CS3481 Fundamentals of Data Science

Assignment 3

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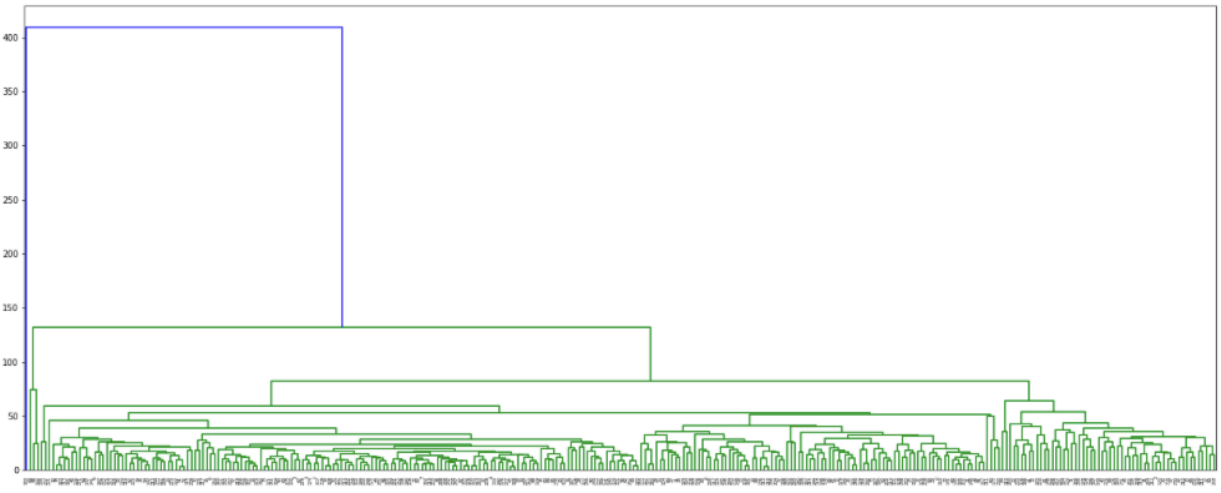
In this project, hierarchical clustering approach is studied using Python. Different versions of clustering are explored and also compared to K-means clustering. Other aspects, such as normalization and eliminating outliers are also discussed and the importance is explained with the help of results and graphs obtained from Python programming. The dataset used is the **Vertebral Column** data set from the UCI Machine Learning Repository. Before performing any clustering algorithm, we first need to test and see how clean is our data, and if we need any pre-processing. As hierarchical clustering is the focus, we use the intermediate version of the approach, group average version, to build the hierarchical clustering model to test the raw data.

Pre-processing

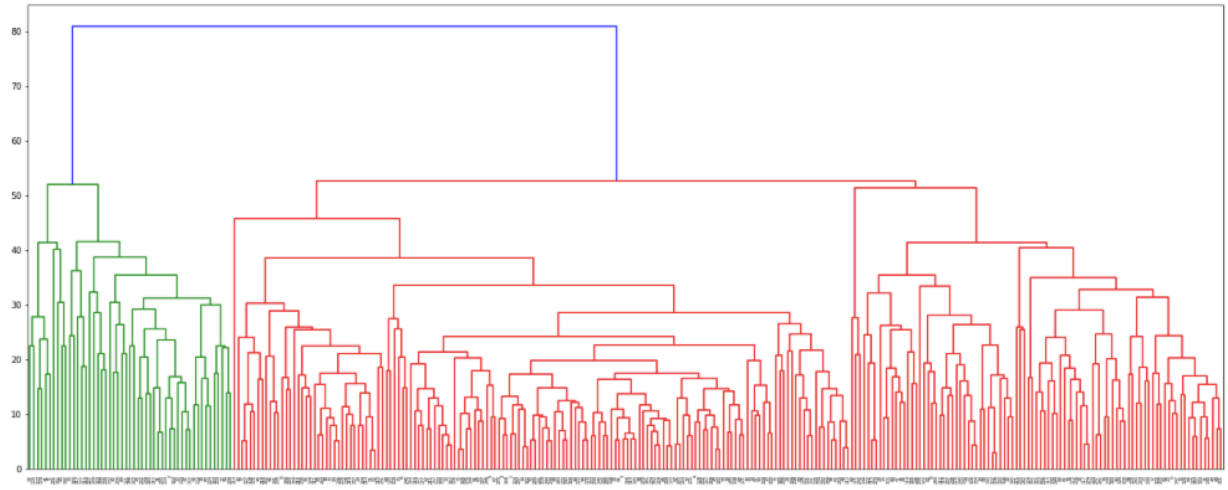
Hierarchical clustering is build using the group average version with the raw data. The resultant dendrogram is shown below.



As shown above, the distances between different clusters at lower level of the dendrogram is less, clusters are not abled to distinguish from each other, and the outliers are affecting the result. The hierarchical clustering dendrogram does not look good as well. It looks messy and unbalanced. As a first step in clustering, the rule of thumb is to normalize/standaradize data as clustering use distance measures such as Euclidean distance. Thus, attributes with larger ranges will automatically have more importance than other attributes, which is false, as we

know, because all attributes must be equally important. The different scales of the numeric data have an undesired effect to the clustering model. Thus normalizing the range of all attributes to scale using min/max or standardize using z-score is important to bring all attributes to similar properties. These two are main normalization techniques. Normalization will improve the clustering result. However, it is not clear, which is better, min-max normalization technique or z-score standardization technique. The former one scales the values between 0 and 1, and the latter one makes sure the values have mean 0, and standard deviation of 1. Both are the main normalization techniques being used in the clustering problems and using any of them arbitrarily is safe enough usually. I am interested in which is better for me so I perform tests to check which one is doing better for this case using the data I have. However, before we test, which two of the normalization technique to use, we first try to eliminate the outliers in our data. It is always good to remove outliers whenever possible to remove unwanted noise. This is done by assuming normal distribution, and using z-score to standardize all the values. We can assume normal distribution because from intuition we know the most important data are usually clustered around the mean and the outliers are the values at the far left or right away from the mean. So we eliminate values, which are 3 standard deviations away to include around 99.7% of the data, as we know from the 68–95–99.7 rule. Any more deviation from this value, I am afraid too many outliers will be included, and any less might delete important information. Anyhow, I have tested 2, and 4 standard deviations, and my hypothesis was correct, so I stuck with using 3 standard deviations.

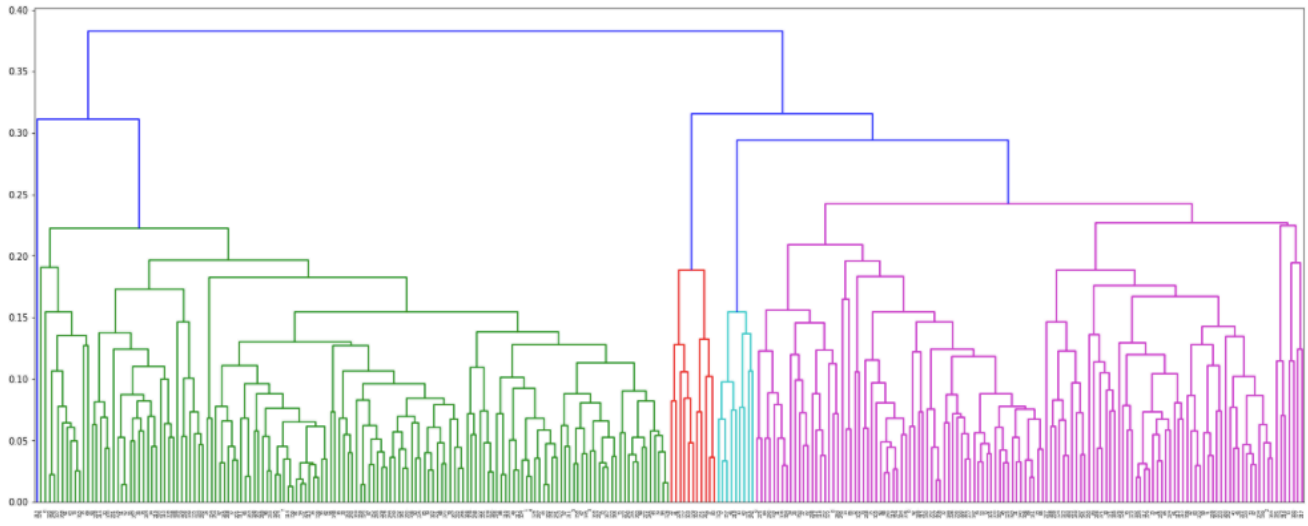
After removing the outliers, the dendrogram changes and the result is shown below.



As seen above, we can see that, eliminating outliers have improved the result greatly compared to earlier result. More clusters are recognized, and the influence of specific outliers forming small cluster is reduced. However, we can

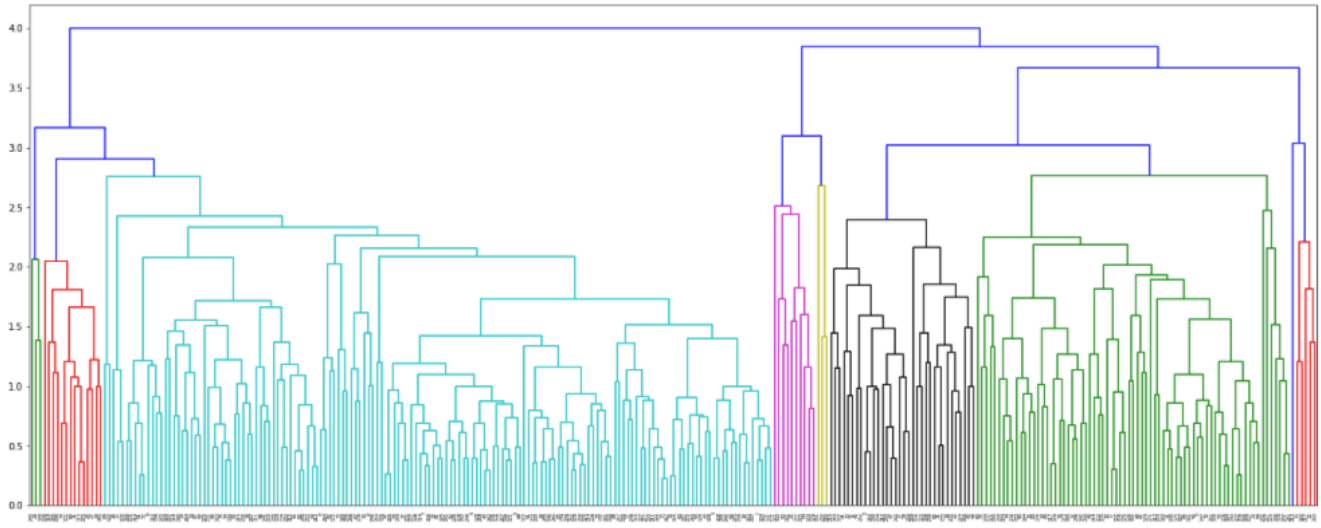
further improve by reducing the importance of large scaled attributes and normalize the data.

Normalization – Method 1 – Min-max normalization

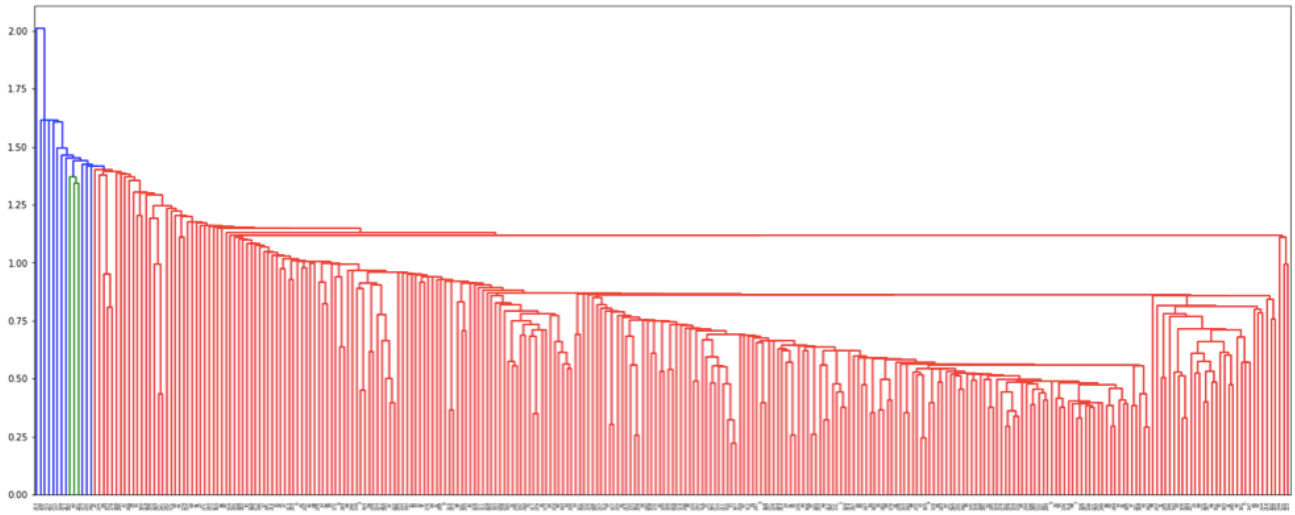


As hypothesized, normalization using min-max normalization technique has improved the clustering result. The model can distinguish between different sets of data points more easily and thus create more distinguishable clusters. This shows that, it can extract more information from the data compared to the previous results.

Normalization – Method 2 – Z-score standardization



Compared to the previous normalization technique, this one is able to extract more information and distinguish more clusters from each other. It can display



much more complicated cluster relationship of the data. Thus, we will use this normalization technique and proceed further to complete the rest of the tasks.

Question 1

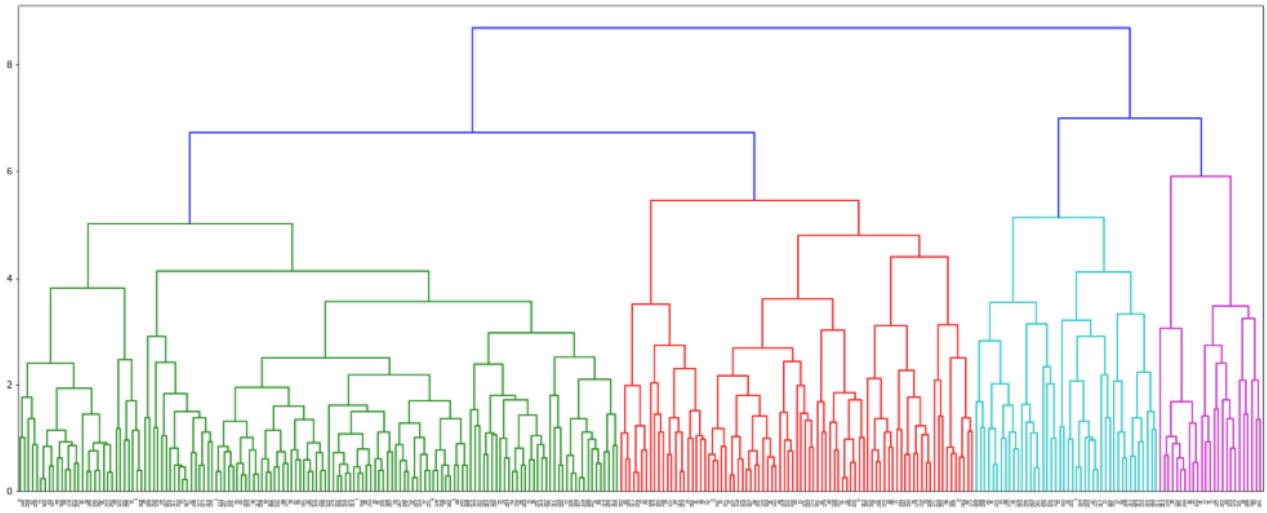
In this part, hierarchical structures are generated using single link, complete link and group average versions of the approach.

Single link

```
In [31]: kclusters1 = fcluster(Z1, 3, criterion='maxclust')
         kclusters1
```

```
Out[31]: 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, 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, 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, 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, 1, 1, 1, 1, 3, 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, 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], dtype=int32)
```

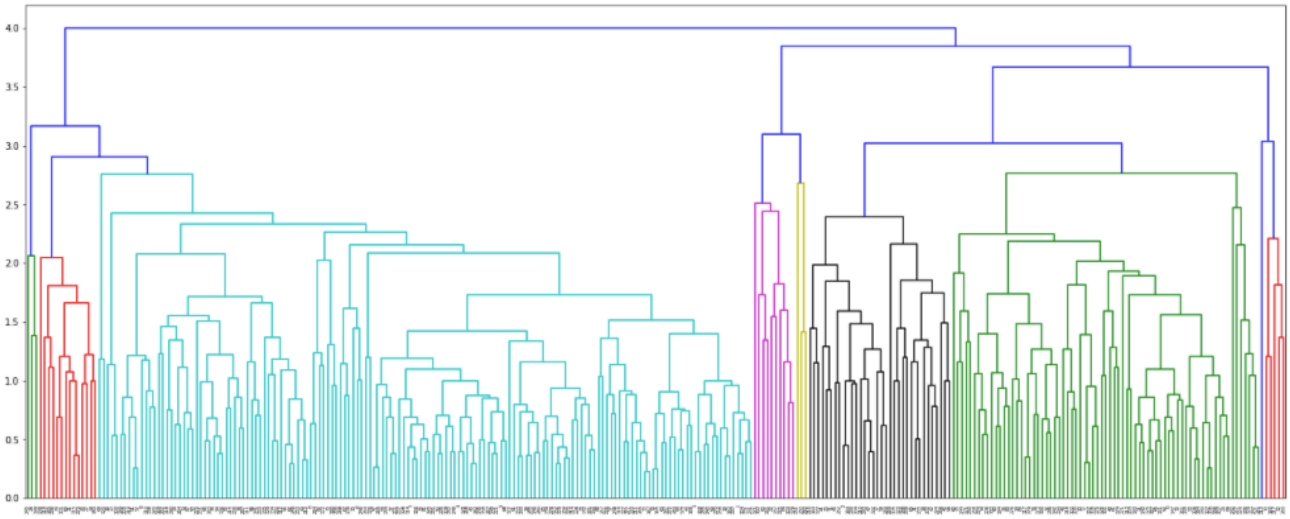
Complete link



```
In [35]: kclusters2 = fcluster(Z2, 3, criterion='maxclust')
         kclusters2
```

```
Out[35]: array([1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 3, 2, 3, 1, 3, 1,
                3, 1, 1, 1, 1, 1, 1, 1, 3, 2, 1, 1, 1, 1, 1, 1, 3, 1, 2, 3, 2, 1,
                1, 2, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1, 2,
                1, 1, 1, 1, 2, 3, 1, 1, 1, 1, 1, 1, 1, 1, 3, 1, 1, 1, 3, 1, 1, 1,
                1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 3, 1, 1, 3, 1, 2, 1, 1, 1, 1,
                1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 3, 1, 2, 2, 1, 1, 1, 1, 1, 1, 1,
                3, 1, 1, 1, 1, 3, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
                1, 1, 1, 1, 1, 1, 2, 1, 1, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
                1, 2, 1, 3, 1, 3, 1, 1, 1, 1, 2, 1, 2, 1, 1, 1, 3, 1, 1, 1, 1, 1,
                1, 1, 1, 1, 2, 2, 2, 1, 1, 1, 1, 1, 2, 1, 1, 3, 3, 1, 2, 2, 1, 1,
                1, 1, 2, 2, 2, 3, 1, 2, 3, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1,
                2, 1, 3, 1, 1, 2, 1, 1, 1, 2, 2, 1, 1, 2, 1, 1, 1, 2, 2, 3, 1, 1,
                1, 1, 3, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1,
                1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1], dtype=int32)
```

Group average



```
In [40]: kclusters3 = fcluster(Z3, 3, criterion='maxclust')
         kclusters3

Out[40]: array([3, 1, 3, 1, 1, 1, 1, 1, 1, 1, 3, 1, 3, 1, 3, 1, 1, 3, 3, 1, 1, 3,
                2, 3, 1, 3, 1, 1, 1, 1, 3, 3, 3, 1, 1, 3, 1, 1, 1, 1, 3, 3, 3, 1,
                1, 3, 3, 3, 3, 1, 1, 1, 1, 3, 1, 1, 1, 1, 1, 3, 3, 3, 1, 1, 1, 3,
                3, 1, 1, 1, 3, 3, 3, 1, 3, 1, 3, 3, 1, 1, 2, 1, 1, 3, 2, 1, 3, 1,
                1, 3, 3, 1, 3, 1, 1, 1, 1, 1, 3, 1, 1, 1, 3, 2, 1, 3, 3, 3, 3, 1,
                1, 1, 1, 3, 1, 1, 1, 3, 1, 1, 1, 2, 1, 3, 3, 3, 3, 1, 1, 1, 3, 1,
                1, 1, 1, 1, 1, 2, 1, 3, 3, 1, 3, 3, 3, 1, 1, 3, 1, 1, 1, 3, 1, 1,
                1, 1, 1, 3, 1, 1, 3, 3, 1, 3, 3, 1, 1, 1, 1, 1, 1, 3, 1, 3, 3, 3,
                1, 3, 1, 2, 1, 1, 1, 3, 3, 1, 3, 3, 3, 1, 3, 3, 2, 3, 3, 1, 3, 1,
                1, 1, 3, 1, 3, 3, 3, 1, 3, 3, 3, 1, 3, 1, 1, 3, 1, 1, 3, 3, 3, 1,
                1, 1, 3, 3, 3, 2, 1, 3, 1, 1, 3, 1, 1, 1, 1, 1, 3, 1, 1, 3, 1, 1,
                3, 1, 1, 1, 1, 3, 1, 1, 2, 2, 3, 1, 1, 3, 1, 1, 3, 3, 3, 2, 1, 1,
                1, 1, 3, 1, 1, 3, 1, 3, 1, 1, 3, 1, 3, 1, 1, 3, 1, 3, 2, 1, 1, 1,
                1, 1, 1, 1, 1, 1, 1, 3, 3, 1, 1, 1], dtype=int32)
```

Comparison between the 3 different versions

Dendrograms, and the partitional clustering solutions of the hierarchical clustering with 3 clusters are obtained. Partitional clustering is obtained by cutting the dendrogram at a certain level, which basically results in partitional clustering. As seen from the result, single link is not doing as good as complete and average versions of the model. Complete and average versions can extract more information from data and distinguish clusters from each other more readily than single link version. Different colors are used to differentiate the clusters in the dendrogram. There are more colors in complete and average versions. As seen from the analysis through the “fcluster” method, in partitional clustering with 3 cluster partitions, single link version classifies most of the data into cluster "1", and there is little or no cluster "2" and "3" at all. In complete version, there is some more variety and has more cluster "2" and "3", although cluster "1" is still the most among the 3 clusters. And in the group version, there's much more of "3" or "2" compared to previous 2 versions. So the average version of Hierarchical clustering has more uniform number of cluster "1", "2" and "3". Thus it can distinguish different clusters more uniformly. In conclusion, the intermediate version of single link and complete link, which is the average version, is a more appropriate method of performing Hierarchical clustering in this case. Also, the complete link version is ranked second best, and the single link version is the worse among all 3 undoubtedly.

Question 2

I will choose complete link and average versions of the Hierarchical clustering to identify possible patterns and investigate the type of information we can get from the results obtained. Single link version is not going to be studied as it gives very poor representational data and information. Between complete and

average versions, it can be seen that in general the group version connected between clusters at lower level of the dendrogram with much less distance values and this can intuitively mean that group version could recognize smaller colonies more easily and label them as distinguishable clusters. This is why, there are more colors in the dendrogram and more clusters. At higher level of the dendrogram, it can be seen that complete version has distance values between different clusters much larger, than that of group version, this is because complete version defines the minimum distance as the largest distance of any two point of two clusters. For complete version, it can be seen that the clustering could recognize 4 main clusters each of reasonable size. However the cluster size gradually decreases as seen from the dendrogram among its clusters. This gives the information that, there are 4 main clusters of different gradually decreasing sizes. For average version, it recognizes around 9 clusters, and it's seen that it can distinguish more specific clusters. It can be thought that, the 4 main clusters in complete version have parts where another clusters can be formed which can be seen from the average version. This shows that there's some variety in the data itself in the 4 main clusters in complete version. For complete version, the difference of the distance values of the merges between the higher and lower levels of dendrogram is large. This signifies, smaller, similar clusters are grouped first, and the larger clusters, which are further from each other, are grouped last. This is what we want in clustering. However this relationship is not as apparent in the group version, so this could be an indicator that complete version is better. If the data is interpreted at 2-cluster level of dendrogram, the average version has 2 clusters of somewhat more equal size of clusters. However, it's quite unequal for the complete version. But when the two clusters are merged into one, the distance value of the merge for average version is much less than that of complete version. This implies, grouping the data into 2 equal sizes does not show the proper cluster information because clusters are supposed to show that differences in data in the form of clusters. The higher the distance value, the higher the difference between the clusters. Thus, the larger distance values usually, signifies a correct clustering of data as we want to distinguish between different types of data in terms of clusters as much as possible.

Question 3

In this part, comparison is done by comparing the number of data points in the clusters. For example, for 3-cluster problem, cluster A, B and C are just named to differentiate 3 different clusters and compared to another method of clustering. The cluster A in the new method does not refer to the same type of class label of cluster A from another method. The names are just to differentiate the 3 different clusters. And the amount of data points in the clusters is used to

compare and see how similar are the proportions. This can easily and roughly tell us how good the clustering method is performing or how similar it is to another clustering method by comparing the proportions of data points in the clusters from one model/clustering method to that of another. 3 clusters will be used only as the class labels in the original dataset has 3 labels, so we want to compare how well the different methods can cluster data into 3 clusters. The performance of partitional clustering solution derived from hierarchical clustering will be compared to that of K-means and the proportions of original class labels will be used to check which is performing better. Both, the complete and average versions of hierarchical clustering will be used to test.

Complete link version

```
kclusters2 = fcluster(Z2, 3, criterion='maxclust')
kk = list(kclusters2)
print("From clustering solutions:")
print("Cluster A: ", kk.count(1))
print("Cluster B: ", kk.count(2))
print("Cluster C: ", kk.count(3))
```

```
From clustering solutions:
Cluster A:  229
Cluster B:  44
Cluster C:  25
```

```
km2 = KMeans(n_clusters=3)
km2.fit(X)
kk = list(km2.labels_)
print("From K-means:")
print("Cluster A: ", kk.count(0))
print("Cluster B: ", kk.count(1))
print("Cluster C: ", kk.count(2))
```

```
Cluster A:  108
Cluster B:  56
Cluster C:  134
```

```
kk = list(Y_train)
print("From original set of class labels:")
print("Cluster A: ", kk.count('DH'))
print("Cluster B: ", kk.count('SL'))
print("Cluster C: ", kk.count('NO'))
```

```
From original set of class labels:
Cluster A:  60
Cluster B:  150
Cluster C:  100
```

(a) Comparing for 3-cluster problem, between the partitional clustering solution derived from hierarchical clustering and k-means, it can be observed that k-means distributes the data points between the 3 clusters more evenly. In the clustering solution, the cluster A has abnormally more data points.

(b) By comparing the 3 partitional clustering solution and K-means to the original class labels of the dataset, we can see how well the clustering algorithms clustered the data properly with correct proportions. Judging from the labels from the original dataset, one cluster has 60 data points, one has 150, and the last one has 100. I didn't eliminate the outliers from the original set before counting the number of data points belonging to the 3 different classes because it is small compared to the size of the dataset of only 12 outlying points. I just need to compare the proportions to have the general idea and conclusion I want to get. From the original class labels, we find that two clusters need to have large number of data points and the difference in the number of data points between each cluster is around 50 roughly. Comparing these facts with the two clustering models, K-means is performing relatively better.

Group average version

```
kclusters3 = fcluster(Z3, 3, criterion='maxclust')
kk = list(kclusters3)
print("From clustering solutions:")
print("Cluster A: ", kk.count(1))
print("Cluster B: ", kk.count(2))
print("Cluster C: ", kk.count(3))
```

```
From clustering solutions:
Cluster A:  172
Cluster B:  13
Cluster C:  113
```

```
km2 = KMeans(n_clusters=3)
km2.fit(X)
kk = list(km2.labels_)
print("From K-means:")
print("Cluster A: ", kk.count(0))
print("Cluster B: ", kk.count(1))
print("Cluster C: ", kk.count(2))
```

```
From K-means:
Cluster A:  56
Cluster B:  134
Cluster C:  108
```

```
kk = list(Y_train)
print("From original set of class labels:")
print("Cluster A: ", kk.count('DH'))
print("Cluster B: ", kk.count('SL'))
print("Cluster C: ", kk.count('NO'))
```

```
From original set of class labels:
Cluster A:  60
Cluster B:  150
Cluster C:  100
```

(a) The derived clustering solution is performing more similar to that of k-means in this case, as not only one cluster has abnormally high number of data points, but two clusters have, which is similar to that of K-means. Still, in the clustering solution the size of the largest cluster is much larger than the smallest cluster. The smallest cluster has abnormally small number of data points. This uneven proportion is not as apparent in K-means. K-means is distributing the data points more evenly.

(b) Comparing the two methods of clustering to proportions of class labels from the original dataset, we can see that K-means is giving clusters, which have proportions much similar to that of original dataset class labels. The smallest cluster in K-means has 56 data points, which is very close to proportion of the smallest class in the original dataset, which is 60. The largest cluster in K-means is 134 and the largest proportion of the class is supposed to be with 150 data points which is much more close to that of what clustering solutions is giving which is 172 data points. Similarly, for the medium cluster, the number of data points for K-means is closer to the original set, compared to the derived clustering solution from hierarchical clustering.

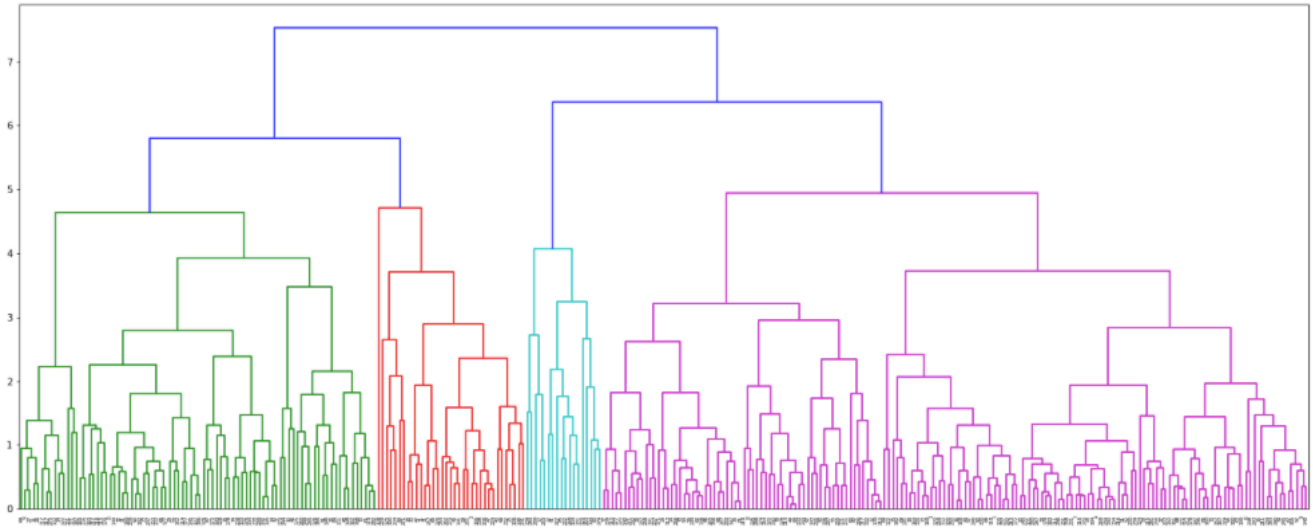
In conclusion, K-means is performing better than the partitional clustering solutions derived from the hierarchical clustering method in both complete version and average version.

Question 4

In this part, different subsets of attributes from the dataset are selected and hierarchical clustering is performed on the new subset and then compared to the original hierarchical clustering structure. I will create subsets, each will have 4 attributes, by eliminating 2 of the attributes. An arbitrary simple subset selection I used is by eliminating the first 2 attributes first, then the next two, and finally, the last two. This way, each attribute is eliminated only once and is considered in the subset twice so it's fair. Many other combinations can also form but this is good enough to generalize and simplify. The hierarchical clustering version I will stick to is the complete link version because it generalizes the data clustering well. Its performance isn't poor nor the clustering are so detailed that higher level, general information is missed.

Round 1 – Eliminate attribute 0,1

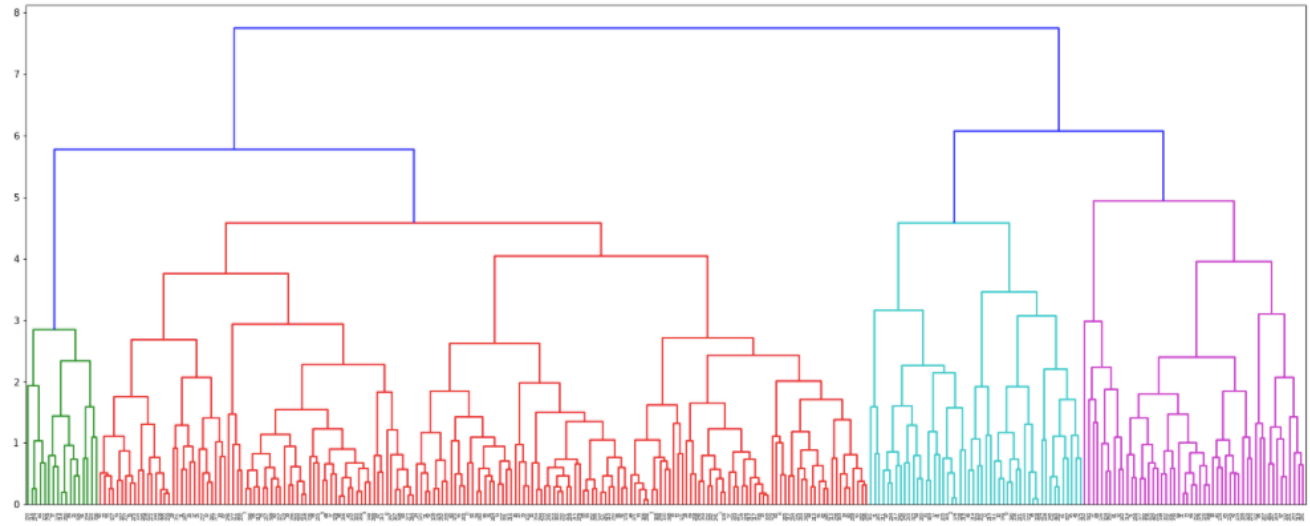
After eliminating the first two attributes, the resultant hierarchical clustering is shown below.



Comparing the result from the subset dataset to the original clustering, it can be seen that again, 4 main clusters are found but are of different proportions than that of original one. The distance values of the clusters at higher level of the dendrogram are smaller in the new result. This shows that, the original clustering could cluster data more properly for data, which are apart.

Round 2 – Eliminate attribute 2,3

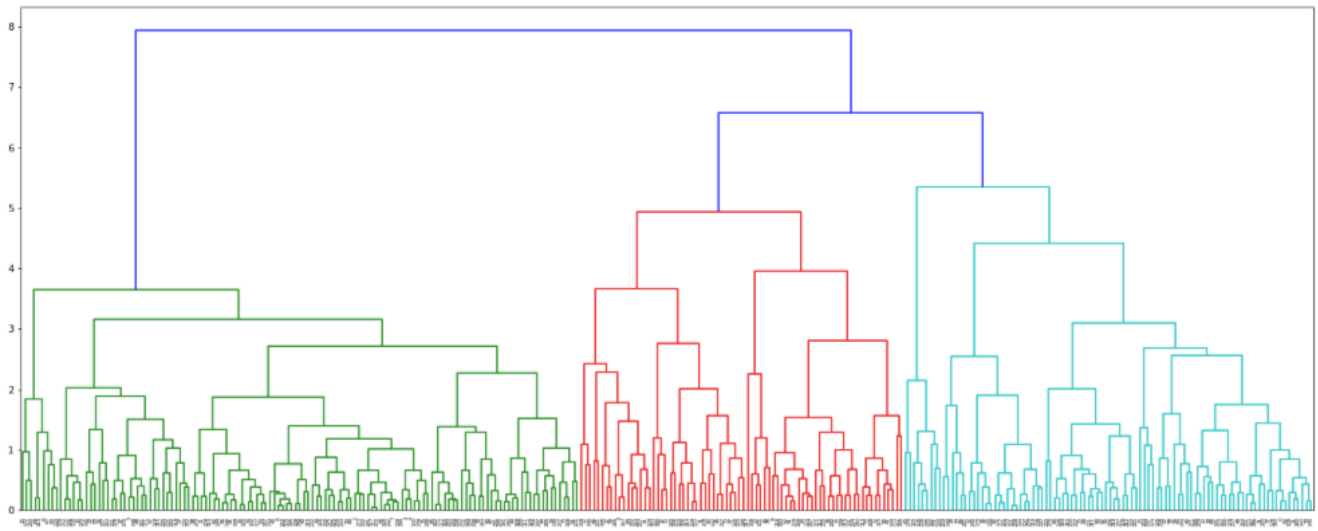
After eliminating the middle two attributes, the resultant hierarchical clustering is shown below.



For the new result, it has shown that it can still show 4 main clusters, but one of them is shrunk considerably, and its data points joined the neighboring cluster. On the other half of the data, the clusters remain almost the same. Thus, this shows that, there's a clear decline in cluster recognition affecting a very specific group of data points.

Round 3 – Eliminate attribute 4,5

After eliminating the last two attributes, the resultant hierarchical clustering is shown below.



The result of this new clustering is quite pleasing to see as there are 3 clear distinct clusters formed. And all of them are in relatively good size indicating that it doesn't include small clusters of outliers, but large cluster group of data points belonging to a distinct group. Also, we know that the original dataset, there are 3 labels, so this new result can show/predict that more relatively. I think it's because, decrease in number of attributes, resulted in less complication of clustering the data, so the clustering could be generalized more easily to represent the whole data. The new clustering recognizes 3 main clusters represented by the 3 colors, which is 1 less than the original clustering. Cutting the dendrogram at 3-cluster level, depicts the original proportion of class labels pretty well.

Appendix

In [56]:

```
import pandas as pd
import numpy as np
from sklearn import tree
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import accuracy_score
from sklearn.metrics import confusion_matrix
import graphviz

# Assignment 2
from sklearn.ensemble import RandomForestClassifier
from sklearn.naive_bayes import GaussianNB

# Assignment 3
from matplotlib import pyplot as plt
from scipy.cluster.hierarchy import dendrogram, linkage, fcluster
from sklearn.cluster import KMeans
from sklearn.preprocessing import normalize
from scipy import stats
```

In [57]:

```
data = pd.read_csv('../../Desktop/CS3481- Fundamentals of Data Science/vertebr
al_column_data/column_3C.dat', sep=' ', header=None)
data.columns = ['pelvic_incidence numeric', 'pelvic_tilt numeric', 'lumbar_lor
dosis_angle numeric', 'sacral_slope numeric', 'pelvic_radius numeric','degree_
spondylolisthesis numeric','class']
features = ['pelvic_incidence numeric', 'pelvic_tilt numeric', 'lumbar_lordosi
s_angle numeric', 'sacral_slope numeric', 'pelvic_radius numeric','degree_spon
dylolisthesis numeric']
classes = ['disk hernia (DH)', 'spondylolisthesis (SL)', 'normal (NO)']
```

In [58]:

```
X=data.iloc[:,0:6].values
Y=data.iloc[:,6].values
#print (len(data))
#print (data.shape)
```

In [59]:

```
X_train, X_test, Y_train, Y_test = train_test_split(X,Y,test_size=0,random_sta
te=10,shuffle=True)
```

In [60]:

```
X = X_train
```

In [ ]:

```

```

In [14]:

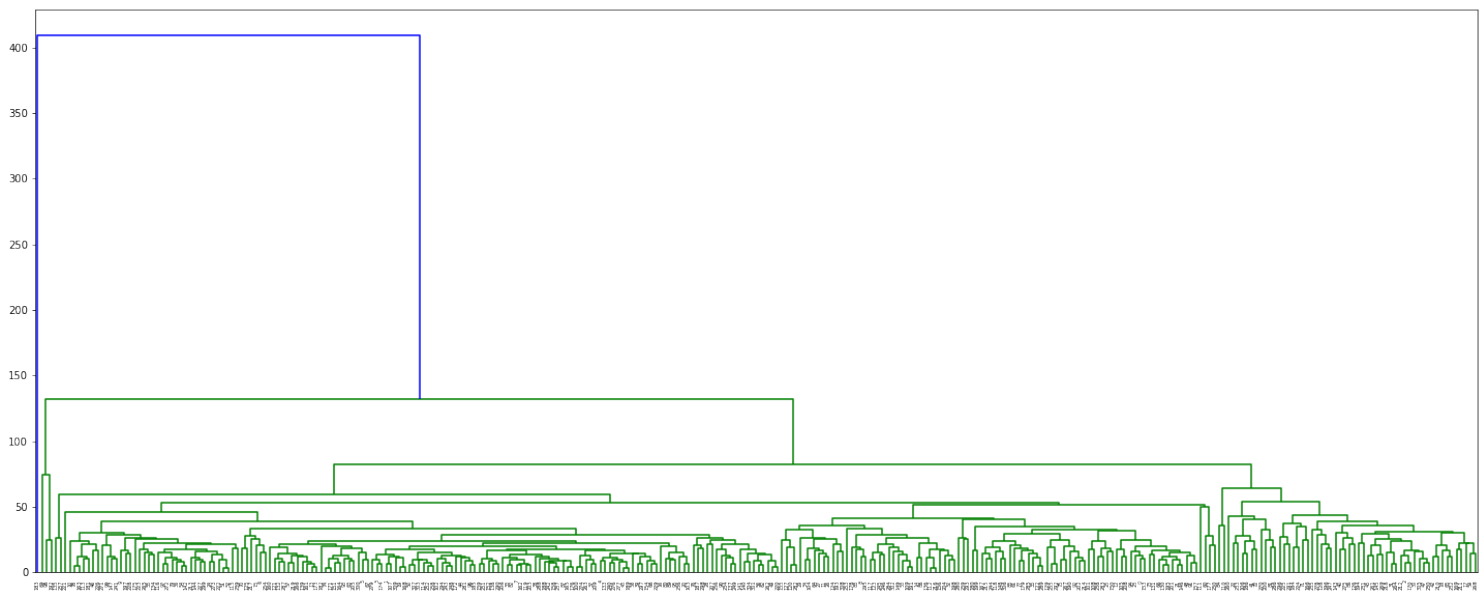
```
# Before performing any clustering algorithm, we first test and see how is our data is and if we need any
# pre-processing. As hierarchical clustering is performed first, we use group average version to build the
# clustering model as it's the intetimediate of single link and complete linkt to use it to test how is our raw data
```

In [15]:

```
Z = linkage(X, 'average')
```

In [16]:

```
plt.figure(figsize=(25, 10))
dendrogram(Z)
plt.show()
```



In [17]:

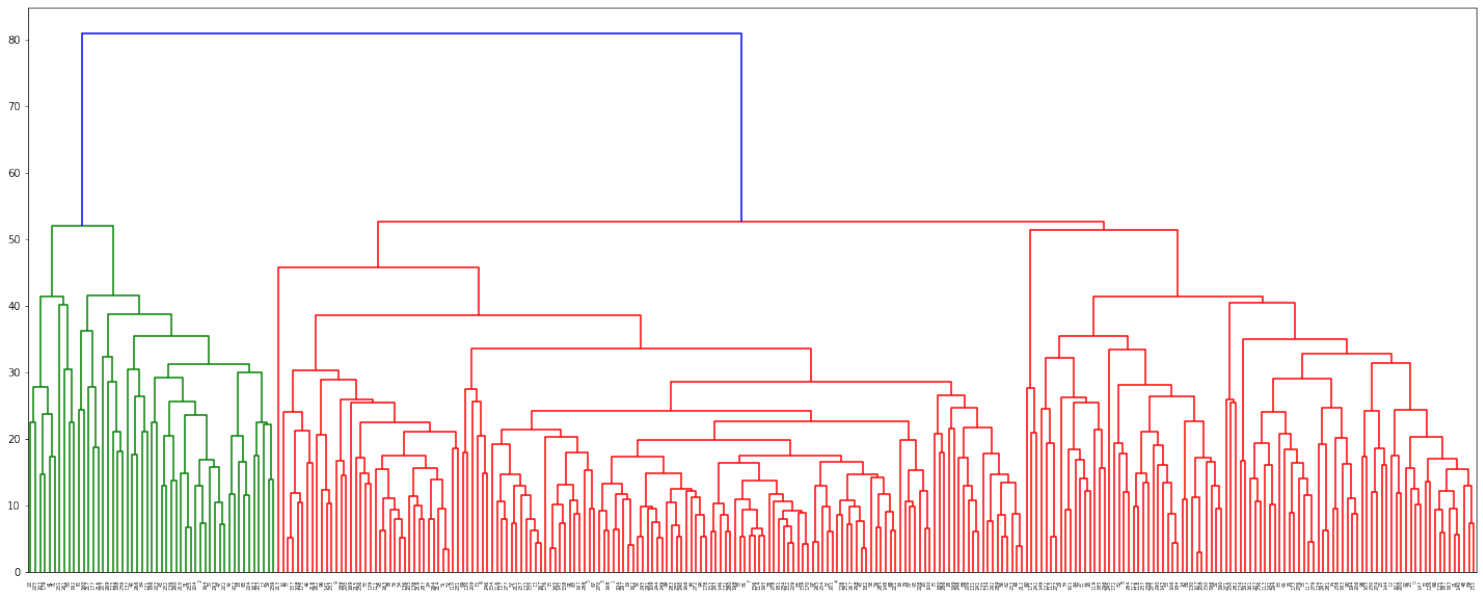
```
# As shown above, the distances between different clusters at lower level of t
he tree is less, clusters are not
# abled to distinguihed from each other, and the outliers are affecting the re
sult. The hierarchical clustering
# dendrogram resulted does not look good as well. As a first step in clusterin
g, the rule of thumb is to
# normalize/standaradize data as clustering uses distance meatures such as
# Euclidean distance. Thus, attributes with larger ranges will automatically h
ave more importance than other
# attributes which is false as we know, because all attributes must be equally
important. Thus normalizing the range
# of all attributes to scale using min/max or standardize using z-score is imp
ortant to bring all attributes to
# similar properties. These two are main normalization techniques. Normalizati
on will improve the clustering result.
# However, it is not clear, which is better, min-max normalization technique o
r z-score standardization technique.
# The former one scales the values between 0 and 1, and the latter one makes s
ure the values have mean 0, and
# standard deviation of 1. Both are normalization techniques in general, just
that standardization is also used in
# some cases as a terminology.
# However, before we test, which two of the normalization technique to use, we
first try to eliminate the outliers in
# our data. This is done by assuming normal distribution, and using z-score to
standardize all the values. We can
# assume normal distribution because from intuition we know the most important
data are usually clustered around the
# mean and the outliers are are the values at the far left or right away from
the mean. So we eliminate values which
# are 3 standard deviations away to include around 99.7% of the data as we kno
w from the 68–95–99.7 rule. Any more
# from this value, I am afraid too much outliers will be included, and any les
s must delete important information as
# well. I have tested 2, and 4, and my hypothesis was correct, so I sticked to
3.
```

In [18]:

```
# Eliminating outliers
```

In [19]:

```
df = pd.DataFrame(data=X)
df = df[(np.abs(stats.zscore(df)) < 3).all(axis=1)]
X = df.values
Z = linkage(X, 'average')
plt.figure(figsize=(25, 10))
dendrogram(Z)
plt.show()
```

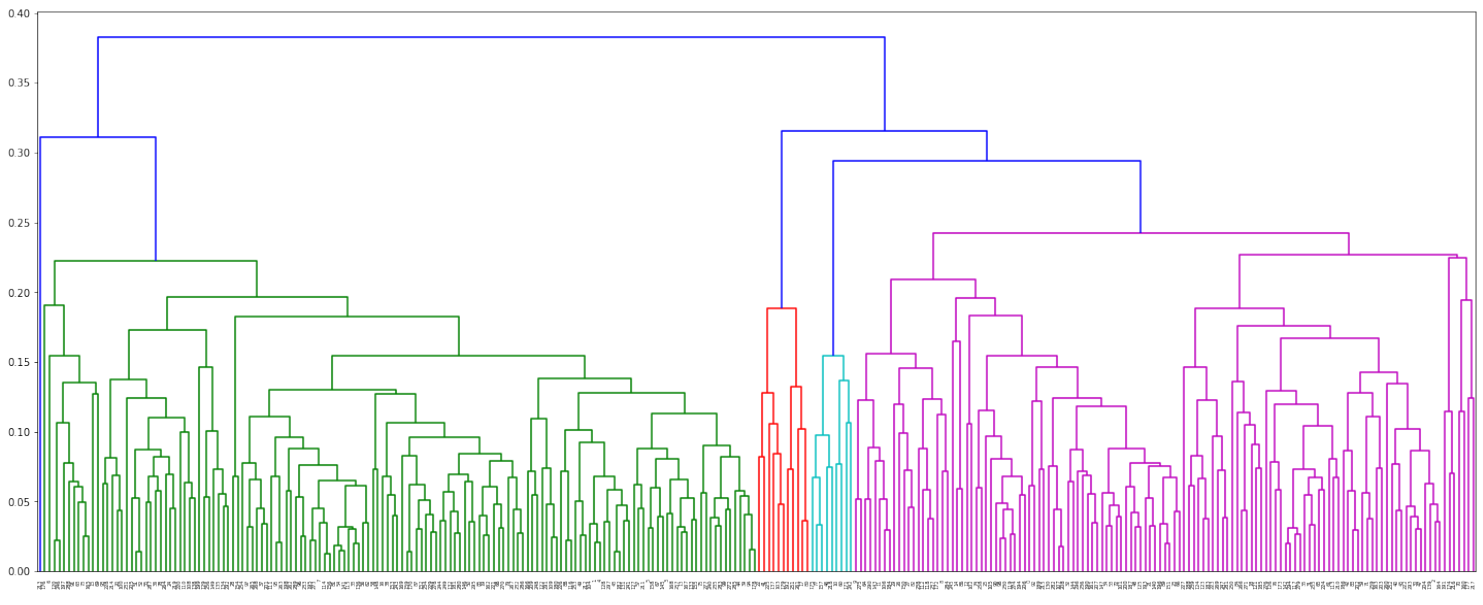


In [20]:

```
# As seen above, we can see that, eliminating outliers have improved the resul
t greatly compared to earlier result.
# However, we can furthur improve by reducing the imporsmotance of large scale
d attributes and normalize the data.
```

In [21]:

```
# First method of normalization - Scale to value between 0-1 --> min-max norma
lization
Xa = normalize(X)
Z = linkage(Xa, 'average')
plt.figure(figsize=(25, 10))
dendrogram(Z)
plt.show()
```



In [22]:

```
# As seen above, normalization has improved the clustering result. The model c
an distingush between different sets
# of data more easily and thus create more distinguishable clusters. Thus, it
can extract more information from the
# data.
```

In [23]:

```
# Second method of normalization - Standardize to mean 0, variance 1 --> z-sco
re normalization
```

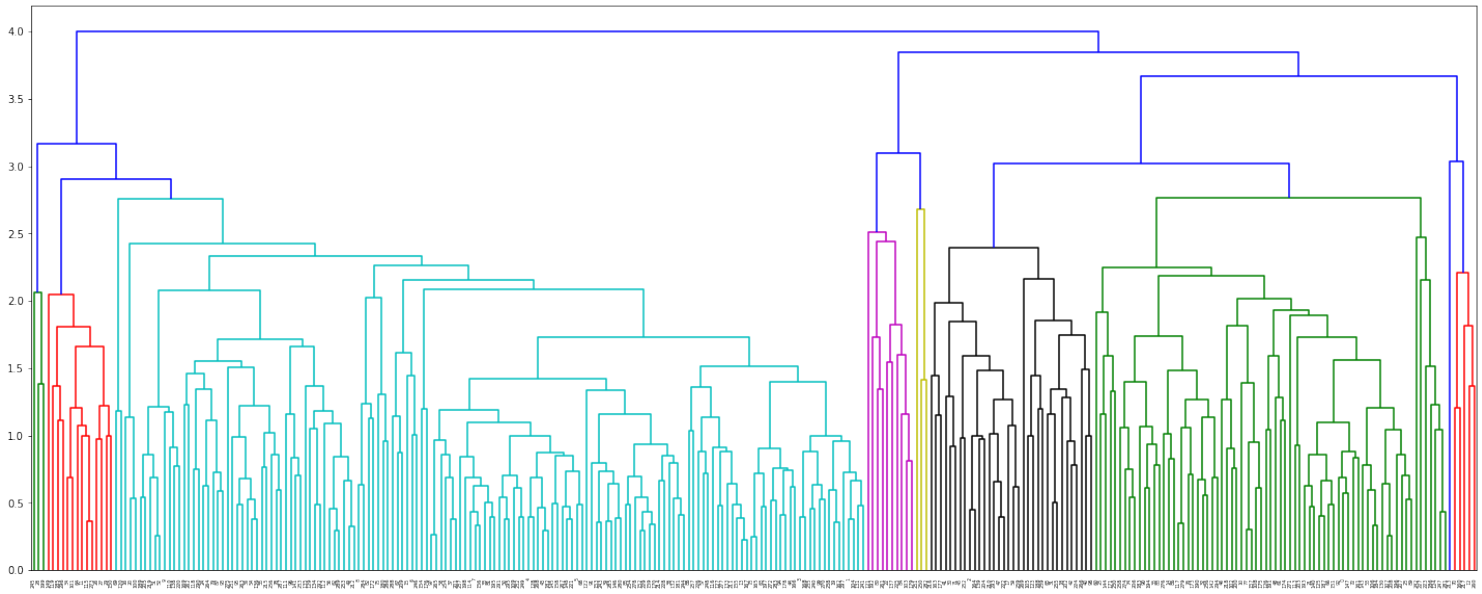
In [ ]:

```

```

In [24]:

```
Xb = stats.zscore(X)
Z = linkage(Xb, 'average')
plt.figure(figsize=(25, 10))
dendrogram(Z)
plt.show()
```



In [25]:

```
# Compared to the previous normalization technique, this one is able to extrac
t more information, distinguish more
# clusters from each other. So we will use  this normalization technique and p
roceed further.
```

In [9]:

```
X = X_train
df = pd.DataFrame(data=X)
df = df[(np.abs(stats.zscore(df)) < 3).all(axis=1)]
X = df.values
X = stats.zscore(X)
```

In [ ]:

```

```

In [ ]:

```
# Question 1
```

In [27]:

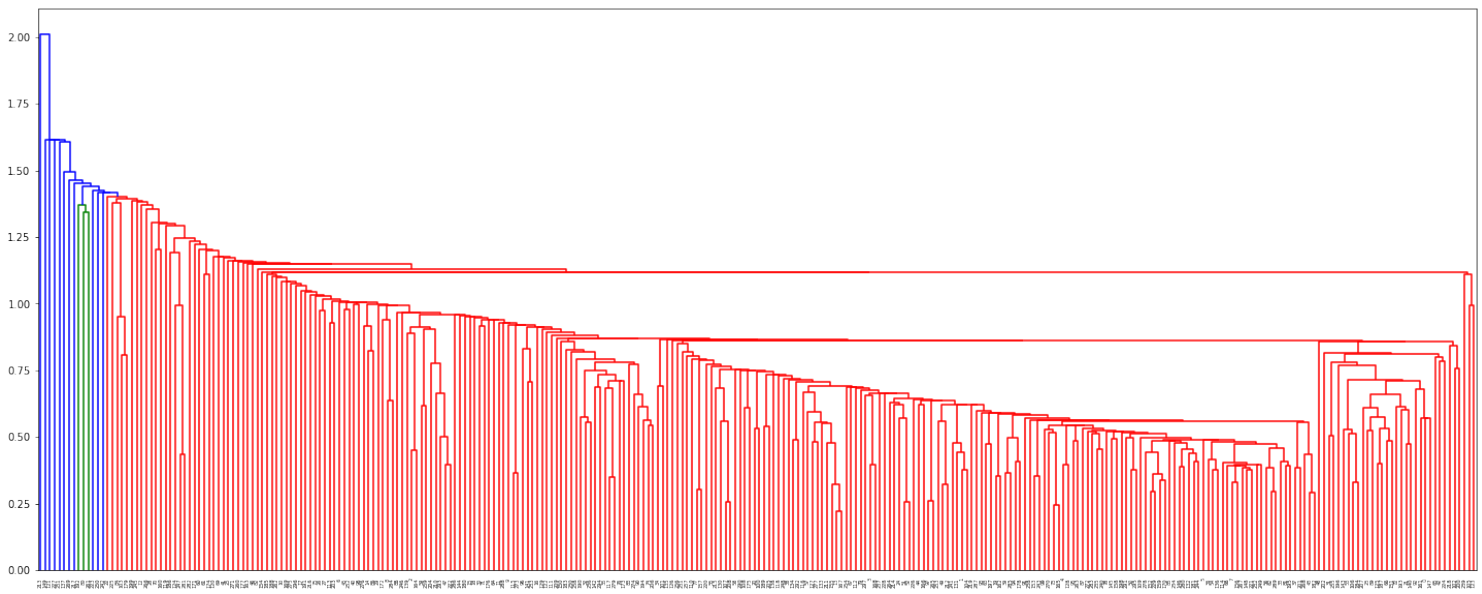
```
# Single link Hierarchical clustering
```

In [28]:

```
Z1 = linkage(X, 'single')
```

In [29]:

```
plt.figure(figsize=(25, 10))
dendrogram(Z1)
plt.show()
```



In [31]:

```
kclusters1 = fcluster(Z1, 3, criterion='maxclust')
kclusters1
```

Out[31]:

```
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, 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, 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, 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, 1, 1, 1, 1, 3, 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, 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], dtype=int32)
```

In [ ]:

```

```

In [32]:

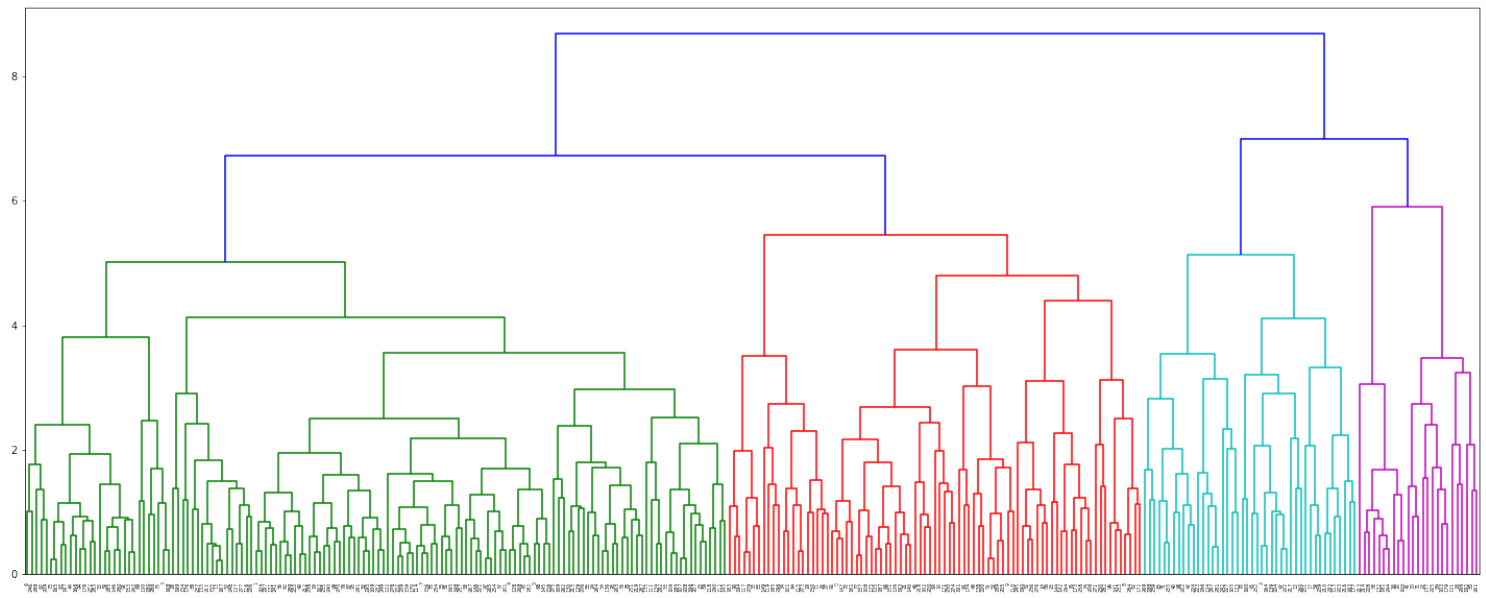
```
# Complete link Hierarchical clustering
```

In [33]:

```
Z2 = linkage(X, 'complete')
```

In [34]:

```
plt.figure(figsize=(25, 10))
dendrogram(Z2)
plt.show()
```



In [35]:

```
kclusters2 = fcluster(Z2, 3, criterion='maxclust')
kclusters2
```

Out[35]:

```
array([1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 3, 2, 3, 1,
       3, 1,
       3, 1, 1, 1, 1, 1, 1, 1, 3, 2, 1, 1, 1, 1, 1, 1, 3, 1, 2, 3,
       2, 1,
       1, 2, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1,
       1, 2,
       1, 1, 1, 1, 2, 3, 1, 1, 1, 1, 1, 1, 1, 1, 3, 1, 1, 1, 3, 1,
       1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 3, 1, 1, 3, 1, 2, 1, 1,
       1, 1,
       1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 3, 1, 2, 2, 1, 1, 1, 1, 1,
       1, 1,
       3, 1, 1, 1, 1, 3, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1,
       1, 1, 1, 1, 1, 1, 2, 1, 1, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1,
       1, 2, 1, 3, 1, 3, 1, 1, 1, 1, 2, 1, 2, 1, 1, 1, 3, 1, 1, 1,
       1, 1,
       1, 1, 1, 1, 2, 2, 2, 1, 1, 1, 1, 1, 2, 1, 1, 3, 3, 1, 2, 2,
       1, 1,
       1, 1, 2, 2, 2, 3, 1, 2, 3, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2,
       1, 1,
       2, 1, 3, 1, 1, 2, 1, 1, 1, 2, 2, 1, 1, 2, 1, 1, 1, 2, 2, 3,
       1, 1,
       1, 1, 3, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1,
       1, 1,
       1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1], dtype=int32)
```

In [ ]:

```
```

In [36]:

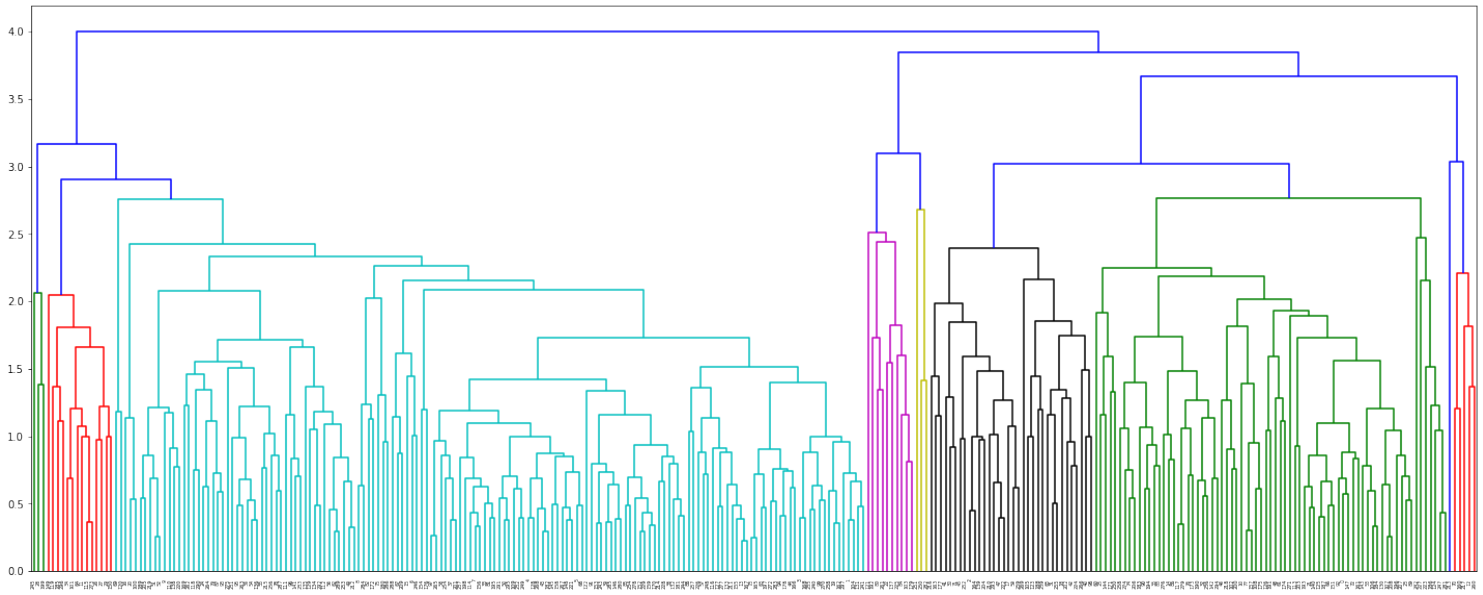
```
# Group average Hierarchical clustering
```

In [38]:

```
Z3 = linkage(X, 'average')
```

In [39]:

```
plt.figure(figsize=(25, 10))
dendrogram(Z3)
plt.show()
```



In [40]:

```
kclusters3 = fcluster(Z3, 3, criterion='maxclust')
kclusters3
```

Out[40]:

```
array([3, 1, 3, 1, 1, 1, 1, 1, 1, 1, 3, 1, 3, 1, 3, 1, 1, 3, 3, 1,
1, 3,
       2, 3, 1, 3, 1, 1, 1, 1, 3, 3, 3, 1, 1, 3, 1, 1, 1, 1, 3, 3,
3, 1,
       1, 3, 3, 3, 3, 1, 1, 1, 1, 3, 1, 1, 1, 1, 1, 3, 3, 3, 1, 1,
1, 3,
       3, 1, 1, 1, 3, 3, 3, 1, 3, 1, 3, 3, 1, 1, 2, 1, 1, 3, 2, 1,
3, 1,
       1, 3, 3, 1, 3, 1, 1, 1, 1, 1, 3, 1, 1, 1, 3, 2, 1, 3, 3, 3,
3, 1,
       1, 1, 1, 3, 1, 1, 1, 3, 1, 1, 1, 2, 1, 3, 3, 3, 3, 1, 1, 1,
3, 1,
       1, 1, 1, 1, 1, 2, 1, 3, 3, 1, 3, 3, 3, 1, 1, 3, 1, 1, 1, 3,
1, 1,
       1, 1, 1, 3, 1, 1, 3, 3, 1, 3, 3, 1, 1, 1, 1, 1, 1, 3, 1, 3,
3, 3,
       1, 3, 1, 2, 1, 1, 1, 3, 3, 1, 3, 3, 3, 1, 3, 3, 2, 3, 3, 1,
3, 1,
       1, 1, 3, 1, 3, 3, 3, 1, 3, 3, 3, 1, 3, 1, 1, 3, 1, 1, 3, 3,
3, 1,
       1, 1, 3, 3, 3, 2, 1, 3, 1, 1, 3, 1, 1, 1, 1, 1, 3, 1, 1, 3,
1, 1,
       3, 1, 1, 1, 1, 3, 1, 1, 2, 2, 3, 1, 1, 3, 1, 1, 3, 3, 3, 2,
1, 1,
       1, 1, 3, 1, 1, 3, 1, 3, 1, 1, 3, 1, 3, 1, 1, 3, 1, 3, 2, 1,
1, 1,
       1, 1, 1, 1, 1, 1, 1, 3, 3, 1, 1, 1], dtype=int32)
```

In [ ]:

```

```

In [41]:

```
# Comparisons between the 3 different versions of hierarchical clustering
```

In [43]:

```
# As seen from the dendrogram and also from the partitional clustering of the
hierarchical clustering with 3 clusters
# by cutting the dendrogram at a certain level which basically results in part
itional clustering, single link
# is not doing as good as complete and average versions of the model. Complete
and average versions can extract more
# information from data and distinguish clusters from each other more readily
than single link version. In dendrogram,
# it can be seen form the different colors present to differentiate the cluste
rs. There are more colors in complete
# and average versions. And in partitional clustering, with 3 cluster partitio
ns, single link version
# classifies most of the data into cluster "1", and there is little or no clus
ter "2" and "3" at all. In complete
# version, there is some more variety and has more cluster "2" and "3", althou
gh cluster "1" is still the most among
# the 3 clusters. And in group version, there's much more of "3" or "2" comapa
red to previous 2 versions. So average
# version of Hierarchical clustering has more uniform number of cluster "1", "
2" and "3". Thus it can distinguish
# different clusters more uniformly. In conclusion, the intermediate version o
f single link and complete link,
# which is the average version is a more appropriate method of performing Hier
archical clusterin in this case.
# Also, complete link version is ranked second best, and single link version i
s the worse among all 3.
```

In [ ]:

```

```

In [44]:

```
# Question 2
```

In [ ]:

```
# I will choose complete link and average versions of the Hierarchical cluster
ing to identify possible patterns and
# investigate the type of information we can get from the results obtained. Si
ngle link version is not going to be
# studied as it gives very poor representational data and information.
# Between complete and average versions, it can be seen that in general the gr
oup version connected between clusters at
# lowever level of the dendrogram with much less distance values and this can
intuitively mean that group version
# could recognize smaller colonies more easily and lable them as distinguishab
le clusters. This is why, there are
# more colors in the dendrogram and more clusters. At higher level of the dend
rogram , it can be seen that complete
# version has distance values of different clusters much larger, than that of
group, this is because complete version
# defines the minimum distance as the largest distance of any two point of two
clusters.
# For complete version, it can be seen that the clustering could recognize 4 m
ain clusters each of reasonable size.
# However the cluster size gradually decreases as seen from the dendogram amon
g its clusters. This gives the
# information that, there are 4 main clusters of different gradually decreasin
g sizes.
# For average version, it recognizes around 9 clusters, and it's seen that it
can distinguish more specific clusters.
# It can be thought that, the 4 main clusters in complete version have parts w
here another clusters can be formed
# which can be seen from the average version. This shows that there's some var
iety in the data itself in the 4 main
# clusters in complete version.
# For complete version, the difference of the distance values of the merges be
tween the higher and lower levels of
# dendrogram is large. This signifies, smaller similar clusters are grouped fi
rst, and the larger clusters which
# are futhur from each other are grouped last. This is what we want in cluster
ing. However this relationship is not
# as apparent in group version, so this could be an indicator that complete ve
rsion is better.
# If the data is interepreted at 2 cluster level of dendrogram, the average ve
rsion has 2 clusters of somewhat more
# equal size of clusters. However, it's quite unequal for the complete version
. But when the two clusters are grouped
# into one, the distance value for average version is much less than that of c
omplete version. This implies,
# grouping the data into 2 equal sizes does not show the proper cluster inform
ation because clusters are supposed to
# show that differences in data in the form of clusters. The higher the distan
ce value, the higher the difference
# between the clusters. Thus, the larger distance values usually, signifies a
correct clustering of data as we want
# to distinguish between different types of data in terms of clusters as much
as possible.
```

In [ ]:

```

```

In [106]:

```
# Question 3
```

In [ ]:

```
# The comparision done in this question is done by comparing the number of dat
a points in the clusters. For example,
# in 3 clusters, cluster A, B and C are just named to differentiate 3 differen
t clusters and compared to another
# method. But the cluster A in the new method does not refer to the same type
of class label of cluster A from another
# method. The names are just to differentiate the 3 different clusters. And th
e amount of data points in the clusters
# is used to compare and see how similar are the proportions. This can easily
and roughly tell us how good the
# clustering method is performing or similar to another clustering method by c
omparing the proportions of data points
# in the clusters from one model/clustering method to that of another
# 3 clusters will be used only as the class labels in the original dataset has
3 labels
# The performance of partitional clustering derived from hierarchical clusteri
ng will be compared to that of K-means
# and the proportions of original class labels will be used to check which is
performing better. Both, the complete
# and average versions of hierarchical clustering will be used to test.
```

In [107]:

```
# For complete link version
```

In [177]:

```
kclusters2 = fcluster(Z2, 3, criterion='maxclust')
kk = list(kclusters2)
print("From clustering solutions:")
print("Cluster A: ", kk.count(1))
print("Cluster B: ", kk.count(2))
print("Cluster C: ", kk.count(3))
```

```
From clustering solutions:
Cluster A:  229
Cluster B:  44
Cluster C:  25
```

In [109]:

```
km2 = KMeans(n_clusters=3)
km2.fit(X)
kk = list(km2.labels_)
print("From K-means:")
print("Cluster A: ", kk.count(0))
print("Cluster B: ", kk.count(1))
print("Cluster C: ", kk.count(2))
```

```
Cluster A:  108
Cluster B:  56
Cluster C:  134
```

In [144]:

```
kk = list(Y_train)
print("From original set of class labels:")
print("Cluster A: ", kk.count('DH'))
print("Cluster B: ", kk.count('SL'))
print("Cluster C: ", kk.count('NO'))
```

```
From original set of class labels:
Cluster A:  60
Cluster B:  150
Cluster C:  100
```

In [ ]:

```
# (a)
# Comapring for 3 clusters, the partitional clusterings derived from hierarchi
cal clusterings and k-means, it can be
# observed that k-means distributes the data points between the 3 clusters mor
e evenly. In the clustering solution
# the cluster A has abnormally more data points.
# (b)
# By comparing the 3 partitional clustering solution and K-means to the origin
al class labels of the dataset, we can
# see how well the clustering algorithms clustered the data properly with corr
ect proportions.
# Judging from the labels from the original dataset, one cluster has 60 data p
oints, one has 150, and the last one
# has 100. I didn't eliminate the outliers because it is small compared to the
original dataset size of only 12 points
# I just need to compare the proportions to have the conclusion I want to get.
Thus, two clusters need to have large
# number of data points and the difference in the number of data points betwee
n each clusters is around 50 roughly.
# Comparing these facts with the two clustering models, K-means is performing
relatively better.
```

In [ ]:

In [147]:

```
# For average version
```

In [153]:

```
kclusters3 = fcluster(Z3, 3, criterion='maxclust')
kk = list(kclusters3)
print("From clustering solutions:")
print("Cluster A: ", kk.count(1))
print("Cluster B: ", kk.count(2))
print("Cluster C: ", kk.count(3))
```

```
From clustering solutions:
Cluster A:  172
Cluster B:  13
Cluster C:  113
```

In [172]:

```
km2 = KMeans(n_clusters=3)
km2.fit(X)
kk = list(km2.labels_)
print("From K-means:")
print("Cluster A: ", kk.count(0))
print("Cluster B: ", kk.count(1))
print("Cluster C: ", kk.count(2))
```

```
From K-means:
Cluster A:  56
Cluster B:  134
Cluster C:  108
```

In [178]:

```
kk = list(Y_train)
print("From original set of class labels:")
print("Cluster A: ", kk.count('DH'))
print("Cluster B: ", kk.count('SL'))
print("Cluster C: ", kk.count('NO'))
```

```
From original set of class labels:
Cluster A:  60
Cluster B:  150
Cluster C:  100
```

In [180]:

```
# (a)
# The derived clustering solution, is performing more similar to that of k-mea
ns in this case, as not only one cluster
# abnormally has high number of data points, but two clusters have, which is s
imilar to that of K-means. But still,
# in the clustering solution the size of the largest cluster is much larger th
an the smallest cluster. The
# smallest cluster has abnotmally small number of data points. K-means is dist
ributing the data points more evenly.
# (b)
# Comparing the two models to proportions of class labels from the original da
taset, we can see that K-means is
# giving clusters which have proportions much similar to that of original data
set class labels. The smallest cluster
# in K-means has 56 data points in K-means very close to original small cluste
r value of 60 and the largest cluster
# is 134 to the original value of 150, which is much more close to that of wha
t clustering solutions is giving which
# is 172. Similarly, for the medium cluster, the number of data points is more
closer to the original set, for K-means
```

In [183]:

```
# In conclusion, K-means is performing better than the partitional clusterin s
olutions derived from the hierarchical
# clustering method in both complete version and average version.
```

In [ ]:

```

```

In [184]:

```
# Question 4
```

In [83]:

```
# In this part, different subsets of attributes from the dataset are selected
and hierarchical clustering is performed
# on the new subset and then compared to the original hierarchical clustering
structure. I will create subsets,
# each will have 4 attributes, by eliminating 2 of the attributes. An arbitrar
y simple subset selection I used is
# by eliminating the first 2 attributes first, then the next two, and finally,
the last two. This way, each
# attribute is eliminated once only and is considered in the subset twice so i
t's fair. Many other combinations can
# also form but this is good enough to generalize. The hierarchical clustering
version I will stick to is the complete
# link version because it generalizes the data clustering well, its performanc
e isn't poor nor the clsuterings are
# so detailed.
```

In [85]:

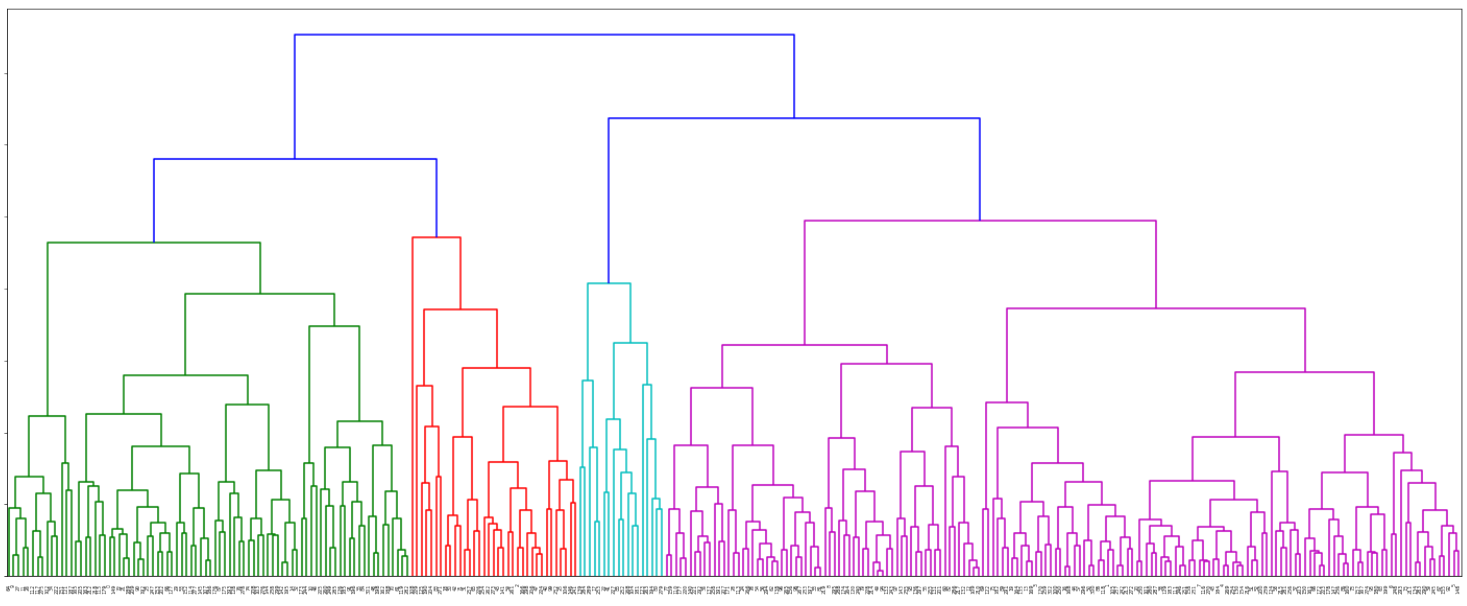
```
# Round 1 - Eliminate 0,1
```

In [81]:

```
X = X_train
df = pd.DataFrame(data=X)
df.columns = features
del df[features[0]]
del df[features[1]]
df = df[(np.abs(stats.zscore(df)) < 3).all(axis=1)]
XX = df.values
XX = stats.zscore(XX)
```

In [84]:

```
ZZ1 = linkage(XX, 'complete')
plt.figure(figsize=(25, 10))
dendrogram(ZZ1)
plt.show()
```



In [ ]:

```
# Comparing the result from the subset dataset to the original clustering, it
can be seen that again, 4 main clusters
# are found but are of different proportions than that of original one. The di
satance values of the clusters at
# higher level of the dendrogram is smaller in the new result this shows that,
the original clusterings could
# cluster data more properly for data which are apart.
```

In [ ]:

```

```

In [90]:

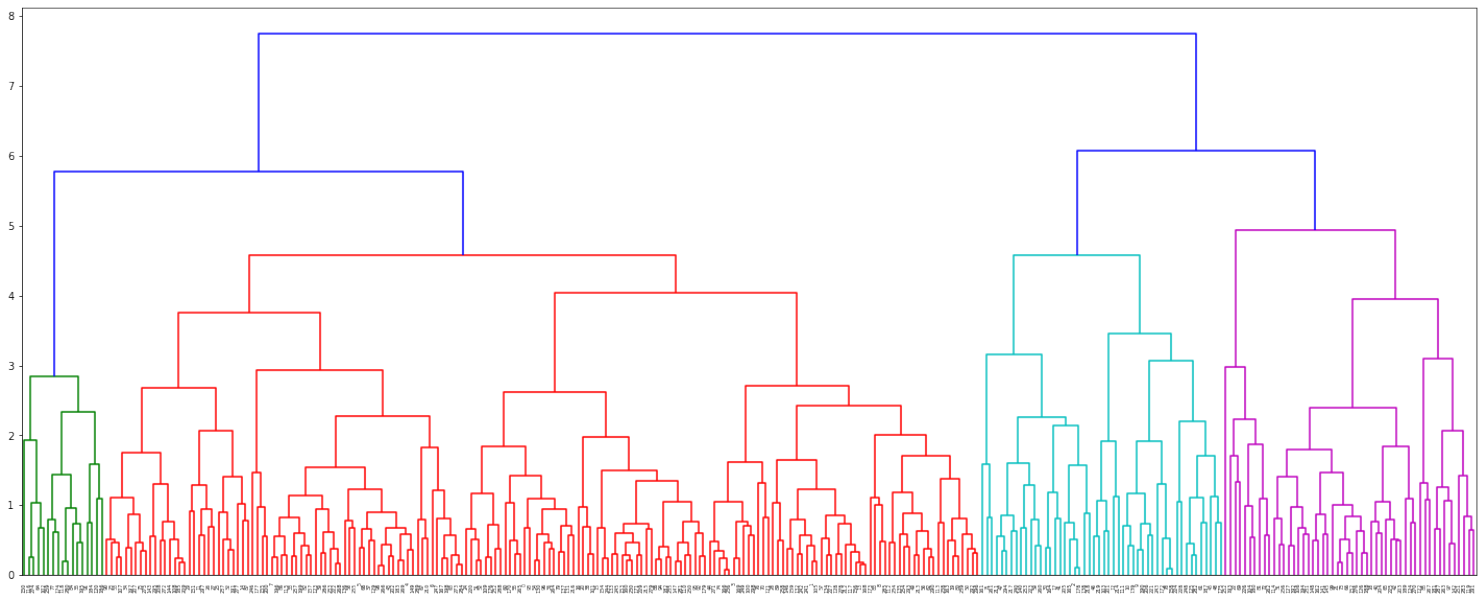
```
# Round 2 - Eliminate 2,3
```

In [91]:

```
X = X_train
df = pd.DataFrame(data=X)
df.columns = features
del df[features[2]]
del df[features[3]]
df = df[(np.abs(stats.zscore(df)) < 3).all(axis=1)]
XX = df.values
XX = stats.zscore(XX)
```

In [92]:

```
ZZ2 = linkage(XX, 'complete')
plt.figure(figsize=(25, 10))
dendrogram(ZZ2)
plt.show()
```



In [ ]:

```
# For the new result, it has shown that it can still show 4 main clusters, but one of them is shrunk considerably,
# and its data points joined the neighbouring cluster. On the other half of the data, the clusters remain almost the
# same. Thus, this shows that, there's a clear decline in cluster recognizition affecting a very specific group
# of data points.
```

In [ ]:

```

```

In [93]:

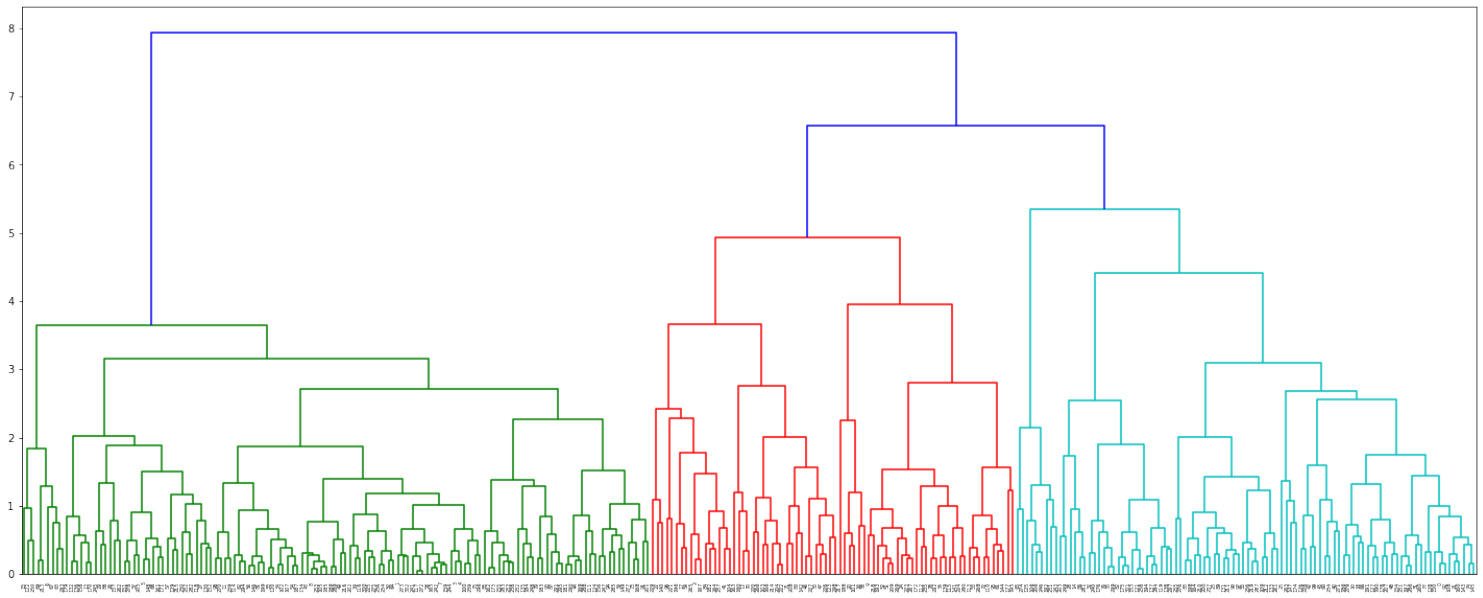
```
# Round 3 - Eliminate 4,5
```

In [94]:

```
X = X_train
df = pd.DataFrame(data=X)
df.columns = features
del df[features[4]]
del df[features[5]]
df = df[(np.abs(stats.zscore(df)) < 3).all(axis=1)]
XX = df.values
XX = stats.zscore(XX)
```

In [95]:

```
ZZ3 = linkage(XX, 'complete')
plt.figure(figsize=(25, 10))
dendrogram(ZZ3)
plt.show()
```



In [96]:

```
# The result of this new clustering is quite pleasing to see as there are clea
r 3 distinct clusters formed. And all
# of them are in relatively good size indicating, it's not a small cluster of
outliers, but group of data points
# belonging to a dinstint group. Also, we know that the original dataset, ther
e are 3 labels, so this new result
# can show/predict that more relatively. I think it's because, as decrease in
number of attributes, resulted in
# less complication of clustering the data, so the clustering could be general
ized more easily to represent the
# whole data. The new clustering recognizes 3 main clusters represented by the
3 colors which is 1 less than the
# original clustering.
```

In [ ]:

```

```

In [ ]:

```

```

In [ ]:

In [ ]: