Principal Component Analysis(PCA)

```
1 import matplotlib.pyplot as plt
2 import numpy as np
3 import pandas as pd
4 %matplotlib inline
1 from sklearn.datasets import load_breast_cancer
1 cancer=load_breast_cancer()
1 cancer.keys()
   dict_keys(['data', 'target', 'frame', 'target_names', 'DESCR', 'feature_names', 'filename', 'data_module'])
1 print(cancer['DESCR'])
       area (worst):
                                           185.2 4254.0
       smoothness (worst):
                                           0.071 0.223
       compactness (worst):
                                           0.027 1.058
                                           0.0 1.252
       concavity (worst):
       concave points (worst):
                                           0.0
                                                   0.291
       symmetry (worst):
                                           0.156 0.664
       fractal dimension (worst):
                                           0.055 0.208
       ______
       :Missing Attribute Values: None
       :Class Distribution: 212 - Malignant, 357 - Benign
       :Creator: Dr. William H. Wolberg, W. Nick Street, Olvi L. Mangasarian
       :Donor: Nick Street
       :Date: November, 1995
   This is a copy of UCI ML Breast Cancer Wisconsin (Diagnostic) datasets.
   https://goo.gl/U2Uwz2
   Features are computed from a digitized image of a fine needle
   aspirate (FNA) of a breast mass. They describe
   characteristics of the cell nuclei present in the image.
   Separating plane described above was obtained using
   Multisurface Method-Tree (MSM-T) [K. P. Bennett, "Decision Tree
   Construction Via Linear Programming." Proceedings of the 4th
   Midwest Artificial Intelligence and Cognitive Science Society,
   pp. 97-101, 1992], a classification method which uses linear
   programming to construct a decision tree. Relevant features
   were selected using an exhaustive search in the space of 1-4
   features and 1-3 separating planes.
   The actual linear program used to obtain the separating plane
   in the 3-dimensional space is that described in:
   [K. P. Bennett and O. L. Mangasarian: "Robust Linear
   Programming Discrimination of Two Linearly Inseparable Sets",
   Optimization Methods and Software 1, 1992, 23-34].
   This database is also available through the UW CS ftp server:
   ftp ftp.cs.wisc.edu
   cd math-prog/cpo-dataset/machine-learn/WDBC/
    .. topic:: References
      - W.N. Street, W.H. Wolberg and O.L. Mangasarian. Nuclear feature extraction
        for breast tumor diagnosis. IS&T/SPIE 1993 International Symposium on
        Electronic Imaging: Science and Technology, volume 1905, pages 861-870,
        San Jose, CA, 1993.
      - O.L. Mangasarian, W.N. Street and W.H. Wolberg. Breast cancer diagnosis and
        prognosis via linear programming. Operations Research, 43(4), pages 570-577,
       - W.H. Wolberg, W.N. Street, and O.L. Mangasarian. Machine learning techniques
        to diagnose breast cancer from fine-needle aspirates. Cancer Letters 77 (1994)
        163-171.
```

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

1 df.head(5)

| dimensio      |  |
|---------------|--|
| 0.2419 0.0787 | 71   |
| 0.1812 0.0566 | 67   |
| 0.2069 0.0599 | 99   |
| 0.2597 0.0974 | 14   |
| 0.1809 0.0588 | 33   |
| 5             | 0.2419 0.0787<br>0.1812 0.0566<br>0.2069 0.0598<br>0.2597 0.0974 |

```
5 rows × 30 columns
     1
1 from sklearn.preprocessing import MinMaxScaler
1 from sklearn.preprocessing import StandardScaler
1 scaler=StandardScaler()
2 scaler.fit(df)
    StandardScaler()
1 scaled_data=scaler.transform(df)
1 scaled_data
    \verb"array" ([[ \ 1.09706398, \ -2.07333501, \ \ 1.26993369, \ \ldots, \ \ 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]])
1 from sklearn.decomposition import PCA
1 pca=PCA(n_components=2)
1 pca.fit(scaled_data)
    PCA(n_components=2)
1 x_pca=pca.transform(scaled_data)
1 scaled_data.shape
    (569, 30)
1 x_pca.shape
    (569, 2)
1 scaled_data
```

```
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]])
1 x_pca
     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]])
1 plt.figure(figsize=(8,6))
2 plt.scatter(x_pca[:,0],x_pca[:,1],c=cancer['target'])
3 plt.xlabel('First principle component')
4 plt.ylabel('Second principle component')
```

## Arr Text(0, 0.5, 'Second principle component')

