

```
In [51]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from sklearn import datasets, linear_model
from sklearn.metrics import mean_squared_error
import seaborn as sns
```

```
In [52]: dia=pd.read_csv('diabetes.csv')
dia
```

Out[52]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1
...
763	10	101	76	48	180	32.9	0.171	63	0
764	2	122	70	27	0	36.8	0.340	27	0
765	5	121	72	23	112	26.2	0.245	30	0
766	1	126	60	0	0	30.1	0.349	47	1
767	1	93	70	31	0	30.4	0.315	23	0

768 rows × 9 columns

```
In [53]: dia.head()
```

Out[53]:

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

```
In [54]: dia.tail()
```

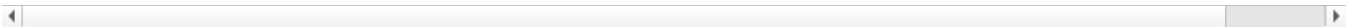
Out[54]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
763	10	101	76	48	180	32.9	0.171	63	0
764	2	122	70	27	0	36.8	0.340	27	0
765	5	121	72	23	112	26.2	0.245	30	0
766	1	126	60	0	0	30.1	0.349	47	1
767	1	93	70	31	0	30.4	0.315	23	0

```
In [55]: dia.describe()
```

Out[55]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
count	768.000000	768.000000	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	0.471876	33.240885	0.346535
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329	11.760232	0.477297
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	21.000000	0.000000
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750	24.000000	0.000000
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500	29.000000	0.000000
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.626250	41.000000	0.000000
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81.000000	1.000000



```
In [56]: dia.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
```

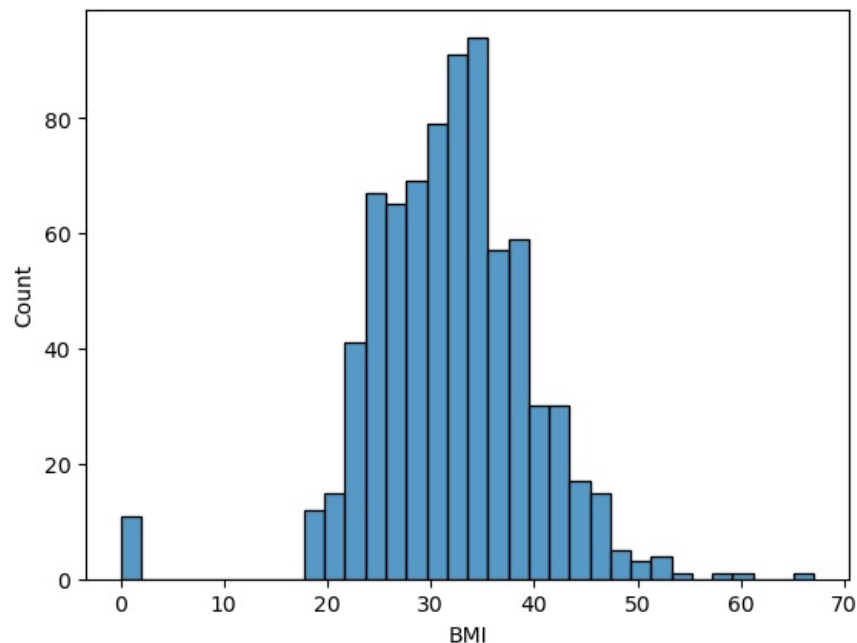
```
In [57]: dia.keys()
```

```
Out[57]: Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
               'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
              dtype='object')
```

```
In [58]: sns.histplot(dia,x='BMI')
```

C:\Users\ajaykanth\anaconda3\Lib\site-packages\seaborn_oldcore.py:1119: FutureWarning: use_inf_as_na option is deprecated and will be removed in a future version. Convert inf values to NaN before operating instead.
with pd.option_context('mode.use_inf_as_na', True):

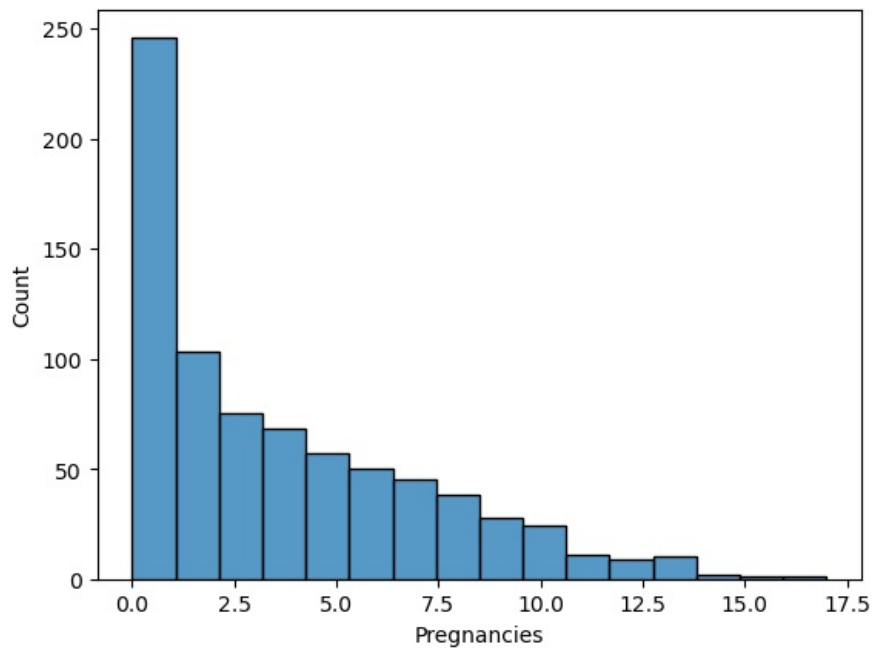
```
Out[58]: <Axes: xlabel='BMI', ylabel='Count'>
```



```
In [59]: sns.histplot(dia,x='Pregnancies')
```

C:\Users\ajaykanth\anaconda3\Lib\site-packages\seaborn_oldcore.py:1119: FutureWarning: use_inf_as_na option is deprecated and will be removed in a future version. Convert inf values to NaN before operating instead.
with pd.option_context('mode.use_inf_as_na', True):

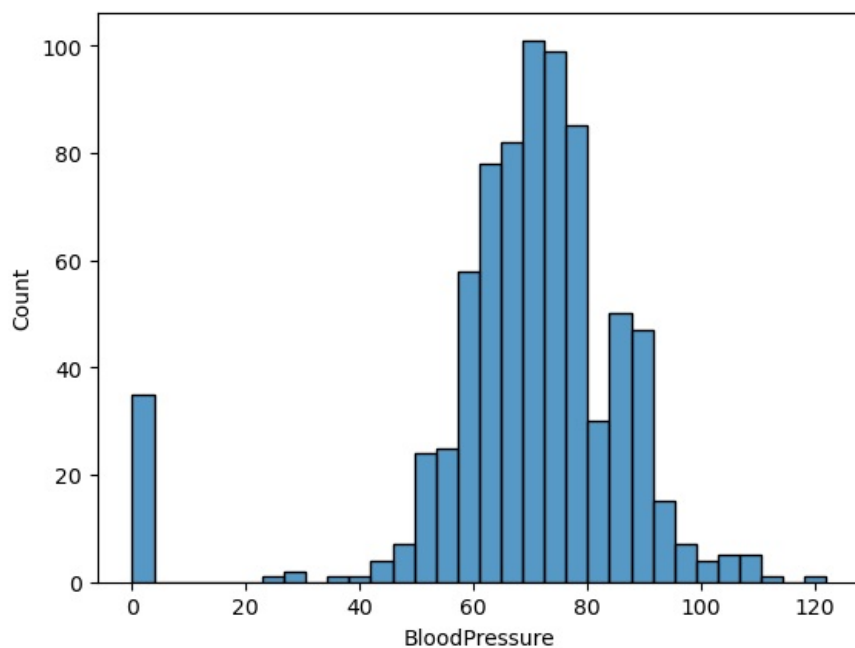
```
Out[59]: <Axes: xlabel='Pregnancies', ylabel='Count'>
```



```
In [60]: sns.histplot(dia,x='BloodPressure')
```

C:\Users\ajaykanth\anaconda3\Lib\site-packages\seaborn_oldcore.py:1119: FutureWarning: use_inf_as_na option is deprecated and will be removed in a future version. Convert inf values to NaN before operating instead.
with pd.option_context('mode.use_inf_as_na', True):

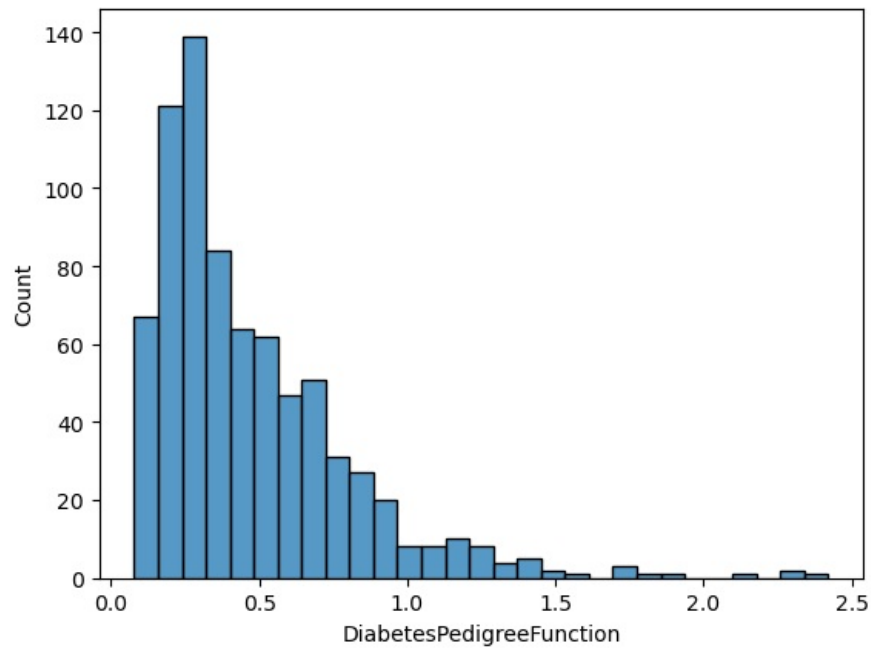
```
Out[60]: <Axes: xlabel='BloodPressure', ylabel='Count'>
```



```
In [61]: sns.histplot(dia,x='DiabetesPedigreeFunction')
```

```
C:\Users\ajaykanth\anaconda3\Lib\site-packages\seaborn\_oldcore.py:1119: FutureWarning: use_inf_as_na option is deprecated and will be removed in a future version. Convert inf values to NaN before operating instead.  
with pd.option_context('mode.use_inf_as_na', True):
```

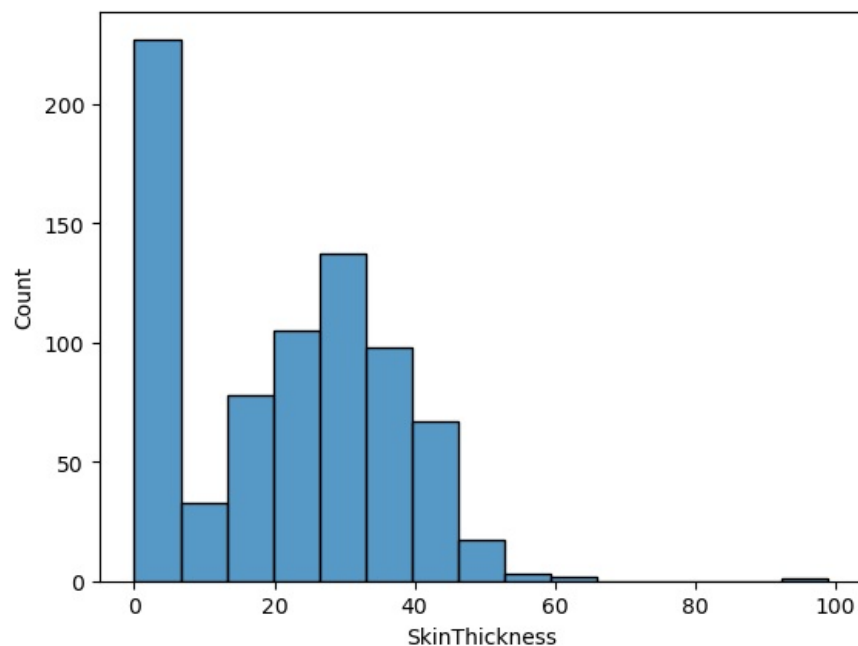
```
Out[61]: <Axes: xlabel='DiabetesPedigreeFunction', ylabel='Count'>
```



```
In [62]: sns.histplot(dia,x='SkinThickness')
```

```
C:\Users\ajaykanth\anaconda3\Lib\site-packages\seaborn\_oldcore.py:1119: FutureWarning: use_inf_as_na option is deprecated and will be removed in a future version. Convert inf values to NaN before operating instead.  
with pd.option_context('mode.use_inf_as_na', True):
```

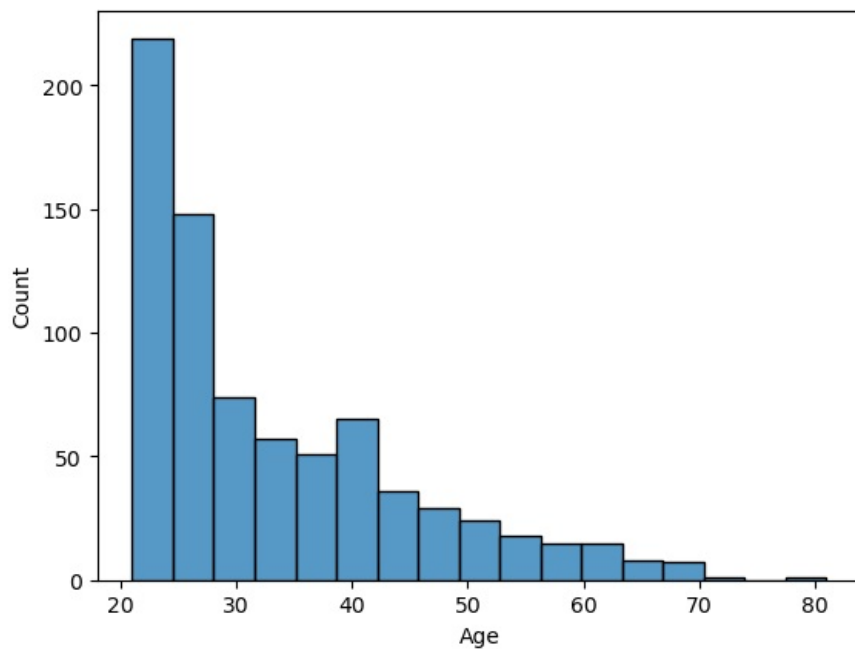
```
Out[62]: <Axes: xlabel='SkinThickness', ylabel='Count'>
```



```
In [63]: sns.histplot(dia,x='Age')
```

```
C:\Users\ajaykanth\anaconda3\Lib\site-packages\seaborn\_oldcore.py:1119: FutureWarning: use_inf_as_na option is deprecated and will be removed in a future version. Convert inf values to NaN before operating instead.  
with pd.option_context('mode.use_inf_as_na', True):
```

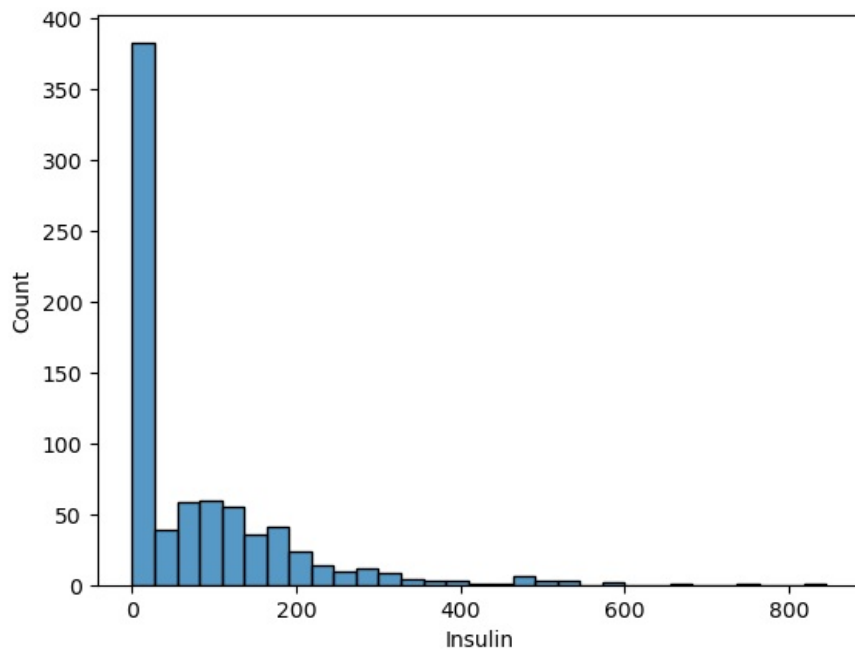
```
Out[63]: <Axes: xlabel='Age', ylabel='Count'>
```



```
In [64]: sns.histplot(dia,x='Insulin')
```

C:\Users\ajaykanth\anaconda3\Lib\site-packages\seaborn_oldcore.py:1119: FutureWarning: use_inf_as_na option is deprecated and will be removed in a future version. Convert inf values to NaN before operating instead.
with pd.option_context('mode.use_inf_as_na', True):

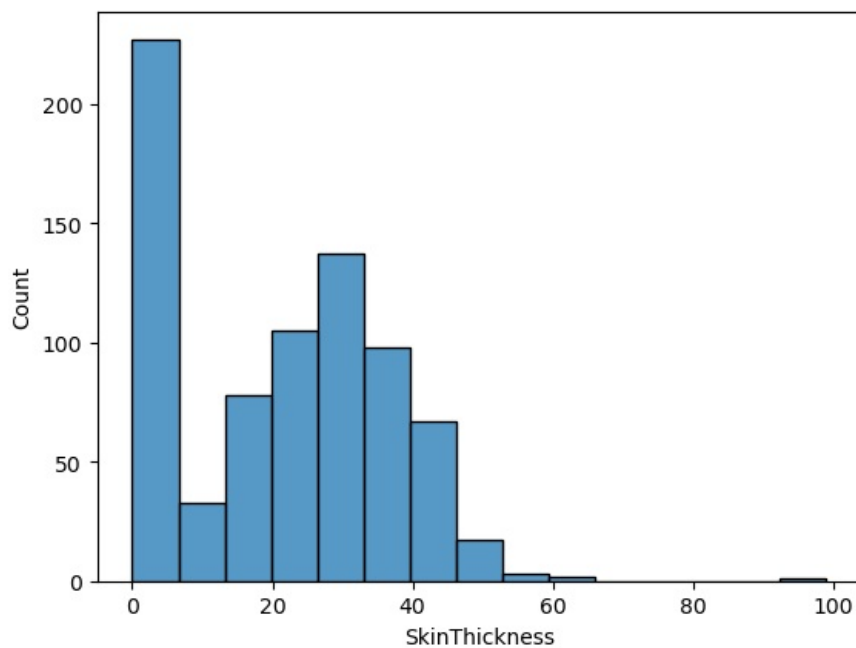
```
Out[64]: <Axes: xlabel='Insulin', ylabel='Count'>
```



```
In [65]: sns.histplot(dia,x='SkinThickness')
```

C:\Users\ajaykanth\anaconda3\Lib\site-packages\seaborn_oldcore.py:1119: FutureWarning: use_inf_as_na option is deprecated and will be removed in a future version. Convert inf values to NaN before operating instead.
with pd.option_context('mode.use_inf_as_na', True):

```
Out[65]: <Axes: xlabel='SkinThickness', ylabel='Count'>
```



```
In [66]: dia_X=dia
          dia_X
```

```
Out[66]:
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1
...
763	10	101	76	48	180	32.9	0.171	63	0
764	2	122	70	27	0	36.8	0.340	27	0
765	5	121	72	23	112	26.2	0.245	30	0
766	1	126	60	0	0	30.1	0.349	47	1
767	1	93	70	31	0	30.4	0.315	23	0

768 rows × 9 columns

```
In [67]: dia_X_train=dia_X[:-30]
          dia_X_test=dia_X[-30:]
          dia_y_train=dia_X[:-30]
          dia_y_test=dia_X[-30:]
```

```
In [68]: model=linear_model.LinearRegression()
          model.fit(dia_X_train,dia_y_train)
```

```
Out[68]:
```

▼ LinearRegression

LinearRegression()

```
In [69]: dia_y_predicted=model.predict(dia_X_test)
          print('mean square error :',mean_squared_error(dia_y_predicted,dia_y_test))
```

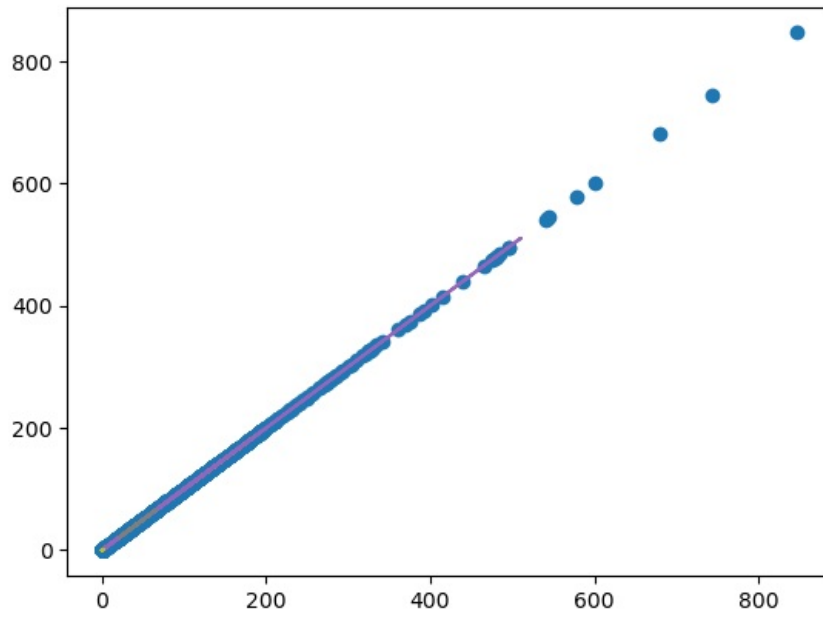
mean square error : 3.7073180087291624e-28

```
In [70]: model.coef_
          model.intercept_
```

```
Out[70]: array([-1.77635684e-15, -9.94759830e-14, -5.68434189e-14,  7.10542736e-15,
                -1.27897692e-13,  1.42108547e-14, -2.77555756e-16, -2.84217094e-14,
                -3.88578059e-15])
```

```
In [71]: plt.scatter(dia_X_train,dia_y_train)
```

```
plt.plot(dia_y_predicted,dia_X_test)  
plt.show()
```



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