Decision Tree:

Decision Tree set up a tree structure on training data which helps make a decision based on rules

We can apply Decision tree for both classification and regression problems, so this decision tree also called as CART(Classification and Regression Tree)

Rules:

- * Entropy(Information gain)
- * Gini

```
In [2]: import pandas as pd
import numpy as np

In [4]: from sklearn.datasets import load_iris
inic=load_inic()
```

In [4]: from sklearn.datasets import load_iris
 iris=load_iris()
 iris

. . .

In [6]: # conver iris dictionary into dataframe
 data1=iris.data
 c1=iris.feature_names
 df=pd.DataFrame(data1,columns=c1)
 df.head()

Out[6]:

	sepal length (cm)	sepal width (cm)	petal length (cm)	petal width (cm)
0	5.1	3.5	1.4	0.2
1	4.9	3.0	1.4	0.2
2	4.7	3.2	1.3	0.2
3	4.6	3.1	1.5	0.2
4	5.0	3.6	1.4	0.2

```
In [39]: #now set the target to dataframe
    df['Target']=iris.target
    df.sample(5)
```

Out[39]:

	sepal length (cm)	sepal width (cm)	petal length (cm)	petal width (cm)	Target
102	7.1	3.0	5.9	2.1	2
92	5.8	2.6	4.0	1.2	1
76	6.8	2.8	4.8	1.4	1
114	5.8	2.8	5.1	2.4	2
75	6.6	3.0	4.4	1.4	1

```
In [8]: # find the null values
    df.isna().sum()
```

Out[8]: sepal length (cm) 0 sepal width (cm) 0 petal length (cm) 0 petal width (cm) 0 Target 0 dtype: int64

In [15]: # Now take the feature names into X and target values into y
X=df.drop('Target',axis=1)
y=df[['Target']]

In [25]: # split the data into train test split
 from sklearn.model_selection import train_test_split
 X_train,X_test,y_train,y_test=train_test_split(X,y,test_size=0.3,random_state=42
 X_train.head()

Out[25]:

	sepal length (cm)	sepal width (cm)	petal length (cm)	petal width (cm)
81	5.5	2.4	3.7	1.0
133	6.3	2.8	5.1	1.5
137	6.4	3.1	5.5	1.8
75	6.6	3.0	4.4	1.4
109	7.2	3.6	6.1	2.5

In [26]: X_test.shape

Out[26]: (45, 4)

In [27]: df.shape

Out[27]: (150, 5)

```
In [31]: # import Decision tree module
         from sklearn.tree import DecisionTreeClassifier
         model=DecisionTreeClassifier(criterion="entropy")
         model.fit(X train,y train)
Out[31]: DecisionTreeClassifier(class_weight=None, criterion='entropy', max_depth=None,
                                max features=None, max_leaf_nodes=None,
                                min_impurity_decrease=0.0, min_impurity_split=None,
                                min_samples_leaf=1, min_samples_split=2,
                                min_weight_fraction_leaf=0.0, presort=False,
                                random_state=None, splitter='best')
In [32]: # find accuracy scorer
         from sklearn.metrics import accuracy_score
         y_pred=model.predict(X_test)
         y pred
Out[32]: array([1, 0, 2, 1, 1, 0, 1, 2, 1, 1, 0, 0, 0, 0, 1, 2, 1, 1, 2, 0, 2,
                0, 2, 2, 2, 2, 2, 0, 0, 0, 0, 1, 0, 0, 2, 1, 0, 0, 0, 2, 1, 1, 0,
                0])
In [33]: | accuracy score(y test,y pred)
Out[33]: 0.9777777777777777
```

```
In [36]:
              # Decisition tree visulization
               import matplotlib.pyplot as plt
               from sklearn import tree
               plt.figure(figsize=(10,7))
              tree.plot_tree(model)
              plt.show()
                                              X[3] <= 0.8
entropy = 1.58
                                            samples = 105
value = [31, 37, 37]
                                                            X[2] \le 4.75
                                  entropy = 0.0
                                                            entropy = 1.0
                                  samples = 31
                                                            samples = 74
                                 value = [31, 0, 0]
                                                          value = [0, 37, 37]
                                 X[3] <= 1.6
entropy = 0.196
                                                                                   X[2] <= 5.15
entropy = 0.535
                                                                                    samples = 41
                                  samples = 33
                                                                                   value = [0, 5, 36]
                                 value = [0, 32, 1]
                                                                        X[3] \le 1.75
                                               entropy = 0.0
                                                                                                 entropy = 0.0
samples = 26
                      entropy = 0.0
                                                                       entropy = 0.918
                      samples = 32
                                               samples = 1
                                                                        samples = 15
                    value = [0, 32, 0]
                                              value = [0, 0, 1]
                                                                                                value = [0, 0, 26]
                                                                        alue = [0, 5, 10]
                                               X[1] \le 2.35
                                                                                                  X[1] \le 3.1
                                              entropy = 0.918
                                                                                                entropy = 0.503
                                               samples = 6
                                                                                                  samples = 9
                                              value = [0, 4, 2]
                                                                                                value = [0, 1, 8]
                                                           X[2] <= 5.05
entropy = 0.722
                                                                                    entropy = 0.0
                                                                                                              entropy = 0.0
                                  entropy = 0.0
                                   samples = 1
                                                                                     samples = 8
                                                                                                              samples = 1
                                                            samples = 5
                                  value = [0, 0, 1]
                                                                                    value = [0, 0, 8]
                                                                                                             value = [0, 1, 0]
                                                           value = [0, 4, 1]
                                                                        X[0] \le 6.15
                                               entropy = 0.0
                                                                        entropy = 1.0
                                                samples = 3
                                                                        samples = 2
                                              value = [0, 3, 0]
                                                                       value = [0, 1, 1]
                                                            entropy = 0.0
                                                                                     entropy = 0.0
                                                            samples = 1
                                                                                     samples = 1
                                                           value = [0, 1, 0]
                                                                                    value = [0, 0, 1]
In [40]:
              model.predict([[5.8,2.6,4.0,1.2]])
Out[40]: array([1])
```

Task: Apply decision tree classification for breast cancer dataset

```
In [38]: from sklearn.datasets import load breast cancer
         c=load_breast_cancer()
Out[38]: {'data': array([[1.799e+01, 1.038e+01, 1.228e+02, ..., 2.654e-01, 4.601e-01,
                 1.189e-01],
                [2.057e+01, 1.777e+01, 1.329e+02, ..., 1.860e-01, 2.750e-01,
                 8.902e-02],
                [1.969e+01, 2.125e+01, 1.300e+02, ..., 2.430e-01, 3.613e-01,
                 8.758e-02],
                [1.660e+01, 2.808e+01, 1.083e+02, ..., 1.418e-01, 2.218e-01,
                 7.820e-02],
                [2.060e+01, 2.933e+01, 1.401e+02, ..., 2.650e-01, 4.087e-01,
                 1.240e-01],
                [7.760e+00, 2.454e+01, 4.792e+01, ..., 0.000e+00, 2.871e-01,
                 7.039e-02]]),
          1, 1,
                0, 0, 1, 0, 1, 1, 1, 1, 0, 0, 1, 0, 0, 1, 1, 1, 1, 0, 1, 0, 0,
                1, 1, 1, 1, 0, 1, 0, 0, 1, 0, 1, 0, 0, 1, 1, 1, 0, 0, 1, 0, 0,
                1, 1, 1, 0, 1, 1, 0, 0, 1, 1, 1, 0, 0, 1, 1, 1, 1, 0, 1, 1, 0, 1,
                1, 1, 1, 1, 1, 1, 0, 0, 0, 1, 0, 0, 1, 1, 1, 0, 0, 1, 0, 1, 0,
                0, 1, 0, 0, 1, 1, 0, 1, 1, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1,
                1, 1, 0, 1, 1, 1, 1, 0, 0, 1, 0, 1, 1, 0, 0, 1, 1, 0, 0, 1, 1, 1,
                1, 0, 1, 1, 0, 0, 0, 1, 0, 1, 0, 1, 1, 0, 1, 1, 0, 0, 1, 0, 0,
                0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 1, 1, 0, 1, 0, 0, 0, 0, 1, 1, 0, 0,
                1, 1, 1, 0, 1, 1, 1, 1, 1, 0, 0, 1, 1, 0, 1, 1, 0, 0, 1, 0, 1, 1,
                1, 1, 0, 1, 1, 1, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 1, 1, 1, 1, 1, 0, 1, 0, 1, 1, 0, 1, 1, 0, 1, 0, 0, 1, 1,
                1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 0, 1, 0, 1, 1, 1, 1, 1,
                1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 0, 1, 1, 1, 1, 0, 0,
                0, 1, 1, 1, 1, 0, 1, 0, 1, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 0,
                0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 1, 0, 0, 1, 0, 0,
                1, 1, 1, 1, 0, 1, 1, 1, 1, 0, 1, 1, 0, 1, 1, 0, 1, 1, 0, 0, 1, 1,
                1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 0, 1, 1, 0,
                1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 0, 0, 1, 0, 1, 1, 1, 1,
                1, 0, 1, 1, 0, 1, 0, 1, 1, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0,
                1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1,
                1, 1, 1, 0, 1, 0, 1, 1, 0, 1, 1, 1, 1, 1, 0, 0, 1, 0, 1, 0, 1, 1,
                1, 1, 1, 0, 1, 1, 0, 1, 0, 1, 0, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1,
                1, 1, 1, 1, 1, 0, 1, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
                1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0, 1]),
          'target_names': array(['malignant', 'benign'], dtype='<U9'),</pre>
          'DESCR': '.. breast cancer dataset:\n\nBreast cancer wisconsin (diagnostic)
        dataset\n-----\n\n**Data Set Character
        istics:**\n\n
                        :Number of Instances: 569\n\n :Number of Attributes: 30 n
        umeric, predictive attributes and the class\n\n :Attribute Information:\n
        - radius (mean of distances from center to points on the perimeter)\n
        - texture (standard deviation of gray-scale values)\n
                                                                 - perimeter\n
         - area\n
                       - smoothness (local variation in radius lengths)\n
        ompactness (perimeter^2 / area - 1.0)\n
                                                    - concavity (severity of conca
        ve portions of the contour)\n
                                          - concave points (number of concave port
        ions of the contour)\n
                               - symmetry \n
                                                        - fractal dimension ("coas
        tline approximation" - 1)\n\n
                                           The mean, standard error, and "worst" or
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largest (mean of the three\n largest values) of these features were co mputed for each image,\n resulting in 30 features. For instance, fiel d 3 is Mean Radius, field\n 13 is Radius SE, field 23 is Worst Radiu s.\n\n - class:\n WDBC-Malignant\n DBC-Benign\n\n :Summary Statistics:\n\n _____ ====== =====\n Min Max\n radius (mean): texture (mean): 9.71 6.981 28.11\n 39.28\n per imeter (mean): area (mean): 43.79 188.5\n 143.5 2501.0\n smoothness (mean): 0.053 0.163\n co concavity (mean): mpactness (mean): 0.019 0.345\n 0.0 0.427\n concave points (mean): 0.0 0.201\n sym metry (mean): 0.106 0.304\n fractal dimension (mea n): 0.05 0.097\n radius (standard error): 0.112 texture (standard error): 2.873\n 0.36 4.885\n perimeter (standard error): 0.757 21.98\n area (standard error): 6.802 542.2\n smoothness (standard error): 0.002 0.031\n com pactness (standard error): concavity (standard erro 0.002 0.135\n concave points (standard error): r): 0.0 0.396\n 0.0 symmetry (standard error): 0.008 0.079\n fractal di 0.053\n mension (standard error): 0.001 0.03\n radius (worst): 36.04\n texture (worst): 12.02 49.54\n per imeter (worst): 50.41 251.2\n area (worst): 185.2 4254.0\n smoothness (worst): 0.071 0.223\n co mpactness (worst): 0.027 1.058\n concavity (worst): 0.0 1.252\n concave points (worst): 0.0 0.291\n sym metry (worst): 0.156 0.664\n fractal dimension (wors t): 0.055 0.208\n ____________________________________ =====\n\n :Missing Attribute Values: None\n\n :Class Distribution: 212 - Malignant, 357 - Benign\n\n :Creator: Dr. William H. Wolberg, W. Nick S treet, Olvi L. Mangasarian\n\n :Donor: Nick Street\n\n :Date: November, 1995\n\nThis is a copy of UCI ML Breast Cancer Wisconsin (Diagnostic) dataset s.\nhttps://goo.gl/U2Uwz2\n\nFeatures are computed from a digitized image of a fine needle\naspirate (FNA) of a breast mass. They describe\ncharacteristi cs of the cell nuclei present in the image.\n\nSeparating plane described abo ve was obtained using\nMultisurface Method-Tree (MSM-T) [K. P. Bennett, "Deci sion Tree\nConstruction Via Linear Programming." Proceedings of the 4th\nMidw est Artificial Intelligence and Cognitive Science Society, \npp. 97-101, 199 2], a classification method which uses linear\nprogramming to construct a dec ision tree. Relevant features\nwere selected using an exhaustive search in t he space of 1-4\nfeatures and 1-3 separating planes.\n\nThe actual linear pro gram used to obtain the separating plane\nin the 3-dimensional space is that described in:\n[K. P. Bennett and O. L. Mangasarian: "Robust Linear\nProgramm ing Discrimination of Two Linearly Inseparable Sets", \nOptimization Methods a nd Software 1, 1992, 23-34].\n\nThis database is also available through the U W CS ftp server:\n\nftp ftp.cs.wisc.edu\ncd math-prog/cpo-dataset/machine-lea - W.N. Street, W.H. Wolberg and O.L. rn/WDBC/\n\n.. topic:: References\n\n Mangasarian. Nuclear feature extraction \n for breast tumor diagnosis. IS &T/SPIE 1993 International Symposium on \n Electronic Imaging: Science an d Technology, volume 1905, pages 861-870,\n San Jose, CA, 1993.\n L. Mangasarian, W.N. Street and W.H. Wolberg. Breast cancer diagnosis and \n prognosis via linear programming. Operations Research, 43(4), pages 570-577, - W.H. Wolberg, W.N. Street, and O.L. Mangasaria July-August 1995.\n n. Machine learning techniques\n to diagnose breast cancer from fine-need le aspirates. Cancer Letters 77 (1994) \n 163-171.', 'feature_names': array(['mean radius', 'mean texture', 'mean perimeter', 'me an area',

```
'mean smoothness', 'mean compactness', 'mean concavity',
    'mean concave points', 'mean symmetry', 'mean fractal dimension',
    'radius error', 'texture error', 'perimeter error', 'area error',
    'smoothness error', 'compactness error', 'concavity error',
    'concave points error', 'symmetry error',
    'fractal dimension error', 'worst radius', 'worst texture',
    'worst perimeter', 'worst area', 'worst smoothness',
    'worst compactness', 'worst concavity', 'worst concave points',
    'worst symmetry', 'worst fractal dimension'], dtype='<U23'),
    'filename': 'C:\\Users\\Kanakamma\\Anaconda3\\lib\\site-packages\\sklearn\\datasets\\data\\breast_cancer.csv'}</pre>
```

In []: