

Practical No. 02

Aim : To perform and analysis for Normal Distribution on given dataset

In [6]:

```
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#Roll no. : 77 (BDA-B77)  
#Section : B  
#Subject : PE-II
```

In [8]:

```
import os  
import pandas as pd
```

In [10]:

```
os.getcwd()
```

Out[10]:

```
'C:\\Users\\USER'
```

In [12]:

```
os.chdir("C:\\Users\\USER\\Desktop")
```

In [14]:

```
data = pd.read_csv("diabetes.csv")
```

In [16]:

```
data.head()
```

Out[16]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
0	6	148	72	35	0	33.6	0.627	50
1	1	85	66	29	0	26.6	0.351	31
2	8	183	64	0	0	23.3	0.672	32
3	1	89	66	23	94	28.1	0.167	21
4	0	137	40	35	168	43.1	2.288	33

In [18]:

```
data.tail()
```

Out[18]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Ag
763	10	101	76	48	180	32.9	0.171	6
764	2	122	70	27	0	36.8	0.340	2
765	5	121	72	23	112	26.2	0.245	3
766	1	126	60	0	0	30.1	0.349	4
767	1	93	70	31	0	30.4	0.315	2

In [20]:

```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
```

```
RangeIndex: 768 entries, 0 to 767
```

```
Data columns (total 9 columns):
```

#	Column	Non-Null Count	Dtype
0	Pregnancies	768 non-null	int64
1	Glucose	768 non-null	int64
2	BloodPressure	768 non-null	int64
3	SkinThickness	768 non-null	int64
4	Insulin	768 non-null	int64
5	BMI	768 non-null	float64
6	DiabetesPedigreeFunction	768 non-null	float64
7	Age	768 non-null	int64
8	Outcome	768 non-null	int64

```
dtypes: float64(2), int64(7)
```

```
memory usage: 54.1 KB
```

```
In [22]:
```

```
data.describe()
```

```
Out[22]:
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	0.471072
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331335
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.367500
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.497500
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.622500
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.015000

```
In [24]:
```

```
data.shape
```

```
Out[24]:
```

```
(768, 9)
```

```
In [26]:
```

```
data.size
```

```
Out[26]:
```

```
6912
```

```
In [28]:
```

```
data.ndim
```

```
Out[28]:
```

```
2
```

```
In [30]:
```

```
data.columns
```

```
Out[30]:
```

```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',  
      'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],  
      dtype='object')
```

Data pre-processing, data-cleaning, missing value treatment

In [33]:

```
data.isna()
```

Out[33]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	False	False	False	False	False	False	False	False	False
1	False	False	False	False	False	False	False	False	False
2	False	False	False	False	False	False	False	False	False
3	False	False	False	False	False	False	False	False	False
4	False	False	False	False	False	False	False	False	False
...
763	False	False	False	False	False	False	False	False	False
764	False	False	False	False	False	False	False	False	False
765	False	False	False	False	False	False	False	False	False
766	False	False	False	False	False	False	False	False	False
767	False	False	False	False	False	False	False	False	False

768 rows × 9 columns

In [35]:

```
data.isna().any()
```

Out[35]:

```
Pregnancies      False  
Glucose          False  
BloodPressure    False  
SkinThickness    False  
Insulin          False  
BMI              False  
DiabetesPedigreeFunction  False  
Age              False  
Outcome          False  
dtype: bool
```

In [37]:

```
data.isna().sum()
```

Out[37]:

```
Pregnancies      0  
Glucose          0  
BloodPressure    0  
SkinThickness    0  
Insulin          0  
BMI              0  
DiabetesPedigreeFunction  0
```

```
Age                                0
Outcome                           0
dtype: int64
```

In [39]:

```
import seaborn as sns
import matplotlib.pyplot as plt
```

In [41]:

```
sns.distplot(data,bins=20)
plt.show()
```

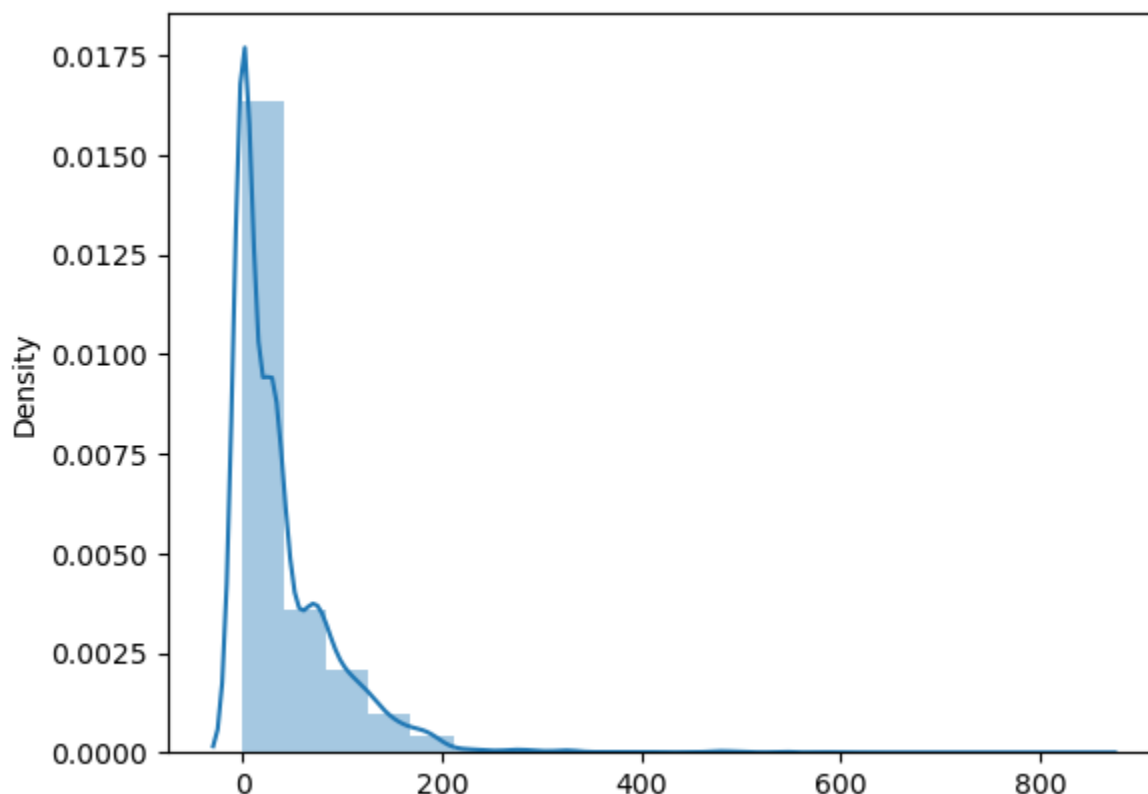
C:\Users\USER\AppData\Local\Temp\ipykernel_15968\1706651633.py:1: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.

Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level function for histograms).

For a guide to updating your code to use the new functions, please see <https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751>

```
sns.distplot(data,bins=20)
```



In [43]:

```
sns.distplot(data['Glucose'],bins=20)
plt.show()
```

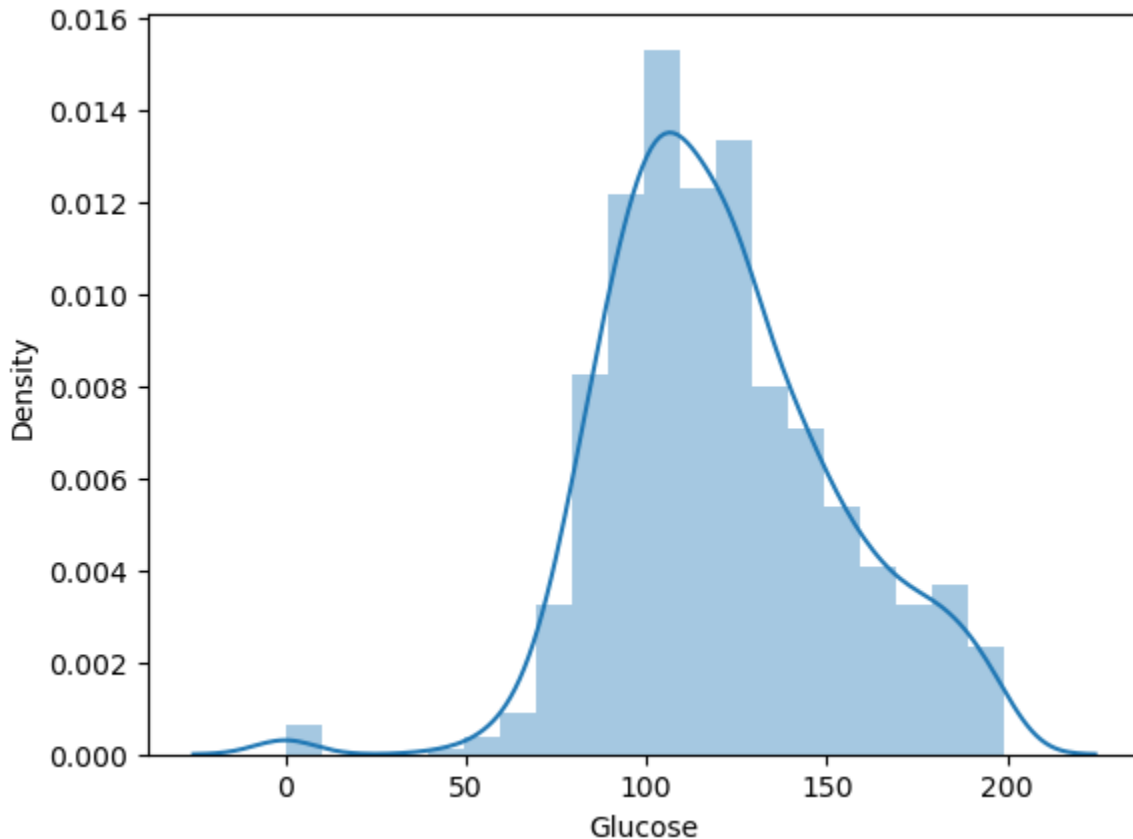
C:\Users\USER\AppData\Local\Temp\ipykernel_15968\1093375177.py:1: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.

Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level function for histograms).

For a guide to updating your code to use the new functions, please see <https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751>

```
sns.distplot(data['Glucose'], bins=20)
```



In [45]:

```
sns.distplot(data['Age'], bins=20)  
plt.show()
```

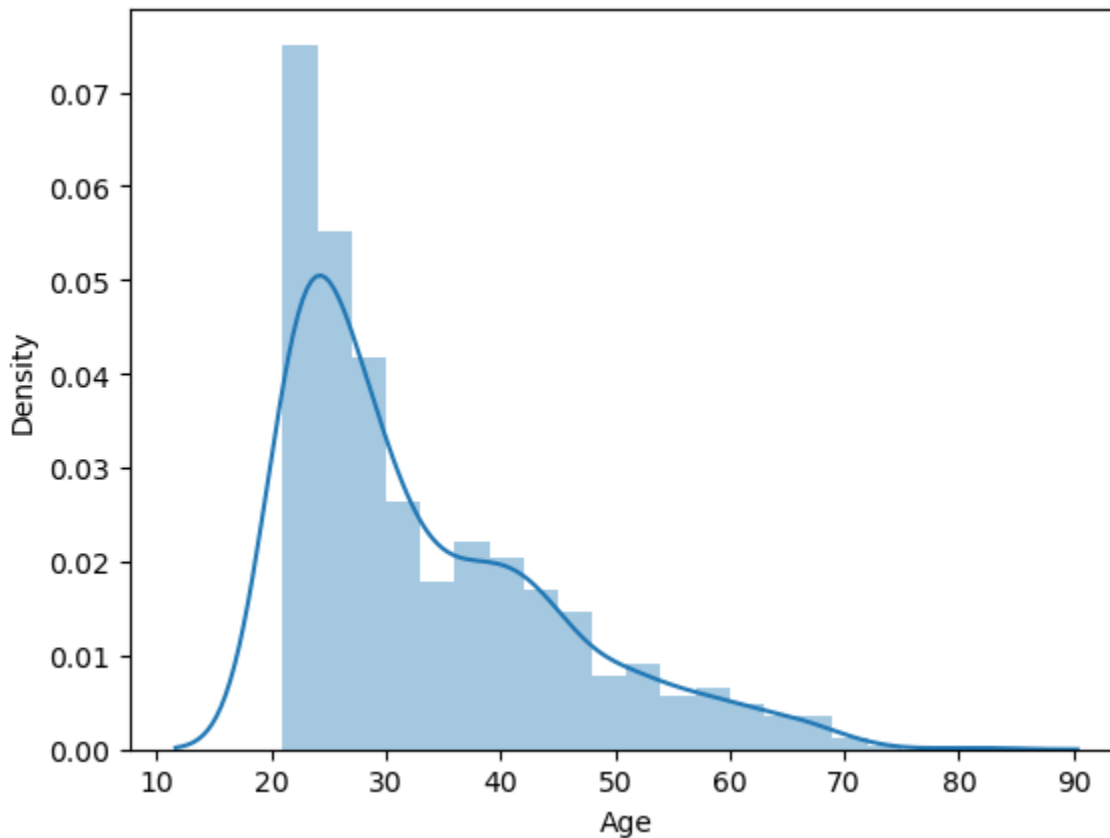
C:\Users\USER\AppData\Local\Temp\ipykernel_15968\713659080.py:1: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.

Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level function for histograms).

For a guide to updating your code to use the new functions, please see <https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751>

```
sns.distplot(data['Age'], bins=20)
```



In [47]:

```
sns.distplot(data['BloodPressure'], bins = 20)
plt.show()
```

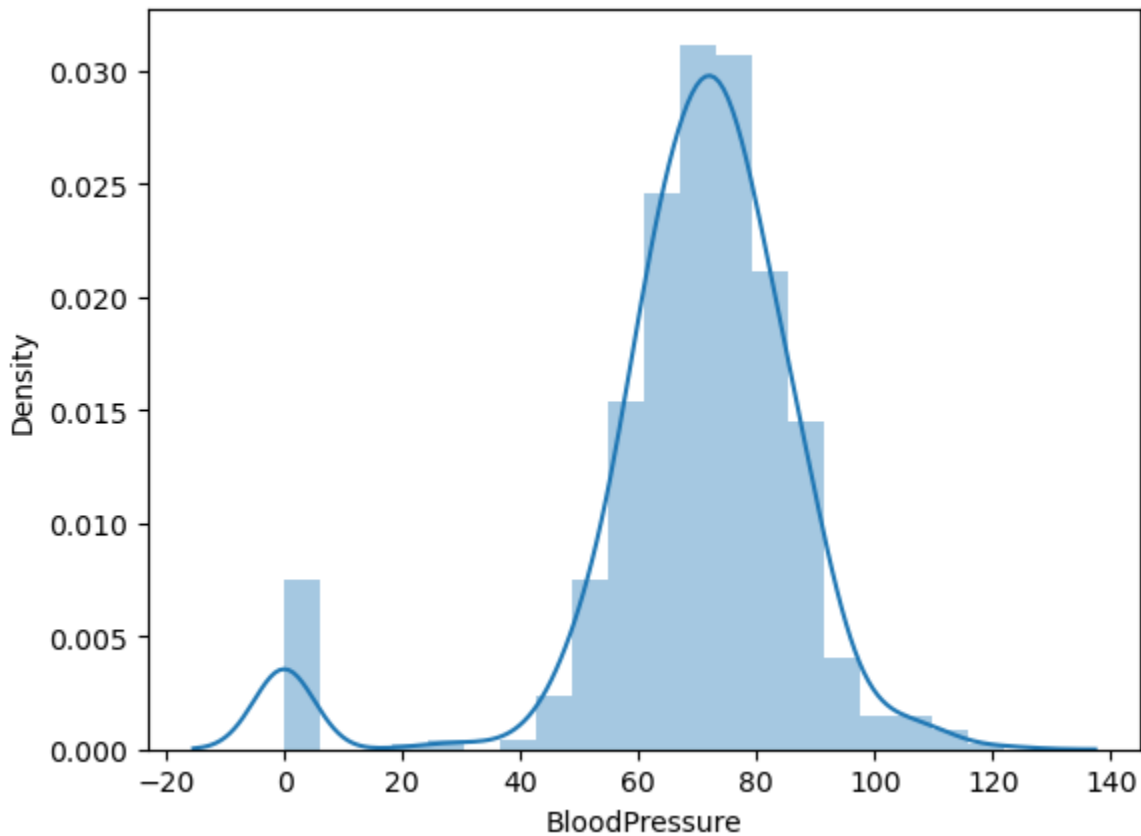
C:\Users\USER\AppData\Local\Temp\ipykernel_15968\1074119919.py:1: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.

Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level function for histograms).

For a guide to updating your code to use the new functions, please see <https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751>

```
sns.distplot(data['BloodPressure'], bins = 20)
```



In [49]:

```
sns.distplot(data['SkinThickness'], bins = 20)  
plt.show()
```

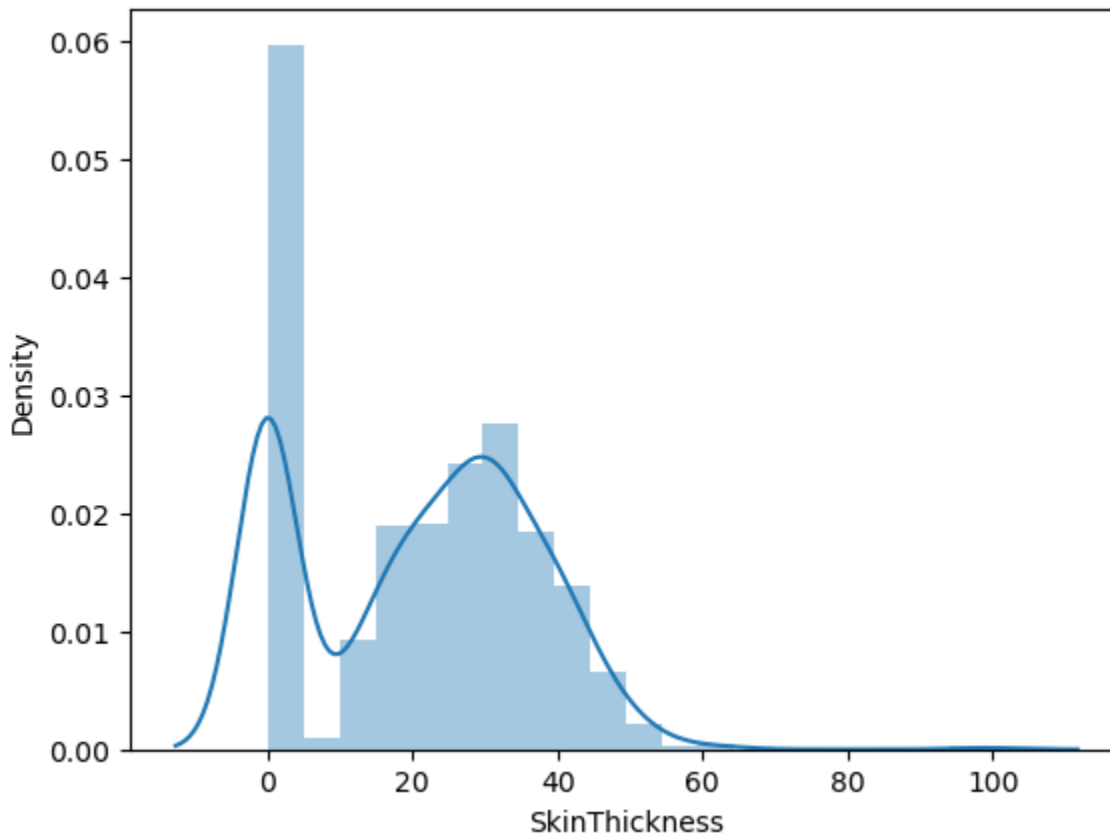
C:\Users\USER\AppData\Local\Temp\ipykernel_15968\3091487386.py:1: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.

Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level function for histograms).

For a guide to updating your code to use the new functions, please see <https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751>

```
sns.distplot(data['SkinThickness'], bins = 20)
```

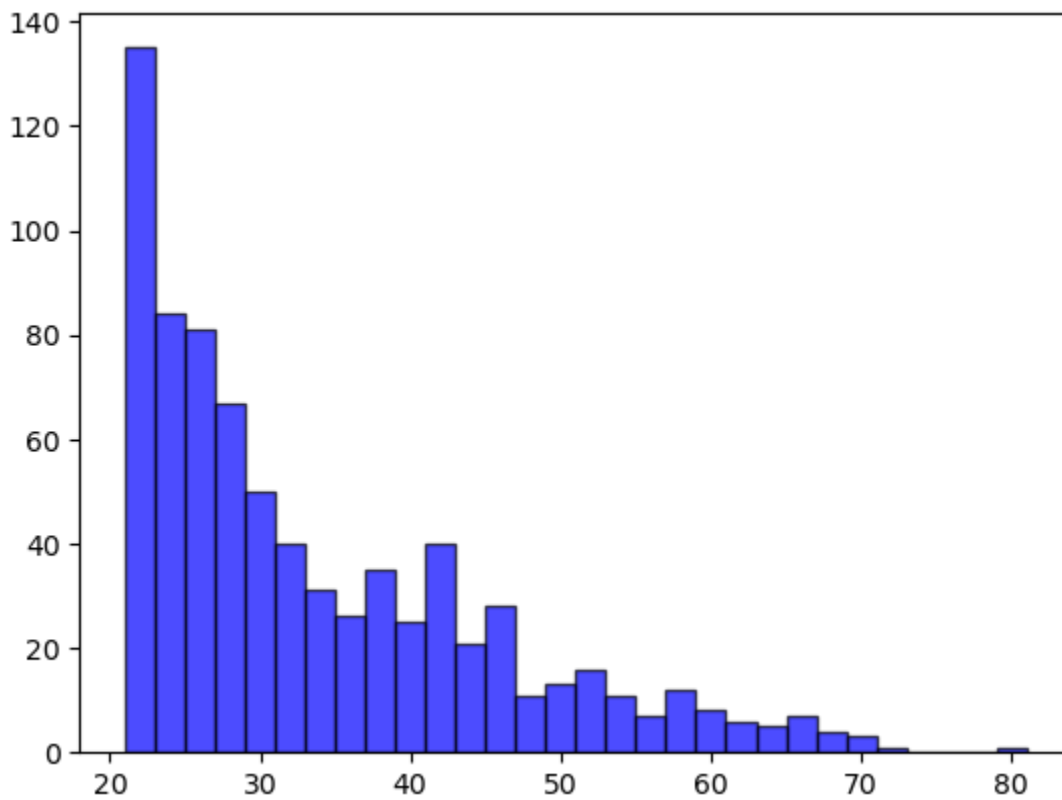


In [51]:

```
plt.hist(data['Age'], bins=30, color='blue', edgecolor='black', alpha=0.7)
```

Out[51]:

```
(array([135., 84., 81., 67., 50., 40., 31., 26., 35., 25., 40.,
        21., 28., 11., 13., 16., 11., 7., 12., 8., 6., 5.,
        7., 4., 3., 1., 0., 0., 0., 1.]),
 array([21., 23., 25., 27., 29., 31., 33., 35., 37., 39., 41., 43., 45.,
        47., 49., 51., 53., 55., 57., 59., 61., 63., 65., 67., 69., 71.,
        73., 75., 77., 79., 81.]),
 <BarContainer object of 30 artists>)
```

Q-Q (Quantile-Quantile) plot is a graphical tool that compares the distribution of a dataset to a theoretical normal distribution to check if the data follows normality

In [55]:

```
import scipy.stats as stats
import matplotlib.pyplot as plt

plt.figure(figsize=(6,6))
stats.probplot(data['Age'], dist="norm", plot=plt)
plt.title("Q-Q Plot")
plt.show()
```

Q-Q Plot

