In [1]:
```python
import numpy as np
import pandas as pd
from matplotlib import pyplot as plt
from sklearn.cluster import KMeans
from sklearn.preprocessing import StandardScaler
from sklearn import preprocessing
import seaborn as sns
from sklearn.decomposition import PCA
import scipy.cluster.hierarchy as sch
from sklearn.cluster import AgglomerativeClustering
from scipy.cluster.hierarchy import linkage
```

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

In [3]:
```python
df1 = df.iloc[:, 1:]
```

In [4]:
```python
df1.head()
```

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

In [5]:
```python
df1.describe()
```

Out[5]:

	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
mean	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	0.811827	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	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%	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%	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%	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	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

Correlation

In [6]:
```python
cor = df1.corr()
```

In [7]:
```python
cor.style.background_gradient(cmap='coolwarm')
```

Out[7]:

	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proanthocyanins	Color	Hue	Dilution	Proline
Alcohol	1.000000	0.094397	0.211545	-0.310235	0.270798	0.289101	0.236815	-0.155929	0.136698	0.546364	-0.071747	0.072343	0.643720
Malic	0.094397	1.000000	0.164045	0.288500	-0.054575	-0.335167	-0.411007	0.292977	-0.220746	0.248985	-0.561296	-0.368710	-0.192011
Ash	0.211545	0.164045	1.000000	0.443367	0.286587	0.128980	0.115077	0.186230	0.009652	0.258887	-0.074667	0.003911	0.223626
Alcalinity	-0.310235	0.288500	0.443367	1.000000	-0.083333	-0.321113	-0.351370	0.361922	-0.197327	0.018732	-0.273955	-0.276769	-0.440597
Magnesium	0.270798	-0.054575	0.286587	-0.083333	1.000000	0.214401	0.195784	-0.256294	0.236441	0.199950	0.055398	0.066004	0.393351
Phenols	0.289101	-0.335167	0.128980	-0.321113	0.214401	1.000000	0.864564	-0.449935	0.612413	-0.055136	0.433681	0.699949	0.498115
Flavanoids	0.236815	-0.411007	0.115077	-0.351370	0.195784	0.864564	1.000000	-0.537900	0.652692	-0.172379	0.543479	0.787194	0.494193
Nonflavanoids	-0.155929	0.292977	0.186230	0.361922	-0.256294	-0.449935	-0.537900	1.000000	-0.365845	0.139057	-0.262640	-0.503270	-0.311385
Proanthocyanins	0.136698	-0.220746	0.009652	-0.197327	0.236441	0.612413	0.652692	-0.365845	1.000000	-0.025250	0.295544	0.519067	0.330417
Color	0.546364	0.248985	0.258887	0.018732	0.199950	-0.055136	-0.172379	0.139057	-0.025250	1.000000	-0.521813	-0.428815	0.316100
Hue	-0.071747	-0.561296	-0.074667	-0.273955	0.055398	0.433681	0.543479	-0.262640	0.295544	-0.521813	1.000000	0.565468	0.236183
Dilution	0.072343	-0.368710	0.003911	-0.276769	0.066004	0.699949	0.787194	-0.503270	0.519067	-0.428815	0.565468	1.000000	0.312761
Proline	0.643720	-0.192011	0.223626	-0.440597	0.393351	0.498115	0.494193	-0.311385	0.330417	0.316100	0.236183	0.312761	1.000000

There are some quite correlation between variables. For example the correlation between flavanoids and dilution is pretty high (78%). Thus we can remove that variable from our dataset. However this method is long and tedious. Hence we PCA method for Dimensionality Reduction

Dimensionality Reduction with PCA

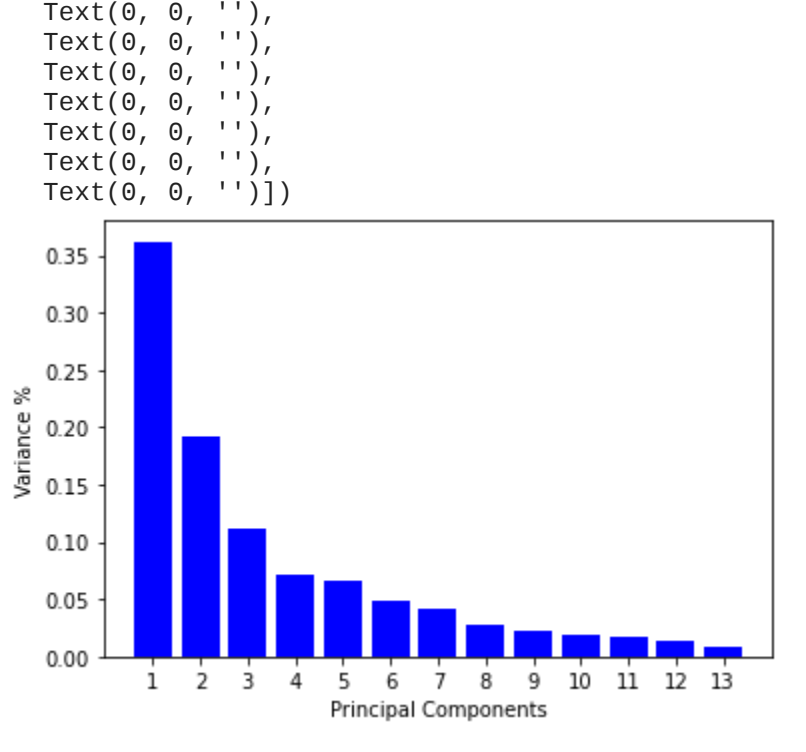
In [8]:
```python
# normalizing the data
df_norm = StandardScaler().fit_transform(df1)
```

In [9]:
```python
pca = PCA(n_components=13)
```

In [10]:
```python
principalComponents = pca.fit_transform(df_norm)
```

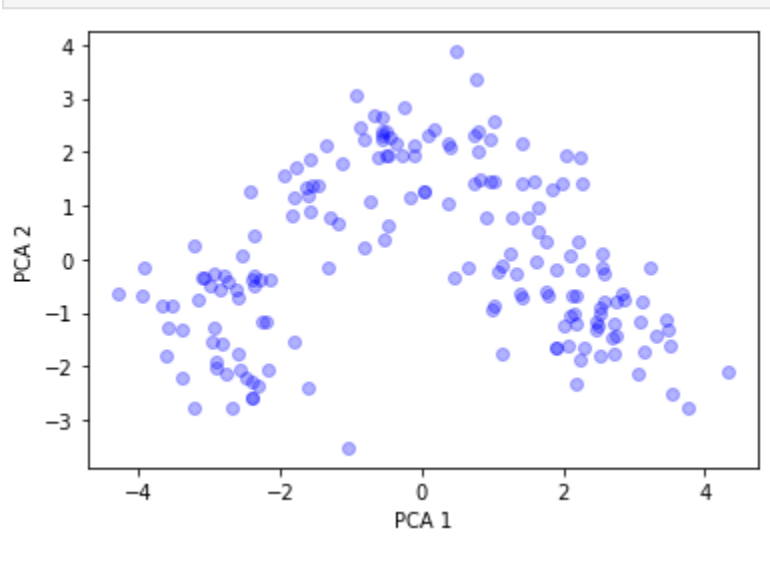
In [11]:
```python
PC = range(1, pca.n_components_+1)
plt.bar(PC, pca.explained_variance_ratio_, color='blue')
plt.xlabel('Principal Components')
plt.ylabel('Variance %')
plt.xticks(PC)
```

Out[11]:
```
([<matplotlib.axis.XTick at 0x1ed9ab34220>,
  <matplotlib.axis.XTick at 0x1ed9ab341f0>,
  <matplotlib.axis.XTick at 0x1ed9a863160>,
  <matplotlib.axis.XTick at 0x1ed9ab70f10>,
  <matplotlib.axis.XTick at 0x1ed9ab82460>,
  <matplotlib.axis.XTick at 0x1ed9ab82970>,
  <matplotlib.axis.XTick at 0x1ed9ab82e80>,
  <matplotlib.axis.XTick at 0x1ed9ab843d0>,
  <matplotlib.axis.XTick at 0x1ed9ab848e0>,
  <matplotlib.axis.XTick at 0x1ed9ab84df0>,
  <matplotlib.axis.XTick at 0x1ed9ab89340>,
  <matplotlib.axis.XTick at 0x1ed9ab89850>,
  <matplotlib.axis.XTick at 0x1ed9ab84460>],
 [Text(0, 0, ''),
  Text(0, 0, ''),
  Text(0, 0, ''),
  Text(0, 0, ''),
  Text(0, 0, ''),
  Text(0, 0, ''),
  Text(0, 0, ''),
  Text(0, 0, ''),
  Text(0, 0, ''),
  Text(0, 0, ''),
  Text(0, 0, ''),
  Text(0, 0, ''),
  Text(0, 0, '')])
```



In [12]:
```python
PCA_components = pd.DataFrame(principalComponents)
```

In [13]:
```python
plt.scatter(PCA_components[0], PCA_components[1], alpha=.3, color='blue')
plt.xlabel('PCA 1')
plt.ylabel('PCA 2')
plt.show()
```



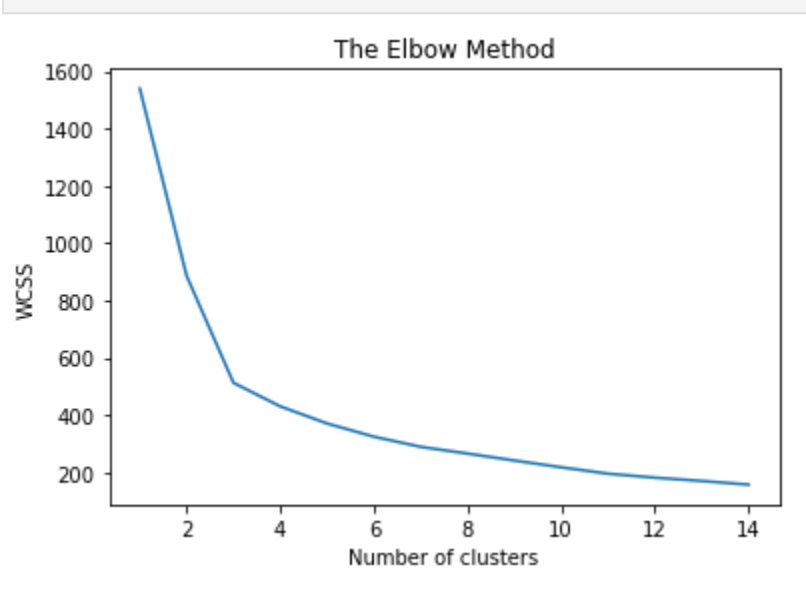
As shown in the bar graph, the most of varianve is put in the first 2 components. Since there is not much variance present from 3rd component, lets just the first 2 componets in our analysis. The scatter plot given an indication that there may be 3 clusters present

Finding out the optimal number of clusters

In [14]:
```python
wcss = []
```

In [15]:
```python
for i in range(1, 15):
    kmeans = KMeans(n_clusters = i, init = 'k-means++', random_state = 42)
    kmeans.fit(PCA_components.iloc[:,:3])
    wcss.append(kmeans.inertia_)
```

In [16]:
```python
plt.plot(range(1, 15), wcss)
plt.title('The Elbow Method')
plt.xlabel('Number of clusters')
plt.ylabel('WCSS')
plt.show()
```



The scree plot levels off at k=3 and let's use it to determine the clusters

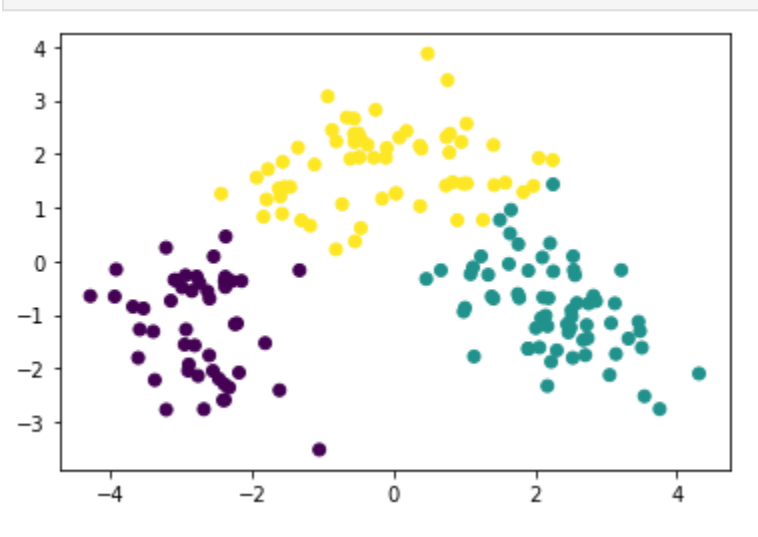
K clusters

In [18]:
```python
model = KMeans(n_clusters=3)
model.fit(PCA_components.iloc[:,:2])
```

Out[18]: KMeans(n_clusters=3)

In [19]:
```python
labels = model.predict(PCA_components.iloc[:,:2])
```

In [20]:
```python
plt.scatter(PCA_components[0], PCA_components[1], c=labels)
plt.show()
```



In [21]:
```python
k_new_df=pd.DataFrame(principalComponents[:,0:2])
```

In [23]:
```python
model_k = KMeans(n_clusters=3)
model_k.fit(k_new_df)
```

Out[23]: KMeans(n_clusters=3)

In [24]:
```python
model_k.labels_
```

Out[24]:
```
array([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, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 0, 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, 0, 1, 1, 1, 1, 1, 1, 1, 1, 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])
```

In [25]:
```python
md=pd.Series(model_k.labels_)
```

In [26]:
```python
df1['clust']=md
```

In [27]:
```python
k_new_df.head()
```

Out[27]:

	0	1
0	3.316751	-1.443463
1	2.209465	0.333393
2	2.516740	-1.031151
3	3.757066	-2.756372
4	1.008908	-0.869831

In [28]:
```python
df1.groupby(df1.clust).mean()
```

Out[28]:

clust	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proanthocyanins	Color	Hue	Dilution	Proline
0	13.659219	1.975781	2.463750	17.596875	107.312500	2.859688	3.012656	0.290000	1.921719	5.406250	1.069688	3.157188	1082.562500
1	12.238308	1.931385	2.219385	19.898462	92.830769	2.204308	1.989231	0.365538	1.587692	2.992615	1.051631	2.769231	506.353846
2	13.151633	3.344490	2.434694	21.438776	99.020408	1.678163	0.797959	0.450816	1.163061	7.343265	0.685918	1.690204	627.551020

H clusters

In [29]:
```python
model2 = AgglomerativeClustering(n_clusters=3, affinity='euclidean', linkage='ward')
```

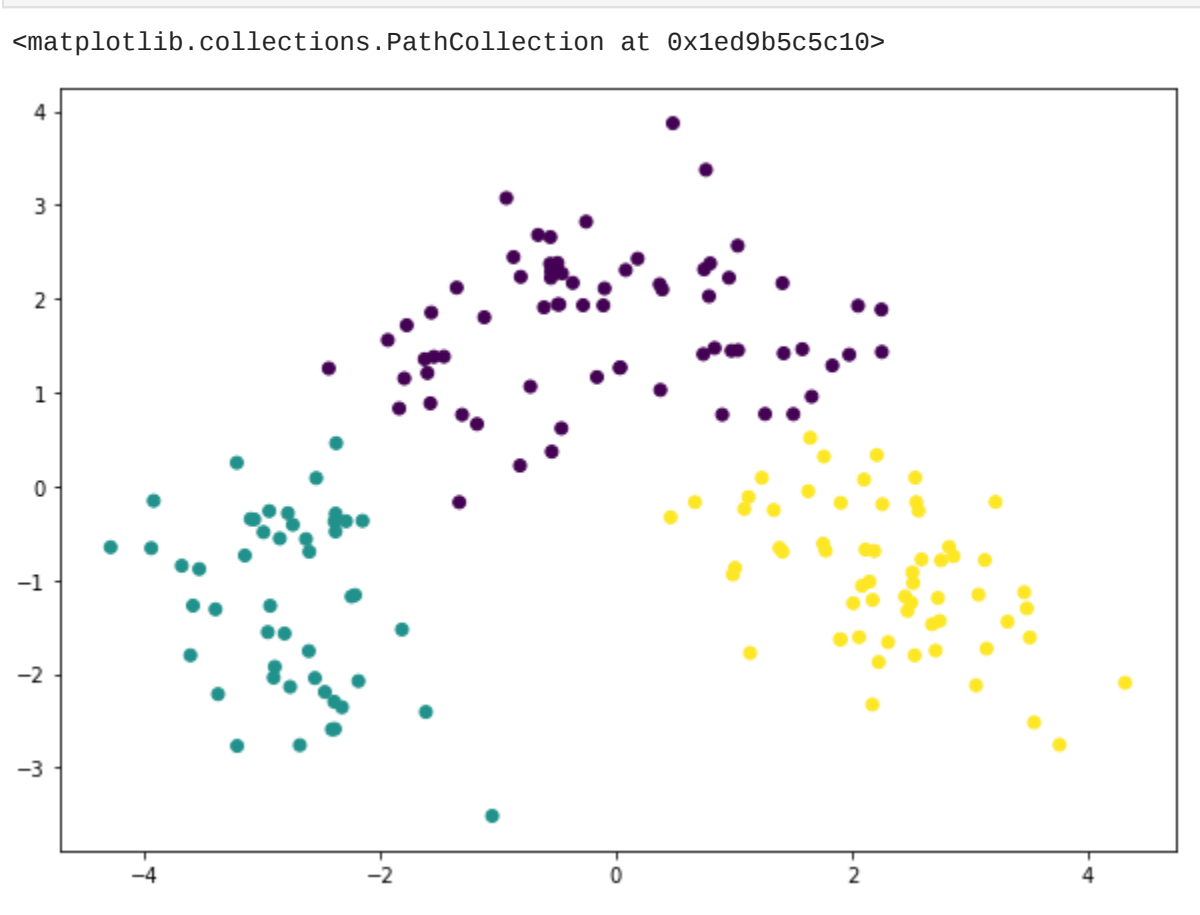
In [30]:
```python
h_cluster = model2.fit(PCA_components.iloc[:,:2])
```

In [31]:
```python
labels2 = model2.labels_
```

In [32]:
```python
X = PCA_components.iloc[:,:1]
Y = PCA_components.iloc[:,1:2]
```

In [33]:
```python
plt.figure(figsize=(10, 7))
plt.scatter(X, Y, c=labels2)
```

Out[33]: <matplotlib.collections.PathCollection at 0x1ed9b5c5c10>



In [34]:
```python
h_new_df=pd.DataFrame(principalComponents[:,0:2])
```

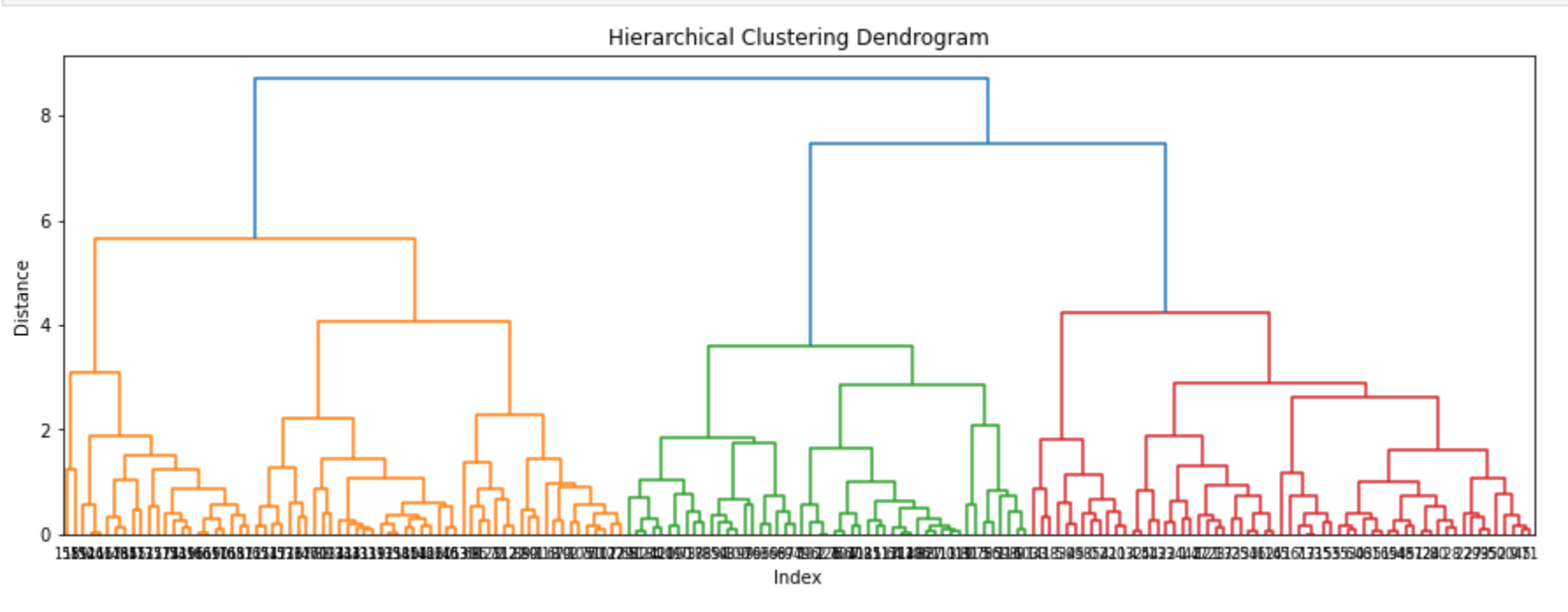
In [35]:
```python
h_new_df.head()
```

Out[35]:

	0	1
0	3.316751	-1.443463
1	2.209465	0.333393
2	2.516740	-1.031151
3	3.757066	-2.756372
4	1.008908	-0.869831

In [36]:
```python
hcf = linkage(h_new_df,method="complete",metric="euclidean")
```

In [37]:
```python
plt.figure(figsize=(15, 5));plt.title('Hierarchical Clustering Dendrogram');plt.xlabel('Index');plt.ylabel('Distance')
sch.dendrogram(
    hcf,
    leaf_rotation=0.,
    leaf_font_size=8.,
)
plt.show()
```



In [38]:
```python
h_complete = AgglomerativeClustering(n_clusters=5,linkage='complete',affinity = "euclidean").fit(h_new_df)
```

In [39]:
```python
h_complete.labels_
```

Out[39]:
```
array([4, 3, 3, 4, 3, 4, 3, 3, 3, 3, 4, 3, 3, 4, 4, 3, 3, 3, 4, 3, 3, 3,
       3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 2, 4, 3, 3, 4, 3,
       3, 3, 3, 3, 3, 4, 3, 3, 4, 3, 3, 3, 3, 3, 4, 2, 0, 0, 2, 2, 2, 2,
       2, 2, 0, 2, 0, 2, 0, 3, 2, 2, 2, 0, 2, 2, 2, 2, 2, 0, 2, 2, 2, 2,
       0, 2, 0, 0, 0, 2, 2, 3, 0, 2, 2, 2, 2, 2, 2, 2, 2, 0, 2, 0, 2, 2,
       2, 2, 0, 2, 2, 2, 2, 2, 0, 2, 2, 3, 0, 0, 2, 2, 2, 0, 2, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 1, 1, 1, 1, 1,
       0, 1, 1, 0, 1, 1, 0, 1, 0, 0, 1, 0, 1, 1, 1, 1, 0, 0, 1, 1, 1, 1,
       1, 1], dtype=int64)
```

In [40]:
```python
cluster_labels=pd.Series(h_complete.labels_)
```

In [41]:
```python
df1['clust']=cluster_labels
```

In [42]:
```python
df1.head()
```

Out[42]:

	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proanthocyanins	Color	Hue	Dilution	Proline	clust
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	4
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	3
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
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
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	3

In [43]:
```python
df1.groupby(df1.clust).mean()
```

Out[43]:

clust	Alcohol	Malic	Ash	Alcalinity	Magnesium	Phenols	Flavanoids	Nonflavanoids	Proanthocyanins	Color	Hue	Dilution	Proline
0	12.686222	2.924000	2.380667	20.966667	95.000000	1.691556	1.088222	0.469556	1.090889	4.613556	0.824578	2.021111	571.444444
1	13.420435	3.390435	2.486087	21.847826	103.130435	1.777391	0.897826	0.428696	1.406522	9.203043	0.640000	1.640870	654.782609
2	12.238163	1.713061	2.165714	19.528571	92.061224	2.395510	2.204694	0.318163	1.713061	2.992653	1.096327	2.913265	509.755102
3	13.573265	2.016531	2.481429	18.069388	107.795918	2.758571	2.887551	0.296122	1.868980	5.175510	1.065510	3.166939	1055.551020
4	14.150000	1.963333	2.435000	15.150000	109.500000	3.248333	3.505833	0.276667	2.185000	6.735000	1.055833	3.188333	1289.333333

Conclusion

Using PCA we reduced the variables to only 2 from 13 and use clustering classification, we can safely assume that there exists 3 cluster in the wine data sets

In [ ]: