Importing the required python modules and reading the dataset

In [1]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
warnings.filterwarnings("ignore")
```

In [2]:
```
df=pd.read_csv('drug200.csv')
```

In [3]:
```
df
```

Out[3]:

	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 [4]:
```
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
```

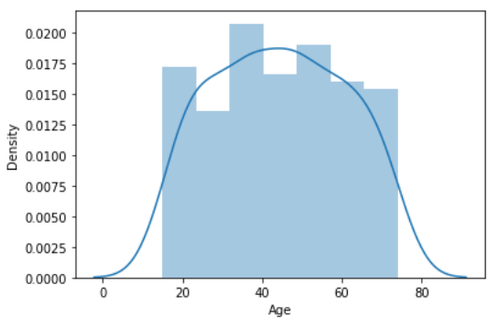
From above info we can see that the dataset has 200 rows in which there are no null values and 6 columns in total. Also the datatype of the columns are correct as per the values containing in it

In [5]:
```
df.describe()
```

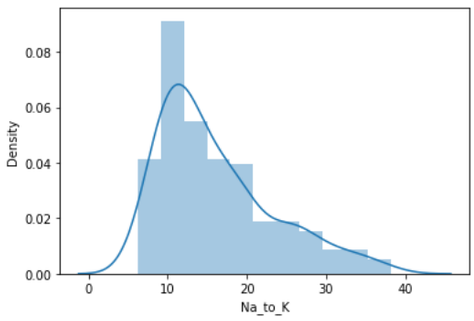
Out[5]:

	Age	Na_to_K
count	200.000000	200.000000
mean	44.315000	16.084485
std	16.544315	7.223956
min	15.000000	6.269000
25%	31.000000	10.445500
50%	45.000000	13.936500
75%	58.000000	19.380000
max	74.000000	38.247000

In [6]:
```
sns.distplot(df['Age'])
plt.show()
```

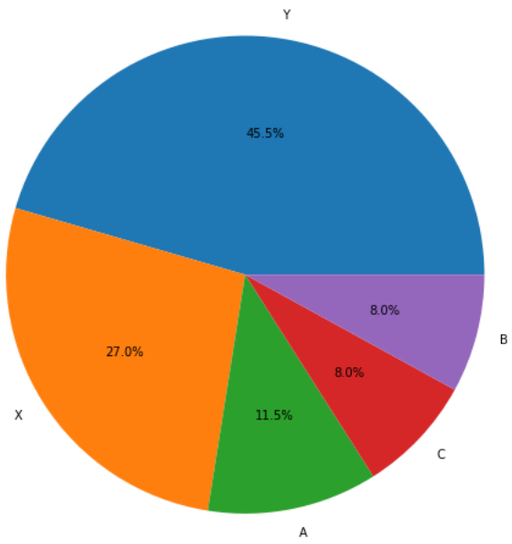


In [7]:
```
sns.distplot(df['Na_to_K'])
plt.show()
```



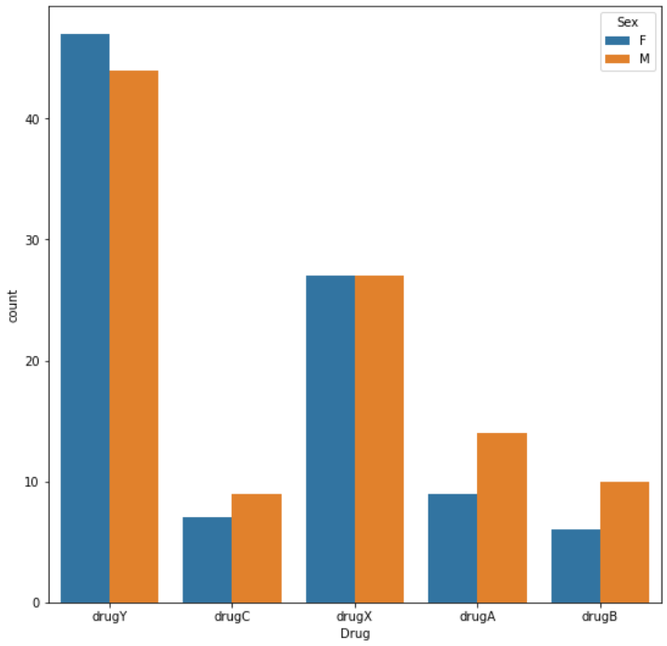
From the above histogram plots and the describe function we can see that the data in Age column is uniformly distributed as seen that the mean and median values are close to each other where as there are some outliers in Na_to_K column

In [8]:
```
plt.figure(figsize=(9,9))
plt.pie(df['Drug'].value_counts(),labels=['Y','X','A','C','B'],autopct='%1.1f%%')
plt.show()
```



The above pie chart shows that most of the patient responded to drug Y i.e. 45.5% and going in descending order X,A,C,B which are 27%,11.5%,8%,8% respectively

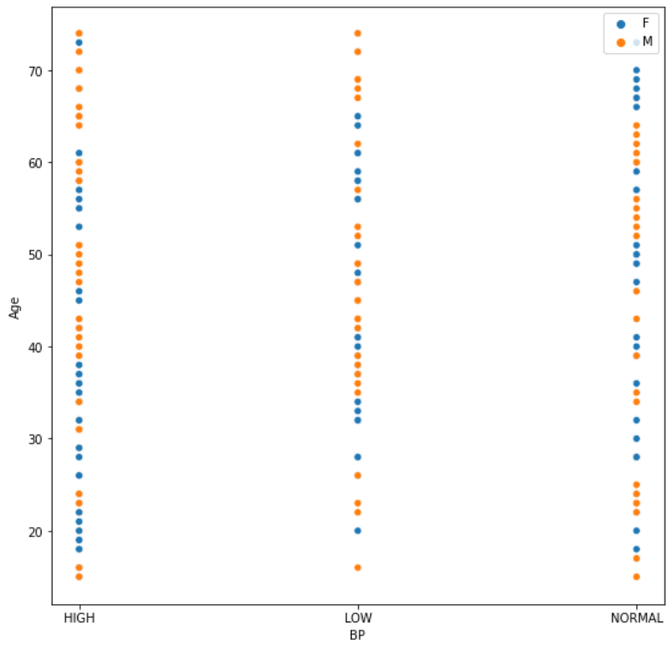
In [9]:
```
plt.figure(figsize=(9,9))
sns.countplot(data=df,x='Drug',hue='Sex')
plt.show()
```



Here in the countplot we can see that as most persons responded to drug Y which is around 45% of total,both genders have equal response to drug Y.It is

also same in case of drug X. But in remaining drugs which are A,B and C males responded more positively than females

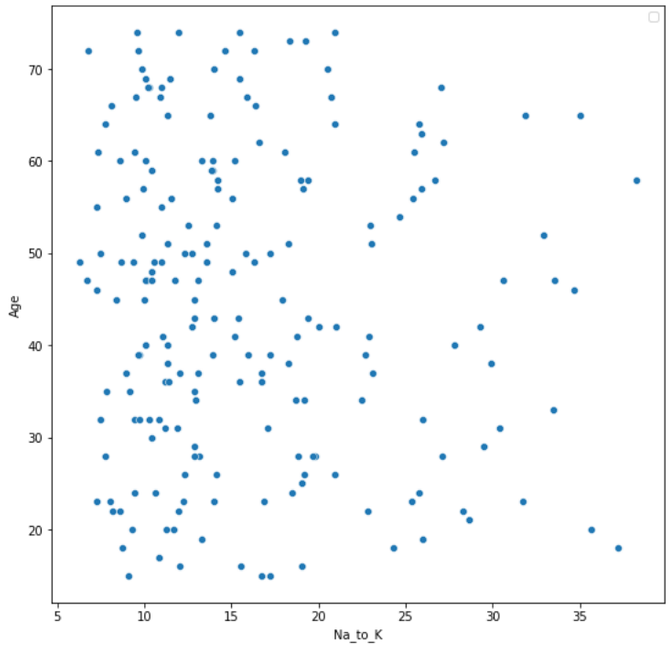
In [10]:
```
plt.figure(figsize=(9,9))
sns.scatterplot(data=df,x='BP',y='Age',hue='Sex')
plt.legend()
plt.show()
```



The above scatter plot shows that the blood pressure categores between male and female are evenly scattered i.e there are both males and females present evenly across all 3 categories

In [11]:
```
plt.figure(figsize=(9,9))
sns.scatterplot(data=df,x='Na_to_K',y='Age')
plt.legend()
plt.show()
```

```
No artists with labels found to put in legend.  Note that artists whose label start with an underscore are ignored when legend
() is called with no argument.
```



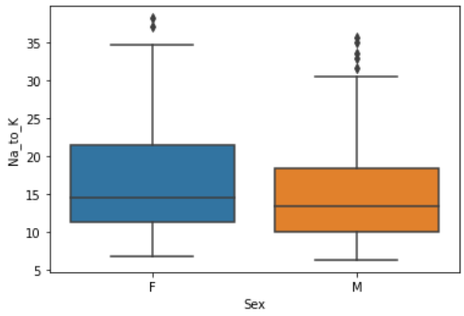
The above scatterplot shows us that there is not relationship between features i.e. both Age and Na_to_K ratio columns are independent of each other

In [12]:
```
df.corr()
```

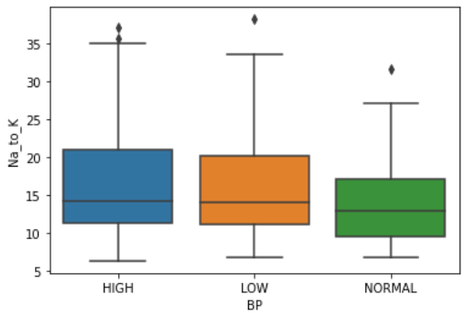
Out[12]:

	Age	Na_to_K
Age	1.000000	-0.063119
Na_to_K	-0.063119	1.000000

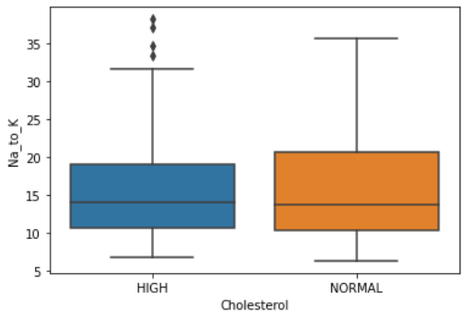
In [13]:
```
sns.boxplot(data=df,x='Sex',y='Na_to_K')
plt.show()
```



In [14]:
```
sns.boxplot(data=df,x='BP',y='Na_to_K')
plt.show()
```



In [15]:
```
sns.boxplot(data=df,x='Cholesterol',y='Na_to_K')
plt.show()
```



Of the above boxplots most of outliers lie when Na_to_K ration is compared to Gender column so we will remove only that

In [16]:
```
df[(df['Sex']=='M')&(df['Na_to_K']>30)]
```

Out[16]:

	Age	Sex	BP	Cholesterol	Na_to_K	Drug
22	47	M	LOW	NORMAL	30.568	drugY
26	31	M	HIGH	HIGH	30.366	drugY
48	23	M	NORMAL	HIGH	31.686	drugY
98	20	M	HIGH	NORMAL	35.639	drugY
128	47	M	LOW	NORMAL	33.542	drugY
131	52	M	LOW	NORMAL	32.922	drugY
188	65	M	HIGH	NORMAL	34.997	drugY

In [17]:
```
df[(df['Sex']=='F')&(df['Na_to_K']>35)]
```

Out[17]:

	Age	Sex	BP	Cholesterol	Na_to_K	Drug
96	58	F	LOW	HIGH	38.247	drugY
184	18	F	HIGH	HIGH	37.188	drugY

In [18]:
```
df.drop([22,26,48,98,128,131,188,96,184],inplace=True)
```

In [19]:
```
df
```

Out[19]:

	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

191 rows × 6 columns

Separating Input and Output variables

In [20]:
```
x=df.iloc[:,:-1]
y=df.iloc[:,-1:]
```

In [21]:
```
x
```

Out[21]:

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

191 rows × 5 columns

In [22]:
```
y
```

Out[22]:

	Drug
0	drugY
1	drugC
2	drugC
3	drugX
4	drugY
...	...
195	drugC
196	drugC
197	drugX
198	drugX
199	drugX

191 rows × 1 columns

Encoding Categorical Data

In [23]:
```
from sklearn.preprocessing import OrdinalEncoder
oe=OrdinalEncoder()
```

In [24]:
```
x[['Sex','BP','Cholesterol']]=oe.fit_transform(x[['Sex','BP','Cholesterol']])
```

In [25]:
```
x
```

Out[25]:

	Age	Sex	BP	Cholesterol	Na_to_K
0	23	0.0	0.0	0.0	25.355
1	47	1.0	1.0	0.0	13.093
2	47	1.0	1.0	0.0	10.114
3	28	0.0	2.0	0.0	7.798
4	61	0.0	1.0	0.0	18.043
...	...	...	...	...	...
195	56	0.0	1.0	0.0	11.567
196	16	1.0	1.0	0.0	12.006
197	52	1.0	2.0	0.0	9.894
198	23	1.0	2.0	1.0	14.020
199	40	0.0	1.0	1.0	11.349

191 rows × 5 columns

Splitting the dataset and Applying ML algorithm

In [26]:
```
from sklearn.model_selection import train_test_split
xtrain,xtest,ytrain,ytest=train_test_split(x,y,test_size=0.2,random_state=0)
```

In [27]:
```
from sklearn.naive_bayes import GaussianNB,MultinomialNB,BernoulliNB
from sklearn.metrics import classification_report
```

In [28]:
```
from sklearn.neighbors import KNeighborsClassifier
from sklearn.svm import SVC
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.linear_model import LogisticRegression
```

In [29]:
```
def mymodel(model):
    model.fit(xtrain,ytrain)
    ypred=model.predict(xtest)

    train=model.score(xtrain,ytrain)
    test=model.score(xtest,ytest)

    print(f"Training Accuracy:- {train}\n Testing Accuracy:- {test}")
    print(classification_report(ytest,ypred))

    return model
```

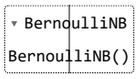
In [30]:
```
mymodel(BernoulliNB())
```

```
Training Accuracy:- 0.5131578947368421
 Testing Accuracy:- 0.5128205128205128
              precision    recall  f1-score   support

       drugA       0.00      0.00      0.00         6
       drugB       0.00      0.00      0.00         2
       drugC       0.00      0.00      0.00         3
       drugX       0.82      0.60      0.69        15
       drugY       0.39      0.85      0.54        13

    accuracy                           0.51        39
   macro avg       0.24      0.29      0.25        39
weighted avg       0.45      0.51      0.45        39
```

Out[30]:



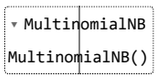
In [31]:
```
mymodel(MultinomialNB())
```

```
Training Accuracy:- 0.6644736842105263
 Testing Accuracy:- 0.6410256410256411
              precision    recall  f1-score   support

       drugA       0.67      0.33      0.44         6
       drugB       1.00      1.00      1.00         2
       drugC       0.00      0.00      0.00         3
       drugX       0.77      0.67      0.71        15
       drugY       0.55      0.85      0.67        13

    accuracy                           0.64        39
   macro avg       0.60      0.57      0.57        39
weighted avg       0.63      0.64      0.62        39
```

Out[31]:



In [32]:
```
mymodel(GaussianNB())
```

```
Training Accuracy:- 0.8618421052631579
 Testing Accuracy:- 0.8205128205128205
              precision    recall  f1-score   support

       drugA       0.60      1.00      0.75         6
       drugB       0.67      1.00      0.80         2
       drugC       0.75      1.00      0.86         3
       drugX       1.00      0.93      0.97        15
       drugY       0.88      0.54      0.67        13

    accuracy                           0.82        39
   macro avg       0.78      0.89      0.81        39
weighted avg       0.86      0.82      0.82        39
```

Out[32]:
```
GaussianNB
GaussianNB()
```

In [33]:
```
mymodel(KNeighborsClassifier())
```

```
Training Accuracy:- 0.7960526315789473
 Testing Accuracy:- 0.5897435897435898
              precision    recall  f1-score   support

       drugA       0.44      0.67      0.53         6
       drugB       0.00      0.00      0.00         2
       drugC       0.00      0.00      0.00         3
       drugX       0.50      0.40      0.44        15
       drugY       0.93      1.00      0.96        13

    accuracy                           0.59        39
   macro avg       0.37      0.41      0.39        39
weighted avg       0.57      0.59      0.57        39
```

Out[33]:
```
KNeighborsClassifier
KNeighborsClassifier()
```

In [34]:
```
mymodel(LogisticRegression())
```

```
Training Accuracy:- 0.881578947368421
 Testing Accuracy:- 0.8974358974358975
              precision    recall  f1-score   support

       drugA       0.80      0.67      0.73         6
       drugB       1.00      1.00      1.00         2
       drugC       1.00      0.67      0.80         3
       drugX       0.94      1.00      0.97        15
       drugY       0.86      0.92      0.89        13

    accuracy                           0.90        39
   macro avg       0.92      0.85      0.88        39
weighted avg       0.90      0.90      0.89        39
```

Out[34]:
```
LogisticRegression
LogisticRegression()
```

In [35]:
```
mymodel(SVC())
```

```
Training Accuracy:- 0.6776315789473685
 Testing Accuracy:- 0.6923076923076923
              precision    recall  f1-score   support

       drugA       0.00      0.00      0.00         6
       drugB       0.00      0.00      0.00         2
       drugC       0.00      0.00      0.00         3
       drugX       0.56      0.93      0.70        15
       drugY       0.93      1.00      0.96        13

    accuracy                           0.69        39
   macro avg       0.30      0.39      0.33        39
weighted avg       0.52      0.69      0.59        39
```

Out[35]:
```
SVC
SVC()
```

In [36]:
```
mymodel(DecisionTreeClassifier())
```

```
Training Accuracy:- 1.0
 Testing Accuracy:- 0.9743589743589743
              precision    recall  f1-score   support

       drugA       1.00      1.00      1.00         6
       drugB       1.00      1.00      1.00         2
       drugC       1.00      1.00      1.00         3
       drugX       1.00      0.93      0.97        15
       drugY       0.93      1.00      0.96        13

    accuracy                           0.97        39
   macro avg       0.99      0.99      0.99        39
weighted avg       0.98      0.97      0.97        39
```

Out[36]:
```
DecisionTreeClassifier
DecisionTreeClassifier()
```

In [37]:
```
mymodel(RandomForestClassifier())
```

```
Training Accuracy:- 1.0
 Testing Accuracy:- 0.9743589743589743
              precision    recall  f1-score   support

       drugA       1.00      1.00      1.00         6
       drugB       1.00      1.00      1.00         2
       drugC       1.00      1.00      1.00         3
       drugX       1.00      0.93      0.97        15
       drugY       0.93      1.00      0.96        13

    accuracy                           0.97        39
   macro avg       0.99      0.99      0.99        39
weighted avg       0.98      0.97      0.97        39
```

Out[37]:

RandomForestClassifier

RandomForestClassifier()

In [38]:
```
from sklearn.model_selection import GridSearchCV
```

In [39]:
```
param={'max_depth':range(1,30),
      'min_samples_leaf':range(1,20,),
      'min_samples_split':range(3,20)}
```

In [40]:
```
grid=GridSearchCV(RandomForestClassifier(),param,verbose=2)
```

In [41]:
```
#grid.fit(xtrain,ytrain)
```

In [42]:
```
#grid.best_params_
```

In [43]:
```
mymodel(RandomForestClassifier(max_depth=5,min_samples_leaf=2,min_samples_split=3))
```

```
Training Accuracy:- 1.0
 Testing Accuracy:- 0.9743589743589743
              precision    recall  f1-score   support

       drugA       1.00      1.00      1.00         6
       drugB       1.00      1.00      1.00         2
       drugC       1.00      1.00      1.00         3
       drugX       1.00      0.93      0.97        15
       drugY       0.93      1.00      0.96        13

    accuracy                           0.97        39
   macro avg       0.99      0.99      0.99        39
weighted avg       0.98      0.97      0.97        39
```

Out[43]:

RandomForestClassifier

RandomForestClassifier(max_depth=5, min_samples_leaf=2, min_samples_split=3)

In [44]:
```
from sklearn.ensemble import AdaBoostClassifier,GradientBoostingClassifier
from xgboost import XGBClassifier
```

In [45]:
```
mymodel(AdaBoostClassifier())
```

```
Training Accuracy:- 0.8223684210526315
 Testing Accuracy:- 0.8461538461538461
              precision    recall  f1-score   support

       drugA       0.75      1.00      0.86         6
       drugB       0.00      0.00      0.00         2
       drugC       0.00      0.00      0.00         3
       drugX       0.82      0.93      0.87        15
       drugY       0.93      1.00      0.96        13

    accuracy                           0.85        39
   macro avg       0.50      0.59      0.54        39
weighted avg       0.74      0.85      0.79        39
```

Out[45]:

AdaBoostClassifier

AdaBoostClassifier()

In [46]:
```
mymodel(GradientBoostingClassifier())
```

```
Training Accuracy:- 1.0
 Testing Accuracy:- 0.9743589743589743
              precision    recall  f1-score   support

       drugA       1.00      1.00      1.00         6
       drugB       1.00      1.00      1.00         2
       drugC       1.00      1.00      1.00         3
       drugX       1.00      0.93      0.97        15
       drugY       0.93      1.00      0.96        13

    accuracy                           0.97        39
   macro avg       0.99      0.99      0.99        39
weighted avg       0.98      0.97      0.97        39
```

Out[46]:

GradientBoostingClassifier

GradientBoostingClassifier()

After applying multiple algorithms it is seen that Logsitic Regression performs the best on this dataset

In [47]:
```
logreg=LogisticRegression()
```

In [48]:
```
logreg.fit(xtrain,ytrain)
```

Out[48]:
```
LogisticRegression
LogisticRegression()
```

Predicting new values

In [49]:
```
def new():
    age=int(input('Enter Age '))
    gen=input('Enter Gender ')
    bp=input('Enter Blood Pressure status ')
    c=input('Enter Cholesterol status ')
    nk=float(input('Enter Na_to_K value '))

    n=[age,gen,bp,c,nk]
    n[1],n[2],n[3]=oe.transform([[n[1],n[2],n[3]]])[0]
    a=logreg.predict([n])[0]
    print(f'\n{a} is recommended for the patient')
```

In [50]:
```
new()
```

```
Enter Age 26
Enter Gender M
Enter Blood Pressure status NORMAL
Enter Cholesterol status HIGH
Enter Na_to_K value 25.222

drugY is recommended for the patient
```

In [ ]:
```

```