Name : Naman Thaker

Roll no : 20BCE529

Subject : Data Mining

Division D

Practical 6

I'll explain the steps involved in PCA with codes without implemeting scikit-learn and with using Scikit-Learn.

1)First import all the necessary libraries

```
import numpy as np
import pandas as pd
import matplotlib as mpl
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
```

2)Loading the dataset

To import the dataset we will use Pandas library.It is the best Python library to play with the dataset and has a lot of functionalities.

```
df = pd.read_csv('HR_comma_sep.csv')
```

```
columns_names=df.columns.tolist()
print("Columns names:")
print(columns_names)
```

```
Columns names:
['satisfaction_level', 'last_evaluation', 'number_project', 'average_montly_hours',
```

df.columns.tolist() fetches all the columns and then convert it into list type.This step is just to check out all the column names in our data.Columns are also called as features of our datasets.

```
df.shape
```

```
(14999, 10)
```

```
df.head()
```

	satisfaction_level	last_evaluation	number_project	average_montly_hours	time_s
0	0.38	0.53	2	157	
1	0.80	0.86	5	262	
2	0.11	0.88	7	272	
3	0.72	0.87	5	223	
4	0.37	0.52	2	159	

df.head() displays first five rows of our datasets.

```
df.corr()
```

	satisfaction_level	last_evaluation	number_project	average_m
satisfaction_level	1.000000	0.105021	-0.142970	
last_evaluation	0.105021	1.000000	0.349333	
number_project	-0.142970	0.349333	1.000000	
average_montly_hours	-0.020048	0.339742	0.417211	
time_spend_company	-0.100866	0.131591	0.196786	
Work_accident	0.058697	-0.007104	-0.004741	
left	-0.388375	0.006567	0.023787	
promotion_last_5years	0.025605	-0.008684	-0.006064	

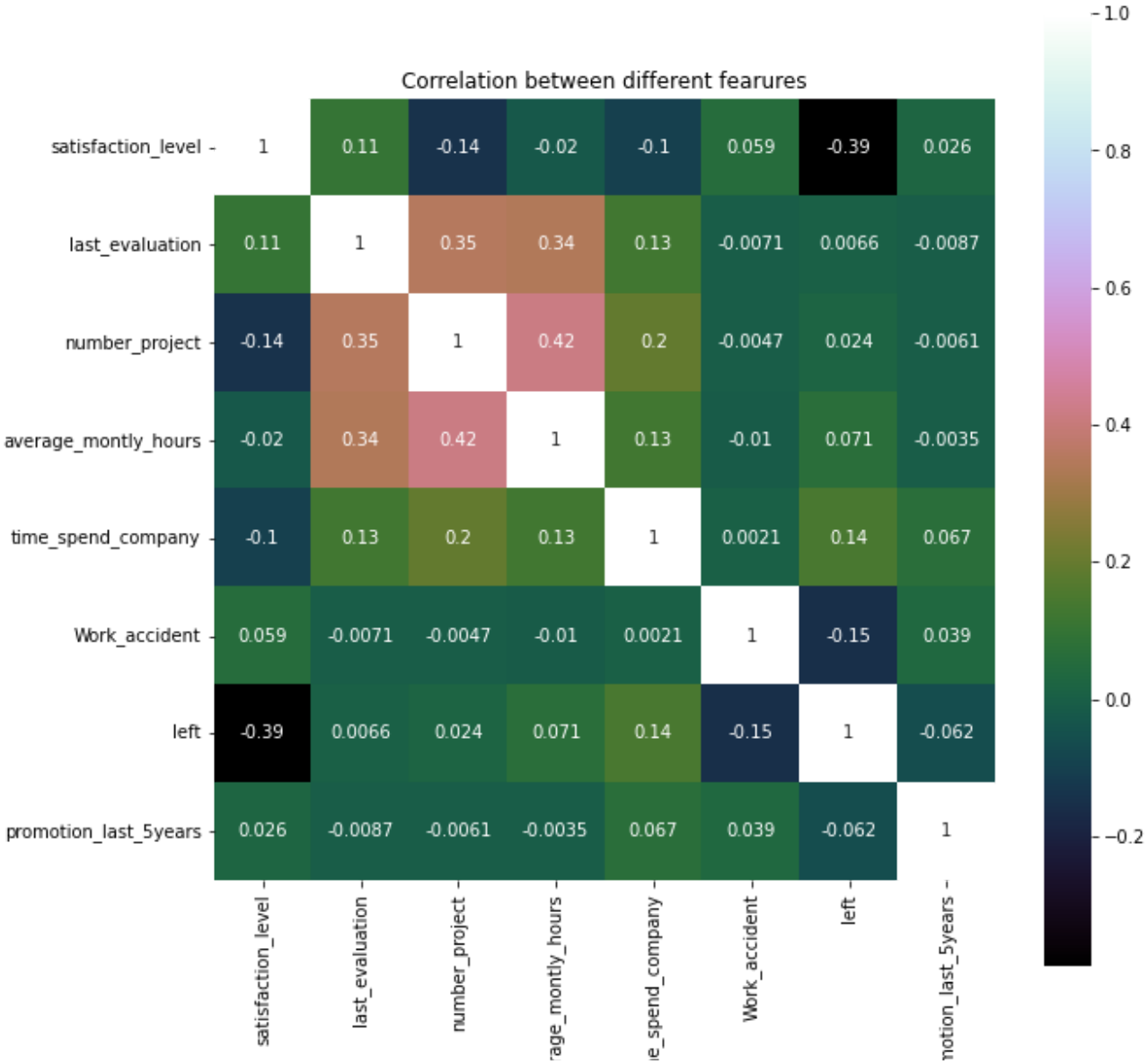
df.corr() compute pairwise correlation of columns.Correlation shows how the two variables are related to each other.Positive values shows as one variable increases other variable increases as well. Negative values shows as one variable increases other variable decreases.Bigger the values,more strongly two varibles are correlated and viceversa.

Visualising correlation using Seaborn library

```
correlation = df.corr()
plt.figure(figsize=(10,10))
sns.heatmap(correlation, vmax=1, square=True,annot=True,cmap='cubehelix')

plt.title('Correlation between different fearures')
```

```
Text(0.5, 1.0, 'Correlation between different fearures')
```



Doing some visualisation before moving onto PCA

```
df['sales'].unique()
```

```
array(['sales', 'accounting', 'hr', 'technical', 'support', 'management',
       'IT', 'product_mng', 'marketing', 'RandD'], dtype=object)
```

Here we are printing all the unique values in **sales** columns

```
sales=df.groupby('sales').sum()
sales
```

sales	satisfaction_level	last_evaluation	number_project	average_montly_hou
IT	758.46	879.55	4683	248
RandD	487.80	560.44	3033	158(
accounting	446.51	550.49	2934	154:
hr	442.52	523.84	2701	146{
management	391.45	456.12	2432	126'
marketing	530.76	614.23	3164	171(

```
df['sales'].unique()
```

```
array(['sales', 'accounting', 'hr', 'technical', 'support', 'management',
       'IT', 'product_mng', 'marketing', 'RandD'], dtype=object)
```

```
groupby_sales=df.groupby('sales').mean()
groupby_sales
```

sales	satisfaction_level	last_evaluation	number_project	average_montly_hou
IT	0.618142	0.716830	3.816626	202.215(
RandD	0.619822	0.712122	3.853875	200.800(
accounting	0.582151	0.717718	3.825293	201.162(
hr	0.598809	0.708850	3.654939	198.684'
management	0.621349	0.724000	3.860317	201.249:
marketing	0.618601	0.715886	3.687646	199.385'
product_mng	0.619634	0.714756	3.807095	199.965(
sales	0.614447	0.709717	3.776329	200.911:
support	0.618300	0.723109	3.803948	200.758'
technical	0.607897	0.721099	3.877941	202.497-

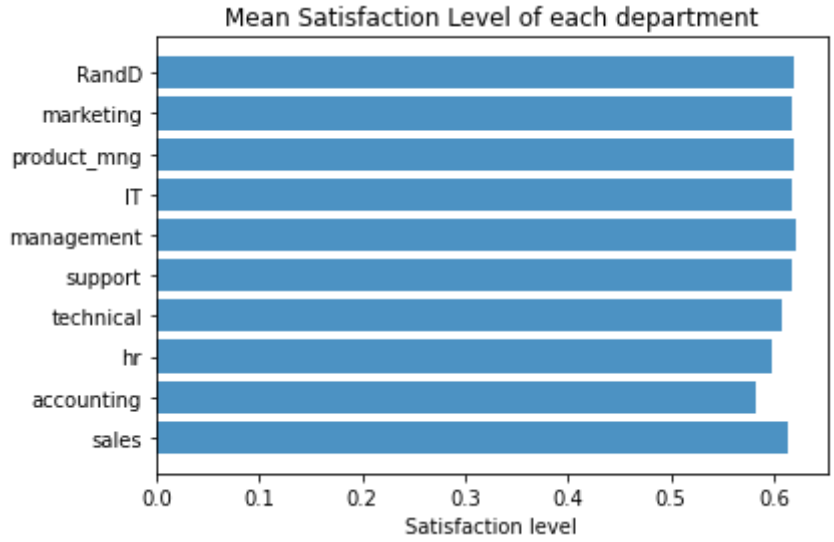
```
IT=groupby_sales['satisfaction_level'].IT
RandD=groupby_sales['satisfaction_level'].RandD
accounting=groupby_sales['satisfaction_level'].accounting
hr=groupby_sales['satisfaction_level'].hr
management=groupby_sales['satisfaction_level'].management
marketing=groupby_sales['satisfaction_level'].marketing
product_mng=groupby_sales['satisfaction_level'].product_mng
sales=groupby_sales['satisfaction_level'].sales
support=groupby_sales['satisfaction_level'].support
technical=groupby_sales['satisfaction_level'].technical
technical
```

```
0.6078970588235294
```

```
department_name=('sales', 'accounting', 'hr', 'technical', 'support', 'management',
       'IT', 'product_mng', 'marketing', 'RandD')
department=(sales, accounting, hr, technical, support, management,
       IT, product_mng, marketing, RandD)
y_pos = np.arange(len(department))
x=np.arange(0,1,0.1)

plt.barh(y_pos, department, align='center', alpha=0.8)
plt.yticks(y_pos,department_name )
plt.xlabel('Satisfaction level')
plt.title('Mean Satisfaction Level of each department')
```

```
Text(0.5, 1.0, 'Mean Satisfaction Level of each department')
```



Principal Component Analysis

```
df.head()
```

	satisfaction_level	last_evaluation	number_project	average_montly_hours	time_s
0	0.38	0.53	2	157	
1	0.80	0.86	5	262	
2	0.11	0.88	7	272	
3	0.72	0.87	5	223	
4	0.37	0.52	2	159	

```
df_drop=df.drop(labels=['sales','salary'],axis=1)
df_drop.head()
```

	satisfaction_level	last_evaluation	number_project	average_montly_hours	time_s
0	0.38	0.53	2	157	
1	0.80	0.86	5	262	
2	0.11	0.88	7	272	
3	0.72	0.87	5	223	
4	0.37	0.52	2	159	

df.drop() is the method to drop the columns in our dataframe

Now we need to bring "left" column to the front as it is the label and not the feature.

```
cols = df_drop.columns.tolist()
cols
```

```
['satisfaction_level',
 'last_evaluation',
 'number_project',
 'average_montly_hours',
 'time_spend_company',
 'Work_accident',
 'left',
 'promotion_last_5years']
```

```
cols.insert(0, cols.pop(cols.index('left')))
```

```
cols
```

```
['left',
 'satisfaction_level',
 'last_evaluation',
 'number_project',
 'average_montly_hours',
 'time_spend_company',
 'Work_accident',
 'promotion_last_5years']
```

```
df_drop = df_drop.reindex(columns= cols)
```

By using df_drop.reindex(columns= cols) we are converting list to columns again

Now we are separating features of our dataframe from the labels.

```
X = df_drop.iloc[:,1:8].values
y = df_drop.iloc[:,0].values
X
```

```
array([[0.38, 0.53, 2.  , ..., 3.  , 0.  , 0.  ],
       [0.8 , 0.86, 5.  , ..., 6.  , 0.  , 0.  ],
       [0.11, 0.88, 7.  , ..., 4.  , 0.  , 0.  ],
       ...,
       [0.37, 0.53, 2.  , ..., 3.  , 0.  , 0.  ],
       [0.11, 0.96, 6.  , ..., 4.  , 0.  , 0.  ],
       [0.37, 0.52, 2.  , ..., 3.  , 0.  , 0.  ]])
```

```
y
```

```
array([1, 1, 1, ..., 1, 1, 1])
```

```
np.shape(X)
```

```
(14999, 7)
```

Thus X is now matrix with 14999 rows and 7 columns

```
np.shape(y)
```

```
(14999,)
```

y is now matrix with 14999 rows and 1 column

4) Data Standardisation

Standardization refers to shifting the distribution of each attribute to have a mean of zero and a standard deviation of one (unit variance). It is useful to standardize attributes for a model. Standardization of datasets is a common requirement for many machine learning estimators implemented in scikit-learn; they might behave badly if the individual features do not more or less look like standard normally distributed data

```
from sklearn.preprocessing import StandardScaler
X_std = StandardScaler().fit_transform(X)
```

5) Computing Eigenvectors and Eigenvalues:

Before computing Eigen vectors and values we need to calculate covariance matrix.

Covariance matrix

```
mean_vec = np.mean(X_std, axis=0)
```

```
cov_mat = (X_std - mean_vec).T.dot((X_std - mean_vec))
print('Covariance matrix \n%s' %cov_mat)
```

```
Covariance matrix
[[ 1.          0.10502121 -0.14296959 -0.02004811 -0.10086607  0.05869724
   0.02560519]
 [ 0.10502121  1.          0.34933259  0.3397418   0.13159072 -0.00710429
  -0.00868377]
 [-0.14296959  0.34933259  1.          0.41721063  0.19678589 -0.00474055
  -0.00606396]
 [-0.02004811  0.3397418   0.41721063  1.          0.12775491 -0.01014289
  -0.00354441]
 [-0.10086607  0.13159072  0.19678589  0.12775491  1.          0.00212042
   0.06743293]
 [ 0.05869724 -0.00710429 -0.00474055 -0.01014289  0.00212042  1.
   0.03924543]
 [ 0.02560519 -0.00868377 -0.00606396 -0.00354441  0.06743293  0.03924543
   1.        ]]
```

```
print('NumPy covariance matrix: \n%s' %np.cov(X_std.T))
```

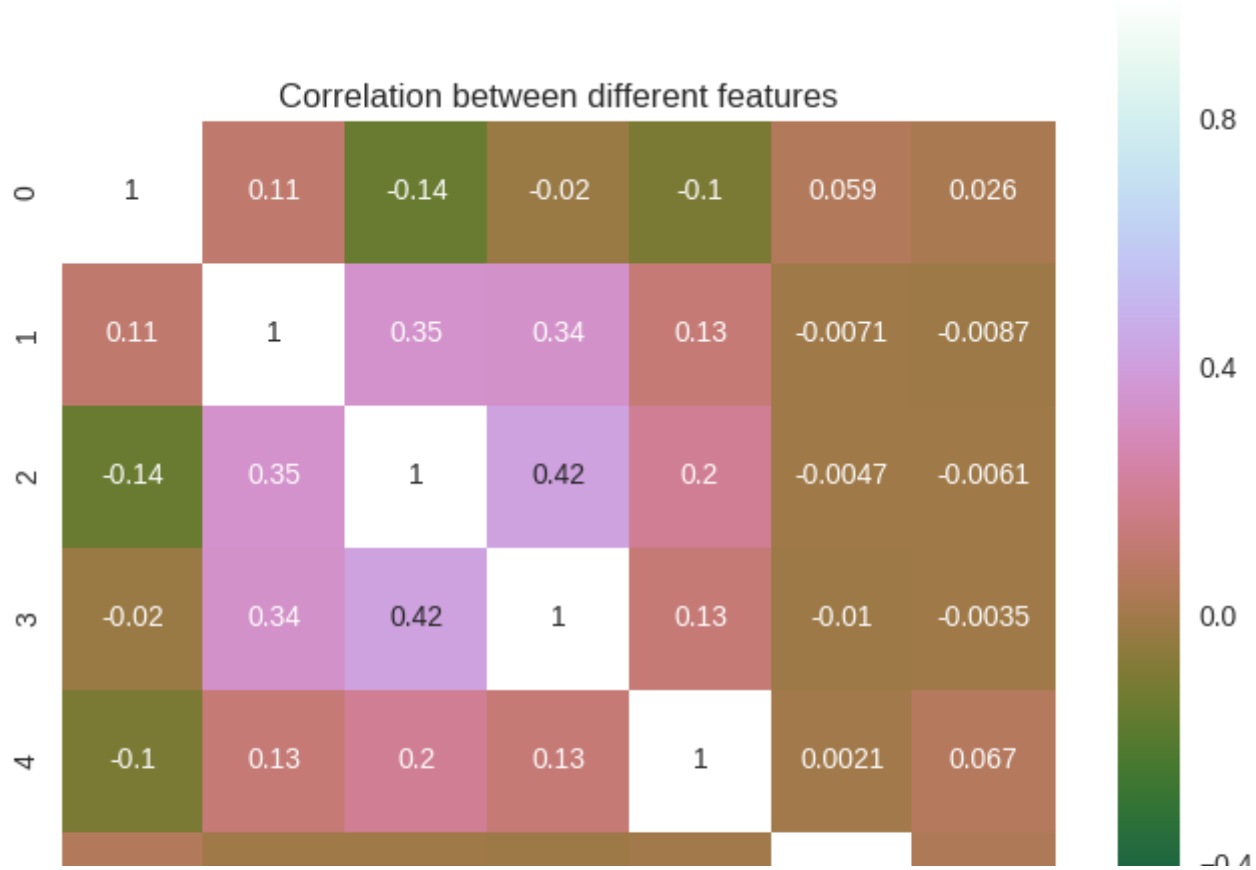
```
NumPy covariance matrix:
[[ 1.00006668  0.10502822 -0.14297912 -0.02004945 -0.1008728   0.05870115
   0.02560689]
 [ 0.10502822  1.00006668  0.34935588  0.33976445  0.1315995  -0.00710476
  -0.00868435]
 [-0.14297912  0.34935588  1.00006668  0.41723845  0.19679901 -0.00474086
  -0.00606436]
 [-0.02004945  0.33976445  0.41723845  1.00006668  0.12776343 -0.01014356
  -0.00354465]
 [-0.1008728   0.1315995   0.19679901  0.12776343  1.00006668  0.00212056
   0.06743742]
 [ 0.05870115 -0.00710476 -0.00474086 -0.01014356  0.00212056  1.00006668
   0.03924805]
 [ 0.02560689 -0.00868435 -0.00606436 -0.00354465  0.06743742  0.03924805
   1.00006668]]
```

Equivalently we could have used Numpy np.cov to calculate covariance matrix

```
plt.figure(figsize=(8,8))
sns.heatmap(cov_mat, vmax=1, square=True,annot=True,cmap='cubehelix')

plt.title('Correlation between different features')
```

```
<matplotlib.text.Text at 0x7fa70e8007b8>
```



Eigen decomposition of the covariance matrix

```
eig_vals, eig_vecs = np.linalg.eig(cov_mat)

print('Eigenvectors \n%s' %eig_vecs)
print('\nEigenvalues \n%s' %eig_vals)
```

```
Eigenvectors
[[-0.08797699 -0.29189921  0.27784886  0.33637135  0.79752505  0.26786864
  -0.09438973]
 [ 0.50695734  0.30996609 -0.70780994  0.07393548  0.33180877  0.1101505
  -0.13499526]
 [ 0.5788351  -0.77736008 -0.00657105 -0.19677589 -0.10338032 -0.10336241
  -0.02293518]
 [ 0.54901653  0.45787675  0.63497294 -0.25170987  0.10388959 -0.01034922
  -0.10714981]
 [ 0.31354922  0.05287224  0.12200054  0.78782241 -0.28404472  0.04036861
   0.42547869]
 [-0.01930249  0.04433104 -0.03622859 -0.05762997  0.37489883 -0.8048393
   0.45245222]
 [ 0.00996933  0.00391698 -0.04873036 -0.39411153  0.10557298  0.50589173
   0.75836313]]

Eigenvalues
[ 1.83017431  0.54823098  0.63363587  0.84548166  1.12659606  0.95598647
  1.06036136]
```

```
# 6) Selecting Principal Components¶
```

6) Selecting Principal Components

T In order to decide which eigenvector(s) can dropped without losing too much information for the construction of lower-dimensional subspace, we need to inspect the corresponding eigenvalues: The eigenvectors with the lowest eigenvalues bear the least information about the distribution of the data; those are the ones can be dropped.

```
# Make a list of (eigenvalue, eigenvector) tuples
eig_pairs = [(np.abs(eig_vals[i]), eig_vecs[:,i]) for i in range(len(eig_vals))]

# Sort the (eigenvalue, eigenvector) tuples from high to low
eig_pairs.sort(key=lambda x: x[0], reverse=True)

# Visually confirm that the list is correctly sorted by decreasing eigenvalues
print('Eigenvalues in descending order:')
for i in eig_pairs:
    print(i[0])
```

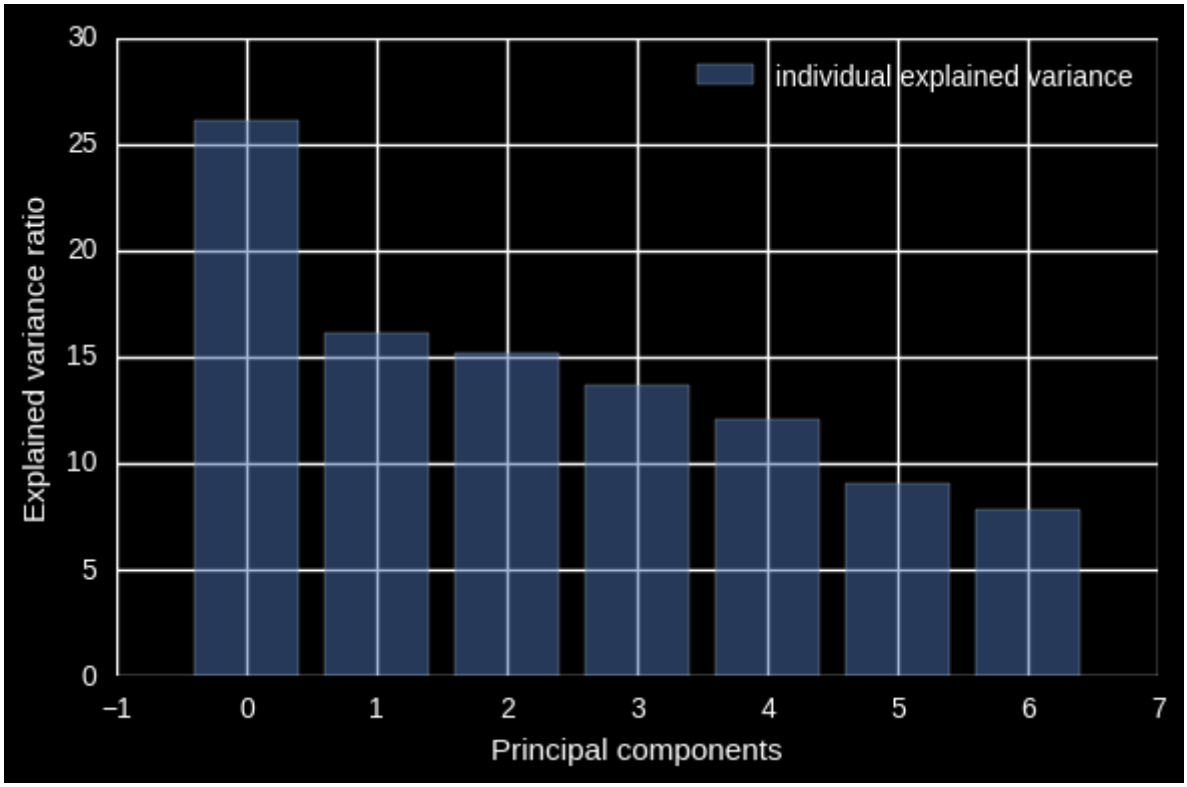
```
 Eigenvalues in descending order:
 1.83017431388
 1.12659606399
 1.06036136228
 0.955986474007
 0.845481663714
 0.633635874483
 0.548230976542
```

Explained Variance After sorting the eigenpairs, the next question is "how many principal components are we going to choose for our new feature subspace?" A useful measure is the so-called "explained variance," which can be calculated from the eigenvalues. The explained variance tells us how much information (variance) can be attributed to each of the principal components.

```
tot = sum(eig_vals)
var_exp = [(i / tot)*100 for i in sorted(eig_vals, reverse=True)]


with plt.style.context('dark_background'):
    plt.figure(figsize=(6, 4))

    plt.bar(range(7), var_exp, alpha=0.5, align='center',
            label='individual explained variance')
    plt.ylabel('Explained variance ratio')
    plt.xlabel('Principal components')
    plt.legend(loc='best')
    plt.tight_layout()
```



The plot above clearly shows that maximum variance (somewhere around 26%) can be explained by the first principal component alone. The second,third,fourth and fifth principal component share almost equal amount of information.Comparatively 6th and 7th components share less amount of information as compared to the rest of the Principal components.But those information cannot be ignored since they both contribute almost 17% of the data.But we can drop the last component as it has less than 10% of the variance

Projection Matrix

The construction of the projection matrix that will be used to transform the Human resouces analytics data onto the new feature subspace. **Suppose only 1st and 2nd principal component shares the maximum amount of information say around 90%**.Hence we can drop other components. Here, we are reducing the 7-dimensional feature space to a 2-dimensional feature subspace, by choosing the “top 2” eigenvectors with the highest eigenvalues to construct our d×k-dimensional eigenvector matrix W

```
matrix_w = np.hstack((eig_pairs[0][1].reshape(7,1),
                      eig_pairs[1][1].reshape(7,1)
                    ))
print('Matrix W:\n', matrix_w)
```

```
Matrix W:
 [[-0.08797699  0.79752505]
 [ 0.50695734  0.33180877]
 [ 0.5788351  -0.10338032]
 [ 0.54901653  0.10388959]
 [ 0.31354922 -0.28404472]
```

```
[-0.01930249  0.37489883]
[ 0.00996933  0.10557298]]
```

Projection Onto the New Feature Space In this last step we will use the 7×2-dimensional projection matrix W to transform our samples onto the new subspace via the equation **Y=X×W**

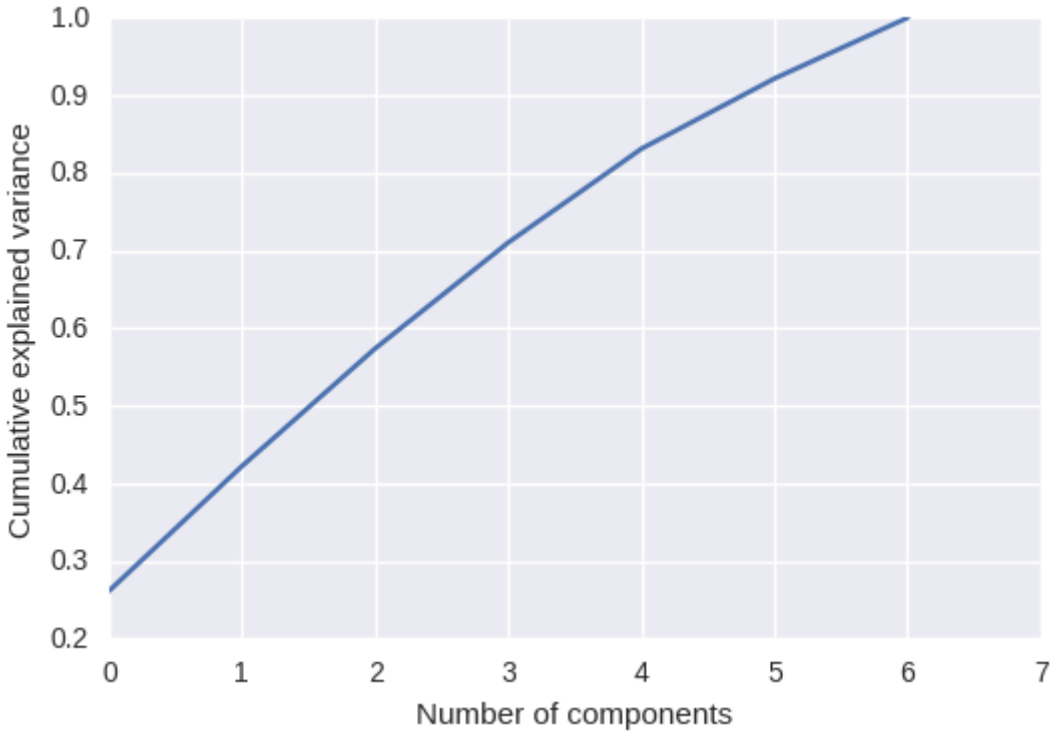
```
Y = X_std.dot(matrix_w)
Y
```

```
array([[-1.90035018, -1.12083103],
       [ 2.1358322 ,  0.2493369 ],
       [ 3.05891625, -1.68312693],
       ...,
       [-2.0507165 , -1.182032  ],
       [ 2.91418496, -1.42752606],
       [-1.91543672, -1.17021407]])
```

PCA in scikit-learn

```
from sklearn.decomposition import PCA
pca = PCA().fit(X_std)
plt.plot(np.cumsum(pca.explained_variance_ratio_))
plt.xlim(0,7,1)
plt.xlabel('Number of components')
plt.ylabel('Cumulative explained variance')
```

```
<matplotlib.text.Text at 0x7fa70c0ac2b0>
```



The above plot shows almost 90% variance by the first 6 components. Therfore we can drop 7th component.

```
from sklearn.decomposition import PCA
sklearn_pca = PCA(n_components=6)
Y_sklearn = sklearn_pca.fit_transform(X_std)
```

```
print(Y_sklearn)
```

```
[[-1.90035018 -1.12083103 -0.0797787   0.03228437 -0.07256447  0.06063013]
 [ 2.1358322   0.2493369   0.0936161   0.50676925  1.2487747  -0.61378158]
 [ 3.05891625 -1.68312693 -0.301682   -0.4488635  -1.12495888  0.29066929]
 ...,
 [-2.0507165  -1.182032   -0.04594506  0.02441143 -0.01553247  0.24980658]
 [ 2.91418496 -1.42752606 -0.36333357 -0.31517759 -0.97107375  0.51444624]
 [-1.91543672 -1.17021407 -0.07024077  0.01486762 -0.09545357  0.01773844]]
```

```
Y_sklearn.shape
```

```
(14999, 6)
```

Thus Principal Component Analysis is used to remove the redundant features from the datasets without losing much information.These features are low dimensional in nature.The first component has the highest variance followed by second, third and so on.PCA works best on data set having 3 or higher dimensions. Because, with higher dimensions, it becomes increasingly difficult to make interpretations from the resultant cloud of data.