```
In [1]: import numpy as np
import pandas as pd
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier
```

In [2]: df=pd.read_csv(r"C:\Users\LENOVO\Downloads\drug200.csv")
df

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
195	56	F	LOW	HIGH	11.567	drugC
196	16	М	LOW	HIGH	12.006	drugC
197	52	М	NORMAL	HIGH	9.894	drugX
198	23	М	NORMAL	NORMAL	14.020	drugX
199	40	F	LOW	NORMAL	11.349	drugX

200 rows × 6 columns

In [3]: df.shape

Out[3]: (200, 6)

In [4]: df.head()

Out[4]:

		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 [5]: df.shape

Out[5]: (200, 6)

```
In [6]: df.describe
 Out[6]: <bound method NDFrame.describe of
                                                   Age Sex
                                                                 BP Cholesterol Na to K
                                                                                             Drug
                23
                     F
                           HIGH
                                       HIGH
                                               25.355
                                                       drugY
          1
                47
                     Μ
                            LOW
                                       HIGH
                                               13.093
                                                       drugC
          2
                47
                     Μ
                            LOW
                                       HIGH
                                               10.114
                                                       drugC
          3
                                                7.798
                28
                     F
                         NORMAL
                                                       drugX
                                       HIGH
          4
                61
                     F
                            LOW
                                       HIGH
                                               18.043
                                                       drugY
                            . . .
                                        . . .
                                                  . . .
          195
                     F
                                               11.567
                                                       drugC
                56
                            LOW
                                       HIGH
          196
                16
                     Μ
                            LOW
                                       HIGH
                                               12.006
                                                       drugC
          197
                52
                     Μ
                        NORMAL
                                       HIGH
                                                9.894
                                                       drugX
                         NORMAL
          198
                23
                     Μ
                                     NORMAL
                                               14.020
                                                       drugX
          199
                40
                     F
                            LOW
                                     NORMAL
                                               11.349
                                                       drugX
          [200 rows x 6 columns]>
         df.info()
 In [7]:
          <class 'pandas.core.frame.DataFrame'>
          RangeIndex: 200 entries, 0 to 199
          Data columns (total 6 columns):
                             Non-Null Count Dtype
               Column
                             -----
                                              _ _ _ _ _
          ---
           0
                             200 non-null
                                              int64
               Age
                             200 non-null
           1
               Sex
                                              object
           2
                             200 non-null
                                              object
                                              object
           3
               Cholesterol
                             200 non-null
               Na_to_K
                             200 non-null
                                              float64
           4
           5
                             200 non-null
                                              object
               Drug
          dtypes: float64(1), int64(1), object(4)
          memory usage: 9.5+ KB
 In [8]: df.isna().sum()
 Out[8]: Age
                          0
                          0
          Sex
          ΒP
                          0
                          0
          Cholesterol
          Na_to_K
                          0
                          0
          Drug
          dtype: int64
 In [9]: df['BP'].value_counts()
 Out[9]: BP
          HIGH
                    77
          LOW
                    64
          NORMAL
                    59
          Name: count, dtype: int64
In [10]: df['Cholesterol'].value_counts()
Out[10]: Cholesterol
          HIGH
                    103
          NORMAL
                     97
          Name: count, dtype: int64
```

```
In [11]: df['Drug'].value_counts()
Out[11]: Drug
         drugY
                   91
         drugX
                   54
         drugA
                   23
         drugC
                   16
         drugB
                   16
         Name: count, dtype: int64
In [12]: df['Na_to_K'].value_counts()
Out[12]: Na_to_K
         12.006
                    2
         18.295
                    2
         25.355
                    1
         11.939
                    1
         16.347
                    1
                   . .
         24.658
                   1
         24.276
                    1
         13.967
                    1
         19.675
                    1
         11.349
                    1
         Name: count, Length: 198, dtype: int64
In [13]: convert={"Sex":{"F":1,"M":0}}
         df=df.replace(convert)
```

Out[13]:

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

200 rows × 6 columns

```
In [14]: convert={"Cholesterol":{"HIGH":1,"NORMAL":0}}
    df=df.replace(convert)
    df
```

Out[14]:

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

200 rows × 6 columns

```
In [15]: x=["Sex","Cholesterol"]
    y=["Yes","No"]
    all_inputs=df[x]
    all_classes=df["BP"]
```

```
In [16]: (x_train,x_test,y_train,y_test)=train_test_split(all_inputs,all_classes,test_size=0.25
```

```
In [17]: clf=DecisionTreeClassifier(random_state=0)
```

```
In [18]: clf.fit(x_train,y_train)
```

Out[18]:

DecisionTreeClassifier

DecisionTreeClassifier(random_state=0)

```
In [20]: score=clf.score(x_test,y_test)
print(score)
```

0.38

```
In [ ]:
```