In [1]:
```
import matplotlib.pyplot as plt
import pandas as pd
import numpy as np
import seaborn as sns
from sklearn.datasets import load_breast_cancer
from sklearn.preprocessing import StandardScaler
from sklearn.decomposition import PCA
%matplotlib inline
```

In [2]:
```
cancer=load_breast_cancer()
cancer.keys()
```

Out[2]:
```
dict_keys(['data', 'target', 'frame', 'target_names', 'DESCR', 'feature_na
mes', 'filename'])
```

In [3]:
```
print(cancer['DESCR'])
```

...

In [4]:
```
df=pd.DataFrame(cancer['data'],columns=cancer['feature_names'])
```

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

...

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

...

In [8]:
```
scaler=StandardScaler()
scaler.fit(df)
```

Out[8]:
```
StandardScaler()
```

standardScaler is a preprocessing technique in scikit-learn used for standardizing features by removing the mean and scaling to unit variance.

In [10]:
```
scaled_data=scaler.transform(df)
scaled_data
```

Out[10]:
```
array([[ 1.09706398, -2.07333501,  1.26993369, ...,  2.29607613,
         2.75062224,  1.93701461],
       [ 1.82982061, -0.35363241,  1.68595471, ...,  1.0870843 ,
        -0.24388967,  0.28118999],
       [ 1.57988811,  0.45618695,  1.56650313, ...,  1.95500035,
         1.152255  ,  0.20139121],
       ...,
       [ 0.70228425,  2.0455738 ,  0.67267578, ...,  0.41406869,
        -1.10454895, -0.31840916],
       [ 1.83834103,  2.33645719,  1.98252415, ...,  2.28998549,
         1.91908301,  2.21963528],
       [-1.80840125,  1.22179204, -1.81438851, ..., -1.74506282,
        -0.04813821, -0.75120669]])
```

In [11]:
```
pca=PCA(n_components=2)
pca.fit(scaled_data)
```

Out[11]:
```
PCA(n_components=2)
```

In [12]:
```
x_pca=pca.transform(scaled_data)
x_pca.shape
```

Out[12]:
```
(569, 2)
```

In [13]:
```
x_pca
```

Out[13]:
```
array([[ 9.19283683,  1.94858307],
       [ 2.3878018 , -3.76817174],
       [ 5.73389628, -1.0751738 ],
       ...,
       [ 1.25617928, -1.90229671],
       [10.37479406,  1.67201011],
       [-5.4752433 , -0.67063679]])
```

In [ ]:
```

```