In [1]:
```
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 [2]:
```
wine = pd.read_csv('wine.csv')
wine
```

Out[2]:

	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 [3]:
```
wine['Type'].value_counts()
```

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

In [4]:
```
wine2 = wine.drop(['Type'], axis=1)
wine2
```

Out[4]:

	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 [5]:
```
wine2.shape
```

Out[5]:
```
(178, 13)
```

In [6]:
```
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: 18.1 KB
```

In [7]:
```
wine2.dtypes
```

Out[7]:
```
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
```

In [8]:
```
# converting data to numpy array
wine_ary = wine2.values
wine_ary
```

Out[8]:
```
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 [9]:
```
# Normalizing the numerical data
wine_norm=scale(wine_ary)
wine_norm
```

Out[9]:
```
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 [10]:
```
# Applying PCA Fit Transform to Dataset
pca = PCA(n_components=13)

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

Out[10]:
```
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 [11]:
```
pca.components_
```

Out[11]:
```
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]])
```

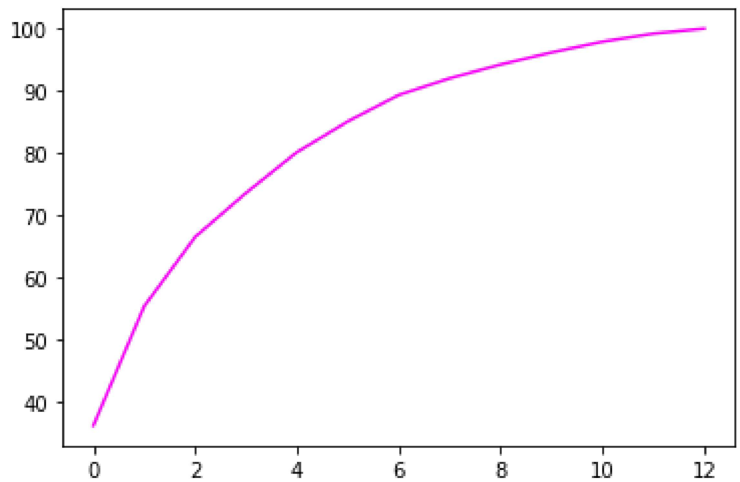
In [12]:
```
# The amount of variance that each PCA has
var=pca.explained_variance_ratio_
var
```

Out[12]:
```
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 [13]:
```
# Cummulative variance of each PCA
var1 = np.cumsum(np.round(var, 4)*100)
var1
```

Out[13]:
```
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 [14]:
```
plt.plot(var1, color='magenta')
plt.show()
```



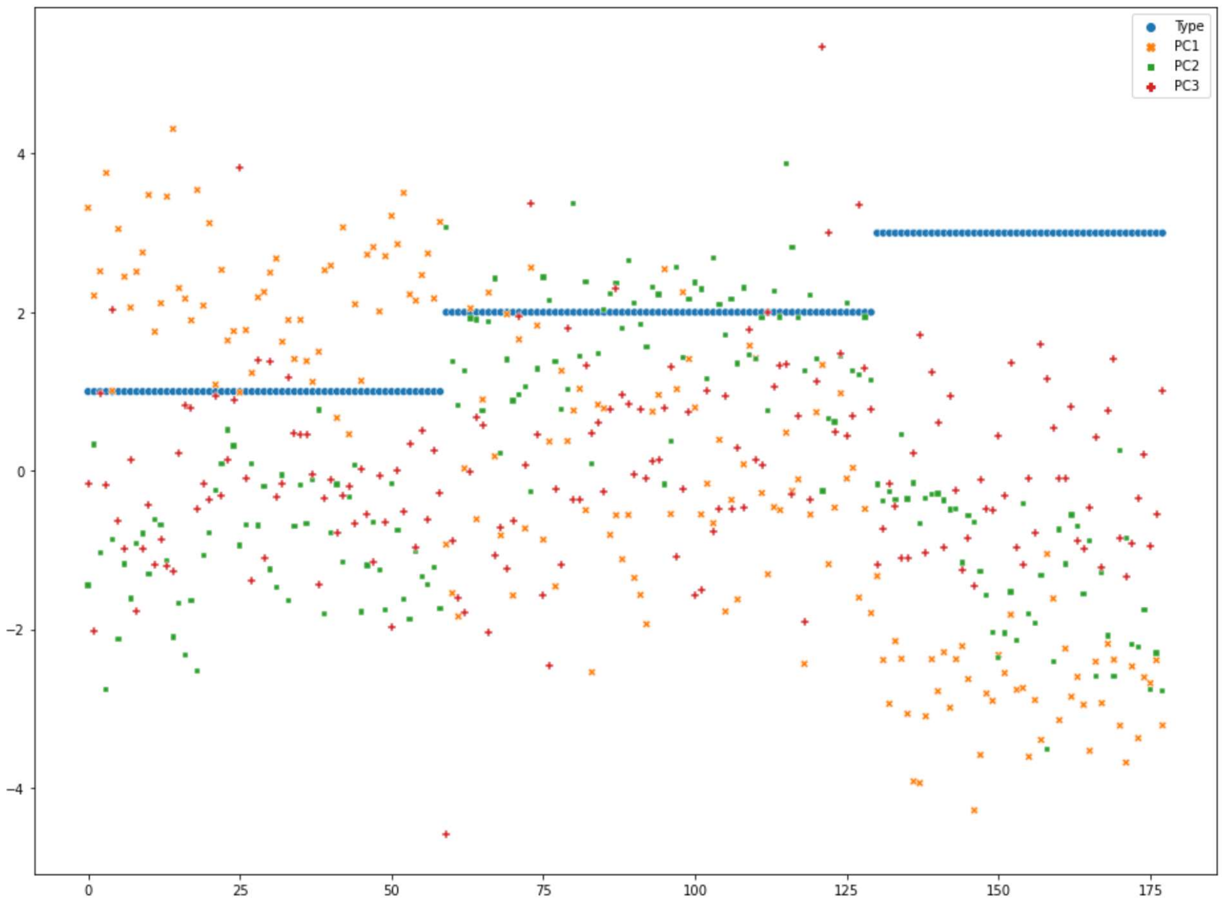
In [15]:
```
final_df=pd.concat([wine['Type'],pd.DataFrame(wine_pca[:,0:3], columns=['PC1', 'F
final_df
```

Out[15]:

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

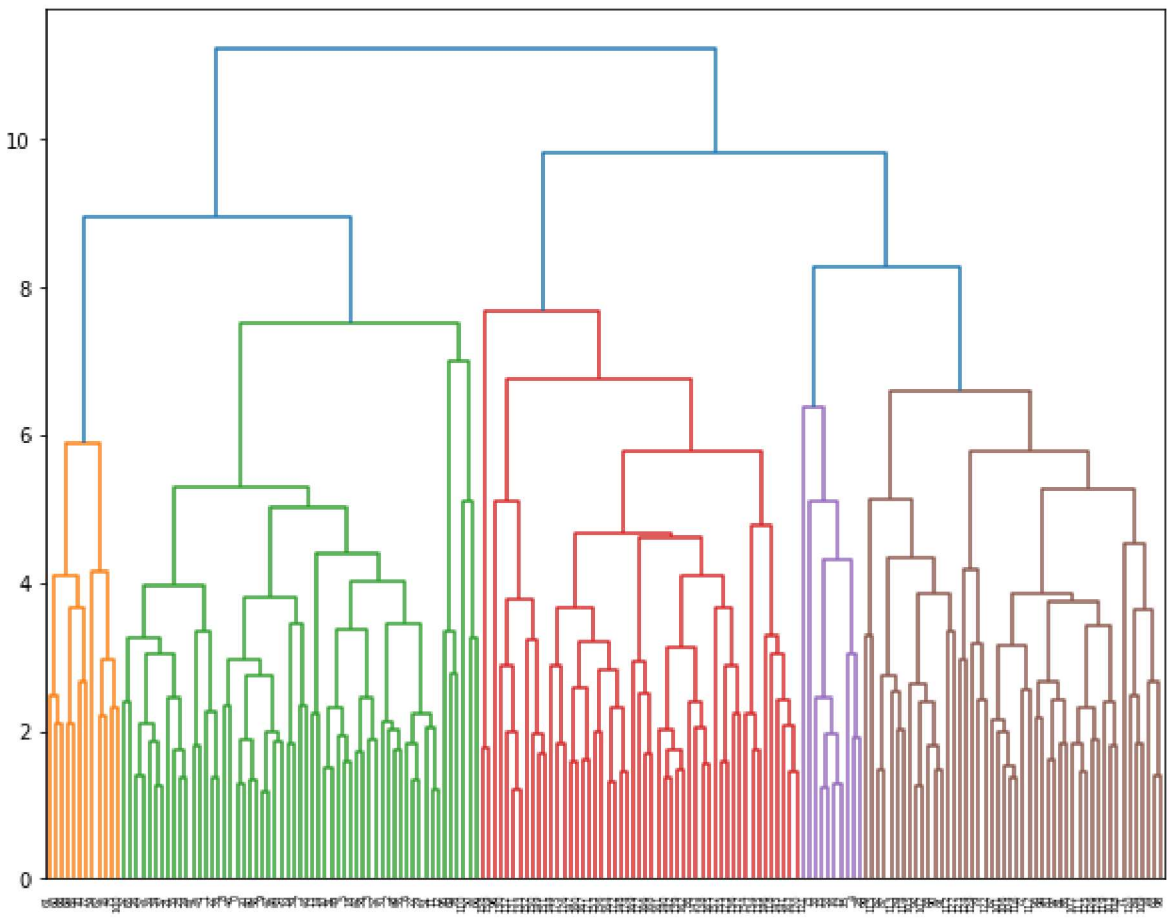


Checking with other Clustering Algorithms

1. Hierarchical Clustering

In [18]:
```
import scipy.cluster.hierarchy as sch
from sklearn.cluster import AgglomerativeClustering
from sklearn.preprocessing import normalize
```

In [19]:
```
plt.figure(figsize=(10,8))
dendrogram=sch.dendrogram(sch.linkage(wine_norm,'complete'))
```



In [20]:
```
hclusters=AgglomerativeClustering(n_clusters=3, affinity='euclidean', linkage='wa
hclusters
```

Out[20]:
```
AgglomerativeClustering(n_clusters=3)
```

In [21]:
```
y=pd.DataFrame(hclusters.fit_predict(wine_norm),columns=['clustersid'])
y['clustersid'].value_counts()
```

Out[21]:
```
2    64
0    58
1    56
Name: clustersid, dtype: int64
```

In [22]:
```
wine3=wine.copy()
wine3['clustersid']=hclusters.labels_
wine3
```

Out[22]:

	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	

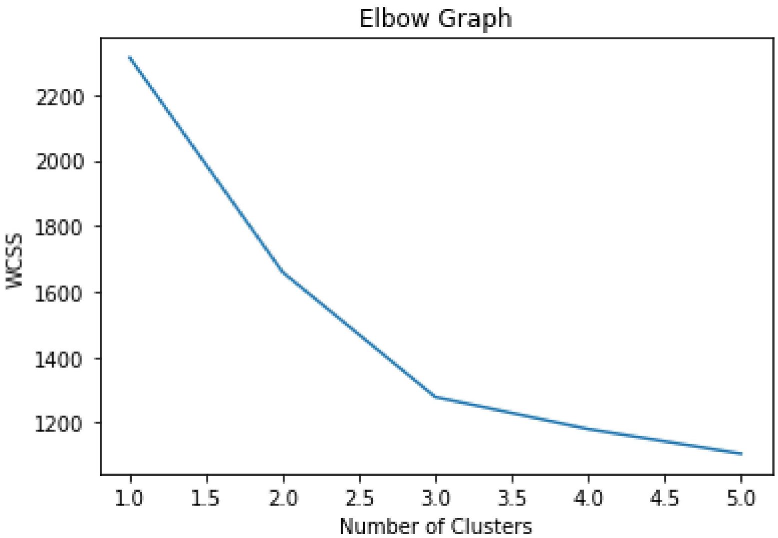
178 rows × 15 columns

2. K-Means Clustering

In [23]:
```
from sklearn.cluster import KMeans
```

In [24]:
```
wcss=[]
for i in range(1,6):
    kmeans=KMeans(n_clusters=i, random_state=2)
    kmeans.fit(wine_norm)
    wcss.append(kmeans.inertia_)
```

In [25]:
```
plt.plot(range(1,6), wcss)
plt.title('Elbow Graph')
plt.xlabel('Number of Clusters')
plt.ylabel('WCSS')
plt.show()
```



In [26]:
```
# Cluster algorithm using K=3
clusters3=KMeans(3, random_state=30).fit(wine_norm)
clusters3
```

Out[26]:
```
KMeans(n_clusters=3, random_state=30)
```

In [27]:
```
clusters3.labels_
```

Out[27]:
```
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, 1, 1, 0, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 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 [29]:
```
wine4=wine.copy()
wine4['clusters3id']=clusters3.labels_
wine4
```

Out[29]:

	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 [30]:
```
wine4['clusters3id'].value_counts()
```

Out[30]:
```
1    65
2    62
0    51
Name: clusters3id, dtype: int64
```

In [ ]: