# Hierarchial and K-means Clustering

## 21BAI1533 Zeel Mehta

In [103]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
```

In [104]:
```
from sklearn import datasets
iris=pd.read_csv('/Users/zeelmehta/Desktop/FALL INTER 23/ML/Decisio
```

In [105]:
```
iris
```

Out[105]:

| | Id | SepalLengthCm | SepalWidthCm | PetalLengthCm | PetalWidthCm | Species |
|---|---|---|---|---|---|---|
| **0** | 1 | 5.1 | 3.5 | 1.4 | 0.2 | Iris-setosa |
| **1** | 2 | 4.9 | 3.0 | 1.4 | 0.2 | Iris-setosa |
| **2** | 3 | 4.7 | 3.2 | 1.3 | 0.2 | Iris-setosa |
| **3** | 4 | 4.6 | 3.1 | 1.5 | 0.2 | Iris-setosa |
| **4** | 5 | 5.0 | 3.6 | 1.4 | 0.2 | Iris-setosa |
| **...** | ... | ... | ... | ... | ... | ... |
| **145** | 146 | 6.7 | 3.0 | 5.2 | 2.3 | Iris-virginica |
| **146** | 147 | 6.3 | 2.5 | 5.0 | 1.9 | Iris-virginica |
| **147** | 148 | 6.5 | 3.0 | 5.2 | 2.0 | Iris-virginica |
| **148** | 149 | 6.2 | 3.4 | 5.4 | 2.3 | Iris-virginica |
| **149** | 150 | 5.9 | 3.0 | 5.1 | 1.8 | Iris-virginica |

150 rows × 6 columns

In [106]:
```
x=iris.iloc[:, [0, 1, 2, 3]].values
x
```

```
[  6. ,   5.4,   3.9,   1.7],
[  7. ,   4.6,   3.4,   1.4],
[  8. ,   5. ,   3.4,   1.5],
[  9. ,   4.4,   2.9,   1.4],
[ 10. ,   4.9,   3.1,   1.5],
[ 11. ,   5.4,   3.7,   1.5],
[ 12. ,   4.8,   3.4,   1.6],
[ 13. ,   4.8,   3. ,   1.4],
[ 14. ,   4.3,   3. ,   1.1],
[ 15. ,   5.8,   4. ,   1.2],
[ 16. ,   5.7,   4.4,   1.5],
[ 17. ,   5.4,   3.9,   1.3],
[ 18. ,   5.1,   3.5,   1.4],
[ 19. ,   5.7,   3.8,   1.7],
[ 20. ,   5.1,   3.8,   1.5],
[ 21. ,   5.4,   3.4,   1.7],
[ 22. ,   5.1,   3.7,   1.5],
[ 23. ,   4.6,   3.6,   1. ],
[ 24. ,   5.1,   3.3,   1.7],
[ 25. ,   4.8,   3.4,   1.9],
```

In [107]:
```
iris.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 150 entries, 0 to 149
Data columns (total 6 columns):
 #   Column         Non-Null Count  Dtype
---  ------         --------------  -----
 0   Id             150 non-null    int64
 1   SepalLengthCm  150 non-null    float64
 2   SepalWidthCm   150 non-null    float64
 3   PetalLengthCm  150 non-null    float64
 4   PetalWidthCm   150 non-null    float64
 5   Species        150 non-null    object
dtypes: float64(4), int64(1), object(1)
memory usage: 7.2+ KB
```

In [108]:
```
iris[0:10]
```

Out[108]:

| | Id | SepalLengthCm | SepalWidthCm | PetalLengthCm | PetalWidthCm | Species |
|---|---|---|---|---|---|---|
| **0** | 1 | 5.1 | 3.5 | 1.4 | 0.2 | Iris-setosa |
| **1** | 2 | 4.9 | 3.0 | 1.4 | 0.2 | Iris-setosa |
| **2** | 3 | 4.7 | 3.2 | 1.3 | 0.2 | Iris-setosa |
| **3** | 4 | 4.6 | 3.1 | 1.5 | 0.2 | Iris-setosa |
| **4** | 5 | 5.0 | 3.6 | 1.4 | 0.2 | Iris-setosa |
| **5** | 6 | 5.4 | 3.9 | 1.7 | 0.4 | Iris-setosa |
| **6** | 7 | 4.6 | 3.4 | 1.4 | 0.3 | Iris-setosa |
| **7** | 8 | 5.0 | 3.4 | 1.5 | 0.2 | Iris-setosa |
| **8** | 9 | 4.4 | 2.9 | 1.4 | 0.2 | Iris-setosa |
| **9** | 10 | 4.9 | 3.1 | 1.5 | 0.1 | Iris-setosa |

In [109]:
```
iriso=pd.crosstab(index=iris["Species"],columns="count")
```

In [110]:
```
iriso
```

Out[110]:

| col_0 | count |
|---|---|
| **Species** | |
| **Iris-setosa** | 50 |
| **Iris-versicolor** | 50 |
| **Iris-virginica** | 50 |

In [111]:
```
irissetosa=iris.loc[iris["Species"]=="Iris-setosa"]
irissetosa.head()
```

Out[111]:

| | Id | SepalLengthCm | SepalWidthCm | PetalLengthCm | PetalWidthCm | Species |
|---|---|---|---|---|---|---|
| **0** | 1 | 5.1 | 3.5 | 1.4 | 0.2 | Iris-setosa |
| **1** | 2 | 4.9 | 3.0 | 1.4 | 0.2 | Iris-setosa |
| **2** | 3 | 4.7 | 3.2 | 1.3 | 0.2 | Iris-setosa |
| **3** | 4 | 4.6 | 3.1 | 1.5 | 0.2 | Iris-setosa |
| **4** | 5 | 5.0 | 3.6 | 1.4 | 0.2 | Iris-setosa |

In [112]:
```
irisvirginica=iris.loc[iris["Species"]=="Iris-virginica"]
irisvirginica.head()
```

Out[112]:

| | Id | SepalLengthCm | SepalWidthCm | PetalLengthCm | PetalWidthCm | Species |
|---|---|---|---|---|---|---|
| **100** | 101 | 6.3 | 3.3 | 6.0 | 2.5 | Iris-virginica |
| **101** | 102 | 5.8 | 2.7 | 5.1 | 1.9 | Iris-virginica |
| **102** | 103 | 7.1 | 3.0 | 5.9 | 2.1 | Iris-virginica |
| **103** | 104 | 6.3 | 2.9 | 5.6 | 1.8 | Iris-virginica |
| **104** | 105 | 6.5 | 3.0 | 5.8 | 2.2 | Iris-virginica |

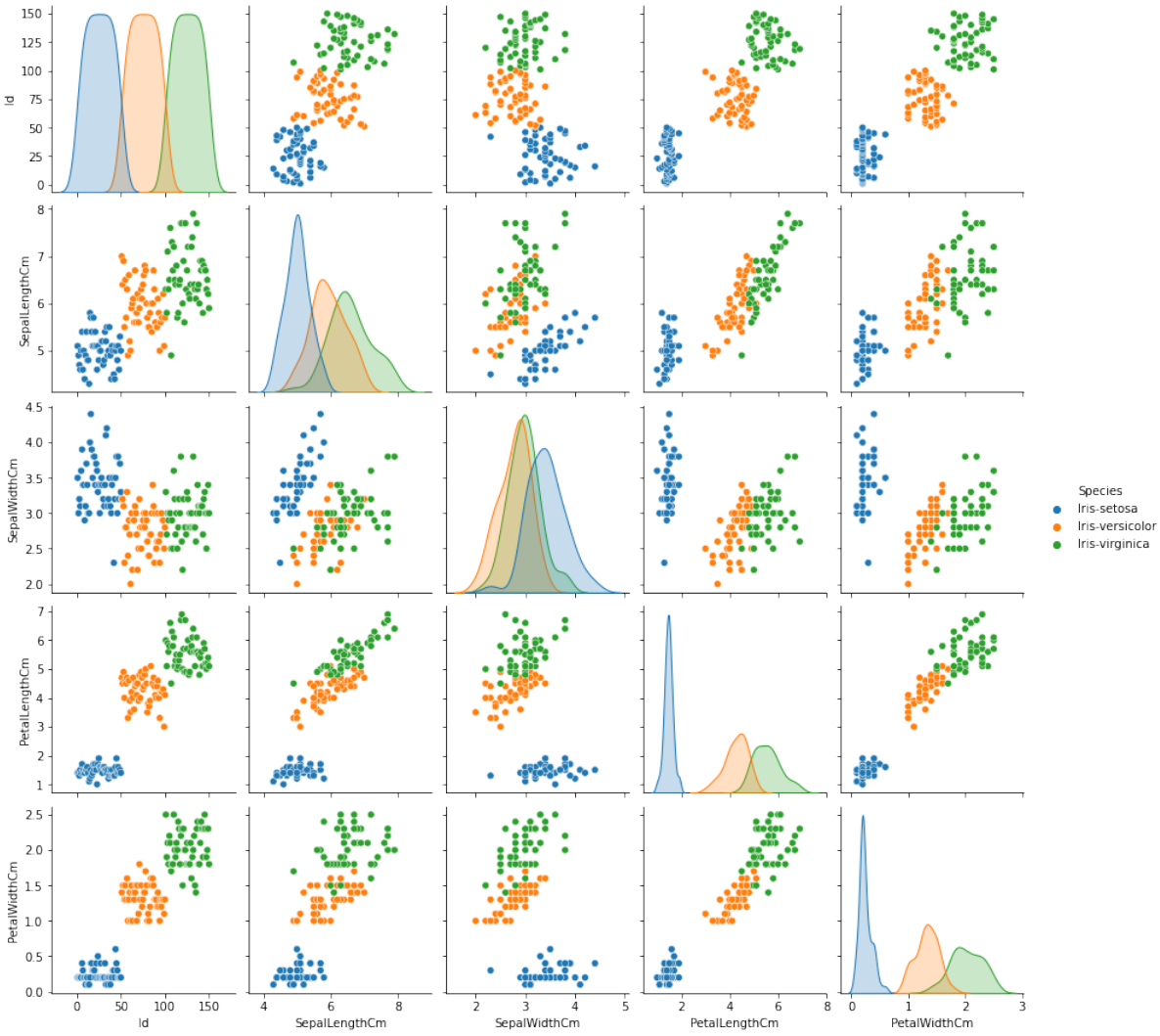
In [113]:
```
irisversi=iris.loc[iris["Species"]=="Iris-versicolor"]
irisversi.head()
```

Out[113]:

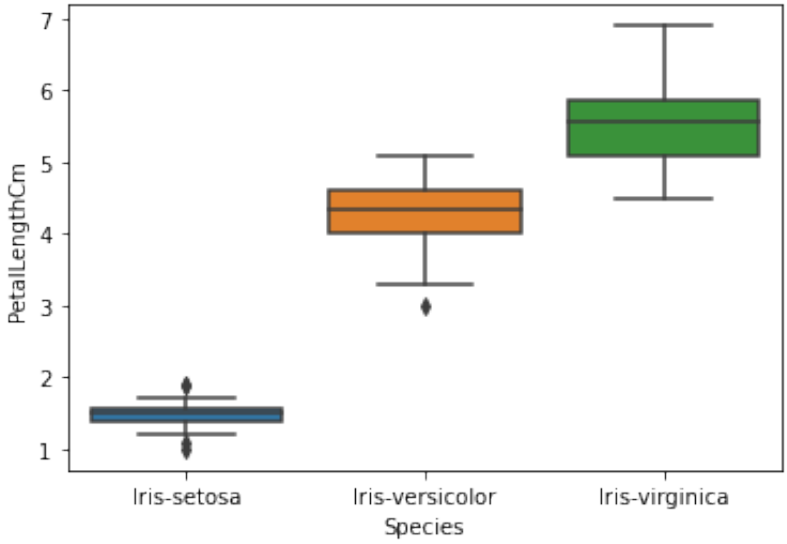
| | Id | SepalLengthCm | SepalWidthCm | PetalLengthCm | PetalWidthCm | Species |
|---|---|---|---|---|---|---|
| **50** | 51 | 7.0 | 3.2 | 4.7 | 1.4 | Iris-versicolor |
| **51** | 52 | 6.4 | 3.2 | 4.5 | 1.5 | Iris-versicolor |
| **52** | 53 | 6.9 | 3.1 | 4.9 | 1.5 | Iris-versicolor |
| **53** | 54 | 5.5 | 2.3 | 4.0 | 1.3 | Iris-versicolor |
| **54** | 55 | 6.5 | 2.8 | 4.6 | 1.5 | Iris-versicolor |

In [114]:
```
sns.pairplot(iris,hue="Species")
```

Out[114]: <seaborn.axisgrid.PairGrid at 0x17cd06af0>




In [115]:
```
sns.boxplot(x="Species",y="PetalLengthCm",data=iris)
plt.show()
```

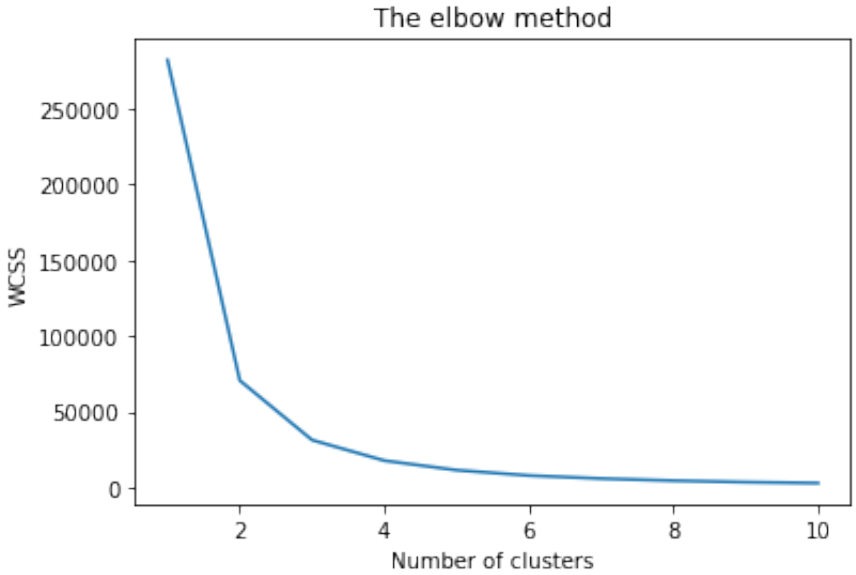


# K means

In [116]:
```
from sklearn.cluster import KMeans
wcss = []
```

In [117]:
```
for i in range(1, 11):
    kmeans = KMeans(n_clusters = i, init = 'k-means++', max_iter =
    kmeans.fit(x)
    wcss.append(kmeans.inertia_)
```

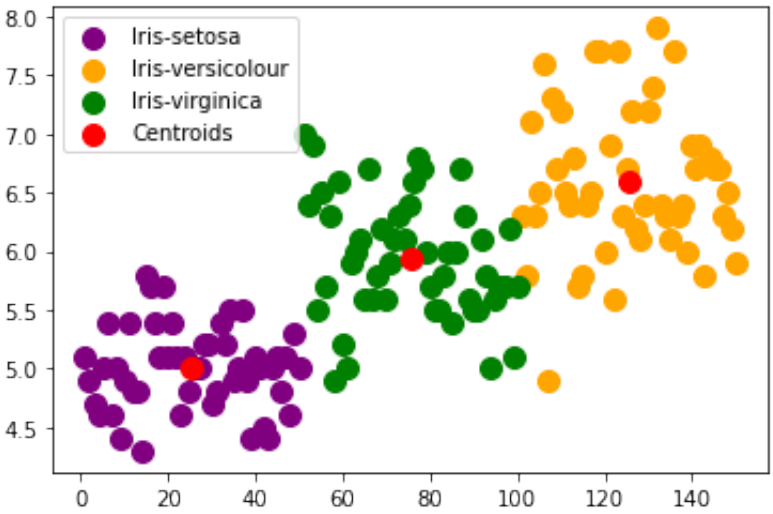
In [118]:
```
plt.plot(range(1, 11), wcss)
plt.title('The elbow method')
plt.xlabel('Number of clusters')
plt.ylabel('WCSS') #within cluster sum of squares
plt.show()
```



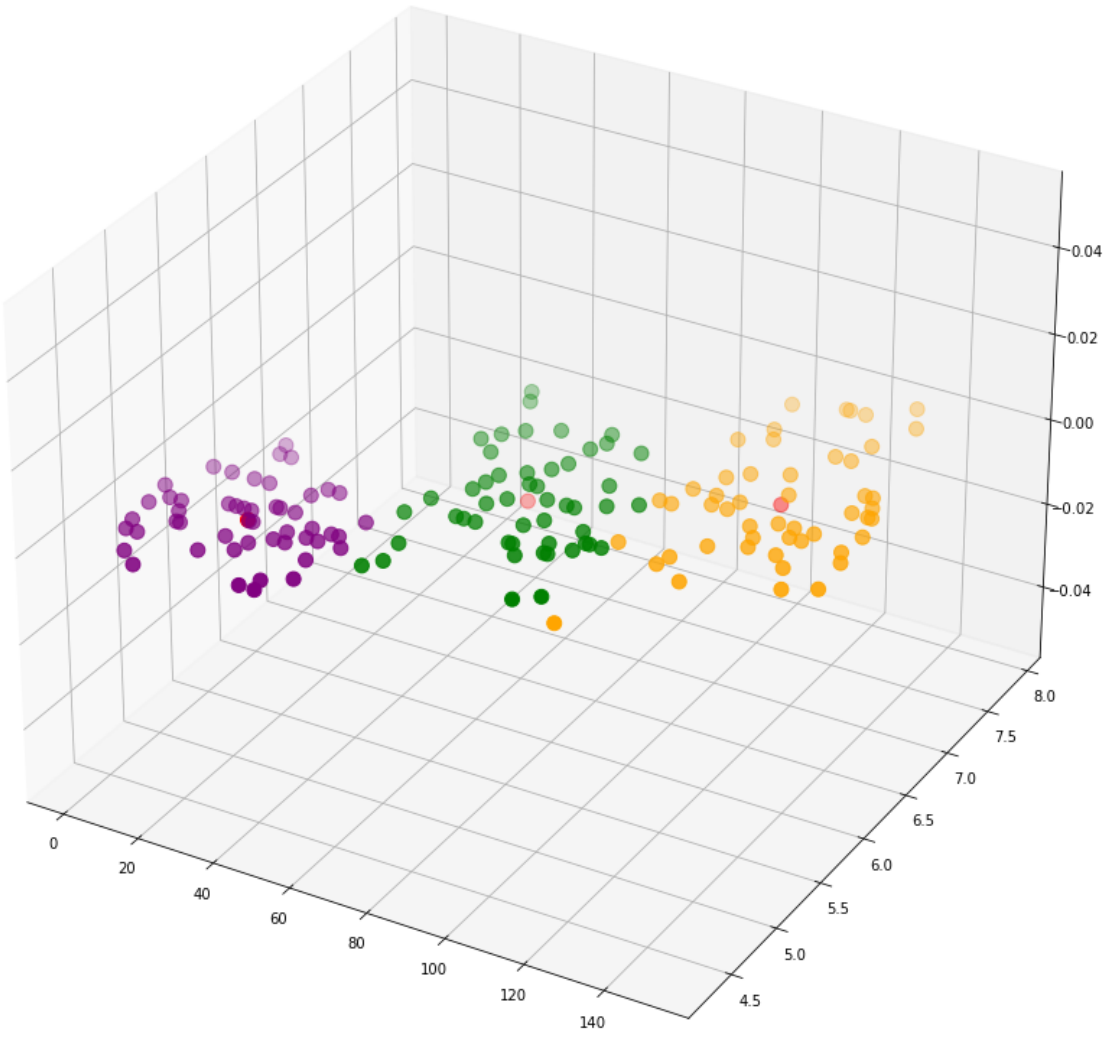

In [119]:
```
kmeans = KMeans(n_clusters = 3, init = 'k-means++', max_iter = 300,
y_kmeans = kmeans.fit_predict(x)
```

In [120]:
```
plt.scatter(x[y_kmeans == 0, 0], x[y_kmeans == 0, 1], s = 100, c =
plt.scatter(x[y_kmeans == 1, 0], x[y_kmeans == 1, 1], s = 100, c =
plt.scatter(x[y_kmeans == 2, 0], x[y_kmeans == 2, 1], s = 100, c =
plt.scatter(kmeans.cluster_centers_[:, 0], kmeans.cluster_centers_[
plt.legend()
```

Out[120]:
```
<matplotlib.legend.Legend at 0x1393c3490>
```



In [121]:
```
fig = plt.figure(figsize = (15,15))
ax = fig.add_subplot(111, projection='3d')
plt.scatter(x[y_kmeans == 0, 0], x[y_kmeans == 0, 1], s = 100, c =
plt.scatter(x[y_kmeans == 1, 0], x[y_kmeans == 1, 1], s = 100, c =
plt.scatter(x[y_kmeans == 2, 0], x[y_kmeans == 2, 1], s = 100, c =
plt.scatter(kmeans.cluster_centers_[:, 0], kmeans.cluster_centers_[
plt.show()
```

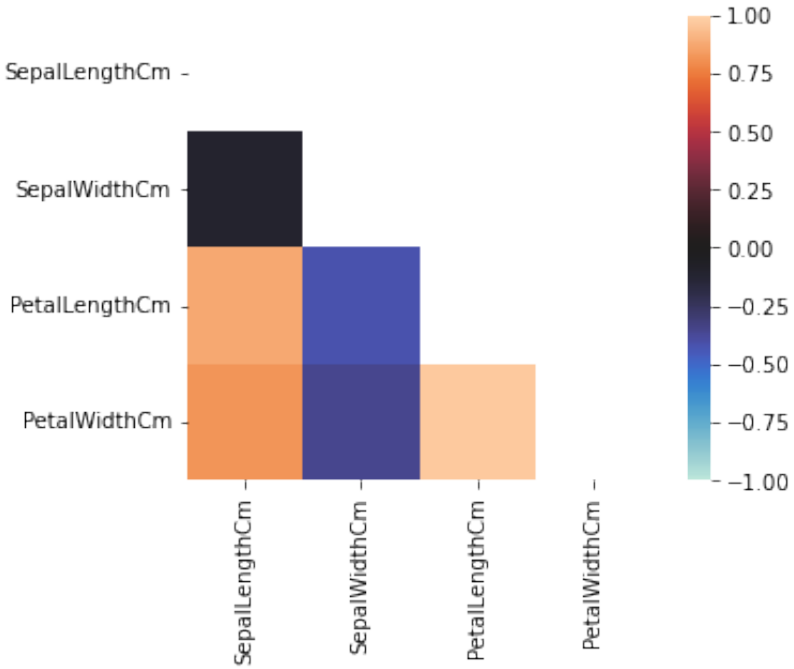



# HIERARCHIAL CLUSTERING

In [122]:
```
matcorr = iris.iloc[:,~iris.columns.isin(['Id','Species'])].corr()
mask = np.zeros_like(matcorr, dtype=np.bool)
mask[np.triu_indices_from(mask)] = True
```

```
/var/folders/72/3kxng2yd5yn203b626zw3kpc0000gn/T/ipykernel_11074/3
622765179.py:2: DeprecationWarning: `np.bool` is a deprecated alia
s for the builtin `bool`. To silence this warning, use `bool` by i
tself. Doing this will not modify any behavior and is safe. If you
specifically wanted the numpy scalar type, use `np.bool_` here.
Deprecated in NumPy 1.20; for more details and guidance: https://n
umpy.org/devdocs/release/1.20.0-notes.html#deprecations
(https://numpy.org/devdocs/release/1.20.0-notes.html#deprecations)
  mask = np.zeros_like(matcorr, dtype=np.bool)
```

In [123]:
```
sns.heatmap(matcorr, mask=mask, vmin=-1, vmax=1, center=0, square=T
```

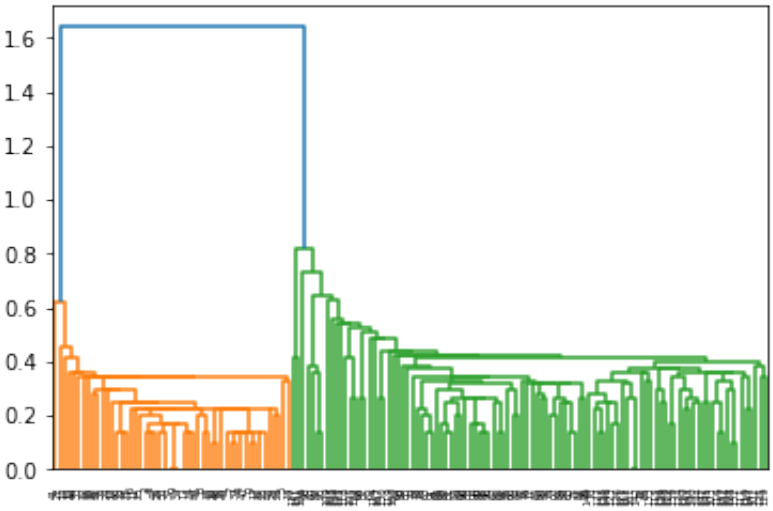



In [124]:
```
from scipy.cluster.hierarchy import dendrogram, linkage
```

## single linkage

In [125]:
```
dist_sin = linkage(iris.loc[:,["SepalLengthCm","SepalWidthCm","Peta
```

In [126]:
```
dendrogram(dist_sin, leaf_rotation=90)
plt.figure(figsize=(18,6))
plt.show()
```




```
<Figure size 1296x432 with 0 Axes>
```

In [127]:
```
from scipy.cluster.hierarchy import fcluster
iris_SM=iris.copy()
```

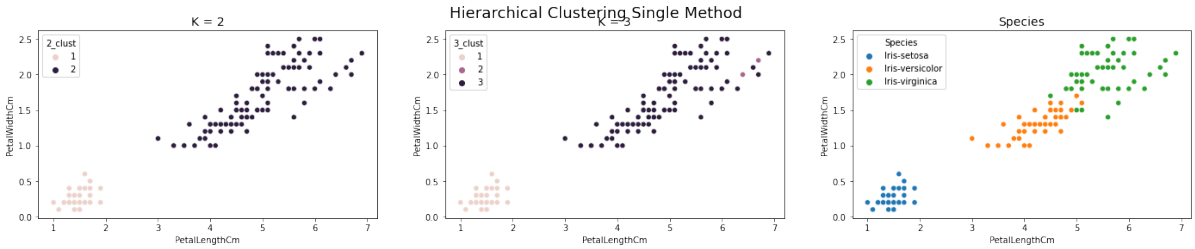
In [128]:
```
iris_SM['2_clust']=fcluster(dist_sin,2, criterion='maxclust')
iris_SM['3_clust']=fcluster(dist_sin,3, criterion='maxclust')
iris_SM.head()
```

Out[128]:

| | Id | SepalLengthCm | SepalWidthCm | PetalLengthCm | PetalWidthCm | Species | 2_clust | 3_ |
|---|---|---|---|---|---|---|---|---|
| **0** | 1 | 5.1 | 3.5 | 1.4 | 0.2 | Iris-setosa | 1 | |
| **1** | 2 | 4.9 | 3.0 | 1.4 | 0.2 | Iris-setosa | 1 | |
| **2** | 3 | 4.7 | 3.2 | 1.3 | 0.2 | Iris-setosa | 1 | |
| **3** | 4 | 4.6 | 3.1 | 1.5 | 0.2 | Iris-setosa | 1 | |
| **4** | 5 | 5.0 | 3.6 | 1.4 | 0.2 | Iris-setosa | 1 | |

In [129]:
```
plt.figure(figsize=(24,4))

plt.suptitle("Hierarchical Clustering Single Method",fontsize=18)

plt.subplot(1,3,1)
plt.title("K = 2",fontsize=14)
sns.scatterplot(x="PetalLengthCm",y="PetalWidthCm", data=iris_SM, h

plt.subplot(1,3,2)
plt.title("K = 3",fontsize=14)
sns.scatterplot(x="PetalLengthCm",y="PetalWidthCm", data=iris_SM, h

plt.subplot(1,3,3)
plt.title("Species",fontsize=14)
sns.scatterplot(x="PetalLengthCm",y="PetalWidthCm", data=iris_SM, h
```

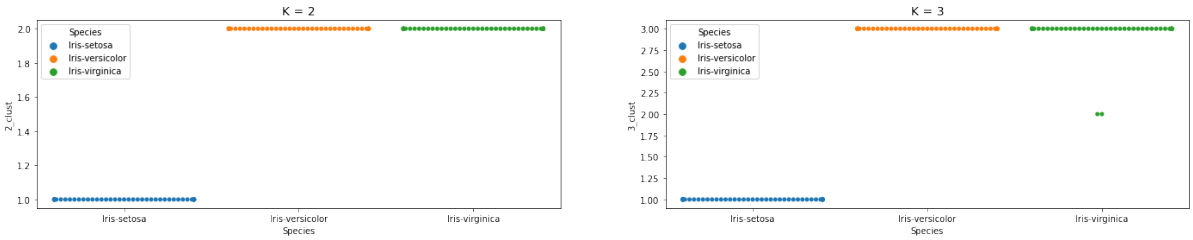
Out[129]:
```
<AxesSubplot:title={'center':'Species'}, xlabel='PetalLengthCm', y
label='PetalWidthCm'>
```



In [130]:
```
plt.figure(figsize=(24,4))
plt.subplot(1,2,1)
plt.title("K = 2",fontsize=14)
sns.swarmplot(x="Species",y="2_clust", data=iris_SM, hue="Species")

plt.subplot(1,2,2)
plt.title("K = 3",fontsize=14)
sns.swarmplot(x="Species",y="3_clust", data=iris_SM, hue="Species")
```

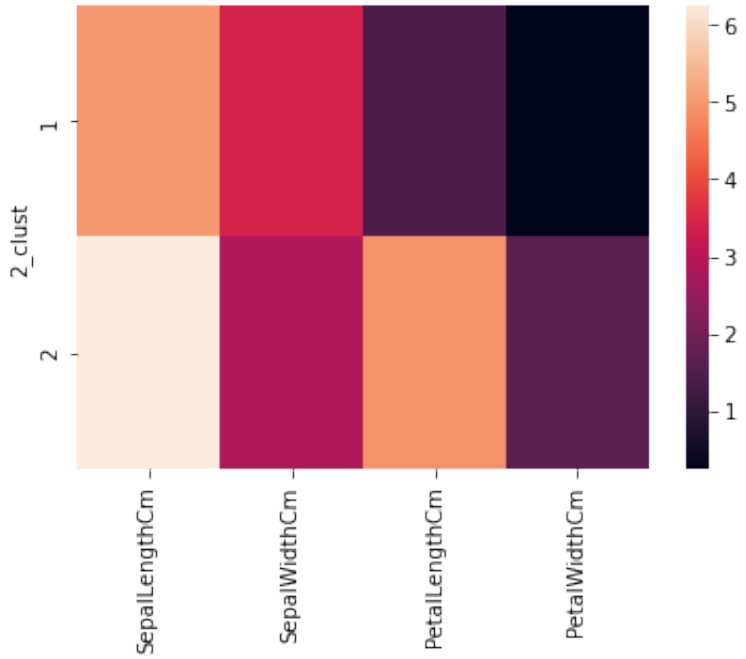
```
/Users/zeelmehta/opt/anaconda3/lib/python3.9/site-packages/seaborn
/categorical.py:1296: UserWarning: 38.0% of the points cannot be p
laced; you may want to decrease the size of the markers or use str
ipplot.
  warnings.warn(msg, UserWarning)
/Users/zeelmehta/opt/anaconda3/lib/python3.9/site-packages/seaborn
/categorical.py:1296: UserWarning: 38.0% of the points cannot be p
laced; you may want to decrease the size of the markers or use str
ipplot.
  warnings.warn(msg, UserWarning)
/Users/zeelmehta/opt/anaconda3/lib/python3.9/site-packages/seaborn
/categorical.py:1296: UserWarning: 34.0% of the points cannot be p
laced; you may want to decrease the size of the markers or use str
ipplot.
  warnings.warn(msg, UserWarning)
```

Out[130]:
```
<AxesSubplot:title={'center':'K = 3'}, xlabel='Species', ylabel='3
_clust'>
```



In [131]:
```
loc[:,["SepalLengthCm","SepalWidthCm","PetalLengthCm","PetalWidthCm'
```

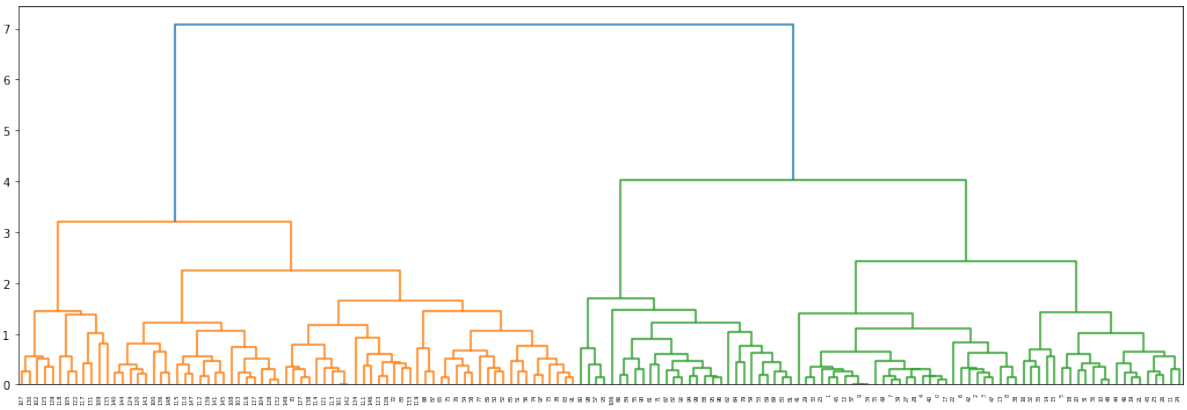
Out[131]: <AxesSubplot:ylabel='2_clust'>




## Complete linkage

In [132]:
```
dist_comp = linkage(iris.loc[:,["SepalLengthCm","SepalWidthCm","Pet
```

In [133]:
```
plt.figure(figsize=(18,6))
dendrogram(dist_comp, leaf_rotation=90)
plt.show()
```



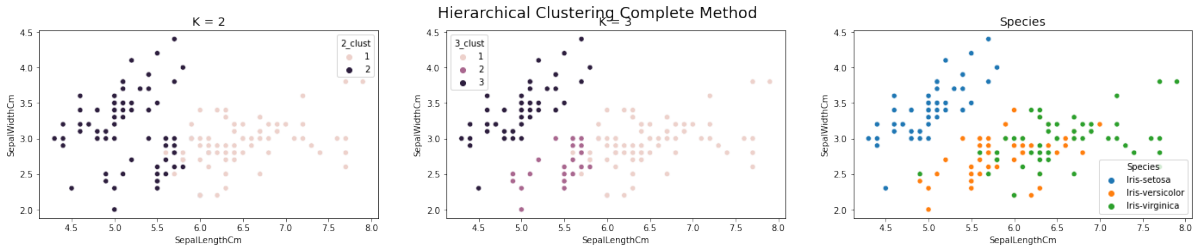
In [134]:
```
iris_CM=iris.copy()
iris_CM['2_clust']=fcluster(dist_comp,2, criterion='maxclust')
iris_CM['3_clust']=fcluster(dist_comp,3, criterion='maxclust')
iris_CM.head()
```

Out[134]:

| | Id | SepalLengthCm | SepalWidthCm | PetalLengthCm | PetalWidthCm | Species | 2_clust | 3_ |
|---|---|---|---|---|---|---|---|---|
| **0** | 1 | 5.1 | 3.5 | 1.4 | 0.2 | Iris-setosa | 2 | |
| **1** | 2 | 4.9 | 3.0 | 1.4 | 0.2 | Iris-setosa | 2 | |
| **2** | 3 | 4.7 | 3.2 | 1.3 | 0.2 | Iris-setosa | 2 | |
| **3** | 4 | 4.6 | 3.1 | 1.5 | 0.2 | Iris-setosa | 2 | |
| **4** | 5 | 5.0 | 3.6 | 1.4 | 0.2 | Iris-setosa | 2 | |

In [135]:
```
plt.figure(figsize=(24,4))

plt.suptitle("Hierarchical Clustering Complete Method",fontsize=18)

plt.subplot(1,3,1)
plt.title("K = 2",fontsize=14)
sns.scatterplot(x="SepalLengthCm",y="SepalWidthCm", data=iris_CM, h

plt.subplot(1,3,2)
plt.title("K = 3",fontsize=14)
sns.scatterplot(x="SepalLengthCm",y="SepalWidthCm", data=iris_CM, h

plt.subplot(1,3,3)
plt.title("Species",fontsize=14)
sns.scatterplot(x="SepalLengthCm",y="SepalWidthCm", data=iris_CM, h
```

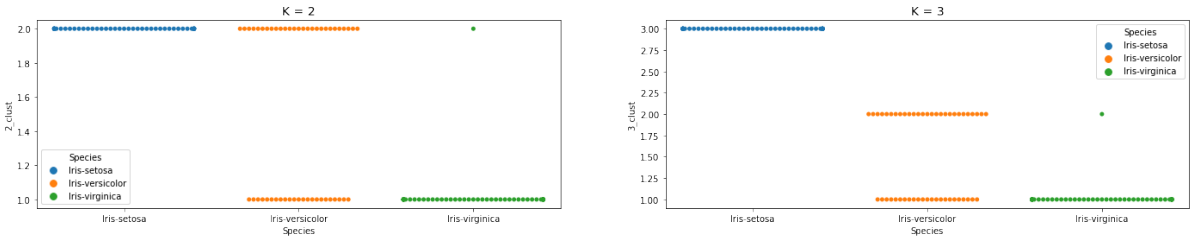
Out[135]:
```
<AxesSubplot:title={'center':'Species'}, xlabel='SepalLengthCm', y
label='SepalWidthCm'>
```



In [136]:
```
plt.figure(figsize=(24,4))
plt.subplot(1,2,1)
plt.title("K = 2",fontsize=14)
sns.swarmplot(x="Species",y="2_clust", data=iris_CM, hue="Species")

plt.subplot(1,2,2)
plt.title("K = 3",fontsize=14)
sns.swarmplot(x="Species",y="3_clust", data=iris_CM, hue="Species")
```

```
/Users/zeelmehta/opt/anaconda3/lib/python3.9/site-packages/seaborn
/categorical.py:1296: UserWarning: 38.0% of the points cannot be p
laced; you may want to decrease the size of the markers or use str
ipplot.
  warnings.warn(msg, UserWarning)
/Users/zeelmehta/opt/anaconda3/lib/python3.9/site-packages/seaborn
/categorical.py:1296: UserWarning: 36.0% of the points cannot be p
laced; you may want to decrease the size of the markers or use str
ipplot.
  warnings.warn(msg, UserWarning)
/Users/zeelmehta/opt/anaconda3/lib/python3.9/site-packages/seaborn
/categorical.py:1296: UserWarning: 38.0% of the points cannot be p
laced; you may want to decrease the size of the markers or use str
ipplot.
  warnings.warn(msg, UserWarning)
/Users/zeelmehta/opt/anaconda3/lib/python3.9/site-packages/seaborn
/categorical.py:1296: UserWarning: 36.0% of the points cannot be p
laced; you may want to decrease the size of the markers or use str
ipplot.
  warnings.warn(msg, UserWarning)
```

Out[136]:
```
<AxesSubplot:title={'center':'K = 3'}, xlabel='Species', ylabel='3
_clust'>
```



In [137]:
```
loc[:,["SepalLengthCm","SepalWidthCm","PetalLengthCm","PetalWidthCm'
```

Out[137]: <AxesSubplot:ylabel='3_clust'>