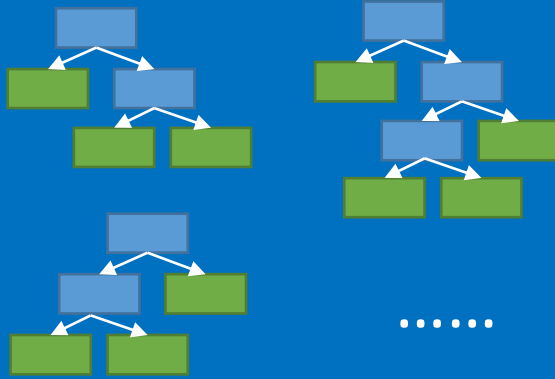


Feature importance – Gini based method

Sijin Zhang

Impurity based feature importance

Future 1	Future 2	Future 3	Target



Assuming that we have a bunch of samples, and through Bagging we created many decision trees

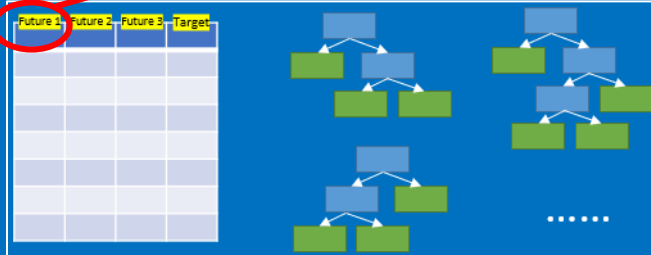
Impurity based feature importance



Usually the importance is estimated as below:

- For each feature
 - For each tree
 - Compute impurity decrease
 - Weighted by number of samples at node
 - Averaged over all trees
- Normalize the results if needed

Impurity based feature importance



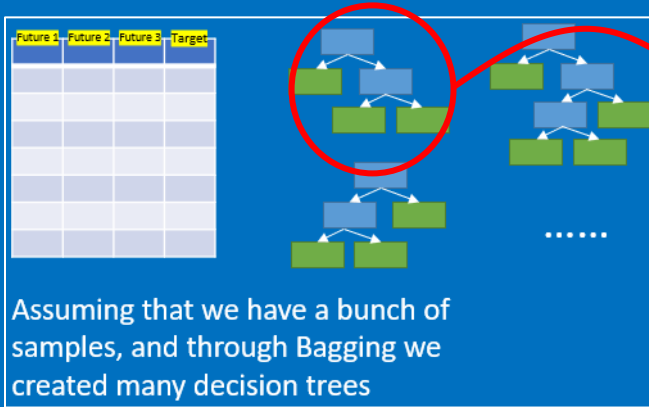
Assuming that we have a bunch of samples, and through Bagging we created many decision trees

Usually the importance

- For each feature
- For each tree
 - Compute impurity decrease
 - Weighted by number of samples at node
- Averaged over all trees
- Normalize the results if needed

For example, we have 3 features in this example, let's look at feature 1, "F1"

Impurity based feature importance




Usually the importance is estimated as below:

- For each feature **F1**
 - For each tree **Let's look at the first tree**
 - Compute impurity decrease
 - Weighted by number of samples at node
 - Averaged over all trees
 - Normalize the results if needed

Impurity based feature importance




Usually the importance is estimated as below:

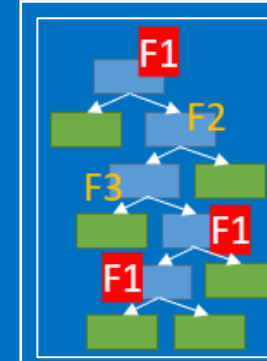
- For each feature **F1**
 - For each tree 
 - Compute impurity decrease
 - Weighted by number of samples at node
 - Averaged over all trees
- Normalize the results if needed

Impurity based feature importance



Usually the importance is estimated as below:

- For each feature **F1**
 - For each tree
 - Compute impurity decrease
 - Weighted by number of samples at node
 - Averaged over all trees
- Normalize the results if needed




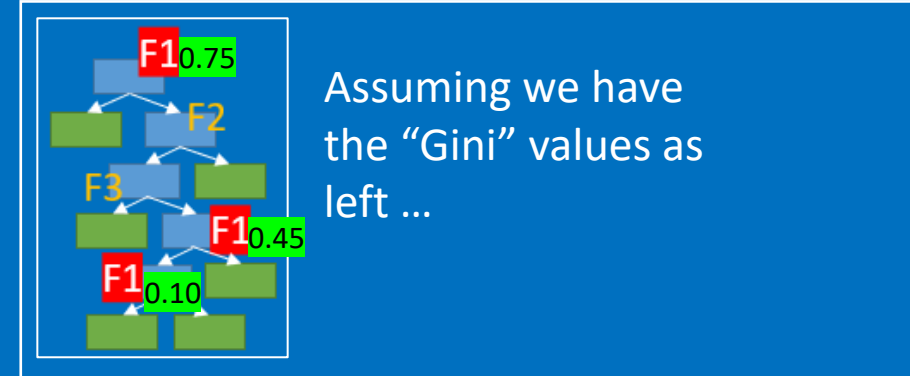
Assuming we have 5 levels of tree, and 3 "F1" features are included.

Impurity based feature importance



Usually the importance is estimated as below:

- For each feature **F1**
 - For each tree 
 - Compute impurity decrease
 - Weighted by number of samples at node
 - Averaged over all trees
- Normalize the results if needed



Impurity based feature importance



Usually the importance is estimated as below:

- For each feature

F1

- For each tree

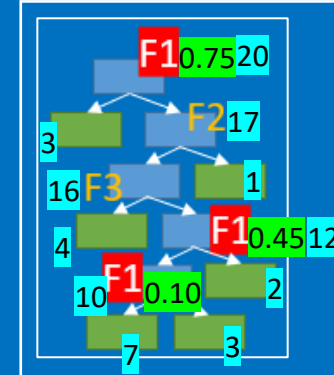


- Compute impurity decrease

- Weighted by number of samples at node

- Averaged over all trees

- Normalize the results if needed



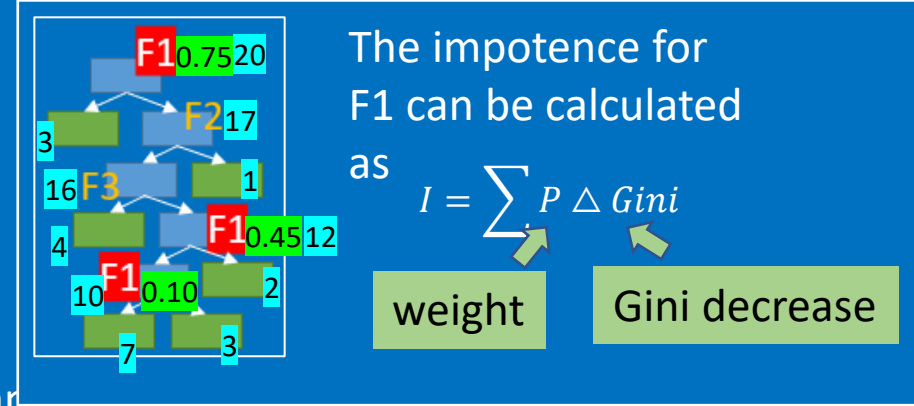
Assuming that in total we have 20 samples, and the samples that each node has is shown left

Impurity based feature importance



Usually the importance is estimated as below:


- For each feature **F1**
 - For each tree
 - Compute impurity decrease
 - Weighted by number of samples at node
 - Averaged over all trees
- Normalize the results if needed

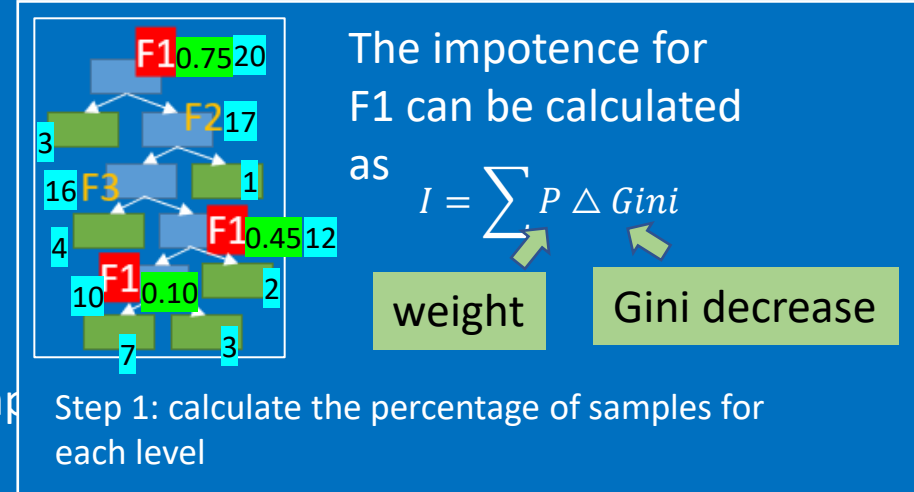


Impurity based feature importance

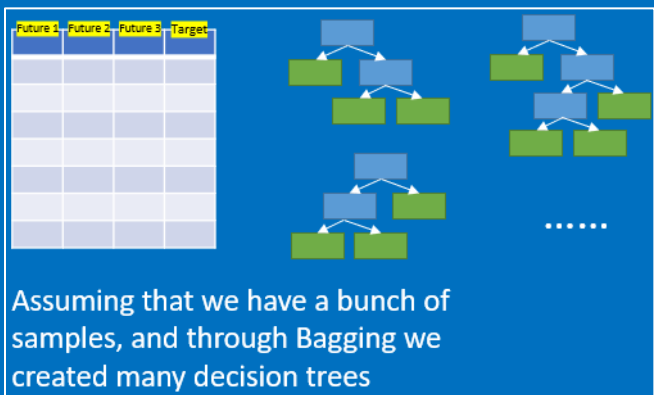


Usually the importance is estimated as below:

- For each feature **F1**
 - For each tree
 - Compute impurity decrease
 - Weighted by number of samples
 - Averaged over all trees
- Normalize the results if needed

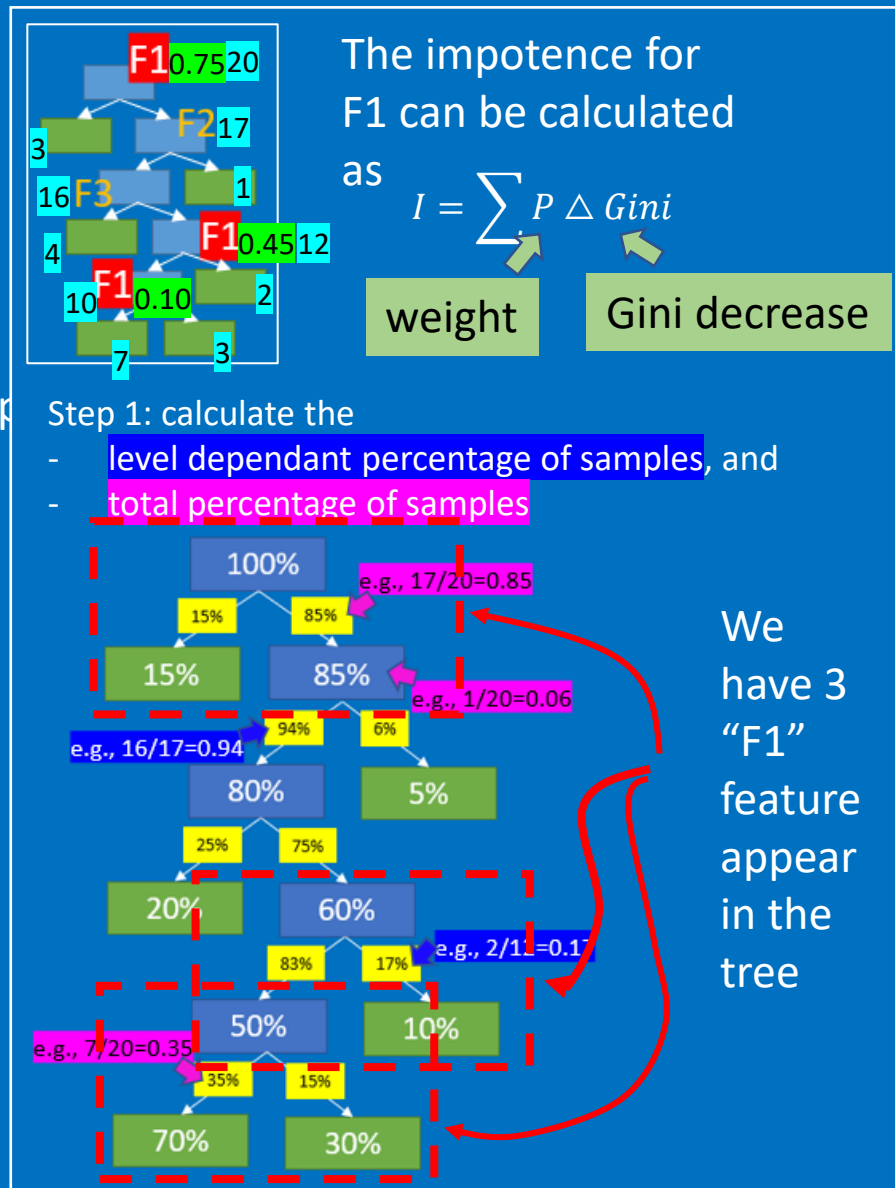


Impurity based feature importance

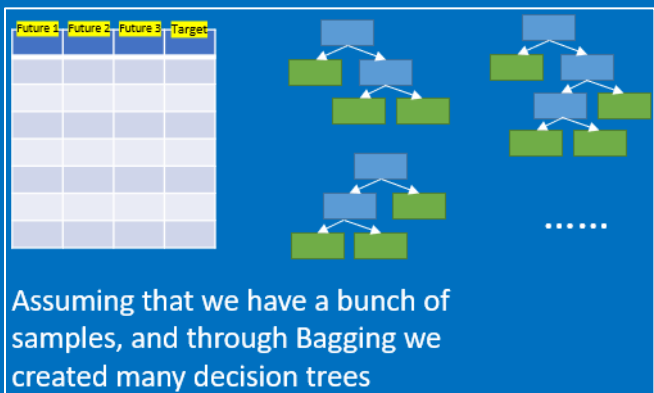


Usually the importance is estimated as below:

- For each feature **F1**
 - For each tree
 - Compute impurity decrease
 - Weighted by number of samples
 - Averaged over all trees
- Normalize the results if needed



Impurity based feature importance



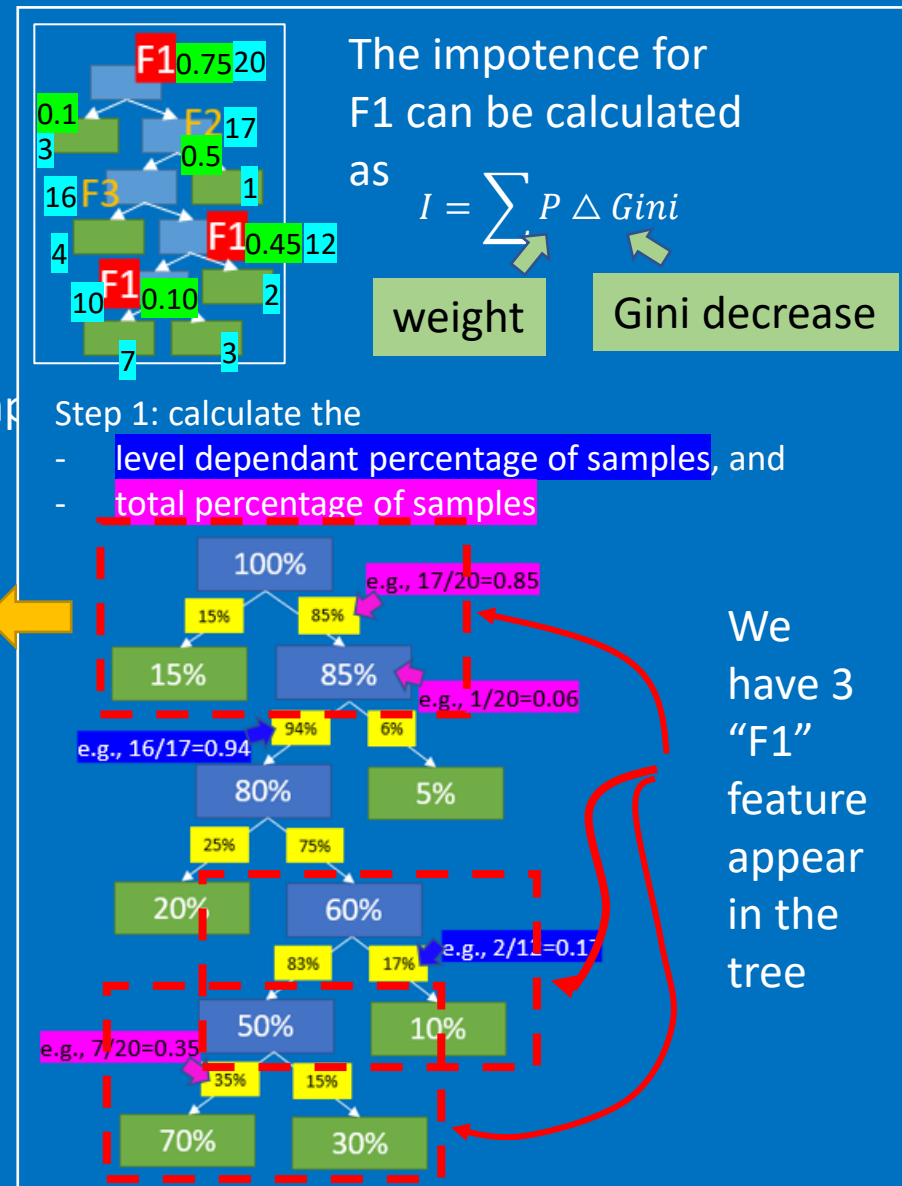
Usually the importance is estimated as below:

- For each feature **F1**
 - For each tree
 - Compute impurity decrease
 - Weighted by number of samples

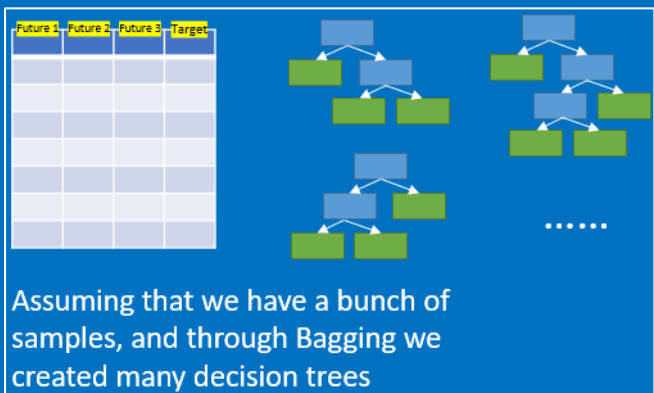
We can calculate $\Delta Gini$ as

$$\Delta Gini_1 = 0.75 - (0.85 \times 0.5 + 0.15 \times 0.1) = 0.31$$

Node Gini Total percentage of samples Next node Gini Total percentage of samples Next leaf Gini Total percentage of samples



Impurity based feature importance



Usually the importance is estimated as below:

- For each feature **F1**
 - For each tree
 - Compute impurity decrease
 - Weighted by number of samples

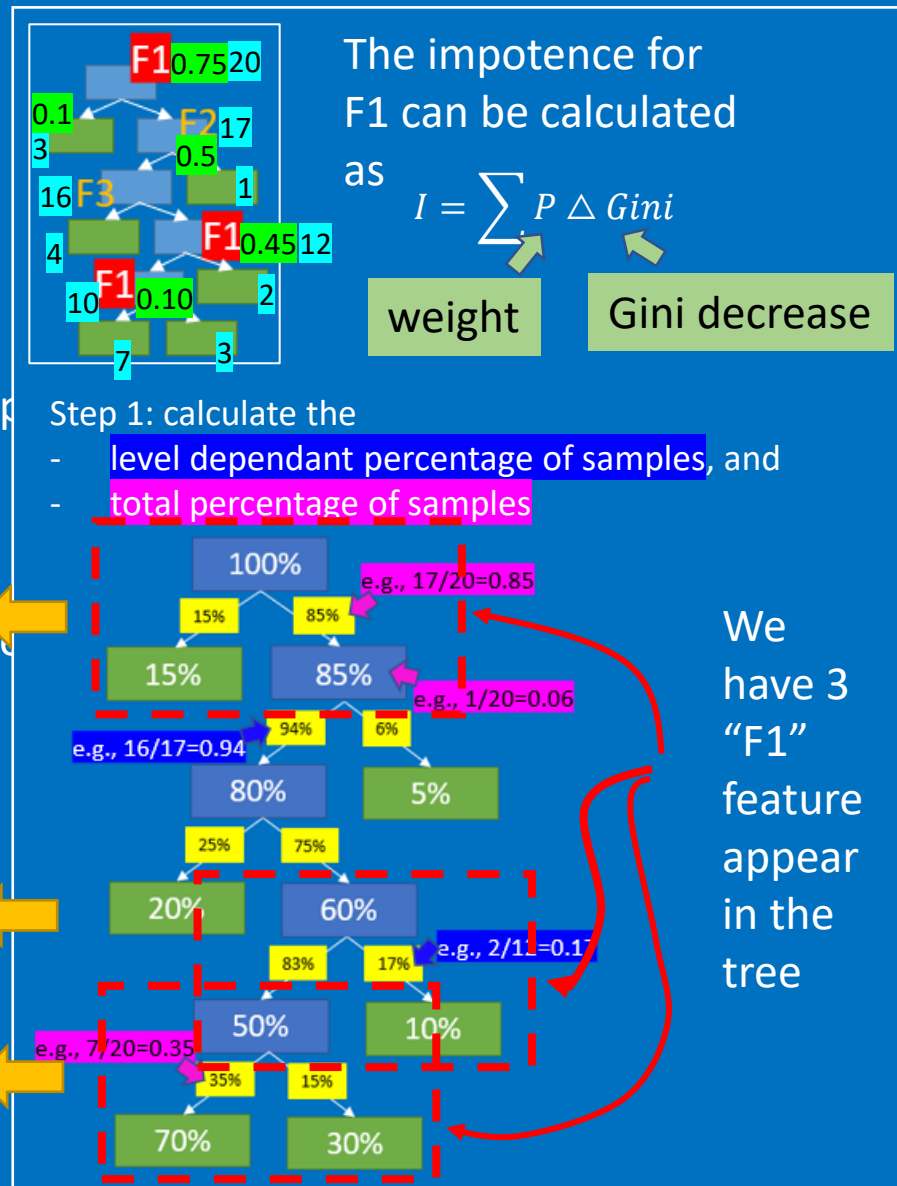
We can calculate $\Delta Gini$ as

$$\Delta Gini_1 = 0.75 - (0.85 \times 0.5 + 0.15 \times 0.1) = 0.31$$

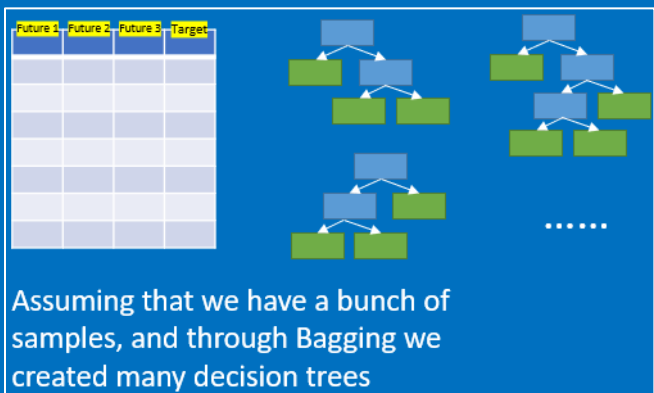
Node Gini Total percentage of samples Next node Gini Total percentage of samples Next leaf Gini Total percentage of samples

$$\Delta Gini_2 = 0.25$$

$$\Delta Gini_3 = 0.1$$



Impurity based feature importance



Usually the importance is estimated as below:

- For each feature **F1**
 - For each tree
 - Compute impurity decrease
 - Weighted by number of samples

Level dependant percentage of samples

100%

We can calculate $\Delta Gini$ as

$$\Delta Gini_1 = 0.75 - (0.85 \times 0.5 + 0.15 \times 0.1) = 0.31$$

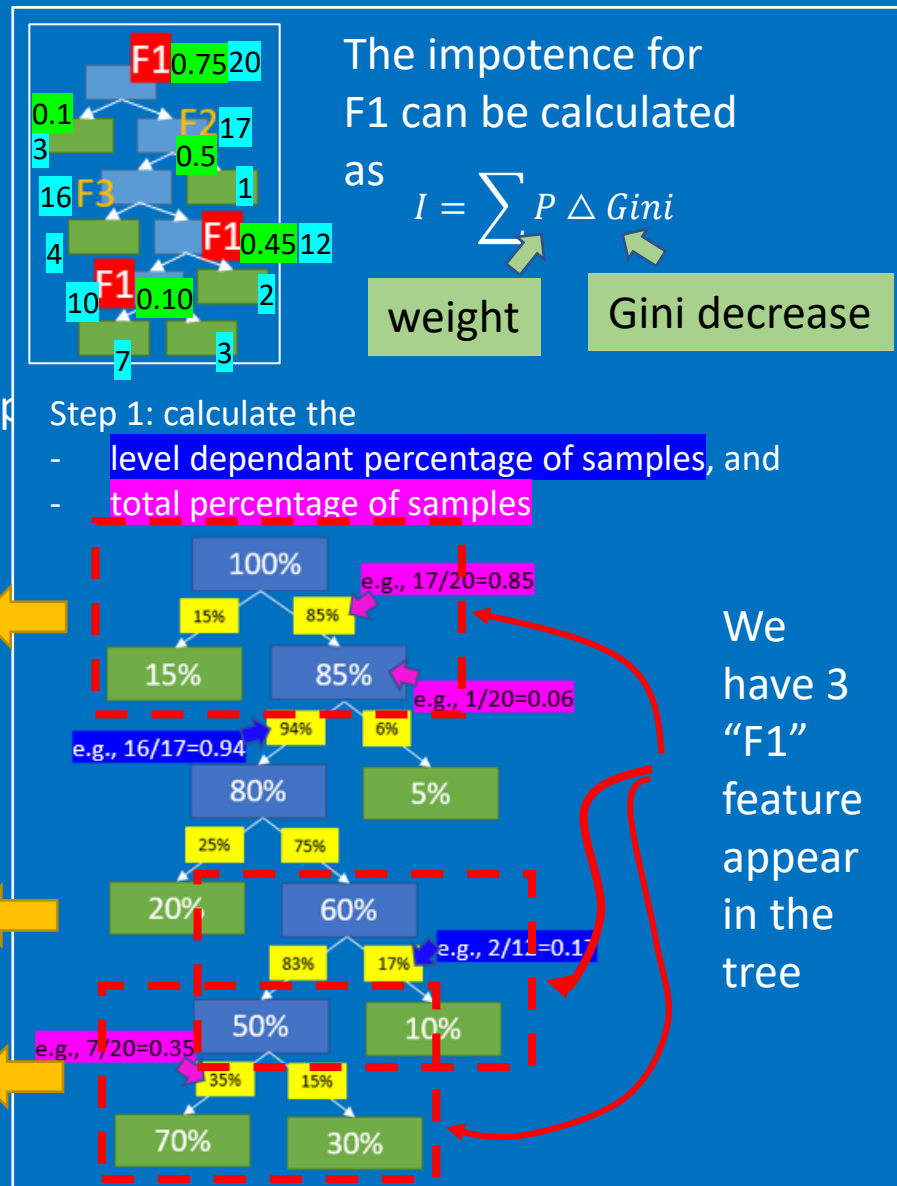
Node Gini Next node Gini Next leaf Gini
Total percentage of samples Total percentage of samples

60%

$$\Delta Gini_2 = 0.25$$

50%


$$\Delta Gini_3 = 0.1$$



Impurity based feature importance



Usually the importance is estimated as below:

- For each feature **F1**
 - For each tree
 - Compute impurity decrease
 - Weighted by number of samples

We can calculate $\Delta Gini$ as

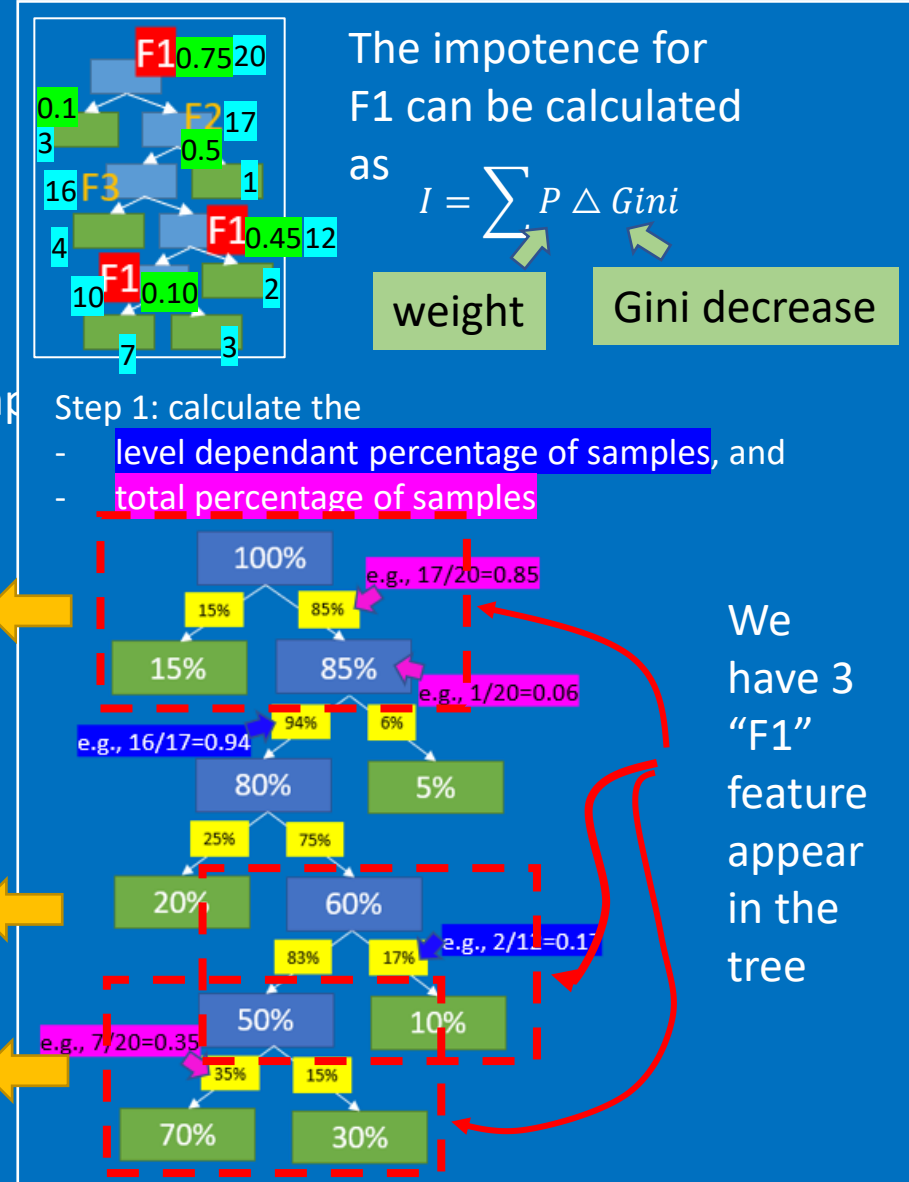
$$\Delta Gini_1 = 0.75 - (0.85 \times 0.5 + 0.15 \times 0.1) = 0.31$$

Node Gini Next node Gini Next leaf Gini
Total percentage of samples Total percentage of samples

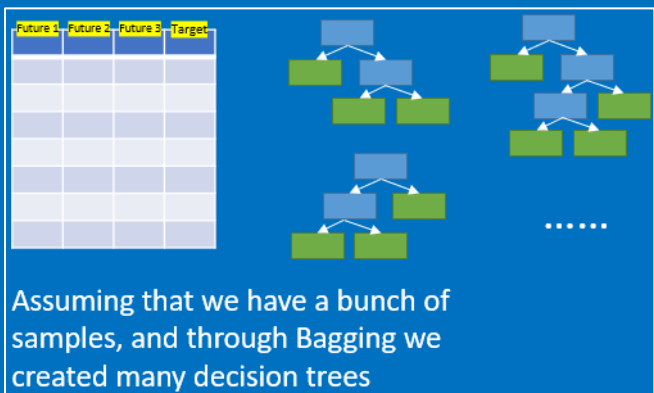
100%

$$\begin{aligned} I_{F_1} &= 1 \times 0.31 \\ &+ 0.6 \times 0.25 \\ &+ 0.5 \times 0.1 \\ &= 0.51 \end{aligned}$$

The importance for F1



Impurity based feature importance



Usually the importance is estimated as below:

- For each feature

F1

- For each tree



- Compute impurity decrease
- Weighted by number of samples at node



- Averaged over all trees

We go through all the trees with the last step, and average the results

- Normalize the results if needed


We through all the features for the above process, and normalize the results.
For example, we can divide the averaged results by the number of trees being used ...

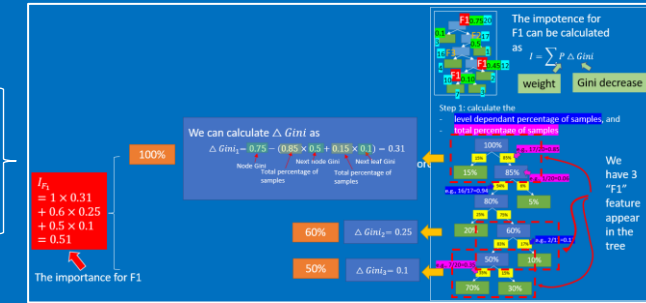
The high the value, the more important that the feature is

Impurity based feature importance



Usually the importance is estimated as below:

- For each feature **F1**
 - For each tree 
 - Compute impurity decrease
 - Weighted by number of samples at node



- Averaged over all trees

We go through all the trees with the last step, and average the results
- Normalize the results if needed

We through all the features for the above process, and normalize the results. For example, we can divide the averaged results by the number of trees being used ...

Eventually, the higher the value, the more important the feature is