Decision Tree Practise

Drug Dataset

In [1]:

```
import pandas as pd

df = pd.read_csv('datasets/drug.csv')
df.head()
```

Out[1]:

	Age	Sex	BP	Cholesterol	Na_to_K	Drug
0	23	F	HIGH	HIGH	25.355	drugY
1	47	M	LOW	HIGH	13.093	drugC
2	47	M	LOW	HIGH	10.114	drugC
3	28	F	NORMAL	HIGH	7.798	drugX
4	61	F	LOW	HIGH	18.043	drugY

In [2]:

```
df.shape
```

Out[2]:

```
(200, 6)
```

In [3]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 200 entries, 0 to 199
Data columns (total 6 columns):
Age            200 non-null int64
Sex            200 non-null object
BP             200 non-null object
Cholesterol    200 non-null object
Na_to_K        200 non-null float64
Drug           200 non-null object
dtypes: float64(1), int64(1), object(4)
memory usage: 9.5+ KB
```

In [4]:

```
df['BP'].value_counts()
```

Out[4]:

```
HIGH      77
LOW       64
NORMAL    59
Name: BP, dtype: int64
```

In [5]:

```
df['Cholesterol'].value_counts()
```

Out[5]:

```
HIGH      103
NORMAL     97
Name: Cholesterol, dtype: int64
```

In [6]:

```
cls_names = df['Drug'].value_counts().index
cls_names
```

Out[6]:

```
Index(['drugY', 'drugX', 'drugA', 'drugB', 'drugC'], dtype='object')
```

In [7]:

```
df.columns
```

Out[7]:

```
Index(['Age', 'Sex', 'BP', 'Cholesterol', 'Na_to_K', 'Drug'], dtype='objec
t')
```

In [8]:

```
from sklearn.preprocessing import LabelEncoder
def lb():
    lbc = LabelEncoder()
    for col in df.columns:
        df[col] = lbc.fit_transform(df[col])
    return
lb()
```

In [9]:

```
df.head()
```

Out[9]:

	Age	Sex	BP	Cholesterol	Na_to_K	Drug
0	8	0	0	0	167	4
1	30	1	1	0	89	2
2	30	1	1	0	43	2
3	12	0	2	0	10	3
4	44	0	1	0	133	4

In [10]:

```
X = df.drop('Drug',axis = 1)
Y = df['Drug']
```

In [11]:

```
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)
```

In [12]:

```
from sklearn.tree import DecisionTreeClassifier
tree_clf = DecisionTreeClassifier(max_depth = 3)
tree_clf.fit(X_train,Y_train)
```

Out[12]:

```
DecisionTreeClassifier(class_weight=None, criterion='gini', max_depth=3,
            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=Non
e,
            splitter='best')
```

In [13]:

```
Y_pred = tree_clf.predict(X_test)
from sklearn.metrics import confusion_matrix,accuracy_score

confusion_matrix(Y_test,Y_pred)
```

Out[13]:

```
array([[ 7,  0,  0,  0,  0],
       [ 0,  3,  0,  0,  0],
       [ 0,  0,  0,  6,  0],
       [ 0,  0,  0, 18,  0],
       [ 0,  0,  0,  0, 26]], dtype=int64)
```

In [14]:

```
accuracy_score(Y_test,Y_pred)
```

Out[14]:

```
0.9
```

In [15]:

```
from sklearn.tree import export_graphviz

export_graphviz(tree_clf,out_file='diabetes.dot',class_names=cls_names,
                rounded=True,filled=True)
```

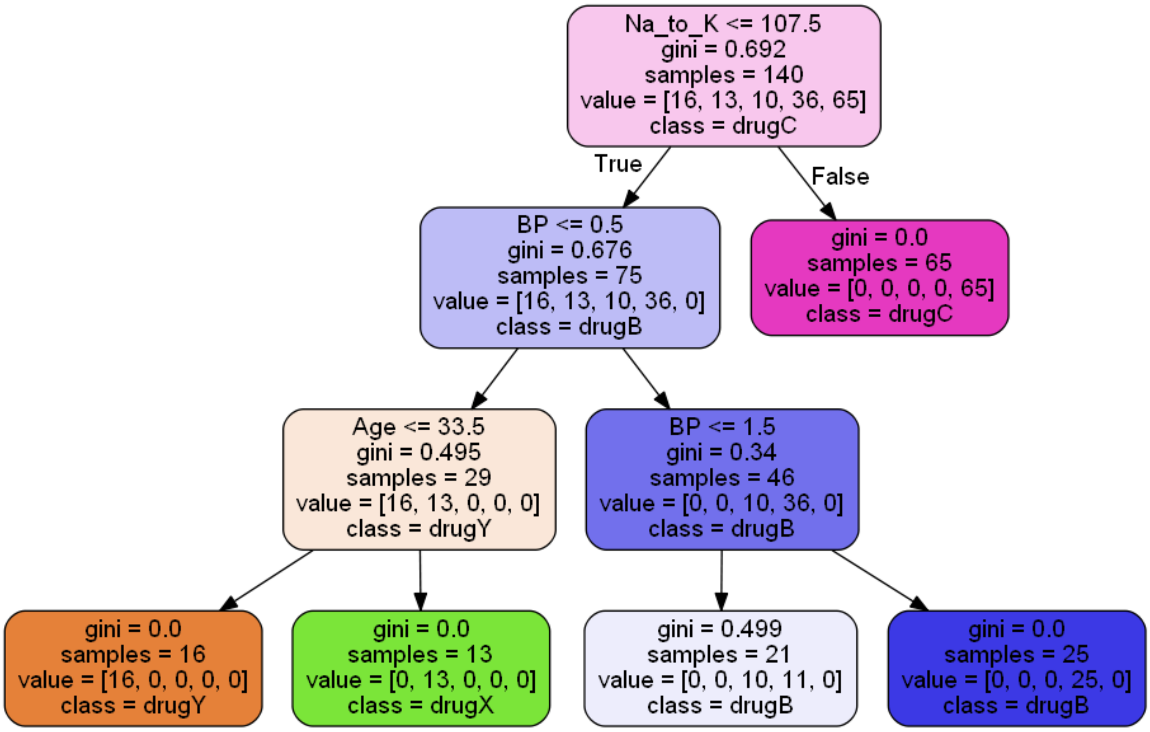
In [16]:

```
from sklearn.externals.six import StringIO
from IPython.display import Image
import pydotplus
import os
os.environ["PATH"]+=os.environ['PATH']+';'+r'C:\Users\Jesus\Anaconda3\Lib\site-packages\graphviz-2.38\release\bin'
```

In [17]:

```
dot_data = StringIO()
export_graphviz(tree_clf,out_file=dot_data,filled=True, rounded=True,feature_names=X_train.columns,
                class_names = cls_names)
graph = pydotplus.graph_from_dot_data(dot_data.getvalue())
Image(graph.create_png())
```

Out[17]:



Random Forest Classifier

Pima Indians Diabetes Database (https://www.kaggle.com/uciml/pima-indians-diabetes-database)

Predict the onset of diabetes based on diagnostic measures

Context

This dataset is originally from the National Institute of Diabetes and Digestive and Kidney Diseases. The objective of the dataset is to diagnostically predict whether or not a patient has diabetes, based on certain diagnostic measurements included in the dataset. Several constraints were placed on the selection of these instances from a larger database. In particular, all patients here are females at least 21 years old of Pima Indian heritage.

Content

The datasets consists of several medical predictor variables and one target variable, Outcome. Predictor variables includes the number of pregnancies the patient has had, their BMI, insulin level, age, and so on.

About this dataset

The datasets consist of several medical predictor (independent) variables and one target (dependent) variable, Outcome. Independent variables include the number of pregnancies the patient has had, their BMI, insulin level, age, and so on.

Features	Description
Pregnancies	Number of times pregnant
Glucose	Plasma glucose concentration a 2 hours in an oral glucose tolerance test
BloodPressure	Diastolic blood pressure (mm Hg)
SkinThickness	Triceps skin fold thickness (mm)
Insulin	2-Hour serum insulin (mu U/ml)
BMI	Body mass index **(weight in kg/(height in m)^2)**
Diabetes	PedigreeFunctionDiabetes pedigree function
Age	Age (years)
Outcome	Class variable (0 or 1) 268 of 768 are 1, the others are 0

In [18]:

```
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt



df = pd.read_csv('datasets/diabetes.csv')
df.head()
```

Out[18]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunc
0	6	148	72	35	0	33.6	0.
1	1	85	66	29	0	26.6	0.
2	8	183	64	0	0	23.3	0.
3	1	89	66	23	94	28.1	0.
4	0	137	40	35	168	43.1	2.

In [19]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
Pregnancies                 768 non-null int64
Glucose                     768 non-null int64
BloodPressure               768 non-null int64
SkinThickness               768 non-null int64
Insulin                     768 non-null int64
BMI                         768 non-null float64
DiabetesPedigreeFunction    768 non-null float64
Age                         768 non-null int64
Outcome                     768 non-null int64
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
```

In [20]:

```
df.shape
```

Out[20]:

```
(768, 9)
```

In [21]:

```
df.isnull().sum()
```

Out[21]:

```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

In [22]:

```
df.describe()
```

Out[22]:

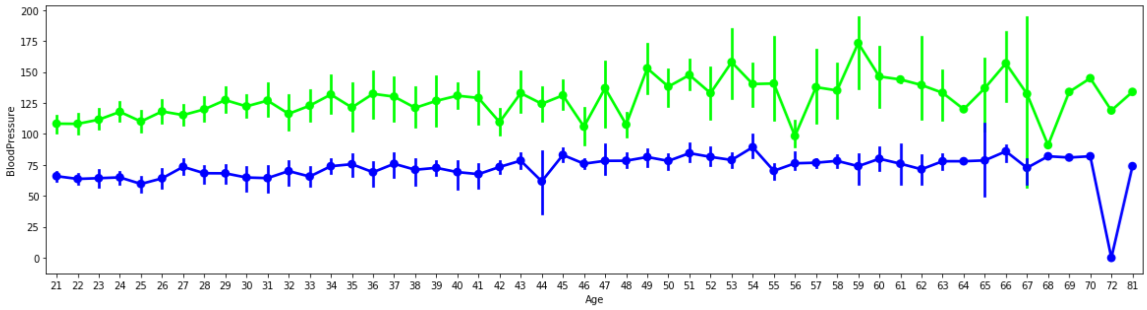
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	Diak
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	

In [23]:

```
plt.figure(figsize=(20,5))
sns.pointplot(x='Age',y='Glucose',data=df,color='lime',alpha=0.8)
sns.pointplot(x='Age',y='BloodPressure',data=df,color='blue',alpha=0.8)
```

Out[23]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x2b11c367320>
```



In [24]:

```
X = df.drop('Outcome',axis = 1)
Y = df['Outcome']
```

In [25]:

```
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
)
```

In [26]:

```
from sklearn.ensemble import RandomForestClassifier

rfc = RandomForestClassifier()
rfc.fit(X_train,Y_train)
```

```
C:\Users\Jesus\Anaconda3\lib\site-packages\sklearn\ensemble\forest.py:246:
FutureWarning: The default value of n_estimators will change from 10 in ve
rsion 0.20 to 100 in 0.22.
  "10 in version 0.20 to 100 in 0.22.", FutureWarning)
```

Out[26]:

```
RandomForestClassifier(bootstrap=True, class_weight=None, criterion='gin
i',
            max_depth=None, max_features='auto', 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, n_estimators=10, n_jobs=None,
            oob_score=False, random_state=None, verbose=0,
            warm_start=False)
```

In [27]:

```
Y_pred = rfc.predict(X_test)
```

In [28]:

```
from sklearn.metrics import accuracy_score

accuracy_score(Y_test,Y_pred)
```

Out[28]:

```
0.7402597402597403
```