In [1]:
```
# import libraries

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]:
```
# import Dataset

wine_data = pd.read_csv('wine.csv')
wine_data
```

Out[2]:

	Type	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proanthocyanins	Color	Hue	Dilution	Prol
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	10
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	10
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	11
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	14
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	7
...	...	...	...	...	...	...	...	...	...	...	...	...	...	
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	7
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	7
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	8
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	8
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	5

178 rows × 14 columns

In [3]:
```
wine_data['Type'].value_counts()
```

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

In [4]:
```
wine_data_1 = wine_data.iloc[:,1:]
wine_data_1
```

Out[4]:

	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 [5]:
```
wine_data_1.shape
```

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

In [6]:
```
1 wine_data_1.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 [9]:
```
1 wine_data_arr = wine_data_1.values # Converting data to numpy array
2 wine_data_arr
```

Out[9]:
```
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 [11]:
```
wine_data_norm = scale(wine_data_arr) # normalizing the numerical data
wine_data_norm
```

Out[11]:
```
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 [12]:

```
# Applying PCA Fit Transform to Dataset

pca = PCA(n_components=13)

wine_data_pca = pca.fit_transform(wine_data_norm)
wine_data_pca
```

Out[12]:

```
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 [13]:

```
# PCA components matrix or covariance matrix

pca.components_
```

Out[13]:

```
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 [14]:

```
# the amount of variance each PCA has

var = pca.explained_variance_ratio_
var
```

Out[14]:

```
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 [15]:

```
# cumulative variance of each PCA

var1 = np.cumsum(np.round(var,4)*100)
var1
```

Out[15]:

```
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])
```

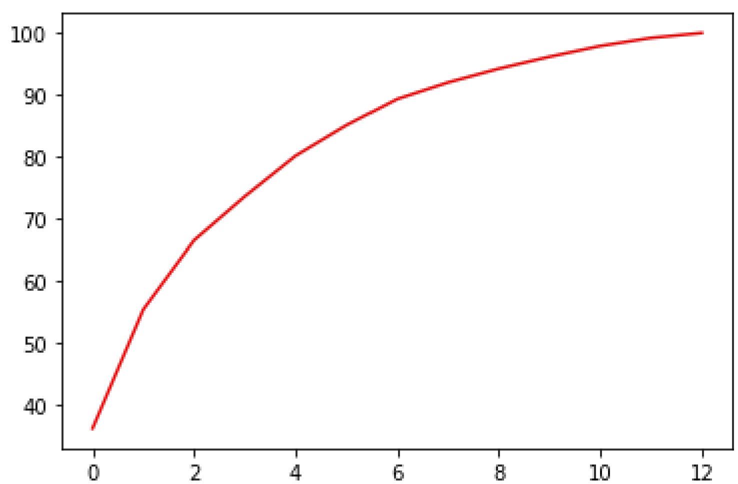
In [16]:

```
# Variance plot for PCA components obtained

plt.plot(var1,color='red')
```

Out[16]:

```
[<matplotlib.lines.Line2D at 0x202477b5eb0>]
```



In [17]:

```
# Final Dataframe

final_df = pd.concat([wine_data['Type'],pd.DataFrame(wine_data_pca[:,0:3],columns=['PC1','PC2','PC3'])],axi:
final_df
```

Out[17]:

	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 [18]:
```
# Visualizng the PCA

fig=plt.figure(figsize=(15,10))
sns.scatterplot(data=final_df)
```

Out[18]: <AxesSubplot:>

Checking with Other Clustering Algorithms

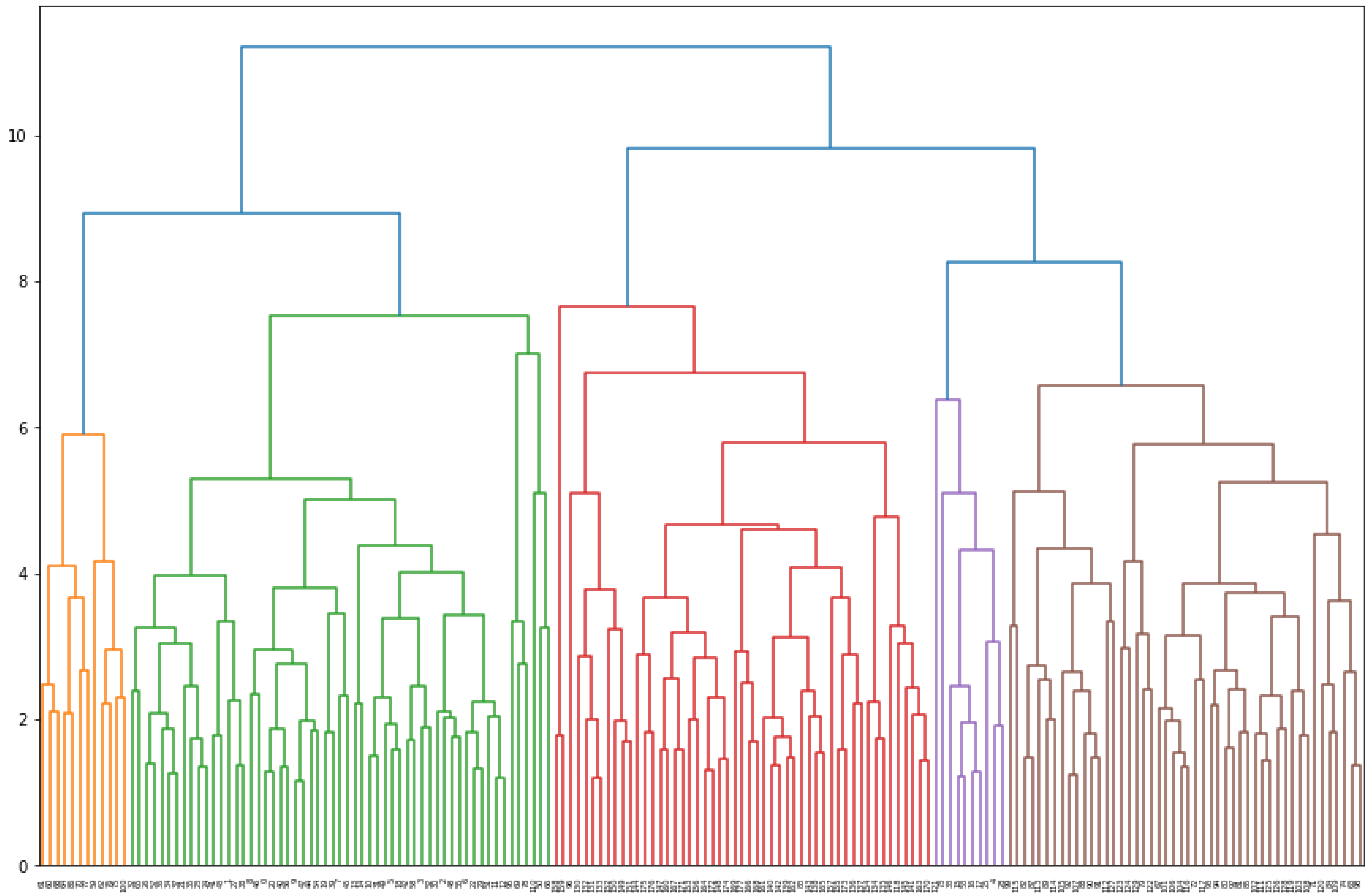
1) hierarchical clustering

In [27]:
```
import scipy.cluster.hierarchy as sch
from scipy.cluster.hierarchy import dendrogram, linkage
from sklearn.cluster import AgglomerativeClustering
```

In [30]:

```
# creating dendogram with normalized data

plt.figure(figsize=(15,10))
dendr0gram = sch.dendrogram(sch.linkage(wine_data_norm,'complete'))
```



In [31]:
```
# cluster creation (y)

hclusters=AgglomerativeClustering(n_clusters=3,affinity='euclidean',linkage='ward')
hclusters
```

Out[31]:
```
AgglomerativeClustering(n_clusters=3)
```

In [32]:
```
y=pd.DataFrame(hclusters.fit_predict(wine_data_norm),columns=['clustersid'])
y['clustersid'].value_counts()
```

Out[32]:
```
2    64
0    58
1    56
Name: clustersid, dtype: int64
```

In [33]:
```
# Adding clusters to dataset
wine_data_2=wine_data.copy()
wine_data_2['clustersid']=hclusters.labels_
wine_data_2
```

Out[33]:

	Type	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proanthocyanins	Color	Hue	Dilution	Prol
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	10
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	10
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	11
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	14
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	7
...	...	...	...	...	...	...	...	...	...	...	...	...	...	
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	7
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	7
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	8
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	8
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	5

178 rows × 15 columns

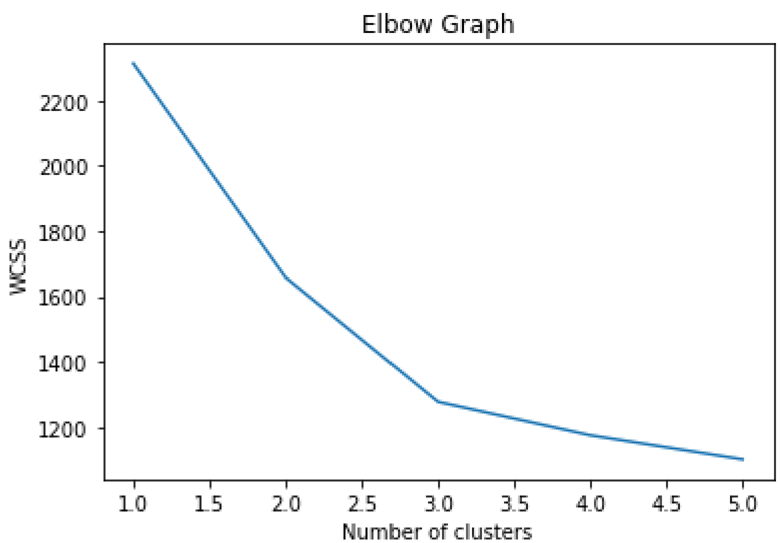
2) K-Means Clustering

In [36]:
```
# Import Libraries
from sklearn.cluster import KMeans

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

In [37]:
```
# within-cluster sum-of-squares criterion
wcss=[]
for i in range (1,6):
    kmeans=KMeans(n_clusters=i,random_state=2)
    kmeans.fit(wine_data_norm)
    wcss.append(kmeans.inertia_)
```

In [38]:
```
# 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 custer algorithm using k=3

In [39]:
```
# Cluster algorithm using K=3
clusters3=KMeans(3,random_state=30).fit(wine_data_norm)
clusters3
```

Out[39]:
```
KMeans(n_clusters=3, random_state=30)
```

In [40]:

```
clusters3.labels_
```

Out[40]:

```
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 [41]:

```
# Assign clusters to the data set
wine_data_3=wine_data.copy()
wine_data_3['clusters3id']=clusters3.labels_
wine_data_3
```

Out[41]:

	Type	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proanthocyanins	Color	Hue	Dilution	Prol
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	10
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	10
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	11
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	14
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	7
...	...	...	...	...	...	...	...	...	...	...	...	...	...	
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	7
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	7
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	8
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	8
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	5

178 rows × 15 columns

In [42]:
```
wine_data_3['clusters3id'].value_counts()
```

Out[42]:
```
2    65
1    62
0    51
Name: clusters3id, dtype: int64
```

In [ ]:
```

```