PCA Assignment

Data Set : Wine

1. Import Necessary libraries

In [1]:
```
import pandas as pd
import numpy as np

import matplotlib.pyplot as plt
import seaborn as sns
```

2. Import Data

In [2]:
```
liquor = pd.read_csv('wine.csv')
liquor
```

Out[2]:

	Type	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proanthocyanins	Color	Hue	Dilution	Proline
0	1	14.23	1.71	2.43	15.6	127	2.80	3.06	0.28	2.29	5.64	1.04	3.92	1065
1	1	13.20	1.78	2.14	11.2	100	2.65	2.76	0.26	1.28	4.38	1.05	3.40	1050
2	1	13.16	2.36	2.67	18.6	101	2.80	3.24	0.30	2.81	5.68	1.03	3.17	1185
3	1	14.37	1.95	2.50	16.8	113	3.85	3.49	0.24	2.18	7.80	0.86	3.45	1480
4	1	13.24	2.59	2.87	21.0	118	2.80	2.69	0.39	1.82	4.32	1.04	2.93	735
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
173	3	13.71	5.65	2.45	20.5	95	1.68	0.61	0.52	1.06	7.70	0.64	1.74	740
174	3	13.40	3.91	2.48	23.0	102	1.80	0.75	0.43	1.41	7.30	0.70	1.56	750
175	3	13.27	4.28	2.26	20.0	120	1.59	0.69	0.43	1.35	10.20	0.59	1.56	835
176	3	13.17	2.59	2.37	20.0	120	1.65	0.68	0.53	1.46	9.30	0.60	1.62	840
177	3	14.13	4.10	2.74	24.5	96	2.05	0.76	0.56	1.35	9.20	0.61	1.60	560

178 rows × 14 columns

3. Data Understanding

In [3]:
```
liquor.head()
```

Out[3]:

	Type	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proanthocyanins	Color	Hue	Dilution	Proline
0	1	14.23	1.71	2.43	15.6	127	2.80	3.06	0.28	2.29	5.64	1.04	3.92	1065
1	1	13.20	1.78	2.14	11.2	100	2.65	2.76	0.26	1.28	4.38	1.05	3.40	1050
2	1	13.16	2.36	2.67	18.6	101	2.80	3.24	0.30	2.81	5.68	1.03	3.17	1185
3	1	14.37	1.95	2.50	16.8	113	3.85	3.49	0.24	2.18	7.80	0.86	3.45	1480
4	1	13.24	2.59	2.87	21.0	118	2.80	2.69	0.39	1.82	4.32	1.04	2.93	735

In [4]:
```
liquor.shape
```

Out[4]:
```
(178, 14)
```

In [5]:
```
liquor.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 178 entries, 0 to 177
Data columns (total 14 columns):
 #   Column           Non-Null Count  Dtype
---  ------           --------------  -----
 0   Type             178 non-null    int64
 1   Alcohol          178 non-null    float64
 2   Malic            178 non-null    float64
 3   Ash              178 non-null    float64
 4   Alcalinity       178 non-null    float64
 5   Magnesium        178 non-null    int64
 6   Phenols          178 non-null    float64
 7   Flavanoids       178 non-null    float64
 8   Nonflavanoids    178 non-null    float64
 9   Proanthocyanins  178 non-null    float64
 10  Color            178 non-null    float64
 11  Hue              178 non-null    float64
 12  Dilution         178 non-null    float64
 13  Proline          178 non-null    int64
dtypes: float64(11), int64(3)
memory usage: 19.6 KB
```

In [6]:
```
liquor.isna().sum()
```

Out[6]:
```
Type               0
Alcohol            0
Malic              0
Ash                0
Alcalinity         0
Magnesium          0
Phenols            0
Flavanoids         0
Nonflavanoids      0
Proanthocyanins    0
Color              0
Hue                0
Dilution           0
Proline            0
dtype: int64
```

In [7]:
```
liquor.describe()
```

Out[7]:

	Type	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proanthocyanins	Color	Hue	Dilution	Proline
count	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000
mean	1.938202	13.000618	2.336348	2.366517	19.494944	99.741573	2.295112	2.029270	0.361854	1.590899	5.058090	0.957449	2.611685	746.893258
std	0.775035	0.811827	1.117146	0.274344	3.339564	14.282484	0.625851	0.998859	0.124453	0.572359	2.318286	0.228572	0.709990	314.907474
min	1.000000	11.030000	0.740000	1.360000	10.600000	70.000000	0.980000	0.340000	0.130000	0.410000	1.280000	0.480000	1.270000	278.000000
25%	1.000000	12.362500	1.602500	2.210000	17.200000	88.000000	1.742500	1.205000	0.270000	1.250000	3.220000	0.782500	1.937500	500.500000
50%	2.000000	13.050000	1.865000	2.360000	19.500000	98.000000	2.355000	2.135000	0.340000	1.555000	4.690000	0.965000	2.780000	673.500000
75%	3.000000	13.677500	3.082500	2.557500	21.500000	107.000000	2.800000	2.875000	0.437500	1.950000	6.200000	1.120000	3.170000	985.000000
max	3.000000	14.830000	5.800000	3.230000	30.000000	162.000000	3.880000	5.080000	0.660000	3.580000	13.000000	1.710000	4.000000	1680.000000

In [8]:
```
liquor.dtypes
```

Out[8]:
```
Type                 int64
Alcohol            float64
Malic              float64
Ash                float64
Alcalinity         float64
Magnesium            int64
Phenols            float64
Flavanoids         float64
Nonflavanoids      float64
Proanthocyanins    float64
Color              float64
Hue                float64
Dilution           float64
Proline              int64
dtype: object
```

4. Performing PCA

STEP 1 = Perform Scaling on the Data :

For Scaling = 1. First import StandardScalar ,

1. Separate the features from the target ,
2. Scale the features

In [9]:
```
from sklearn.preprocessing import scale
```

In [10]:
```
data = liquor.iloc[:, 1:]
```

In [11]:
```
# Converting into numpy array
liquor_array = data.values
liquor_array
```

Out[11]:
```
array([[1.423e+01, 1.710e+00, 2.430e+00, ..., 1.040e+00, 3.920e+00,
        1.065e+03],
       [1.320e+01, 1.780e+00, 2.140e+00, ..., 1.050e+00, 3.400e+00,
        1.050e+03],
       [1.316e+01, 2.360e+00, 2.670e+00, ..., 1.030e+00, 3.170e+00,
        1.185e+03],
       ...,
       [1.327e+01, 4.280e+00, 2.260e+00, ..., 5.900e-01, 1.560e+00,
        8.350e+02],
       [1.317e+01, 2.590e+00, 2.370e+00, ..., 6.000e-01, 1.620e+00,
        8.400e+02],
       [1.413e+01, 4.100e+00, 2.740e+00, ..., 6.100e-01, 1.600e+00,
        5.600e+02]])
```

In [12]:
```
# Normalizing data
liquor_norm = scale(liquor_array)
liquor_norm
```

Out[12]:
```
array([[ 1.51861254, -0.5622498 ,  0.23205254, ...,  0.36217728,
         1.84791957,  1.01300893],
       [ 0.24628963, -0.49941338, -0.82799632, ...,  0.40605066,
         1.1134493 ,  0.96524152],
       [ 0.19687903,  0.02123125,  1.10933436, ...,  0.31830389,
         0.78858745,  1.39514818],
       ...,
       [ 0.33275817,  1.74474449, -0.38935541, ..., -1.61212515,
        -1.48544548,  0.28057537],
       [ 0.20923168,  0.22769377,  0.01273209, ..., -1.56825176,
        -1.40069891,  0.29649784],
       [ 1.39508604,  1.58316512,  1.36520822, ..., -1.52437837,
        -1.42894777, -0.59516041]])
```

In [13]:
```
from sklearn.decomposition import PCA
from sklearn import preprocessing
```

In [14]:
```
PCA = PCA()
```

In [15]:
```
pca_liquor = PCA.fit_transform(liquor_norm)
pca_liquor
```

Out[15]:
```
array([[ 3.31675081e+00, -1.44346263e+00, -1.65739045e-01, ...,
        -4.51563395e-01,  5.40810414e-01, -6.62386309e-02],
       [ 2.20946492e+00,  3.33392887e-01, -2.02645737e+00, ...,
        -1.42657306e-01,  3.88237741e-01,  3.63650247e-03],
       [ 2.51674015e+00, -1.03115130e+00,  9.82818670e-01, ...,
        -2.86672847e-01,  5.83573183e-04,  2.17165104e-02],
       ...,
       [-2.67783946e+00, -2.76089913e+00, -9.40941877e-01, ...,
         5.12492025e-01,  6.98766451e-01,  7.20776948e-02],
       [-2.38701709e+00, -2.29734668e+00, -5.50696197e-01, ...,
         2.99821968e-01,  3.39820654e-01, -2.18657605e-02],
       [-3.20875816e+00, -2.76891957e+00,  1.01391366e+00, ...,
        -2.29964331e-01, -1.88787963e-01, -3.23964720e-01]])
```

STEP 2 = Explaining the Variance Using Principal Component :

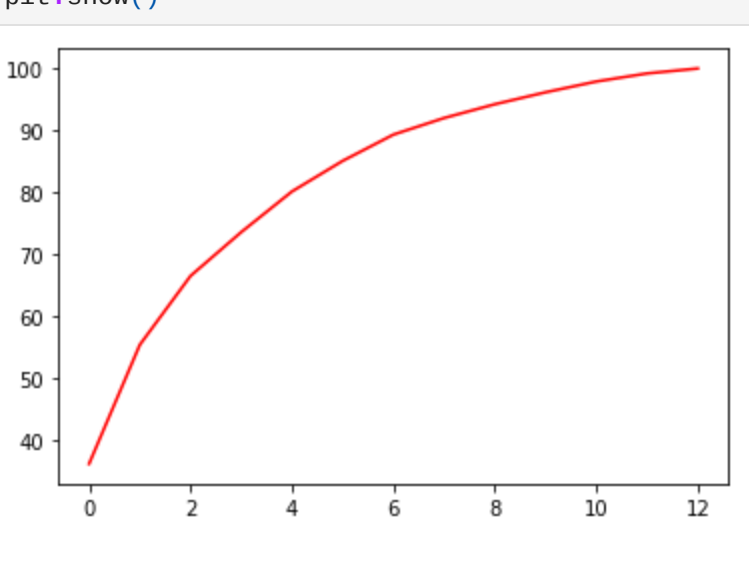
In [16]:
```
# The amount of variance that each PCA explains is
liquor_var = PCA.explained_variance_ratio_
liquor_var
```

Out[16]:
```
array([0.36198848, 0.1920749 , 0.11123631, 0.0706903 , 0.06563294,
       0.04935823, 0.04238679, 0.02680749, 0.02222153, 0.01930019,
       0.01736836, 0.01298233, 0.00795215])
```

In [17]:
```
# Cumulative variance
liquor_cum_var = np.cumsum(np.round(PCA.explained_variance_ratio_, decimals = 4)*100)
liquor_cum_var
```

Out[17]:
```
array([ 36.2 ,  55.41,  66.53,  73.6 ,  80.16,  85.1 ,  89.34,  92.02,
        94.24,  96.17,  97.91,  99.21, 100.01])
```

In [18]:
```
# Variance plot for PCA components obtained
plt.plot(liquor_cum_var, color = "red")
plt.show()
```



STEP 3 = Combine the Target and the Principal Components :

In [19]:
```
#create data frame from pca1 and pca2

df_liquor = pd.concat([pd.DataFrame(pca_liquor[:, 0:3], columns = ['PC1','PC2','PC3']), liquor[['Type']]], axis = 1)
df_liquor
```

Out[19]:

	PC1	PC2	PC3	Type
0	3.316751	-1.443463	-0.165739	1
1	2.209465	0.333393	-2.026457	1
2	2.516740	-1.031151	0.982819	1
3	3.757066	-2.756372	-0.176192	1
4	1.008908	-0.869831	2.026688	1
...	...	...	...	...
173	-3.370524	-2.216289	-0.342570	3
174	-2.601956	-1.757229	0.207581	3
175	-2.677839	-2.760899	-0.940942	3
176	-2.387017	-2.297347	-0.550696	3
177	-3.208758	-2.768920	1.013914	3

178 rows × 4 columns

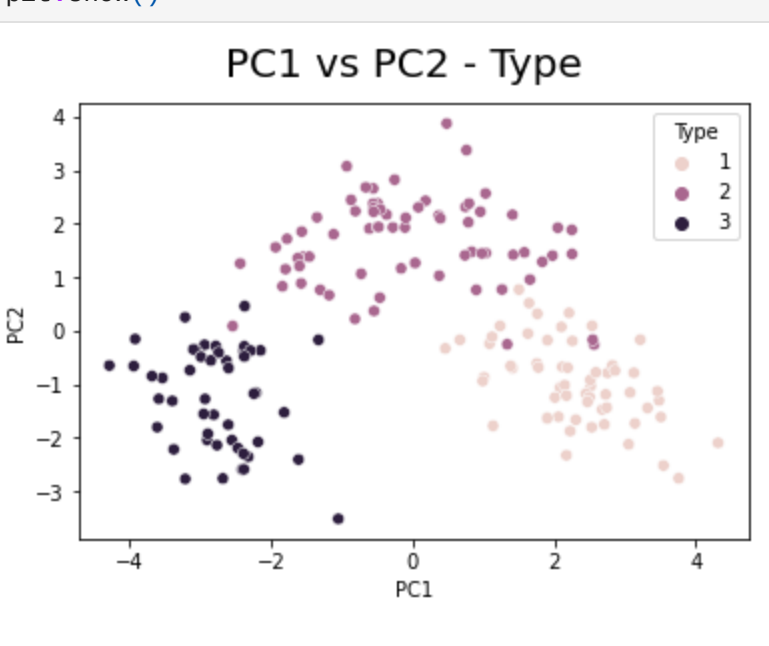
In [20]:
```
df_liquor['Type'].value_counts()
```

Out[20]:
```
2    71
1    59
3    48
Name: Type, dtype: int64
```

STEP 4 = Plot the Principal Components on 2D :

In [21]:
```
plt.suptitle('PC1 vs PC2 - Type', size = 20)

sns.scatterplot(data = df_liquor, x = 'PC1', y = 'PC2', hue = 'Type')
plt.show()
```



5. Clustering

Clustering a Data Frame with PC1, PC2 and PC3

(a) Hierarchical Clustering

STEP 1 = Data Pre-processing :

In [22]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

import warnings
warnings.filterwarnings('ignore')
```

In [23]:
```
liquor = pd.read_csv('wine.csv')
liquor.head()
```

Out[23]:

	Type	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proanthocyanins	Color	Hue	Dilution	Proline
0	1	14.23	1.71	2.43	15.6	127	2.80	3.06	0.28	2.29	5.64	1.04	3.92	1065
1	1	13.20	1.78	2.14	11.2	100	2.65	2.76	0.26	1.28	4.38	1.05	3.40	1050
2	1	13.16	2.36	2.67	18.6	101	2.80	3.24	0.30	2.81	5.68	1.03	3.17	1185
3	1	14.37	1.95	2.50	16.8	113	3.85	3.49	0.24	2.18	7.80	0.86	3.45	1480
4	1	13.24	2.59	2.87	21.0	118	2.80	2.69	0.39	1.82	4.32	1.04	2.93	735

In [24]:
```
liquor_x_1 = pd.DataFrame(pca_liquor[:, 0:3], columns = ['PC1','PC2', 'PC3'])
liquor_x_1
```

Out[24]:

	PC1	PC2	PC3
0	3.316751	-1.443463	-0.165739
1	2.209465	0.333393	-2.026457
2	2.516740	-1.031151	0.982819
3	3.757066	-2.756372	-0.176192
4	1.008908	-0.869831	2.026688
...	...	...	...
173	-3.370524	-2.216289	-0.342570
174	-2.601956	-1.757229	0.207581
175	-2.677839	-2.760899	-0.940942
176	-2.387017	-2.297347	-0.550696
177	-3.208758	-2.768920	1.013914

178 rows × 3 columns

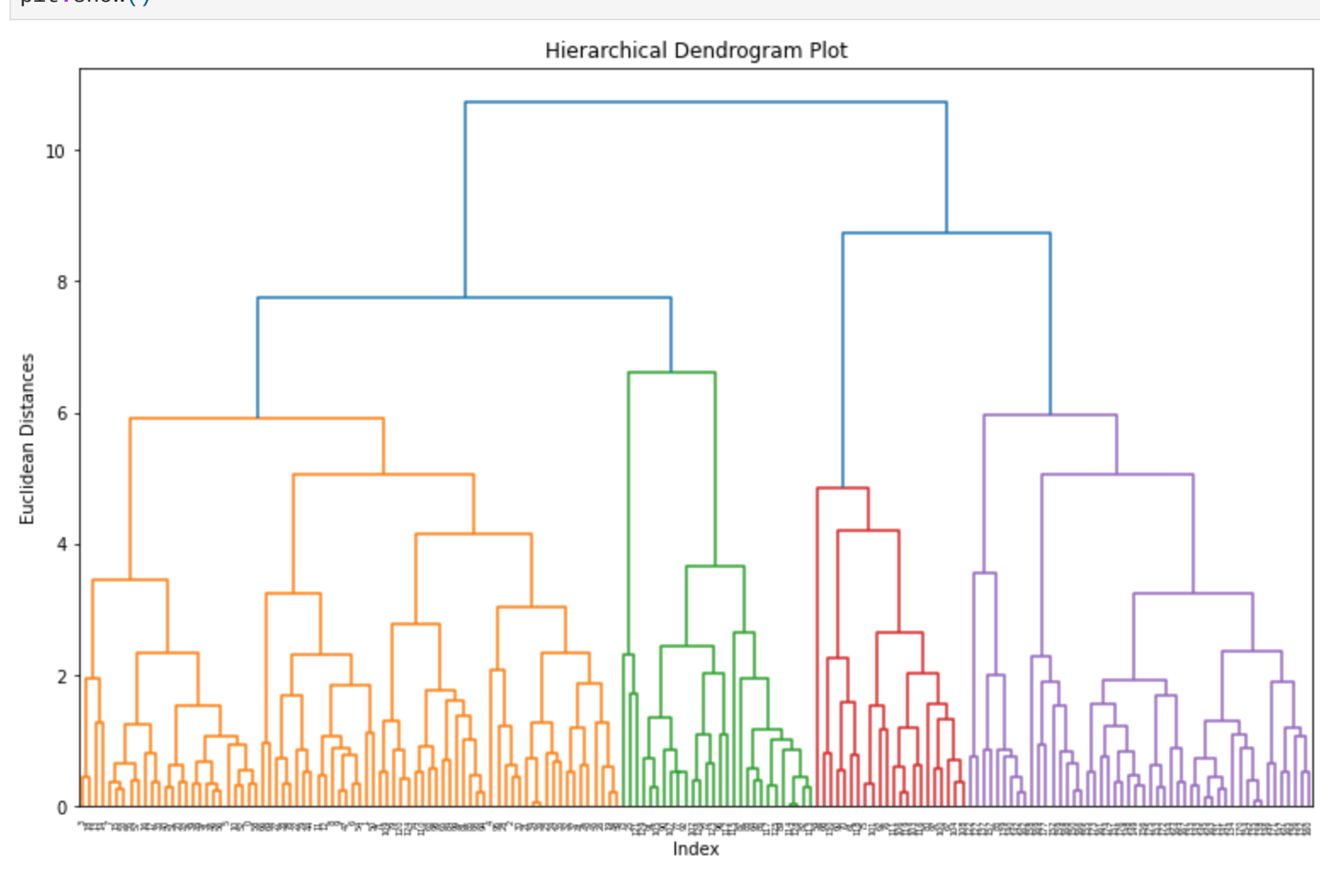
STEP 2 = Finding the optimal number of clusters using the Dendrogram :

In [25]:
```
from scipy.cluster.hierarchy import linkage
import scipy.cluster.hierarchy as sch
```

In [26]:
```
# create dendrogram
x = linkage(liquor_x_1, method = 'complete',metric = 'euclidean')

plt.figure(figsize = (13, 8))
plt.title('Hierarchical Dendrogram Plot')
plt.xlabel('Index')
plt.ylabel('Euclidean Distances')

sch.dendrogram(x)
plt.show()
```



STEP 3 = Training the hierarchical clustering model :

In [27]:
```
from sklearn.cluster import AgglomerativeClustering
```

In [28]:
```
hc = AgglomerativeClustering(n_clusters = 3, affinity = 'euclidean', linkage = 'ward')
hc
```

Out[28]:
```
AgglomerativeClustering(n_clusters=3)
```

In [29]:
```
x_hc = hc.fit_predict(liquor_x_1)
x_hc
```

Out[29]:
```
array([2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 0, 0, 0, 0, 0, 0, 0,
       2, 0, 0, 2, 0, 0, 0, 2, 0, 0, 0, 0, 2, 0, 0, 0, 0, 1, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 2, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 2, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1,
       1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1], dtype=int64)
```

In [30]:
```
add_Clusters = pd.DataFrame(x_hc, columns = ['Clusters_1'])
add_Clusters.head()
```

Out[30]:

	Clusters_1
0	2
1	2
2	2
3	2
4	2

In [31]:
```
liquor_x_1['Clusters_1'] = add_Clusters
liquor_x_1
```

Out[31]:

	PC1	PC2	PC3	Clusters_1
0	3.316751	-1.443463	-0.165739	2
1	2.209465	0.333393	-2.026457	2
2	2.516740	-1.031151	0.982819	2
3	3.757066	-2.756372	-0.176192	2
4	1.008908	-0.869831	2.026688	2
...	...	...	...	...
173	-3.370524	-2.216289	-0.342570	1
174	-2.601956	-1.757229	0.207581	1
175	-2.677839	-2.760899	-0.940942	1
176	-2.387017	-2.297347	-0.550696	1
177	-3.208758	-2.768920	1.013914	1

178 rows × 4 columns

STEP 4 = Clusters with Number of Records :

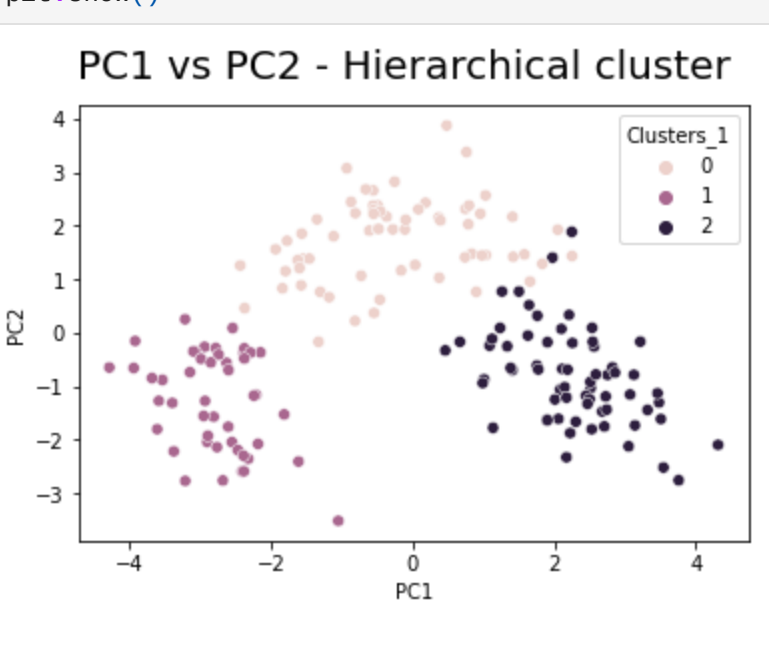
In [32]:
```
liquor_x_1['Clusters_1'].value_counts()
```

Out[32]:
```
0    66
2    65
1    47
Name: Clusters_1, dtype: int64
```

STEP 5 = Plot the Principal Components of Hierarchical in 2D :

In [33]:
```
plt.suptitle('PC1 vs PC2 - Hierarchical cluster', size = 20)

sns.scatterplot(data = liquor_x_1, x = 'PC1', y = 'PC2', hue = 'Clusters_1')
plt.show()
```



(b) K-MEANS

STEP 1 = Data Pre-processing :

In [34]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

import warnings
warnings.filterwarnings('ignore')
```

In [35]:
```
liquor = pd.read_csv('wine.csv')
liquor.head()
```

Out[35]:

	Type	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proanthocyanins	Color	Hue	Dilution	Proline
0	1	14.23	1.71	2.43	15.6	127	2.80	3.06	0.28	2.29	5.64	1.04	3.92	1065
1	1	13.20	1.78	2.14	11.2	100	2.65	2.76	0.26	1.28	4.38	1.05	3.40	1050
2	1	13.16	2.36	2.67	18.6	101	2.80	3.24	0.30	2.81	5.68	1.03	3.17	1185
3	1	14.37	1.95	2.50	16.8	113	3.85	3.49	0.24	2.18	7.80	0.86	3.45	1480
4	1	13.24	2.59	2.87	21.0	118	2.80	2.69	0.39	1.82	4.32	1.04	2.93	735

In [36]:
```
liquor_x_1 = pd.DataFrame(pca_liquor[:, 0:3], columns = ['PC1','PC2', 'PC3'])
liquor_x_1
```

Out[36]:

	PC1	PC2	PC3
0	3.316751	-1.443463	-0.165739
1	2.209465	0.333393	-2.026457
2	2.516740	-1.031151	0.982819
3	3.757066	-2.756372	-0.176192
4	1.008908	-0.869831	2.026688
...	...	...	...
173	-3.370524	-2.216289	-0.342570
174	-2.601956	-1.757229	0.207581
175	-2.677839	-2.760899	-0.940942
176	-2.387017	-2.297347	-0.550696
177	-3.208758	-2.768920	1.013914

178 rows × 3 columns

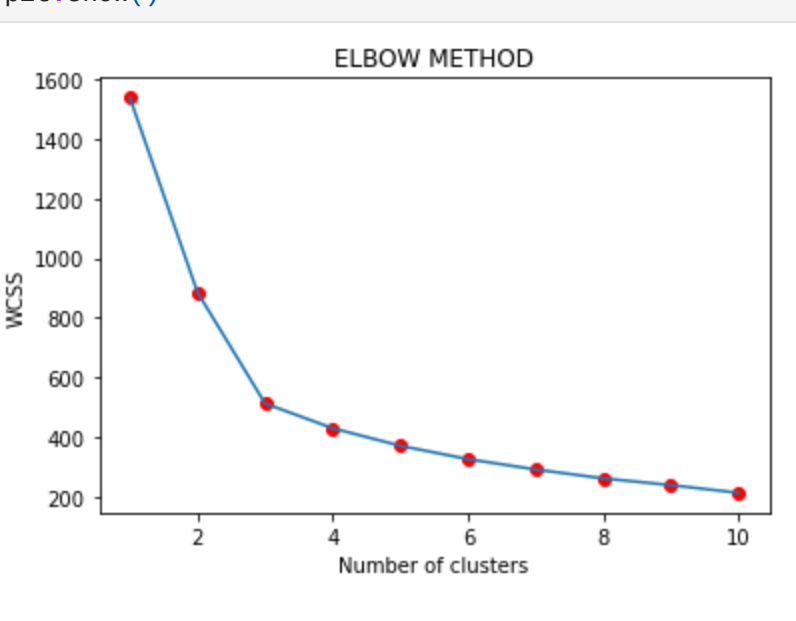
STEP 2 = Finding the optimal number of clusters using the Elbow Method :

In [37]:
```
from matplotlib import pyplot as plt
from sklearn.cluster import KMeans
```

In [38]:
```
wcss = []
for i in range(1, 11):
    kmeans = KMeans(n_clusters = i,random_state = 0)
    kmeans.fit(liquor_x_1)
    wcss.append(kmeans.inertia_)
wcss
```

Out[38]:
```
[1539.5034801883066,
 886.1611364823499,
 512.9995067661521,
 429.8030732473654,
 371.02394449456744,
 326.2768904959661,
 291.52701349085964,
 261.6843759885969,
 239.04461949060345,
 213.23994073321188]
```

In [39]:
```
plt.plot(range(1, 11), wcss)
plt.scatter(range(1, 11), wcss,color = 'red')
plt.title('ELBOW METHOD')
plt.xlabel('Number of clusters')
plt.ylabel('WCSS')
plt.show()
```



STEP 3 = Training the K - means clustering model :

In [40]:
```
km = KMeans(3, random_state = 42)
km.fit(liquor_x_1)
```

Out[40]:
```
KMeans(n_clusters=3, random_state=42)
```

In [41]:
```
km.labels_
```

Out[41]:
```
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 2, 0, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 1, 2, 2, 2, 2, 2, 2, 2, 2, 2, 0, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 1, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 0, 2, 2, 1, 2, 2, 2, 2, 2, 2, 2, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0])
```

In [42]:
```
liquor_x_1 = liquor_x_1.copy()
liquor_x_1['Clusters_2'] = km.labels_
liquor_x_1
```

Out[42]:

	PC1	PC2	PC3	Clusters_2
0	3.316751	-1.443463	-0.165739	1
1	2.209465	0.333393	-2.026457	1
2	2.516740	-1.031151	0.982819	1
3	3.757066	-2.756372	-0.176192	1
4	1.008908	-0.869831	2.026688	1
...	...	...	...	...
173	-3.370524	-2.216289	-0.342570	0
174	-2.601956	-1.757229	0.207581	0
175	-2.677839	-2.760899	-0.940942	0
176	-2.387017	-2.297347	-0.550696	0
177	-3.208758	-2.768920	1.013914	0

178 rows × 4 columns

STEP 4 = Clusters with Number of Records :

In [43]:
```
liquor_x_1['Clusters_2'].value_counts()
```

Out[43]:
```
2    65
1    62
0    51
Name: Clusters_2, dtype: int64
```

STEP 5 = Plot the Principal Components of KMEANS in 2D :¶

In [44]:
```
plt.suptitle('PC1 vs PC2 - K means clusters', size = 20)

sns.scatterplot(data = liquor_x_1, x = 'PC1', y = 'PC2', hue = 'Clusters_2')
plt.show()
```