Clas-Decision-Trees-drug-py-v1

July 14, 2020

Decision Trees

In this lab exercise, you will learn a popular machine learning algorithm, Decision Tree. You will use this classification algorithm to build a model from historical data of patients, and their response to different medications. Then you use the trained decision tree to predict the class of a unknown patient, or to find a proper drug for a new patient.

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```

Import the Following Libraries:

numpy (as np)

pandas

DecisionTreeClassifier from sklearn.tree

[1]:
```
import numpy as np
import pandas as pd
from sklearn.tree import DecisionTreeClassifier
```

```
<h2>About the dataset</h2>
Imagine that you are a medical researcher compiling data for a study. You have collected data a
<br>
<br>
Part of your job is to build a model to find out which drug might be appropriate for a future p
<br>
<br>
It is a sample of binary classifier, and you can use the training part of the dataset
to build a decision tree, and then use it to predict the class of a unknown patient, or to pres
```

<h2>Downloading the Data</h2>
To download the data, we will use !wget to download it from IBM Object Storage.

[2]:
```
!wget -O drug200.csv https://s3-api.us-geo.objectstorage.softlayer.net/
↪cf-courses-data/CognitiveClass/ML0101ENv3/labs/drug200.csv
```

```
--2020-07-14 13:07:20--  https://s3-api.us-geo.objectstorage.softlayer.net/cf-
courses-data/CognitiveClass/ML0101ENv3/labs/drug200.csv
Resolving s3-api.us-geo.objectstorage.softlayer.net (s3-api.us-
geo.objectstorage.softlayer.net)… 67.228.254.196
Connecting to s3-api.us-geo.objectstorage.softlayer.net (s3-api.us-
geo.objectstorage.softlayer.net)|67.228.254.196|:443… connected.
HTTP request sent, awaiting response… 200 OK
Length: 6027 (5.9K) [text/csv]
Saving to: ‘drug200.csv’

drug200.csv         100%[===================>]   5.89K  --.-KB/s    in 0s

2020-07-14 13:07:20 (11.7 MB/s) - ‘drug200.csv’ saved [6027/6027]
```

Did you know? When it comes to Machine Learning, you will likely be working with large datasets. As a business, where can you host your data? IBM is offering a unique opportunity for businesses, with 10 Tb of IBM Cloud Object Storage: Sign up now for free

now, read data using pandas dataframe:

[5]:
```
my_data = pd.read_csv("drug200.csv",delimiter=",")
my_data[0:5]
```

[5]:

	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

<h3>Practice</h3>
What is the size of data?

[6]:
```
my_data.shape
```

[6]: (200, 6)

<h2>Pre-processing</h2>

Using my_data as the Drug.csv data read by pandas, declare the following variables:

X as the Feature Matrix (data of my_data)

y as the response vector (target)

Remove the column containing the target name since it doesn't contain numeric values.

[7]:
```
X = my_data[['Age', 'Sex', 'BP', 'Cholesterol', 'Na_to_K']].values
X[0:5]
```

[7]:
```
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)
```

As you may figure out, some features in this dataset are categorical such as **Sex** or **BP**. Unfortunately, Sklearn Decision Trees do not handle categorical variables. But still we can convert these features to numerical values. **pandas.get_dummies()** Convert categorical variable into dummy/indicator variables.

[8]:
```
from sklearn import preprocessing
le_sex = preprocessing.LabelEncoder()
le_sex.fit(['F','M'])
X[:,1] = le_sex.transform(X[:,1])


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


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

X[0:5]
```

[8]:
```
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)
```

Now we can fill the target variable.

[9]:
```
y = my_data["Drug"]
y[0:5]
```

[9]:
```
0    drugY
1    drugC
2    drugC
3    drugX
```

```
4    drugY
Name: Drug, dtype: object
```

<h2>Setting up the Decision Tree</h2>
We will be using train/test split on our decision tree. Let's import train_tes

[10]:
```
from sklearn.model_selection import train_test_split
```

Now train_test_split will return 4 different parameters. We will name them: X_trainset, X_testset, y_trainset, y_testset The train_test_split will need the parameters: X, y, test_size=0.3, and random_state=3. The X and y are the arrays required before the split, the test_size represents the ratio of the testing dataset, and the random_state ensures that we obtain the same splits.

[11]:
```
X_trainset, X_testset, y_trainset, y_testset = train_test_split(X, y,␣
↪test_size=0.3, random_state=3)
```

Practice

Print the shape of X_trainset and y_trainset. Ensure that the dimensions match

[14]:
```
print("shape of X_trainset:", X_trainset.shape)
print("shape of y_trainset:", y_trainset.shape)
```

```
shape of X_trainset: (140, 5)
shape of y_trainset: (140,)
```

Print the shape of X_testset and y_testset. Ensure that the dimensions match

[15]:
```
print("shape of X_trainset:", X_testset.shape)
print("shape of y_trainset:", y_testset.shape)
```

```
shape of X_trainset: (60, 5)
shape of y_trainset: (60,)
```

<h2>Modeling</h2>
We will first create an instance of the DecisionTreeClassifier called drugTree.<
Inside of the classifier, specify criterion="entropy" so we can see the information g

[16]:
```
drugTree = DecisionTreeClassifier(criterion="entropy", max_depth = 4)
drugTree # it shows the default parameters
```

[16]:
```
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')
```

Next, we will fit the data with the training feature matrix X_trainset and training response vector y_trainset

[17]:
```
drugTree.fit(X_trainset,y_trainset)
```

[17]:
```
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')
```

```
<h2>Prediction</h2>
Let's make some <b>predictions</b> on the testing dataset and store it into a variable called
```

[18]:
```
predTree = drugTree.predict(X_testset)
```

You can print out predTree and y_testset if you want to visually compare the prediction to the actual values.

[19]:
```
print (predTree [0:5])
print (y_testset [0:5])
```

```
['drugY' 'drugX' 'drugX' 'drugX' 'drugX']
40     drugY
51     drugX
139    drugX
197    drugX
170    drugX
Name: Drug, dtype: object
```

```
<h2>Evaluation</h2>
Next, let's import <b>metrics</b> from sklearn and check the accuracy of our model.
```

[20]:
```
from sklearn import metrics
import matplotlib.pyplot as plt
print("DecisionTrees's Accuracy: ", metrics.accuracy_score(y_testset, predTree))
```

```
DecisionTrees's Accuracy:  0.9833333333333333
```

Accuracy classification score computes subset accuracy: the set of labels predicted for a sample must exactly match the corresponding set of labels in y_true.

In multilabel classification, the function returns the subset accuracy. If the entire set of predicted labels for a sample strictly match with the true set of labels, then the subset accuracy is 1.0; otherwise it is 0.0.

0.1 Practice

Can you calculate the accuracy score without sklearn ?

[ ]:
```
# your code here
```

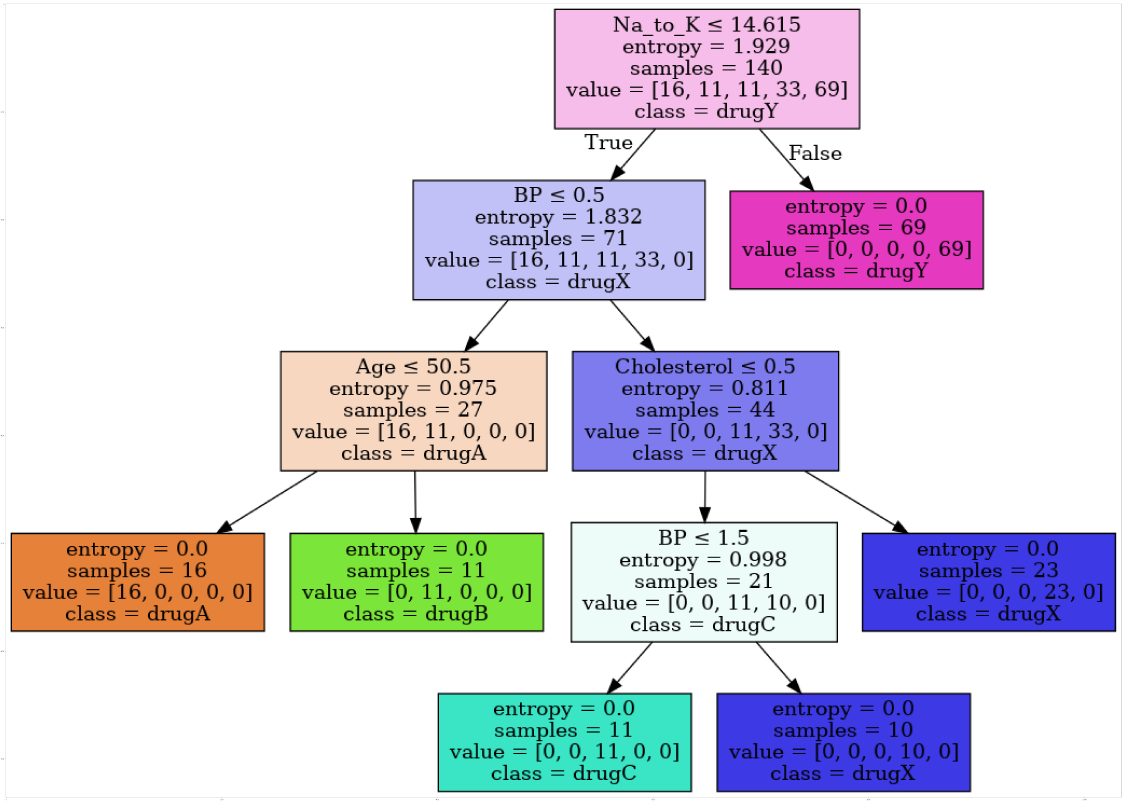
<h2>Visualization</h2>
Lets visualize the tree

[21]:
```
# Notice: You might need to uncomment and install the pydotplus and graphviz␣
 ↪libraries if you have not installed these before
# !conda install -c conda-forge pydotplus -y
# !conda install -c conda-forge python-graphviz -y
```

[22]:
```
from sklearn.externals.six import StringIO
import pydotplus
import matplotlib.image as mpimg
from sklearn import tree
%matplotlib inline
```

[23]:
```
dot_data = StringIO()
filename = "drugtree.png"
featureNames = my_data.columns[0:5]
targetNames = my_data["Drug"].unique().tolist()
out=tree.export_graphviz(drugTree,feature_names=featureNames,␣
 ↪out_file=dot_data, class_names= np.unique(y_trainset), filled=True, ␣
 ↪special_characters=True,rotate=False)
graph = pydotplus.graph_from_dot_data(dot_data.getvalue())
graph.write_png(filename)
img = mpimg.imread(filename)
plt.figure(figsize=(100, 200))
plt.imshow(img,interpolation='nearest')
```

[23]:
```
<matplotlib.image.AxesImage at 0x7f5e91483e10>
```



Want to learn more?

IBM SPSS Modeler is a comprehensive analytics platform that has many machine learning algorithms. It has been designed to bring predictive intelligence to decisions made by individuals, by groups, by systems – by your enterprise as a whole. A free trial is available through this course, available here: SPSS Modeler

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Thanks for completing this lesson!

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Saeed Aghabozorgi, PhD is a Data Scientist in IBM with a track record of developing enterprise level applications that substantially increases clients' ability to turn data into actionable knowledge. He is a researcher in data mining field and expert in developing advanced analytic methods like machine learning and statistical modelling on large datasets.