Skill 5

Title : Perform Principal Component Analysis on Wine Dataset ¶

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In [ ]:

```

```

PCA (Principal Component Analysis)

The goal of PCA is to identify and detect the correlation between attributes.
If there is a strong correlation and it is found.Then PCA reduces the dimensionality.
PCA, is a dimensionality-reduction method that is often used to reduce the dimensionality of large data sets,
by transforming a large set of variables into a smaller.

In [1]:

```
#Importing all necesary libraries

import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.preprocessing import scale
```

In [2]:

```
#Read dataset

df = pd.read_csv("wine.csv")
```

In [3]:

```
df.head()
```

Out[3]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcoh
0	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	9
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970	3.26	0.65	9
3	11.2	0.28	0.56	1.9	0.075	17.0	60.0	0.9980	3.16	0.58	9
4	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9

In [4]:

```
#Checking null value or not

df.isnull().sum()
```

Out[4]:

```
fixed acidity           0
volatile acidity        0
citric acid             0
residual sugar          0
chlorides               0
free sulfur dioxide     0
total sulfur dioxide    0
density                 0
pH                      0
sulphates               0
alcohol                 0
quality                 0
dtype: int64
```

In [5]:

```
#Checking the dimensions
df.shape
```

Out[5]:

```
(1596, 12)
```

In [6]:

```
#Separating dependent and independent variable.
X = df.iloc[:, 1:11].values
y = df.iloc[:, 11].values
```

In [7]:

```
X
```

Out[7]:

```
array([[ 0.7  ,  0.   ,  1.9  , ...,  3.51 ,  0.56 ,  9.4  ],
       [ 0.88 ,  0.   ,  2.6  , ...,  3.2  ,  0.68 ,  9.8  ],
       [ 0.76 ,  0.04 ,  2.3  , ...,  3.26 ,  0.65 ,  9.8  ],
       ...,
       [ 0.51 ,  0.13 ,  2.3  , ...,  3.42 ,  0.75 , 11.   ],
       [ 0.645,  0.12 ,  2.   , ...,  3.57 ,  0.71 , 10.2  ],
       [ 0.31 ,  0.47 ,  3.6  , ...,  3.39 ,  0.66 , 11.   ]])
```

In [8]:

```
y
```

Out[8]:

```
array([5, 5, 5, ..., 6, 5, 6], dtype=int64)
```

In [9]:

```
# Splitting the dataset into the Training set and Test set

from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.2, random_state = 0
```

In [10]:

```
# Feature Scaling

from sklearn.preprocessing import StandardScaler
sc = StandardScaler()
X_train = sc.fit_transform(X_train)
X_test = sc.transform(X_test)
```

In [11]:

```
# Applying PCA

from sklearn.decomposition import PCA
pca = PCA(n_components = 3)
X_train = pca.fit_transform(X_train)
X_test = pca.transform(X_test)
explained_variance = pca.explained_variance_ratio_
```

In [12]:

```
print(explained_variance)
```

```
[0.24819062 0.19304757 0.14756741]
```

In [13]:

```
x_pca=pca.transform(X)
```

In [ ]:

In [14]:

```
# Final Dataframe
final_df=pd.concat([pd.DataFrame(x_pca[:,0:3],columns=['PC1','PC2','PC3'])],axis=1)
final_df
```

Out[14]:

	PC1	PC2	PC3
0	3.924200	19.765460	23.148248
1	10.704833	43.021444	43.178490
2	7.669154	31.672135	33.089507
3	9.126063	35.221215	36.601071
4	3.924200	19.765460	23.148248
...	...	...	...
1591	7.301446	34.091879	38.265743
1592	8.998656	40.604585	44.940013
1593	6.470954	30.453449	35.533107
1594	7.350085	34.205518	38.153066
1595	6.311552	26.490060	30.985035

1596 rows × 3 columns

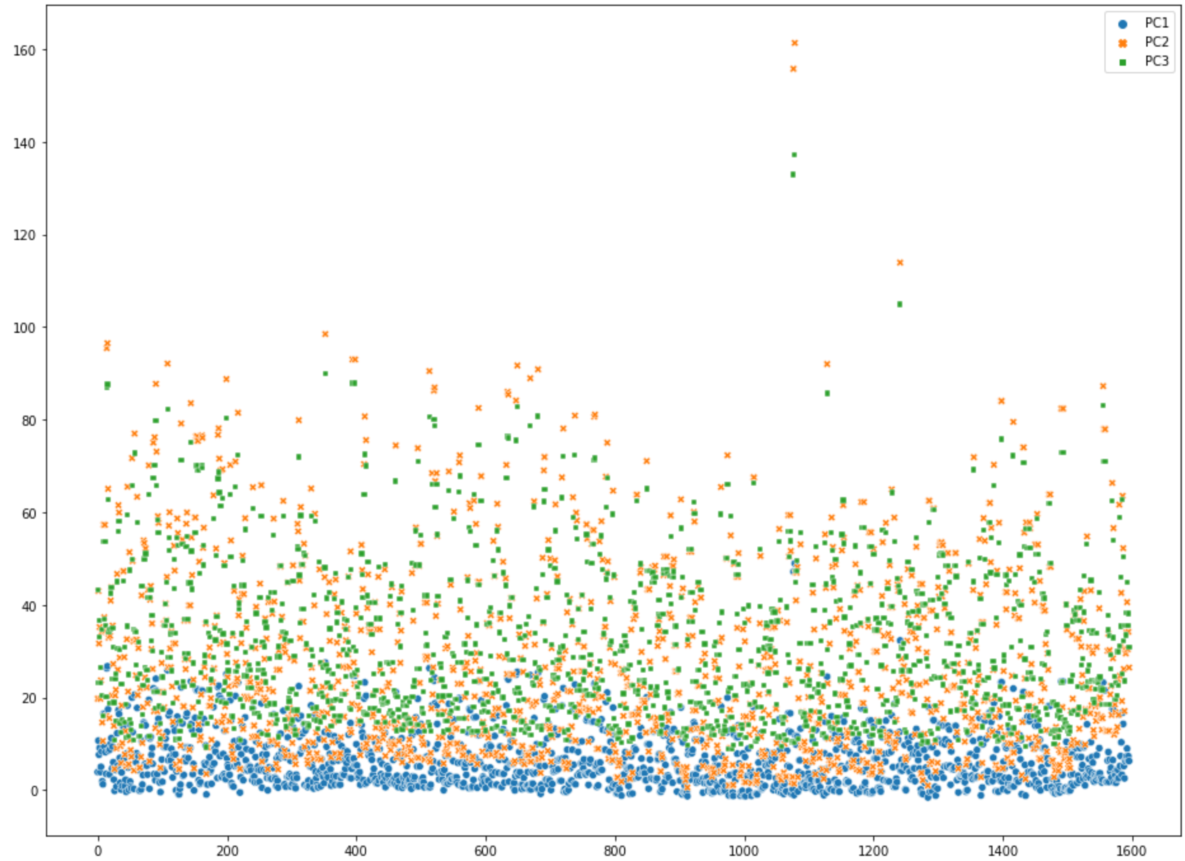
In [15]:

```
# Visualization of PCAs

fig=plt.figure(figsize=(16,12))
sns.scatterplot(data=final_df)
```

Out[15]:

```
<AxesSubplot:>
```



In [ ]:

```

```

K-Means Clustering

In [16]:

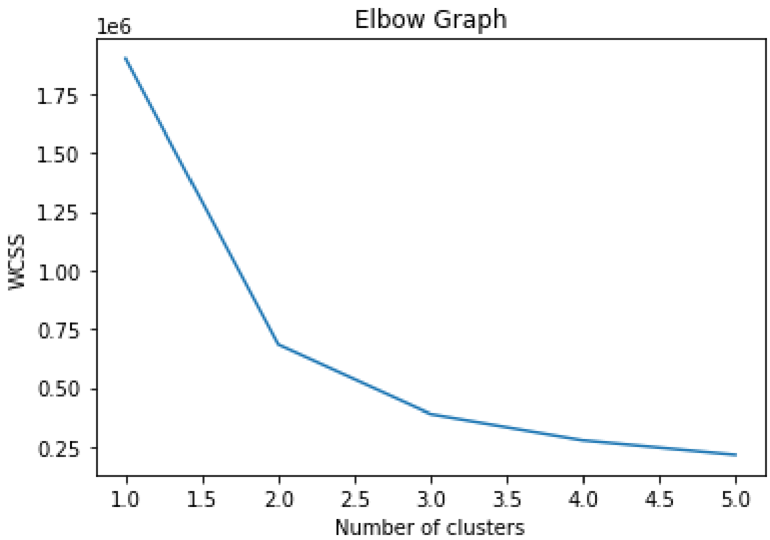
```
from sklearn.cluster import KMeans
```

In [17]:

```
wcss=[]
for i in range (1,6):
    kmeans=KMeans(n_clusters=i,random_state=2)
    kmeans.fit(X)
    wcss.append(kmeans.inertia_)
```

In [18]:

```
plt.plot(range(1,6),wcss)
plt.title('Elbow Graph')
plt.xlabel('Number of clusters')
plt.ylabel('WCSS')
plt.show()
```



In [19]:

```
# Cluster algorithm using K=3
clusters3=KMeans(3,random_state=30).fit(X)
clusters3
```

Out[19]:

```
KMeans(n_clusters=3, random_state=30)
```

In [20]:

```
clusters3.labels_
```

Out[20]:

```
array([0, 2, 2, ..., 2, 2, 2])
```

In [21]:

```
clusters3.n_iter_
```

Out[21]:

```
13
```

In [22]:

```
clusters3.cluster_centers_
```

Out[22]:

```
array([[5.19666255e-01, 2.68825711e-01, 2.36186650e+00, 8.45315204e-02,
        8.98269468e+00, 2.23288010e+01, 9.96620519e-01, 3.31123609e+00,
        6.46897404e-01, 1.05773383e+01],
       [5.72293388e-01, 2.75413223e-01, 3.23181818e+00, 8.82851240e-02,
        2.61053719e+01, 1.08173554e+02, 9.96929545e-01, 3.29152893e+00,
        6.46322314e-01, 1.00084711e+01],
       [5.20568807e-01, 2.70146789e-01, 2.48422018e+00, 9.04440367e-02,
        2.15146789e+01, 5.46495413e+01, 9.96845119e-01, 3.32198165e+00,
        6.74935780e-01, 1.03725382e+01]])
```

In [23]:

```
data=df
data["Final Label"]=clusters3.labels_
data
```

Out[23]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	al
0	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	
1	7.8	0.880	0.00	2.6	0.098	25.0	67.0	0.99680	3.20	0.68	
2	7.8	0.760	0.04	2.3	0.092	15.0	54.0	0.99700	3.26	0.65	
3	11.2	0.280	0.56	1.9	0.075	17.0	60.0	0.99800	3.16	0.58	
4	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	
...	...	...	...	...	...	...	...	...	...	...	
1591	6.2	0.600	0.08	2.0	0.090	32.0	44.0	0.99490	3.45	0.58	
1592	5.9	0.550	0.10	2.2	0.062	39.0	51.0	0.99512	3.52	0.76	
1593	6.3	0.510	0.13	2.3	0.076	29.0	40.0	0.99574	3.42	0.75	
1594	5.9	0.645	0.12	2.0	0.075	32.0	44.0	0.99547	3.57	0.71	
1595	6.0	0.310	0.47	3.6	0.067	18.0	42.0	0.99549	3.39	0.66	

1596 rows × 13 columns

In [24]:

```
data['Final Label'].value_counts()
```

Out[24]:

```
0    810
2    545
1    241
Name: Final Label, dtype: int64
```

In [ ]:

```
```

Hierarchical Clustering

In [25]:

```
import scipy.cluster.hierarchy as sch
from sklearn.cluster import AgglomerativeClustering
from sklearn.preprocessing import normalize
```

In [26]:

```
# Converting data to numpy array
wine_ary=df.values
wine_ary
```

Out[26]:

```
array([[ 7.4  ,  0.7  ,  0.   , ...,  9.4  ,  5.   ,  0.   ],
       [ 7.8  ,  0.88 ,  0.   , ...,  9.8  ,  5.   ,  2.   ],
       [ 7.8  ,  0.76 ,  0.04 , ...,  9.8  ,  5.   ,  2.   ],
       ...,
       [ 6.3  ,  0.51 ,  0.13 , ..., 11.   ,  6.   ,  2.   ],
       [ 5.9  ,  0.645,  0.12 , ..., 10.2  ,  5.   ,  2.   ],
       [ 6.   ,  0.31 ,  0.47 , ..., 11.   ,  6.   ,  2.   ]])
```

In [27]:

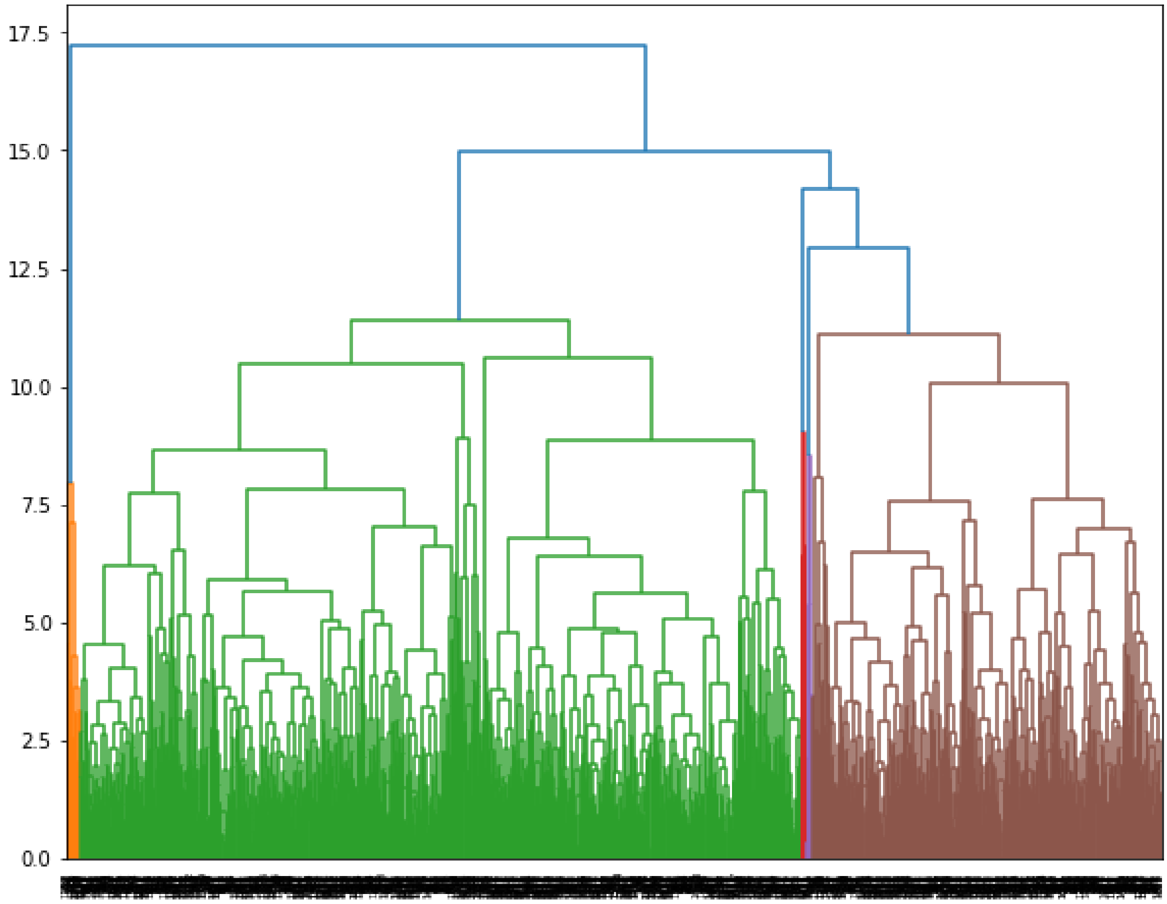
```
# Normalizing the numerical data
wine_norm=scale(wine_ary)
wine_norm
```

Out[27]:

```
array([[-0.52790985,  0.96050573, -1.3943694 , ..., -0.96331098,
        -0.7897822 , -0.92015369],
       [-0.29691763,  1.9654189 , -1.3943694 , ..., -0.58596616,
        -0.7897822 ,  1.28655598],
       [-0.29691763,  1.29547678, -1.18800687, ..., -0.58596616,
        -0.7897822 ,  1.28655598],
       ...,
       [-1.16313844, -0.10023596, -0.72369117, ...,  0.54606832,
         0.44964002,  1.28655598],
       [-1.39413066,  0.65344892, -0.7752818 , ..., -0.20862133,
        -0.7897822 ,  1.28655598],
       [-1.33638261, -1.21680616,  1.03039037, ...,  0.54606832,
         0.44964002,  1.28655598]])
```

In [28]:

```
plt.figure(figsize=(10,8))
dendrogram=sch.dendrogram(sch.linkage(wine_norm,'complete'))
```



In [29]:

```
# Create Clusters (y)
hclusters=AgglomerativeClustering(n_clusters=3,affinity='euclidean',linkage='ward')
hclusters
```

Out[29]:

```
AgglomerativeClustering(n_clusters=3)
```

In [30]:

```
y=pd.DataFrame(hclusters.fit_predict(wine_norm),columns=['clustersid'])
y['clustersid'].value_counts()
```

Out[30]:

```
1    767
0    425
2    404
Name: clustersid, dtype: int64
```

In [31]:

```
# Adding clusters to dataset
wine=df.copy()
wine['clustersid']=hclusters.labels_
wine
```

Out[31]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	al
0	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	
1	7.8	0.880	0.00	2.6	0.098	25.0	67.0	0.99680	3.20	0.68	
2	7.8	0.760	0.04	2.3	0.092	15.0	54.0	0.99700	3.26	0.65	
3	11.2	0.280	0.56	1.9	0.075	17.0	60.0	0.99800	3.16	0.58	
4	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	
...	...	...	...	...	...	...	...	...	...	...	
1591	6.2	0.600	0.08	2.0	0.090	32.0	44.0	0.99490	3.45	0.58	
1592	5.9	0.550	0.10	2.2	0.062	39.0	51.0	0.99512	3.52	0.76	
1593	6.3	0.510	0.13	2.3	0.076	29.0	40.0	0.99574	3.42	0.75	
1594	5.9	0.645	0.12	2.0	0.075	32.0	44.0	0.99547	3.57	0.71	
1595	6.0	0.310	0.47	3.6	0.067	18.0	42.0	0.99549	3.39	0.66	

1596 rows × 14 columns

In [ ]:

In [ ]:

In [ ]:

In [ ]: