Homework 3 (100 points)

The goal of this homework is to practice techniques relating to GMM and SVD.

Exercise 1 (25 points)

In this exercise we will implement 1-dimensional GMM clustering algorithm from scratch. A GMM distribution is composed of k components, each characterized by:

- 1. A mixture proportion
- 2. A mean for its Normal Distribution
- 3. A variance for its Normal Distribution

So, to generate a dataset that follows a GMM dsitrbution we need a list of those parameters. In this exercise we will use a class called Component to capture the parameters for a given component. And a GMM will be a list of Component s.

```
In [1]: class Component:
    def __init__(self, mixture_prop, mean, variance):
        self.mixture_prop = mixture_prop
        self.mean = mean
        self.variance = variance

example_gmm = [Component(.5, 5, 1), Component(.5, 8, 1)]
```

a) Complete the function below to validate and generate a dataset following a GMM distribution, given a specified set of GMM parameters as above and a size. You may only use the methods already imported in the cell. (10pts)

```
In [2]:
        from numpy.random import normal, uniform
        def generate_gmm_dataset(gmm_params, size):
            if not is_valid_gmm(gmm_params):
                raise ValueError("GMM parameters are invalid")
            dataset = []
            for _ in range(size):
                comp = get_random_component(gmm_params)
                # mean_j, var_j of comp
                mean_j = comp.mean
                var_j = comp.variance
                dataset += [normal(mean_j, var_j)]
            return dataset
        def is_valid_gmm(gmm_params):
                Checks that the sum of the mixture
                proportions is 1
            if abs(sum([comp.mixture_prop for comp in gmm_params]) -1) != 0:
                print("is_valid_gmm returns false")
            return True
        def get_random_component(gmm_params):
                returns component with prob
                proportional to mixture_prop
            u = uniform()
            prob_sum = 0
            for comp in gmm_params:
                prob_sum += comp.mixture_prop
                if u <= prob_sum:</pre>
                    return comp
            return gmm_params[-1]
        # test your code: this should return a list of 10 numbers similar to worksheet 8
        data = generate_gmm_dataset(example_gmm, 10)
        print(data)
```

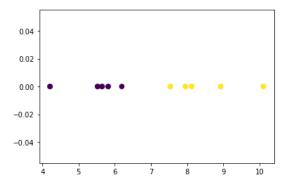
[7.9490908318149245, 5.522271509604284, 5.8156020180488355, 10.100229133797184, 5.646674466932788, 8.120996406941904, 7.531 112991672513, 4.207668559673417, 8.920073382539059, 6.191570682802771]

b) Finish the implementation below of the Expectation-Maximization Algorithm. Only use methods that have been imported in the cell. (15pts)

```
In [3]:
        from scipy.stats import norm
        from numpy import array, argmax
        import matplotlib.pyplot as plt
        from sklearn.cluster import KMeans
        def gmm init(k, dataset):
            kmeans = KMeans(k, init='k-means++').fit(X=array(dataset).reshape(-1, 1))
            gmm_params = []
            for _ in range(k):
                mean_j = kmeans.cluster_centers_[_][0]
                var_j = kmeans.inertia_/(k* len(dataset))
                mixture prop = 1/k
                gmm_params.append(Component(mixture_prop, mean_j, var_j))
            return gmm_params
        def compute_gmm(k, dataset, probs):
               Compute P(C_j), mean_j, var_j
            gmm params = []
            for j in range(k):
                probs_j = array([p[j] for p in probs])
                mixture_prop_j = probs_j.mean()
                mean_j = (probs_j * dataset).sum()/ probs_j.sum()
                var j = (probs j * (dataset - mean j)**2).sum() / probs j.sum()
                gmm_params.append(Component(mixture_prop_j, mean_j, var_j))
            return gmm_params
        def compute_probs(k, dataset, gmm_params):
                For all x_i in dataset, compute P(C_j | X_i)
                = P(X i \mid C j)P(C j) / P(X i) for all C j
                return the list of lists of all P(C_j | X_i)
                for all x_i in dataset.
            probs = []
            for x in dataset:
               px = sum([comp.mixture_prop* norm(comp.mean, comp.variance).pdf(x) for comp in gmm_params])
                p x given c = [comp.mixture prop* norm(comp.mean, comp.variance).pdf(x)/ px for comp in gmm params]
                probs.append(p_x_given_c)
            return probs
        def expectation_maximization(k, dataset, iterations):
                Repeat for a set number of iterations.
            gmm_params = gmm_init(k, dataset)
            for _ in range(iterations):
                # expectation step
                probs = compute_probs(k, dataset, gmm_params)
                # maximization step
                gmm_params = compute_gmm(k, dataset, probs)
            return probs, gmm_params
        # for testing: you should see smaller sized points
        # near the boundary of a cluster if it is close to another cluster
        probs, gmm p = expectation maximization(2, data, 3)
        labels = [argmax(array(p)) for p in probs] # create a hard assignment
        size = 50 * array(probs).max(1) ** 2 # square to emphasize the difference
        plt.scatter(data, [0.0 for _ in range(len(data))], c=labels, cmap='viridis', s=size)
        plt.show()
        /opt/homebrew/lib/python3.9/site-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will
```

change from 10 to 'auto' in 1.4. Set the value of `n_init` explicitly to suppress the warning

warnings.warn(



Notes:

- 1. your code should work with any number of components, each with reasonable parameters.
- 2. your code should work for 1 to about 5 iterations of the EM algorithm. It may not work for iterations over 10 because the math we are doing may overflow and create nans that's ok / don't worry about it.
- 3. worksheet 7 is your friend

Exercise 2 (50 points)

a) Fetch the "mnist_784" data and store is as a .csv (that way you don't have to fetch it every time - which takes about 30s). (2.5 points)

```
import matplotlib.pyplot as plt
from sklearn.datasets import fetch_openml

X, y = fetch_openml(name="mnist_784", version=1, return_X_y=True, as_frame=False)

# your code here
import pandas as pd

df = pd.DataFrame(X, y)
# df.to csv('mnist_784.csv', index=False)
```

/opt/homebrew/lib/python3.9/site-packages/sklearn/datasets/_openml.py:932: FutureWarning: The default value of `parser` will change from `'liac-arff'` to `'auto'` in 1.4. You can set `parser='auto'` to silence this warning. Therefore, an `ImportE rror` will be raised from 1.4 if the dataset is dense and pandas is not installed. Note that the pandas parser may return d ifferent data types. See the Notes Section in fetch_openml's API doc for details.

warn(

b) Plot the singular value plot for a single example of the 0 digit (2.5 points)

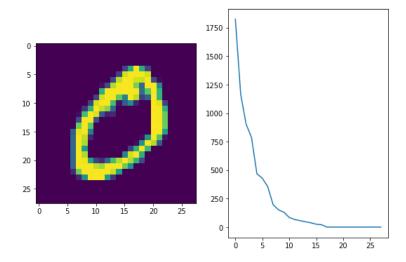
```
In [2]: import numpy as np
singular_value = []
for i in range(len(X)):
    if y[i] == '0':
        singular_value = X[i]
        break

image = singular_value.reshape(28, 28)

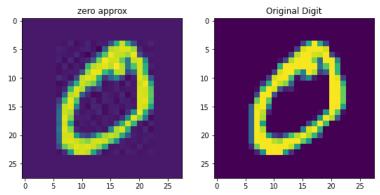
u, s, vh = np.linalg.svd(image)
fig, ax = plt.subplots(1, 2,figsize=(9, 6))

ax[0].imshow(image)
ax[1].plot(s)
```

Out[2]: [<matplotlib.lines.Line2D at 0x14c8cf1f0>]



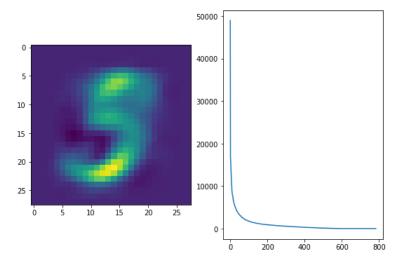
c) Just like we did in class with the image of the boat: By setting some singular values to 0, plot the approximation of an image of a 0 digit next to the original image. (10 points)



d) Consider the entire dataset as a matrix. Perform SVD and explain why / how you chose a particular rank. Note: you may not be able to run this on the entire dataset in a reasonable amount of time so you may take a small random sample for this and the following questions. (5 points)

```
In [6]: # print(X.shape)
        # print(X[:1000].reshape(-1, 28,28).shape)
        # print(X.shape)
        \# X = X.reshape(-1, 28, 28)
        # # print(X.shape)
        # u1, s1, vh1 = np.linalg.svd(X[:1000], full matrices = False)
        # print(X[:1000].shape)
        # # print(u1.shape)
        # # print(s1.shape)
        # # print(vh1.shape)
        # rank = 10
        # scopy1 =s1.copy()
        # scopy1[rank:]=0
        # dataset_approx = u1.dot(np.diag(scopy1)).dot(vh1)
        # fig, ax = plt.subplots(1, 2, figsize=(9, 6))
        # # ax[0].imshow(dataset approx[0])
        # ax[1].plot(s1)
        #*****************
        # zero image1 = u1.dot(np.diag(scopy1)).dot(vt1).reshape(-1, 28,28)
        # print(zero_image1.shape)
        # ax1[0].imshow(zero_image1.reshape(28, 28))
        # ax1[1].plot(s1)
        # plt.figure(figsize=(9,6))
        # plt.subplot(1,2,1)
        # plt.imshow(dataset approx[0].reshape(28, 28))
        # plt.title('dataset approx')
        # plt.subplot(1,2,2)
        # plt.imshow(image)
        # plt.title('Original Digit')
        # plt.show()
        u1, s1, v1 = np.linalg.svd(X[:1000], full matrices=False)
        rank = 10
        slcopy = sl.copy()
        s1copy[rank:]=0.0
        datasetApprox = u1.dot(np.diag(s1copy)).dot(v1).reshape(-1,28,28)
        fig, ax = plt.subplots(1, 2,figsize=(9, 6))
        ax[0].imshow(datasetApprox[0].reshape(28,28))
        ax[1].plot(s1)
```

Out[6]: [<matplotlib.lines.Line2D at 0x14df2fbe0>]



From the plot, we can see that the singular values decay rapidly, indicating that we can retain most of the information by choosing a relatively low rank. 10 is a good choice since the elbow is about 10 in the plot

e) As in homework 2, using Kmeans on this new dataset, cluster the images from d) using 10 clusters and plot the centroid of each cluster. Note: the centroids should be represented as images. (10 points)

```
In [8]: from sklearn.cluster import KMeans
    #had to redo the new dataset, the dimension of the dataset in 1d does not fit here.
    zero_image2 = u1.dot(np.diag(scopy1)).dot(vt1)

kmeans_new_ds= KMeans(n_clusters=10)
    clusters_new_ds = kmeans_new_ds.fit_predict(zero_image2)
    centroids_new_ds = kmeans_new_ds.cluster_centers_

centroids_new_copy = centroids_new_ds.reshape(10, 28, 28)

fig, ax = plt.subplots(1,10)
    for i in range(10):
        ax[i].imshow(centroids_new_copy[i])
```

/opt/homebrew/lib/python3.9/site-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10 to 'auto' in 1.4. Set the value of `n_init` explicitly to suppress the warning warnings.warn(



f) Repeat e) on the original dataset (if you used a subset of the dataset, keep using that same subset). Comment on any differences (or lack thereof) you observe between the centroids. (5 points)

```
In [9]: kmeans_old_ds= KMeans(n_clusters=10)
    clusters_old_ds = kmeans_old_ds.fit_predict(X)
    centroids_old_ds = kmeans_old_ds.cluster_centers_

centroids_copy = centroids_old_ds.reshape(10, 28, 28)

fig, ax = plt.subplots(1,10)
    for i in range(10):
        ax[i].imshow(centroids_copy[i])
```

/opt/homebrew/lib/python3.9/site-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10 to 'auto' in 1.4. Set the value of `n_init` explicitly to suppress the warning warnings.warn(

0.00000000e+00, 0.00000000e+00, 0.00000000e+00], [1.02674393e-16, 3.49401441e-13, -2.76044478e-13, ..., 0.00000000e+00, 0.00000000e+00, 0.00000000e+00])

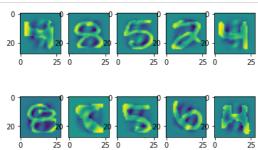
both datasets are not doing good job custering data points of number 4 and 5 since we can see both 4 and 5 are missing from two graphs. In addition, the numbers shown in 1e are slightly more blured than the ones in 1f since 1e has the approximation of the dataset.

g) Create a matrix (let's call it 0) that is the difference between the original dataset and the rank-10 approximation of the dataset. (5 points)

h) The largest (using euclidean distance from the origin) rows of the matrix o could be considered anomalous data points. Briefly explain why. Plot the 10 images responsible for the 10 largest rows of that matrix o . (10 points)

```
In [12]: origins = [0 for i in range(0.shape[1])] #Origion for each cluster is 0
    eucli_dist = [(np.linalg.norm(0[_]- origins)) for _ in range (0.shape[0])]
    # eucli_dist
    eucli_dist_array = np.array(eucli_dist)

# eucli_dist_array
sorted_array = np.argsort(eucli_dist_array)
top_ten = sorted_array[-10: ]
# top_ten
fig, ax = plt.subplots(2,5)
ax = ax.flatten()
for i in range(10):
    ax[i].imshow(0[top_ten[i]].reshape(28, 28))
```



the largest 10 rows of the matrix are really anomalous since the 10 numbers shown above are really wonky. They are the outliers that make our results less accurate.

Exercise 3 (25pts)

For this question we will re-use the "mnist_784" dataset.

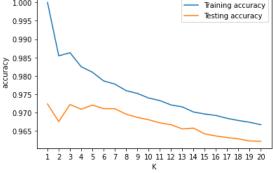
a) Begin by creating a training and testing datasest from our dataset, with a 80-20 ratio, and random_state=1. You can use the train_test_split function from sklearn. By holding out a portion of the dataset we can evaluate how our model generalizes to unseen data (i.e. data it did not learn from). - 2 Points

```
In [33]: from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=1)
# X_train
# X_test
y_train
# y_test
```

- Out[33]: array(['9', '7', '1', ..., '5', '0', '0'], dtype=object)
 - b) For K ranging from 1 to 20:
 - 1. train a KNN on the training data 2 points
 - 2. record the training and testing accuracy 2 points

Plot a graph of the training and testing set accuracy as a function of the number of neighbors K (on the same plot). Which value of K is optimal? Briefly explain. - 4 points

```
In [40]: from sklearn.neighbors import KNeighborsClassifier
         from sklearn.metrics import accuracy_score
         indices_for_x = []
         train acc = []
         test_acc = []
         optimal = 0
         knn optimal = None
         optimal K =1
         for i in range(1, 21):
             indices_for_x.append(i)
             knn = KNeighborsClassifier(n neighbors=i)
             knn.fit(X_train, y_train)
             perdict y train = knn.predict(X train)
             accuracy1 = accuracy_score(y_train, perdict_y_train)
             train_acc.append(accuracy1)
             perdict_y_test = knn.predict(X_test)
             accuracy2 = accuracy_score(y_test, perdict_y_test)
             test_acc.append(accuracy2)
             print("K is", i, ", accuracy for training data is", accuracy1, ", accuracy for testing data is", accuracy2)
             if accuracy2> optimal:
                 optimal = accuracy2
                 optimal K = i
                 knn_optimal = knn
         print("optimal K is", optimal_K)
         plt.xlabel("K")
         plt.ylabel("accuracy")
         plt.xticks(np.arange(1,21,1))
         plt.plot(indices for x, train acc, label = 'Training accuracy')
         plt.plot(indices_for_x, test_acc, label = 'Testing accuracy')
         plt.legend()
         plt.show()
         K is 1 , accuracy for training data is 1.0 , accuracy for testing data is 0.9723571428571428
         K is 2 , accuracy for training data is 0.9854642857142857 , accuracy for testing data is 0.9675714285714285
         K is 3 , accuracy for training data is 0.9863035714285714 , accuracy for testing data is 0.9722142857142857
         K is 4 , accuracy for training data is 0.9825 , accuracy for testing data is 0.9709285714285715
         K is 5 , accuracy for training data is 0.981 , accuracy for testing data is 0.9720714285714286
         K is 6 , accuracy for training data is 0.978625 , accuracy for testing data is 0.9710714285714286
         K is 7 , accuracy for training data is 0.9777678571428572 , accuracy for testing data is 0.9710714285714286
         K is 8 , accuracy for training data is 0.9759821428571429 , accuracy for testing data is 0.9695714285714285
         K is 9 , accuracy for training data is 0.9752321428571429 , accuracy for testing data is 0.9687142857142857
         K is 10 , accuracy for training data is 0.9739821428571429 , accuracy for testing data is 0.9680714285714286
         K is 11 , accuracy for training data is 0.9732857142857143 , accuracy for testing data is 0.9672142857142857
         K is 12 , accuracy for training data is 0.9720892857142858 , accuracy for testing data is 0.9667142857142857
         K is 13 , accuracy for training data is 0.9715714285714285 , accuracy for testing data is 0.9655714285714285
         K is 14 , accuracy for training data is 0.9701785714285714 , accuracy for testing data is 0.9657857142857142
         K is 15 , accuracy for training data is 0.969625 , accuracy for testing data is 0.9642142857142857
         K is 16 , accuracy for training data is 0.9692321428571429 , accuracy for testing data is 0.9636428571428571
         K is 17 , accuracy for training data is 0.9684464285714286 , accuracy for testing data is 0.9632142857142857
         K is 18 , accuracy for training data is 0.9678571428571429 , accuracy for testing data is 0.9628571428571429
         K is 19 , accuracy for training data is 0.967375 , accuracy for testing data is 0.9622857142857143
         K is 20 , accuracy for training data is 0.9667142857142857 , accuracy for testing data is 0.9622142857142857
         optimal K is 1
            1.000
                                             Training accuracy
                                            Testing accuracy
            0.995
            0.990
```



c) Using the best model from b), pick an image at random and plot it next to its K nearest neighbors (5pts)

```
In [41]: import random
    random_image = random.randrange(len(X_test))

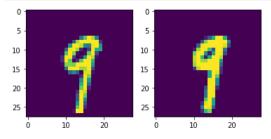
neighbor = knn_optimal.kneighbors([X_test[random_image]],return_distance=False)

plt.subplot(1,2,1)
    plt.imshow([X_test[random_image]][0].reshape(28, 28))

i = 2
    for n in neighbor[0]:
        plt.subplot(1,2,i)
        plt.imshow(X_train[n].reshape(28, 28))

        i += 1

plt.show()
```



```
In [ ]: # random_image_index = random.randint(0,10)
# random_image_index
```

Out[68]: 0

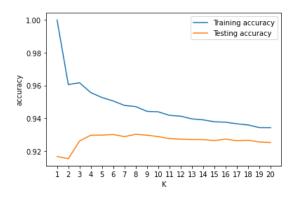
d) Using a dimensionality reduction technique discussed in class, reduce the dimensionality of the dataset before applying a KNN model. Repeat b) and discuss similarities and differences to the previous model. Briefly discuss your choice of dimension and why you think the performance / accuracy of the model has changed. (10 points)

```
In [37]: from sklearn.pipeline import make_pipeline
         from sklearn.decomposition import PCA
         #origional b
         from sklearn.neighbors import KNeighborsClassifier
         from sklearn.metrics import accuracy score
         indices_for_x = []
         train_acc = []
         test_acc = []
         optimal = 0
         knn optimal = None
         for i in range(1, 21):
             indices_for_x.append(i)
             dimensionality reduction = PCA(n components = 10) #add pca as dimension reduction technique here
             knn = KNeighborsClassifier(n_neighbors=i)
             model = make_pipeline(dimensionality_reduction, knn)
             model.fit(X_train, y_train)
             perdict y train = model.predict(X train)
             accuracy1 = accuracy_score(y_train, perdict_y_train)
             train acc.append(accuracy1)
             perdict_y_test = model.predict(X_test)
             accuracy2 = accuracy score(y test, perdict y test)
             test_acc.append(accuracy2)
             print("K is", i, ", accuracy for training data is", accuracy1, ", accuracy for testing data is", accuracy2)
             if accuracy2> optimal:
                 optimal = accuracy2
                 optimal K = i
                 knn optimal = model
         print("optimal K is", optimal_K)
         plt.xlabel("K")
         plt.ylabel("accuracy")
         plt.xticks(np.arange(1,21,1))
         plt.plot(indices for x, train acc, label = 'Training accuracy')
         plt.plot(indices_for_x, test_acc, label = 'Testing accuracy')
         plt.legend()
         plt.show()
         K is 1 , accuracy for training data is 1.0 , accuracy for testing data is 0.9166428571428571
         K is 2 , accuracy for training data is 0.9605535714285715 , accuracy for testing data is 0.9152857142857143
         K is 3 , accuracy for training data is 0.9616428571428571 , accuracy for testing data is 0.9260714285714285
         K is 4 , accuracy for training data is 0.9556428571428571 , accuracy for testing data is 0.9296428571428571
         K is 5 , accuracy for training data is 0.9526428571428571 , accuracy for testing data is 0.9297142857142857
         K is 6 , accuracy for training data is 0.9505 , accuracy for testing data is 0.9300714285714285
         K is 7 , accuracy for training data is 0.9478214285714286 , accuracy for testing data is 0.9287857142857143
         K is 8 , accuracy for training data is 0.9470892857142857 , accuracy for testing data is 0.9302142857142857
         K is 9 , accuracy for training data is 0.9441964285714286 , accuracy for testing data is 0.9296428571428571
         K is 10 , accuracy for training data is 0.9439107142857143 , accuracy for testing data is 0.9287857142857143
         K is 11 , accuracy for training data is 0.9417678571428572 , accuracy for testing data is 0.9275714285714286
         K is 12 , accuracy for training data is 0.94125 , accuracy for testing data is 0.9272142857142858
         K is 13 , accuracy for training data is 0.9396071428571429 , accuracy for testing data is 0.927
         K is 14 , accuracy for training data is 0.939 , accuracy for testing data is 0.927
         K is 15 , accuracy for training data is 0.9378392857142858 , accuracy for testing data is 0.9263571428571429
         K is 16 , accuracy for training data is 0.9375892857142857 , accuracy for testing data is 0.9272857142857143
```

K is 17, accuracy for training data is 0.9366071428571429, accuracy for testing data is 0.9262857142857143 K is 18, accuracy for training data is 0.9359107142857143, accuracy for testing data is 0.9265714285714286

K is 19, accuracy for training data is 0.9342857142857143, accuracy for testing data is 0.9255 K is 20, accuracy for training data is 0.93425, accuracy for testing data is 0.9252142857142858

optimal K is 8



From the two graphs, we can say the two methods give really similar trend. KNN method tells us when K=1, the accuracy is the highest. PCA method tells us when K=8, the accuracy is the highest. Two graphs show the accuracies drop significantly at K=2 and goes back up at 3. For the second method, we have the highest accuracies slightly lower than the ones in 3b. For dimensionality reduction, I chose to use PCA as the method. It is rather a fast process and isn't computationally that expensive than running KNN on the whole dataset since i've reduced the dimension to 10

Bonus (20 points)

Complete the code below to support N-dimensional GMM clustering. Only use the methods imported below. Please take a look at the comments and docstrings for more info.

```
In [9]: from numpy import array, argmax
        import matplotlib.pyplot as plt
        from sklearn.cluster import KMeans
        from scipy.stats import multivariate_normal
        from numpy.random import multivariate normal, uniform
        class Component:
            def __init__(self, mixture_prop, mean, variance):
                self.mixture_prop = mixture_prop
                self.mean = mean
                self.variance = variance
        nd_gmm = [
            Component(.25, [-1, 1], [[1, 0], [0, 1]]),
            Component(.50, [0, 0], [[1, 0], [0, 1]]),
            Component(.25, [1, 1], [[1, 0], [0, 1]])
        def get_random_component(gmm_params):
                returns component with prob
                proportional to mixture prop
            u = uniform()
            prob sum = 0
            for comp in gmm_params:
                prob_sum += comp.mixture_prop
                if u <= prob_sum:</pre>
                   return comp
            return gmm_params[-1]
        def generate_nd_gmm_dataset(gmm_params, size):
            if not is valid nd gmm(gmm params):
                raise ValueError("GMM parameters are invalid")
            dataset = []
            for _ in range(size):
                comp = get_random_component(gmm_params)
                mean_j = comp.mean
                var_j = comp.variance
                dataset += [normal(mean_j, var_j)]
            return array(dataset) # this should be a numpy array instead of a list
        def is_valid_nd_gmm(gmm_params):
                Check that all the dimensions are consistent
                accross all components
            dimension = len(gmm_params[0].mean)
            mean_j = comp.mean
            var_j = comp.variance
            for comp in qmm params:
                if len(mean_j) != dimension or var_j.shape != (dimension, dimension):
            return is_valid_gmm(gmm_params) # checks if mixture components add to 1
        def is_valid_gmm(gmm_params):
                Checks that the sum of the mixture
                proportions is 1
            if abs(sum([comp.mixture prop for comp in gmm params]) -1) != 0:
                print("is_valid_gmm returns false")
            return True
        def gmm_nd_init(k, dataset):
            kmeans = KMeans(k, init='k-means++').fit(X=array(dataset).reshape(-1, 1))
            gmm_params = []
            for _ in range(k):
                mean_j = kmeans.cluster_centers_[_][0]
                var_j = kmeans.inertia_/(k* len(dataset))
                mixture_prop = 1/k
                gmm_params.append(Component(mixture_prop, mean_j, var_j))
            return gmm_params
        def compute_nd_gmm(k, dataset, probs):
                Compute P(C_j), mean_j, var_j
```

```
Here mean_j is a vector and var_j is a matrix
   gmm_params = []
   n_dim = dataset.shape[1]
   for i in range(k):
       weight = sum(probs[:, i]) / len(dataset)
       mean = np.zeros(n dim)
       for j in range(len(dataset)):
           mean += probs[j, i] * dataset[j]
       mean /= sum(probs[:, i])
        covariance = np.zeros((n_dim, n_dim))
        for j in range(len(dataset)):
            diff = dataset[j] - mean
            covariance += probs[j, i] * (diff.reshape(-1, 1) @ diff.reshape(1, -1))
        covariance /= sum(probs[:, i])
       gmm_params.append(Component(weight, mean, covariance))
def compute_nd_probs(k, dataset, gmm_params):
       For all x_i in dataset, compute P(C_j | X_i)
        = P(X_i \mid C_j)P(C_j) / P(X_i) for all C_j
       return the list of lists of all P(C_j | X_i)
       for all x_i in dataset.
       Here x i are vectors
   probs = []
   for x in dataset:
        px = 0
        for comp in gmm params:
           px += comp.mixture_prop * multivariate_normal.pdf(x, comp.mean, comp.variance)
        row = [comp.mixture_prop * multivariate_normal.pdf(x, comp.mean, comp.variance) / px for comp in gmm_params]
   return probs
def expectation_maximization_nd(k, dataset, iterations):
      Repeat for a set number of iterations.
   gmm params = gmm nd init(k, dataset)
    for _ in range(iterations):
        # expectation step
       probs = compute_nd_probs(k, dataset, gmm_params)
        # maximization step
        gmm_params = compute_nd_gmm(k, dataset, probs)
   return probs, gmm params
data = generate_nd_gmm_dataset(nd_gmm, 100)
probs, gmm_p = expectation_maximization_nd(2, data, 3)
labels = [argmax(array(p)) for p in probs] # create a hard assignment
size = 50 * array(probs).max(1) ** 2
plt.scatter(data[:, 0], data[:, 1], c=labels, cmap='viridis', s=size)
plt.show()
```

UnboundLocalError Traceback (most recent call last)

/Users/tassychen/Desktop/2023Spring/cs506/hw/homework-3-tassychen/homework3.ipynb Cell 39 in <module>

- <a href='vscode-notebook-cell:/Users/tassychen/Desktop/2023Spring/cs506/hw/homework-3-tassychen/homework3.ipynb#X53sZml
 sZQ%3D%3D?line=136'>137 gmm params = compute nd gmm(k, dataset, probs)
- <a href='vscode-notebook-cell:/Users/tassychen/Desktop/2023Spring/cs506/hw/homework-3-tassychen/homework3.ipynb#X53sZml
 sZQ%3D%3D?line=138'>139 return probs, gmm_params
- --> 142 data = generate_nd_gmm_dataset(nd_gmm, 100)
- <a href='vscode-notebook-cell:/Users/tassychen/Desktop/2023Spring/cs506/hw/homework-3-tassychen/homework3.ipynb#X53sZml
 sZQ%3D%3D?line=142'>143 probs, gmm_p = expectation_maximization_nd(2, data, 3)
- <a href='vscode-notebook-cell:/Users/tassychen/Desktop/2023Spring/cs506/hw/homework-3-tassychen/homework3.ipynb#X53sZml
 sZQ%3D%3D?line=143'>144 labels = [argmax(array(p)) for p in probs] # create a hard assignment
- /Users/tassychen/Desktop/2023Spring/cs506/hw/homework-3-tassychen/homework3.ipynb Cell 39 in generate_nd_gmm_dataset(gmm_pa rams, size)
- 31 def generate_nd_gmm_dataset(gmm params, size):
- ---> 32 if not is_valid_nd_gmm(gmm_params):
- <a href='vscode-notebook-cell:/Users/tassychen/Desktop/2023Spring/cs506/hw/homework-3-tassychen/homework3.ipynb#X53sZm
 lsZQ%3D%3D?line=32'>33 raise ValueError("GMM parameters are invalid")
- <a href='vscode-notebook-cell:/Users/tassychen/Desktop/2023Spring/cs506/hw/homework-3-tassychen/homework3.ipynb#X53sZm
 lsZQ%3D%3D?line=34'>35 dataset = []
- /Users/tassychen/Desktop/2023Spring/cs506/hw/homework-3-tassychen/homework3.ipynb Cell 39 in is_valid_nd_gmm(gmm_params)
- 46 '''
- <a href='vscode-notebook-cell:/Users/tassychen/Desktop/2023Spring/cs506/hw/homework-3-tassychen/homework3.ipynb#X53sZm
 lsZQ%3D%3D?line=46'>47 Check that all the dimensions are consistent
- 48 accross all components
- 49 '''
- <a href='vscode-notebook-cell:/Users/tassychen/Desktop/2023Spring/cs506/hw/homework-3-tassychen/homework3.ipynb#X53sZm
 lsZQ%3D%3D?line=49'>50 dimension = len(gmm_params[0].mean)
- ---> 51 mean_j = comp.mean
- $\label{localizero} $$\an f='vscode-notebook-cell:/Users/tassychen/Desktop/2023Spring/cs506/hw/homework-3-tassychen/homework3.ipynb$$X53sZmlsZQ%3D%3D?line=51'>52 var_j = comp.variance$
- 53 for comp in gmm params:

UnboundLocalError: local variable 'comp' referenced before assignment