CSE17040 - Evaluation Lab

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1 Lab 9 - Evaluation Lab

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1.1 Exploratory Data Analysis

[1]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
%matplotlib inline

from scipy.spatial import distance
from sklearn.preprocessing import LabelEncoder
from sklearn.cluster import DBSCAN, KMeans
from sklearn.decomposition import PCA
from sklearn.metrics import homogeneity_score, completeness_score,␣
↪v_measure_score, adjusted_rand_score
from sklearn.metrics import adjusted_mutual_info_score, silhouette_score
```

1.1.1 Reading and Understanding the Data

[2]:
```
df = pd.read_csv('pima-indians-diabetes.csv', skiprows=9, header=None)
df.head()
```

[2]:

	0	1	2	3	4	5	6	7	8
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

[3]:
```
df.columns = ['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness',␣
↪'Insulin','BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome']
df.head()
```

[3]:
```
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
0            6      148             72             35        0  33.6
1            1       85             66             29        0  26.6
2            8      183             64              0        0  23.3
3            1       89             66             23       94  28.1
4            0      137             40             35      168  43.1

   DiabetesPedigreeFunction  Age  Outcome
0                     0.627   50        1
1                     0.351   31        0
2                     0.672   32        1
3                     0.167   21        0
4                     2.288   33        1
```

1.1.2 Data cleaning

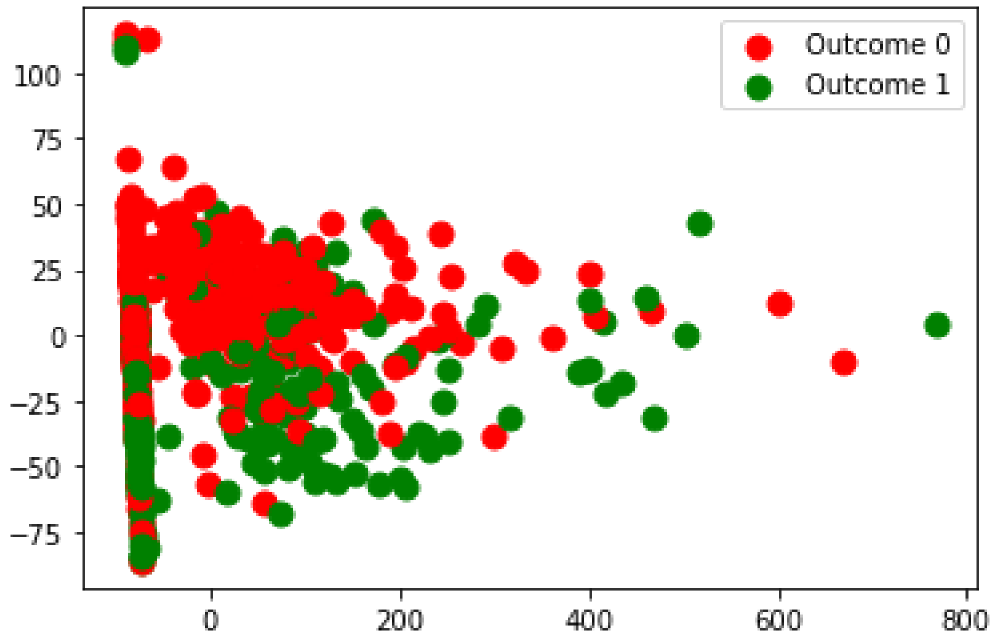
[4]:
```
df.isnull().sum()
```

[4]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

1.1.3 Data Preparation

[5]:
```
X=PCA(n_components=2).fit(df.drop(columns=['Outcome']))
X=X.transform(df.drop(columns=['Outcome']))
y = df['Outcome'].values
```

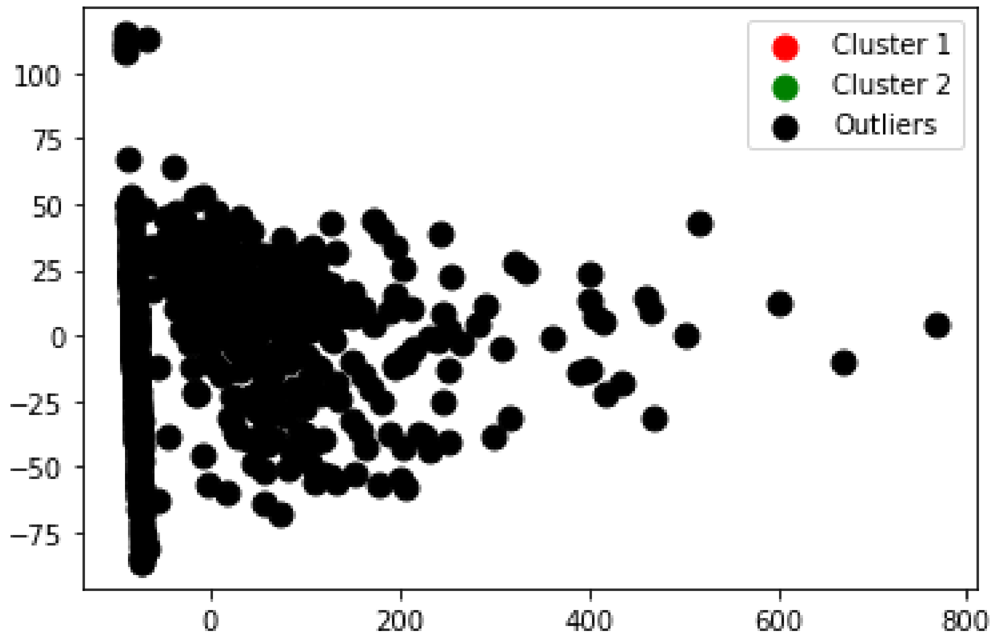
[6]:
```
for i in range(0, X.shape[0]):
    if y[i] == 0:
        p1 = plt.scatter(X[i, 0], X[i, 1], s = 80, c = 'red')
    elif y[i] == 1:
        p2 = plt.scatter(X[i, 0], X[i, 1], s = 80, c = 'green')
plt.legend([p1,p2],['Outcome 0', 'Outcome 1'])
plt.show()
```



1.2 Analyze the Clusters in data using DBSCAN

[7]:
```
db = DBSCAN(eps=0.8, min_samples=19)
model = db.fit(X)
pred = model.labels_
```

[8]:
```
for i in range(0, X.shape[0]):
    if pred[i] == 0:
        p1 = plt.scatter(X[i, 0], X[i, 1], s = 80, c = 'red')
    elif pred[i] == 1:
        p2 = plt.scatter(X[i, 0], X[i, 1], s = 80, c = 'green')
    else:
        p3 = plt.scatter(X[i, 0], X[i, 1], s = 80, c = 'black')
plt.legend([p1,p2,p3],['Cluster 1', 'Cluster 2', 'Outliers'])
plt.show()
```



1.2.1 How successful has the clustering been in this regard?

With the give parameters (Eps=0.8, minPts=19), DBSCAN fails to capture any similarities in order to form a cluster. This is because there is no point in the dataset such that the distance between the point and its neighboring 19 points are less than 0.8

1.2.2 Looking at each class individually, can you spot the particular class that is well identified by the clustering? Classes that are poorly identified?

No, since every point in the dataset is considered as a noise, no distinct clusters can be seen

1.2.3 Which classes are mostly confused with each other?

All the classes were confused because of choosing wrong hyperparameters

[9]:

```
p1 = X[0]
p2 = X[1]
d = distance.euclidean(p1, p2)
print("Euclidean distance: ",d)
```

```
Euclidean distance:  65.19836603412135
```

The distance between two points in the dataset is very much greater than 0.18. There does not exist 19 points which are closer than 0.18. This is the reason why DBSCAN considers every point as noise and thereby fails in clustering

1.2.4 Find the clustering parameters

[10]:
```
n_clusters_ = len(set(pred)) - (1 if -1 in pred else 0)
n_noise_ = list(pred).count(-1)
```

[11]:
```
print('Estimated number of clusters      : %d' % n_clusters_)
print('Estimated number of noise points : %d' % n_noise_)
print("Homogeneity                      : %0.3f" %  homogeneity_score(y, pred))
print("Completeness                     : %0.3f" %  completeness_score(y, pred))
print("V-measure                        : %0.3f" %  v_measure_score(y, pred))
print("Adjusted Rand Index              : %0.3f" %  adjusted_rand_score(y,␣
 ↪pred))
print("Adjusted Mutual Information      : %0.3f" % ␣
 ↪adjusted_mutual_info_score(y, pred))
# print("Silhouette Coefficient           : %0.3f" %  silhouette_score(X, pred))
```

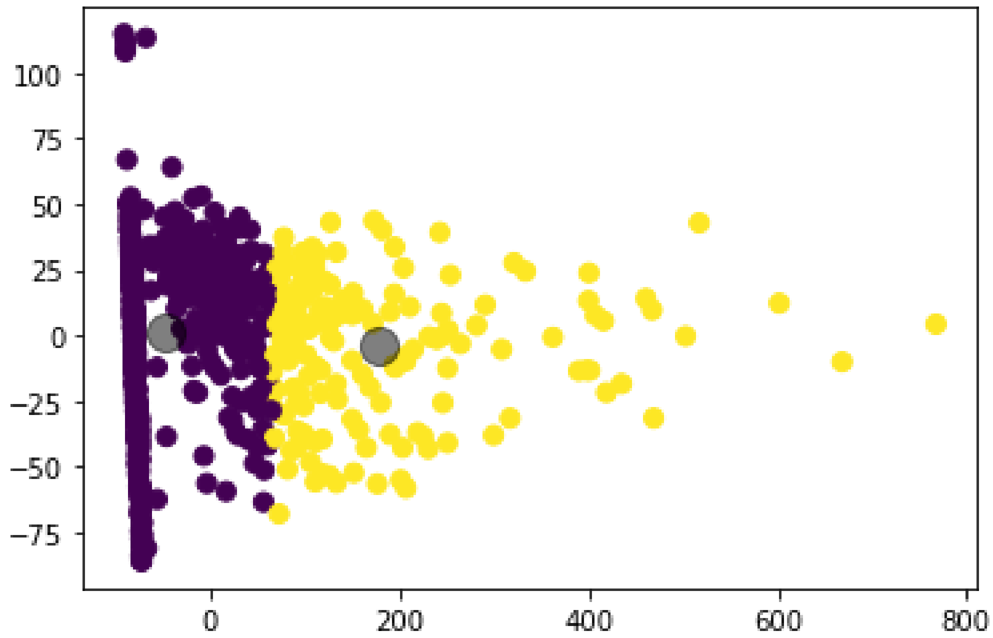
```
Estimated number of clusters     : 0
Estimated number of noise points : 768
Homogeneity                      : 0.000
Completeness                     : 1.000
V-measure                        : 0.000
Adjusted Rand Index              : 0.000
Adjusted Mutual Information      : 0.000
```

1.3 Compare the results with K-means

[12]:
```
kmeans = KMeans(n_clusters=2)
kmeans.fit(X)
pred = kmeans.predict(X)
```

[13]:
```
plt.scatter(X[:, 0], X[:, 1], c=pred, s=50, cmap='viridis')
centers = kmeans.cluster_centers_
plt.scatter(centers[:, 0], centers[:, 1], c='black', s=200, alpha=0.5)
```

[13]: <matplotlib.collections.PathCollection at 0x7fde60ec1950>



[14]:
```
n_clusters_ = len(set(pred)) - (1 if -1 in pred else 0)
n_noise_ = list(pred).count(-1)
```

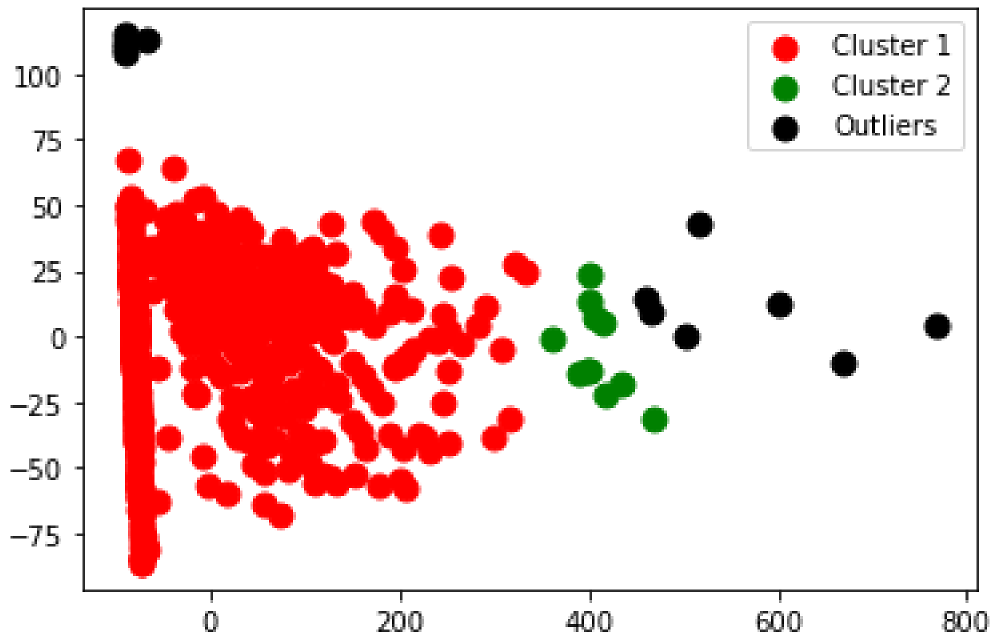
[15]:
```
print('Estimated number of clusters      : %d' % n_clusters_)
print('Estimated number of noise points : %d' % n_noise_)
print("Homogeneity                       : %0.3f" %  homogeneity_score(y, pred))
print("Completeness                      : %0.3f" %  completeness_score(y, pred))
print("V-measure                         : %0.3f" %  v_measure_score(y, pred))
print("Adjusted Rand Index               : %0.3f" %  adjusted_rand_score(y,␣
 ↪pred))
print("Adjusted Mutual Information       : %0.3f" % ␣
 ↪adjusted_mutual_info_score(y, pred))
print("Silhouette Coefficient            : %0.3f" %  silhouette_score(X, pred))
```

```
Estimated number of clusters     : 2
Estimated number of noise points : 0
Homogeneity                      : 0.026
Completeness                     : 0.033
V-measure                        : 0.029
Adjusted Rand Index              : 0.074
Adjusted Mutual Information      : 0.028
Silhouette Coefficient           : 0.614
```

Difference Even if there exists an outlier, KMeans clustering is affected.So none of the points are considered as noise and therefore, in the given scenario, with the given hyperparameters, KMeans actually performs better than DBSCAN.

[16]:
```
db = DBSCAN(eps=40, min_samples=6)
model = db.fit(X)
pred = model.labels_
```

[17]:
```
for i in range(0, X.shape[0]):
    if pred[i] == 0:
        p1 = plt.scatter(X[i, 0], X[i, 1], s = 80, c = 'red')
    elif pred[i] == 1:
        p2 = plt.scatter(X[i, 0], X[i, 1], s = 80, c = 'green')
    else:
        p3 = plt.scatter(X[i, 0], X[i, 1], s = 80, c = 'black')
plt.legend([p1,p2,p3],['Cluster 1', 'Cluster 2', 'Outliers'])
plt.show()
```



[18]:
```
from collections import Counter
Counter(df['Outcome'].values)
```

[18]: Counter({1: 268, 0: 500})

[19]:
```
n_clusters_ = len(set(pred)) - (1 if -1 in pred else 0)
n_noise_ = list(pred).count(-1)
print('Estimated number of clusters      : %d' % n_clusters_)
print('Estimated number of noise points : %d' % n_noise_)
print("Homogeneity                        : %0.3f" %  homogeneity_score(y, pred))
print("Completeness                       : %0.3f" %  completeness_score(y, pred))
print("V-measure                          : %0.3f" %  v_measure_score(y, pred))
```

```
print("Adjusted Rand Index              : %0.3f" %  adjusted_rand_score(y,␣
 ↪pred))
print("Adjusted Mutual Information      : %0.3f" % ␣
 ↪adjusted_mutual_info_score(y, pred))
print("Silhouette Coefficient           : %0.3f" %  silhouette_score(X, pred))
```

```
Estimated number of clusters     : 2
Estimated number of noise points : 12
Homogeneity                      : 0.008
Completeness                     : 0.033
V-measure                        : 0.013
Adjusted Rand Index              : 0.020
Adjusted Mutual Information      : 0.009
Silhouette Coefficient           : 0.670
```

After changing the hyperparameters, the DBSCAN algorithm seems to be working better than the KMeans itself. This exercise shows how important choosing the correct value of hyperparameters are.