In [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
```

Part A

Question 1: Group Info

Group Name: Plum

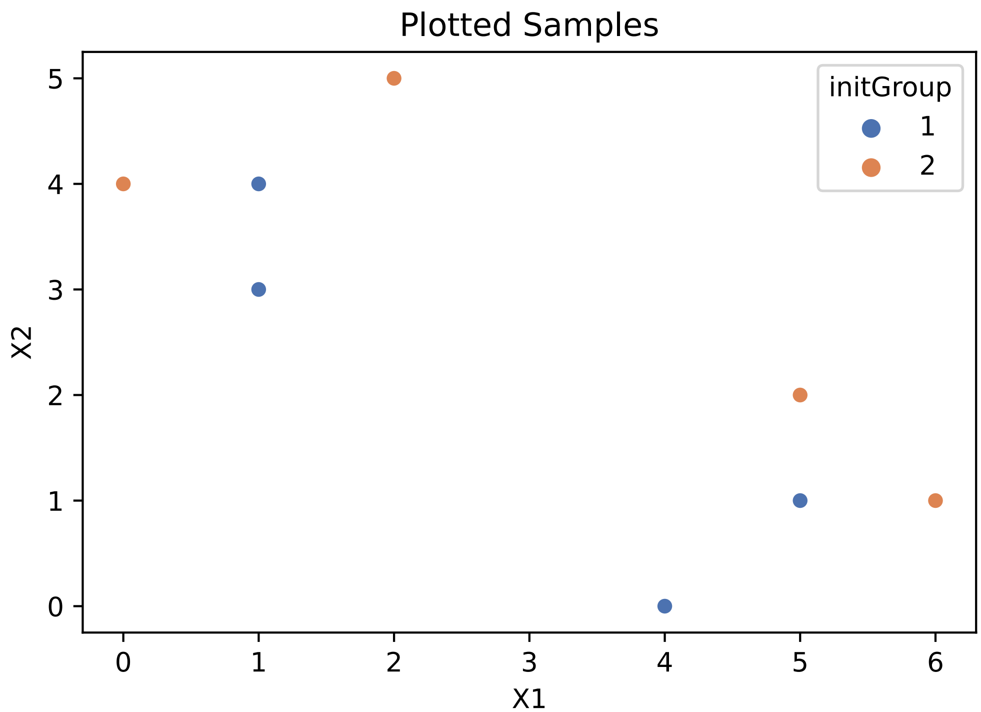
Group Member: Eric Grant

Question 2: K-Means Clustering

(a)

In [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="dee
plot.set(xlabel="X1", ylabel="X2")
plt.title("Plotted Samples")
plt.show()
```



(b + c)

In [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

(d)

In [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],

    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

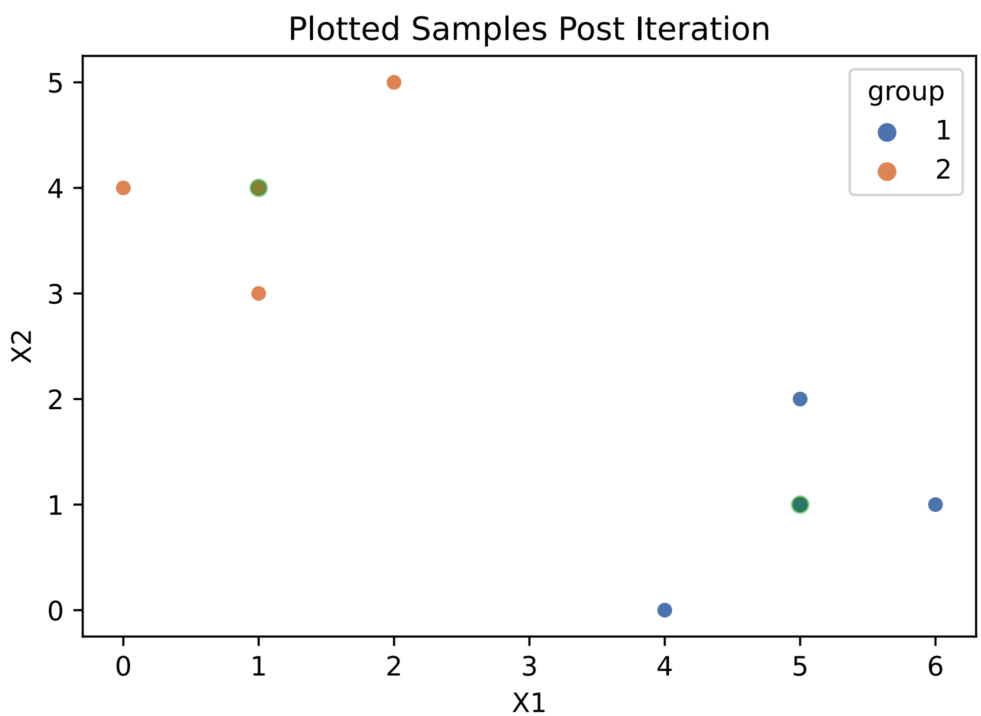
	sample	group
0	1	2
1	2	2

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

(e)

Green points are centroids

In [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()
```



Question 3: Hierarchical Clustering

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

(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

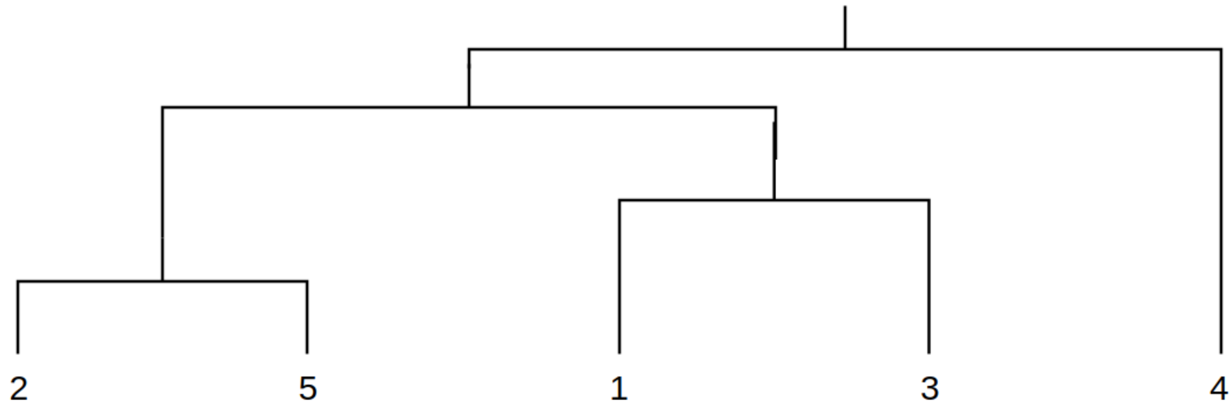
	13	25	4
13	0	-	-
25	0.6	0	-
4	0.7	0.8	0

Step 3. Combine 13 and 25

	1325	4
1325	0	-
4	0.8	0

Step 4. Combine 1325 and 4

	13254
13254	0



(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

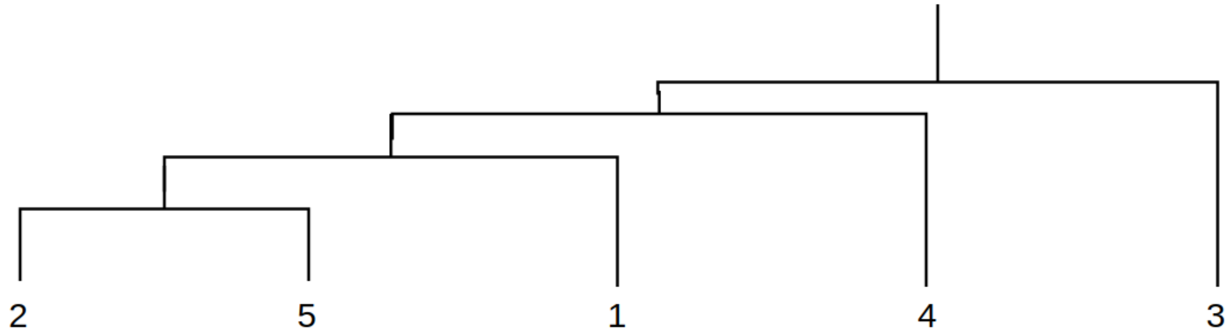
	125	3	4
125	0	-	-
3	0.4	0	-
4	0.35	0.45	0

Step 3. Combine 125 and 4

	1254	3
1254	0	-
3	0.4	0

Step 4. Combine 1254 and 3

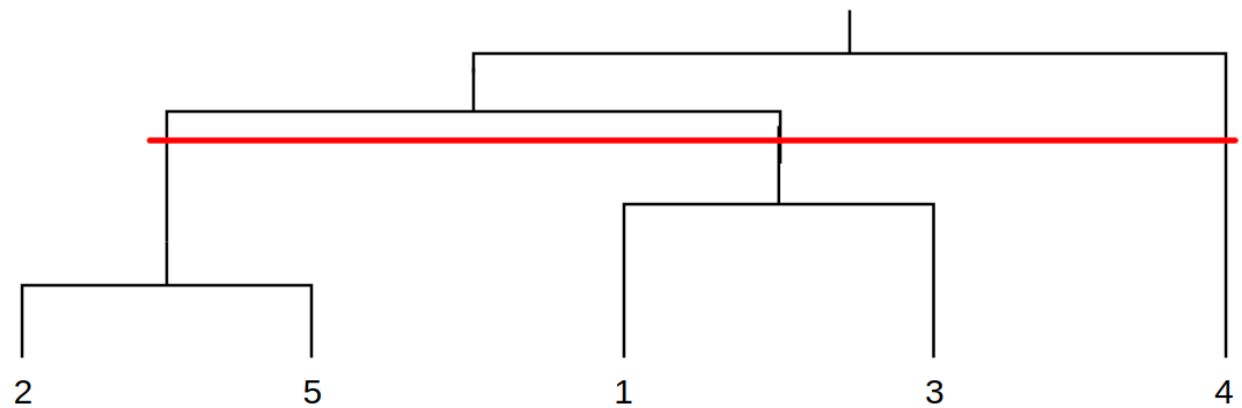
	12543
12543	0



(c)

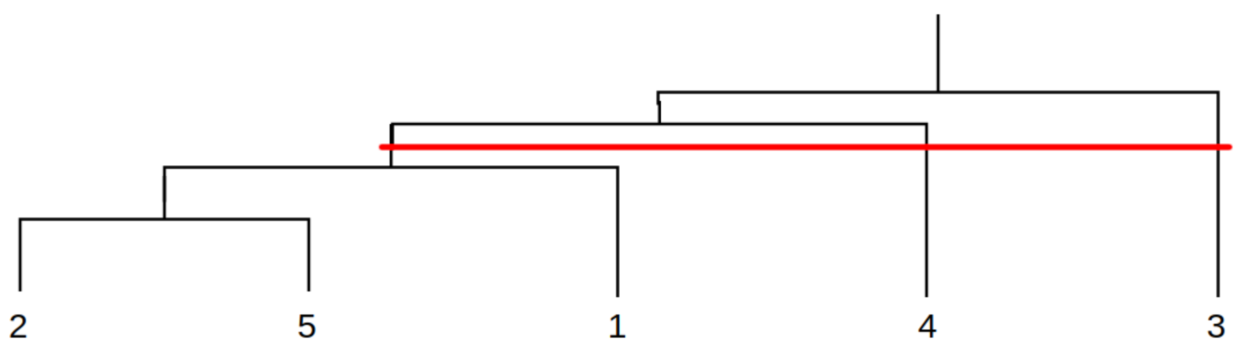
Complete Linkage Clusters:

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



Single Linkage Clusters:

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



Part B

Question 4: Normalized Values

In [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

Question 5: Distances

(a)

In [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(
    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

(b)

In [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
```

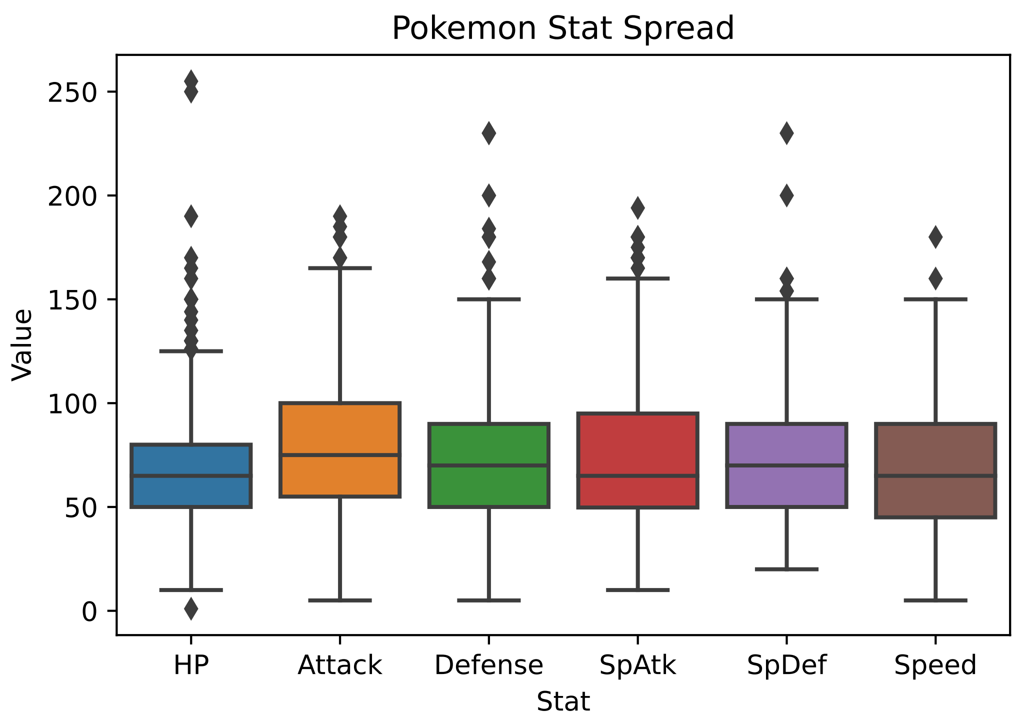
	sample	euc
0	x1	0.378686
1	x2	0.826868
2	x3	0.372773
3	x4	0.839446
4	x5	0.793450

Question 6: Pokemon Data & Grouping

(a)

In [9]:

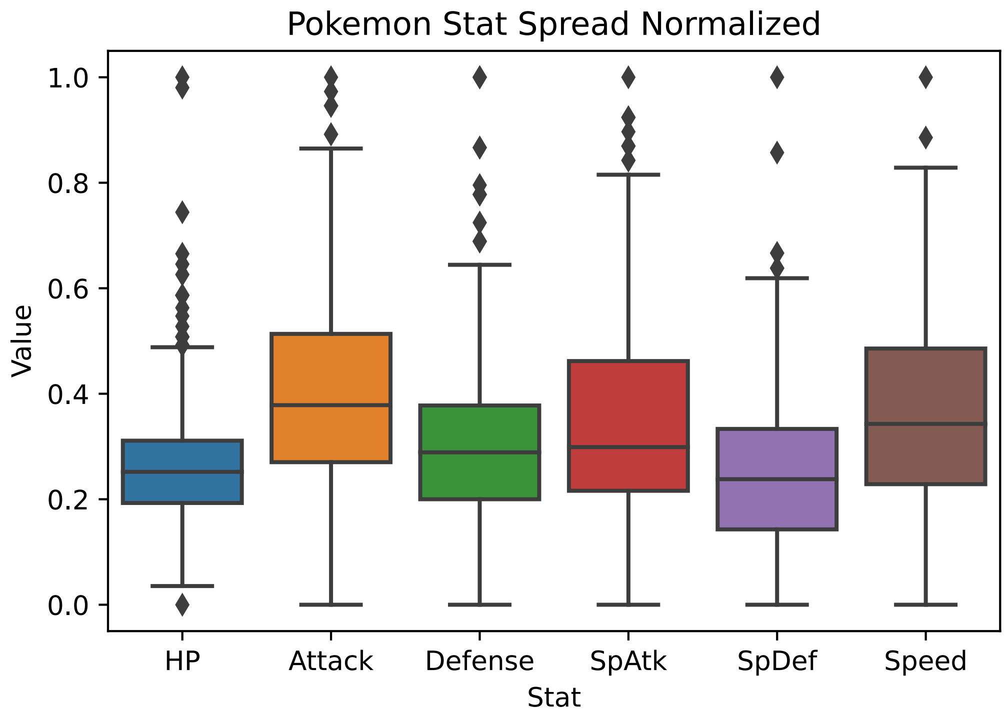
```
pokemon = pd.read_csv("Pokemon.csv", sep=",", engine="python")
stats = ["HP","Attack","Defense","SpAtk","SpDef","Speed"]
plot = sb.boxplot(x="variable", y="value", data=pd.melt(pokemon[stats]))
plot.set(xlabel="Stat", ylabel="Value")
plot.set_title("Pokemon Stat Spread")
plt.show()
```



(b)

In [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()
```



(c)

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

(d)

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

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

(e)

In [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

(f)

In [14]:

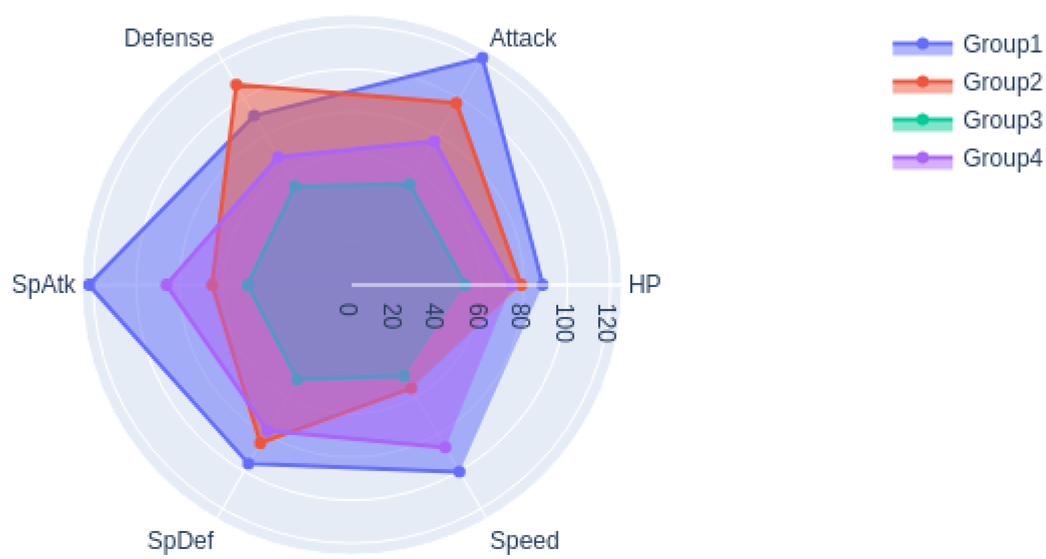
```
orig = scaler.inverse_transform(statCentroids[stats])
statCentroidsOrig = pd.DataFrame(data=orig, columns=stats)
display(statCentroidsOrig)
```

	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

(g)

In [20]:

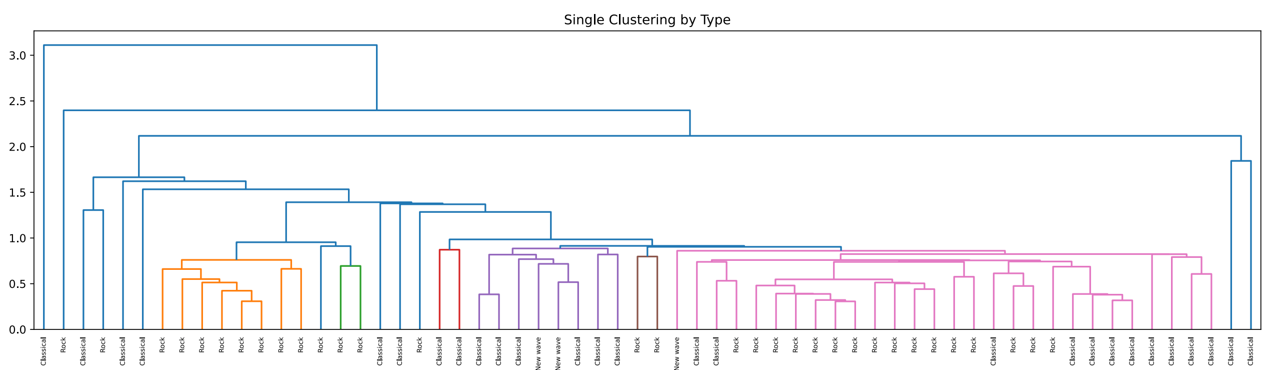
```
fig = go.Figure()
for n in range(0,k):
    gName = "Group" + str(n+1)
    fig.add_trace(go.Scatterpolar(
        r=statCentroidsOrig.iloc[n],
        theta=stats,
        fill="toself",
        name=gName
    ))
fig.show()
```

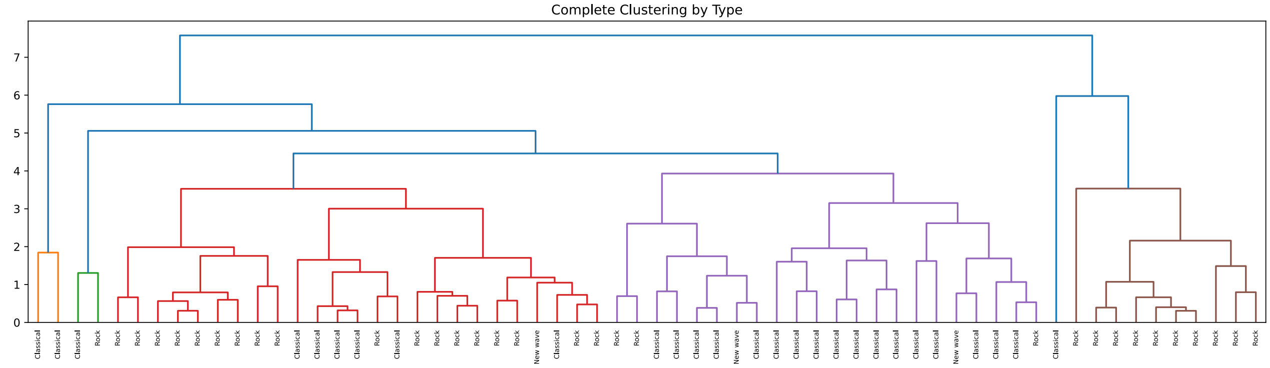


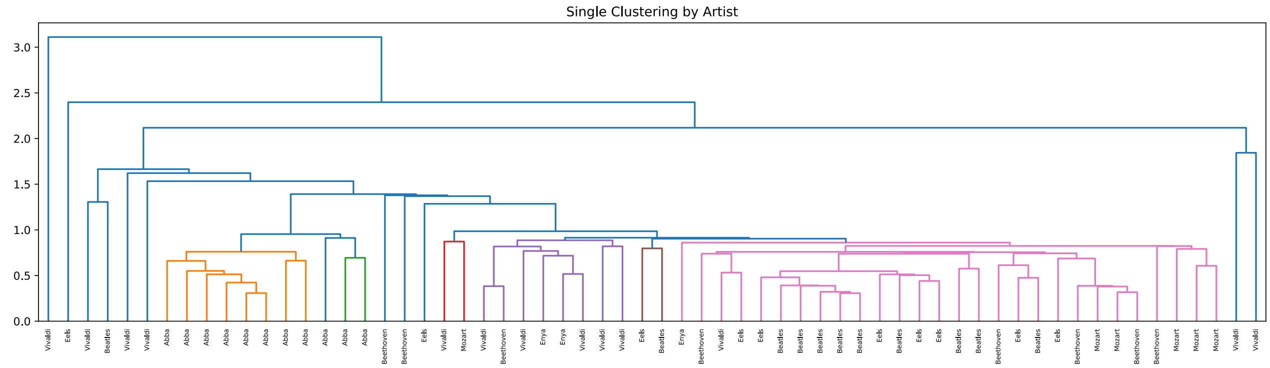
Question 7: Music Data

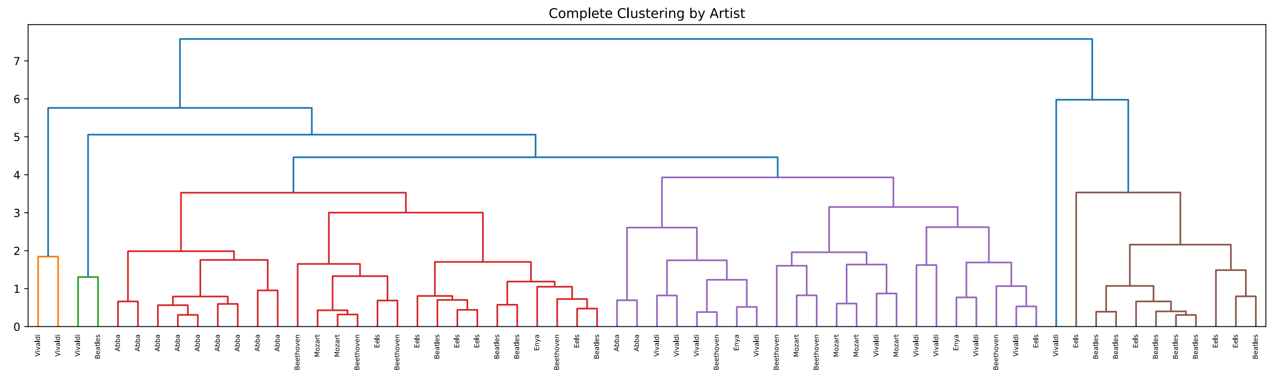
In [16]:

```
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,
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
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=.
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
plt.show()

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