

pca-21mis1152

February 21, 2024

21MIS1152 Rajeev Sekar

```
[16]: # Import necessary libraries
import pandas as pd
from sklearn.preprocessing import StandardScaler
from sklearn.decomposition import PCA
import seaborn as sns
```

Loading the dataset

```
[17]: df=pd.read_csv("BC.csv")
df.head()
```

```
[17]:
```

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	
0	842302	M	17.99	10.38	122.80	1001.0	\
1	842517	M	20.57	17.77	132.90	1326.0	
2	84300903	M	19.69	21.25	130.00	1203.0	
3	84348301	M	11.42	20.38	77.58	386.1	
4	84358402	M	20.29	14.34	135.10	1297.0	

	smoothness_mean	compactness_mean	concavity_mean	concave	points_mean	
0	0.11840	0.27760	0.3001		0.14710	\
1	0.08474	0.07864	0.0869		0.07017	
2	0.10960	0.15990	0.1974		0.12790	
3	0.14250	0.28390	0.2414		0.10520	
4	0.10030	0.13280	0.1980		0.10430	

...	texture_worst	perimeter_worst	area_worst	smoothness_worst	
0	17.33	184.60	2019.0	0.1622	\
1	23.41	158.80	1956.0	0.1238	
2	25.53	152.50	1709.0	0.1444	
3	26.50	98.87	567.7	0.2098	
4	16.67	152.20	1575.0	0.1374	

	compactness_worst	concavity_worst	concave	points_worst	symmetry_worst	
0	0.6656	0.7119		0.2654	0.4601	\
1	0.1866	0.2416		0.1860	0.2750	
2	0.4245	0.4504		0.2430	0.3613	

3	0.8663	0.6869	0.2575	0.6638
4	0.2050	0.4000	0.1625	0.2364

	fractal_dimension_worst	Unnamed: 32
0	0.11890	NaN
1	0.08902	NaN
2	0.08758	NaN
3	0.17300	NaN
4	0.07678	NaN

[5 rows x 33 columns]

Data preprocessing

```
[18]: #First col is id, it is dropped and the last col is unnamed, that is also
      ↪dropped
      df = df.iloc[:,1:-1]
      df.head()
```

```
[18]:  diagnosis  radius_mean  texture_mean  perimeter_mean  area_mean
0         M         17.99         10.38         122.80        1001.0  \
1         M         20.57         17.77         132.90        1326.0
2         M         19.69         21.25         130.00        1203.0
3         M         11.42         20.38          77.58         386.1
4         M         20.29         14.34         135.10        1297.0
```

	smoothness_mean	compactness_mean	concavity_mean	concave points_mean
0	0.11840	0.27760	0.3001	0.14710 \
1	0.08474	0.07864	0.0869	0.07017
2	0.10960	0.15990	0.1974	0.12790
3	0.14250	0.28390	0.2414	0.10520
4	0.10030	0.13280	0.1980	0.10430

	symmetry_mean	...	radius_worst	texture_worst	perimeter_worst
0	0.2419	...	25.38	17.33	184.60 \
1	0.1812	...	24.99	23.41	158.80
2	0.2069	...	23.57	25.53	152.50
3	0.2597	...	14.91	26.50	98.87
4	0.1809	...	22.54	16.67	152.20

	area_worst	smoothness_worst	compactness_worst	concavity_worst
0	2019.0	0.1622	0.6656	0.7119 \
1	1956.0	0.1238	0.1866	0.2416
2	1709.0	0.1444	0.4245	0.4504
3	567.7	0.2098	0.8663	0.6869
4	1575.0	0.1374	0.2050	0.4000

	concave points_worst	symmetry_worst	fractal_dimension_worst
0	0.2654	0.4601	0.11890
1	0.1860	0.2750	0.08902
2	0.2430	0.3613	0.08758
3	0.2575	0.6638	0.17300
4	0.1625	0.2364	0.07678

[5 rows x 31 columns]

```
[19]: df.shape
```

```
[19]: (569, 31)
```

```
[21]: #Separating the feature and target columns
X=df.iloc[:,1:]
Y=df["diagnosis"]
X.head()
```

```
[21]:
```

	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean
0	17.99	10.38	122.80	1001.0	0.11840 \
1	20.57	17.77	132.90	1326.0	0.08474
2	19.69	21.25	130.00	1203.0	0.10960
3	11.42	20.38	77.58	386.1	0.14250
4	20.29	14.34	135.10	1297.0	0.10030

	compactness_mean	concavity_mean	concave points_mean	symmetry_mean
0	0.27760	0.3001	0.14710	0.2419 \
1	0.07864	0.0869	0.07017	0.1812
2	0.15990	0.1974	0.12790	0.2069
3	0.28390	0.2414	0.10520	0.2597
4	0.13280	0.1980	0.10430	0.1809

	fractal_dimension_mean	...	radius_worst	texture_worst	perimeter_worst
0	0.07871	...	25.38	17.33	184.60 \
1	0.05667	...	24.99	23.41	158.80
2	0.05999	...	23.57	25.53	152.50
3	0.09744	...	14.91	26.50	98.87
4	0.05883	...	22.54	16.67	152.20

	area_worst	smoothness_worst	compactness_worst	concavity_worst
0	2019.0	0.1622	0.6656	0.7119 \
1	1956.0	0.1238	0.1866	0.2416
2	1709.0	0.1444	0.4245	0.4504
3	567.7	0.2098	0.8663	0.6869
4	1575.0	0.1374	0.2050	0.4000

	concave points_worst	symmetry_worst	fractal_dimension_worst
--	----------------------	----------------	-------------------------

0	0.2654	0.4601	0.11890
1	0.1860	0.2750	0.08902
2	0.2430	0.3613	0.08758
3	0.2575	0.6638	0.17300
4	0.1625	0.2364	0.07678

[5 rows x 30 columns]

There are totally 30 features in this dataset all of which are numerical. We standardize the dataset first then apply PCA to reduce 30 features to 2 principle components

Scaling the data

```
[24]: scalar = StandardScaler()
X = pd.DataFrame(scalar.fit_transform(X)) #scaling the data
X.head()
```

```
[24]:
```

	0	1	2	3	4	5	6	
0	1.097064	-2.073335	1.269934	0.984375	1.568466	3.283515	2.652874	\
1	1.829821	-0.353632	1.685955	1.908708	-0.826962	-0.487072	-0.023846	
2	1.579888	0.456187	1.566503	1.558884	0.942210	1.052926	1.363478	
3	-0.768909	0.253732	-0.592687	-0.764464	3.283553	3.402909	1.915897	
4	1.750297	-1.151816	1.776573	1.826229	0.280372	0.539340	1.371011	

	7	8	9	...	20	21	22	23	
0	2.532475	2.217515	2.255747	...	1.886690	-1.359293	2.303601	2.001237	\
1	0.548144	0.001392	-0.868652	...	1.805927	-0.369203	1.535126	1.890489	
2	2.037231	0.939685	-0.398008	...	1.511870	-0.023974	1.347475	1.456285	
3	1.451707	2.867383	4.910919	...	-0.281464	0.133984	-0.249939	-0.550021	
4	1.428493	-0.009560	-0.562450	...	1.298575	-1.466770	1.338539	1.220724	

	24	25	26	27	28	29
0	1.307686	2.616665	2.109526	2.296076	2.750622	1.937015
1	-0.375612	-0.430444	-0.146749	1.087084	-0.243890	0.281190
2	0.527407	1.082932	0.854974	1.955000	1.152255	0.201391
3	3.394275	3.893397	1.989588	2.175786	6.046041	4.935010
4	0.220556	-0.313395	0.613179	0.729259	-0.868353	-0.397100

[5 rows x 30 columns]

PCA is applied to reduce 30 features to 2 principle components

```
[28]: from sklearn.decomposition import PCA
pca_breast = PCA(n_components=2)
X_PCA = pca_breast.fit_transform(X)
X_PCA
```

```
[28]: 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]])
```

```
[30]: PCA_df = pd.DataFrame(data = X_PCA
                           , columns = ['principal component 1', 'principal component 2'])
PCA_df.head()
```

```
[30]:   principal component 1  principal component 2
0              9.192837              1.948583
1              2.387802             -3.768172
2              5.733896             -1.075174
3              7.122953             10.275589
4              3.935302             -1.948072
```

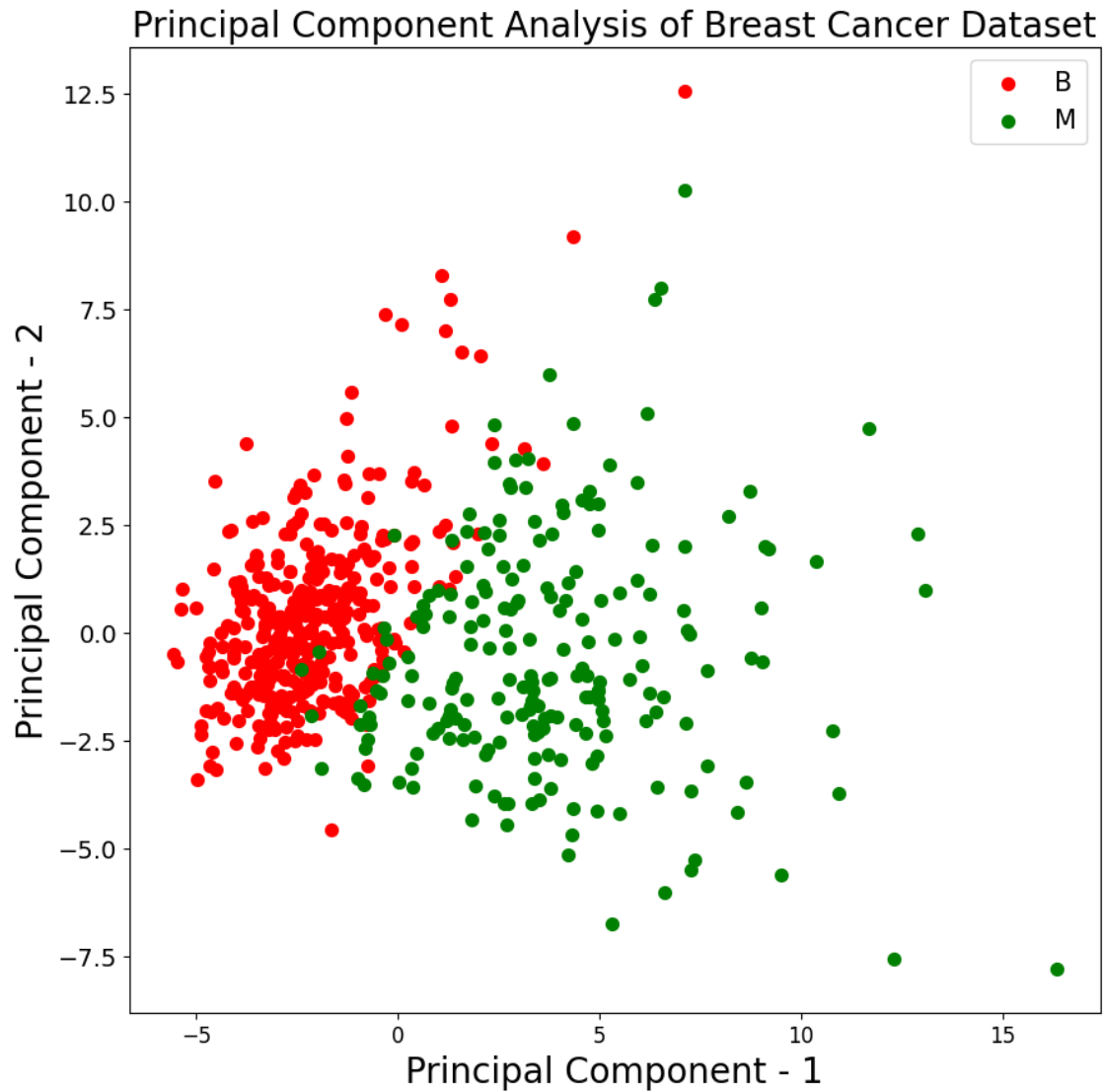
Plotting the benign and malignant data points with respect to the PCs to check how much information is retained from the original dataset

```
[32]: import matplotlib.pyplot as plt
plt.figure()
plt.figure(figsize=(10,10))
plt.xticks(fontsize=12)
plt.yticks(fontsize=14)
plt.xlabel('Principal Component - 1',fontsize=20)
plt.ylabel('Principal Component - 2',fontsize=20)
plt.title("Principal Component Analysis of Breast Cancer Dataset",fontsize=20)
targets = ['B', 'M']
colors = ['r', 'g']
for target, color in zip(targets,colors):
    indicesToKeep = Y == target
    plt.scatter(PCA_df.loc[indicesToKeep, 'principal component 1']
               , PCA_df.loc[indicesToKeep, 'principal component 2'], c = color,
               s = 50)

plt.legend(targets,prop={'size': 15})
```

```
[32]: <matplotlib.legend.Legend at 0x216da5a6ed0>
```

```
<Figure size 640x480 with 0 Axes>
```



We can see that the 2 classes (benign and malignant) is projected in 2d whereas actually it had 30 features and the data points are to a great extent, linearly separable \Rightarrow the meaning of the features is not lost to an extent where it affects the diagnosis

[]: