CS145 Howework 4

Important Note: HW4 is due on **11:59 PM PT, Nov 20 (Friday, Week 7)**. Please submit through GradeScope.

Print Out Your Name and UID

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Before You Start

You need to first create HW4 conda environment by the given `cs145hw4.yml` file, which provides the name and necessary packages for this tasks. If you have `conda` properly installed, you may create, activate or deactivate by the following commands:

```
conda env create -f cs145hw4.yml
conda activate hw4
conda deactivate
```

OR

```
conda env create --name NAMEOFYOURCHOICE -f cs145hw4.yml
conda activate NAMEOFYOURCHOICE
conda deactivate
```

To view the list of your environments, use the following command:

```
conda env list
```

More useful information about managing environments can be found here.

You may also quickly review the usage of basic Python and Numpy package, if needed in coding for matrix operations.

In this notebook, you must not delete any code cells in this notebook. If you change any code outside the blocks (such as some important hyperparameters) that you are allowed to edit (between STRART/END YOUR CODE HERE), you need to highlight these changes. You may add some additional cells to help explain your results and observations.

In [1]:
```
import numpy as np
import pandas as pd
import sys
import random
import math
import matplotlib.pyplot as plt
from scipy.stats import multivariate_normal
```

```
%load_ext autoreload
%autoreload 2
```

If you can successfully run the code above, there will be no problem for environment setting.

1. Clustering Evaluation

This workbook will walk you through an example for calculating different clustering metrics.

Note: This is a "question-answer" style problem. You do not need to code anything and you are required to calculate by hand (with a scientific calculator).

Questions

Suppose we want to cluster the following 20 conferences into four areas, with ground truth label and algorithm output label shown in third and fourth column. Please evaluate the quality of the clustering algorithm according to four different metrics respectively.

Questions (please include intermediate steps)

1. Calculate purity.
2. Calculate precision.
3. Calculate recall.
4. Calculate F1-score.
5. Calculate normalized mutual information.

Your answer here:

Note: you can use several code cells to help you compute the results and answer the questions. Again you don't need to do any coding.

Please type your answer here!

In [29]:
```
Y = [3, 3, 1, 1, 1, 4, 3, 3, 4, 2, 4, 2, 1, 2, 3, 2, 1, 2, 4, 4]
Yhat = [2, 2, 3, 3, 3, 4, 2, 2, 3, 1, 4, 1, 3, 1, 2, 1, 2, 1, 4, 4]

for cluster in range(1, 5):
    for y, yhat in zip(Y, Yhat):
        if yhat == cluster:
            print(f'Cluster {cluster}. True label {y}')
    print()
```

```
Cluster 1. True label 2
Cluster 1. True label 2
Cluster 1. True label 2
Cluster 1. True label 2
Cluster 1. True label 2

Cluster 2. True label 3
Cluster 2. True label 3
Cluster 2. True label 3
Cluster 2. True label 3
Cluster 2. True label 3
Cluster 2. True label 1

Cluster 3. True label 1
Cluster 3. True label 1
```

```
Cluster 3. True label 1
Cluster 3. True label 4
Cluster 3. True label 1

Cluster 4. True label 4
Cluster 4. True label 4
Cluster 4. True label 4
Cluster 4. True label 4
```

1

Purity is $\frac{1}{N}\sum_k \max_j |c_k \cap \omega_j|$

$N = 20$ since we have 20 points

For output cluster 1, we have true labels 2, 2, 2, 2 and 2 so all five are correct

For output cluster 2, we have true labels 3, 3, 3, 3, 3, 1 so five out of six are correct

For output cluster 3, we have true labels 1, 1, 1, 1, 4 so four out of five are correct

For output cluster 4, we have all true labels 4 so all four are correct

So, $\sum_k \max_j |c_k \cap \omega_j| = 5 + 5 + 4 + 4 = 18$

Purity is $\frac{18}{20} = 0.9$

In [31]:

```
n = len(Y)
tp, fp, fn, tn = 0, 0, 0, 0
for i in range(n):
    for j in range(i + 1, n):
        if Y[i] == Y[j]:
            if Yhat[i] == Yhat[j]:
                tp += 1
            else:
                fn += 1
        else:
            if Yhat[i] == Yhat[j]:
                fp += 1
            else:
                tn += 1

print(tp, fp, tn, fn)
```

```
32 9 141 8
```

2

$Precision = TP/(TP + FP)$

$TP = 32$, $FP = 9$

$Precision = 32/41 \approx 0.78$

3

$Recall = TP/(TP + FN)$

$TP = 32 \; FP = 8$

$Recall = 32/40 = 0.80$

4

$F_1 = 2 \cdot Precision \cdot Recall/(Precision + Recall)$

$F_1 = 2 \cdot .78 \cdot .8/(.78 + .8)$

$F_1 \approx 0.79$

5

NMI Table:

	C1	C2	C3	C4	Sum
L1	0	1	4	0	5
L2	5	0	0	0	5
L3	0	5	0	0	5
L4	0	0	1	4	5
Sum	5	6	5	4	20

We then apply the NMI formula

$$NMI(C, \Omega) = \frac{I(C, \Omega)}{\sqrt{H(C)H(\Omega)}}$$

To get $I(C, \Omega)$, we calculate the following:

$$\sum_k \sum_j \frac{|c_k \cap \omega_j|}{N} \ln \frac{N|c_k \cap \omega_j|}{|c_k| \cdot |\omega_j|}$$

To get $H(\Omega)$, we calculate the following:

$$\sum_j \frac{|\omega_j|}{N} \ln \frac{|\omega_j|}{N}$$

To get $H(C)$, we calculate the following:

$$\sum_k \frac{|c_k|}{N} \ln \frac{|c_k|}{N}$$

Once we calculate the values for I, H_Ω and $H_{C'}$ we get the following:

$I(C, \Omega) \approx 1.13$

$H(\Omega) = \frac{5}{20}\ln\frac{5}{20} + \frac{5}{20}\ln\frac{5}{20} + \frac{5}{20}\ln\frac{5}{20} + \frac{5}{20}\ln\frac{5}{20} \approx -1.39$

$H(\Omega) = \frac{5}{20}\ln\frac{5}{20} + \frac{6}{20}\ln\frac{6}{20} + \frac{5}{20}\ln\frac{5}{20} + \frac{4}{20}\ln\frac{4}{20} \approx -1.38$

Once calculated, we combine them and get

$$NMI(C, \Omega) \approx 0.82$$

2. K-means

In this section, we are going to apply K-means algorithm against two datasets (dataset1.txt, dataset2.txt) with different distributions, respectively.

For each dataset, it contains 3 columns, with the format: x1 \t x2 \t cluster_label. You need to use the first two columns for clustering, and the last column for evaluation.

In [3]:
```
from hw4code.KMeans import KMeans
k = KMeans()
# As a sanity check, we print out a sample of each dataset
dataname1 = "data/dataset1.txt"
dataname2 = "data/dataset2.txt"
k.check_dataloader(dataname1)
k.check_dataloader(dataname2)
```

```
For dataset1: number of datapoints is 150
          x         y  ground_truth_cluster
0 -0.163880 -0.219869                     1
1 -0.886274 -0.356186                     1
2 -0.978910 -0.893314                     1
3 -0.658867 -0.371122                     1
4 -0.072518  0.399157                     1

For dataset2: number of datapoints is 200
          x         y  ground_truth_cluster
0  1.068587  0.136921                     1
1  0.705440  0.393068                     1
2  0.840811 -0.054906                     1
3 -0.923447  0.598501                     1
4  0.784353  0.724743                     1
```

2.1 Coding K-means

Complete the `reassignClusters` and `getCentroid` function in `KMeans.py` .

Print out each output cluster's size and centroid (x,y) for dataset1 and dataset2 respectively.

In [16]:
```
k = KMeans()
#========================#
# STRART YOUR CODE HERE  #
#========================#
k.main(dataname1)
k.main(dataname2)
#========================#
#   END YOUR CODE HERE   #
#========================#
```

```
For dataset1
Iteration :3
Cluster 0 size :50
Centroid [x=2.5737264423871213, y=-0.027462568841232993]
Cluster 1 size :50
Centroid [x=-0.4633368646347212, y=-0.46611409698195794]
Cluster 2 size :50
Centroid [x=0.9888766205736857, y=2.010478965197201]

For dataset2
Iteration :4
Cluster 0 size :102
Centroid [x=1.2708406269481844, y=-0.08583389704900128]
Cluster 1 size :98
Centroid [x=-0.2018593506236788, y=0.5726963240559536]
```

2.2 Purity and NMI Evaluation

Complete the `compute_purity` function in `KMeans.py` .

In order to compute NMI, you need to firstly compute NMI matrix and then do the calculation. That is to complete the `getNMIMatrix` and `calcNMI` functions in `KMeans.py` .

Print out the purity and NMI for each dataset respectively.

In [33]:
```
k = KMeans()
#========================#
# STRART YOUR CODE HERE  #
#========================#
k.main(dataname1, isevaluate=True)
k.main(dataname2, isevaluate=True)
#========================#
#   END YOUR CODE HERE   #
#========================#
```

```
For dataset1
Iteration :3
Purity is 1.000000
NMI is 1.000000
Cluster 0 size :50
Centroid [x=2.5737264423871213, y=-0.027462568841232993]
Cluster 1 size :50
Centroid [x=-0.4633368646347212, y=-0.46611409698195794]
Cluster 2 size :50
Centroid [x=0.9888766205736857, y=2.010478965197201]

For dataset2
Iteration :4
Purity is 0.760000
NMI is 0.205096
Cluster 0 size :102
Centroid [x=1.2708406269481844, y=-0.08583389704900128]
Cluster 1 size :98
Centroid [x=-0.2018593506236788, y=0.5726963240559536]
```

2.3 Visualization

The clustering results for KMeans are saved as `KMeans_dataset1.csv` and `KMeans_dataset2.csv` respectively under your root folder. Plot the clustering results for the two datasets, with different colors representing different clusters.

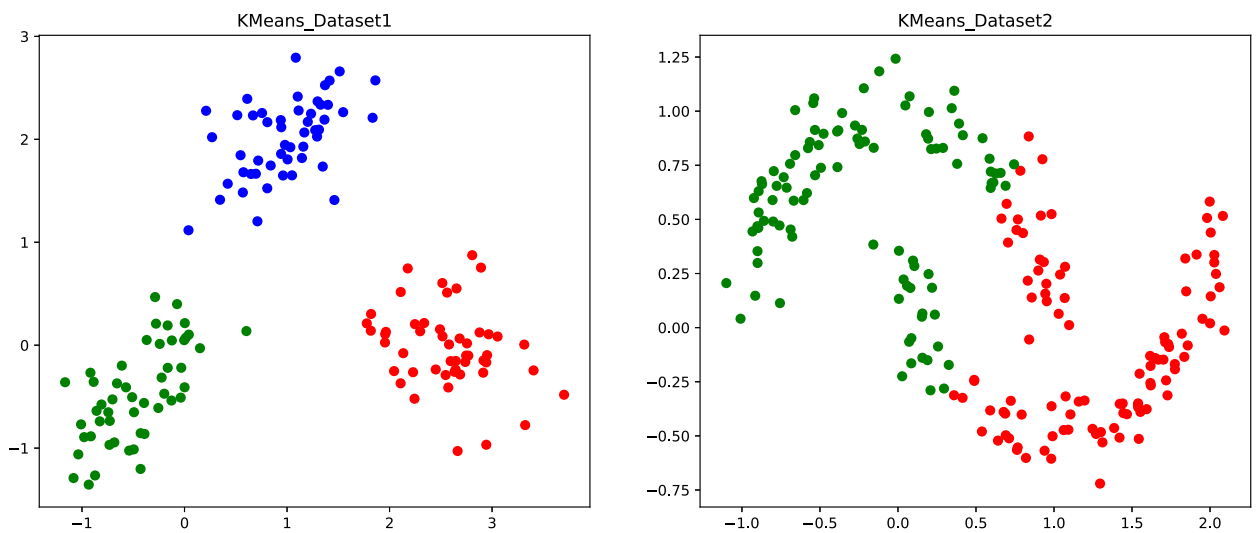
In [45]:
```
CSV_FILE_PATH1 = 'Kmeans_dataset1.csv'
CSV_FILE_PATH2 = 'Kmeans_dataset2.csv'

df1 = pd.read_csv(CSV_FILE_PATH1,header=None,names=['x','y','pred'])
df2 = pd.read_csv(CSV_FILE_PATH2,header=None,names=['x','y','pred'])
fig, [ax0,ax1] = plt.subplots(1, 2, figsize=(15, 6))
ax0.title.set_text("KMeans_Dataset1")
ax1.title.set_text("KMeans_Dataset2")

#========================#
# STRART YOUR CODE HERE  #
#========================#

colors = np.array(['r', 'g', 'b', 'orange'])
ax0.scatter(df1.x, df1.y, color=colors[df1.pred])
ax1.scatter(df2.x, df2.y, color=colors[df2.pred])

#========================#
#   END YOUR CODE HERE   #
#========================#
plt.show()
```



Question

Give the pros and cons of K-means algorithm. (At least one for pro and two for cons to get full marks)

Your answer here

Please type your answer here!

Pros

K-means is quick to train, taking $O(tkn)$ time where n is the number of points, k is the number of clusters, and t is the number of iterations. Generally, k and t are normally far less than n as well.

Additionally, K-means is simple to implement and understand

Cons

K-means can only be applied to continuous spaces (k-modes must be used for categorial data)

Very poor at discovering non-convex shapes (as we just showed!)

3 DBSCAN

In this section, we are going to use DBSCAN for clustering the same two datasets.

3.1 Coding DBSCAN

Complete the `dbscan` function in `DBSCAN.py` . Print out the purity, NMI and cluter size for each dataset respectively.

In [41]:
```
from hw4code.DBSCAN import DBSCAN
d = DBSCAN()
#========================#
# STRART YOUR CODE HERE  #
#========================#
d.main(dataname1)
d.main(dataname2)
#========================#
#   END YOUR CODE HERE   #
#========================#
```

```
For dataset1
Esp :0.3560832705047313
Number of clusters formed :4
Noise points :11
Purity is 0.940000
NMI is 0.959065
Cluster 0 size :49
Cluster 1 size :41
Cluster 2 size :47
Cluster 3 size :4

For dataset2
Esp :0.18652096476712493
Number of clusters formed :3
Noise points :3
Purity is 0.985000
NMI is 0.817349
Cluster 0 size :99
Cluster 1 size :51
Cluster 2 size :47
```

3.2 Visualization

The clustering results for DBSCAN are saved as `DBSCAN_dataset1.csv` and `DBSCAN_dataset2.csv` respectively under your root folder. Plot the clustering results for the two datasets, with different colors representing different clusters.

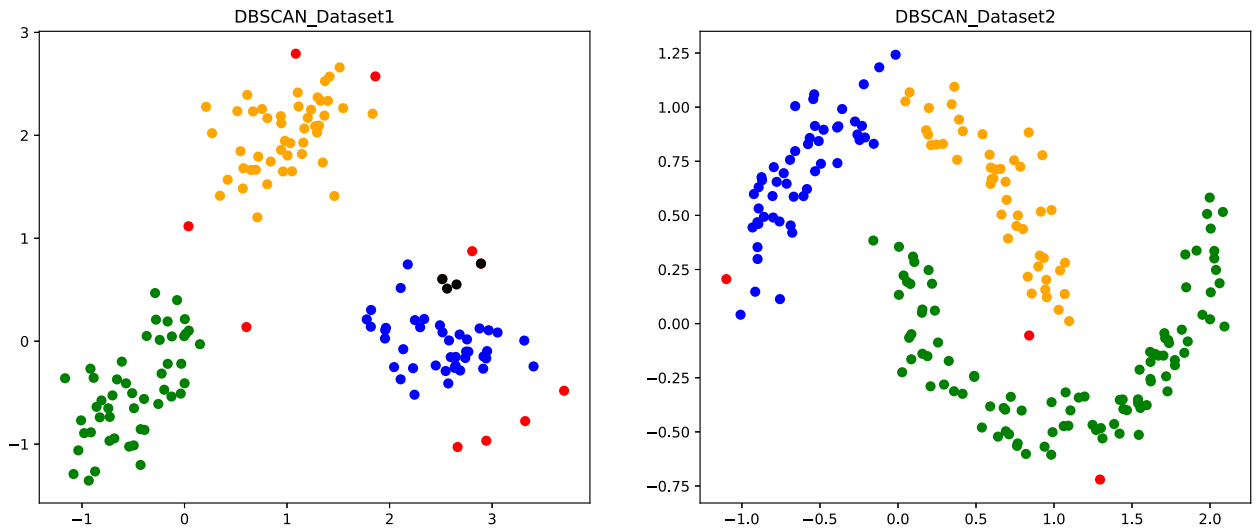
In [44]:
```
CSV_FILE_PATH1 = 'DBSCAN_dataset1.csv'
CSV_FILE_PATH2 = 'DBSCAN_dataset2.csv'

df1 = pd.read_csv(CSV_FILE_PATH1,header=None,names=['x','y','pred'])
df2 = pd.read_csv(CSV_FILE_PATH2,header=None,names=['x','y','pred'])
fig, [ax0,ax1] = plt.subplots(1, 2, figsize=(15, 6))
ax0.title.set_text("DBSCAN_Dataset1")
ax1.title.set_text("DBSCAN_Dataset2")
```

```
#========================#
# STRART YOUR CODE HERE  #
#========================#

colors = np.array(['r', 'g', 'b', 'orange', 'black'])
ax0.scatter(df1.x, df1.y, color=colors[df1.pred])
ax1.scatter(df2.x, df2.y, color=colors[df2.pred])

#========================#
#   END YOUR CODE HERE   #
#========================#
plt.show()
```



Question

Give the pros and cons of DBSCAN algorithm. (At least two for pro and one for cons to get full marks)

Your answer here

Please type your answer here!

Pros

DBSCAN can perform well discovering non-convex shapes (as demonstrated above)

DBSCAN is also very resilient to noise

Cons

Since ϵ must be chosen, it may be very hard to find a reasonable value for it if one doesn't know the scale of the features

Additionally, ϵ and $minPts$ are static values; therefore, clusters with different densities cannot easily and correctly both be identified by DBSCAN.

One last issue that exists for any model that uses a distance metric such as Euclidean is the curse of dimensionality which essentially makes the distance between data points very precise (they almost all end up around the same values) making selection of ϵ virtually impossible

4 GMM

In this section, we are going to use GMM for clustering the same two datasets.

4.1 Coding GMM

Complete the `Estep` and 'Mstep' function in `GMM.py` . Print out the purity, NMI, final mean, covariance and cluter size for each dataset respectively.

In [64]:
```
from hw4code.GMM import GMM
g = GMM()
#========================#
# STRART YOUR CODE HERE  #
#========================#
g.main(dataname1)
g.main(dataname2)
#========================#
#   END YOUR CODE HERE   #
#========================#
```

```
For dataset1
Number of Iterations = 22

After Calculations
Final mean =
-0.46247285694404044
-0.4638749980764899

0.9898929396029765
2.011802723814242

2.57342634413319
-0.027108746076609493


Final covariance =
For Cluster : 1
0.14918910487220216
0.1173463005433889

0.1173463005433889
0.215548612531075


For Cluster : 2
0.16028233507625483
0.07486967581052754

0.07486967581052754
0.13939774162738802


For Cluster : 3
0.18039223672749394
-0.04672614559811056

-0.04672614559811056
```

```
0.15206459963738586


Purity is 1.000000
NMI is 1.000000
Cluster 0 size :50
Cluster 1 size :50
Cluster 2 size :50

For dataset2
Number of Iterations = 95

After Calculations
Final mean =
0.7464905663922625
0.45649665848541027

0.28287851889390897
-0.05970560727188742


Final covariance =
For Cluster : 1
0.7692790765358334
-0.28782809642382123

-0.28782809642382123
0.1901249384356512


For Cluster : 2
0.6828574757628687
-0.30058915994390495

-0.30058915994390495
0.17583559485120057


Purity is 0.690000
NMI is 0.107406
Cluster 0 size :106
Cluster 1 size :94
```

4.2 Visualization

The clustering results for GMM are saved as `GMM_dataset1.csv` and `GMM_dataset2.csv` respectively under your root folder. Plot the clustering results for the two datasets, with different colors representing different clusters.

In [65]:

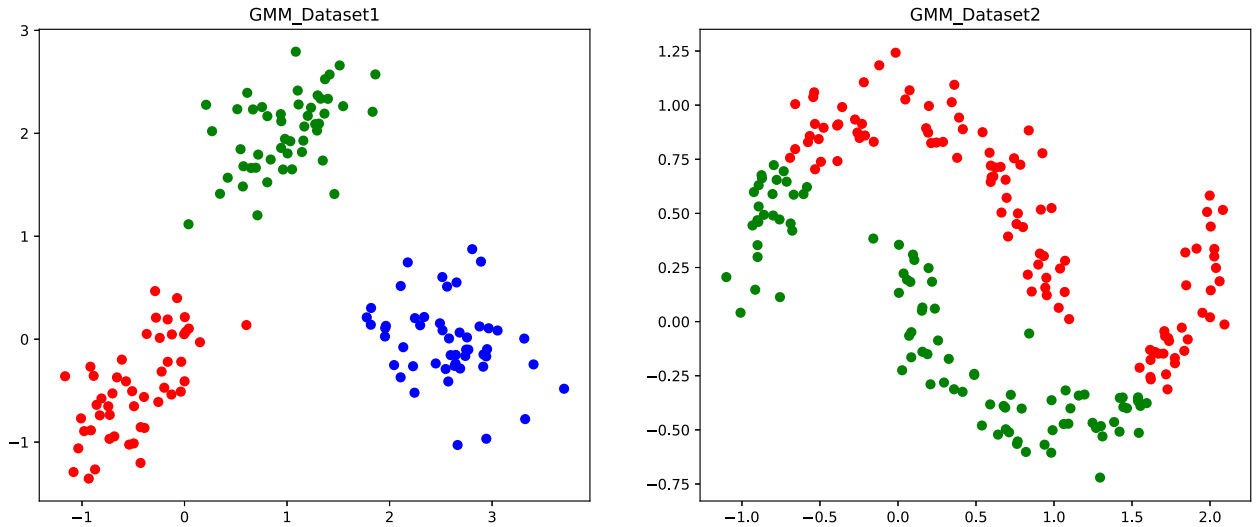
```
CSV_FILE_PATH1 = 'GMM_dataset1.csv'
CSV_FILE_PATH2 = 'GMM_dataset2.csv'

df1 = pd.read_csv(CSV_FILE_PATH1,header=None,names=['x','y','pred'])
df2 = pd.read_csv(CSV_FILE_PATH2,header=None,names=['x','y','pred'])
fig, [ax0,ax1] = plt.subplots(1, 2, figsize=(15, 6))
ax0.title.set_text("GMM_Dataset1")
ax1.title.set_text("GMM_Dataset2")

#========================#
# STRART YOUR CODE HERE  #
#========================#
```

```
colors = np.array(['r', 'g', 'b', 'orange', 'black'])
ax0.scatter(df1.x, df1.y, color=colors[df1.pred])
ax1.scatter(df2.x, df2.y, color=colors[df2.pred])

#=======================#
#   END YOUR CODE HERE   #
#=======================#
plt.show()
```



Questions

1. Give the pros and cons of GMM algorithm. (At least two for pro and two for cons to get full marks)
2. Compare the visualization results from three algorithms, analyze for each dataset why these algorithms would produce such result.

Your answer here:

Please type your answer here!

Pros of GMM

One pro of mixture models is that they can generalize different densities and different cluster sizes simultaneously

Another pro is that is is a simple model with only a few (and fairly explainable) parameters

Cons of GMM

GMM can only create round circular/ovalish shapes.

It is also computationally expensive to train if there are many distributions

Reasoning over dataset1

All three models do fairly well. This makes sense, because all three clusters are consistently dense (good for DBSCAN), have similarly sized clusters (good for K-means), and have roughly circular/oval shaped clusters (good for K-means and GMM)

Reasoning over dataset2

We see GMM and K-means doing pretty poorly while DBSCAN performs excellently. This make sense, becuase the shapes are non-convex, oblong, non-circular shapes. Thus K-means and GMM will struggle significantly to cluster them while DBSCAN can do a good job since the data has a nice, consistent density in the clusters.

5 Bonus Question

Prove that KMeans algorithm would guarantee covergence. (**Hint: prove for each step the loss would descrease.**)

In the first step, we fix the centers and find the assignment of w_{ij} that minimizes J. If there is no better assignment, we leave the assignments as they are.
We note that the only way J changes is if the cluster label of a point changes. If it does, then we know J will decrease because we only change if we can pick an assignment for which the J_i for that point i decreases (and then we pick the label that maximally decreases J_i).

In the second step, we fix the assignments of the points w_{ij}, but then find centers for the clusters that minimize J. We note that the solution to this is closed; we can simply set $\frac{\partial J}{\partial c_j} = 0$. So, we will prove now that when doing this, we end up with the solution we run (where we recenter the clusters based on their center of mass). Thus, we're minimizing J and therefore either decreasing it or leaving it the same.

$$J = \sum_{j=1}^{k} \sum_{i} w_{ij} ||x_i - c_j||^2$$

$$\frac{\partial J}{\partial c_j} = -2 \sum_{i} w_{ij}(x_i - c_j)$$

Setting the derivative equal to zero, we get

$$0 = -2 \sum_{i} w_{ij}(x_i - c_j)$$

$$c_j = \frac{\sum_i w_{ij} x_i}{\sum_i w_{ij}}$$

This is precisely what we do; therefore in step two we minimize J again and monotonically decrease it.

End of Homework 4 :)

After you've finished the homework, please print out the entire `ipynb` notebook and four `py` files into one PDF file. Make sure you include the output of code cells and answers for questions. Prepare submit it to GradeScope. Also this time remember assign the pages to the questions on GradeScope

```python
from hw4code.DataPoints import DataPoints
import random
import sys
import math
import pandas as pd
import numpy as np

# ======================================================================
def sqrt(n):
    return math.sqrt(n)

# ======================================================================
def getEuclideanDist(x1, y1, x2, y2):
    dist = sqrt(pow((x2 - x1), 2) + pow((y2 - y1), 2))
    return dist
# ======================================================================
def compute_purity(clusters,total_points):
    # Calculate purity

    # Create list to store the maximum union number for each output cluster.
    maxLabelCluster = []
    num_clusters = len(clusters)
    # ========================#
    # STRART YOUR CODE HERE  #
    # ========================#
    for cluster in clusters:
        vals, counts = np.unique([dp.label for dp in cluster], return_counts=True)
        maxLabelCluster.append(max(counts))
    # ========================#
    #   END YOUR CODE HERE   #
    # ========================#
    purity = 0.0
    for j in range(num_clusters):
        purity += maxLabelCluster[j]
    purity /= total_points
    print("Purity is %.6f" % purity)

# ======================================================================
def compute_NMI(clusters,noOfLabels):
    # Get the NMI matrix first
    nmiMatrix = getNMIMatrix(clusters, noOfLabels)
    # Get the NMI matrix first
    nmi = calcNMI(nmiMatrix)
    print("NMI is %.6f" % nmi)


# ======================================================================
def getNMIMatrix(clusters, noOfLabels):
    # Matrix shape of [num_true_clusters + 1,num_output_clusters + 1] (example under week6's slide page 9)
    nmiMatrix = [[0 for x in range(len(clusters) + 1)] for y in range(noOfLabels + 1)]
    clusterNo = 0
    for cluster in clusters:
        # Create dictionary {true_class_No: Number of shared elements}
        labelCounts = {}
        # ========================#
        # STRART YOUR CODE HERE  #
        # ========================#
        classes, counts = np.unique([dp.label for dp in cluster], return_counts=True)
```

```python
        labelCounts = dict(zip(classes, counts))
        # ========================#
        #   END YOUR CODE HERE   #
        # ========================#
        labelTotal = 0
        labelCounts_sorted = sorted(labelCounts.items(), key=lambda item: item[1], reverse=True)
        for label, val in labelCounts_sorted:
            nmiMatrix[label - 1][clusterNo] = labelCounts[label]
            labelTotal += labelCounts.get(label)
        # Populate last row (row of summation)
        nmiMatrix[noOfLabels][clusterNo] = labelTotal
        clusterNo += 1
        labelCounts.clear()

    # Populate last col (col of summation)
    lastRowCol = 0
    for i in range(noOfLabels):
        totalRow = 0
        for j in range(len(clusters)):
            totalRow += nmiMatrix[i][j]
        lastRowCol += totalRow
        nmiMatrix[i][len(clusters)] = totalRow

    # Total number of datapoints
    nmiMatrix[noOfLabels][len(clusters)] = lastRowCol

    return nmiMatrix

# ======================================================================
def calcNMI(nmiMatrix):
    # Num of true clusters + 1
    row = len(nmiMatrix)
    # Num of output clusters + 1
    col = len(nmiMatrix[0])
    # Total number of datapoints
    N = nmiMatrix[row - 1][col - 1]
    I = 0.0
    HOmega = 0.0
    HC = 0.0

    for i in range(row - 1):
        for j in range(col - 1):
            # Compute the log part of each pair of clusters within I's formula.
            logPart_I = 1.0
            # ========================#
            # STRART YOUR CODE HERE  #
            # ========================#
            logPart_I = N * nmiMatrix[i][j] / (nmiMatrix[-1][j] * nmiMatrix[i][-1])
            # ========================#
            #   END YOUR CODE HERE   #
            # ========================#

            if logPart_I == 0.0:
                continue
            I += (nmiMatrix[i][j] / float(N)) * math.log(float(logPart_I))
        # Compute HOmega
        # ========================#
        # STRART YOUR CODE HERE  #
        # ========================#
```

```python
        HOmega += nmiMatrix[i][-1] / N * np.log(nmiMatrix[i][-1] / N)
        # ========================#
        #   END YOUR CODE HERE   #
        # ========================#

    #Compute HC
    # ========================#
    # STRART YOUR CODE HERE  #
    # ========================#
    c_row = np.array(nmiMatrix[-1][:-1])
    HC = np.sum((c_row / N) * np.log(c_row/N))
    # ========================#
    #   END YOUR CODE HERE   #
    # ========================#

    return I / math.sqrt(HC * HOmega)




# ======================================================================
class Centroid:
    # ----------------------------------------------------------------------
    def __init__(self, x, y):
        self.x = x
        self.y = y
    # ----------------------------------------------------------------------
    def __eq__(self, other):
        if not type(other) is type(self):
            return False
        if other is self:
            return True
        if other is None:
            return False
        if self.x != other.x:
            return False
        if self.y != other.y:
            return False
        return True
    # ----------------------------------------------------------------------
    def __ne__(self, other):
        result = self.__eq__(other)
        if result is NotImplemented:
            return result
        return not result
    # ----------------------------------------------------------------------
    def toString(self):
        return "Centroid [x=" + str(self.x) + ", y=" + str(self.y) + "]"
    # ----------------------------------------------------------------------
    def __str__(self):
        return self.toString()
    # ----------------------------------------------------------------------
    def __repr__(self):
        return self.toString()
```

```python


# ======================================================================
class KMeans:
    # ------------------------------------------------------------------
    def __init__(self):
        self.K = 0
    # ------------------------------------------------------------------
    def main(self, dataname,isevaluate=False):
        seed = 71
        self.dataname = dataname[5:-4]
        print("\nFor " + self.dataname)
        self.dataSet = self.readDataSet(dataname)
        self.K = DataPoints.getNoOFLabels(self.dataSet)
        random.Random(seed).shuffle(self.dataSet)
        self.kmeans(isevaluate)

    # ------------------------------------------------------------------
    def check_dataloader(self,dataname):

        df = pd.read_table(dataname,sep = "\t", header=None, names=['x','y','ground_truth_cluster'])
        print("\nFor " + dataname[5:-4] + ": number of datapoints is %d" % df.shape[0])
        print(df.head(5))


    # ------------------------------------------------------------------
    def kmeans(self,isevaluate=False):
        clusters = []
        k = 0
        while k < self.K:
            cluster = set()
            clusters.append(cluster)
            k += 1

        # Initially randomly assign points to clusters
        i = 0
        for point in self.dataSet:
            clusters[i % k].add(point)
            i += 1

        # calculate centroid for clusters
        centroids = []
        for j in range(self.K):
            centroids.append(self.getCentroid(clusters[j]))

        self.reassignClusters(self.dataSet, centroids, clusters)

        # continue till converge
        iteration = 0
        while True:
            iteration += 1
            # calculate centroid for clusters
            centroidsNew = []
            for j in range(self.K):
                centroidsNew.append(self.getCentroid(clusters[j]))

            isConverge = False
            for j in range(self.K):
```

```
                if centroidsNew[j] != centroids[j]:
                    isConverge = False
                else:
                    isConverge = True
            if isConverge:
                break

            for j in range(self.K):
                clusters[j] = set()

            self.reassignClusters(self.dataSet, centroidsNew, clusters)
            for j in range(self.K):
                centroids[j] = centroidsNew[j]
        print("Iteration :" + str(iteration))

        if isevaluate:
            # Calculate purity and NMI
            compute_purity(clusters, len(self.dataSet))
            compute_NMI(clusters, self.K)

        # write clusters to file for plotting
        f = open("Kmeans_"+ self.dataname + ".csv", "w")
        for w in range(self.K):
            print("Cluster " + str(w) + " size :" + str(len(clusters[w])))
            print(centroids[w].toString())
            for point in clusters[w]:
                f.write(str(point.x) + "," + str(point.y) + "," + str(w) + "\n")
        f.close()

    # ----------------------------------------------------------------------
    def reassignClusters(self, dataSet, c, clusters):
        # reassign points based on cluster and continue till stable clusters found
        dist = [0.0 for x in range(self.K)]
        for point in dataSet:
            for i in range(self.K):
               dist[i] = getEuclideanDist(point.x, point.y, c[i].x, c[i].y)

            minIndex = self.getMin(dist)
            # assign point to the closest cluster
            # ========================#
            # STRART YOUR CODE HERE  #
            # ========================#

            for cluster in clusters:
                try:
                    cluster.remove(point)
                except KeyError:
                    pass

            clusters[minIndex].add(point)

            # ========================#
            #   END YOUR CODE HERE   #
            # ========================#
    # ----------------------------------------------------------------------
    def getMin(self, dist):
        min = sys.maxsize
        minIndex = -1
        for i in range(len(dist)):
            if dist[i] < min:
```

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                min = dist[i]
                minIndex = i
        return minIndex

    # ------------------------------------------------------------------
    def getCentroid(self, cluster):
        # mean of x and mean of y
        cx = 0
        cy = 0
        # ========================#
        # STRART YOUR CODE HERE  #
        # ========================#
        for dp in cluster:
            cx += dp.x
            cy += dp.y

        cx /= len(cluster)
        cy /= len(cluster)
        # ========================#
        #   END YOUR CODE HERE   #
        # ========================#
        return Centroid(cx, cy)
    # ------------------------------------------------------------------
    @staticmethod
    def readDataSet(filePath):
        dataSet = []
        with open(filePath) as f:
            lines = f.readlines()
        lines = [x.strip() for x in lines]
        for line in lines:
            points = line.split('\t')
            x = float(points[0])
            y = float(points[1])
            label = int(points[2])
            point = DataPoints(x, y, label)
            dataSet.append(point)
        return dataSet

```

```python
from hw4code.KMeans import KMeans,compute_purity,compute_NMI,getEuclideanDist
from hw4code.DataPoints import DataPoints
import random


class DBSCAN:
    # ------------------------------------------------------------------
    def __init__(self):
        self.e = 0.0
        self.minPts = 3
        self.noOfLabels = 0
    # ------------------------------------------------------------------
    def main(self, dataname):
        seed = 71

        self.dataname = dataname[5:-4]
        print("\nFor " + self.dataname)
        self.dataSet = KMeans.readDataSet(dataname)
        random.Random(seed).shuffle(self.dataSet)
        self.noOfLabels = DataPoints.getNoOFLabels(self.dataSet)
        self.e = self.getEpsilon(self.dataSet)
        print("Esp :" + str(self.e))
        self.dbscan(self.dataSet)


    # ------------------------------------------------------------------
    def getEpsilon(self, dataSet):
        distances = []
        sumOfDist = 0.0
        for i in range(len(dataSet)):
            point = dataSet[i]
            for j in range(len(dataSet)):
                if i == j:
                    continue
                pt = dataSet[j]
                dist = getEuclideanDist(point.x, point.y, pt.x, pt.y)
                distances.append(dist)

            distances.sort()
            sumOfDist += distances[7]
            distances = []
        return sumOfDist/len(dataSet)
    # ------------------------------------------------------------------
    def dbscan(self, dataSet):
        clusters = []
        visited = set()
        noise = set()

        # Iterate over data points
        for i in range(len(dataSet)):
            point = dataSet[i]
            if point in visited:
                continue
            visited.add(point)
            N = []
            minPtsNeighbours = 0

            # check which point satisfies minPts condition
            for j in range(len(dataSet)):
                if i==j:
```

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                    continue
                pt = dataSet[j]
                dist = getEuclideanDist(point.x, point.y, pt.x, pt.y)
                if dist <= self.e:
                    minPtsNeighbours += 1
                    N.append(pt)

            if minPtsNeighbours >= self.minPts:
                cluster = set()
                cluster.add(point)
                point.isAssignedToCluster = True

                j = 0
                while j < len(N):
                    point1 = N[j]
                    minPtsNeighbours1 = 0
                    N1 = []
                    if not point1 in visited:
                        visited.add(point1)
                        for l in range(len(dataSet)):
                            pt = dataSet[l]
                            dist = getEuclideanDist(point1.x, point1.y, pt.x, pt.y)
                            if dist <= self.e:
                                minPtsNeighbours1 += 1
                                N1.append(pt)
                        if minPtsNeighbours1 >= self.minPts:
                            self.removeDuplicates(N, N1)

                    # Add point1 is not yet member of any other cluster then add it to cluster
                    # Hint: use self.isAssignedToCluster function to check if a point is assigned to any clusters
                    # ========================#
                    # STRART YOUR CODE HERE  #
                    # ========================#
                    if not point1.isAssignedToCluster:
                        cluster.add(point1)
                        point1.isAssignedToCluster = True
                    # ========================#
                    #   END YOUR CODE HERE   #
                    # ========================#
                    j += 1

                # add cluster to the list of clusters
                clusters.append(cluster)

            else:
                noise.add(point)


        # List clusters
        print("Number of clusters formed :" + str(len(clusters)))
        print("Noise points :" + str(len(noise)))

        # Calculate purity
        compute_purity(clusters,len(self.dataSet))
        compute_NMI(clusters,self.noOfLabels)
        DataPoints.writeToFile(noise, clusters, "DBSCAN_"+ self.dataname + ".csv")
    # ------------------------------------------------------------------
    def removeDuplicates(self, n, n1):
```

```
        for point in n1:
            isDup = False
            for point1 in n:
                if point1 == point:
                    isDup = True
                    break
            if not isDup:
                n.append(point)


```

```python
from hw4code.DataPoints import DataPoints
from hw4code.KMeans import KMeans, compute_purity,compute_NMI
import math
from scipy.stats import multivariate_normal

# ======================================================================
class GMM:
    # ----------------------------------------------------------------------
    def __init__(self):
        self.dataSet = []
        self.K = 0
        self.mean = [[0.0 for x in range(2)] for y in range(3)]
        self.stdDev = [[0.0 for x in range(2)] for y in range(3)]
        self.coVariance = [[[0.0 for x in range(2)] for y in range(2)] for z in range(3)]
        self.W = None
        self.w = None
    # ----------------------------------------------------------------------
    def main(self, dataname):

        self.dataname = dataname[5:-4]
        print("\nFor " + self.dataname)
        self.dataSet = KMeans.readDataSet(dataname)
        self.K = DataPoints.getNoOFLabels(self.dataSet)
        # weight for pair of data and cluster
        self.W = [[0.0 for y in range(self.K)] for x in range(len(self.dataSet))]
        # weight for pair of data and cluster
        self.w = [0.0 for x in range(self.K)]
        self.GMM()

    # ----------------------------------------------------------------------
    def GMM(self):
        clusters = []
        # [num_clusters,2]
        self.mean = [[0.0 for y in range(2)] for x in range(self.K)]
        # [num_clusters,2]
        self.stdDev = [[0.0 for y in range(2)] for x in range(self.K)]
        # [num_clusters,2]
        self.coVariance = [[[0.0 for z in range(2)] for y in range(2)] for x in range(self.K)]
        k = 0
        while k < self.K:
            cluster = set()
            clusters.append(cluster)
            k += 1

        # Initially randomly assign points to clusters
        i = 0
        for point in self.dataSet:
            clusters[i % self.K].add(point)
            i += 1

        # Initially assign equal prior weight for each cluster
        for m in range(self.K):
            self.w[m] = 1.0 / self.K

        # Get Initial mean, std, covariance matrix
        DataPoints.getMean(clusters, self.mean)
        DataPoints.getStdDeviation(clusters, self.mean, self.stdDev)
        DataPoints.getCovariance(clusters, self.mean, self.stdDev, self.coVariance)
```

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        length = 0
        while True:
            mle_old = self.Likelihood()
            self.Estep()
            self.Mstep()
            length += 1
            mle_new = self.Likelihood()

            # convergence condition
            if abs(mle_new - mle_old) / abs(mle_old) < 0.000001:
                break

        print("Number of Iterations = " + str(length))
        print("\nAfter Calculations")
        print("Final mean = ")
        self.printArray(self.mean)
        print("\nFinal covariance = ")
        self.print3D(self.coVariance)

        # Assign points to cluster depending on max prob.
        for j in range(self.K):
            clusters[j] = set()

        i = 0
        for point in self.dataSet:
            index = -1
            prob = 0.0
            for j in range(self.K):
                if self.W[i][j] > prob:
                    index = j
                    prob = self.W[i][j]
            temp = clusters[index]
            temp.add(point)
            i += 1

        # Calculate purity and NMI
        compute_purity(clusters,len(self.dataSet))
        compute_NMI(clusters,self.K)

        # write clusters to file for plotting
        f = open("GMM_" + self.dataname + ".csv", "w")
        for w in range(self.K):
            print("Cluster " + str(w) + " size :" + str(len(clusters[w])))
            for point in clusters[w]:
                f.write(str(point.x) + "," + str(point.y) + "," + str(w) + "\n")
        f.close()
    # ------------------------------------------------------------------
    def Estep(self):
        # Update self.W
        for i in range(len(self.dataSet)):
            denominator = 0.0
            for j in range(self.K):
                gaussian = multivariate_normal(self.mean[j], self.coVariance[j])
                # Compute numerator for self.W[i][j] below
                numerator = 0.0
                # ========================#
                # STRART YOUR CODE HERE  #
                # ========================#

```

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                pt = self.dataSet[i]
                numerator = self.w[j] * gaussian.pdf((pt.x, pt.y))

                # ========================#
                #   END YOUR CODE HERE   #
                # ========================#
                self.W[i][j] = numerator
                denominator += numerator

            # normalize W[i][j] into probabilities
            # ========================#
            # STRART YOUR CODE HERE  #
            # ========================#

            row_weight = sum(self.W[i])
            for j in range(self.K):
                self.W[i][j] /= row_weight

            # ========================#
            #   END YOUR CODE HERE   #
            # ========================#
    # ----------------------------------------------------------------------
    def Mstep(self):
        for j in range(self.K):
            denominator = 0.0
            numerator_x = 0.0
            numerator_y = 0.0
            cov_xy = 0.0
            updatedMean_x = 0.0
            updatedMean_y = 0.0

            # update self.w[j] and self.mean
            for i in range(len(self.dataSet)):
                denominator += self.W[i][j]
                updatedMean_x += self.W[i][j] * self.dataSet[i].x
                updatedMean_y += self.W[i][j] * self.dataSet[i].y

            self.w[j] = denominator / len(self.dataSet)

            #update self.mean
            # ========================#
            # STRART YOUR CODE HERE  #
            # ========================#

            self.mean[j] = [0, 0]

            den = 0
            for i, dp in enumerate(self.dataSet):
                self.mean[j][0] += self.W[i][j] * dp.x
                self.mean[j][1] += self.W[i][j] * dp.y

                den += self.W[i][j]

            self.mean[j][0] /= den
            self.mean[j][1] /= den

            denominator = 0

            # ========================#
            #   END YOUR CODE HERE   #
```

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            # ========================#

            # update covariance matrix
            for i in range(len(self.dataSet)):
                numerator_x += self.W[i][j] * pow((self.dataSet[i].x - self.mean[j][0]), 2)
                numerator_y += self.W[i][j] * pow((self.dataSet[i].y - self.mean[j][1]), 2)
                # Compute conv_xy +=?
                # ========================#
                # STRART YOUR CODE HERE  #
                # ========================#

                cov_xy += self.W[i][j] * (self.dataSet[i].x - self.mean[j][0]) * (self.dataSet[i].y - self.mean[j][1])
                denominator += self.W[i][j]

                # ========================#
                #   END YOUR CODE HERE   #
                # ========================#

            self.stdDev[j][0] = numerator_x / denominator
            self.stdDev[j][1] = numerator_y / denominator


            self.coVariance[j][0][0] = self.stdDev[j][0]
            self.coVariance[j][1][1] = self.stdDev[j][1]
            self.coVariance[j][0][1] = self.coVariance[j][1][0] = cov_xy / denominator
    # ------------------------------------------------------------------
    def Likelihood(self):
        likelihood = 0.0
        for i in range(len(self.dataSet)):
            numerator = 0.0
            for j in range(self.K):
                gaussian = multivariate_normal(self.mean[j], self.coVariance[j])
                numerator += self.w[j] * gaussian.pdf([self.dataSet[i].x, self.dataSet[i].y])
            likelihood += math.log(numerator)
        return likelihood
    # ------------------------------------------------------------------
    def printArray(self, mat):
        for i in range(len(mat)):
            for j in range(len(mat[i])):
                print(str(mat[i][j]) + " "),
            print("")
    # ------------------------------------------------------------------
    def print3D(self, mat):
        for i in range(len(mat)):
            print("For Cluster : " + str((i + 1)))
            for j in range(len(mat[i])):
                for k in range(len(mat[i][j])):
                    print(str(mat[i][j][k]) + " "),
                print("")
            print("")

# ====================================================================
if __name__ == "__main__":
    g = GMM()
    dataname = "dataset1.txt"
```

```
    g.main(dataname)
```