step:1

Importing necessary imports.

```
In [1]: # important imports
    import sys
    import numpy as np
    import pandas as pd
    import matplotlib.pyplot as plt
    from sklearn.tree import DecisionTreeClassifier
    import sklearn.tree as tree
In []:
```

step:2

About Dataset.

In [2]: # downloading the dataset and making a pandas dataframe from the dataset
 df= pd.read_csv('https://cf-courses-data.s3.us.cloud-object-storage.appdomain.cloud
 df.head()

Out[2]:		Age	Sex	ВР	Cholesterol	Na_to_K	Drug
	0	23	F	HIGH	HIGH	25.355	drugY
	1	47	М	LOW	HIGH	13.093	drugC
	2	47	М	LOW	HIGH	10.114	drugC
	3	28	F	NORMAL	HIGH	7.798	drugX
	4	61	F	LOW	HIGH	18.043	drugY

```
In [3]: # inspect the size and important features of the dataset.
df.shape
```

Out[3]: (200, 6)

In [4]: df.info()

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 200 entries, 0 to 199
Data columns (total 6 columns):
    Column
                Non-Null Count Dtype
    -----
                -----
                200 non-null
                               int64
0
    Age
1
    Sex
                200 non-null object
 2
    BP
                200 non-null
                             object
 3
                               object
    Cholesterol 200 non-null
4
                200 non-null
                               float64
    Na_to_K
 5
                               object
    Drug
                200 non-null
dtypes: float64(1), int64(1), object(4)
memory usage: 9.5+ KB
```

what we got?

The dataset contains 6 variables in total. **Age** and **Na_to_K** variables contain numerical values and are continuous variables. Rest of the variables are categorical variables and contain object type i.e. string type values. Our target variable is Drug. The rest are feature variables.

```
In [ ]:
```

step:3

Pre-processing.

```
In [5]: # creating a matrix of feature variables from dataset.
X = df.loc[:,["Age","Sex","BP","Cholesterol","Na_to_K"]]
X.head()
```

```
Out[5]:
            Age Sex
                           BP
                               Cholesterol Na to K
        0
             23
                   F
                         HIGH
                                     HIGH
                                             25.355
                          LOW
         1
             47
                  Μ
                                     HIGH
                                             13.093
        2
             47
                  M
                          LOW
                                     HIGH
                                             10.114
             28
                   F NORMAL
                                     HIGH
                                              7.798
             61
                          LOW
                                     HIGH
                                             18.043
```

```
In [6]: X.shape
Out[6]: (200, 5)
```

As there are categorical values in certain columns, so let us encode them into their numerical values.

```
from sklearn import preprocessing
In [7]:
In [8]: encoder_for_sex = preprocessing.LabelEncoder()
        encoder_for_sex.fit(['F','M'])
        X["Sex"] = encoder for sex.transform(X['Sex'])
In [9]: X.head()
Out[9]:
                           BP
                               Cholesterol Na_to_K
           Age Sex
        0
             23
                   0
                         HIGH
                                     HIGH
                                             25.355
                         LOW
         1
             47
                   1
                                     HIGH
                                             13.093
        2
             47
                   1
                         LOW
                                     HIGH
                                             10.114
        3
             28
                   0 NORMAL
                                     HIGH
                                             7.798
             61
                   0
                         LOW
                                     HIGH
                                             18.043
```

So, now for female there is 0 and for male there is 1 in the dataset X

Doing the same for other variables which contain object type categorical values.

```
In [10]: # doing the same for BP columns
         X['BP'].unique()
Out[10]: array(['HIGH', 'LOW', 'NORMAL'], dtype=object)
In [11]: encoder_for_bp = preprocessing.LabelEncoder()
         encoder_for_bp.fit(['HIGH', 'LOW', 'NORMAL'])
         X["BP"] = encoder_for_bp.transform(X['BP'])
         X.head()
Out[11]:
             Age Sex BP Cholesterol Na_to_K
          0
              23
                    0
                        0
                                HIGH
                                        25.355
          1
              47
                    1
                        1
                                HIGH
                                         13.093
          2
              47
                    1
                        1
                                HIGH
                                        10.114
              28
                        2
                                 HIGH
                    0
                                          7.798
                        1
                                HIGH
              61
                    0
                                         18.043
In [12]: X['BP'].unique()
Out[12]: array([0, 1, 2])
In [13]: # doing the same for Cholesterol feature.
         X['Cholesterol'].unique()
```

```
Out[13]: array(['HIGH', 'NORMAL'], dtype=object)
In [14]: encoder_for_cholesterol = preprocessing.LabelEncoder()
         encoder_for_cholesterol.fit(['HIGH', 'NORMAL'])
         X['Cholesterol'] = encoder_for_cholesterol.transform(X['Cholesterol'])
         X.head()
Out[14]:
            Age Sex BP Cholesterol Na_to_K
                                        25.355
         0
              23
                    0
                        0
         1
              47
                    1
                                   0
                                        13.093
                                        10.114
         2
              47
                    1
                        1
                                   0
              28
                    0
                                         7.798
              61
                    0
                        1
                                   0
                                        18.043
In [15]: X['Cholesterol'].unique()
Out[15]: array([0, 1])
In [16]:
         X array = X.values
In [17]: type(X_array)
Out[17]: numpy.ndarray
In [18]: # making arrray of response variable
         y = df['Drug'].values
In [19]: y[0:5]
Out[19]: array(['drugY', 'drugC', 'drugX', 'drugX'], dtype=object)
         Step:4
         Setting up decision tree
In [20]:
         #making and training and test sets.
In [21]: from sklearn.model_selection import train_test_split
In [22]: x_train,x_test,y_train,y_test = train_test_split(X,y,test_size = 0.25, shuffle=True
In [23]: # printing the size of datasets
         print(x_train.shape)
```

print(y_train.shape)

```
(150, 5)
        (150,)
In [24]: print(x_test.shape)
         print(y_test.shape)
        (50, 5)
        (50,)
In [25]: # Now building our decision tree model
In [26]: decision_tree = DecisionTreeClassifier(criterion='entropy',max_depth=4)
In [27]:
         decision_tree
Out[27]:
                            DecisionTreeClassifier
         DecisionTreeClassifier(criterion='entropy', max_depth=4)
In [28]: decision_tree.fit(x_train,y_train)
Out[28]:
                            DecisionTreeClassifier
         DecisionTreeClassifier(criterion='entropy', max_depth=4)
 In [ ]:
```

Step:5

Making prediction on the test dataset.

```
In [29]: predictions = decision_tree.predict(x_test)
In [30]: # Let us see whether the model works properly or not.
    print(y_test[0:5])
    print(predictions[0:5])

['drugX' 'drugY' 'drugX' 'drugC' 'drugY']
    ['drugX' 'drugY' 'drugX' 'drugC' 'drugY']
    It seems that the model works properly.
In []:
```

Step:6

Model evaluation.

```
In [31]: from sklearn.metrics import accuracy_score
```

```
In [32]: print(f'The accuracy score of the model is: {accuracy_score(y_test,predictions)}')
```

The accuracy score of the model is: 1.0

The accuracy score of 1.0 shows that our model works 100% accurately on the test data.

Step:7

Visualising the model tree.

```
In [33]: # Plot the decision tree using matplotlib
           plt.figure(figsize=(20,10))
           tree.plot_tree(decision_tree, feature_names=["Age","Sex","BP","Cholesterol","Na_to_
           plt.savefig("decision_tree.png") # Save the plot as a PNG file
           plt.show() # Display the plot
                                                                  Na_to_K <= 14.829
                                                                   entropy = 1.938
                                                                    samples = 150
                                                              value = [17, 13, 10, 39, 71]
                                                         BP <= 0.5
                                                                                  entropy = 0.0
                                                      entropy = 1.786
                                                                                  samples = 71
                                                       samples = 79
                                                                              value = [0, 0, 0, 0, 71]
                                                  value = [17, 13, 10, 39, 0]
                             Age <= 50.5
                                                                                   BP <= 1.5
                            entropy = 0.987
                                                                                 entropy = 0.73
                             samples = 30
                                                                                 samples = 49
                         value = [17, 13, 0, 0, 0]
                                                                             value = [0, 0, 10, 39, 0]
                                                                  Cholesterol <= 0.5
                entropy = 0.0
                                          entropy = 0.0
                                                                                               entropy = 0.0
                                                                   entropy = 0.998
                samples = 17
                                          samples = 13
                                                                                               samples = 28
                                                                    samples = 21
             value = [17, 0, 0, 0, 0]
                                      value = [0, 13, 0, 0, 0]
                                                                                           value = [0, 0, 0, 28, 0]
                                                                value = [0, 0, 10, 11, 0]
                                                       entropy = 0.0
                                                                                  entropy = 0.0
                                                                                  samples = 11
                                                       samples = 10
                                                    value = [0, 0, 10, 0, 0]
                                                                              value = [0, 0, 0, 11, 0]
 In [ ]:
```

Step:8

Comparing decesion tree model with KNN model

```
In [34]: from sklearn.neighbors import KNeighborsClassifier
In [35]: knn = KNeighborsClassifier(n_neighbors = 5)
knn.fit(x_train,y_train)
```

Confusion matrix, classification report and accuracy score of KNN model

```
In [38]: print(confusion_matrix(knn_pred,y_test))
       [[ 3 0 2 2
                      0]
        [0 1 2 3 0]
        [00100]
        [ 3 2 1 10 0]
        [ 0 0 0 0 20]]
In [39]: print(classification_report(knn_pred,y_test))
                     precision
                                 recall f1-score
                                                    support
                                                          7
              drugA
                          0.50
                                   0.43
                                             0.46
              drugB
                          0.33
                                   0.17
                                             0.22
                                                          6
              drugC
                          0.17
                                   1.00
                                             0.29
                                                          1
                                             0.65
              drugX
                          0.67
                                   0.62
                                                         16
                          1.00
                                   1.00
              drugY
                                             1.00
                                                         20
           accuracy
                                             0.70
                                                         50
                          0.53
                                   0.64
                                             0.52
                                                         50
          macro avg
       weighted avg
                          0.73
                                   0.70
                                             0.70
                                                         50
In [40]: print(accuracy_score(knn_pred,y_test))
       0.7
In [ ]:
```

confusion matrix , classification report, and accuracy score of Decision Tree model.

```
In [41]: print(confusion_matrix(predictions,y_test))

[[ 6  0  0  0  0]
       [ 0  3  0  0  0]
       [ 0  0  6  0  0]
       [ 0  0  0  15  0]
       [ 0  0  0  0  20]]

In [42]: print(classification_report(predictions,y_test))
```

	precision	recall	f1-score	support
drugA	1.00	1.00	1.00	6
urugA	1.00	1.00	1.00	O
drugB	1.00	1.00	1.00	3
drugC	1.00	1.00	1.00	6
drugX	1.00	1.00	1.00	15
drugY	1.00	1.00	1.00	20
accuracy			1.00	50
macro avg	1.00	1.00	1.00	50
weighted avg	1.00	1.00	1.00	50

Step:9

Conclusion:

From the above two models we can see that the decision tree model gives us the highest accuracy as compared to KNN model on this dataset. Hence we can assume that the decision tree model will perform very well on the unseen data.