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\Sudheer\AppData\Local\Microsoft\Windows\INetCache\IE
df
```

Out[2]:

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

200 rows × 6 columns

In [3]:
```
df.info()
```

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

In [4]:
```
df['BP'].value_counts()
```

Out[4]:
```
BP
HIGH      77
LOW       64
NORMAL    59
Name: count, dtype: int64
```

In [5]:
```
df['Cholesterol'].value_counts()
```

Out[5]:
```
Cholesterol
HIGH      103
NORMAL     97
Name: count, dtype: int64
```

In [6]:
```
convert={"BP":{"LOW":1,"NORMAL":2,"HIGH":3}}
df=df.replace(convert)
df
```

Out[6]:

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

200 rows × 6 columns

In [7]:
```
convert={"Drug":{"drugX":1,"drugY":2,"drugA":3,"drugB":4,"drugC":5}}
df=df.replace(convert)
df
```

Out[7]:

	Age	Sex	BP	Cholesterol	Na_to_K	Drug
0	23	F	3	HIGH	25.355	2
1	47	M	1	HIGH	13.093	5
2	47	M	1	HIGH	10.114	5
3	28	F	2	HIGH	7.798	1
4	61	F	1	HIGH	18.043	2
...	...	...	...	...	...	...
195	56	F	1	HIGH	11.567	5
196	16	M	1	HIGH	12.006	5
197	52	M	2	HIGH	9.894	1
198	23	M	2	NORMAL	14.020	1
199	40	F	1	NORMAL	11.349	1

200 rows × 6 columns

In [8]:
```
x=["Drug","BP"]
y=["M","F"]
all_inputs=df[x]
all_classes=df["Sex"]
```

In [9]:
```
(x_train,x_test,y_train,y_test)=train_test_split(all_inputs,all_classes,test_s
```

In [10]:
```
clf=DecisionTreeClassifier(random_state=0)
```

In [11]:
```
clf.fit(x_train,y_train)
```

Out[11]:
```
DecisionTreeClassifier(random_state=0)
```
In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.
On GitHub, the HTML representation is unable to render, please try loading this page with nbviewer.org.

In [12]:
```
score=clf.score(x_test,y_test)
print(score)
```

```
0.525
```

In [ ]: