```
Pract5.ipynb
             ■ Practical5.ipynb ×
Practical 5 > ■ Practical5.ipynb > M+Prediction of Drug
+ Code + Markdown | ▶ Run All 

□ Clear Outputs of All Cells 
□ Restart | □ Variables □ Outline …
        import pandas as pd
        import numpy as np
        import matplotlib.pyplot as plt
        Loading of data
        df = pd.read_csv("drugclassification.csv")
        Information of data
        df.info()
     ✓ 0.1s
   <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 Cholesterol 200 non-null object
     4 Na_to_K 200 non-null float64
5 Drug 200 non-null object
                        200 non-null
     5
                                           object
          Drug
    dtypes: float64(1), int64(1), object(4)
    memory usage: 9.5+ KB
```

```
■ Practical5.ipynb ×
Pract5.ipynb
Practical 5 > ■ Practical5.ipynb > M+Prediction of Drug
+ Code + Markdown | ▶ Run All ≡ Clear Outputs of All Cells S Restart | ☑ Variables ≡ Outline ···
       Visualising dataframe
       df.head()
                       BP Cholesterol Na_to_K Drug
       Age Sex
        23
             F
                                 HIGH 25.355 DrugY
                    HIGH
                                 HIGH 13.093 drugC
    1
        47
                    LOW
              М
                                 HIGH 10.114 drugC
    2
        47
             M
                     LOW
                                 HIGH 7.798 drugX
        28 F NORMAL
    3
    4 61
                                 HIGH 18.043 DrugY
              F
                     LOW
```

Seperation of input and target data

```
Seperation of input and target data
```

Applying label encoder

```
inputs_val['sex_up'] = sex_up.fit_transform(inputs_val['Sex'])
inputs_val['bp_up'] = bp_up.fit_transform(inputs_val['BP'])
inputs_val['cho_up'] = cho_up.fit_transform(inputs_val['Cholesterol'])

4) \( \square$ 0.7s
```

```
inputs_val
```

	Age	Sex	ВР	Cholesterol	Na_to_K	sex_up	bp_up	cho_up
0	23	F	HIGH	HIGH	25.355	0	0	0
1	47	М	LOW	HIGH	13.093	1	1	0
2	47	М	LOW	HIGH	10.114	1	1	0
3	28	F	NORMAL	HIGH	7.798	0	2	0
4	61	F	LOW	HIGH	18.043	0	1	0
195	56	F	LOW	HIGH	11.567	0	1	0
196	16	М	LOW	HIGH	12.006	1	1	0
197	52	М	NORMAL	HIGH	9.894	1	2	0
198	23	М	NORMAL	NORMAL	14.020	1	2	1
199	40	F	LOW	NORMAL	11.349	0	1	1

200 rows × 8 columns

inputs_n



	Na_to_K	sex_up	bp_up	cho_up
0	25.355	0	0	0
1	13.093	1	1	0
2	10.114	1	1	0
3	7.798	0	2	0
4	18.043	0	1	0
195	11.567	0	1	0
196	12.006	1	1	0
197	9.894	1	2	0
198	14.020	1	2	1
199	11.349	0	1	1

200 rows × 4 columns

```
Formation of decision tree
```

```
from sklearn import tree
dt = tree.DecisionTreeClassifier()

v 0.4s
```

fitting the data into decision tree

DecisionTreeClassifier()

```
dt.score(inputs_n,target_val)

v 0.1s
```

1.0

Prediction of Drug

```
dt.predict([[25.355,0,0,0]])

v 0.3s

C:\Users\astha\AppData\Roaming\Python\Python310\site
names, but DecisionTreeClassifier was fitted with fe
warnings.warn(
array(['DrugY'], dtype=object)

dt.predict([[12.56,0,1,2]])

v 0.4s

C:\Users\astha\AppData\Roaming\Python\Python310\site
names, but DecisionTreeClassifier was fitted with fe
warnings.warn(
array(['drugX'], dtype=object)
```

```
Output exceeds the <a href="mailto:sizellimit">[inst:sizellimit</a>. Open the full output data <a href="mailto:inst:sizellimit">in a text editor</a>
[Text(0.703125, 0.9615384615384616, 'X[0] <= 14.829\ngini = 0.694\nsamples = 200\nvalue = [91, 23, 16, 16, 54]'), Text(0.640625, 0.88461538461538461, 'X[2] <= 0.5\ngini = 0.667\nsamples = 109\nvalue = [0, 23, 16, 16, 54]'), Text(0.40625, 0.8076923076923077, 'X[0] <= 3.316\ngini = 0.484\nsamples = 39\nvalue = [0, 23, 16, 0, 0]'), Text(0.1875, 0.6538461538461539, 'gini = 0.0\nsamples = 31\nvalue = [0, 22, 12, 0, 0]'), Text(0.1875, 0.6538461538461539, 'gini = 0.0\nsamples = 31\nvalue = [0, 3, 0, 0, 0]'), Text(0.1875, 0.5538461538461539, 'X[0] <= 10.24\ngini = 0.475\nsamples = 31\nvalue = [0, 19, 12, 0, 0]'), Text(0.1875, 0.5769230769230769, 'X[0] <= 9.67\ngini = 0.484\nsamples = 10\nvalue = [0, 4, 6, 0, 0]'), Text(0.1875, 0.5769230769230769, 'X[0] <= 9.67\ngini = 0.484\nsamples = 10\nvalue = [0, 4, 6, 0, 0]'), Text(0.1875, 0.5769230769230769, 'X[0] <= 9.67\ngini = 0.484\nsamples = 10\nvalue = [0, 4, 2, 0, 0]'), Text(0.1875, 0.4230769230769231, 'X[0] <= 9.67\ngini = 0.484\nsamples = 10\nvalue = [0, 4, 2, 0, 0]'), Text(0.1875, 0.4230769230769231, 'X[0] <= 9.65\ngini = 0.32\nsamples = 1\nvalue = [0, 4, 1, 0, 0]'), Text(0.1875, 0.4230769230769231, 'X[0] <= 9.615\ngini = 0.5\nsamples = 2\nvalue = [0, 4, 1, 0, 0]'), Text(0.1875, 0.2692307692307692, 'gini = 0.0\nsamples = 1\nvalue = [0, 0, 1, 0, 0]'), Text(0.1875, 0.2692307692307692, 'gini = 0.0\nsamples = 1\nvalue = [0, 1, 0, 0]'), Text(0.25, 0.2692307692307692, 'gini = 0.0\nsamples = 1\nvalue = [0, 1, 0, 0]'), Text(0.25, 0.5, 'gini = 0.0\nsamples = 4\nvalue = [0, 4, 0, 0]'), Text(0.4375, 0.5769230769230769), 'X[0] <= 10.712\ngini = 0.408\nsamples = 2\nvalue = [0, 1, 0, 0]'), Text(0.4375, 0.5, 'gini = 0.0\nsamples = 3\nvalue = [0, 4, 0, 0]'), Text(0.5025, 0.5, 'yin = 0.0\nsamples = 3\nvalue = [0, 0, 0, 0]'), Text(0.5025, 0.5, 'yin = 0.0\nsamples = 3\nvalue = [0, 0, 0, 0]'), Text(0.5025, 0.43015384615384615, 'X[0] <= 11.333\
```

