In [4]:
```python
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.decomposition import PCA
from sklearn.preprocessing import scale
```

In [7]:
```python
# Import Dataset
wine=pd.read_csv('wine.csv')
wine
```

Out[7]:

	Type	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proar
0	1	14.23	1.71	2.43	15.6	127	2.80	3.06	0.28	
1	1	13.20	1.78	2.14	11.2	100	2.65	2.76	0.26	
2	1	13.16	2.36	2.67	18.6	101	2.80	3.24	0.30	
3	1	14.37	1.95	2.50	16.8	113	3.85	3.49	0.24	
4	1	13.24	2.59	2.87	21.0	118	2.80	2.69	0.39	
...	...	...	...	...	...	...	...	...	...	
173	3	13.71	5.65	2.45	20.5	95	1.68	0.61	0.52	
174	3	13.40	3.91	2.48	23.0	102	1.80	0.75	0.43	
175	3	13.27	4.28	2.26	20.0	120	1.59	0.69	0.43	
176	3	13.17	2.59	2.37	20.0	120	1.65	0.68	0.53	
177	3	14.13	4.10	2.74	24.5	96	2.05	0.76	0.56	

178 rows × 14 columns

In [9]:
```python
wine['Type'].value_counts()
```

Out[9]:
```
2    71
1    59
3    48
Name: Type, dtype: int64
```

In [10]:
```
wine2 = wine.iloc[:,1:]
wine2
```

Out[10]:

	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proanthocya
0	14.23	1.71	2.43	15.6	127	2.80	3.06	0.28	
1	13.20	1.78	2.14	11.2	100	2.65	2.76	0.26	
2	13.16	2.36	2.67	18.6	101	2.80	3.24	0.30	
3	14.37	1.95	2.50	16.8	113	3.85	3.49	0.24	
4	13.24	2.59	2.87	21.0	118	2.80	2.69	0.39	
...	...	...	...	...	...	...	...	...	
173	13.71	5.65	2.45	20.5	95	1.68	0.61	0.52	
174	13.40	3.91	2.48	23.0	102	1.80	0.75	0.43	
175	13.27	4.28	2.26	20.0	120	1.59	0.69	0.43	
176	13.17	2.59	2.37	20.0	120	1.65	0.68	0.53	
177	14.13	4.10	2.74	24.5	96	2.05	0.76	0.56	

178 rows × 13 columns

In [11]:
```
wine2.shape
```

Out[11]: (178, 13)

In [12]:
```
wine2.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 [13]:
```
# Converting data to numpy array
wine_ary=wine2.values
wine_ary
```

Out[13]:
```
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 [14]:
```
# Normalizing the numerical data
wine_norm=scale(wine_ary)
wine_norm
```

Out[14]:
```
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 [15]:
```python
# Applying PCA Fit Transform to dataset
pca=PCA(n_components=13)

wine_pca=pca.fit_transform(wine_norm)
wine_pca
```

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]])
```

In [16]:
```python
# PCA Components matrix or covariance Matrix
pca.components_
```

Out[16]:
```
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 [17]:
```python
# The amount of variance that each PCA has
var=pca.explained_variance_ratio_
var
```

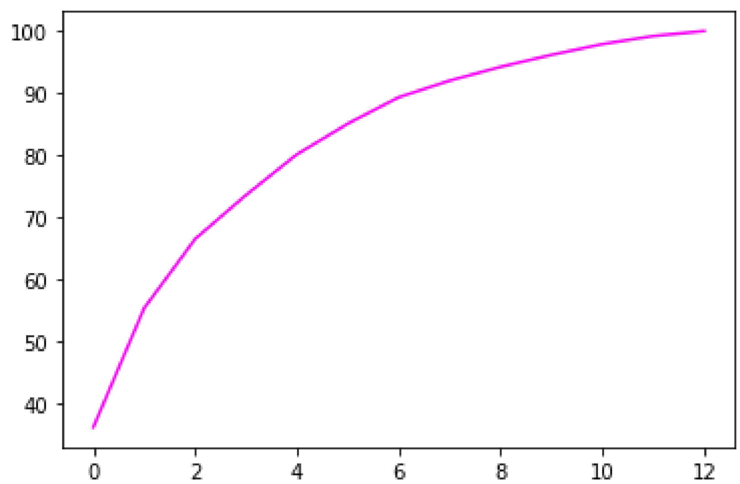
Out[17]:
```
array([0.36198848, 0.1920749 , 0.11123631, 0.0706903 , 0.06563294,
       0.04935823, 0.04238679, 0.02680749, 0.02222153, 0.01930019,
       0.01736836, 0.01298233, 0.00795215])
```

In [18]:
```python
# Cummulative variance of each PCA
var1=np.cumsum(np.round(var,4)*100)
var1
```

Out[18]:
```
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 [13]:
```python
# Variance plot for PCA components obtained
plt.plot(var1,color='magenta')
```

Out[13]:
```
[<matplotlib.lines.Line2D at 0x28af191f3d0>]
```



In [19]:
```python
# Final Dataframe
final_df=pd.concat([wine['Type'],pd.DataFrame(wine_pca[:,0:3],columns=['PC1','PC2
final_df
```

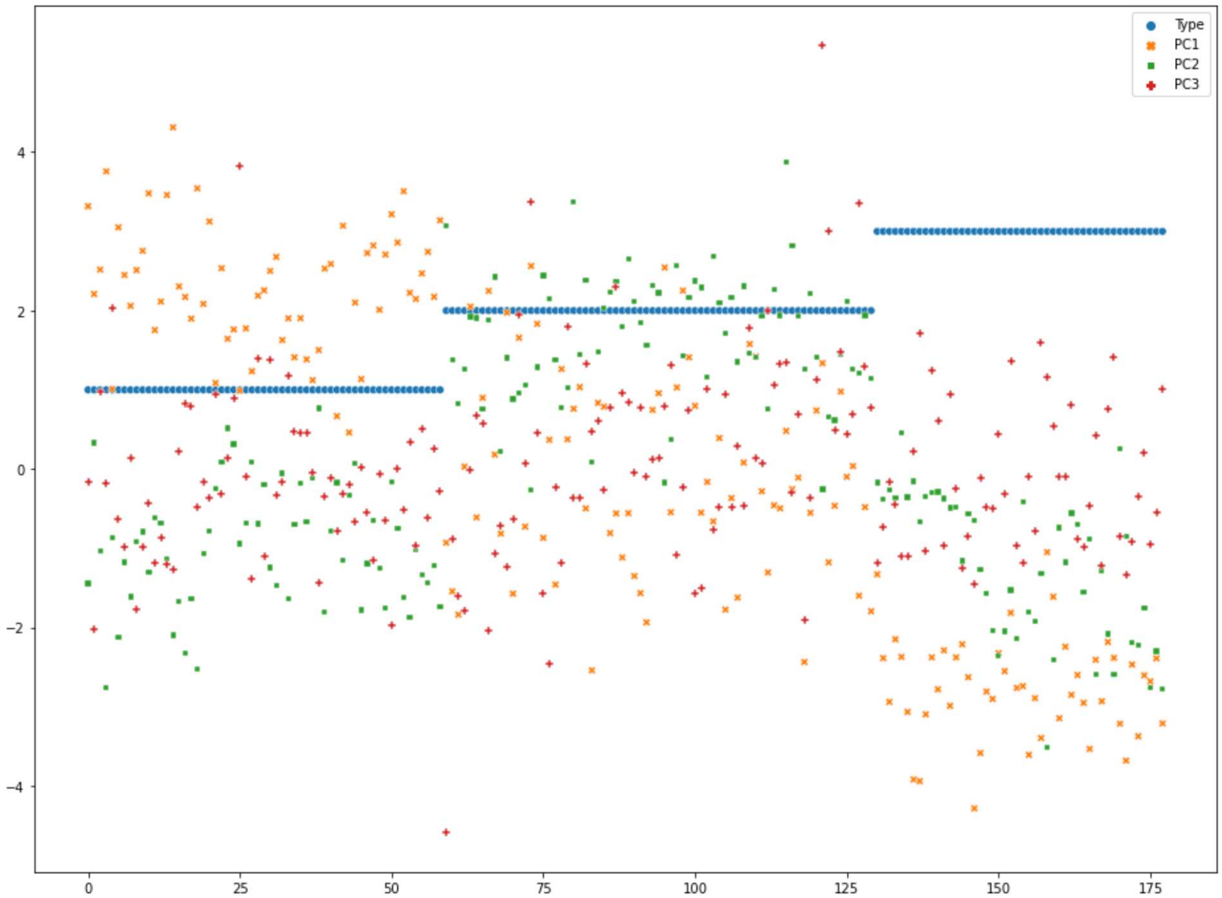
Out[19]:

	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 [20]:
```
# Visualization of PCAs
fig=plt.figure(figsize=(16,12))
sns.scatterplot(data=final_df)
```

Out[20]: <AxesSubplot:>

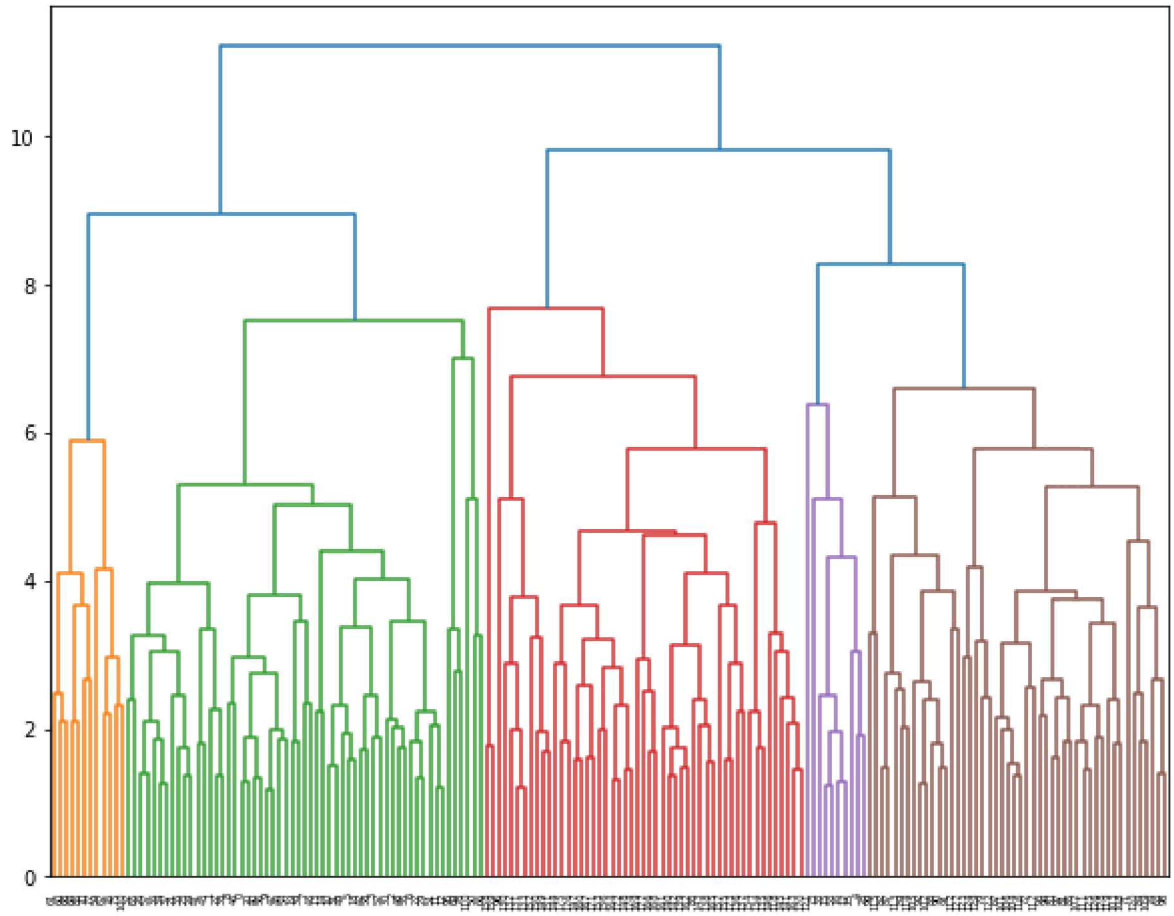


Checking with other Clustering Algorithms

1. Hierarchical Clustering

In [21]:
```
# Import Libraries
import scipy.cluster.hierarchy as sch
from sklearn.cluster import AgglomerativeClustering
from sklearn.preprocessing import normalize
```

In [22]:
```
# As we already have normalized data, create Dendrograms
plt.figure(figsize=(10,8))
dendrogram=sch.dendrogram(sch.linkage(wine_norm,'complete'))
```



In [23]:
```
# Create Clusters (y)
hclusters=AgglomerativeClustering(n_clusters=3,affinity='euclidean',linkage='warc
hclusters
```

Out[23]:
```
AgglomerativeClustering(n_clusters=3)
```

In [24]:
```
y=pd.DataFrame(hclusters.fit_predict(wine_norm),columns=['clustersid'])
y['clustersid'].value_counts()
```

Out[24]:
```
2    64
0    58
1    56
Name: clustersid, dtype: int64
```

In [25]:
```
# Adding clusters to dataset
wine3=wine.copy()
wine3['clustersid']=hclusters.labels_
wine3
```

Out[25]:

	Type	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proar
0	1	14.23	1.71	2.43	15.6	127	2.80	3.06	0.28	
1	1	13.20	1.78	2.14	11.2	100	2.65	2.76	0.26	
2	1	13.16	2.36	2.67	18.6	101	2.80	3.24	0.30	
3	1	14.37	1.95	2.50	16.8	113	3.85	3.49	0.24	
4	1	13.24	2.59	2.87	21.0	118	2.80	2.69	0.39	
...	...	...	...	...	...	...	...	...	...	
173	3	13.71	5.65	2.45	20.5	95	1.68	0.61	0.52	
174	3	13.40	3.91	2.48	23.0	102	1.80	0.75	0.43	
175	3	13.27	4.28	2.26	20.0	120	1.59	0.69	0.43	
176	3	13.17	2.59	2.37	20.0	120	1.65	0.68	0.53	
177	3	14.13	4.10	2.74	24.5	96	2.05	0.76	0.56	

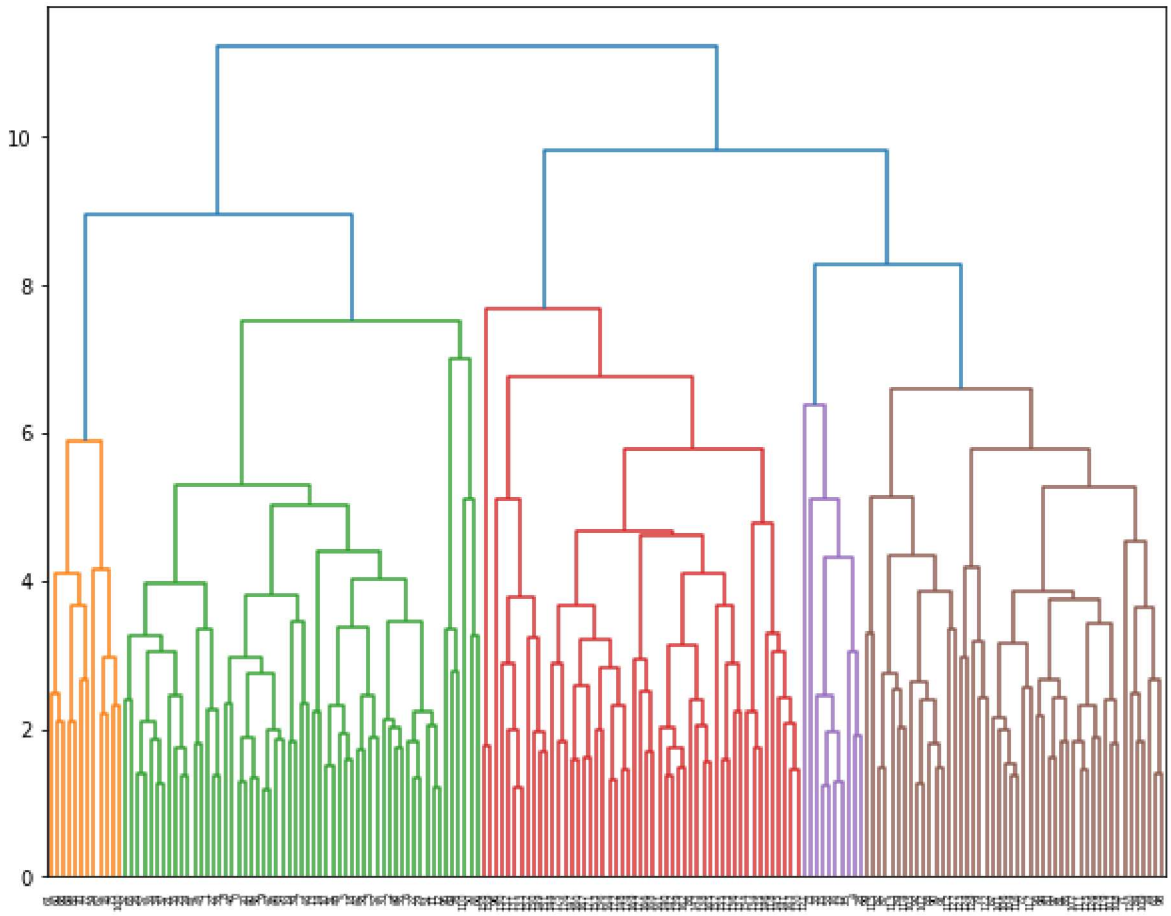
178 rows × 15 columns

In [27]:
```
import scipy.cluster.hierarchy as sch
from sklearn.cluster import AgglomerativeClustering
from sklearn.preprocessing import normalize
```

In [37]:
```
wine3_norm=scale(wine_ary)
wine3_norm
```

Out[37]:
```
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 [38]:
```
plt.figure(figsize=(10,8))
dendrogram=sch.dendrogram(sch.linkage(wine3_norm,'complete'))
```



2. K-Means Clustering

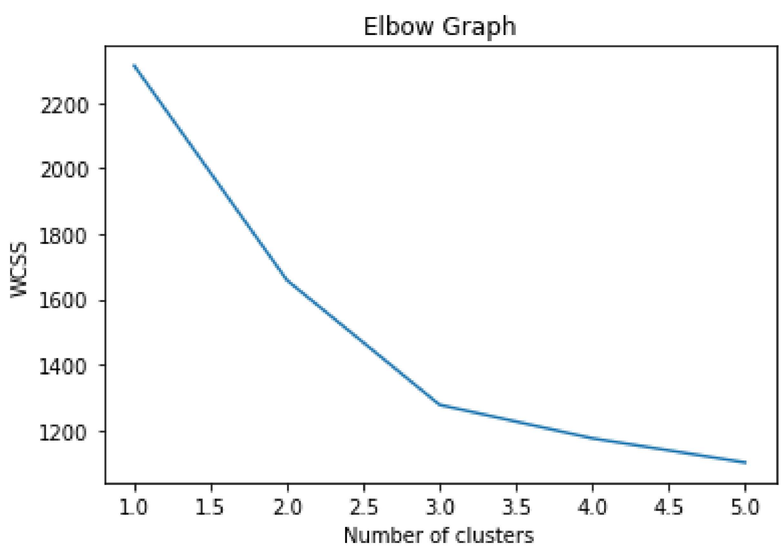
In [29]:
```
# Import Libraries
from sklearn.cluster import KMeans
```

In [30]:
```
# As we already have normalized data
# Use Elbow Graph to find optimum number of  clusters (K value) from K values rar
# The K-means algorithm aims to choose centroids that minimise the inertia, or wi
# random state can be anything from 0 to 42, but the same number to be used every
```

In [31]:
```
# 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_)
```

```
C:\ProgramData\Anaconda3\lib\site-packages\sklearn\cluster\_kmeans.py:881: User
Warning: KMeans is known to have a memory leak on Windows with MKL, when there
are less chunks than available threads. You can avoid it by setting the environ
ment variable OMP_NUM_THREADS=1.
  warnings.warn(
```

In [32]:
```
# 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')
plt.show()
```



Build Cluster algorithm using K=3

In [33]:
```
# Cluster algorithm using K=3
clusters3=KMeans(3,random_state=30).fit(wine_norm)
clusters3
```

Out[33]:
```
KMeans(n_clusters=3, random_state=30)
```

In [34]:
```
clusters3.labels_
```
Out[34]:
```
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 [35]:
```
# Assign clusters to the data set
wine4=wine.copy()
wine4['clusters3id']=clusters3.labels_
wine4
```
Out[35]:

	Type	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proar
0	1	14.23	1.71	2.43	15.6	127	2.80	3.06	0.28	
1	1	13.20	1.78	2.14	11.2	100	2.65	2.76	0.26	
2	1	13.16	2.36	2.67	18.6	101	2.80	3.24	0.30	
3	1	14.37	1.95	2.50	16.8	113	3.85	3.49	0.24	
4	1	13.24	2.59	2.87	21.0	118	2.80	2.69	0.39	
...	...	...	...	...	...	...	...	...	...	
173	3	13.71	5.65	2.45	20.5	95	1.68	0.61	0.52	
174	3	13.40	3.91	2.48	23.0	102	1.80	0.75	0.43	
175	3	13.27	4.28	2.26	20.0	120	1.59	0.69	0.43	
176	3	13.17	2.59	2.37	20.0	120	1.65	0.68	0.53	
177	3	14.13	4.10	2.74	24.5	96	2.05	0.76	0.56	

178 rows × 15 columns

In [36]:
```
wine4['clusters3id'].value_counts()
```
Out[36]:
```
2    65
1    62
0    51
Name: clusters3id, dtype: int64
```

In [ ]: