# Heamnath

# 20104028

# Basic Analysis using Numpy and Pandas

## Importing libraries

In [1]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
```

## importing datasets

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

## To display first 10 rows

In [3]:
```
df.head(10)
```

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 |
| **5** | 22 | F | NORMAL | HIGH | 8.607 | drugX |
| **6** | 49 | F | NORMAL | HIGH | 16.275 | drugY |
| **7** | 41 | M | LOW | HIGH | 11.037 | drugC |
| **8** | 60 | M | NORMAL | HIGH | 15.171 | drugY |
| **9** | 43 | M | LOW | NORMAL | 19.368 | drugY |

# To display last 5 rows

In [4]:
```
df.tail(5)
```

Out[4]:

| | 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 |

# Statistical Summary

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

Out[5]:
```
Age        44.315000
Na_to_K    16.084485
dtype: float64
```

In [6]:
```
df.median()
```

Out[6]:
```
Age        45.0000
Na_to_K    13.9365
dtype: float64
```

In [7]:
```
df.mode()
```

Out[7]:

| | Age | Sex | BP | Cholesterol | Na_to_K | Drug |
|---|---|---|---|---|---|---|
| **0** | 47.0 | M | HIGH | HIGH | 12.006 | drugY |
| **1** | NaN | NaN | NaN | NaN | 18.295 | NaN |

In [8]:
```
df.sum()
```

Out[8]:
```
Age                                                          8863
Sex           FMMFFFFMMMFFMFFFMMMFMMMFFFMFFMFMMFMMMMFMFFMMFF...
BP            HIGHLOWLOWNORMALLOWNORMALNORMALLOWNORMALLOWLOW...
Cholesterol   HIGHHIGHHIGHHIGHHIGHHIGHHIGHHIGHHIGHNORMALHIGH...
Na_to_K                                                3216.897
Drug          drugYdrugCdrugCdrugXdrugYdrugXdrugYdrugCdrugYd...
dtype: object
```

In [9]:
```
df.cumsum()
```

Out[9]:

| | Age | Sex | |
|---|---|---|---|
| **0** | 23 | F | |
| **1** | 70 | FM | |
| **2** | 117 | FMM | |
| **3** | 145 | FMMF | |
| **4** | 206 | FMMFF | |
| **...** | ... | ... | |
| **195** | 8732 | FMMFFFFMMMFFMFFFMMMFMMMFFFMFFMFMMFMMMMFMFFMMFF... | HIGHLOWLOWNORMALLOW |
| **196** | 8748 | FMMFFFFMMMFFMFFFMMMFMMMFFFMFFMFMMFMMMMFMFFMMFF... | HIGHLOWLOWNORMALLOW |
| **197** | 8800 | FMMFFFFMMMFFMFFFMMMFMMMFFFMFFMFMMFMMMMFMFFMMFF... | HIGHLOWLOWNORMALLOW |
| **198** | 8823 | FMMFFFFMMMFFMFFFMMMFMMMFFFMFFMFMMFMMMMFMFFMMFF... | HIGHLOWLOWNORMALLOW |
| **199** | 8863 | FMMFFFFMMMFFMFFFMMMFMMMFFFMFFMFMMFMMMMFMFFMMFF... | HIGHLOWLOWNORMALLOW |

200 rows × 6 columns

In [10]:
```
df.count()
```

Out[10]:
```
Age            200
Sex            200
BP             200
Cholesterol    200
Na_to_K        200
Drug           200
dtype: int64
```

In [11]:
```
df.min()
```

Out[11]:
```
Age              15
Sex               F
BP             HIGH
Cholesterol    HIGH
Na_to_K       6.269
Drug          drugA
dtype: object
```

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

Out[12]:
```
Age              74
Sex               M
BP           NORMAL
Cholesterol  NORMAL
Na_to_K      38.247
Drug          drugY
dtype: object
```

In [13]:
```
from numpy import cov
```

In [14]:
```
cov(df['Age'],df['Na_to_K'])
```

Out[14]:
```
array([[273.71434673,  -7.54375153],
       [ -7.54375153,  52.18553348]])
```

In [15]:
```
from scipy.stats import pearsonr
pearsonr(df['Age'],df['Na_to_K'])
```

Out[15]:
```
(-0.06311949726772592, 0.3745756399034559)
```

In [16]:
```
from scipy.stats import spearmanr
spearmanr(df['Age'],df['Na_to_K'])
```

Out[16]:
```
SpearmanrResult(correlation=-0.047273882688479915, pvalue=0.5062200581387418)
```

In [17]:
```
df.describe()
```

Out[17]:

| | 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 |

# To print no of rows and columns

In [18]:
```
df.shape
```

Out[18]: (200, 6)

# To print total no of elements

In [19]:
```
df.size
```

Out[19]: 1200

# To find the null value

In [20]:
```
df.isna()
```

Out[20]:

| | Age | Sex | BP | Cholesterol | Na_to_K | Drug |
|---|---|---|---|---|---|---|
| **0** | False | False | False | False | False | False |
| **1** | False | False | False | False | False | False |
| **2** | False | False | False | False | False | False |
| **3** | False | False | False | False | False | False |
| **4** | False | False | False | False | False | False |
| **...** | ... | ... | ... | ... | ... | ... |
| **195** | False | False | False | False | False | False |
| **196** | False | False | False | False | False | False |
| **197** | False | False | False | False | False | False |
| **198** | False | False | False | False | False | False |
| **199** | False | False | False | False | False | False |

200 rows × 6 columns

# To fill the missing value

In [21]:
```
df.fillna(value=0)
```

Out[21]:

| | Age | Sex | BP | Cholesterol | Na_to_K | Drug |
|---|---|---|---|---|---|---|
| **0** | 23 | F | HIGH | HIGH | 25.355 | drugY |
| **1** | 47 | M | LOW | HIGH | 13.093 | drugC |

| | Age | Sex | BP | Cholesterol | Na_to_K | Drug |
|---|---|---|---|---|---|---|
| **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

# Print column names

In [22]:
```
df.columns
```

Out[22]:
```
Index(['Age', 'Sex', 'BP', 'Cholesterol', 'Na_to_K', 'Drug'], dtype='object')
```

# To print particular column names

In [23]:
```
data=df[['Age', 'Na_to_K']]
data
```

Out[23]:

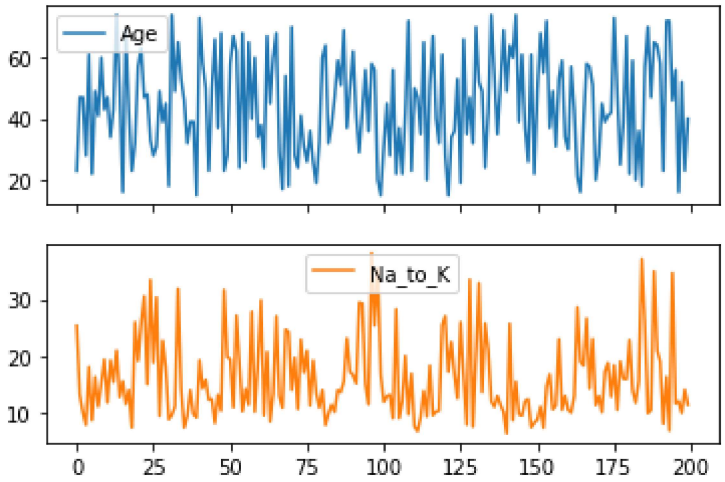
| | Age | Na_to_K |
|---|---|---|
| **0** | 23 | 25.355 |
| **1** | 47 | 13.093 |
| **2** | 47 | 10.114 |
| **3** | 28 | 7.798 |
| **4** | 61 | 18.043 |
| **...** | ... | ... |
| **195** | 56 | 11.567 |
| **196** | 16 | 12.006 |
| **197** | 52 | 9.894 |
| **198** | 23 | 14.020 |
| **199** | 40 | 11.349 |

200 rows × 2 columns

# Line chart with subplots

In [24]:
```
data.plot.line(subplots=True)
```

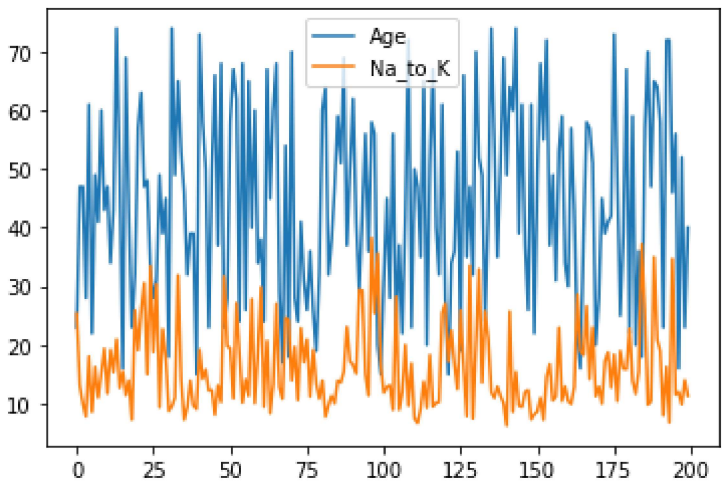
Out[24]:
```
array([<AxesSubplot:>, <AxesSubplot:>], dtype=object)
```




# Line chart

In [25]:
```
data.plot.line()
```

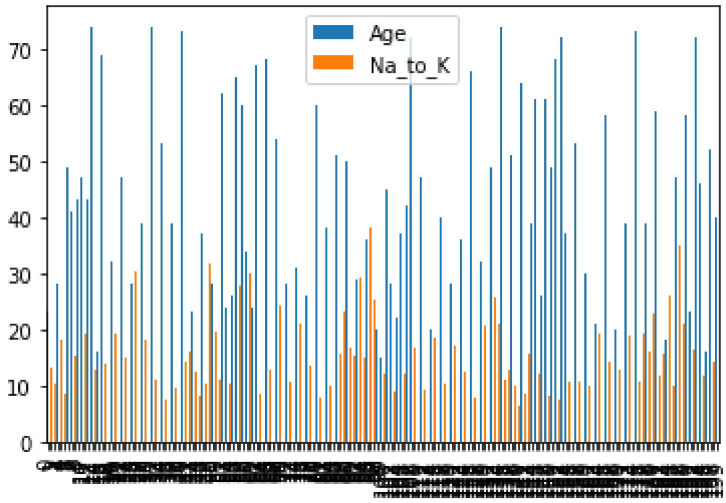
Out[25]:
```
<AxesSubplot:>
```




# Bar chart

In [26]:
```
data.plot.bar()
```

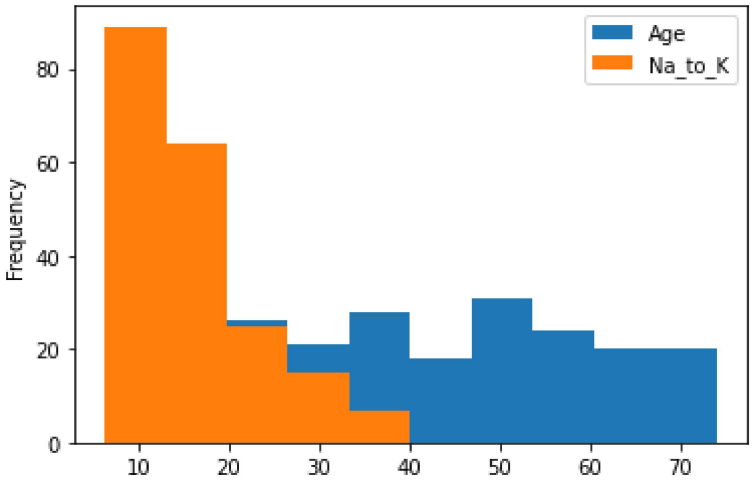
Out[26]:
```
<AxesSubplot:>
```




# Histogram

In [27]:
```
data.plot.hist()
```

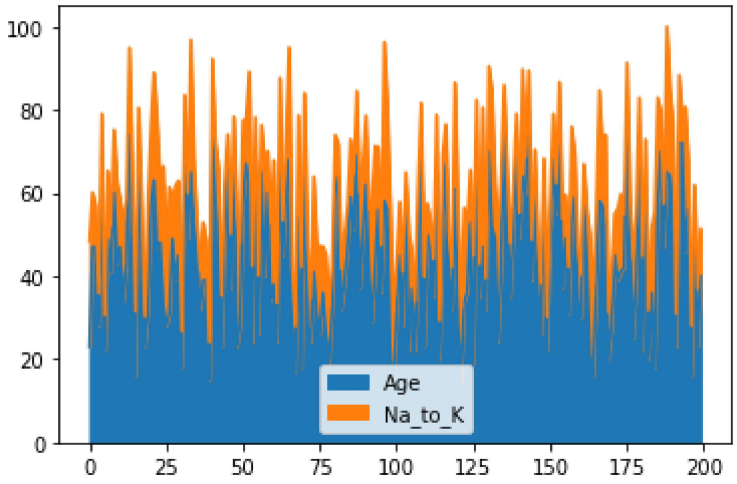
Out[27]: <AxesSubplot:ylabel='Frequency'>




# Area chart

In [28]:
```
data.plot.area()
```

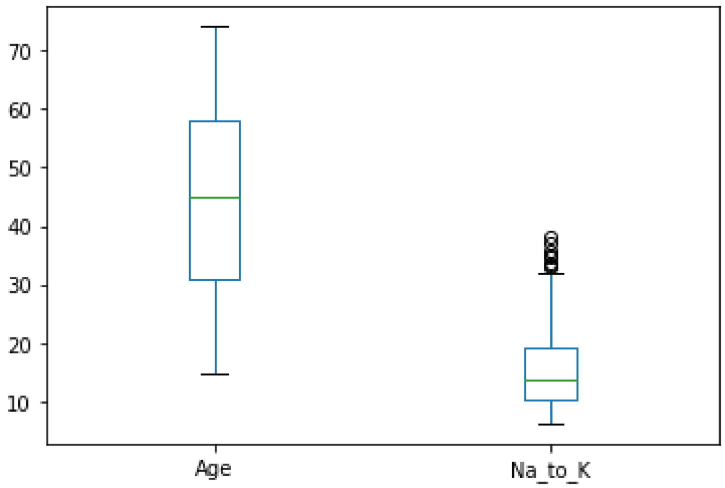
Out[28]: <AxesSubplot:>




# Box chart

In [29]:
```
data.plot.box()
```

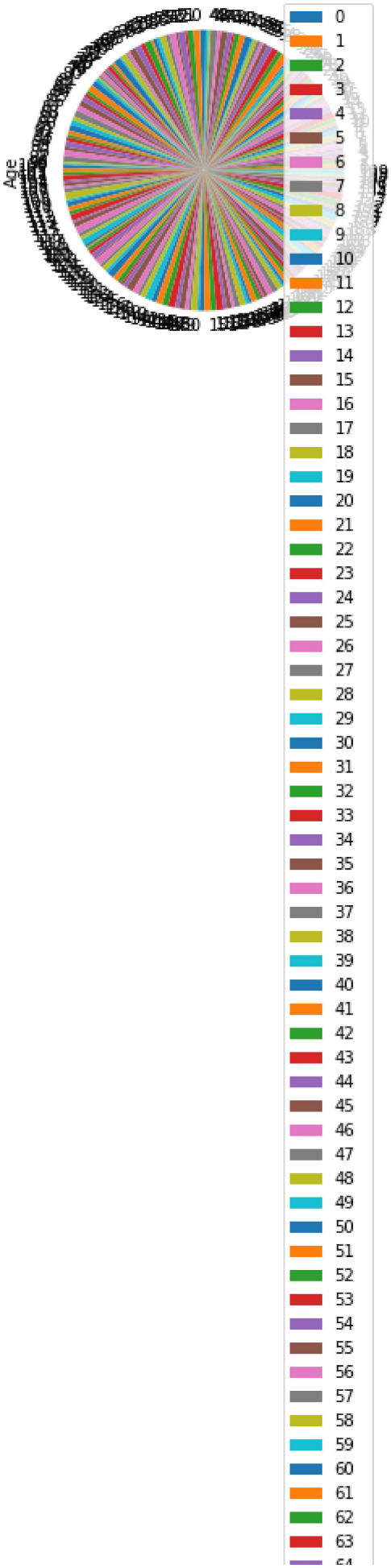
Out[29]: <AxesSubplot:>




# Pie chart

In [30]:
```
data.plot.pie(y='Age')
```

Out[30]: <AxesSubplot:ylabel='Age'>


Age
0
1
2
3
4
5
6
7
8
9
10
11
12
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14
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16
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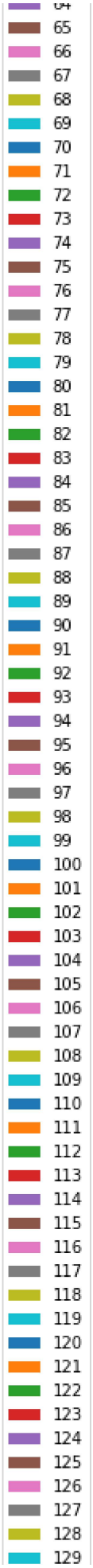
63


64
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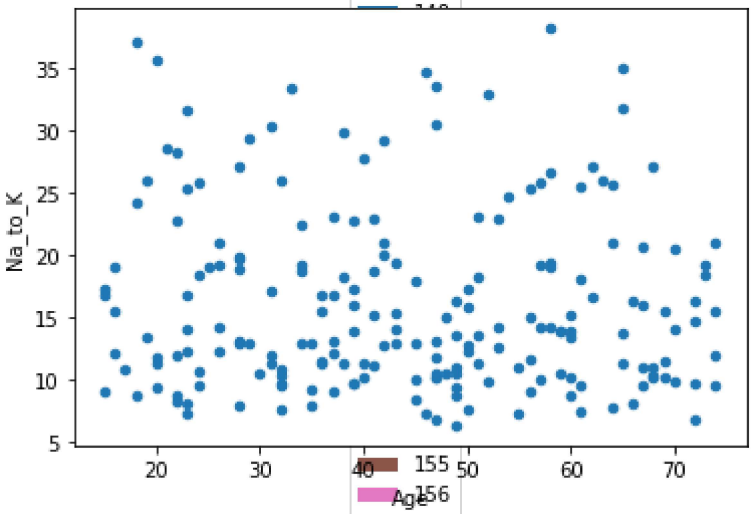
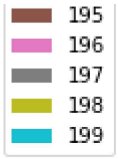
129

# Scatter chart

In [31]:
```
data.plot.scatter(x='Age',y='Na_to_K')
```

Out[31]: <AxesSubplot:xlabel='Age', ylabel='Na_to_K'>




195
196
197
198
199