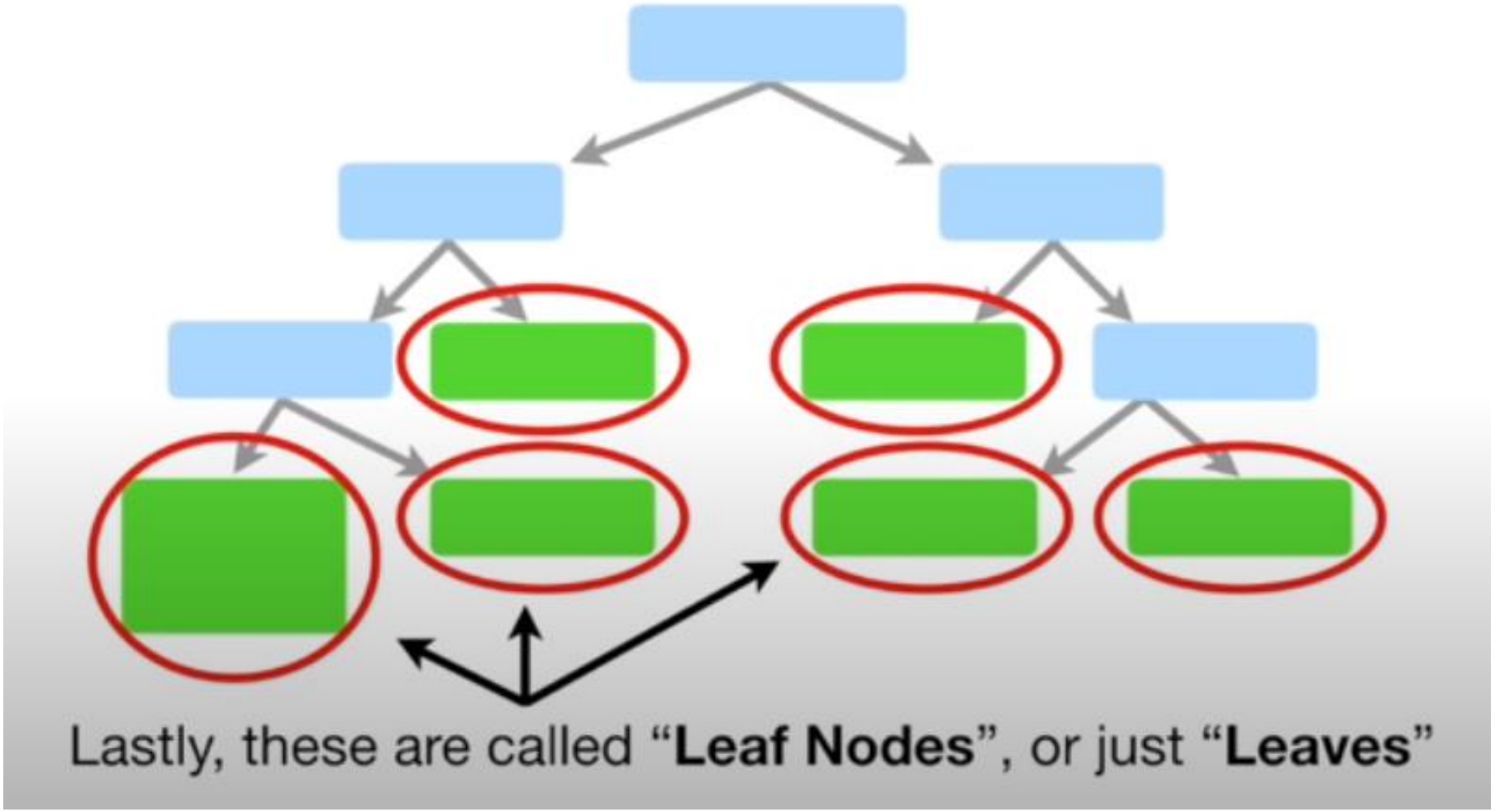
https://www.youtube.com/watch?v=7VeUPuFGJHk

Decision trees: Internal Nodes (Nodes)



https://www.youtube.com/watch?v=7VeUPuFGJHk

Decision trees: Leaf Nodes (Leaves)



https://www.youtube.com/watch?v=7VeUPuFGJHk

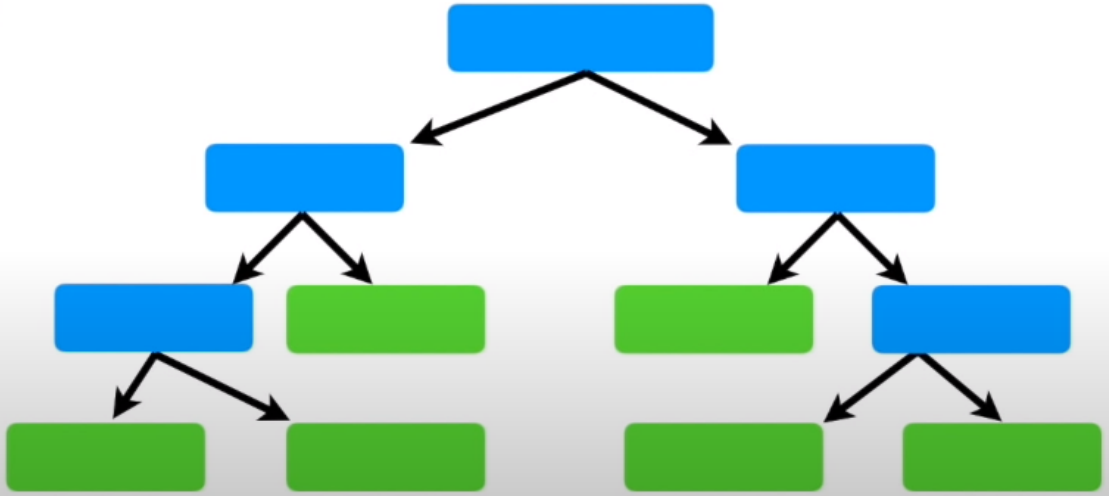
Example

In this example, we want to create a tree that uses **chest pain**, **good blood circulation** and **blocked artery status** to predict…

…whether or not a patient has heart disease.

Chest Pain	Good Blood Circulation	Blocked Arteries	Heart Disease
No	No	No	No
Yes	Yes	Yes	Yes
Yes	Yes	No	No
Yes	No	???	Yes
etc…	etc…	etc…	etc…

The first thing we want to know is whether **Chest Pain**, **Good Blood Circulation** or **Blocked Arteries** should be at the very top of our tree.



3:41 / 17:21

https://www.youtube.com/watch?v=7VeUPuFGJHk

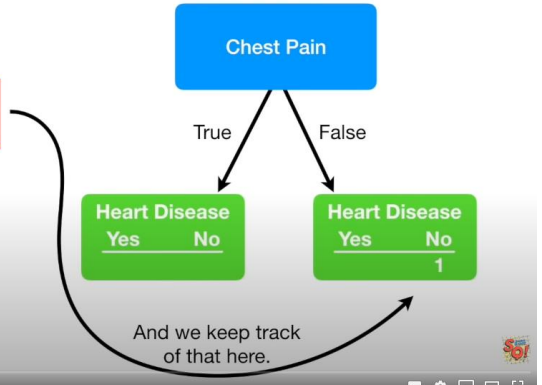
We start by looking at how well **Chest Pain** alone predicts heart disease…

Chest Pain	Good Blood Circulation	Blocked Arteries	Heart Disease
No	No	No	No
Yes	Yes	Yes	Yes
Yes	Yes	No	No
Yes	No	???	Yes
etc…	etc…	etc…	etc…

4:05 / 17:21

The first patient does not have chest pain and does not have heart disease.

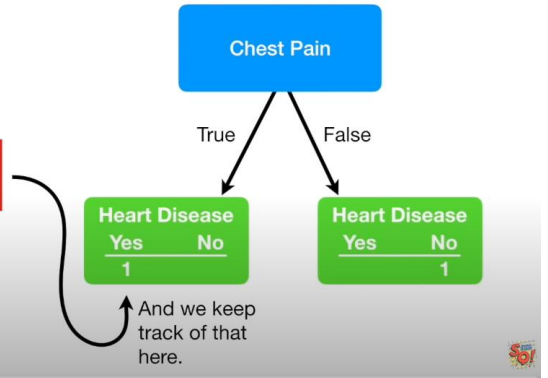
Chest Pain	Good Blood Circulation	Blocked Arteries	Heart Disease
No	No	No	No
Yes	Yes	Yes	Yes
Yes	Yes	No	No
Yes	No	???	Yes
etc…	etc…	etc…	etc…



4:17 / 17:21

The 2nd patient has chest pain and heart disease.

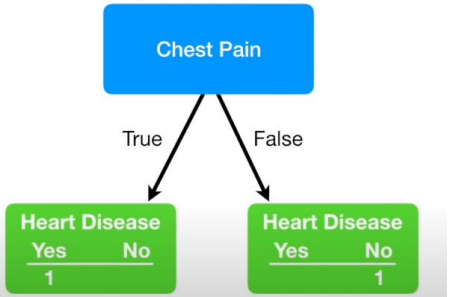
Chest Pain	Good Blood Circulation	Blocked Arteries	Heart Disease
No	No	No	No
Yes	Yes	Yes	Yes
Yes	Yes	No	No
Yes	No	???	Yes
etc…	etc…	etc…	etc…



4:25 / 17:21

The 3rd patient has chest pain but does not have heart disease.

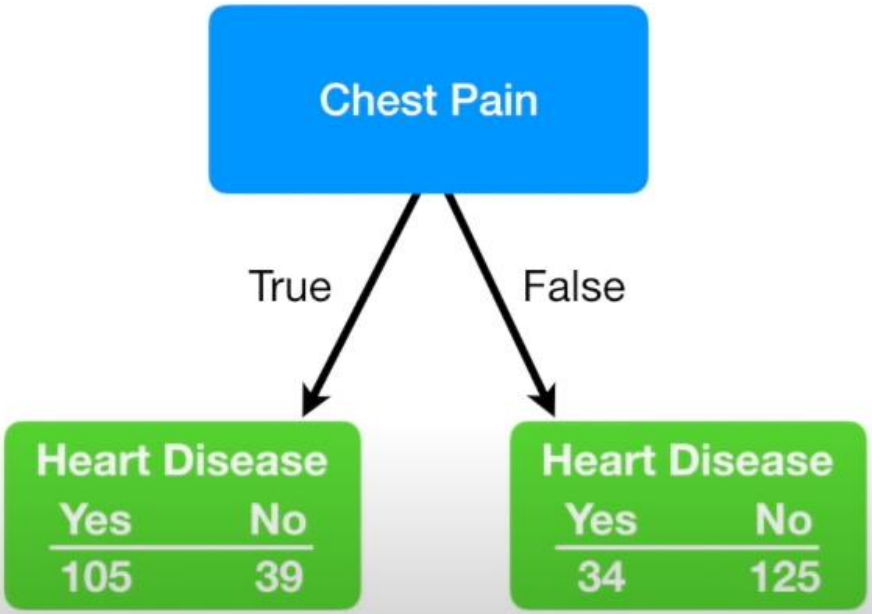
Chest Pain	Good Blood Circulation	Blocked Arteries	Heart Disease
No	No	No	No
Yes	Yes	Yes	Yes
Yes	Yes	No	No
Yes	No	???	Yes
etc…	etc…	etc…	etc…



4:31 / 17:21

https://www.youtube.com/watch?v=7VeUPuFGJHk

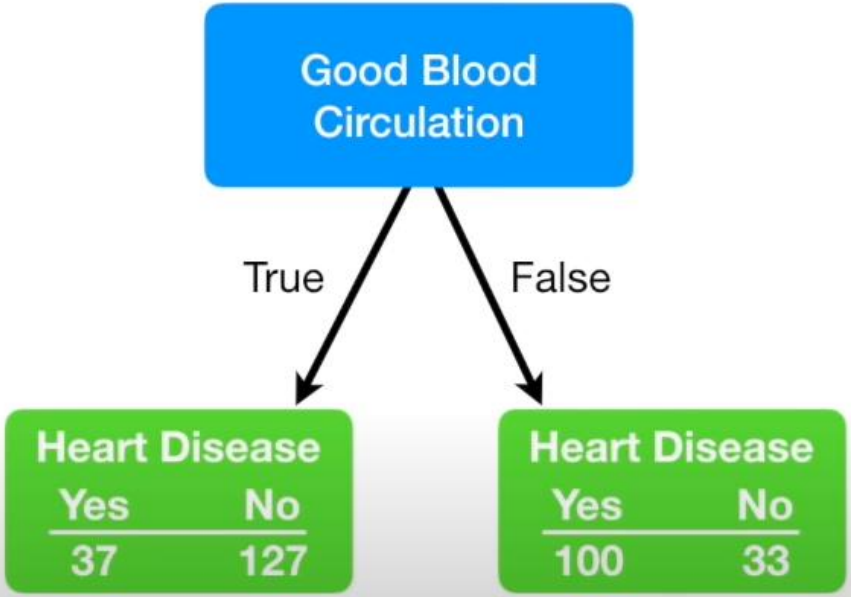
Chest Pain	Good Blood Circulation	Blocked Arteries	Heart Disease
No	No	No	No
Yes	Yes	Yes	Yes
Yes	Yes	No	No
Yes	No	???	Yes
etc…	etc…	etc…	etc…



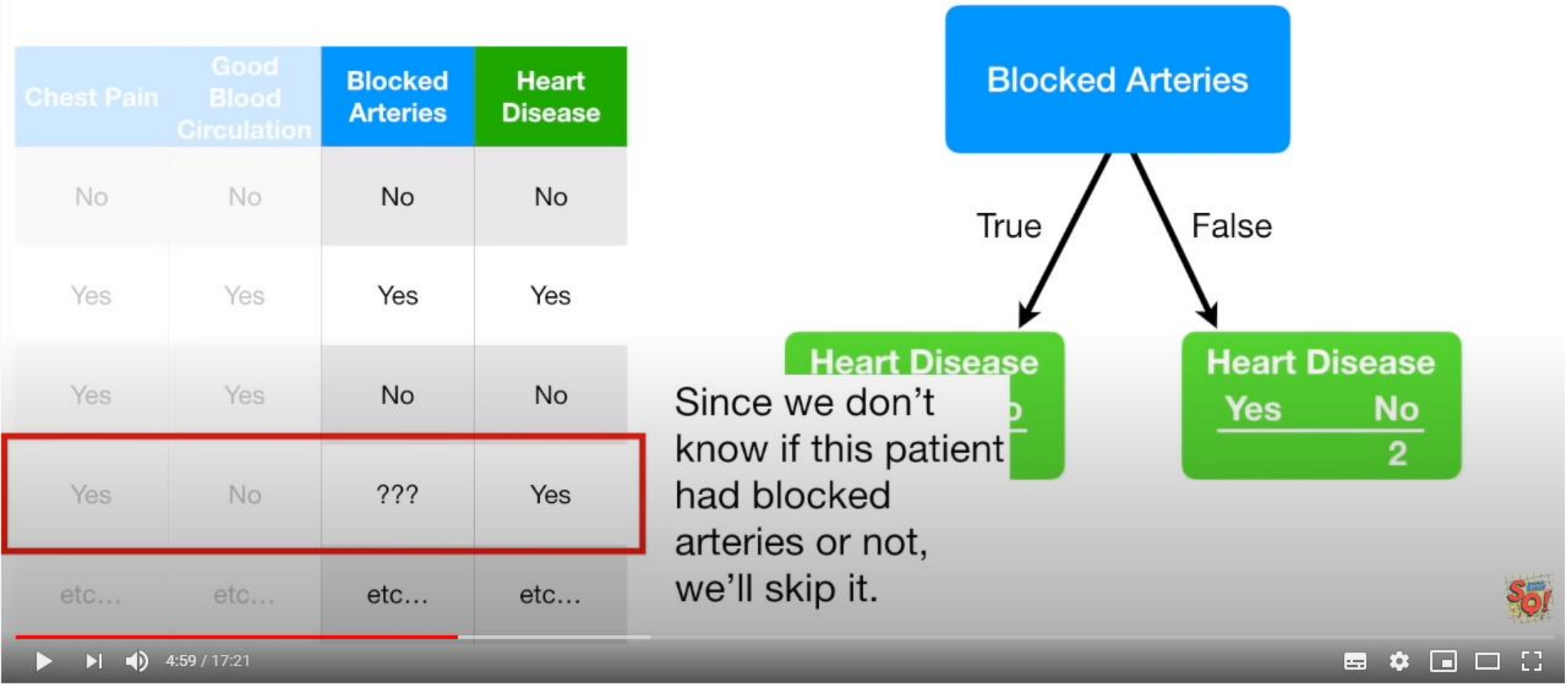
Ultimately, we look at chest pain and heart disease for all 303 patients in this study.

Now we do the exact same thing for **Good Blood Circulation**.

Chest Pain	Good Blood Circulation	Blocked Arteries	Heart Disease
No	No	No	No
Yes	Yes	Yes	Yes
Yes	Yes	No	No
Yes	No	???	Yes
etc…	etc…	etc…	etc…



Decision trees: Missing data

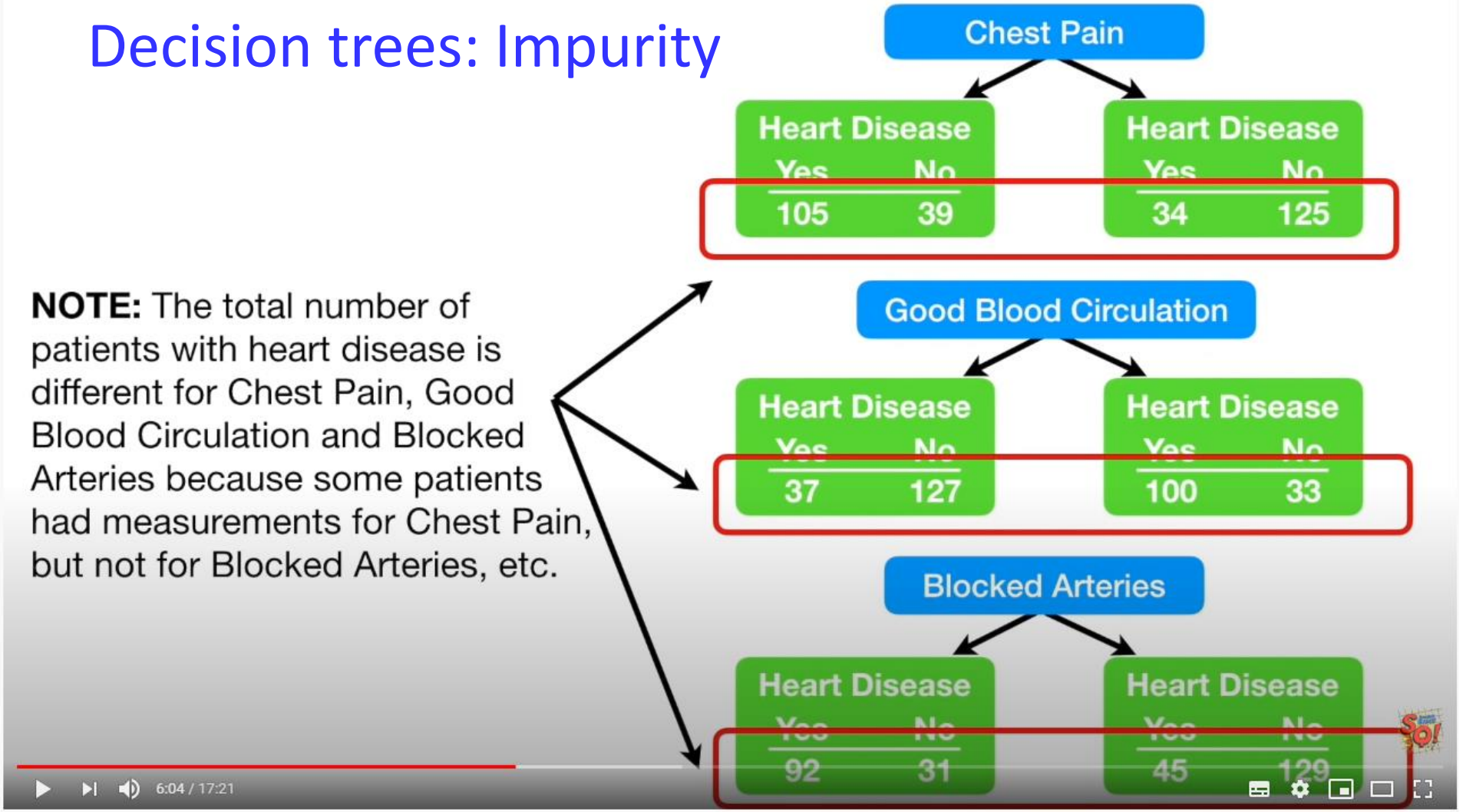


However, there are alternatives that I'll discuss in a follow up video.

Decision trees: Missing data

https://www.youtube.com/watch?v=wpNl-JwwplA&t=183s

Decision trees: Impurity

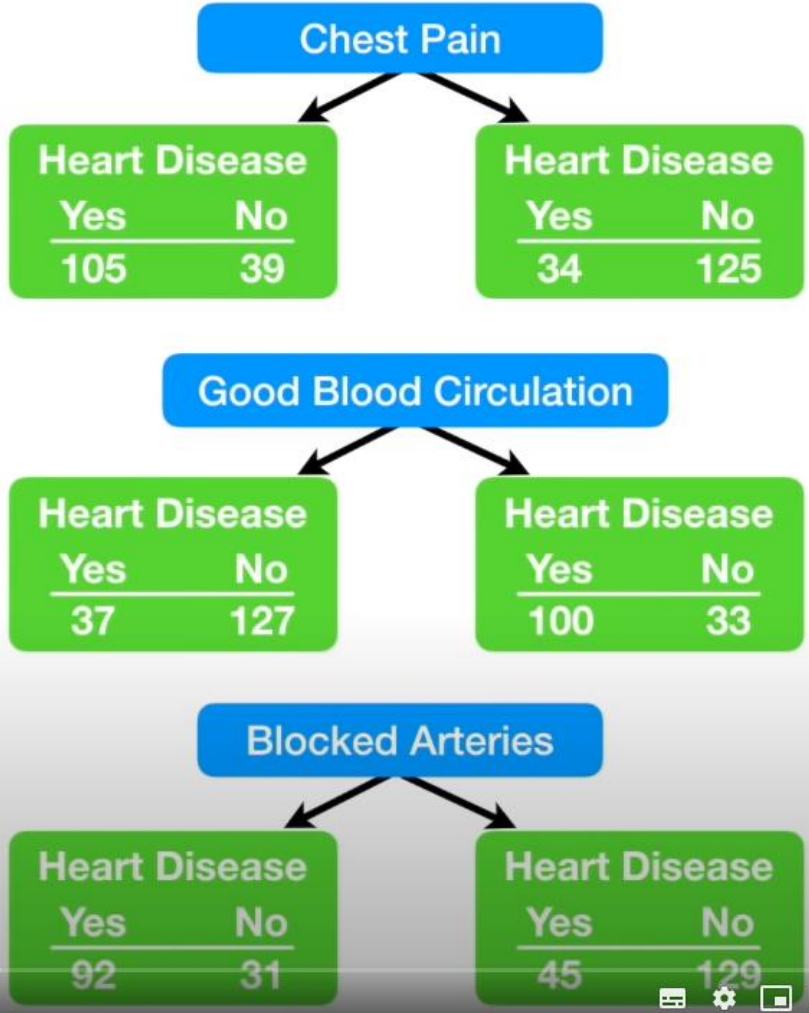


Because none of the leaf nodes are 100% "YES Heart Disease" or 100% "NO Heart Disease", they are all considered "**impure**".

Decision trees: Impurity

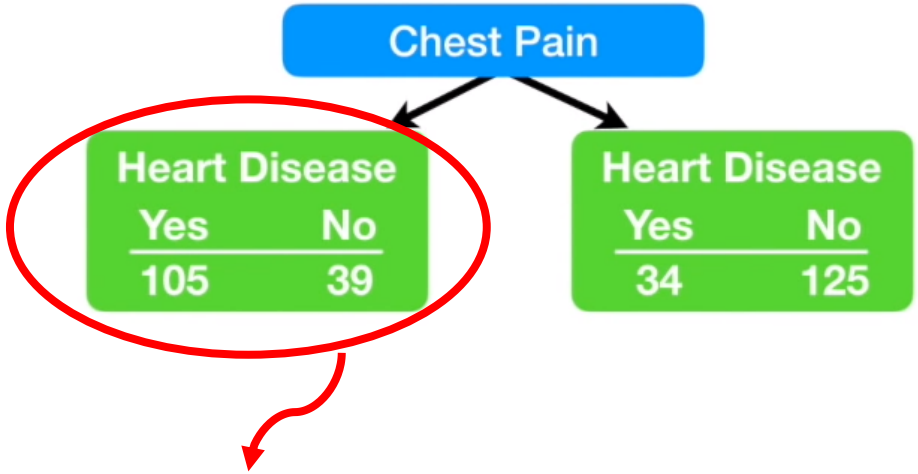
Because none of the leaf nodes are 100% "YES Heart Disease" or 100% "NO Heart Disease", they are all considered "**impure**".

To determine which separation is best, we need a way to measure and compare "**impurity**".



Decision trees: Gini Impurity

Impurity=0 是最佳



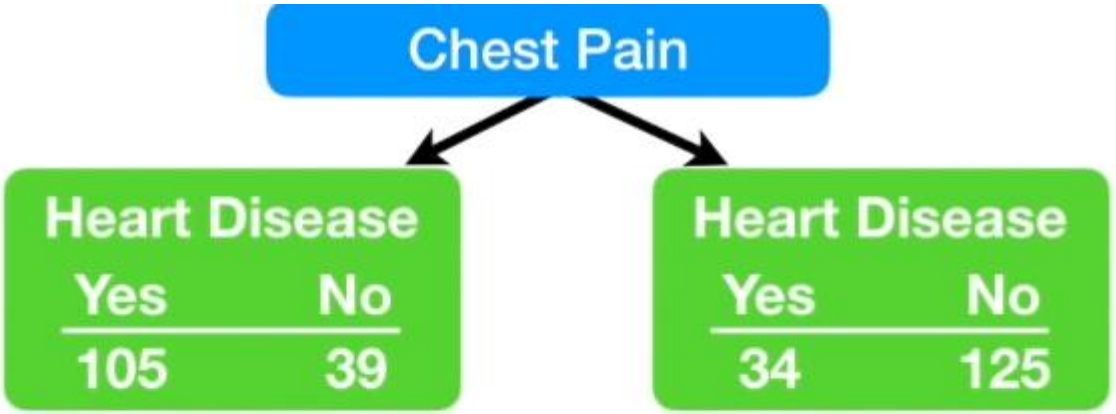
For this leaf, the Gini impurity = 1 - (the probability of "yes")^2 - (the probability of "no")^2

$$= 1 - \left(\frac{105}{105 + 39}\right)^2 - \left(\frac{39}{105 + 39}\right)^2$$

$$= 0.395$$

7:43 / 17:21

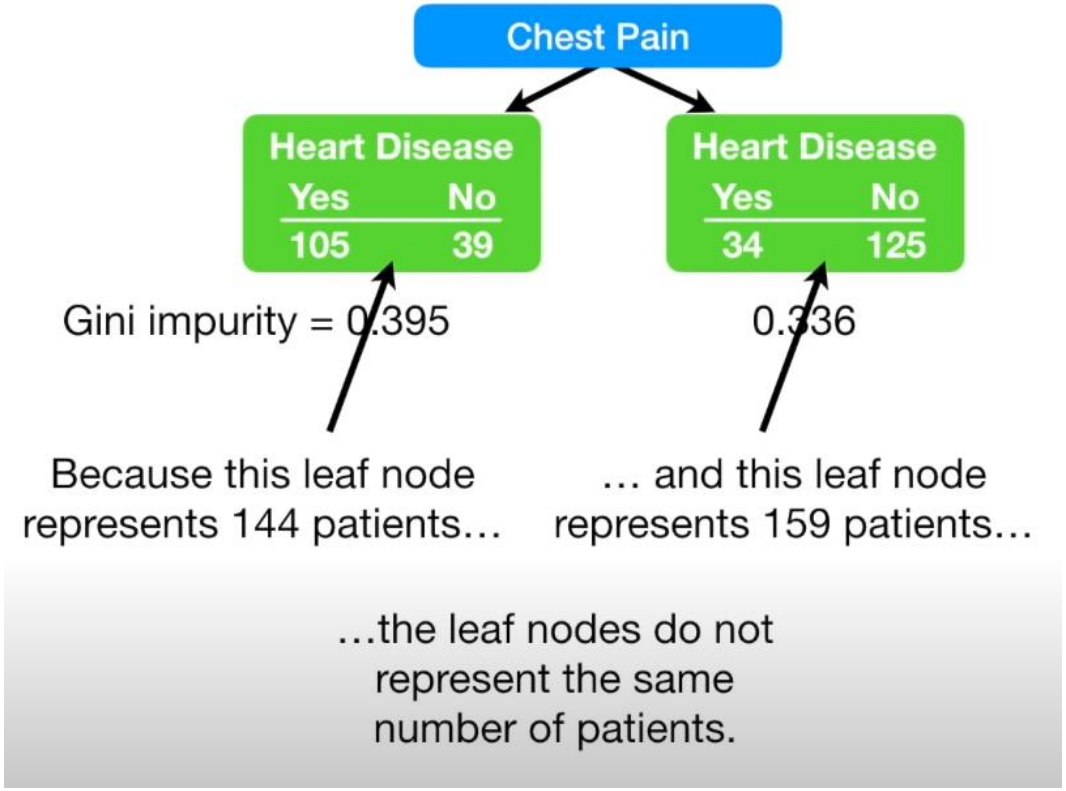
https://www.youtube.com/watch?v=7VeUPuFGJHk



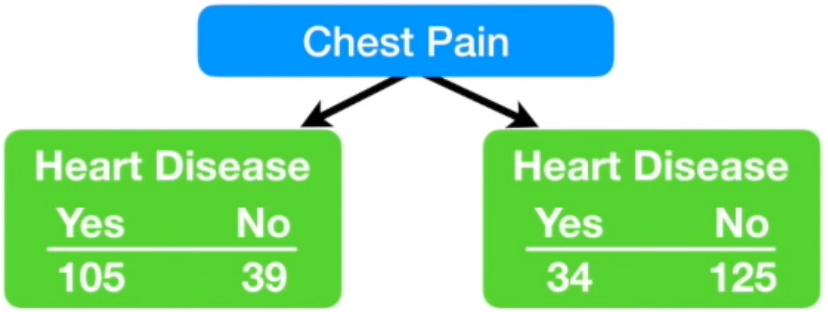
Gini impurity = 0.395

0.336

Now that we have measured the Gini impurity for both leaf nodes, we can calculate the total Gini impurity for using Chest Pain to separate patients with and without heart disease.



Thus, the total Gini impurity for using Chest Pain to separate patients with and without heart disease is the **weighted average of the leaf node impurities**.



Gini impurity = 0.395

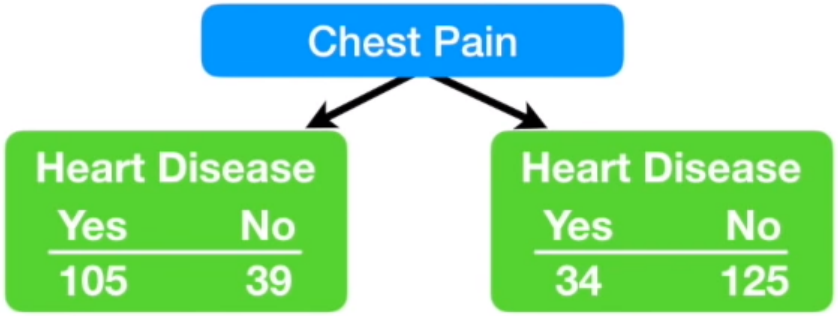
0.336

Gini impurity for Chest Pain = weighted average of Gini impurities for the leaf nodes

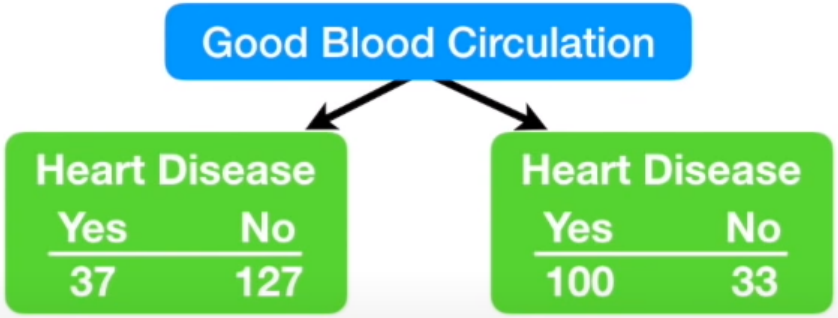
$$= \left(\frac{144}{144 + 159}\right) 0.395 + \left(\frac{159}{144 + 159}\right) 0.336$$

$$= 0.364$$

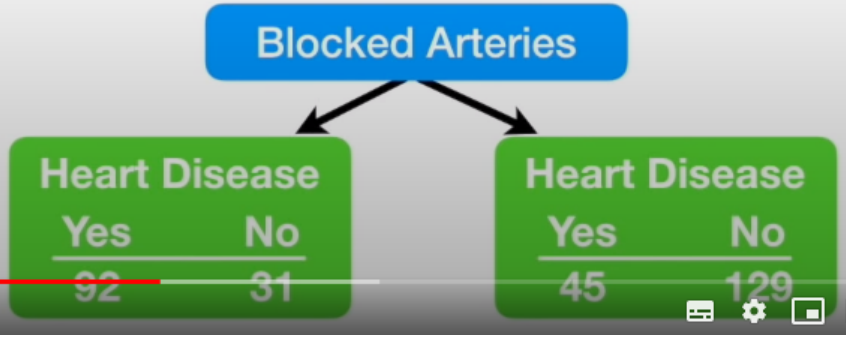
Gini impurity for Chest Pain = 0.364



Gini impurity for Good Blood Circulation = 0.360



Gini impurity for Blocked Arteries = 0.381



10:08 / 17:21

https://www.youtube.com/watch?v=7VeUPuFGJHk

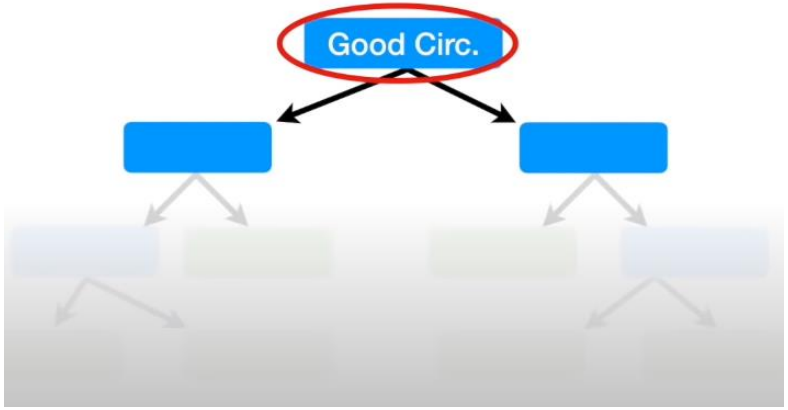
The lowest impurity separates the patients with/without HD the best

Gini impurity for Chest Pain = 0.364

Gini impurity for Good Blood Circulation = 0.360

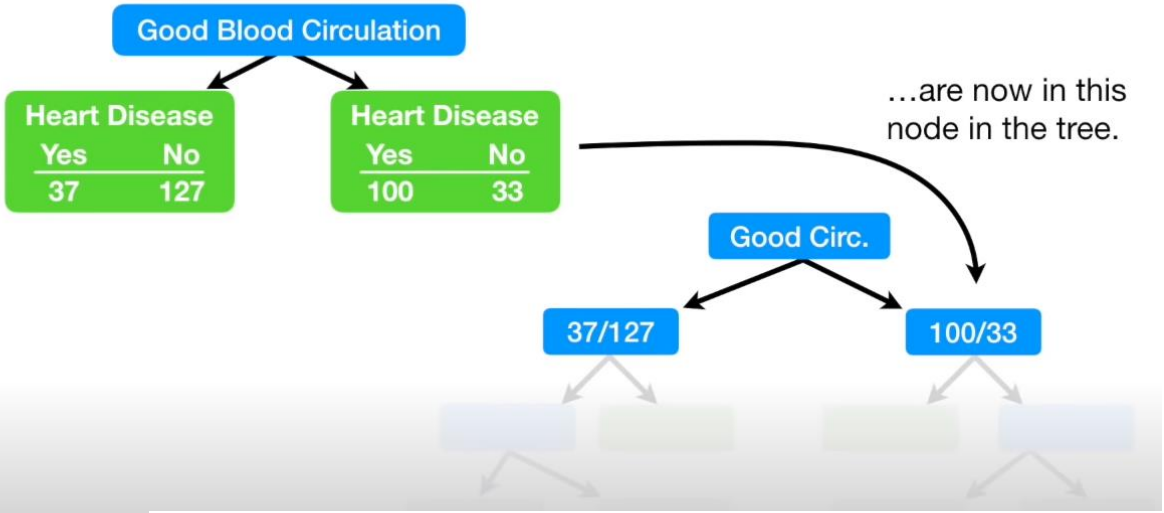
Gini impurity for Blocked Arteries = 0.381

…so we will use it at the root of the tree.

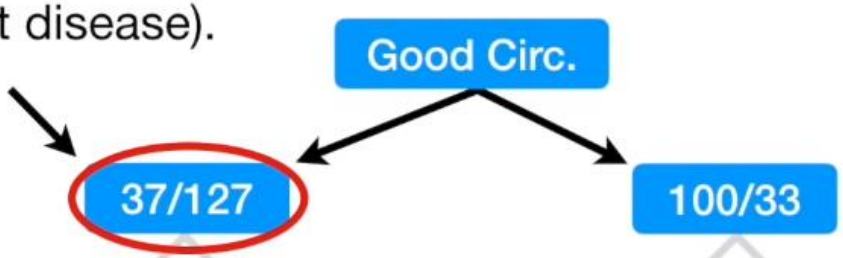


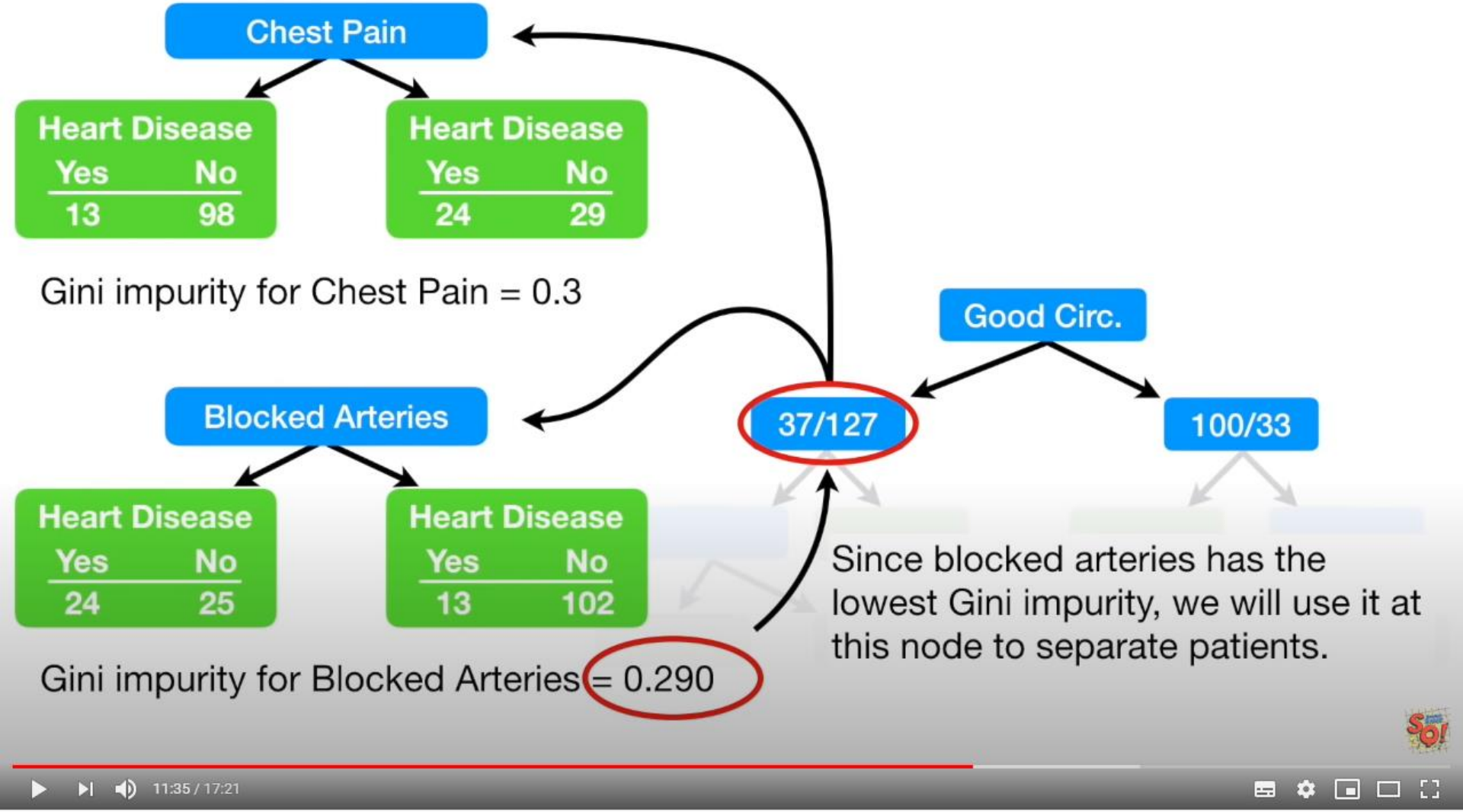
Good Blood Circulation has the lowest impurity (it separates patients with and without heart disease the best)…

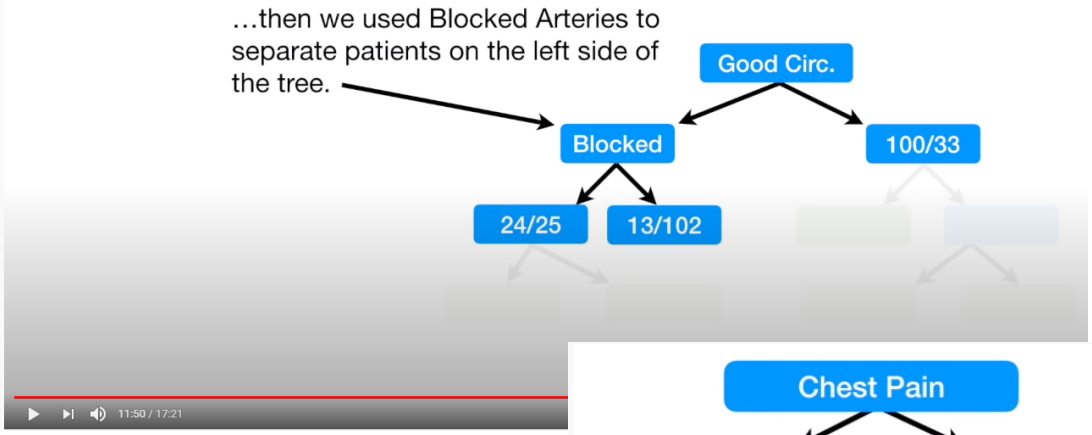
https://www.youtube.com/watch?v=7VeUPuFGJHk

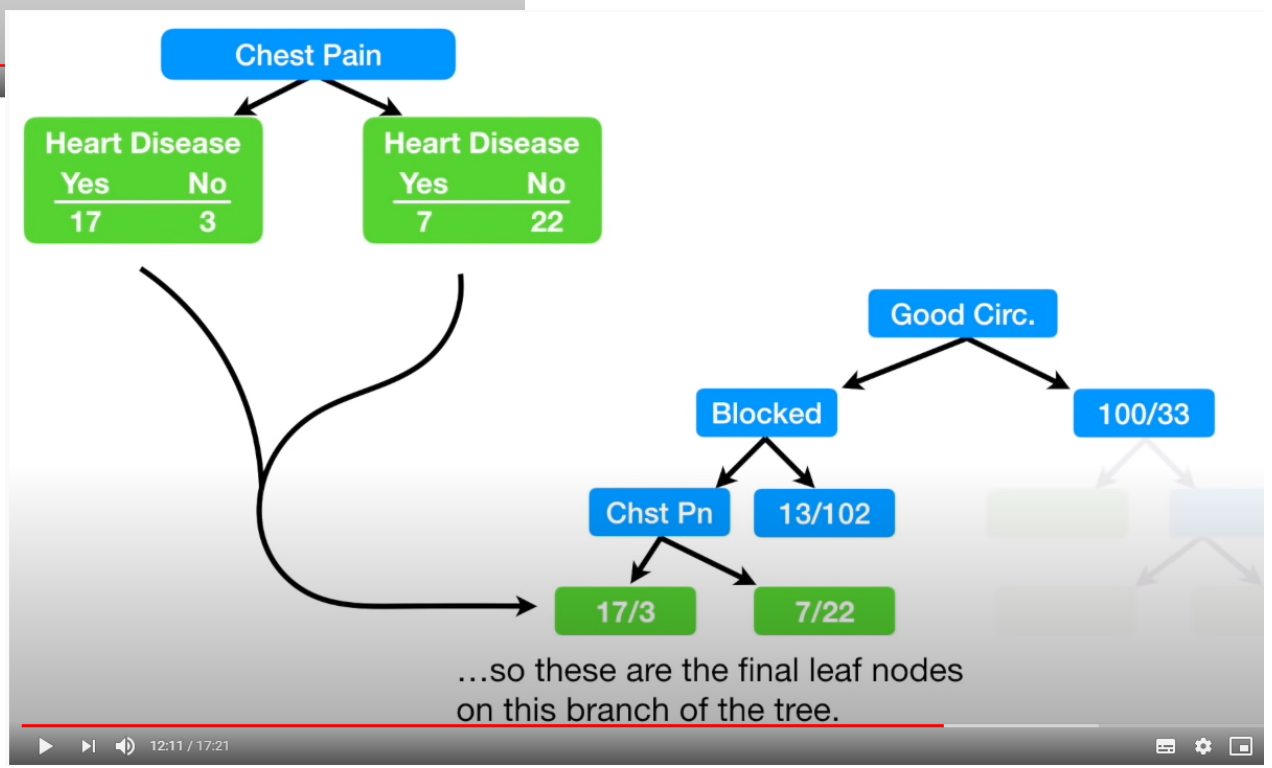


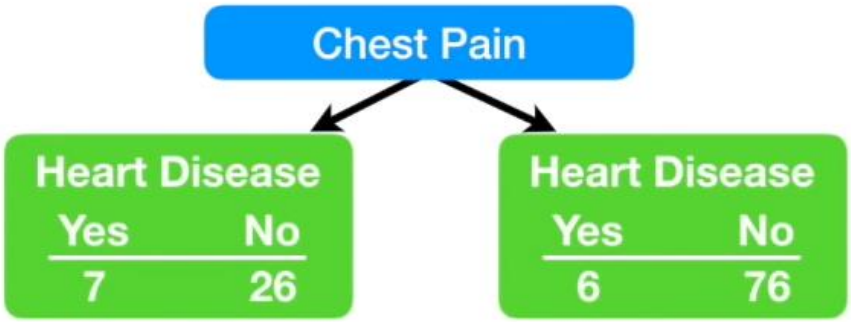
Now we need to figure how well **chest pain** and **blocked arteries** separate these 164 patients (37 with heart disease and 127 without heart disease).




Chest Pain
Heart Disease
Yes No
13 98
Heart Disease
Yes No
24 29
Gini impurity for Chest Pain = 0.3
Good Circ.
Blocked Arteries
37/127
100/33
Heart Disease
Yes No
24 25
Heart Disease
Yes No
13 102
Since blocked arteries has the lowest Gini impurity, we will use it at this node to separate patients.
Gini impurity for Blocked Arteries = 0.290
11:35 / 17:21


…then we used Blocked Arteries to separate patients on the left side of the tree.
Good Circ.
Blocked
100/33
24/25
13/102
11:50 / 17:21


Chest Pain
Heart Disease
Yes No
17 3
Heart Disease
Yes No
7 22
Good Circ.
Blocked
100/33
Chst Pn
13/102
17/3
7/22
…so these are the final leaf nodes on this branch of the tree.
12:11 / 17:21



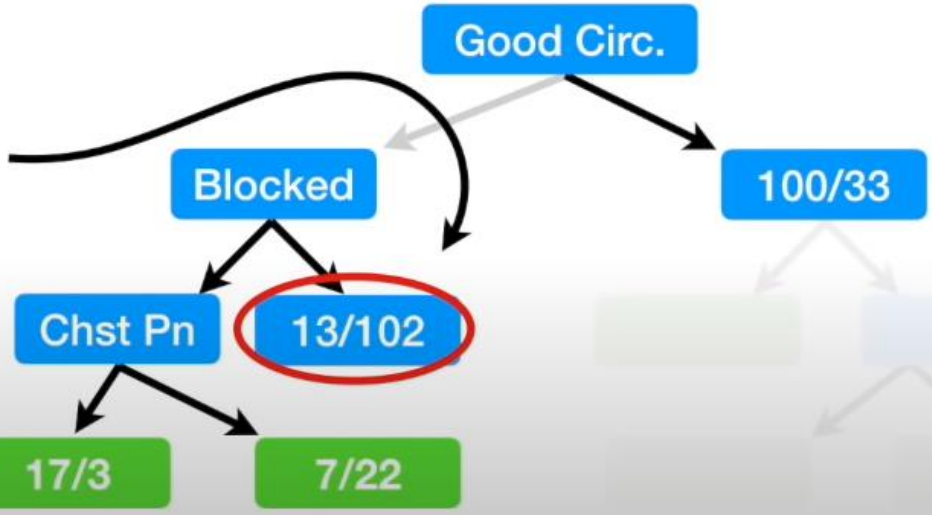
Gini impurity for Chest Pain = 0.29

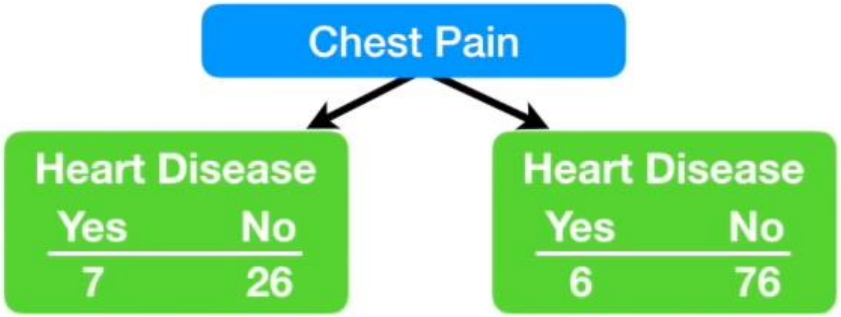
The Gini impurity for this node, before using chest pain to separate patients is…

= 1 - (the probability of "yes")^2
- (the probability of "no")^2

$$= 1 - \left(\frac{13}{13 + 102}\right)^2 - \left(\frac{102}{13 + 102}\right)^2$$

= 0.2





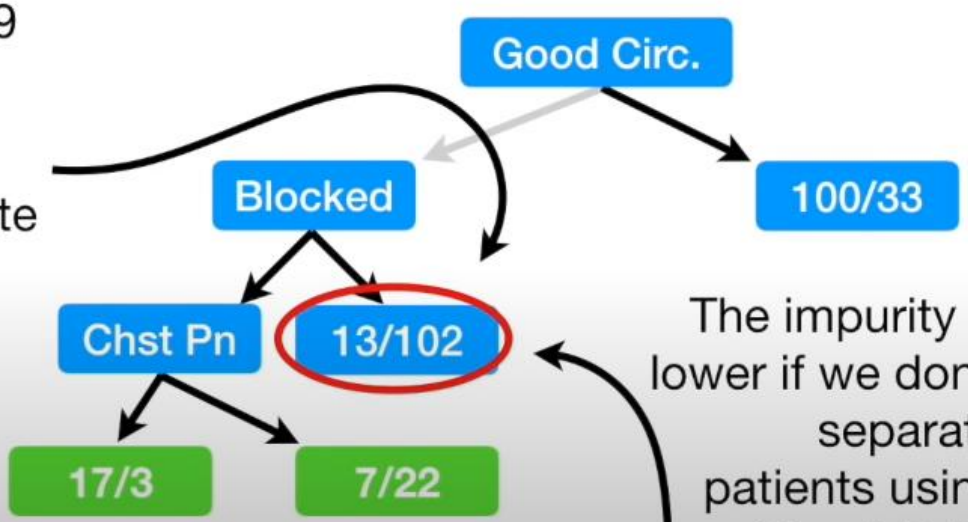
Gini impurity for Chest Pain = 0.29

The Gini impurity for this node, before using chest pain to separate patients is…

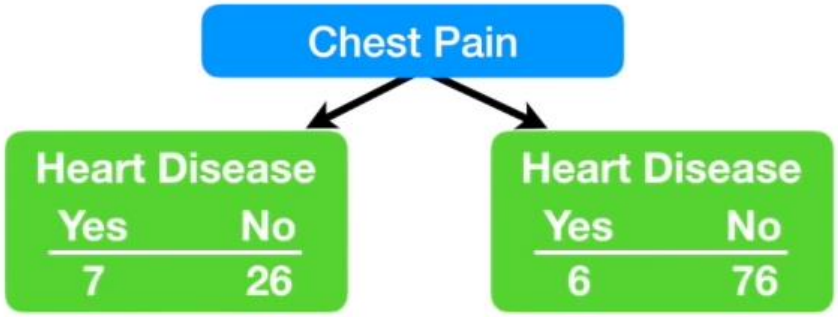
= 1 - (the probability of "yes")^2
- (the probability of "no")^2

$$= 1 - \left(\frac{13}{13 + 102}\right)^2 - \left(\frac{102}{13 + 102}\right)^2$$

= 0.2



The impurity is lower if we don't separate patients using Chest Pain.



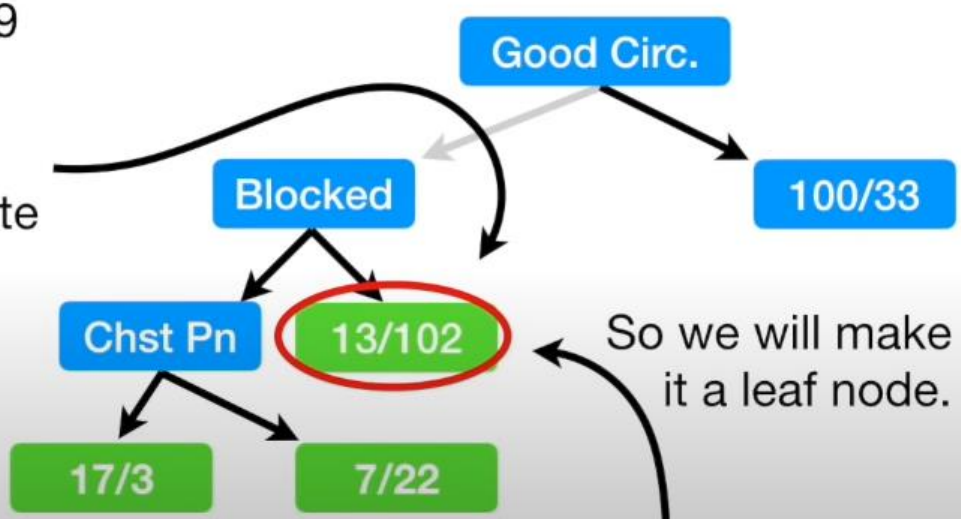
Gini impurity for Chest Pain = 0.29

The Gini impurity for this node, before using chest pain to separate patients is…

= 1 - (the probability of "yes")^2
- (the probability of "no")^2

$$= 1 - \left(\frac{13}{13 + 102}\right)^2 - \left(\frac{102}{13 + 102}\right)^2$$

= 0.2



So we will make it a leaf node.

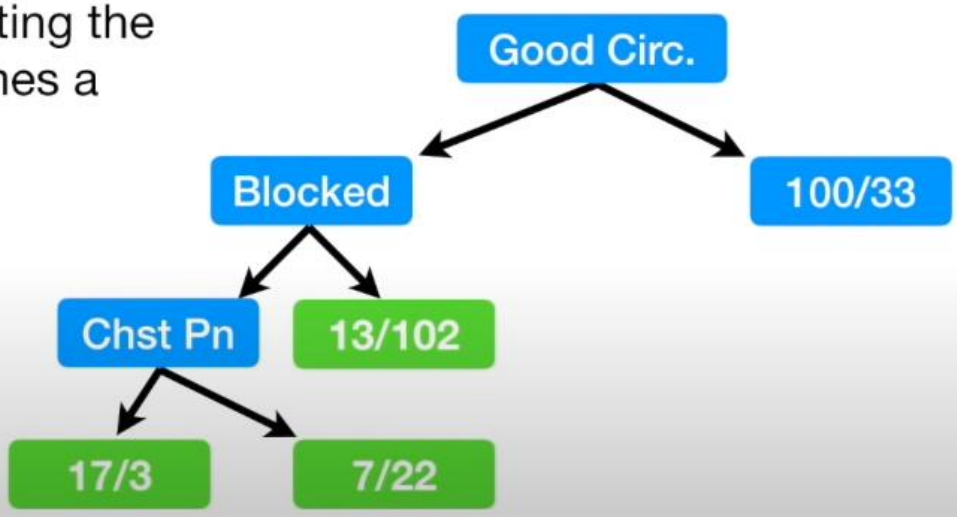
Right side in the example

The good news is that we follow the exact same steps as we did on the left side:

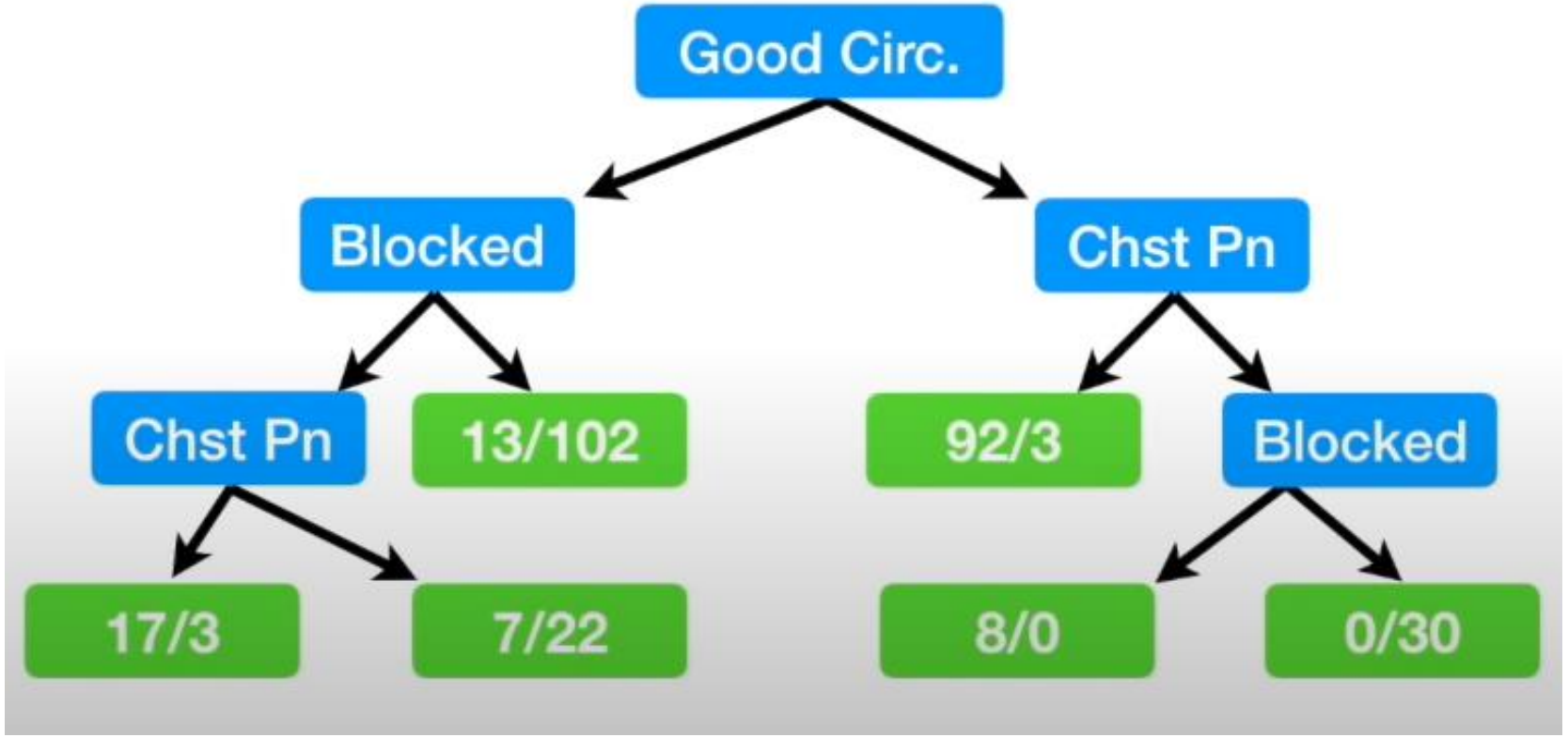
1) Calculate all of the Gini impurity scores.

2) If the node itself has the lowest score, than there is no point in separating the patients any more and it becomes a leaf node.

3) If separating the data results in an improvement, than pick the separation with the lowest impurity value.



Hooray!!! We made a decision tree!!!



So far we've seen how to build a tree with "yes/no" questions at each step…

…but what if we have numeric data, like patient weight?

Weight	Heart Disease
220	Yes
180	Yes
225	Yes
190	No
155	No

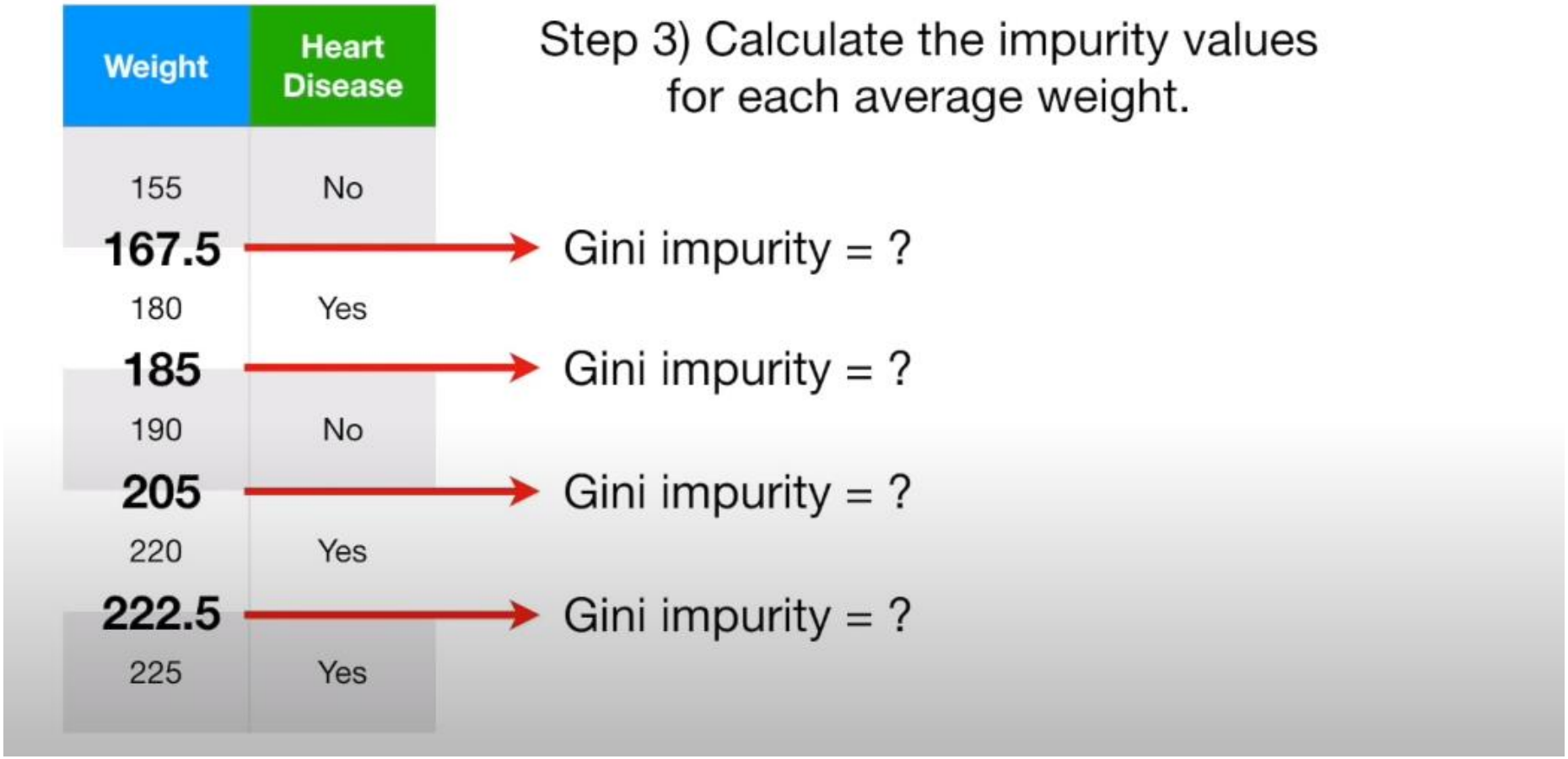
How do we determine what's the best weight to use to divide the patients?

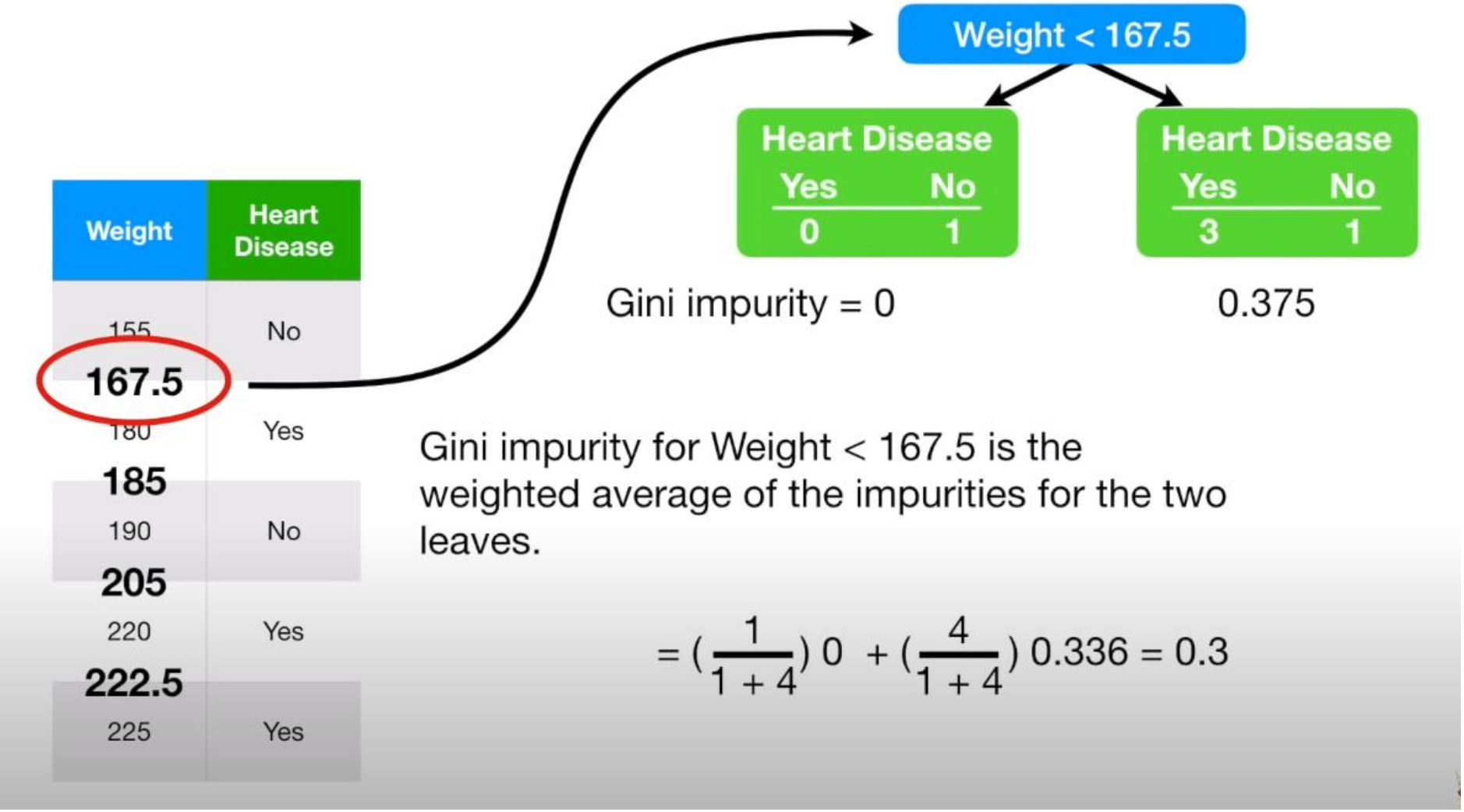
Step 1) Sort the patients by weight, lowest to highest.

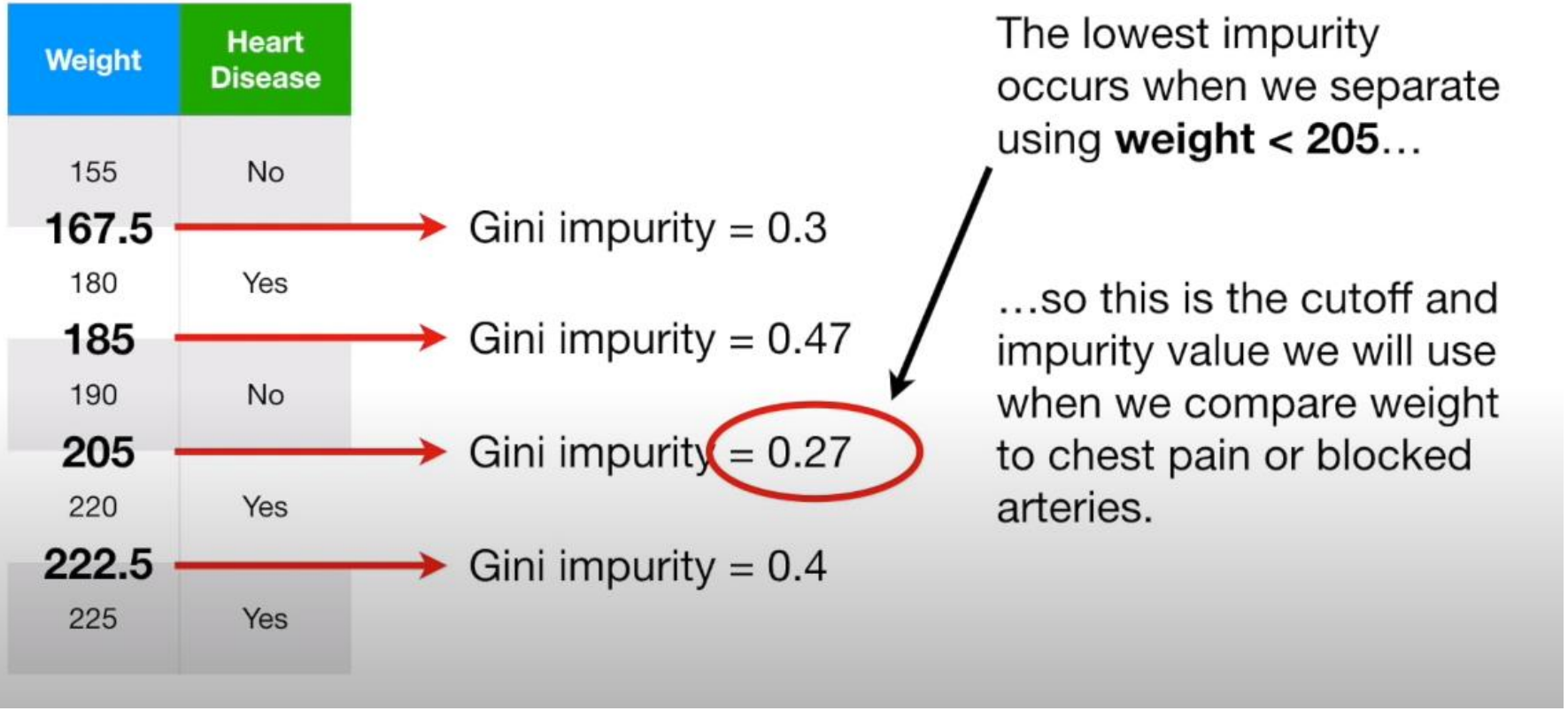
	Weight	Heart Disease
Lowest	155	No
	180	Yes
	190	No
	220	Yes
Highest	225	Yes

Weight	Heart Disease
155	No
167.5	
180	Yes
185	
190	No
205	
220	Yes
222.5	
225	Yes

Step 2) Calculate the average weight for all adjacent patients.


Weight
Heart Disease
155
No
167.5
Gini impurity = ?
180
Yes
185
Gini impurity = ?
190
No
205
Gini impurity = ?
220
Yes
222.5
Gini impurity = ?
225
Yes
Step 3) Calculate the impurity values for each average weight.


Weight < 167.5
Heart Disease
Yes No
0 1
Heart Disease
Yes No
3 1
Gini impurity = 0
0.375
Weight
Heart Disease
155
No
167.5
180
Yes
185
190
No
205
220
Yes
222.5
225
Yes
Gini impurity for Weight < 167.5 is the weighted average of the impurities for the two leaves.
$= (\frac{1}{1+4})\,0 + (\frac{4}{1+4})\,0.336 = 0.3$


Weight
Heart Disease
155
No
167.5
Gini impurity = 0.3
180
Yes
185
Gini impurity = 0.47
190
No
205
Gini impurity = 0.27
220
Yes
222.5
Gini impurity = 0.4
225
Yes
The lowest impurity occurs when we separate using weight < 205…
…so this is the cutoff and impurity value we will use when we compare weight to chest pain or blocked arteries.

Now we've seen how to build a tree with…

1) "yes/no" questions at each step…

2) Numeric data, like patient weight…

Now let's talk about **ranked data**, like "rank my jokes on a scale of 1 to 4", and **multiple choice data**, like "which color do you like, red, blue or green?"

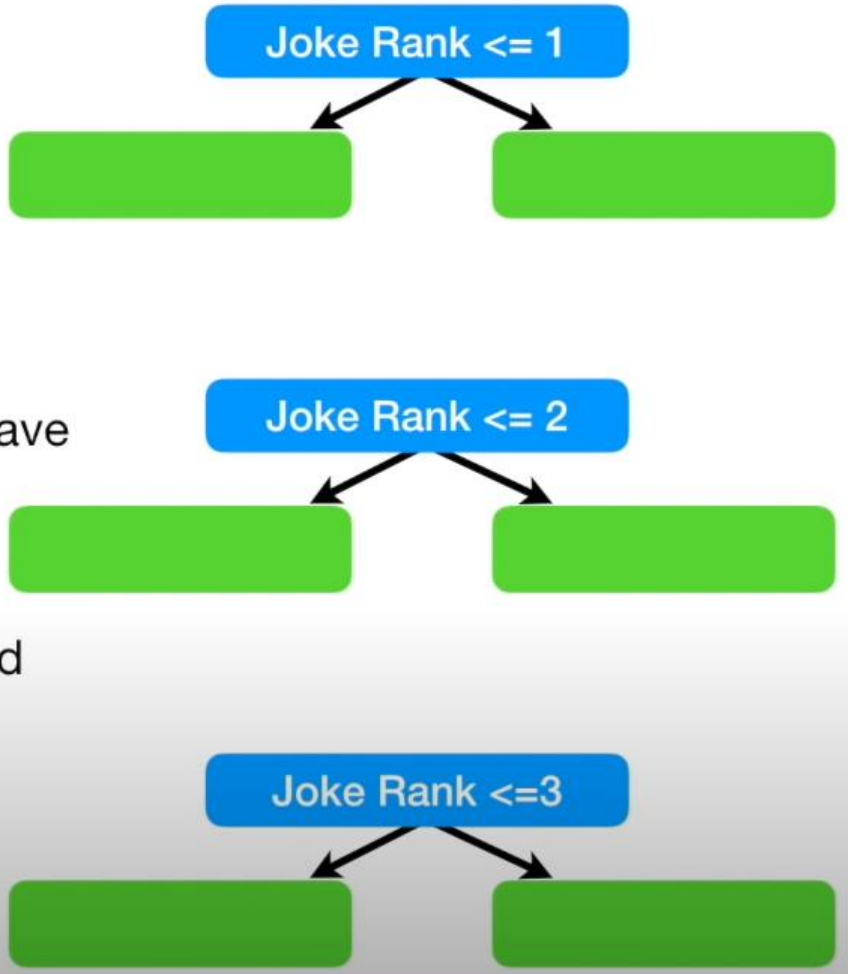
Rank my jokes…	Likes StatQuest
1	Yes
1	No
3	Yes
1	Yes
etc…	etc…

Ranked data is similar to numeric data, except instead now we calculate impurity scores for all of the possible ranks.

So if people could rank my jokes from 1 to 4 (4 being the funniest), we could calculate the following impurity scores…

Rank my jokes…	Likes StatQuest
1	Yes
1	No
3	Yes
1	Yes
etc…	etc…

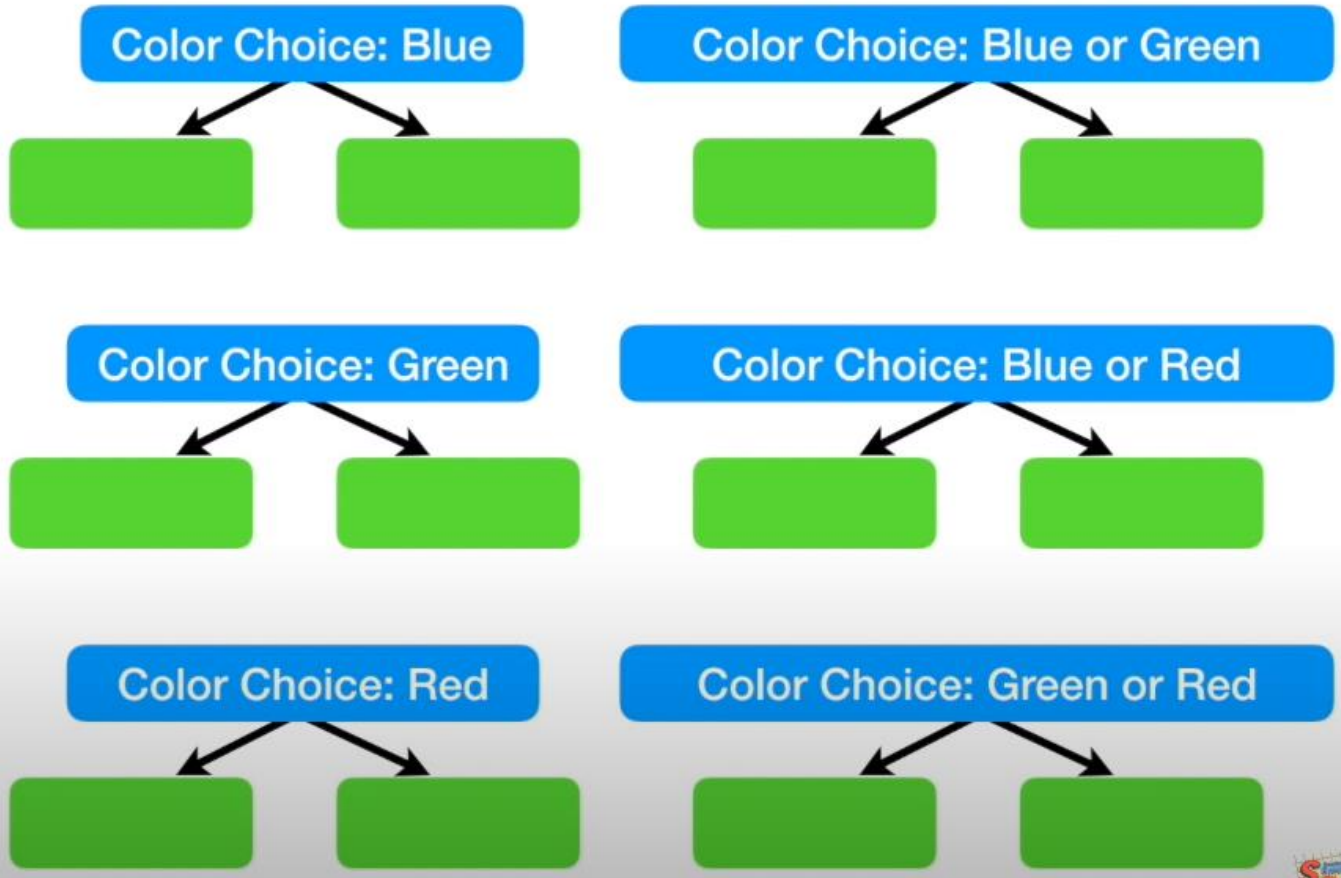
NOTE: We don't have to calculate an impurity score for Joke Rank <= 4 because that would include everyone.



Color Choice	Likes StatQuest
Green	Yes
Blue	No
Red	Yes
Green	Yes
etc…	etc…

When there are **multiple choices**, like "**color choice can be blue, green or red**", you calculate an impurity score for each one as well as each possible combination.

Color Choice	Likes StatQuest
Green	Yes
Blue	No
Red	Yes
Green	Yes
etc…	etc…



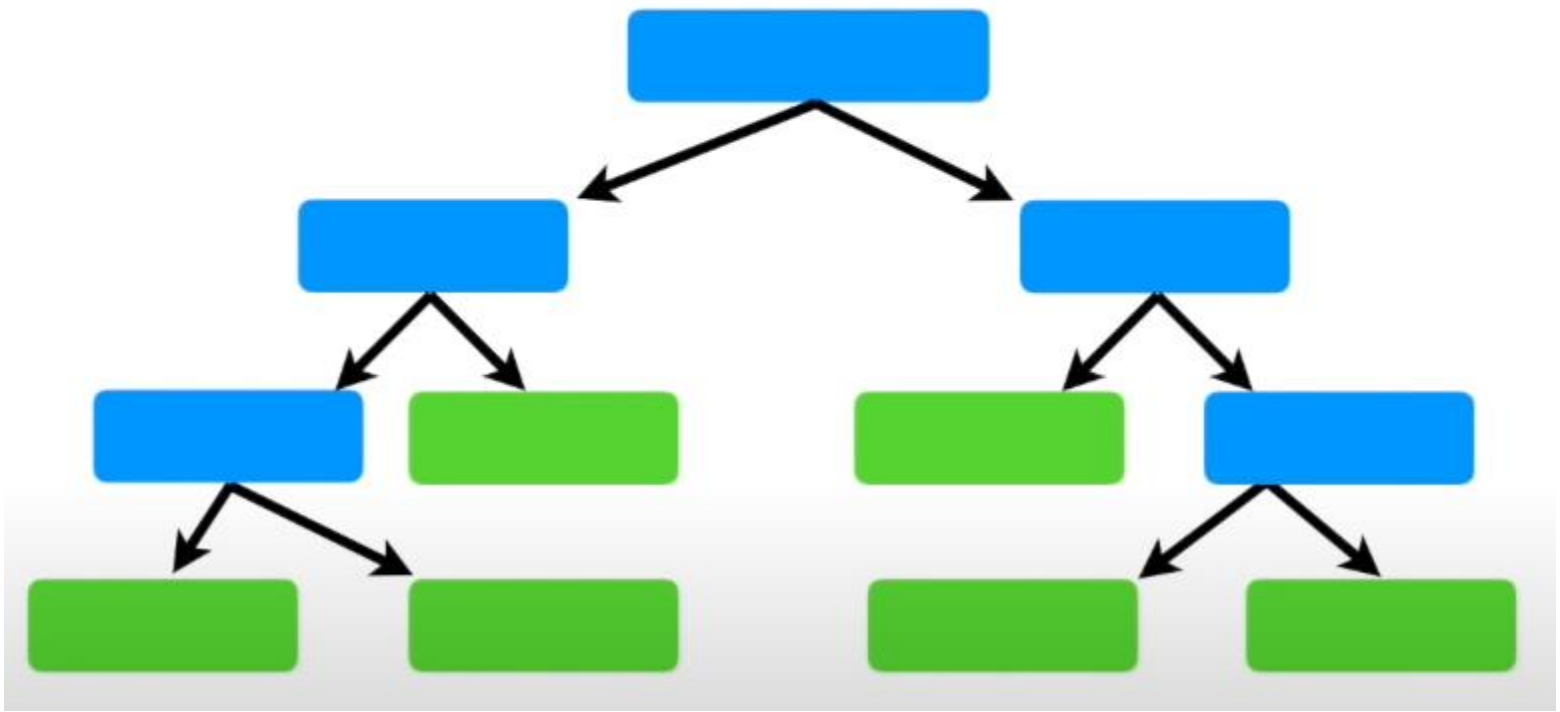
16:43 / 17:21

NOTE: We don't have to calculate an impurity score for "Color Choice: Blue or Green or Red" since that includes everyone.

Random Forests

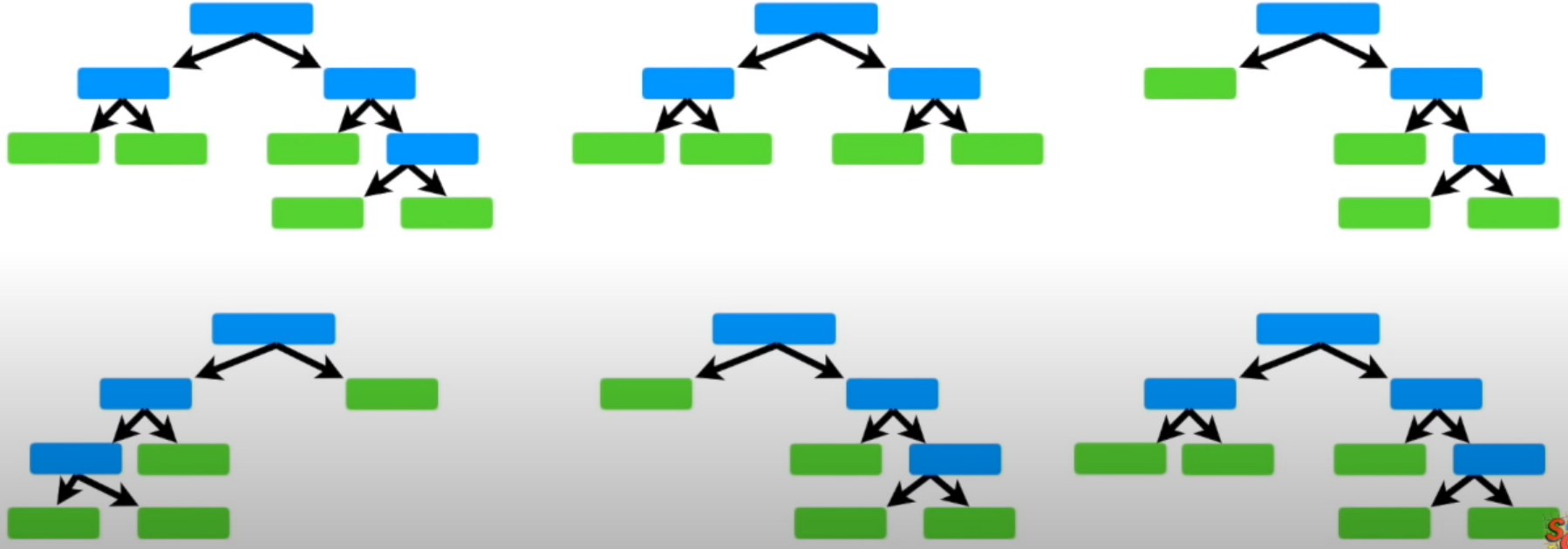
Decision trees 缺點:

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.**



https://www.youtube.com/watch?v=J4Wdy0Wc_xQ

The good news is that **Random Forests** combine the simplicity of decision trees with flexibility resulting in a vast improvement in accuracy.



Random Forests

Step 1: Create 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

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.

Random Forests

Step 1: Create a "bootstrapped" dataset.

Randomly selected samples from the Original 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

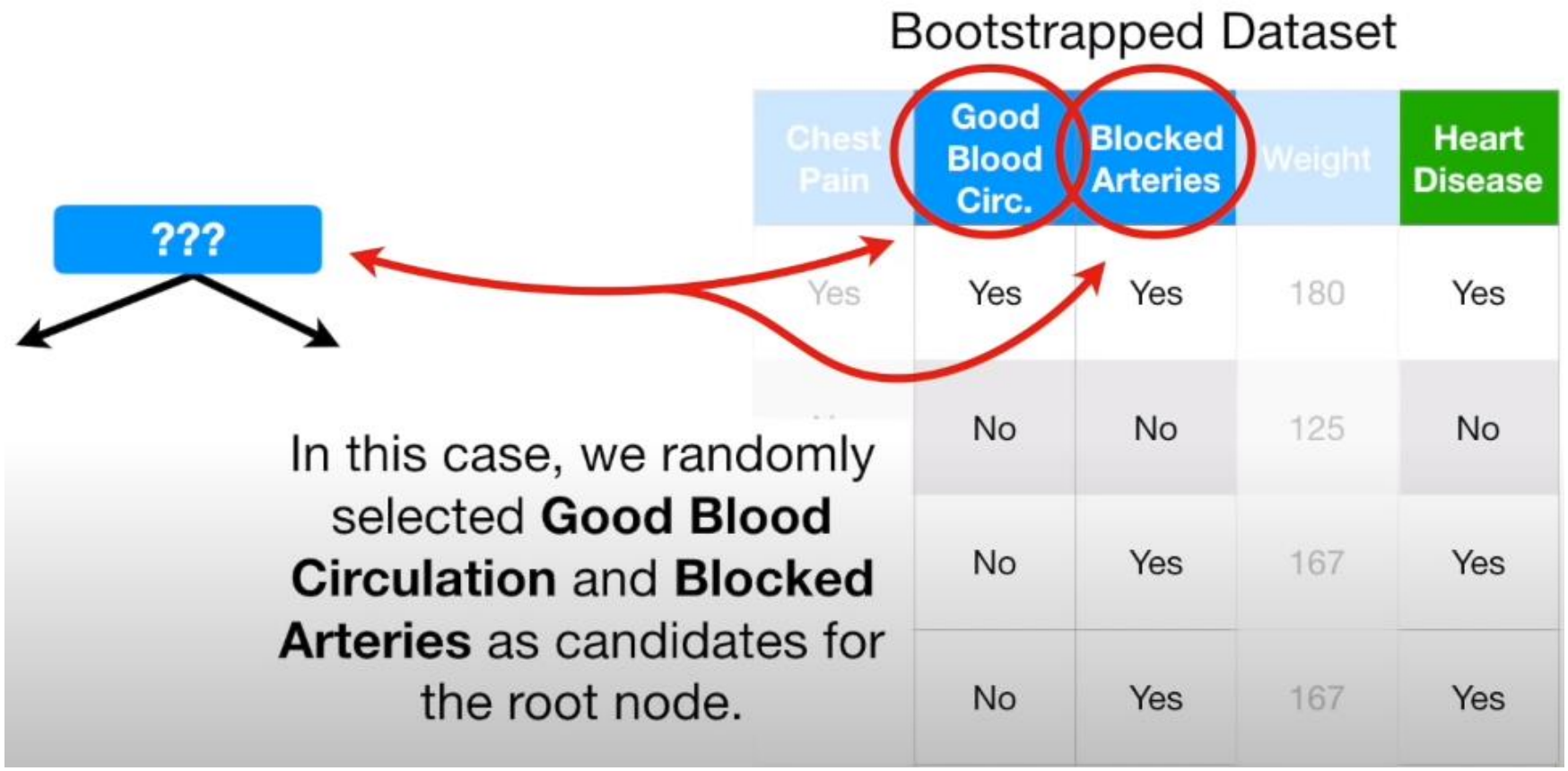
Step 2: Create a decision tree using the bootstrapped dataset, but only use a random subset of variables (or columns) at each step.

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

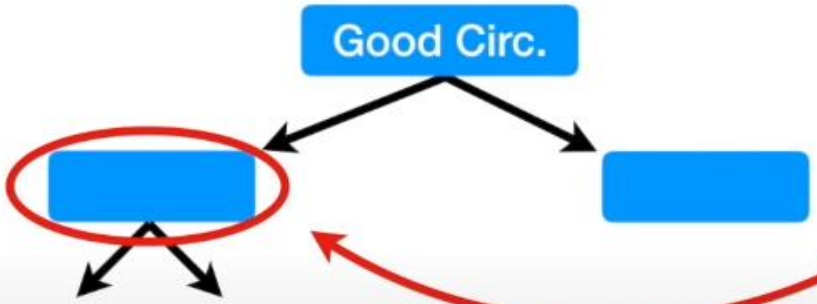


https://www.youtube.com/watch?v=J4Wdy0Wc_xQ

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



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

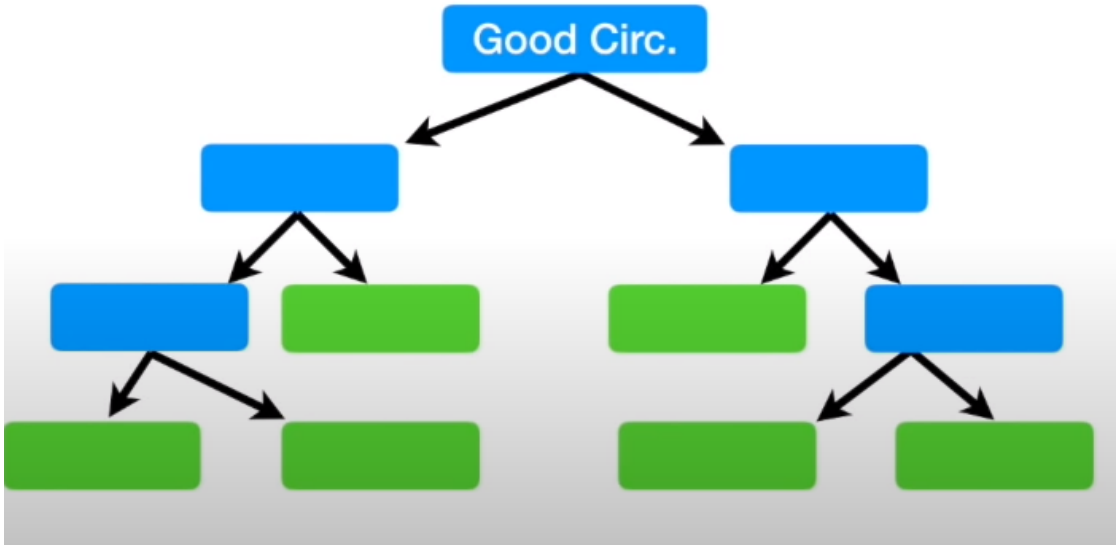
Bootstrapped Dataset

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

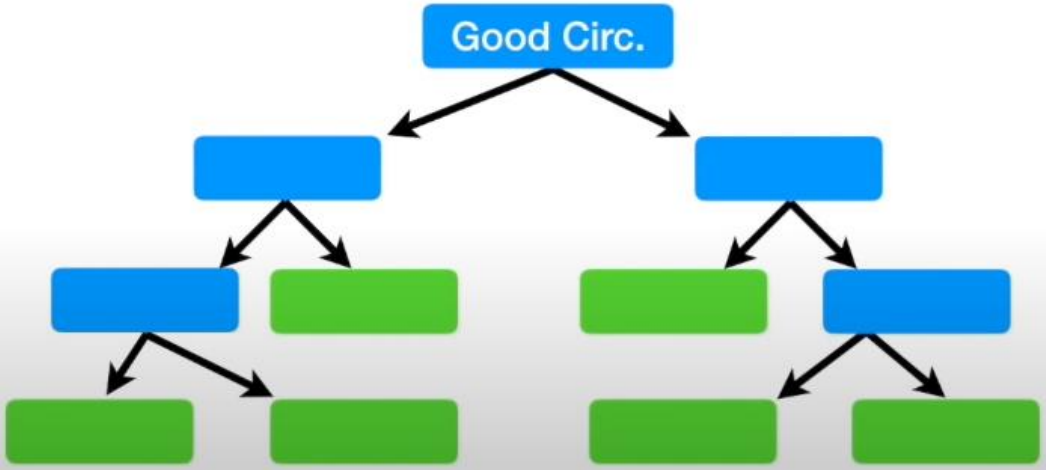
And we just build the tree as usual, but only considering a random subset of variables at each step.



We built a tree…

1) Using a bootstrapped dataset

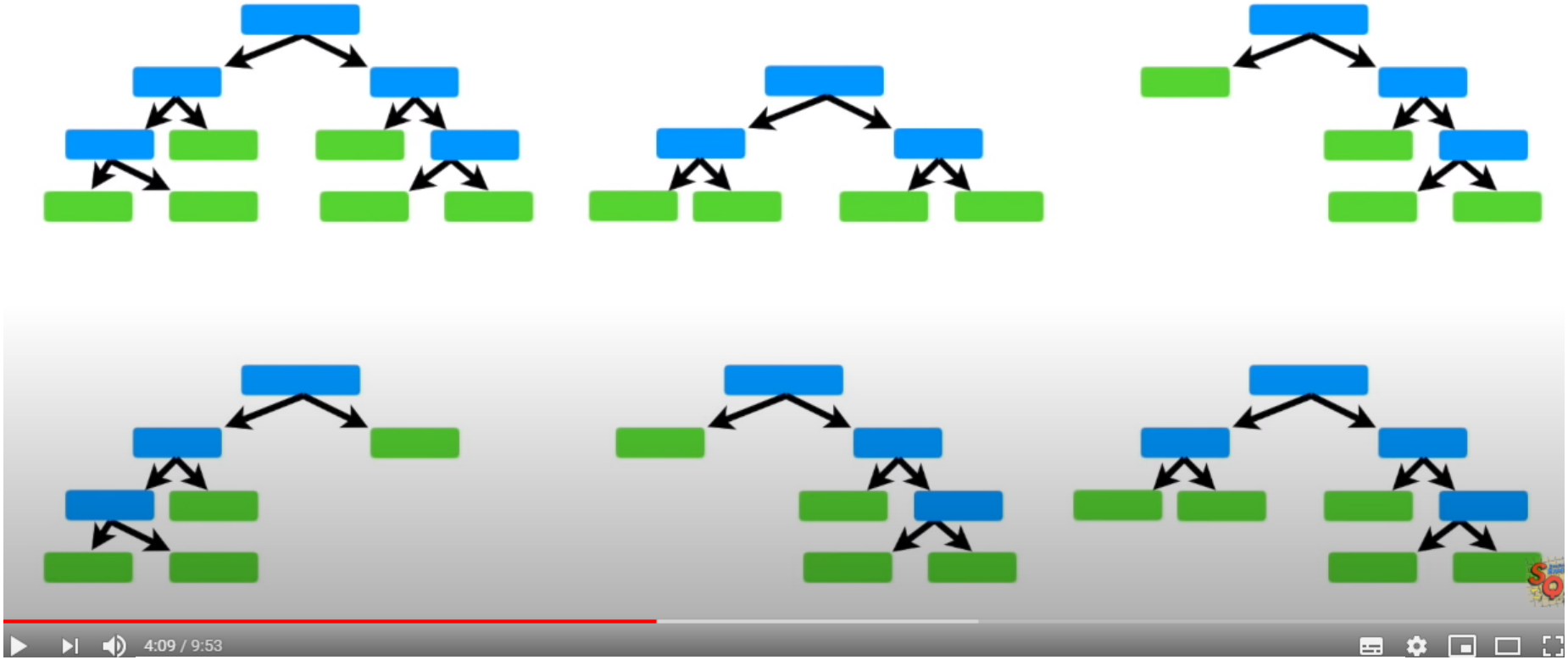
2) Only considering a random a subset of variables at each step.



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

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.

Ideally, you'd do this 100's of times.

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

https://www.youtube.com/watch?v=J4Wdy0Wc_xQ

How to use a Random Forest?

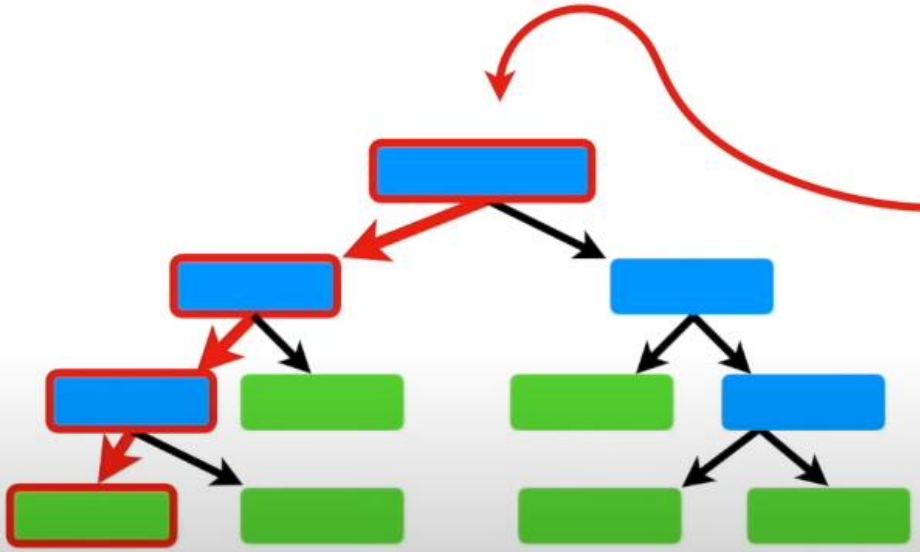
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	No	168	

…we've got all the measurements…

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

https://www.youtube.com/watch?v=J4Wdy0Wc_xQ

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	

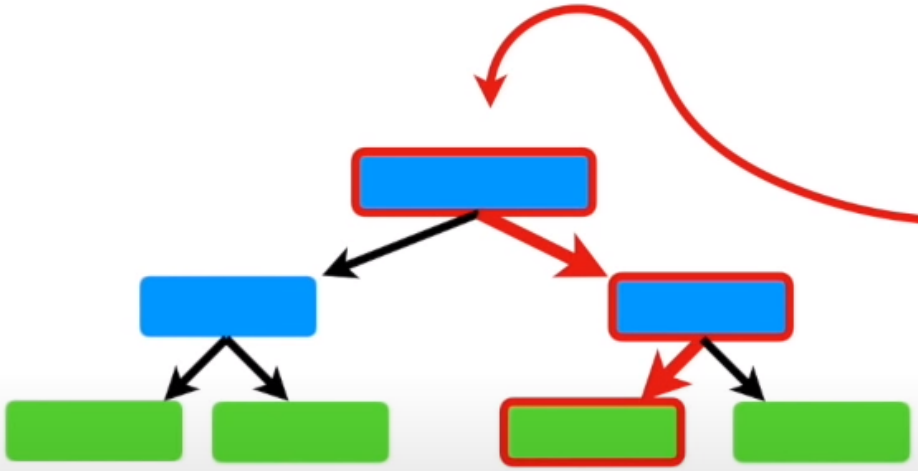
Heart Disease	
Yes	No
1	0

The first tree says "Yes"…

…and we keep track of that here.

https://www.youtube.com/watch?v=J4Wdy0Wc_xQ

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



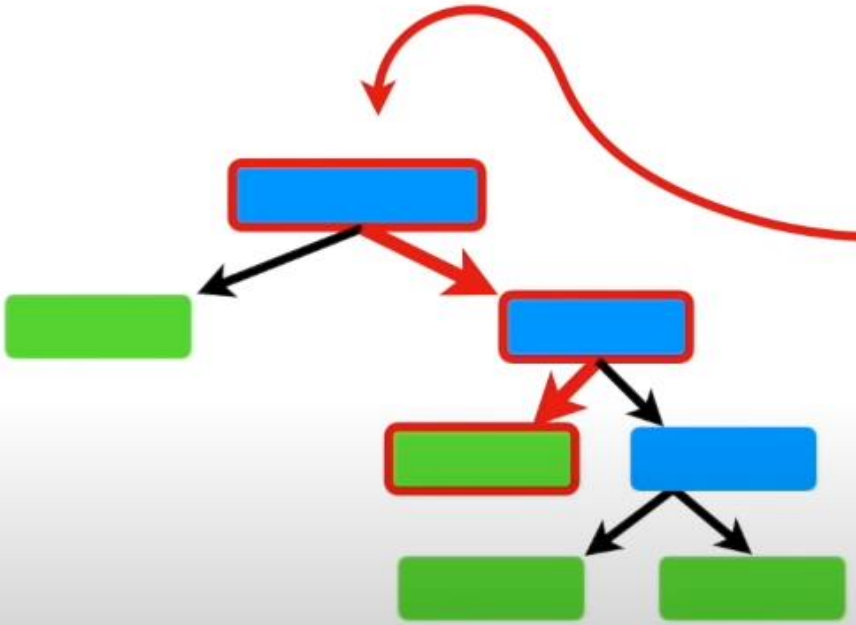
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	No	168	

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
4	1

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

How to use a Random Forest?

→ To predict the patient has heart disease

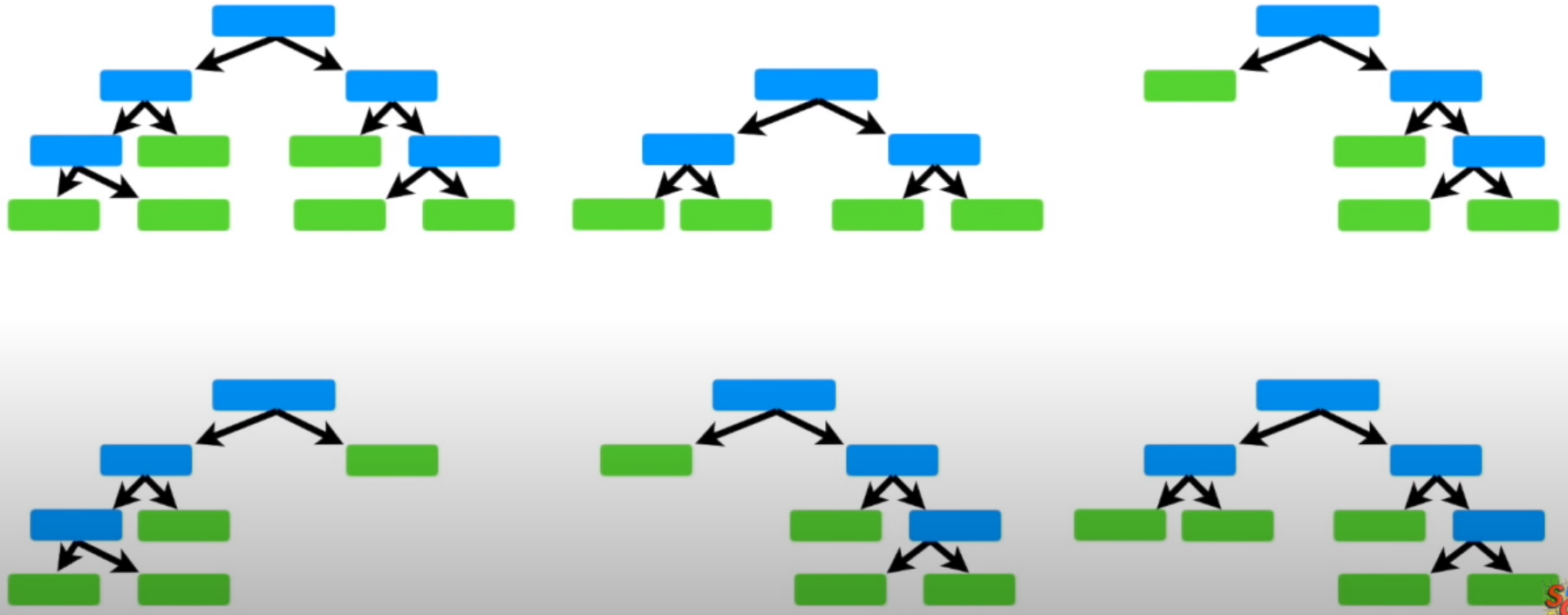
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	No	No	168	**YES**

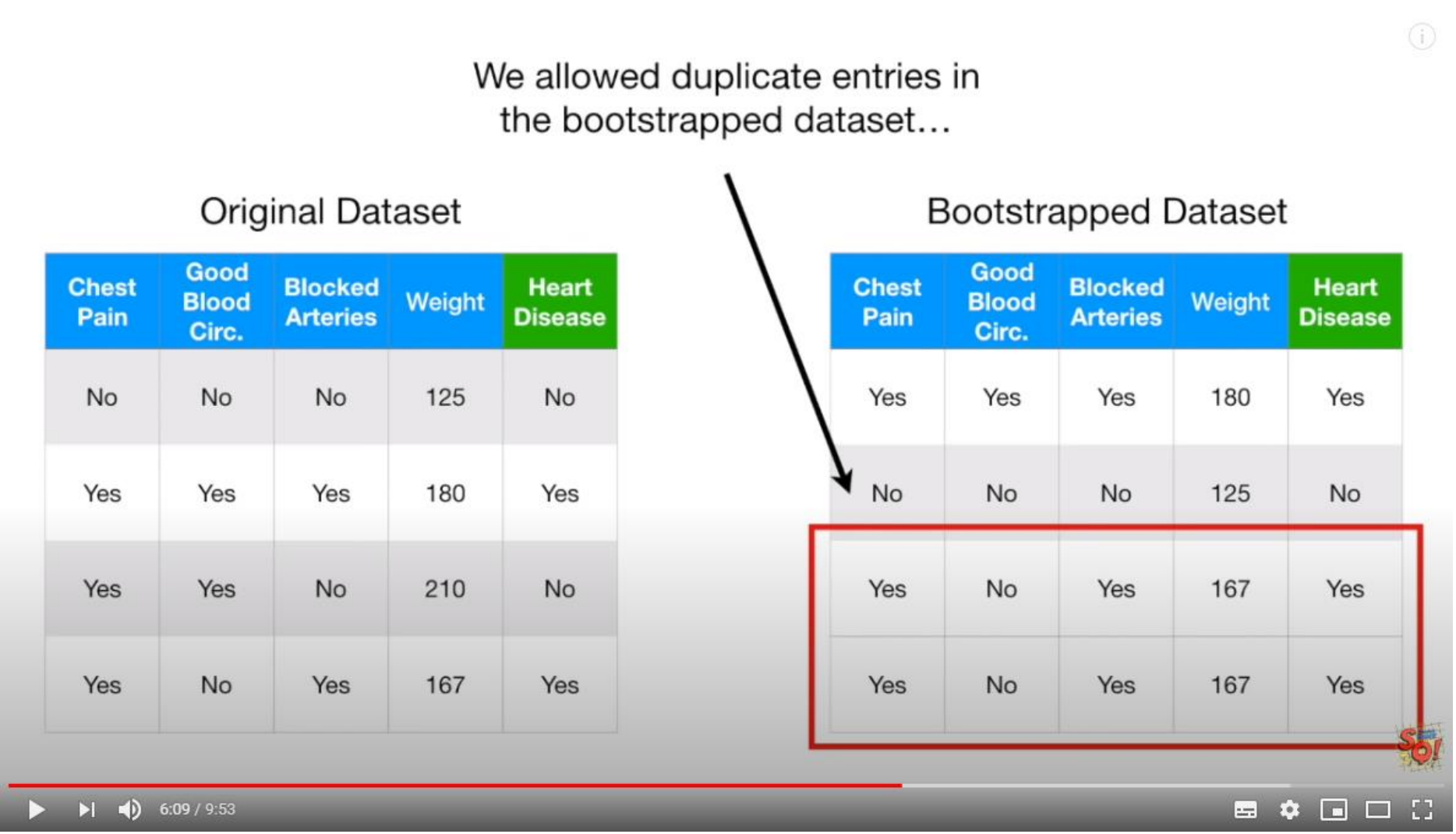
In this case, "**Yes**" received the most votes, so we will conclude that this patient has heart disease.

Bootstrapping the data plus using the **agg**regate to make a decision is called "**Bagging**"

OK, now we've seen how to create and use a random forest…

How do we know if it's any good?




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
6:09 / 9:53

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

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

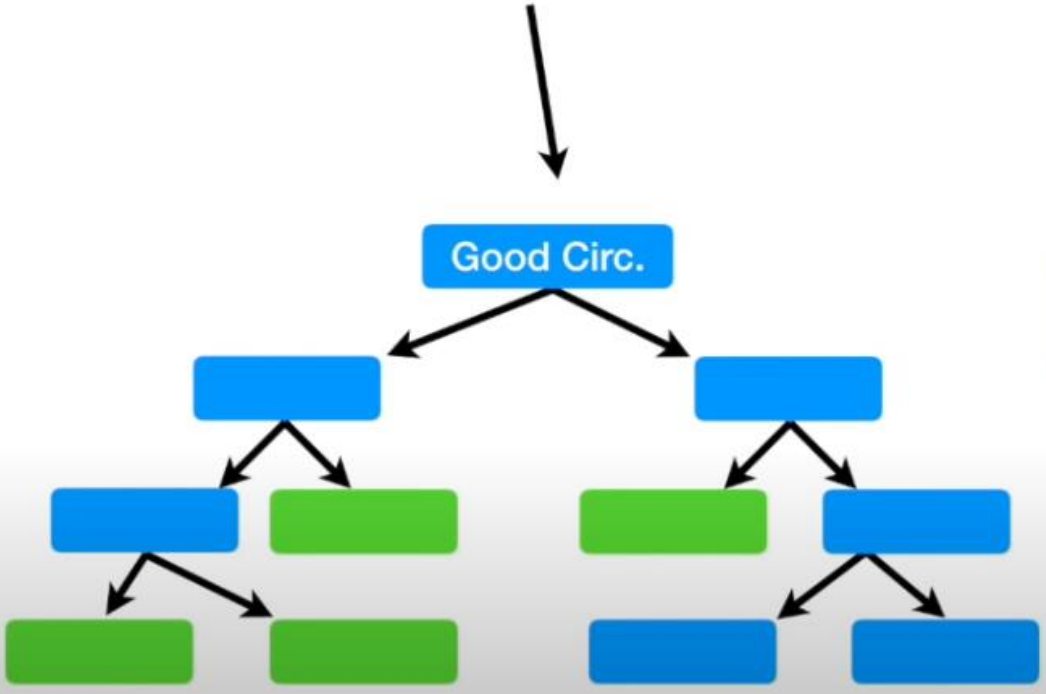
Bootstrapped Dataset

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

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

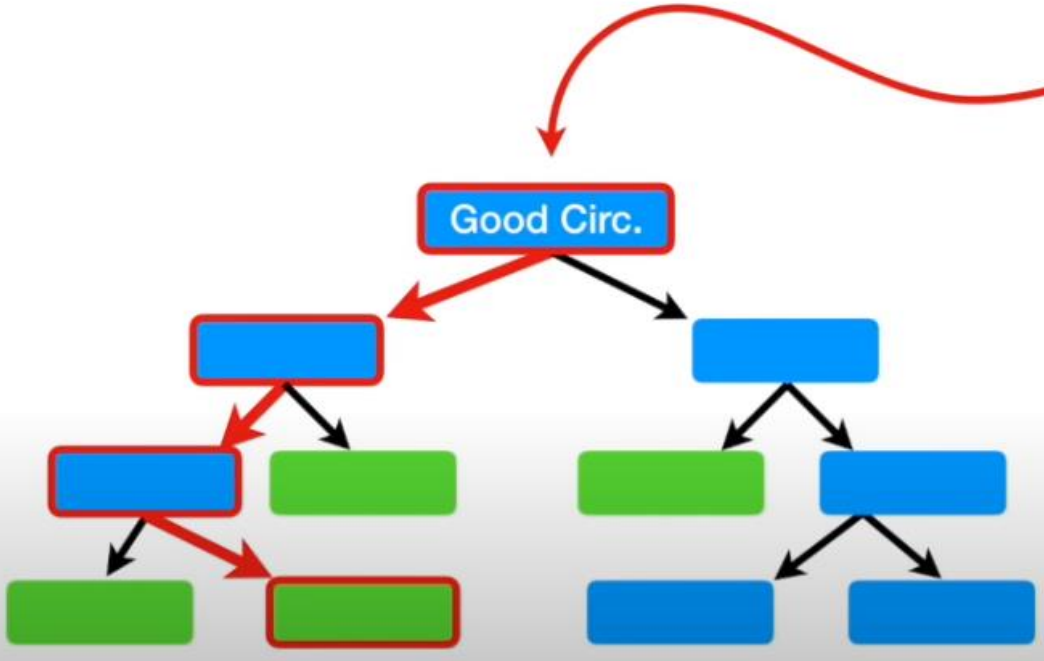
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	Yes	No	210	No

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

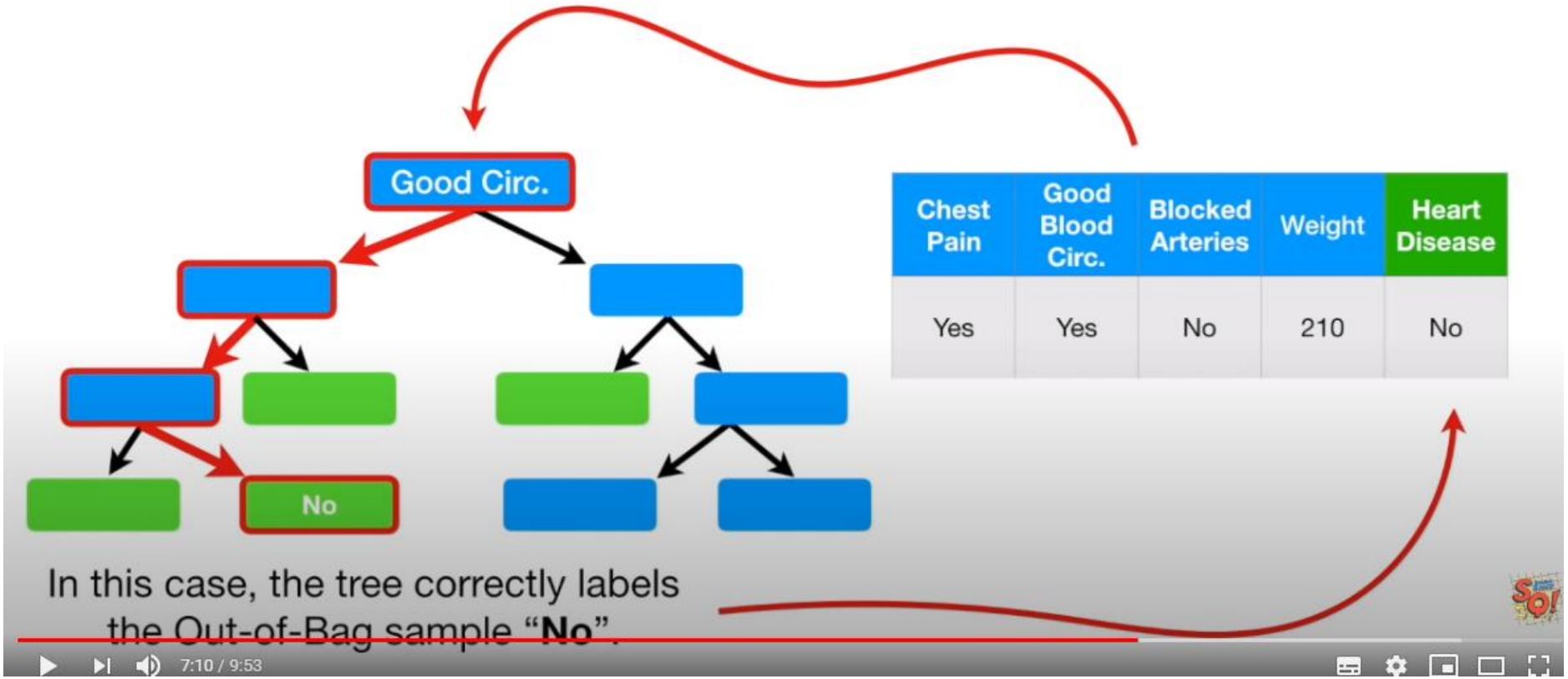


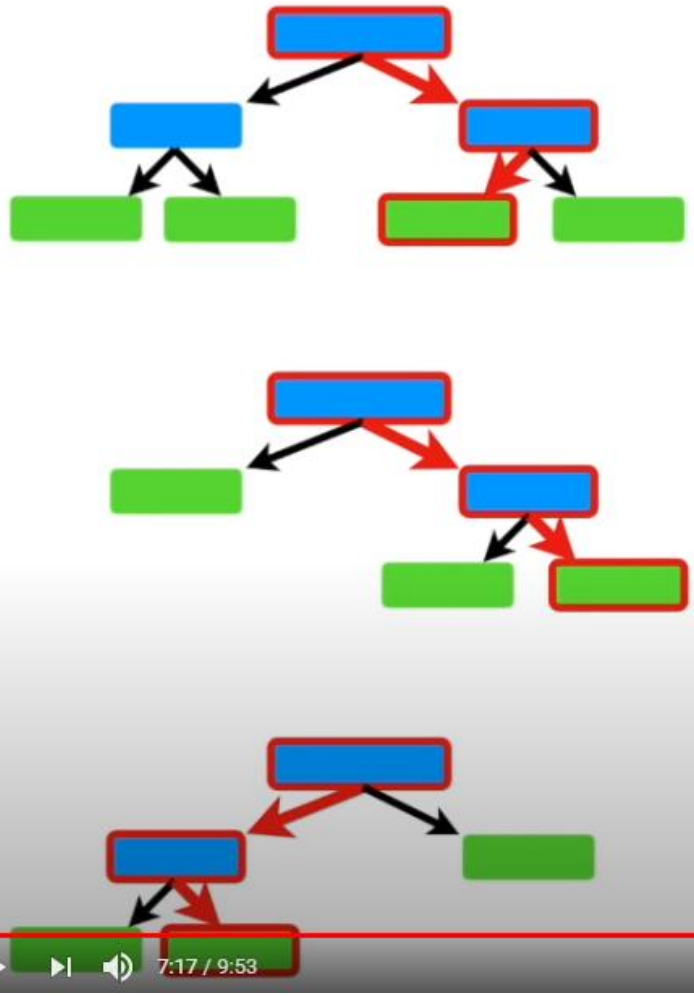
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	Yes	No	210	No

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



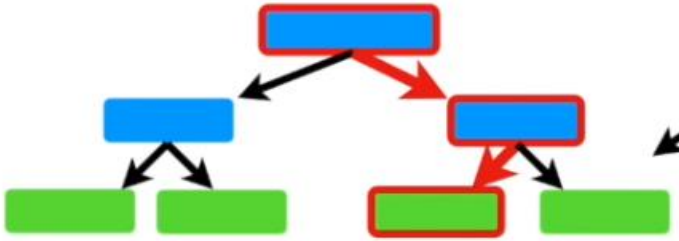
Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease
Yes	Yes	No	210	No


Good Circ.
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".
7:10 / 9:53

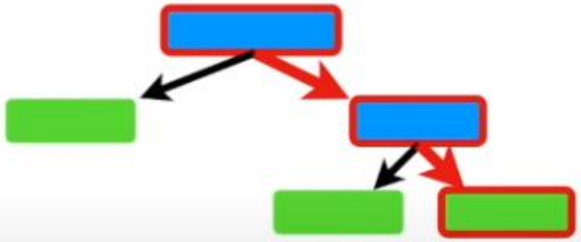


Then we run this Out-Of-Bag sample through all of the other trees that were built without it…

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

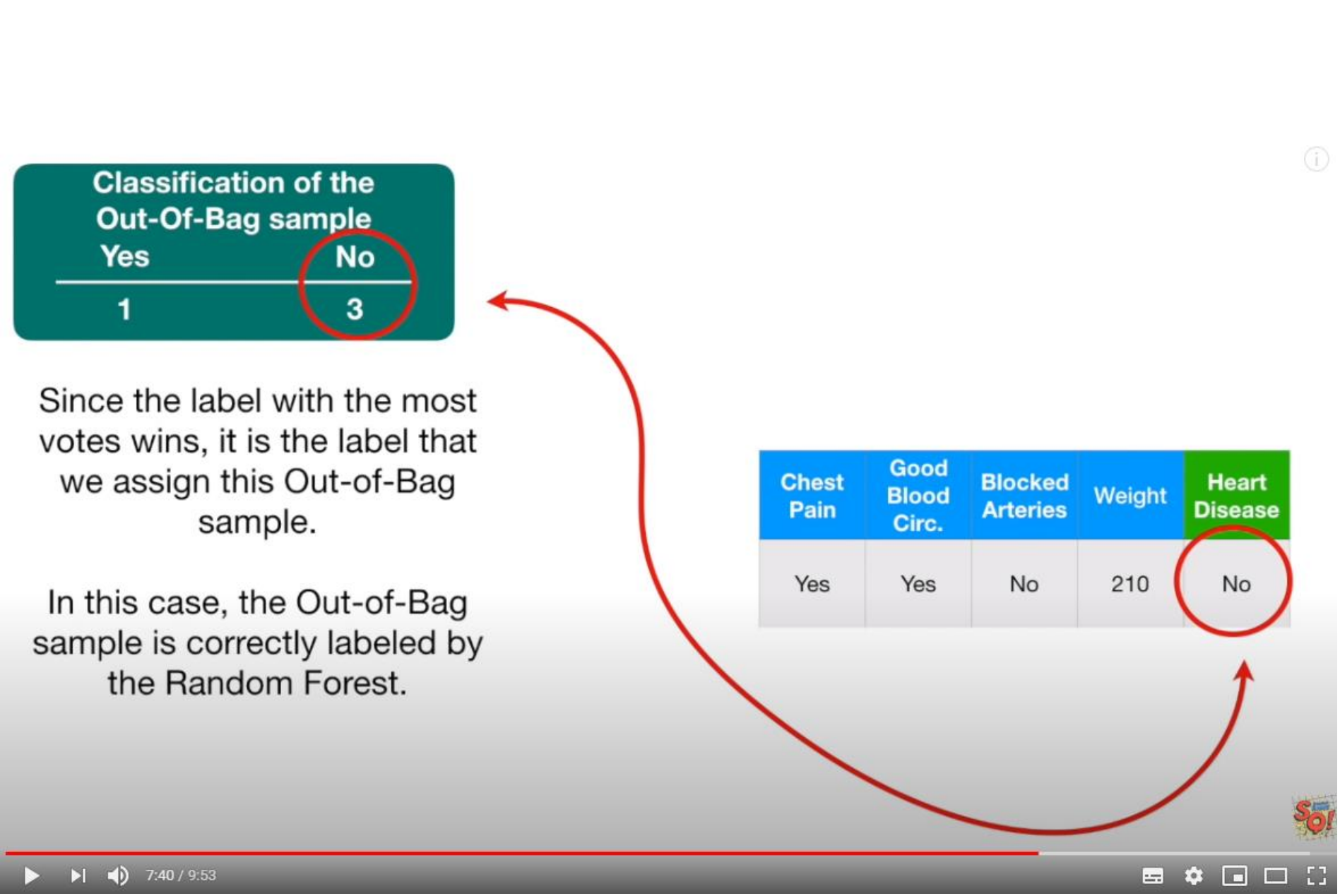


This tree incorrectly labeled the Out-of-Bag sample "**Yes**".



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**".


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
7:40 / 9:53

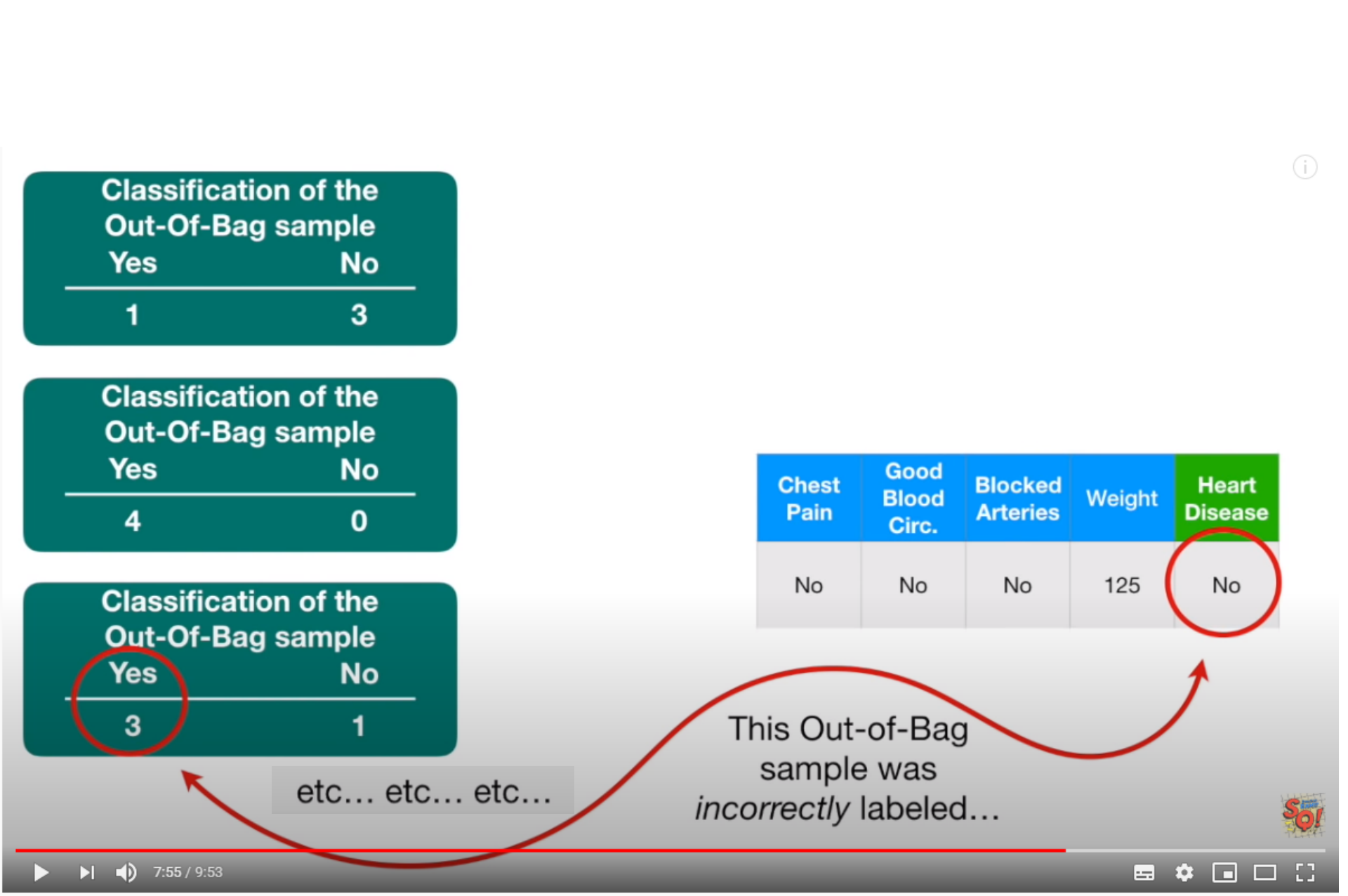
We then do the same thing for all of the other Out-Of-Bag samples for all of the trees.

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

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

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

This Out-of-Bag sample was also correctly 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…
Chest Pain
Good Blood Circ.
Blocked Arteries
Weight
Heart Disease
No
No
No
125
No
This Out-of-Bag sample was *incorrectly* labeled…
7:55 / 9:53

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

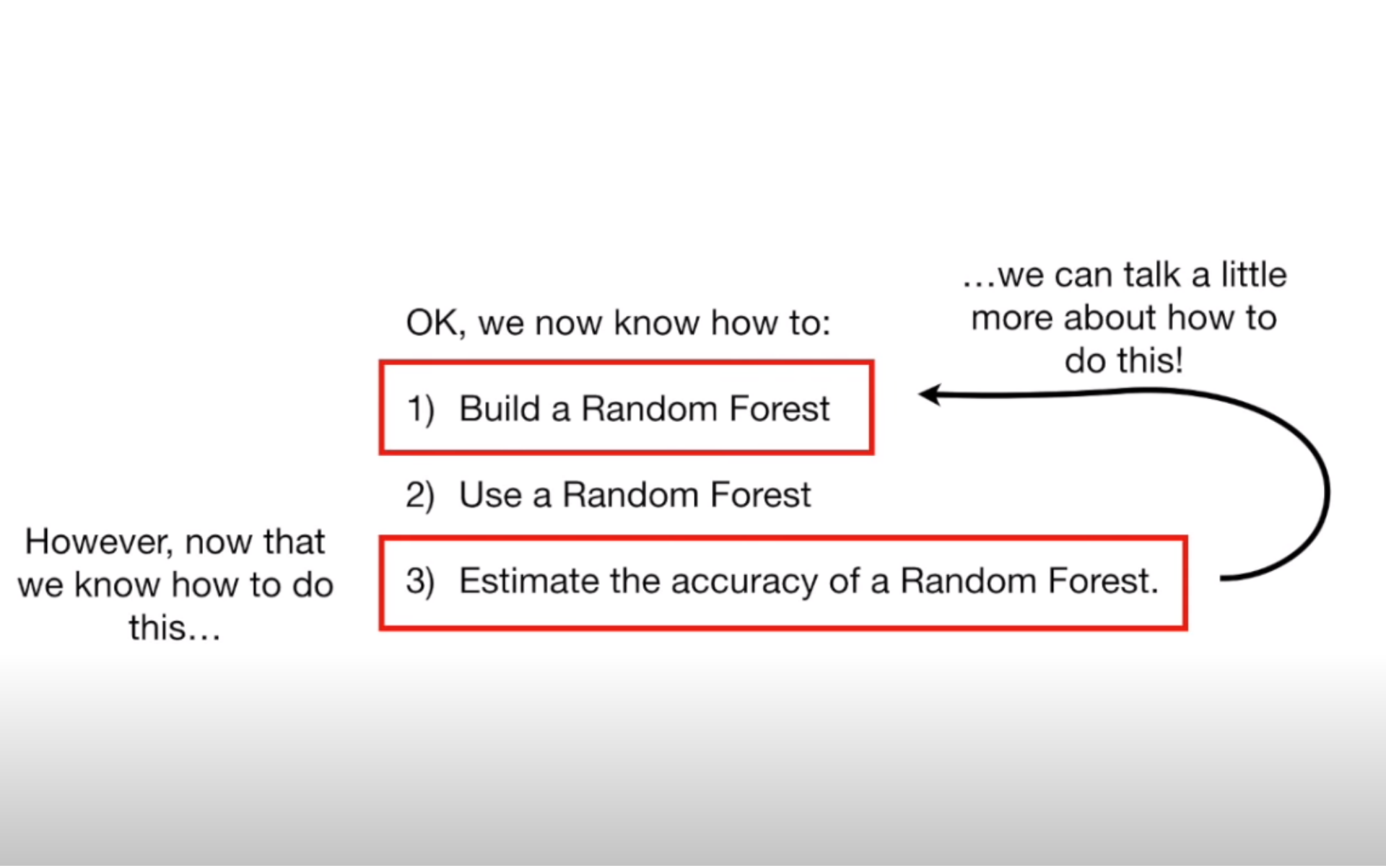
Classification of the Out-Of-Bag sample	
Yes	No
4	0

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**"



https://www.youtube.com/watch?v=J4Wdy0Wc_xQ

Remember when we built our first tree and we only used 2 variables (columns of data) to make a decision 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

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

…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

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

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.

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

Continue … next week