CE066-ML-LAB4-Jaydeep Mahajan

Task 2: Apply algorithm on breast cancer wisconsin dataset - One Hot Encoding of features: and Train test Division 60%-40%

```
from sklearn.datasets import load_breast_cancer
X,y = load_breast_cancer(return_X_y=True)
```

```
print("Features shape : ",X.shape)
print("Label shape: ",y.shape)
```

```
Features shape :  (569, 30)
Label shape:  (569,)
```

```
print(X[0])
```

```
[1.799e+01 1.038e+01 1.228e+02 1.001e+03 1.184e-01 2.776e-01 3.001e-01
 1.471e-01 2.419e-01 7.871e-02 1.095e+00 9.053e-01 8.589e+00 1.534e+02
 6.399e-03 4.904e-02 5.373e-02 1.587e-02 3.003e-02 6.193e-03 2.538e+01
 1.733e+01 1.846e+02 2.019e+03 1.622e-01 6.656e-01 7.119e-01 2.654e-01
 4.601e-01 1.189e-01]
```

+ Code + Text

```
label = ['Benign','Malignant']
print(label[y[0]]) #0 -> Benign 1 ->Malignant
```

```
Benign
```

```
from sklearn.tree import DecisionTreeClassifier
from sklearn import preprocessing
from sklearn.model_selection import train_test_split
from sklearn import metrics
```

```
x_train, x_test, y_train, y_test = train_test_split(X, y, test_size=0.4, random_state=66)
```

```
clf = DecisionTreeClassifier()
clf.fit(x_train, y_train)
y_pred = clf.predict(x_test)
print("Accuracy: ",metrics.accuracy_score(y_test, y_pred))
```

```
Accuracy:  0.9429824561403509
```

```
#create confusion matrix
from sklearn.metrics import confusion_matrix
confusion_matrix(y_test, y_pred)
```

```
array([[ 77,   3],
       [ 10, 138]])
```

```
from sklearn.metrics import precision_score
from sklearn.metrics import recall_score
precision = precision_score(y_test,y_pred)
recall = recall_score(y_test,y_pred)
print('precision: {}'.format(precision))
print('recall: {}'.format(recall))
```

```
precision: 0.9787234042553191
recall: 0.9324324324324325
```

```
y_pred = clf.predict(X[20].reshape(1,-1))
print("Predicted : ",label[int(y_pred)])
print("Actual : ",label[y[20]])
```

```
Predicted :  Malignant
Actual :  Malignant
```

```
load_breast_cancer().feature_names
```

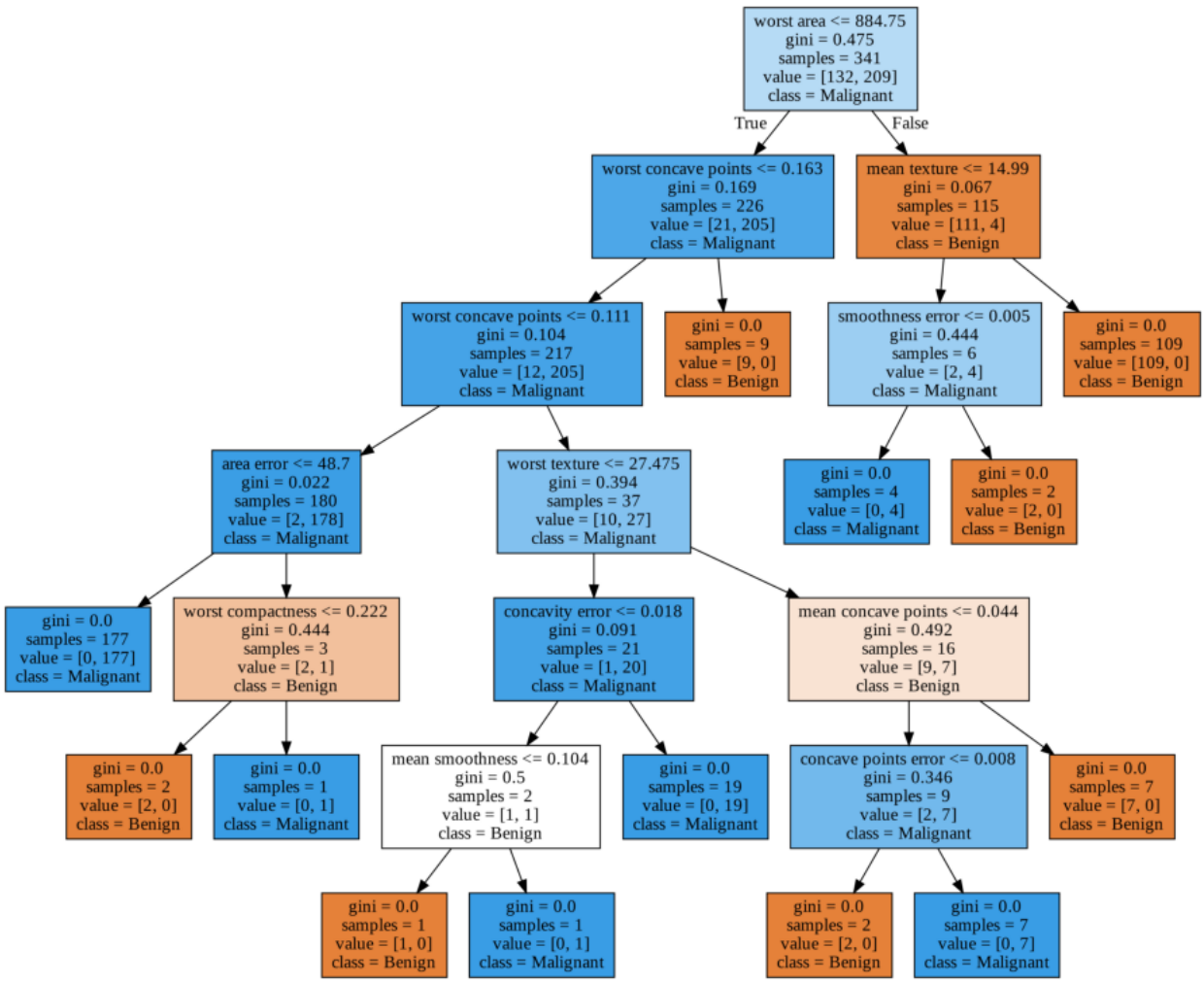
```
array(['mean radius', 'mean texture', 'mean perimeter', 'mean area',
       'mean smoothness', 'mean compactness', 'mean concavity',
       'mean concave points', 'mean symmetry', 'mean fractal dimension',
       'radius error', 'texture error', 'perimeter error', 'area error',
       'smoothness 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')
```

```
from sklearn.tree import export_graphviz
export_graphviz(clf,out_file='tree_entropy.dot',
                feature_names=['mean radius', 'mean texture', 'mean perimeter', 'mean area'
                               'mean smoothness', 'mean compactness', 'mean concavity',
                               'mean concave points', 'mean symmetry', 'mean fractal dimens
                               'radius error', 'texture error', 'perimeter error', 'area er
                               '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 point
                               'worst symmetry', 'worst fractal dimension'],
                class_names=['Benign','Malignant'],
                filled=True)
```

```
#Convert to png
from subprocess import call
call(['dot', '-Tpng', 'tree_entropy.dot', '-o', 'tree_entropy.png', '-Gdpi=600'])
```

```
#Display in python
import matplotlib.pyplot as plt
plt.figure(figsize = (16, 20))
plt.imshow(plt.imread('tree_entropy.png'))
plt.axis('off');
```

```
plt.show();
```


worst area <= 884.75
gini = 0.475
samples = 341
value = [132, 209]
class = Malignant
True
False
worst concave points <= 0.163
gini = 0.169
samples = 226
value = [21, 205]
class = Malignant
mean texture <= 14.99
gini = 0.067
samples = 115
value = [111, 4]
class = Benign
worst concave points <= 0.111
gini = 0.104
samples = 217
value = [12, 205]
class = Malignant
gini = 0.0
samples = 9
value = [9, 0]
class = Benign
smoothness error <= 0.005
gini = 0.444
samples = 6
value = [2, 4]
class = Malignant
gini = 0.0
samples = 109
value = [109, 0]
class = Benign
area error <= 48.7
gini = 0.022
samples = 180
value = [2, 178]
class = Malignant
worst texture <= 27.475
gini = 0.394
samples = 37
value = [10, 27]
class = Malignant
gini = 0.0
samples = 4
value = [0, 4]
class = Malignant
gini = 0.0
samples = 2
value = [2, 0]
class = Benign
gini = 0.0
samples = 177
value = [0, 177]
class = Malignant
worst compactness <= 0.222
gini = 0.444
samples = 3
value = [2, 1]
class = Benign
concavity error <= 0.018
gini = 0.091
samples = 21
value = [1, 20]
class = Malignant
mean concave points <= 0.044
gini = 0.492
samples = 16
value = [9, 7]
class = Benign
gini = 0.0
samples = 2
value = [2, 0]
class = Benign
gini = 0.0
samples = 1
value = [0, 1]
class = Malignant
mean smoothness <= 0.104
gini = 0.5
samples = 2
value = [1, 1]
class = Benign
gini = 0.0
samples = 19
value = [0, 19]
class = Malignant
concave points error <= 0.008
gini = 0.346
samples = 9
value = [2, 7]
class = Malignant
gini = 0.0
samples = 7
value = [7, 0]
class = Benign
gini = 0.0
samples = 1
value = [1, 0]
class = Benign
gini = 0.0
samples = 1
value = [0, 1]
class = Malignant
gini = 0.0
samples = 2
value = [2, 0]
class = Benign
gini = 0.0
samples = 7
value = [0, 7]
class = Malignant