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## *IS LAB- 13*

### ***Decision tree using ID3 Algorithm***

*The decision tree splits the nodes on all available variables and then selects the split which results in most homogeneous sub-nodes. ID3 stands for Iterative Dichotomiser 3. It is one of the many algorithms used to make decision trees. The Algorithm selection is based upon the type of target variables e.g.*

*#C4.5(successor of ID3)*

*#CART(Classification And  
Regression Tree)*

*#CHAID(Chi-square automatic interaction detection Performs multi-level splits when computing classification trees)*

*#MARS(multivariate adaptive regression splines)*

*ID3 Algorithm iteratively divides the features into two or more groups at each step*

### **Steps in ID3 algorithm:**

*#It begins with the original set  $S$  as the root node.*

*#On each iteration of the algorithm, it iterates through the very unused attribute of the set  $S$  and calculates Entropy( $H$ ) and Information gain( $IG$ ) of this attribute.*

*#It then selects the attribute which has the smallest Entropy or Largest*

*Information gain. #The set  $S$  is then split by the selected attribute to*

*produce a subset of the data.*

*#The algorithm continues to recur on each subset, considering only attributes never selected before.*

### **Using a sample dataset of iris flower identification.**

*In [89]:* `import numpy as np  
import pandas as pd  
import matplotlib.pyplot as plt`

In [90]: `input_data=pd.read_csv("Iris.csv")`

In [91]: `input_data.head()`

Out[91]:

		<i>Id</i>	<i>SepalLength</i>	<i>SepalWidth</i>	<i>PetalLengt</i>	<i>PetalWidth</i>	<i>Species</i>
			<i>Cm</i>	<i>Cm</i>	<i>hCm</i>	<i>Cm</i>	
<i>0</i>	<i>1</i>		<i>5.1</i>	<i>3.5</i>	<i>1.4</i>	<i>0.2</i>	<i>Iris-setosa</i>
<i>1</i>	<i>2</i>		<i>4.9</i>	<i>3.0</i>	<i>1.4</i>	<i>0.2</i>	<i>Iris-setosa</i>
<i>2</i>	<i>3</i>		<i>4.7</i>	<i>3.2</i>	<i>1.3</i>	<i>0.2</i>	<i>Iris-setosa</i>
<i>3</i>	<i>4</i>		<i>4.6</i>	<i>3.1</i>	<i>1.5</i>	<i>0.2</i>	<i>Iris-setosa</i>
<i>4</i>	<i>5</i>		<i>5.0</i>	<i>3.6</i>	<i>1.4</i>	<i>0.2</i>	<i>Iris-setosa</i>

In [92]: `eps=np.finfo(float).eps`

## Calculating Entropy of each feature

```
In [93]: def ent(input_data, attribute):  
    target_variables=input_data.Species.unique()  
    variables=input_data[attribute].unique()  
    entropy_attribute=0  
  
    for variable in variables: entropy_each_feature=0  
        for target_variable in target_variables:  
  
            num=len(input_data[attribute][input_data[attribute]==variable])  
            den=len(input_data[attribute][input_data[attribute]==variable])  
            fraction=num/(den+eps)  
  
            entropy_each_feature+= -  
            fraction*log(fraction+eps)  
            fraction2=den/len(input_data)  
            entropy_attribute+= -fraction2*entropy_each_feature
```

```
In [94]: a_entropy={k:ent(input_data,k) for k in input_data.keys()[:-1]} a_entropy
```

```
Out[94]: {'Id': 0.0,  
          'SepalLengthCm': 0.7080248798300978,  
          'SepalWidthCm': 1.0740925365975489,  
          'PetalLengthCm': 0.1386459770753558,  
          'PetalWidthCm': 0.14906466204571406}
```

## Find Information Gain

```
In [95]: def ig(e_dataset, e_attr):  
    return(e_dataset-e_attr)
```

```
In [96]: IG={k:ig(entropy_node,a_entropy[k]) for k in a_entropy}
```

In [97]:

IG

Out[97]: {'Id': 1.584962500721156,  
'SepalLengthCm': 0.8769376208910583,  
'SepalWidthCm': 0.5108699641236072,  
'PetalLengthCm': 1.4463165236458002,  
'PetalWidthCm': 1.435897838675442}

*Find entropy of original dataset S*

In [98]:

```
def find_entropy(input_data):  
    Species=input_data.keys()[:-1]  
    entropy=0  
    values=input_data[Species].unique()  
    for value in values:  
        fraction=input_data[Species].value_counts()[value]/len(input_data[Species])  
        entropy+=-fraction*np.log2(fraction)
```

In [99]:

```
def find_winner(input_data):  
    Entropy_att=[]  
    IG=[]  
    for key in input_data.keys()[:-1]:  
        Entropy_att.append(ent(input_data, key))
```

```
In [100]: def get_subtable(input_data, node, value):  
          return input_data[input_data[node]==value].reset_index(drop=True)
```

```
In [101]: def buildTree(input_data, tree=None):  
          species=input_data.keys()[-1]  
  
          node=find_winner(input_data)  
  
          attValue=np.unique(input_data[node])  
  
          if tree is None: tree={}  
              tree[node]={}  
  
          for value in attValue: subtable=get_subtable(input_data, node, value)  
              clValue, counts=np.unique(subtable['Species'], return_counts=True)  
  
              if len(counts)==1:  
                  tree[node][value]=clValue[0]
```

```

t=buildTree(input_data)

```

```
import pprint
```

```
pprint.pprint(t)
```

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