P2_Grant_Eric

February 17, 2021

[1]:
```
from sklearn.preprocessing import MinMaxScaler
from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import scale
from scipy.cluster import hierarchy
from scipy.cluster.hierarchy import dendrogram
from sklearn import cluster
from sklearn import metrics
from scipy.spatial import distance
from scipy import stats
import sklearn as sk
import pandas as pd
import numpy as np
import matplotlib as mpl
import matplotlib.pyplot as plt
import seaborn as sb
import gapstat as gs
import plotly.express as px
import plotly.graph_objects as go
%matplotlib inline
```

1 Part A

1.1 Question 1

Group Name: Plum

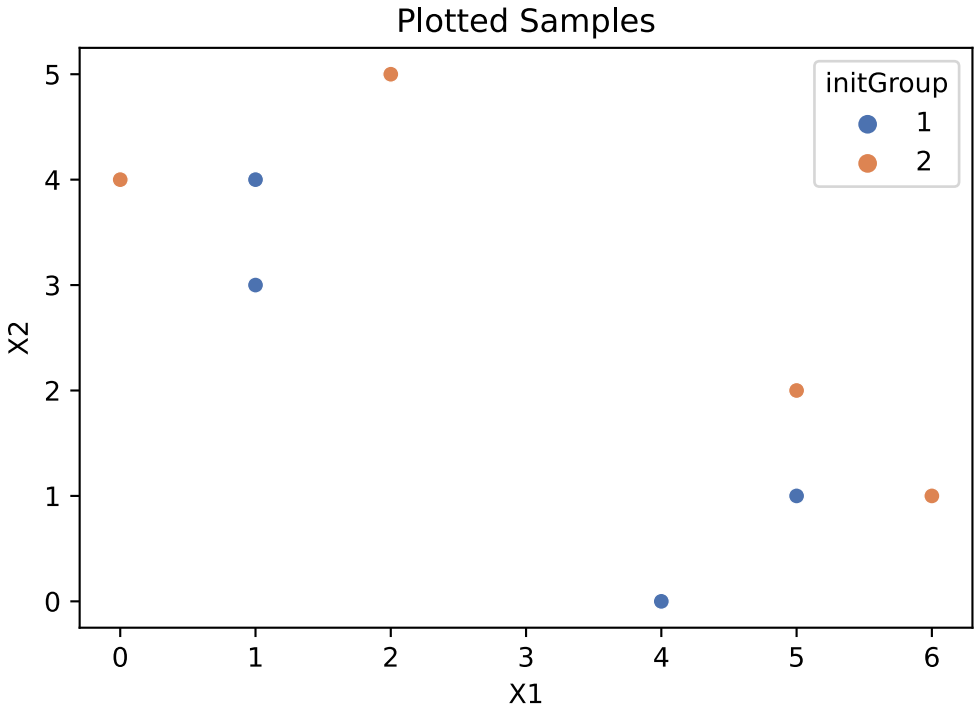
Group Member: Eric Grant

1.2 Question 2: K-Means Clustering

1.2.1 (a)

[2]:
```
points = pd.DataFrame({
    'sample':    [1,2,3,4,5,6,7,8],
    'x1':        [0,1,1,2,4,5,5,6],
    'x2':        [4,3,4,5,0,1,2,1],
    'initGroup': [2,1,1,2,1,1,2,2],
    'group': [2,1,1,2,1,1,2,2]
```

```
})
plot = sb.scatterplot(data=points, x="x1", y="x2", hue="initGroup",␣
 ↪palette="deep")
plot.set(xlabel="X1", ylabel="X2")
plt.title("Plotted Samples")
plt.show()
```



1.2.2 (b + c)

[3]:
```
group1 = points[points["initGroup"] == 1]
group2 = points[points["initGroup"] == 2]

centroid1 = ((sum(group1["x1"])/len(group1)), (sum(group1["x2"])/len(group1)))
centroid2 = ((sum(group2["x1"])/len(group2)), (sum(group2["x2"])/len(group2)))

centroids = pd.DataFrame({
    'group': ["Group1","Group2"],
    'x1': [centroid1[0], centroid2[0]],
    'x2': [centroid1[1], centroid2[1]]
})

for index, row in points.iterrows():
    cord = np.array((row[1],row[2]))
```

```
    distance1 = np.linalg.norm(cord - centroid1)
    distance2 = np.linalg.norm(cord - centroid2)
    if (distance1 < distance2):
        points.at[index,"group"] = 1
    elif (distance1 > distance2):
        points.at[index,"group"] = 2

print("Iteration: 1")
display(centroids)
display(points[["sample","group"]])
```

```
Iteration: 1
```

	group	x1	x2
0	Group1	2.75	2.0
1	Group2	3.25	3.0

	sample	group
0	1	2
1	2	1
2	3	2
3	4	2
4	5	1
5	6	1
6	7	2
7	8	2

1.2.3 (d)

[4]:
```
iteration = 2
while True:
    clone = centroids
    group1 = points[points["group"] == 1]
    group2 = points[points["group"] == 2]
    centroid1 = ((sum(group1["x1"])/len(group1)), (sum(group1["x2"])/
 ↪len(group1)))
    centroid2 = ((sum(group2["x1"])/len(group2)), (sum(group2["x2"])/
 ↪len(group2)))
    centroids = pd.DataFrame({'group': ["Group1","Group2"],'x1': [centroid1[0],␣
 ↪centroid2[0]],'x2': [centroid1[1], centroid2[1]]})

    for index, row in points.iterrows():
        cord = np.array((row[1],row[2]))
        distance1 = np.linalg.norm(cord - centroid1)
        distance2 = np.linalg.norm(cord - centroid2)
        if (distance1 < distance2):
            points.at[index,"group"] = 1
        elif (distance1 > distance2):
```

```
            points.at[index,"group"] = 2

    print("Iteration:", iteration)
    display(centroids)
    display(points[["sample","group"]])
    print()
    iteration += 1

    if (centroids.equals(clone)):
        break
```

```
Iteration: 2
```

	group	x1	x2
0	Group1	3.333333	1.333333
1	Group2	2.800000	3.200000

	sample	group
0	1	2
1	2	2
2	3	2
3	4	2
4	5	1
5	6	1
6	7	1
7	8	1

```
Iteration: 3
```

	group	x1	x2
0	Group1	5.0	1.0
1	Group2	1.0	4.0

	sample	group
0	1	2
1	2	2
2	3	2
3	4	2
4	5	1
5	6	1
6	7	1
7	8	1

```
Iteration: 4
```

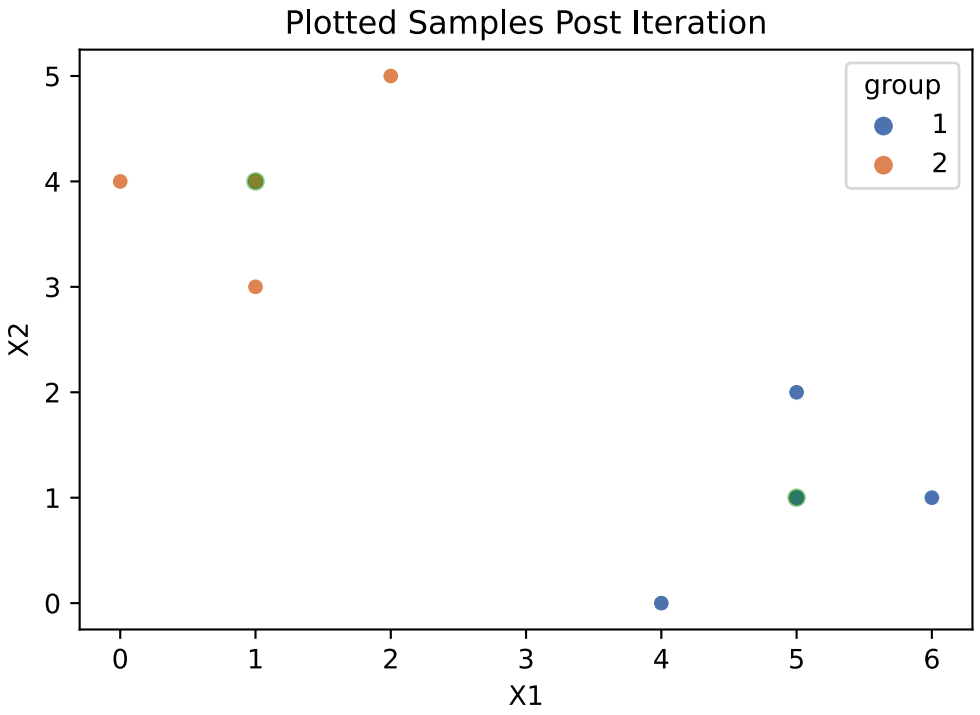
	group	x1	x2
0	Group1	5.0	1.0
1	Group2	1.0	4.0

	sample	group
0	1	2
1	2	2
2	3	2
3	4	2
4	5	1
5	6	1
6	7	1
7	8	1

1.2.4 (e)

Green points are centroids

[5]:
```
plot = sb.scatterplot(data=points, x="x1", y="x2", hue="group", palette="deep")
plot.set(xlabel="X1", ylabel="X2")
plt.title("Plotted Samples Post Iteration")
plt.scatter(x=5, y=1, color='g', alpha=0.4)
plt.scatter(x=1, y=4, color='g', alpha=0.4)
plt.show()
```



1.3 Question 3

Original Data

	1	2	3	4	5
1	0	-	-	-	-
2	0.3	0	-	-	-
3	0.4	0.5	0	-	-
4	0.7	0.8	0.45	0	-
5	0.6	0.2	0.4	0.35	0

1.3.1 (a)

Step 1. Combine 2 and 5

	1	25	3	4
1	0	-	-	-
25	0.6	0	-	-
3	0.4	0.5	0	-
4	0.7	0.8	0.45	0

Step 2. Combine 1 and 3

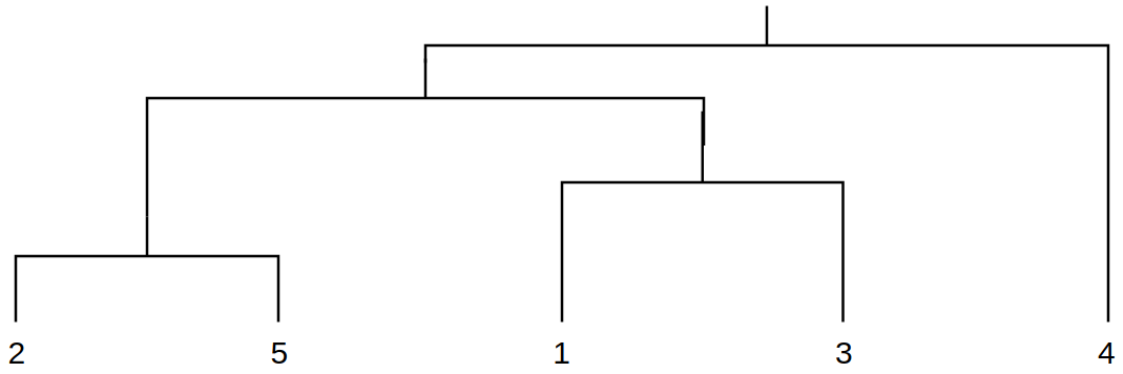
	13	25	4
13	0	-	-
25	0.6	0	-
4	0.7	0.8	0

Step 3. Combine 13 and 25

	1325	4
1325	0	-
4	0.8	0

Step 4. Combine 1325 and 4

	13254
13254	0



1.3.2 (b)

Step 1. Combine 2 and 5

	1	25	3	4
1	0	-	-	-
25	0.3	0	-	-
3	0.4	0.4	0	-
4	0.7	0.35	0.45	0

Step 2. Combine 1 and 25

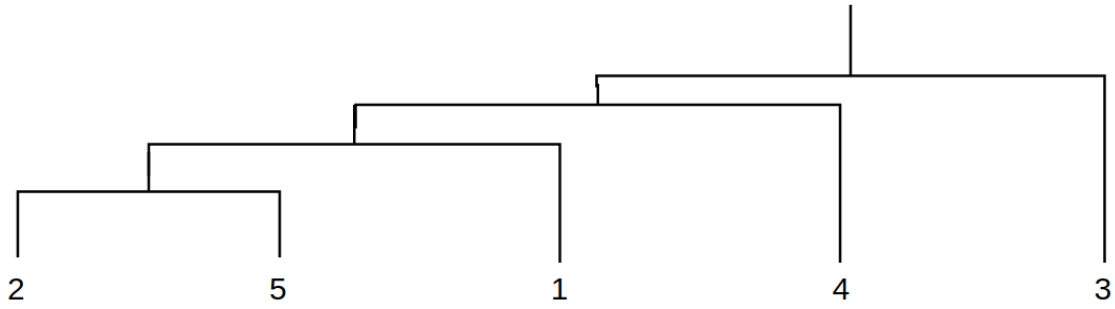
	125	3	4
125	0	-	-
3	0.4	0	-
4	0.35	0.45	0

Step 3. Combine 125 and 4

	1254	3
1254	0	-
3	0.4	0

Step 4. Combine 1254 and 3

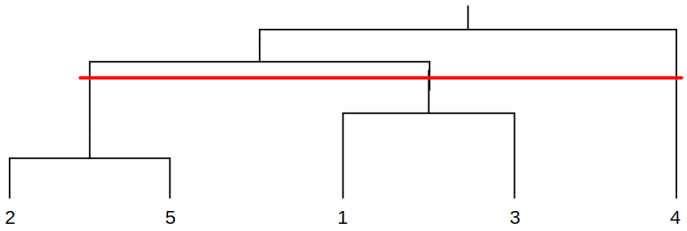
	12543
12543	0



1.3.3 (c)

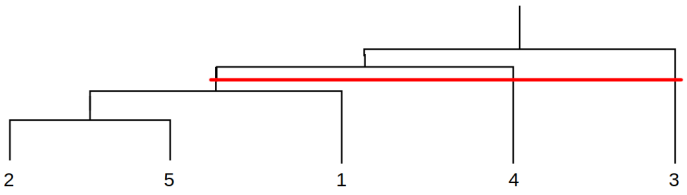
Complete Linkage Clusters:

(2, 5), (1, 3), (4)



Single Linkage Clusters:

(2, 5, 1), (4), (3)



2 Part B

2.1 Question 4

[6]:
```
nums = np.array([20,30,40,60,120]).reshape(-1,1)

scaler = MinMaxScaler()
ns1 = scaler.fit_transform(nums)
scaler = MinMaxScaler([-1,1])
ns2 = scaler.fit_transform(nums)
scaler = StandardScaler()
ns3 = scaler.fit_transform(nums)

normed = pd.DataFrame({
```

```
    "orig": [20,30,40,60,120],
    "minMax": [ns1[0][0],ns1[1][0],ns1[2][0],ns1[3][0],ns1[4][0]],
    "minMaxNeg": [ns2[0][0],ns2[1][0],ns2[2][0],ns2[3][0],ns2[4][0]],
    "z-score": [ns3[0][0],ns3[1][0],ns3[2][0],ns3[3][0],ns3[4][0]]
})

print("Normalized vectors")
display(normed)
```

```
Normalized vectors
```

	orig	minMax	minMaxNeg	z-score
0	20	0.0	-1.0	-0.956325
1	30	0.1	-0.8	-0.675053
2	40	0.2	-0.6	-0.393781
3	60	0.4	-0.2	0.168763
4	120	1.0	1.0	1.856395

2.2 Question 5

2.2.1 (a)

[7]:
```
samples = pd.DataFrame({
    "A": [1.4,1.8,1.3,0.9,1.5],
    "B": [1.3,1.1,1.2,3.3,2.1],
    "C": [2.9,3.2,2.9,3.1,3.3]
})

distances = pd.DataFrame({
    "sample": ["x1","x2","x3","x4","x5"],
    "man": [0.,0.,0.,0.,0.],
    "euc": [0.,0.,0.,0.,0.],
    "min": [0.,0.,0.,0.,0.],
    "sup": [0.,0.,0.,0.,0.],
    "cos": [0.,0.,0.,0.,0.]
})

newP = [1.25,1.74,3.01]

for index, row in samples.iterrows():
    distances.at[index,"man"] = abs(newP[0]-row[0]) + abs(newP[1]-row[1]) +␣
 ↪abs(newP[2]-row[2])
    distances.at[index,"euc"] = np.linalg.norm(newP-row)
    distances.at[index,"min"] = distance.minkowski(newP, row, 3)
    distances.at[index,"sup"] = distance.chebyshev(newP, row)
    distances.at[index,"cos"] = distance.cosine(newP, row)

print("Distances from new point to data points")
```

```
display(distances)
```

```
Distances from new point to data points
```

	sample	man	euc	min	sup	cos
0	x1	0.70	0.477703	0.447958	0.44	0.006975
1	x2	1.38	0.864986	0.757918	0.64	0.025745
2	x3	0.70	0.553353	0.541659	0.54	0.008671
3	x4	2.00	1.601312	1.565950	1.56	0.050270
4	x5	0.90	0.525547	0.442544	0.36	0.001018

2.2.2 (b)

[8]:
```
arrSamples = samples.values
arrNewP = np.array(newP).reshape(1,-1)

scaler = MinMaxScaler()
scaler.fit(arrSamples)

normSamples = scaler.transform(arrSamples)
normSamples = pd.DataFrame(data=normSamples)

normNewP = scaler.transform(arrNewP)[0]

normDistances = pd.DataFrame({
    "sample": ["x1","x2","x3","x4","x5"],
    "euc": [0.,0.,0.,0.,0.]
})
for index, row in normSamples.iterrows():
    normDistances.at[index,"euc"] = np.linalg.norm(normNewP-row)

print("Euclidean Distances with Normalization")
display(normDistances)
```

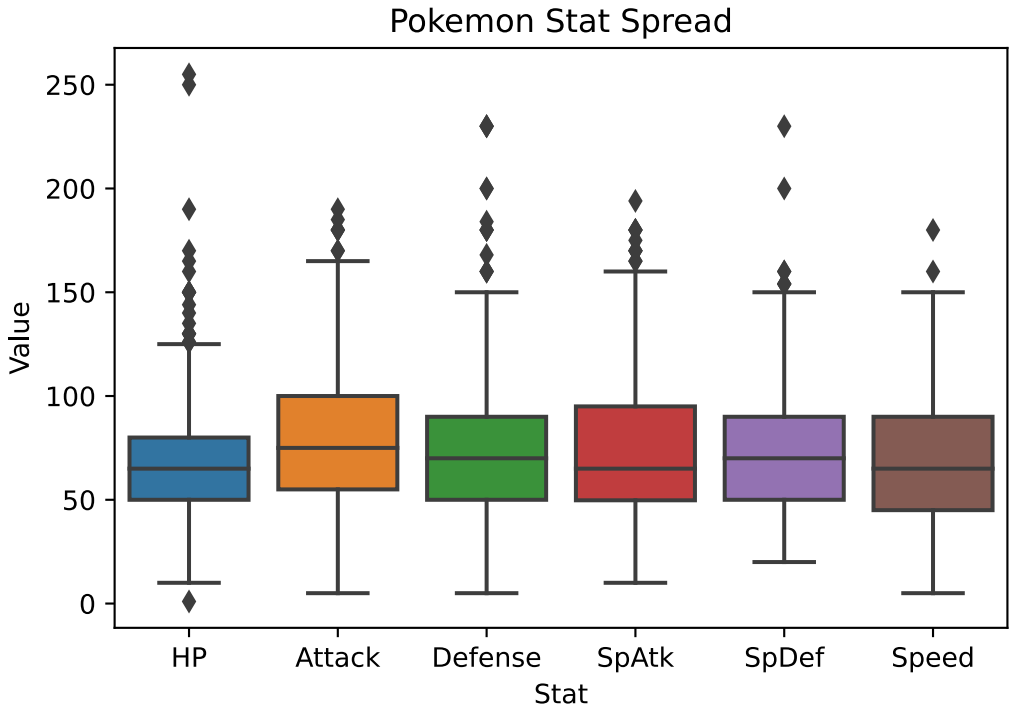
```
Euclidean Distances with Normalization
```

	sample	euc
0	x1	0.378686
1	x2	0.826868
2	x3	0.372773
3	x4	0.839446
4	x5	0.793450

2.3 Question 6

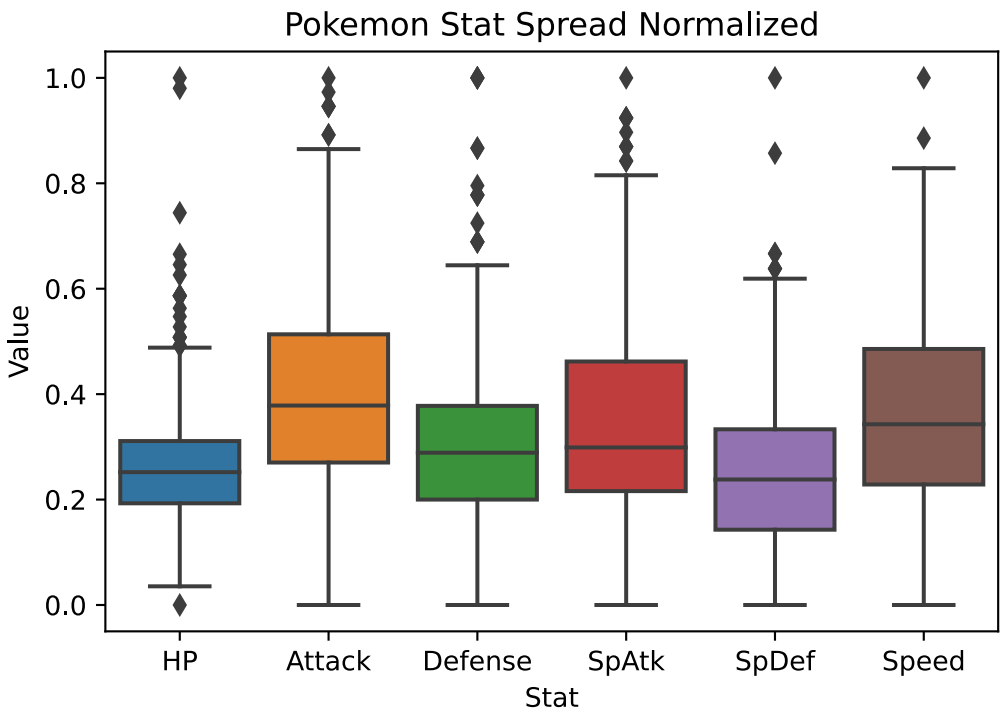
2.3.1 (a)

[9]:
```
pokemon = pd.read_csv("Pokemon.csv", sep=",", engine="python")
stats = ["HP","Attack","Defense","SpAtk","SpDef","Speed"]
plot = sb.boxplot(x="variable", y="value", data=pd.melt(pokemon[stats]))
plot.set(xlabel="Stat", ylabel="Value")
plot.set_title("Pokemon Stat Spread")
plt.show()
```



2.3.2 (b)

[10]:
```
scaler = MinMaxScaler()
scaler.fit(pokemon[stats])
pokemon[stats] = scaler.transform(pokemon[stats])

plot = sb.boxplot(x="variable", y="value", data=pd.melt(pokemon[stats]))
plot.set(xlabel="Stat", ylabel="Value")
plot.set_title("Pokemon Stat Spread Normalized")
plt.show()
```



2.3.3 (c)

[11]:
```
kClusters = []
for n in range(3,9):
    kmeans = cluster.KMeans(n_clusters=n).fit(pokemon[stats])
    kClusters.append(kmeans.cluster_centers_)
```

2.3.4 (d)

[12]:
```
k, labels = gs.gapstat(pokemon[stats])
print("Optimal number of clusters:",k)
```

```
Optimal number of clusters: 4
```

2.3.5 (e)

[13]:
```
statCentroids = pd.DataFrame(data=kClusters[k-3], columns=stats)
display(statCentroids)
```

	HP	Attack	Defense	SpAtk	SpDef	Speed
0	0.344436	0.630041	0.380413	0.608407	0.361188	0.543919
1	0.305436	0.498948	0.454105	0.297937	0.308611	0.287938

```
2  0.203529  0.264016  0.211771  0.207876  0.145214  0.250141
3  0.288217  0.388237  0.281508  0.412852  0.276757  0.468848
```

2.3.6 (f)

[14]:
```
orig = scaler.inverse_transform(statCentroids[stats])
statCentroidsOrig = pd.DataFrame(data=orig, columns=stats)
display(statCentroidsOrig)
```

```
          HP      Attack     Defense       SpAtk      SpDef       Speed
0  88.486726  121.557522   90.592920  121.946903  95.849558  100.185841
1  78.580838   97.305389  107.173653   64.820359  84.808383   55.389222
2  52.696246   53.843003   52.648464   48.249147  50.494881   48.774744
3  74.207048   76.823789   68.339207   85.964758  78.118943   87.048458
```

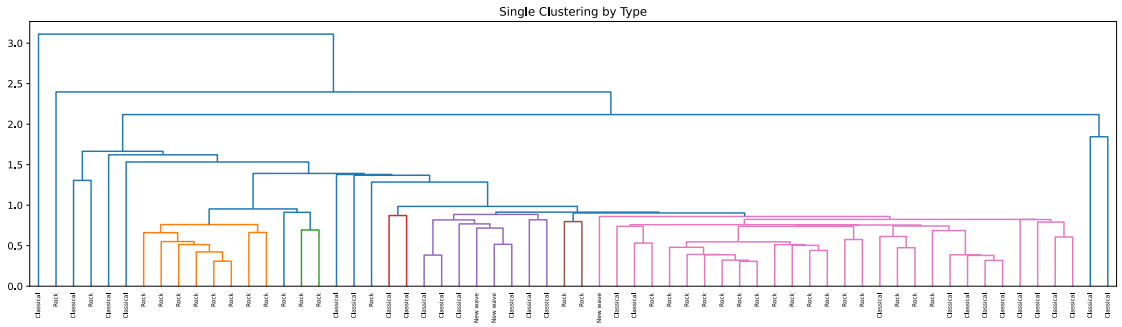
2.3.7 (g)

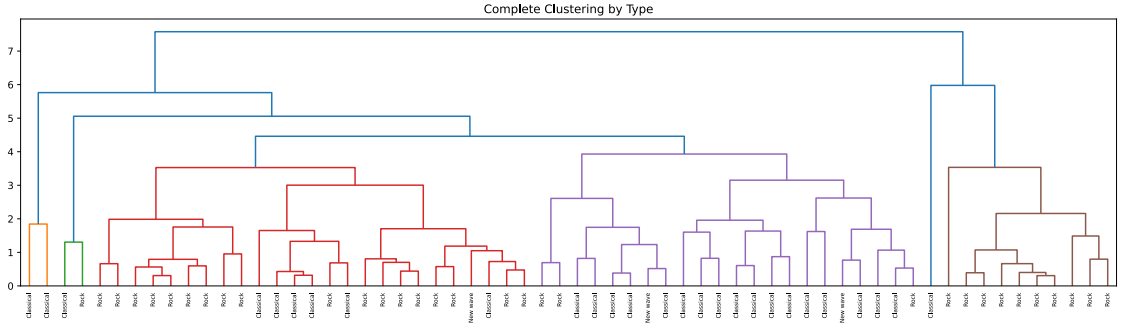
[20]:
```
fig = go.Figure()
for n in range(0,k):
    gName = "Group" + str(n+1)
    fig.add_trace(go.Scatterpolar(
        r=statCentroidsOrig.iloc[n],
        theta=stats,
        fill="toself",
        name=gName
    ))
fig.show()
```

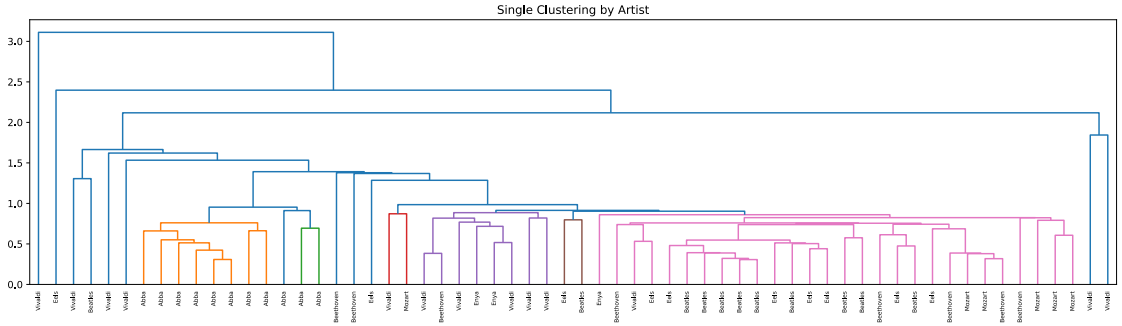
2.4 Question 7

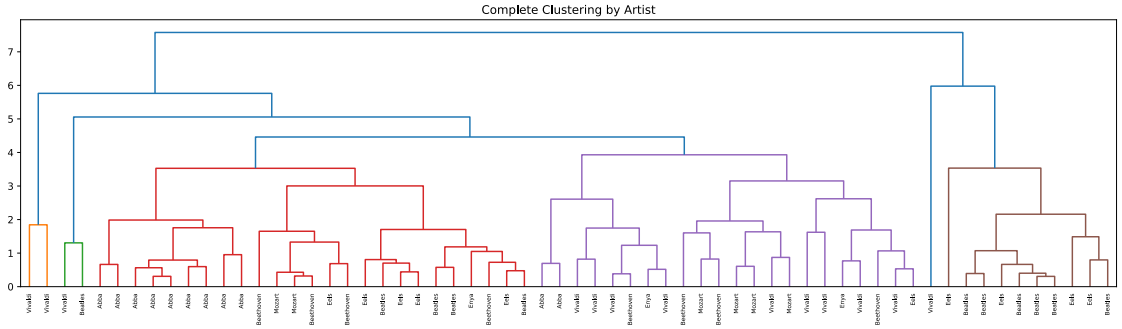
[16]:
```
music = pd.read_csv("music2.csv", sep=",", engine="python")
vals = ["LVar","LAve","LMax","LFEner","LFreq"]
scaler = StandardScaler()
scaler.fit(music[vals])
music[vals] = scaler.transform(music[vals])

single = cluster.AgglomerativeClustering(distance_threshold=0, n_clusters=None,␣
 ↪linkage="single")
single = single.fit(music[vals])
y1 = single.fit_predict(music[vals])
Z1 = hierarchy.linkage(music[vals], 'single')

complete = cluster.AgglomerativeClustering(distance_threshold=0,␣
 ↪n_clusters=None, linkage="complete")
complete = complete.fit(music[vals])
y2 = complete.fit_predict(music[vals])
Z2 = hierarchy.linkage(music[vals], 'complete')
```

```
plt.figure(figsize=(20, 5))
plt.title("Single Clustering by Type")
dn = hierarchy.dendrogram(Z1, labels=music["Type"].to_numpy(), color_threshold=.
 ↪9)
plt.show()

plt.figure(figsize=(20, 5))
plt.title("Complete Clustering by Type")
dn = hierarchy.dendrogram(Z2, labels=music["Type"].to_numpy(), color_threshold=4)

plt.figure(figsize=(20, 5))
plt.title("Single Clustering by Artist")
dn = hierarchy.dendrogram(Z1, labels=music["Artist"].to_numpy(),␣
 ↪color_threshold=.9)
plt.show()

plt.figure(figsize=(20, 5))
plt.title("Complete Clustering by Artist")
dn = hierarchy.dendrogram(Z2, labels=music["Artist"].to_numpy(),␣
 ↪color_threshold=4)
plt.show()
```









I believe that using complete clustering and labeling using the artists gives the best results.

In this case each artist has most of their songs close together with a few outliers that are typically also group near eachother.

This shows artists general vibe and also shows how some songs or group of songs stand out from their usual.