PCA

Perform Principal component analysis and perform cluserting using first 3 principal component scores (both heirarchial and k mean cluserting(scree plot or elbow curve) and obtain optimum number of clusters and check whether we have obtained same number of clusters with the original data (class column we have ignored at the begining who shows it has 3 clusters)df

In [253]:
```
# Import Libraries
import pandas as pd
import numpy as np
from sklearn.decomposition import PCA
import matplotlib.pyplot as plt
from sklearn.preprocessing import scale
```

In [254]:
```
wine=pd.read_csv('wine.csv')
wine
```

Out[254]:

	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

In [255]:
```
print(wine.describe())
wine.head()
```

```
             Type     Alcohol       Malic         Ash  Alcalinity   Magnesium  \
count  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
std      0.775035    0.811827    1.117146    0.274344    3.339564   14.282484
min      1.000000   11.030000    0.740000    1.360000   10.600000   70.000000
25%      1.000000   12.362500    1.602500    2.210000   17.200000   88.000000
50%      2.000000   13.050000    1.865000    2.360000   19.500000   98.000000
75%      3.000000   13.677500    3.082500    2.557500   21.500000  107.000000
max      3.000000   14.830000    5.800000    3.230000   30.000000  162.000000

          Phenols  Flavanoids  Nonflavanoids  Proanthocyanins       Color  \
count  178.000000  178.000000     178.000000       178.000000  178.000000
mean     2.295112    2.029270       0.361854         1.590899    5.058090
std      0.625851    0.998859       0.124453         0.572359    2.318286
min      0.980000    0.340000       0.130000         0.410000    1.280000
25%      1.742500    1.205000       0.270000         1.250000    3.220000
50%      2.355000    2.135000       0.340000         1.555000    4.690000
75%      2.800000    2.875000       0.437500         1.950000    6.200000
max      3.880000    5.080000       0.660000         3.580000   13.000000

              Hue    Dilution      Proline
count  178.000000  178.000000   178.000000
mean     0.957449    2.611685   746.893258
std      0.228572    0.709990   314.907474
min      0.480000    1.270000   278.000000
25%      0.782500    1.937500   500.500000
50%      0.965000    2.780000   673.500000
75%      1.120000    3.170000   985.000000
max      1.710000    4.000000  1680.000000
```

Out[255]:

	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 [256]:
```
wine
```

Out[256]:

	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

In [257]:
```
wine['Type'].value_counts()
```

Out[257]:
```
2    71
1    59
3    48
Name: Type, dtype: int64
```

In [258]:
```
wine = wine.iloc[:,1:]
wine
```

Out[258]:

	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proanthocyanins	Color	Hue	Dilution	Proline
0	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	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	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	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	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	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	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	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	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	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 × 13 columns

In [259]:
```
wine.shape
```

Out[259]:
```
(178, 13)
```

In [260]:
```
wine.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 178 entries, 0 to 177
Data columns (total 13 columns):
 #   Column           Non-Null Count  Dtype  
---  ------           --------------  -----  
 0   Alcohol          178 non-null    float64
 1   Malic            178 non-null    float64
 2   Ash              178 non-null    float64
 3   Alcalinity       178 non-null    float64
 4   Magnesium        178 non-null    int64  
 5   Phenols          178 non-null    float64
 6   Flavanoids       178 non-null    float64
 7   Nonflavanoids    178 non-null    float64
 8   Proanthocyanins  178 non-null    float64
 9   Color            178 non-null    float64
 10  Hue              178 non-null    float64
 11  Dilution         178 non-null    float64
 12  Proline          178 non-null    int64  
dtypes: float64(11), int64(2)
memory usage: 18.2 KB
```

In [261]:
```
# Converting data to numpy array
wine_ary=wine.values
wine_ary
```

Out[261]:
```
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 [262]:
```
# Normalize the numerical data
wine_norm=scale(wine_ary)
wine_norm
```

Out[262]:
```
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]])
```

PCA Implementation

In [263]:
```
#Appling PCA fit transform to dataset
pca = PCA()
pca_values = pca.fit_transform(wine_norm)
pca_values
```

Out[263]:
```
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]])
```

In [264]:
```
# PCA Compoments matrix or convariance Matrix
pca.components_
```

Out[264]:
```
array([[ 0.1443294 , -0.24518758, -0.00205106, -0.23932041,  0.14199204,
         0.39466085,  0.4229343 , -0.2985331 ,  0.31342949, -0.0886167 ,
         0.29671456,  0.37616741,  0.28675223],
       [-0.48365155, -0.22493093, -0.31606881,  0.0105905 , -0.299634  ,
        -0.06503951,  0.00335981, -0.02877949, -0.03930172, -0.52999567,
         0.27923515,  0.16449619, -0.36490283],
       [-0.20738262,  0.08901289,  0.6262239 ,  0.61208035,  0.13075693,
         0.14617896,  0.1506819 ,  0.17036816,  0.14945431, -0.13730621,
         0.08522192,  0.16600459, -0.12674592],
       [-0.0178563 ,  0.53689028, -0.21417556,  0.06085941, -0.35179658,
         0.19806835,  0.15229479, -0.20330102,  0.39905653,  0.06592568,
        -0.42777141,  0.18412074, -0.23207086],
       [-0.26566365,  0.03521363, -0.14302547,  0.06610294,  0.72704851,
        -0.14931841, -0.10902584, -0.50070298,  0.13685982, -0.07643678,
        -0.17361452, -0.10116099, -0.1578688 ],
       [-0.21353865, -0.53681385, -0.15447466,  0.10082451, -0.03814394,
         0.0841223 ,  0.01892002,  0.25859401,  0.53379539,  0.41864414,
        -0.10598274, -0.26585107, -0.11972557],
       [-0.05639636,  0.42052391, -0.14917061, -0.28696914,  0.3228833 ,
        -0.02792498, -0.06068521,  0.59544729,  0.37213935, -0.22771214,
         0.23207564, -0.0447637 ,  0.0768045 ],
       [-0.39613926, -0.06582674,  0.17026002, -0.42797018,  0.15636143,
         0.40593409,  0.18724536,  0.23328465, -0.36822675,  0.03379692,
        -0.43662362,  0.07810789, -0.12002267],
       [ 0.50861912, -0.07528304, -0.30769445,  0.20044931,  0.27140257,
         0.28603452,  0.04957849,  0.19550132, -0.20914487,  0.05621752,
         0.08582839,  0.1372269 , -0.57578611],
       [ 0.21160473, -0.30907994, -0.02712539,  0.05279942,  0.06787022,
        -0.32013135, -0.16315051,  0.21553507,  0.1341839 , -0.29077518,
        -0.52239889,  0.52370587,  0.162116  ],
       [-0.22591696,  0.07648554, -0.49869142,  0.47931378,  0.07128891,
         0.30434119, -0.02569409,  0.11689586, -0.23736257,  0.0318388 ,
        -0.04821201,  0.0464233 ,  0.53926983],
       [-0.26628645,  0.12169604, -0.04962237, -0.05574287,  0.06222011,
        -0.30388245, -0.04289883,  0.04235219, -0.09555303,  0.60422163,
         0.259214  ,  0.60095872, -0.07940162],
       [ 0.01496997,  0.02596375, -0.14121803,  0.09168285,  0.05677422,
        -0.46390791,  0.83225706,  0.11403985, -0.11691707, -0.0119928 ,
        -0.08988884, -0.15671813,  0.01444734]])
```

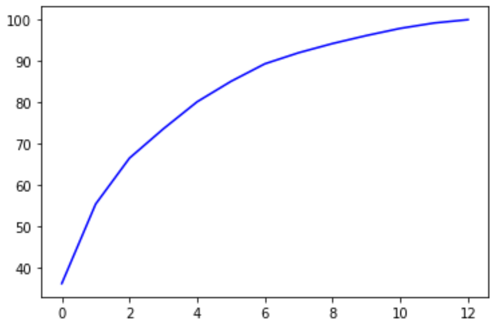
In [265]:
```
# The amount of variance that each PCA has
var = pca.explained_variance_ratio_
var
```

Out[265]:
```
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 [266]:
```
#Cummulative variance of each PCA
var = np.cumsum(np.round(var,decimals=4)*100)
var
```

Out[266]:
```
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 [267]:
```
plt.plot(var,color="blue");
```



In [268]:
```
wine=pd.read_csv('wine.csv')
wine
```

Out[268]:

	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

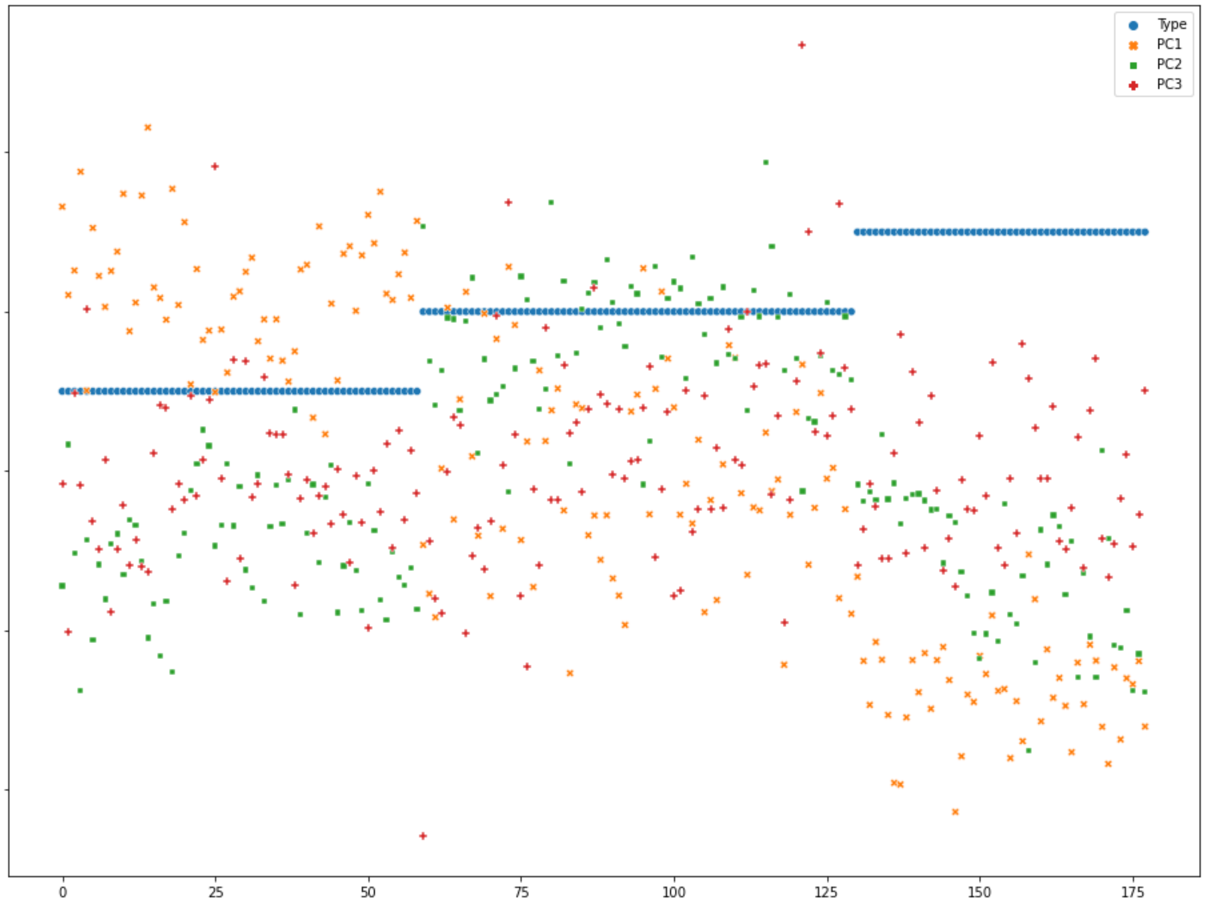
In [269]:
```
# Final DataFrame
final_df=pd.concat([wine['Type'],pd.DataFrame(pca_values[:,0:3],columns=['PC1','PC2','PC3'])],axis=1)
final_df
```

Out[269]:

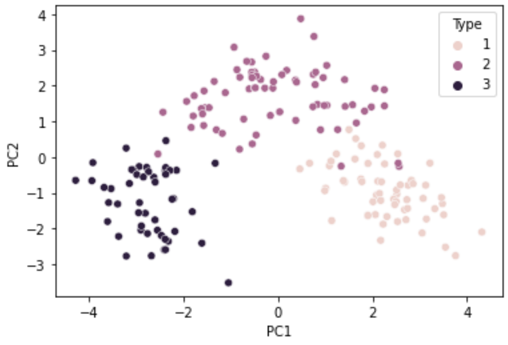
	Type	PC1	PC2	PC3
0	1	3.316751	-1.443463	-0.165739
1	1	2.209465	0.333393	-2.026457
2	1	2.516740	-1.031151	0.982819
3	1	3.757066	-2.756372	-0.176192
4	1	1.008908	-0.869831	2.026688
...	...	...	...	...
173	3	-3.370524	-2.216289	-0.342570
174	3	-2.601956	-1.757229	0.207581
175	3	-2.677839	-2.760899	-0.940942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

178 rows × 4 columns

In [270]:
```python
# Visualization of PCAs
import seaborn as sns
fig=plt.figure(figsize=(16,12))
sns.scatterplot(data=final_df);
```



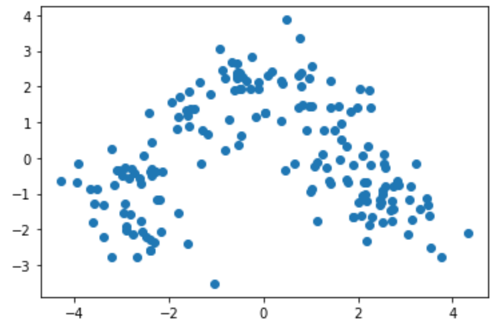
In [271]:
```python
sns.scatterplot(data=final_df,x='PC1',y='PC2',hue='Type');
```



In [272]:
```
pca_values[: ,0:1]
```

Out[272]:
```
array([[ 3.31675081],
       [ 2.20946492],
       [ 2.51674015],
       [ 3.75706561],
       [ 1.00890849],
       [ 3.05025392],
       [ 2.44908967],
       [ 2.05943687],
       [ 2.5108743 ],
       [ 2.75362819],
       [ 3.47973668],
       [ 1.7547529 ],
       [ 2.11346234],
       [ 3.45815682],
       [ 4.31278391],
       [ 2.3051882 ],
       [ 2.17195527],
       [ 1.89897118],
       [ 3.54198508],
```

In [234]:
```
x=pca_values[:,0:1]
y=pca_values[:,1:2]
plt.scatter(x,y);
```

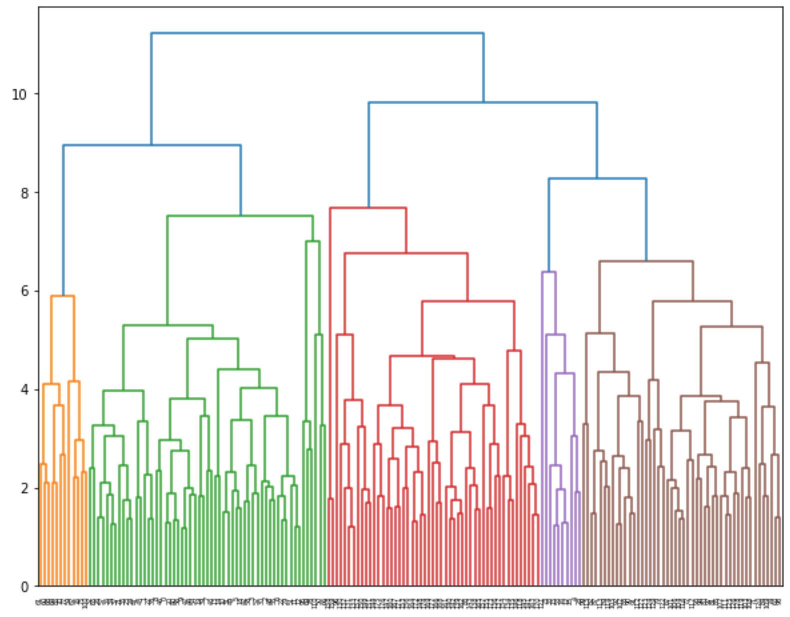


Checking with other clustering Algorithms

Hierarchical Clustering

In [273]:
```
import scipy.cluster.hierarchy as sch
from sklearn.cluster import AgglomerativeClustering
from sklearn.preprocessing import normalize
```

In [274]:
```
# As we already have normalized data,create Dendrograms
plt.figure(figsize=(10,8))
dendrogram=sch.dendrogram(sch.linkage(wine_norm,'complete'))
```



In [275]:
```
#Create Clusters
hclsters=AgglomerativeClustering(n_clusters=3,affinity='euclidean',linkage='ward')
hclsters
```

Out[275]:
```
AgglomerativeClustering(n_clusters=3)
```

In [276]:
```
y=pd.DataFrame(hclsters.fit_predict(wine_norm),columns=['clustersid'])
y['clustersid'].value_counts()
```

Out[276]:
```
2    64
0    58
1    56
Name: clustersid, dtype: int64
```

In [277]:
```
# Adding Clusertsid to dataset
wine2=wine.copy()
wine2['clustersid']=hclsters.labels_
wine2
```

Out[277]:

	Type	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proanthocyanins	Color	Hue	Dilution	Proline	clustersid
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	2
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
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	2
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	2
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	2
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
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	1
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	1
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	1
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	1
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	1

178 rows × 15 columns

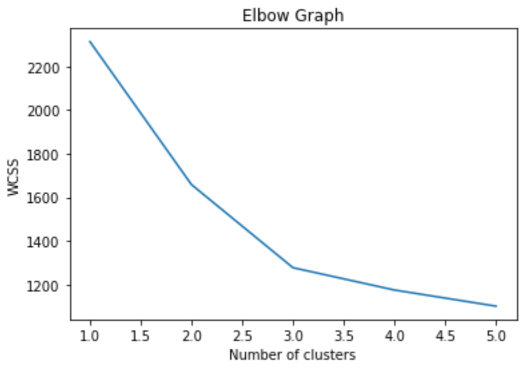
K - Means Clustering

In [278]:
```
from sklearn.cluster import KMeans
import warnings
warnings.filterwarnings('ignore')
```

In [279]:
```
# As we already have normalized data
# Use Elbow Graph tp find optimum number of clusters (K Value) from K values range.
# The K-Means algorithm aims to choose centroids that minimise the inertia, or within - cluster sum-of-square criterion WCSS
# Random state can be anything from 0 to 42,but same number to be used everytime, so that the result don't change
```

In [280]:
```
# within-cluster sum-of-squares criterion
wcss=[]
for i in range (1,6):
    kmeans=KMeans(n_clusters=i,random_state=2)
    kmeans.fit(wine_norm)
    wcss.append(kmeans.inertia_)
```

In [281]:
```
# Plot K values range vs WCSS to get Elbow graph for choosing K (no. of clusters)
plt.plot(range(1,6),wcss)
plt.title('Elbow Graph')
plt.xlabel('Number of clusters')
plt.ylabel('WCSS');
```



Build Cluster Algorithm using

K - 3

In [282]:
```
# Cluster Algorithm using K=3
Cluster3=KMeans(3,random_state=30).fit(wine_norm)
Cluster3
```

Out[282]:
```
KMeans(n_clusters=3, random_state=30)
```

In [283]:
```
Cluster3.labels_
```

Out[283]:
```
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, 0, 2, 2, 1, 2, 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 [284]:
```python
# Assign clusters to the dataset
wine3=wine.copy()
wine3['clusters3id']=Cluster3.labels_
wine3
```

Out[284]:

	Type	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proanthocyanins	Color	Hue	Dilution	Proline	clusters3id
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	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	1
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	1
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	1
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	1
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
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	0
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	0
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	0
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	0
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	0

178 rows × 15 columns

In [285]:
```python
wine3['clusters3id'].value_counts()
```

Out[285]:
```
2    65
1    62
0    51
Name: clusters3id, dtype: int64
```

In [ ]:
```python

```