
# Decision Trees

Estimated time needed: **15** minutes

## Objectives

After completing this lab you will be able to:

- Develop a classification model using Decision Tree Algorithm

In this lab exercise, you will learn a popular machine learning algorithm, Decision Trees. You will use this classification algorithm to build a model from the historical data of patients, and their response to different medications. Then you will 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**

In [20]:
```
import numpy as np
import pandas as pd
from sklearn.tree import DecisionTreeClassifier
```

# About the dataset

Imagine that you are a medical researcher compiling data for a study. You have collected data about a set of patients, all of whom suffered from the same illness. During their course of treatment, each patient responded to one of 5 medications, Drug A, Drug B, Drug c, Drug x and y.

Part of your job is to build a model to find out which drug might be appropriate for a future patient with the same illness. The features of this dataset are Age, Sex, Blood Pressure, and the Cholesterol of the patients, and the target is the drug that each patient responded to.

It is a sample of multiclass 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 prescribe a drug to a new patient.

# Downloading the Data

To download the data, we will use !wget to download it from IBM Object Storage.

In [21]:
```
import wget

url = 'https://cf-courses-data.s3.us.cloud-object-storage.appdomain.cloud/IBMDeveloperSkillsNetwork-ML0101EN-SkillsNetwork/la
myfile = wget.download(url)
```

```
100% [######################################################################################]     5K / 5K
```

!wget -O drug200.csv https://cf-courses-data.s3.us.cloud-object-storage.appdomain.cloud/IBMDeveloperSkillsNetwork-ML0101EN-SkillsNetwork/labs/Module%203/data/drug200.csv

**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 the data using pandas dataframe:

In [22]:
```
my_data = pd.read_csv(myfile, delimiter=",")
my_data[0:5]
```

Out[22]:

| | 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 |

## Practice

What is the size of data?

In [23]:
```
# write your code here

my_data.shape
```

Out[23]:
```
(200, 6)
```

▶ Click here for the solution

# Pre-processing

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.

In [24]:
```
X = my_data[['Age', 'Sex', 'BP', 'Cholesterol', 'Na_to_K']].values
X[0:5]
```

Out[24]:
```
array([[23, 'F', 'HIGH', 'HIGH', 25.355],
       [47, 'M', 'LOW', 'HIGH', 13.093],
       [47, 'M', 'LOW', 'HIGH', 10.114],
       [28, 'F', 'NORMAL', 'HIGH', 7.798],
       [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 does not handle categorical variables. We can still convert these features to numerical values using **pandas.get_dummies()** to convert the categorical variable into dummy/indicator variables.

In [25]:
```
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]
```

Out[25]:
```
array([[23, 0, 0, 0, 25.355],
       [47, 1, 1, 0, 13.093],
       [47, 1, 1, 0, 10.114],
       [28, 0, 2, 0, 7.798],
       [61, 0, 1, 0, 18.043]], dtype=object)
```

Now we can fill the target variable.

In [26]:
```
y = my_data["Drug"]
y[0:5]
```

Out[26]:
```
0    drugY
1    drugC
2    drugC
3    drugX
4    drugY
Name: Drug, dtype: object
```

---

# Setting up the Decision Tree

We will be using **train/test split** on our **decision tree**. Let's import **train_test_split** from **sklearn.cross_validation**.

In [27]:
```
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.

In [28]:
```
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.

In [29]:
```
# your code

print('Shape of X training set {}'.format(X_trainset.shape),'&',' Size of Y training set {}'.format(y_trainset.shape))
```

```
Shape of X training set (140, 5) &  Size of Y training set (140,)
```

▶ Click here for the solution

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

In [30]:
```
# your code

print('Shape of X training set {}'.format(X_testset.shape),'&',' Size of Y training set {}'.format(y_testset.shape))
```

```
Shape of X training set (60, 5) &  Size of Y training set (60,)
```

▶ Click here for the solution

---

# Modeling

We will first create an instance of the **DecisionTreeClassifier** called **drugTree**.
Inside of the classifier, specify *criterion="entropy"* so we can see the information gain of each node.

In [31]:
```
drugTree = DecisionTreeClassifier(criterion="entropy", max_depth = 4)
drugTree # it shows the default parameters
```

Out[31]:
```
DecisionTreeClassifier(criterion='entropy', max_depth=4)
```

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

In [32]:
```
drugTree.fit(X_trainset,y_trainset)
```

Out[32]:
```
DecisionTreeClassifier(criterion='entropy', max_depth=4)
```

# Prediction

Let's make some **predictions** on the testing dataset and store it into a variable called **predTree**.

In [33]:
```
predTree = drugTree.predict(X_testset)
```

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

In [34]:
```
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
```

# Evaluation

Next, let's import **metrics** from sklearn and check the accuracy of our model.

In [35]:
```
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.

# Visualization

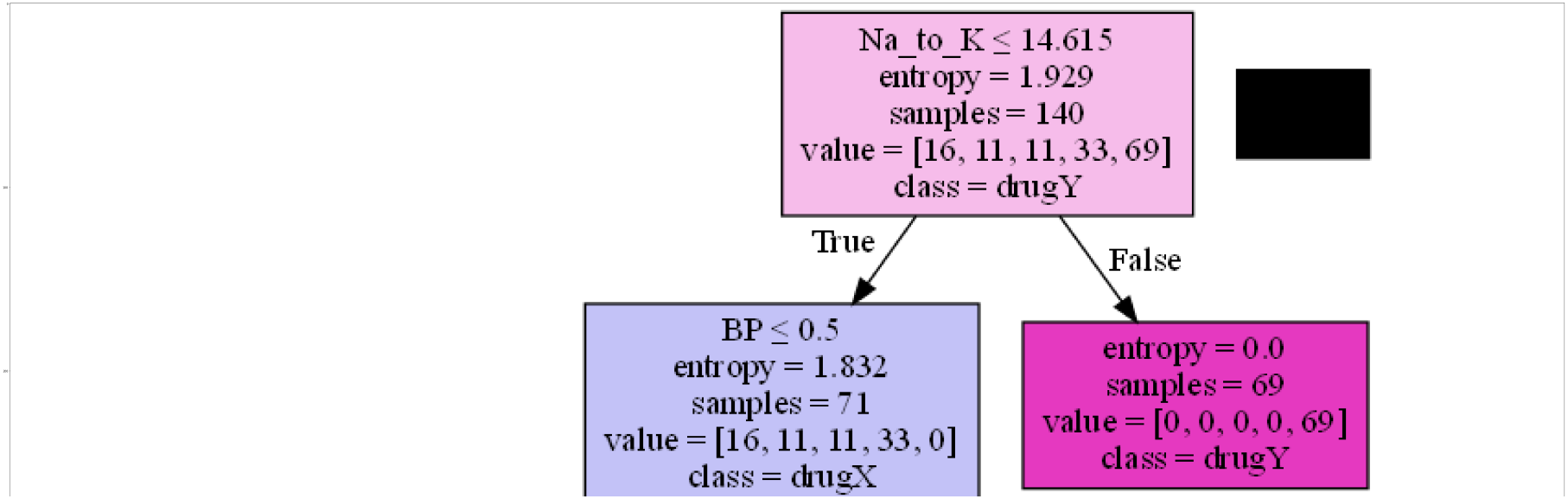
Let's visualize the tree

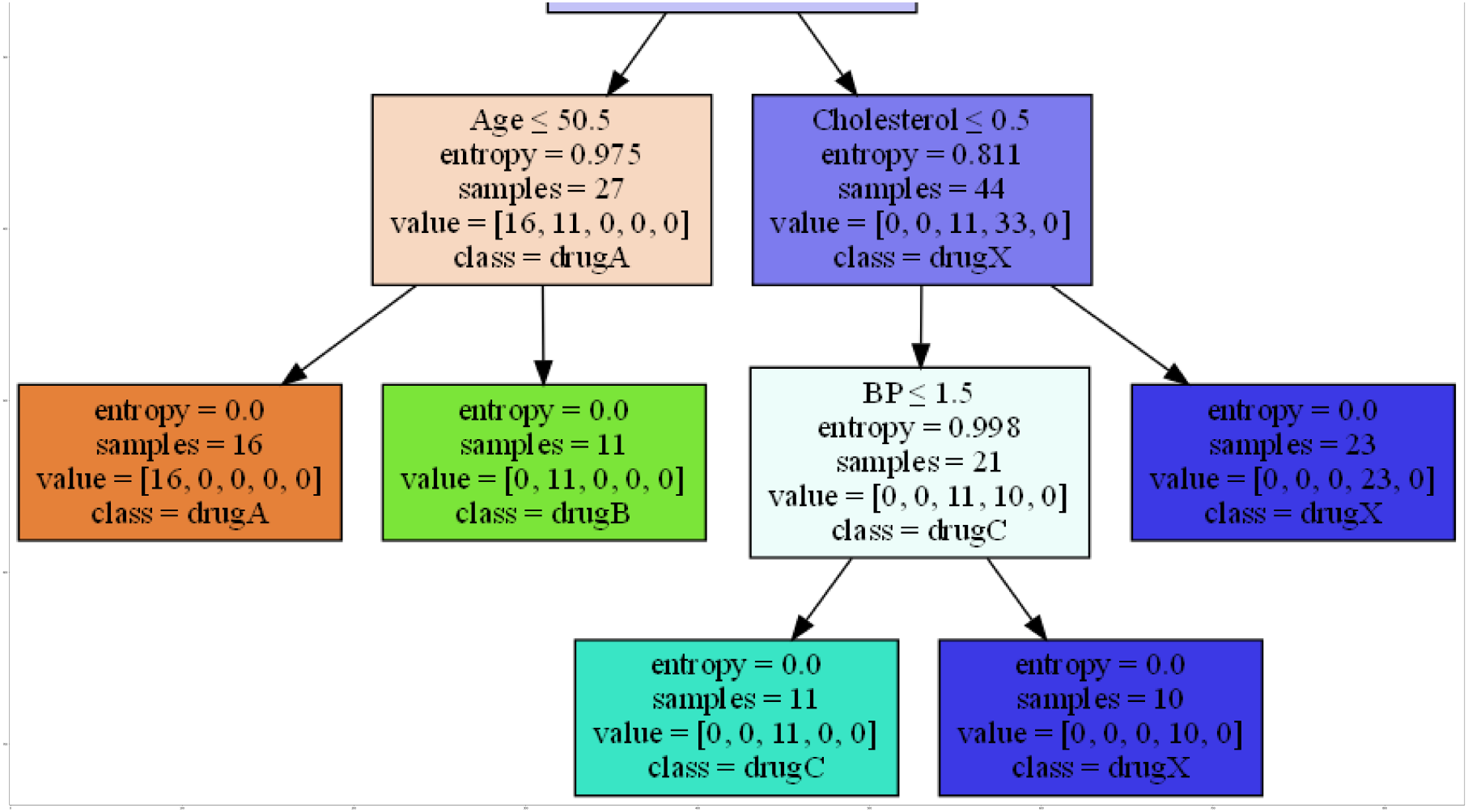
# Notice: You might need to uncomment and install the pydotplus and graphviz libraries if you have not installed these before !conda install -c conda-forge pydotplus -y !conda install -c conda-forge python-graphviz -y

In [38]:
```
from  io import StringIO
import pydotplus
import matplotlib.image as mpimg
from sklearn import tree
%matplotlib inline
```

In [39]:
```
dot_data = StringIO()
filename = "drugtree.png"
featureNames = my_data.columns[0:5]
out=tree.export_graphviz(drugTree,feature_names=featureNames, out_file=dot_data, class_names= np.unique(y_trainset), filled=T
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')
```

Out[39]:
```
<matplotlib.figure.AxesImage at 0x1945b45d8b0>
```






## 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

Also, you can use Watson Studio to run these notebooks faster with bigger datasets. Watson Studio is IBM's leading cloud solution for data scientists, built by data scientists. With Jupyter notebooks, RStudio, Apache Spark and popular libraries pre-packaged in the cloud, Watson