DecisonTree_Abu_Sayad_Hussain

November 18, 2019

Import python packages

```
In [44]: import numpy as np
         import pandas as pd
         from sklearn.tree import DecisionTreeClassifier
         from sklearn import preprocessing
         from sklearn.preprocessing import LabelEncoder
         from sklearn.metrics import confusion_matrix
         from sklearn.model_selection import train_test_split
         from sklearn.metrics import accuracy_score
         import matplotlib.pyplot as plt
         from sklearn.externals.six import StringIO
         import pydotplus
         import matplotlib.image as mpimg
         from sklearn import tree
         %matplotlib inline
```

Uploading CSV data

```
In [45]: my_data = pd.read_csv('drug200.csv', delimiter=',')
         my_data.head()
```

Out[45]:

	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

Pre-Processing the data As the colum names will not be counting we have to remove it And Sex,Bp and Cholestor are nominal value not numeric we have to convert them into Numeric value

```
In [46]: X = my_data[['Age', 'Sex', 'BP', 'Cholesterol', 'Na_to_K']].values
         X[0:5]
```

```
Out[46]: array([[23, 'F', 'HIGH', 'HIGH', 25.355],
                [47, 'M', 'LOW', 'HIGH', 13.093],
                [47, 'M', 'LOW', 'HIGH', 10.113999999999999],
                [28, 'F', 'NORMAL', 'HIGH', 7.797999999999999],
                [61, 'F', 'LOW', 'HIGH', 18.043]], dtype=object)
```

```
In [47]: #Finding out the nomianl values to convert into numeric values
         print(my_data['Sex'].unique())
         print(my_data['BP'].unique())
         print(my_data['Cholesterol'].unique())

['F' 'M']
['HIGH' 'LOW' 'NORMAL']
['HIGH' 'NORMAL']


In [48]: le_sex = preprocessing.LabelEncoder()
         le_sex.fit_transform(['F','M'])
         X[:,1] = le_sex.transform(X[:,1])

         le_bp = preprocessing.LabelEncoder()
         le_bp.fit_transform(['HIGH','LOW','NORMAL'])
         X[:,2] = le_bp.transform(X[:,2])

         le_chol = preprocessing.LabelEncoder()
         le_chol.fit_transform(['HIGH','NORMAL'])
         X[:,3] = le_chol.transform(X[:,3])

         X[0:5]

Out[48]: array([[23, 0, 0, 0, 25.355],
                [47, 1, 1, 0, 13.093],
                [47, 1, 1, 0, 10.113999999999999],
                [28, 0, 2, 0, 7.797999999999999],
                [61, 0, 1, 0, 18.043]], dtype=object)
```

Setting Up the prediction column

```
In [49]: Y = my_data['Drug']
         Y[0:5]

Out[49]: 0    drugY
         1    drugC
         2    drugC
         3    drugX
         4    drugY
         Name: Drug, dtype: object
```

Split the data into train and test datasets

```
In [50]: X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size = 0.2, random_sta
         print(X_train.shape)
         print(Y_train.shape)
         print(X_test.shape)
         print(Y_test.shape)
```

```
(160, 5)
(160,)
(40, 5)
(40,)
```

```
In [51]: drugDTree = DecisionTreeClassifier(criterion='entropy', max_depth=4)
         drugDTree
```

```
Out[51]: DecisionTreeClassifier(class_weight=None, criterion='entropy', max_depth=4,
                                 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 [52]: drugDTree.fit(X_train,Y_train)
```

```
Out[52]: DecisionTreeClassifier(class_weight=None, criterion='entropy', max_depth=4,
                                 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')
```

Prediction time

```
In [53]: y_pred = drugDTree.predict(X_test)
```

```
In [54]: print('Real Data', Y_test[0:5])
         print('Predicted Data', y_pred[0:5])
```

```
Real Data 18     drugC
170    drugX
107    drugY
98     drugY
177    drugY
Name: Drug, dtype: object
Predicted Data ['drugC' 'drugX' 'drugY' 'drugY' 'drugY']
```

Accuracy of the data

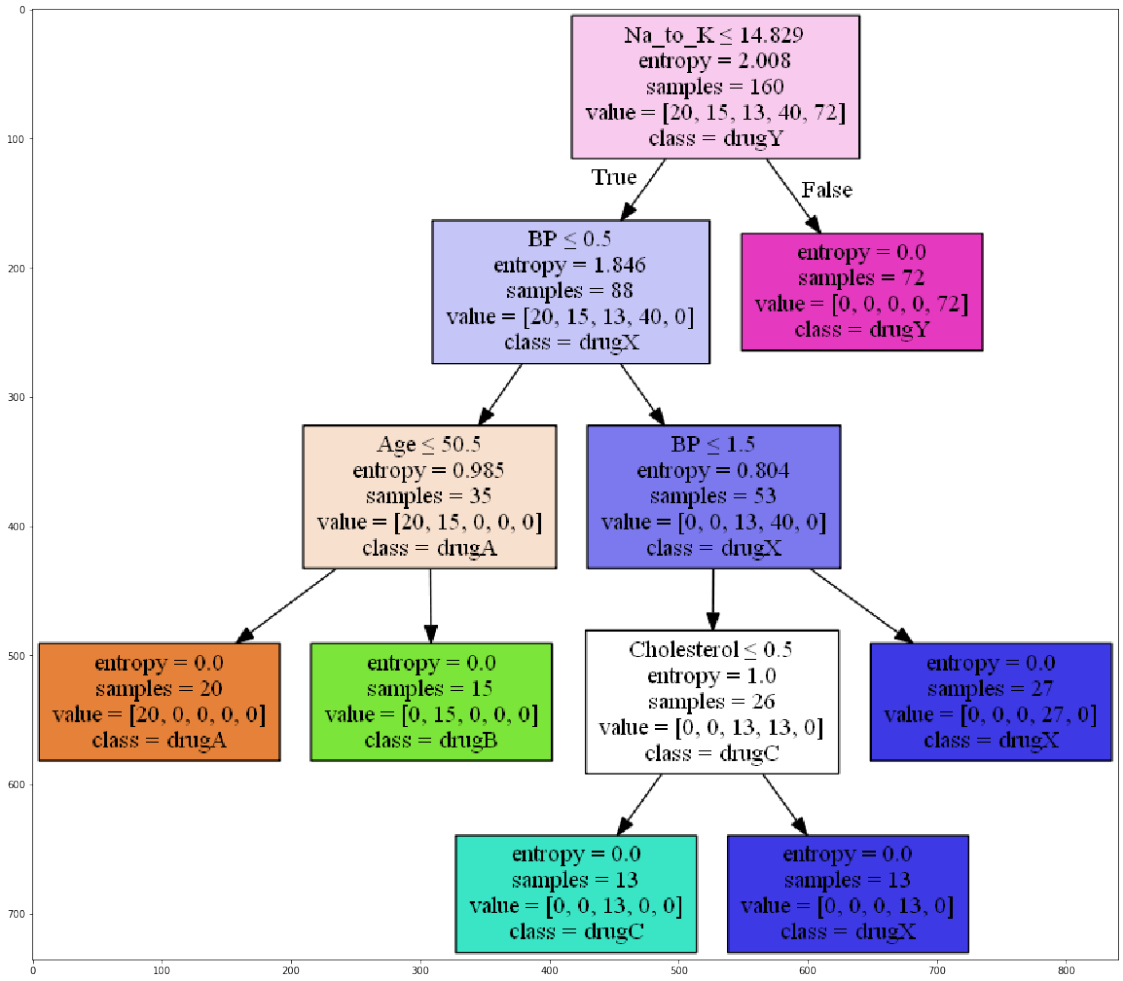
```
In [55]: print('Accuracy Score:',accuracy_score(Y_test,y_pred))
```

```
Accuracy Score: 1.0
```

Visualization

```
In [56]: dot_data = StringIO()
         file_name = 'DrugPredicton.png'
         featuresName = my_data.columns[0:5]
         predicted = my_data['Drug'].unique().tolist()
         out=tree.export_graphviz(drugDTree,feature_names=featuresName, out_file=dot_data, cla
         graph = pydotplus.graph_from_dot_data(dot_data.getvalue())
         graph.write_png(file_name)
         img = mpimg.imread(file_name)
         plt.figure(figsize=(20,40))
         plt.imshow(img, interpolation='nearest')

Out[56]: <matplotlib.image.AxesImage at 0x2d71ef30>
```



Predicting accuracy manually

```
In [91]: confusion = confusion_matrix(Y_test, y_pred)
         i=0
         for var in confusion:
```

```
            tn=var[0]
            fp=var[1]
            fn=var[2]
            tp=var[3]

            accuracy=(tp+tn)/(tn+fp+fn+fp)
            print(accuracy)
            break
```

```
1.0
```

In [ ]: