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\shaha\OneDrive\Desktop\Excel\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.head()

Out[3]:

| | 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 [4]:
```

```
df.tail()
```

Out[4]:

| | Age | Sex | ВР | Cholesterol | Na_to_K | Drug |
|-----|-----|-----|--------|-------------|---------|-------|
| 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 |

In [5]:

```
df.shape
```

Out[5]:

(200, 6)

In [6]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 200 entries, 0 to 199
Data columns (total 6 columns):
```

```
#
    Column
                 Non-Null Count Dtype
                 _____
    -----
_ _ _
0
                 200 non-null
                                int64
    Age
 1
                 200 non-null
                                object
    Sex
 2
                 200 non-null
                                object
 3
    Cholesterol 200 non-null
                                object
 4
    Na_to_K
                 200 non-null
                                float64
 5
                 200 non-null
    Drug
                                object
dtypes: float64(1), int64(1), object(4)
```

memory usage: 9.5+ KB

In [7]:

```
df.isnull().sum()
```

Out[7]:

| Age | 0 |
|--------------|---|
| Sex | 0 |
| BP | 0 |
| Cholesterol | 0 |
| Na_to_K | 0 |
| Drug | 0 |
| dtype: int64 | |

```
In [8]:
df['Sex'].value_counts()
Out[8]:
Sex
Μ
     104
F
      96
Name: count, dtype: int64
In [9]:
df['BP'].value_counts()
Out[9]:
BP
          77
HIGH
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]:

```
convert={'Sex':{"M":0,"F":1}}
df=df.replace(convert)
df
```

Out[12]:

| | Age | Sex | ВР | BP Cholesterol | | 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={'BP':{"HIGH":1,"LOW":0,"NORMAL":2}}
df=df.replace(convert)
df
```

Out[14]:

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

200 rows × 6 columns

In [15]:

```
convert={'Cholesterol':{"HIGH":1,"NORMAL":0}}
df=df.replace(convert)
df
```

Out[15]:

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

200 rows × 6 columns

In [21]:

```
x=["Age","Sex","BP","Cholesterol"]
y=["drugY","drugC","drugX","drugB"]
all_inputs=df[x]
all_classes=df["Drug"]
```

In [22]:

```
(x_train,x_test,y_train,y_test)=train_test_split(all_inputs,all_classes,test_size=0.5)
```

In [23]:

```
clf=DecisionTreeClassifier(random_state=0)
```

In [24]:

```
clf.fit(x_train,y_train)
```

Out[24]:

```
DecisionTreeClassifier
DecisionTreeClassifier(random_state=0)
```

In [25]:
score=clf.score(x_test,y_test)
print(score)

0.49
In []: