HEAMNATH

20104028

In [1]:

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

In [2]:

```
df=pd.read_csv("4_drug200.csv")
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.head()
```

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

DATA CLEANING AND DATA PREPROCESSING

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
```

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]:

```
df.columns
```

Out[6]:

```
Index(['Age', 'Sex', 'BP', 'Cholesterol', 'Na_to_K', 'Drug'], dtype='object')
```

In [7]:

```
df1=df.dropna(axis=1)
df1
```

Out[7]:

	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

	Age	Sex	BP	Cholesterol	Na_to_K	Drug
...	...	...	...	...	...	...
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 [8]:

```
df1.columns
```

Out[8]:

```
Index(['Age', 'Sex', 'BP', 'Cholesterol', 'Na_to_K', 'Drug'], dtype='object')
```

In [9]:

```
df1=df1[['Age','Na_to_K']]
```

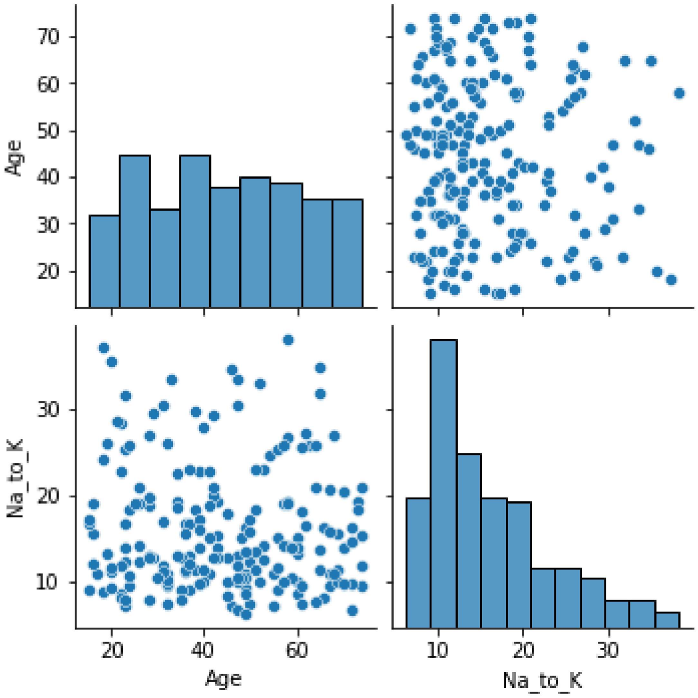
EDA AND VISUALIZATION

In [10]:

```
sns.pairplot(df1)
```

Out[10]:

```
<seaborn.axisgrid.PairGrid at 0x27aa3162b20>
```



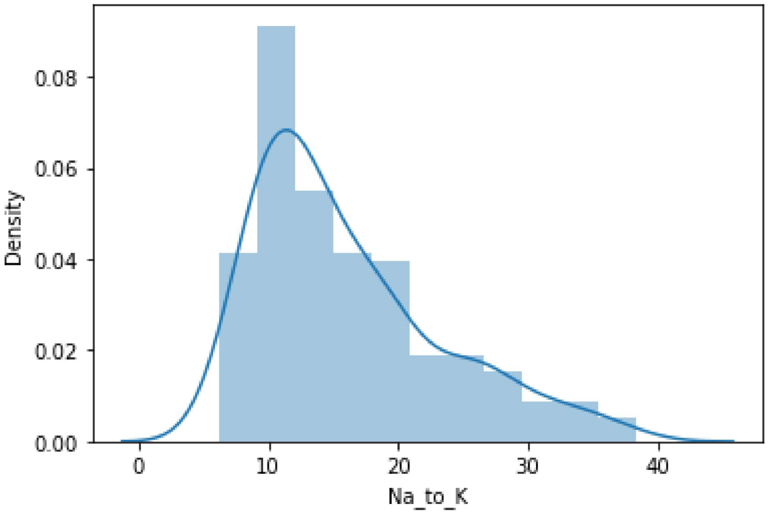
In [11]:

```
sns.distplot(df1['Na_to_K'])
```

```
C:\ProgramData\Anaconda3\lib\site-packages\seaborn\distributions.py:2557: FutureWarning:
`distplot` is a deprecated function and will be removed in a future version. Please adap
t your code to use either `displot` (a figure-level function with similar flexibility) o
r `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```

Out[11]:

```
<AxesSubplot:xlabel='Na_to_K', ylabel='Density'>
```

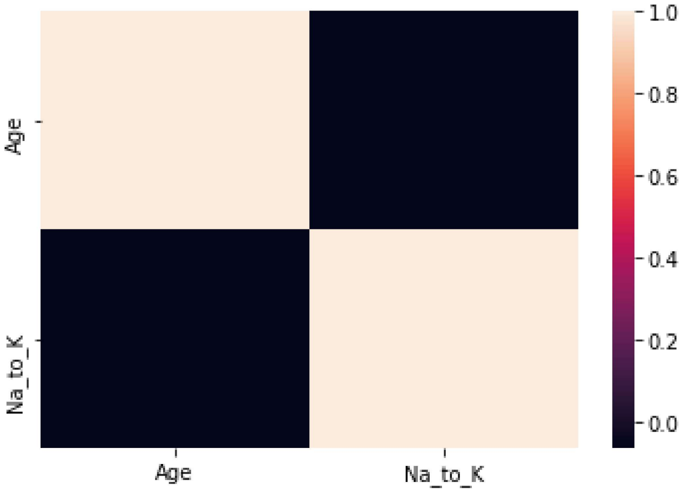


In [12]:

```
sns.heatmap(df1.corr())
```

Out[12]:

```
<AxesSubplot:>
```



TO TRAIN THE MODEL AND MODEL BULDING

In [13]:

```
x=df[['Age','Na_to_K']]
y=df['Na_to_K']
```

In [14]:

```
from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.2)
```

In [15]:

```
from sklearn.linear_model import LinearRegression
lr=LinearRegression()
```

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

```
Out[15]: LinearRegression()
```

```
In [16]: lr.intercept_
```

```
Out[16]: -1.0658141036401503e-14
```

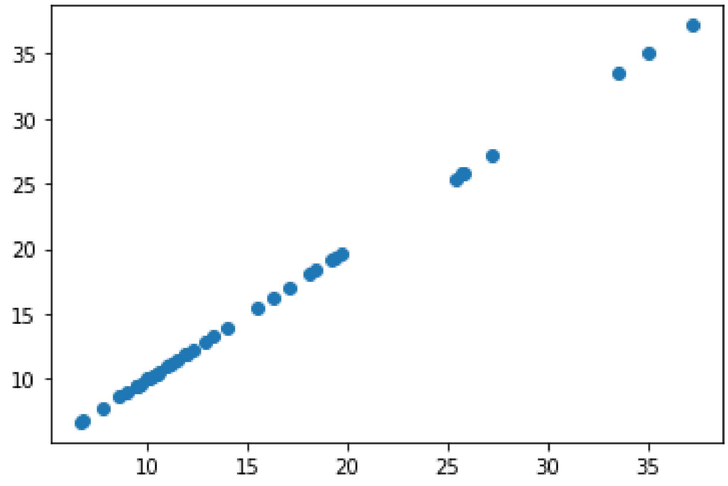
```
In [17]: coeff=pd.DataFrame(lr.coef_,x.columns,columns=['Co-efficient'])
         coeff
```

Out[17]:

	Co-efficient
Age	0.0
Na_to_K	1.0

```
In [18]: prediction =lr.predict(x_test)
         plt.scatter(y_test,prediction)
```

```
Out[18]: <matplotlib.collections.PathCollection at 0x27aa542a670>
```



ACCURACY

```
In [19]: lr.score(x_test,y_test)
```

```
Out[19]: 1.0
```