```
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.datasets import load breast cancer
b = load breast cancer()
bdata = b.data
print(bdata)
print(bdata.shape)
          [[1.799e+01 1.038e+01 1.228e+02 ... 2.654e-01 4.601e-01 1.189e-01]

[2.057e+01 1.777e+01 1.329e+02 ... 1.860e-01 2.750e-01 8.902e-02]

[1.969e+01 2.125e+01 1.300e+02 ... 2.430e-01 3.613e-01 8.758e-02]
           [] .660e+01 2.808e+01 1.083e+02 ... 1.418e-01 2.218e-01 7.820e-02] [] [2.060e+01 2.933e+01 1.401e+02 ... 2.650e-01 4.087e-01 1.240e-01] [] [7.760e+00 2.454e+01 4.792e+01 ... 0.000e+00 2.871e-01 7.039e-02]]
#use of target
blabels = b.target
print(blabels)
print(blabels.shape)
 #reshaping the dataset by adding label to it labels=np.reshape(blabels, (569,1))
final=np.concatenate([bdata, labels], axis=1)
print(final.shape)
         (569, 31)
bdataset = pd.DataFrame(final) \\
print(bdataset)
              17.59 10.58 122.80 1001.0 0.11840 0.27760 0.30010 0.14710 0.2419 20.57 17.77 132.90 1326.0 0.08474 0.07864 0.08690 0.07017 0.1812 19.69 21.25 130.00 1203.0 0.10960 0.15990 0.19740 0.12790 0.2069 11.42 20.38 77.58 386.1 0.14250 0.28390 0.24140 0.10520 0.2597 20.29 14.34 135.10 1297.0 0.10030 0.13280 0.19800 0.10430 0.1809
          565 20.13 28.25 131.20 1261.0 0.09780 0.10340 0.14400 0.09791 0.1752 566 16.60 28.08 108.30 858.1 0.08455 0.10230 0.09251 0.05302 0.1590 567 20.60 29.33 140.10 1265.0 0.11780 0.27700 0.35140 0.15200 0.2397 568 7.76 24.54 47.92 181.0 0.05263 0.04362 0.00000 0.00000 0.1587
         23.41 158.80 1956.0 0.12380 0.18660 0.2416 0.1860 25.53 152.50 1709.0 0.14440 0.42450 0.4504 0.2430
                                26.50 98.87 567.7 0.20980 0.86630 0.6869 0.2575
              0.05883 ... 16.67 152.20 1575.0 0.13740 0.20500 0.4000 0.1625
                                  26.40 166.10 2027.0 0.14100 0.21130 0.4107 0.2216
                                  38.25 155.00 1731.0 0.11660 0.19220 0.3215 0.1628
34.12 126.70 1124.0 0.11390 0.30940 0.3403 0.1418
39.42 184.60 1821.0 0.16500 0.86810 0.9387 0.2650
          566 0.05648
           567 0.07016
           568 0.05884
                                  30.37 59.16 268.6 0.08996 0.06444 0.0000 0.0000
         28 29 30
0 0.4601 0.11890 0.0
1 0.2750 0.08902 0.0
              0.3613 0.08758 0.0
              0.2364 0.07678 0.0
          565 0.2572 0.06637 0.0
566 0.2218 0.07820 0.0
          568 0.2871 0.07039 1.0
          [569 rows x 31 columns]
print(f)
            mean smoothness' 'mean compactness' 'mean concavity
```

'radius error' 'texture error' 'perimeter error' 'area error' 'smoothness error' 'compactness error' 'concavity error'

'concave points error' 'symmetry error' 'fractal dimension error' 'worst radius' 'worst texture' 'worst perimeter' 'worst area'

'worst smoothness' 'worst compactness' 'worst concavity'
'worst concave points' 'worst symmetry' 'worst fractal dimension']

#add the missing labels to it feature_labels = np.append(f, "label")

#embedding the column names in dataframe bdataset.columns = feature_labels

bdataset.head()

									mean symmetry							
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419	0.07871	 17.33	184.60	2019.0	0.1622	0.6656	0.7119
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812	0.05667	 23.41	158.80	1956.0	0.1238	0.1866	0.2416
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2069	0.05999	 25.53	152.50	1709.0	0.1444	0.4245	0.4504
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2597	0.09744	 26.50	98.87	567.7	0.2098	0.8663	0.6869
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1809	0.05883	 16.67	152.20	1575.0	0.1374	0.2050	0.4000

5 rows × 31 columns

#replace the data with values of benign and malignant using .replace function bdataset['label'].replace(0, 'Benign', inplace=True) bdataset['label'].replace(1, 'Malignant', inplace=True) bdataset.tail()

									mean							
564	21.56	22.39	142.00	1479.0	0.11100	0.11590	0.24390	0.13890	0.1726	0.05623	 26.40	166.10	2027.0	0.14100	0.21130	0.410
565	20.13	28.25	131.20	1261.0	0.09780	0.10340	0.14400	0.09791	0.1752	0.05533	 38.25	155.00	1731.0	0.11660	0.19220	0.321
566	16.60	28.08	108.30	858.1	0.08455	0.10230	0.09251	0.05302	0.1590	0.05648	 34.12	126.70	1124.0	0.11390	0.30940	0.340
567	20.60	29.33	140.10	1265.0	0.11780	0.27700	0.35140	0.15200	0.2397	0.07016	 39.42	184.60	1821.0	0.16500	0.86810	0.938
568	7.76	24.54	47.92	181.0	0.05263	0.04362	0.00000	0.00000	0.1587	0.05884	 30.37	59.16	268.6	0.08996	0.06444	0.000

5 rows × 31 column

PCA standardisation

from sklearn.preprocessing import StandardSealer x=bdataset.loc[:, f].values x=StandardSealer().fit_transform(x) print(x.shape)

(569, 30)

print(np.std(x))
print(np.mean(x))

1.0

#convert normalised features into tabular form
feat_cols=['feature'+str(i) for i in range(x.shape[1])]
n = pd.DataFrame(x, columns=feat_cols)
print(n)

```
#projecting 30 dim(cols) space to 2D
from sklearn.decomposition import PCA
p = PCA(n_components=2)
pc_breast = p.fit_transform(x)
breast=pd.DataFrame(data=pc_breast, columns=['PC1', 'PC2'])
                     6.439315 -3.576817
           564
            566
                    1.256179 -1.902297
            568 -5.475243 -0.670637
explained_variance_ratio_ = pc_breast.explained_variance_ratio_
print("explained variation per principal component: {}".format(explained_variance_ratio_))
import matplotlib.pyplot as plt
plt.figure(figsize=(10,10))
plt.xticks(fontsize=12)
plt.yticks(fontsize=14)
plt.xlabel('PC1', fontsize=20)
plt.ylabel('PC2', fontsize=20)
plt.title('PCA of breast cancer dataset', fontsize=20) targets=['Benign', 'Malignant'] colors=['r','g']
for targets, colors in zip(targets, colors):
indicesToKeep = bdataset['label']==targets
plt.scatter(breast.loc[indicesToKeep, 'PC2'], c=colors, s=50 )
plt.legend(targets, prop={'size' :15})
plt.show()
```

568 -1.075813 -1.859019 -1.207552 -1.305831 -1.745063 -0.048138

feature29 1.937015 0.281190 0.201391

4 -0.397100 564 -0.709091

566 -0.318409 567 2.219635

