LAB 4 TASK 2

Apply algorithm on wine dataset - LabelEncoding of features: and Train test Division 66%-34%

In [3]:

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

In [4]:

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

```
Features shape :  (178, 13)
Label shape:  (178,)
```

In [5]:

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

```
[1.423e+01 1.710e+00 2.430e+00 1.560e+01 1.270e+02 2.800e+00 3.060e+00
 2.800e-01 2.290e+00 5.640e+00 1.040e+00 3.920e+00 1.065e+03]
```

In [6]:

```
label = ['Benign','Malignant']
print(label[y[0]])
```

```
Benign
```

In [8]:

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

In [9]:

```
x_train, x_test, y_train, y_test = train_test_split(X, y, test_size=0.34, random_state=134)
```

In [17]:

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

```
Accuracy:  0.819672131147541
```

In [18]:

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

Out[18]:

```
array([[11,  7,  0],
       [ 1, 25,  0],
       [ 1,  2, 14]])
```

In [19]:

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

```
precision: 0.8604826546003017
recall: 0.798726328138093
```

In [26]:

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

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

In [33]:

```
load_wine().target_names
```

Out[33]:

```
array(['class_0', 'class_1', 'class_2'], dtype='<U7')
```

In [34]:

```
load_wine().feature_names
```

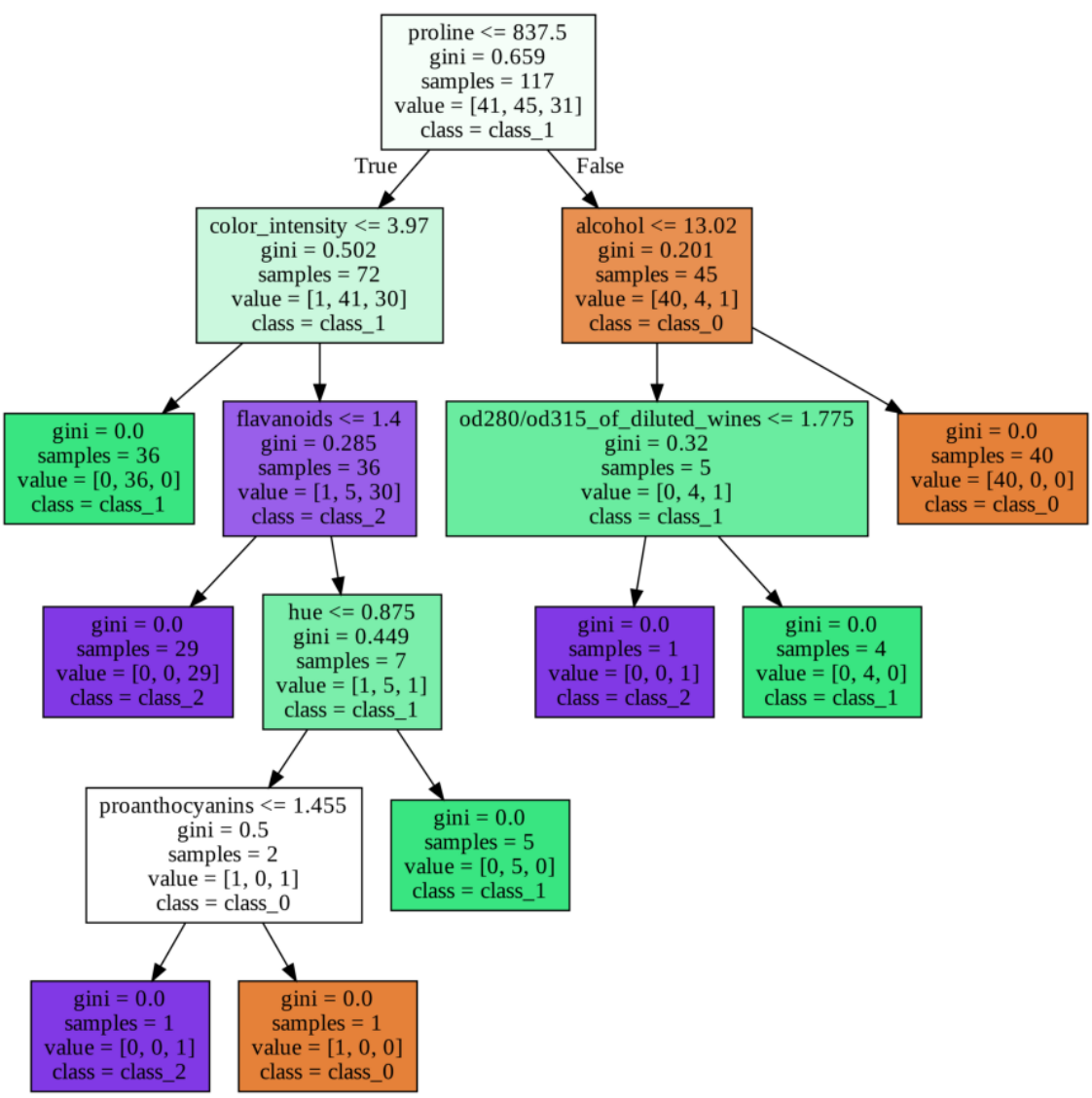
Out[34]:

```
['alcohol',
 'malic_acid',
 'ash',
 'alcalinity_of_ash',
 'magnesium',
 'total_phenols',
 'flavanoids',
 'nonflavanoid_phenols',
 'proanthocyanins',
 'color_intensity',
 'hue',
 'od280/od315_of_diluted_wines',
 'proline']
```

In [32]:

```
from sklearn.tree import export_graphviz
export_graphviz(clf,out_file='tree_entropy.dot',
                feature_names=['alcohol',
                               'malic_acid',
                               'ash',
                               'alcalinity_of_ash',
                               'magnesium',
                               'total_phenols',
                               'flavanoids',
                               'nonflavanoid_phenols',
                               'proanthocyanins',
                               'color_intensity',
                               'hue',
                               'od280/od315_of_diluted_wines',
                               'proline'],
                class_names=['class_0','class_1','class_2'],
                 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();
```


proline <= 837.5
gini = 0.659
samples = 117
value = [41, 45, 31]
class = class_1
True
False
color_intensity <= 3.97
gini = 0.502
samples = 72
value = [1, 41, 30]
class = class_1
alcohol <= 13.02
gini = 0.201
samples = 45
value = [40, 4, 1]
class = class_0
gini = 0.0
samples = 36
value = [0, 36, 0]
class = class_1
flavanoids <= 1.4
gini = 0.285
samples = 36
value = [1, 5, 30]
class = class_2
od280/od315_of_diluted_wines <= 1.775
gini = 0.32
samples = 5
value = [0, 4, 1]
class = class_1
gini = 0.0
samples = 40
value = [40, 0, 0]
class = class_0
gini = 0.0
samples = 29
value = [0, 0, 29]
class = class_2
hue <= 0.875
gini = 0.449
samples = 7
value = [1, 5, 1]
class = class_1
gini = 0.0
samples = 1
value = [0, 0, 1]
class = class_2
gini = 0.0
samples = 4
value = [0, 4, 0]
class = class_1
proanthocyanins <= 1.455
gini = 0.5
samples = 2
value = [1, 0, 1]
class = class_0
gini = 0.0
samples = 5
value = [0, 5, 0]
class = class_1
gini = 0.0
samples = 1
value = [0, 0, 1]
class = class_2
gini = 0.0
samples = 1
value = [1, 0, 0]
class = class_0