Clustering

1. DBSCAN

Using DBSCAN iterate (for-loop) through different values of min_samples (1 to 10) and epsilon (.05 to .5, in steps of .01) to find clusters in the road-data used in the Lesson and calculate the Silohouette Coeff for min_samples and epsilon . Plot *one* line plot with the multiple lines generated from the min_samples and epsilon values. Use a 2D array to store the SilCoeff values, one dimension represents min_samples, the other represents epsilon.

Expecting a plot of epsilon vs sil_score.

```
In [1]: #Import necessary models
    import numpy as np
    import pandas as pd

%matplotlib notebook
    import matplotlib.pyplot as plt
    plt.rcParams['font.size'] = 10

from sklearn.cluster import DBSCAN
    from sklearn import metrics
```

```
In [2]: #Read Dataset
   X = pd.read_csv('3D_spatial_network.txt.gz', header=None, names=['osm', 'lat','lon','alt'])
   X = X.drop(['osm'], axis=1).sample(10000)
   X.describe()
```

Out[2]:

```
lat
                              lon
                                             alt
count 10000.000000
                                   10000.000000
                    10000.000000
mean
           9.720130
                        57.077939
                                       22.259654
           0.630799
                         0.288816
                                       18.595995
  std
  min
           8.146664
                        56.584513
                                       -1.724164
 25%
           9.327763
                        56.841226
                                       7.122218
 50%
           9.883242
                        57.039543
                                       17.600544
 75%
          10.158706
                        57.296597
                                       32.041836
 max
          11.196113
                        57.744022
                                      129.286451
```

```
In [3]: #Normalize the data
    XX = X.copy()
    XX['alt'] = (X.alt - X.alt.mean())/X.alt.std()
    XX['lat'] = (X.lat - X.lat.mean())/X.lat.std()
    XX['lon'] = (X.lon - X.lon.mean())/X.lon.std()
    XX.describe()
```

Out[3]:

| | lat | lon | alt |
|-------|---------------|---------------|---------------|
| count | 1.000000e+04 | 1.000000e+04 | 1.000000e+04 |
| mean | 1.278977e-17 | 2.366107e-16 | -1.818989e-16 |
| std | 1.000000e+00 | 1.000000e+00 | 1.000000e+00 |
| min | -2.494402e+00 | -1.708442e+00 | -1.289730e+00 |
| 25% | -6.220163e-01 | -8.195985e-01 | -8.140159e-01 |
| 50% | 2.585797e-01 | -1.329426e-01 | -2.505437e-01 |
| 75% | 6.952713e-01 | 7.570810e-01 | 5.260370e-01 |
| max | 2.339863e+00 | 2.306250e+00 | 5.755368e+00 |

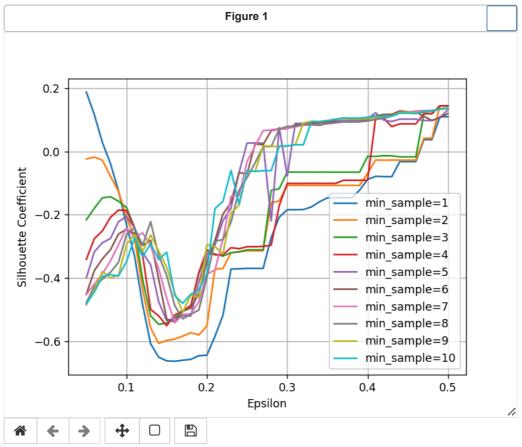
```
In [4]: #generate arrays for minimum samples and epsilons
    min_samples = np.arange(1, 11)
    epsilons = np.arange(0.05, 0.51, 0.01)

In [5]: #generate scores using 'for' loop
    all_scores = []
    for min_sample in min_samples:
        scores = []
        for epsilon in epsilons:
        # define DBSCAN
            dbscan = DBSCAN(eps=epsilon, min_samples=min_sample)
            XX.cluster = dbscan.fit_predict(XX[['lat','lon', 'alt']])
        # calculate silouette score
        score = metrics.silhouette_score(XX[['lon', 'lat', 'alt']], XX.cluster)
        scores.append(score)
```

C:\Users\Kcosm\AppData\Local\Temp\ipykernel_63896\3645285632.py:11: User\Uparning: Pandas doesn't allow co lumns to be created via a new attribute name - see https://pandas.pydata.org/pandas-docs/stable/indexing.html\upartattribute-access (https://pandas.pydata.org/pandas-docs/stable/indexing.html\upartattribute-access)

XX.cluster = dbscan.fit_predict(XX[['lat','lon', 'alt']])

all_scores.append(scores)



Findings

- 1. In every case of minimum sample except minimum sample = 1, Silhouette Coefficients were the lowest between 0.1 and 0.2, and the highest in between 0.4 and 0.5.
- 2. in low epsilons (e < 0.1), low mininum samples were associated with high Silhouette Coefficient
- 3. in epsilons over 0.1, high minimum samples were associated with high Silhouette Coefficient

2. Clustering your own data

Using your own data, find relevant clusters/groups within your data (repeat the above). If your data is labeled with a class that you are attempting to predict, be sure to not use it in training and clustering.

You may use the labels to compare with predictions to show how well the clustering performed using one of the clustering metrics (http://scikit-learn.org/stable/modules/clustering.html#clustering-performance-evaluation).

If you don't have labels, use the silhouette coefficient to show performance. Find the optimal fit for your data but you don't need to be as exhaustive as above.

Additionally, show the clusters in 2D or 3D plots.

As a bonus, try using PCA first to condense your data from N columns to less than N.

Two items are expected:

- Metric Evaluation Plot (like in 1.)
- · Plots of the clustered data

2-A. Preprocessing Data: Heart Failure Clinical Records

• This dataset contains the medical records of 299 patients who had heart failure, collected during their follow-up period, where each patient profile has 13 clinical features.

https://archive.ics.uci.edu/dataset/519/heart+failure+clinical+records (https://archive.ics.uci.edu/dataset/519/heart+failure+clinical+records)

```
In [7]: #Load Dataset as 'df'
    df = pd.read_csv('heart_failure_clinical_records_dataset.csv')
    df.head()
```

Out[7]:

| | age | anaemia | creatinine_phosphokinase | diabetes | ejection_fraction | high_blood_pressure | platelets | serum_creatini |
|---|------|---------|--------------------------|----------|-------------------|---------------------|-----------|----------------|
| 0 | 75.0 | 0 | 582 | 0 | 20 | 1 | 265000.00 | , |
| 1 | 55.0 | 0 | 7861 | 0 | 38 | 0 | 263358.03 | • |
| 2 | 65.0 | 0 | 146 | 0 | 20 | 0 | 162000.00 | |
| 3 | 50.0 | 1 | 111 | 0 | 20 | 0 | 210000.00 | • |
| 4 | 65.0 | 1 | 160 | 1 | 20 | 0 | 327000.00 | 1 |
| 4 | | | | | | | | + |

```
In [8]: #sort three non-binary value columns for clustering as 'df2'
df2 = df[['age', 'serum_sodium', 'ejection_fraction']]
df2.describe()
```

Out[8]:

| | age | serum_soaium | ejection_fraction |
|-------|------------|--------------|-------------------|
| count | 299.000000 | 299.000000 | 299.000000 |
| mean | 60.833893 | 136.625418 | 38.083612 |
| std | 11.894809 | 4.412477 | 11.834841 |
| min | 40.000000 | 113.000000 | 14.000000 |
| 25% | 51.000000 | 134.000000 | 30.000000 |
| 50% | 60.000000 | 137.000000 | 38.000000 |
| 75% | 70.000000 | 140.000000 | 45.000000 |
| max | 95.000000 | 148.000000 | 80.000000 |

```
In [9]: #Normalize dataset as 'df3'
df3 = (df2 - df2.mean()) / df2.std()
df3.describe()
```

Out[9]:

| | age | serum_sodium | ejection_fraction |
|-------|---------------|---------------|-------------------|
| count | 2.990000e+02 | 2.990000e+02 | 2.990000e+02 |
| mean | 5.465713e-16 | -8.703554e-16 | 8.911489e-18 |
| std | 1.000000e+00 | 1.000000e+00 | 1.000000e+00 |
| min | -1.751511e+00 | -5.354230e+00 | -2.034976e+00 |
| 25% | -8.267382e-01 | -5.949987e-01 | -6.830351e-01 |
| 50% | -7.010562e-02 | 8.489153e-02 | -7.064906e-03 |
| 75% | 7.705972e-01 | 7.647817e-01 | 5.844090e-01 |
| max | 2.872354e+00 | 2.577822e+00 | 3.541779e+00 |

2-B. Run DBSCAN and plot the results

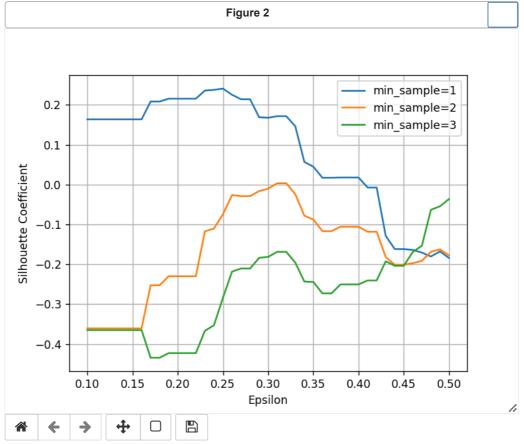
all_scores2.append(scores)

C:\Users\kcosm\AppData\Local\Temp\ipykernel_63896\klein210914201.py:10: User\User\Imp\ipykerning: Pandas doesn't allow columns to be created via a new attribute name - see https://pandas.pydata.org/pandas-docs/stable/indexing.html\u00e4attribute-access (https://pandas.pydata.org/pandas-docs/stable/indexing.html\u00e4attribute-access) df3.cluster = dbscan.fit_predict(df3)

```
In [12]: # Plot lines (x axis = epsilon, y axis = Silhouette Coefficient')
plt.figure()

# Draw multiple lines
for i in all_scores2:
    plt.plot(epsilons2, i)

# Labeling
plt.xlabel('Epsilon')
plt.ylabel('Silhouette Coefficient')
plt.legend(['min_sample=1', 'min_sample=2', 'min_sample=3'])
plt.grid(True)
plt.show()
```



```
In [13]: # How many clusters in Optimal points for minimum_samples = 1?
    dbscan = DBSCAN(eps=0.25, min_samples=1)
    df3.cluster = dbscan.fit_predict(df3)
    len(np.unique(df3.cluster))

Out[13]: 205

In [14]: # How many clusters in Optimal points for minimum_samples = 2?
    dbscan = DBSCAN(eps=0.32, min_samples=2)
    df3.cluster = dbscan.fit_predict(df3)
    len(np.unique(df3.cluster))

Out[14]: 49

In [15]: # How many clusters in Optimal points for minimum_samples = 3?
    dbscan = DBSCAN(eps=0.50, min_samples=3)
    df3.cluster = dbscan.fit_predict(df3)
```

Findings for 2-B

Out[15]: 8

len(np.unique(df3.cluster))

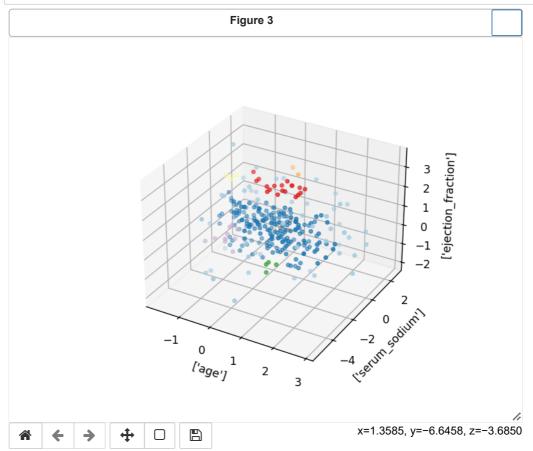
• Although low minimum samples(1, 2) showed higher scores than 3 minimum samples in epsilon under 0.45, the amount of clusters was excessive and thus did not provide meaningful outcome.

• In optimal point of 3 minimum samples, the amount of clusters was 8 and thus would be more meaningful outcome.

2-C. 3D Plot for optimal configuration

- · Axed3D function did not work properly
- Therefore, I used 3D scatterplot referring to matplotlib guide:
 https://matplotlib.org/stable/plot_types/3D/scatter3d_simple.html#sphx-glr-plot-types-3d-scatter3d-simple-py
 (https://matplotlib.org/stable/plot_types/3D/scatter3d_simple.html#sphx-glr-plot-types-3d-scatter3d-simple-py

```
In [16]: fig, ax = plt.subplots(subplot_kw={"projection": "3d"})
ax.scatter(df3['age'], df3['serum_sodium'], df3['ejection_fraction'], c=df3.cluster, s=10, cmap = 'Paired
ax.set(xlabel=['age'], ylabel=['serum_sodium'], zlabel=['ejection_fraction'])
plt.show()
```



2-D(Bonus). use PCA to condense 3D data

explained variance ratio (first two components): [0.39217475 0.34234826]