

pnpe2rbgq

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1 Principal Component Analysis

PCA is a widely covered machine learning method on the web, and there are some great articles about it, but many spend too much time in the weeds on the topic, when most of us just want to know how it works in a simplified way.

Principal component analysis can be broken down into five steps. I'll go through each step, providing logical explanations of what PCA is doing and simplifying mathematical concepts such as standardization, covariance, eigenvectors and eigenvalues without focusing on how to compute them.

```
[5]: import matplotlib.pyplot as plt
import pandas as pd
import numpy as np
import seaborn as sns
%matplotlib inline
```

```
[6]: from sklearn.datasets import load_breast_cancer
```

```
[7]: cancer = load_breast_cancer()
```

```
[8]: cancer.keys()
```

```
[8]: dict_keys(['data', 'target', 'frame', 'target_names', 'DESCR', 'feature_names',
'filename', 'data_module'])
```

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

```
[11]: df.head()
```

```
[11]:   mean radius  mean texture  mean perimeter  mean area  mean smoothness  \
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

      mean compactness  mean concavity  mean concave points  mean symmetry  \
```

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

	mean fractal dimension	...	worst radius	worst texture	worst perimeter \
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

	worst area	worst smoothness	worst compactness	worst concavity \
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

	worst concave points	worst symmetry	worst fractal dimension
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]

```
[12]: from sklearn.preprocessing import StandardScaler
```

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

```
[13]: StandardScaler()
```

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

```
[15]: from sklearn.decomposition import PCA
```

```
[16]: pca = PCA(n_components=2)
```

```
[17]: pca.fit(scaled_data)
```

```
[17]: PCA(n_components=2)
```

```
[18]: x_pca = pca.transform(scaled_data)
```

```
[19]: scaled_data.shape
```

```
[19]: (569, 30)
```

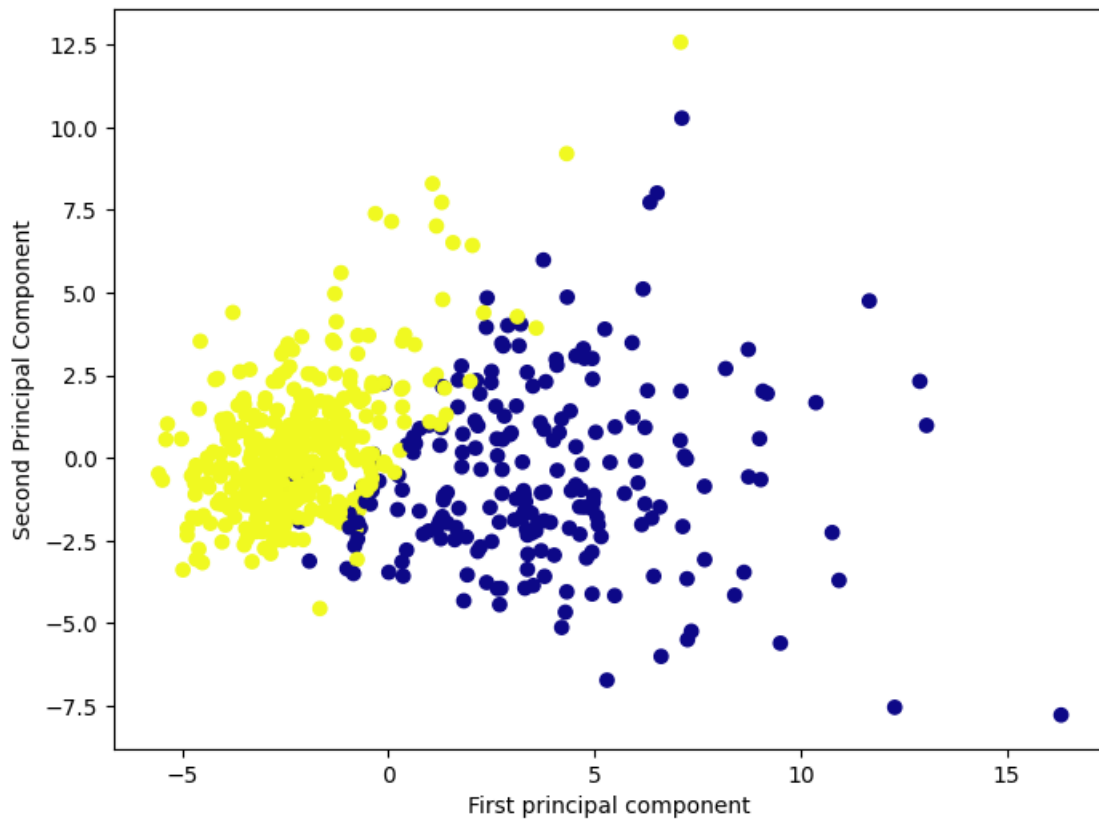
```
[ ]:
```

```
[20]: x_pca.shape
```

```
[20]: (569, 2)
```

```
[21]: plt.figure(figsize=(8,6))  
plt.scatter(x_pca[:,0],x_pca[:,1],c=cancer['target'],cmap='plasma')  
plt.xlabel('First principal component')  
plt.ylabel('Second Principal Component')
```

```
[21]: Text(0, 0.5, 'Second Principal Component')
```



```
[22]: pca.components_
```

```
[22]: array([[ 0.21890244,  0.10372458,  0.22753729,  0.22099499,  0.14258969,  
            0.23928535,  0.25840048,  0.26085376,  0.13816696,  0.06436335,            ...])
```

```

0.20597878, 0.01742803, 0.21132592, 0.20286964, 0.01453145,
0.17039345, 0.15358979, 0.1834174 , 0.04249842, 0.10256832,
0.22799663, 0.10446933, 0.23663968, 0.22487053, 0.12795256,
0.21009588, 0.22876753, 0.25088597, 0.12290456, 0.13178394],
[-0.23385713, -0.05970609, -0.21518136, -0.23107671, 0.18611302,
0.15189161, 0.06016536, -0.0347675 , 0.19034877, 0.36657547,
-0.10555215, 0.08997968, -0.08945723, -0.15229263, 0.20443045,
0.2327159 , 0.19720728, 0.13032156, 0.183848 , 0.28009203,
-0.21986638, -0.0454673 , -0.19987843, -0.21935186, 0.17230435,
0.14359317, 0.09796411, -0.00825724, 0.14188335, 0.27533947]])

```

```
[23]: df_comp = pd.DataFrame(pca.components_, columns=cancer['feature_names'])
```

```
[24]: plt.figure(figsize=(12,6))
sns.heatmap(df_comp, cmap='plasma',)
```

[24]: <Axes: >

