AML Homework 3

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Programming Exercise

Question 1: Eigenface for face recognition

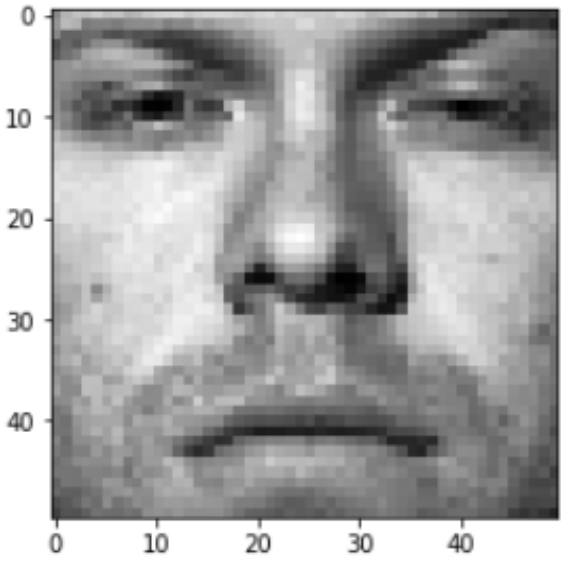
(a) Download the Face Dataset

(b) Load data in matrix

Load the training set into a matrix X

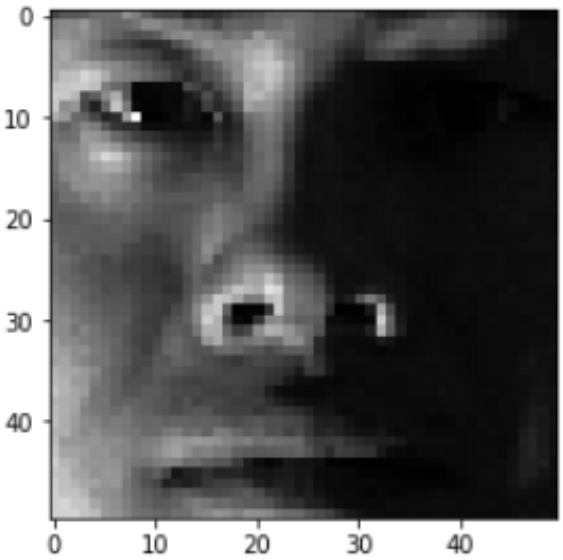
```
#Load traning set and display an image
train_labels, train_data = [], []
for line in open('./faces/train.txt'):
    im = misc.imread(line.strip().split()[0])
    train_data.append(im.reshape(2500,))
    train_labels.append(line.strip().split()[1])
train_data, train_labels = np.array(train_data, dtype=float), np.array(train_labels,
dtype=int)

print (train_data.shape, train_labels.shape)

plt.imshow(train_data[10, :].reshape(50,50), cmap = cm.Greys_r)

plt.show()
```

Pick a face image from X and display that image in grayscale



Do the same thing for the test set

```
#Load test set and display an image
test_labels, test_data = [], []
for line in open('./faces/test.txt'):
    im = misc.imread(line.strip().split()[0])
    test_data.append(im.reshape(2500,))
    test_labels.append(line.strip().split()[1])
test_data, test_labels = np.array(test_data, dtype=float), np.array(test_labels,
dtype=int)

print (test_data.shape, test_labels.shape)

plt.imshow(test_data[10, :].reshape(50,50), cmap = cm.Greys_r)

plt.show()
```

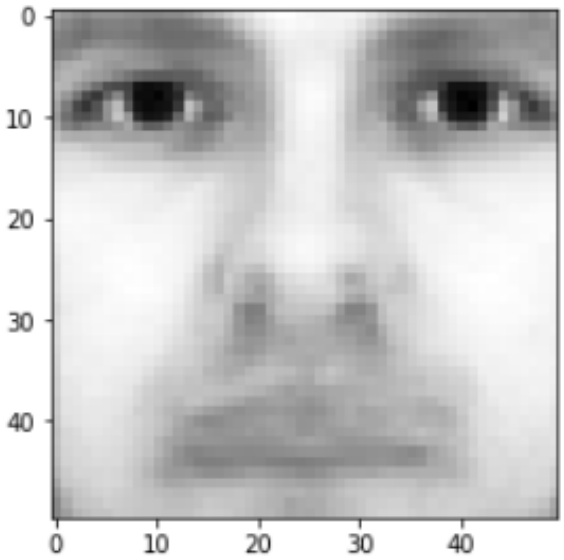


(c) Average Face

Compute the average face

```
avg_Face = []
for i in range(2500):
    tmp = 0
    for row in train_data:
        tmp+=row[i]
    avg_Face.append(tmp/540)

avg_Face = np.array(avg_Face)

plt.imshow(avg_Face.reshape(50,50), cmap = cm.Greys_r)
plt.show()
```

Display the average face

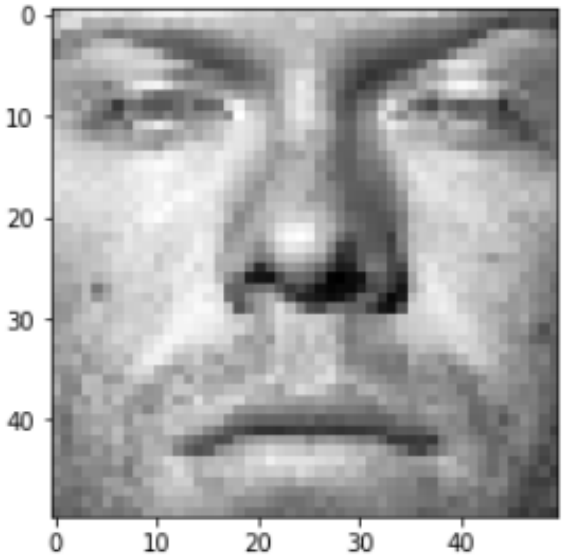


(d) Mean Substraction

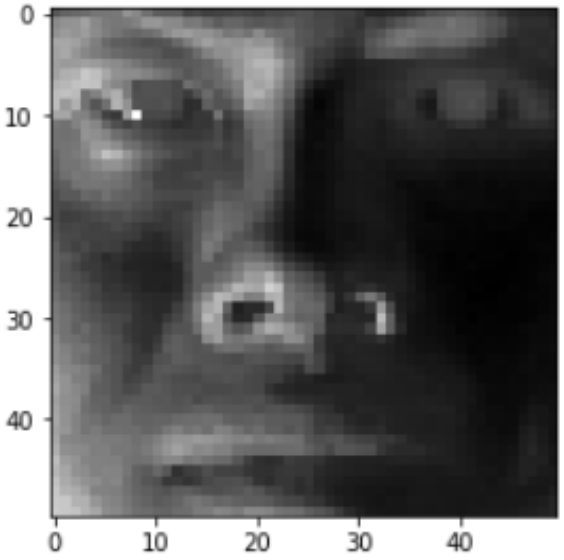
Subtract average face μ from every row in X

```
#Mean subtraction on training data
for row in train_data:
    row -= avg_Face
#mean subtraction on testing data
for row in test_data:
    row -= avg_Face

#Displaying mean-subtracted training image
plt.imshow(train_data[10, :].reshape(50,50), cmap = cm.Greys_r)
plt.show()
#Displaying mean-subtracted testing image
plt.imshow(test_data[10, :].reshape(50,50), cmap = cm.Greys_r)
plt.show()
```

Pick a face image after mean subtraction from the new X and display that image in grayscale



Do the same thing for the test set Xtest using the pre- computed average face μ in (c)

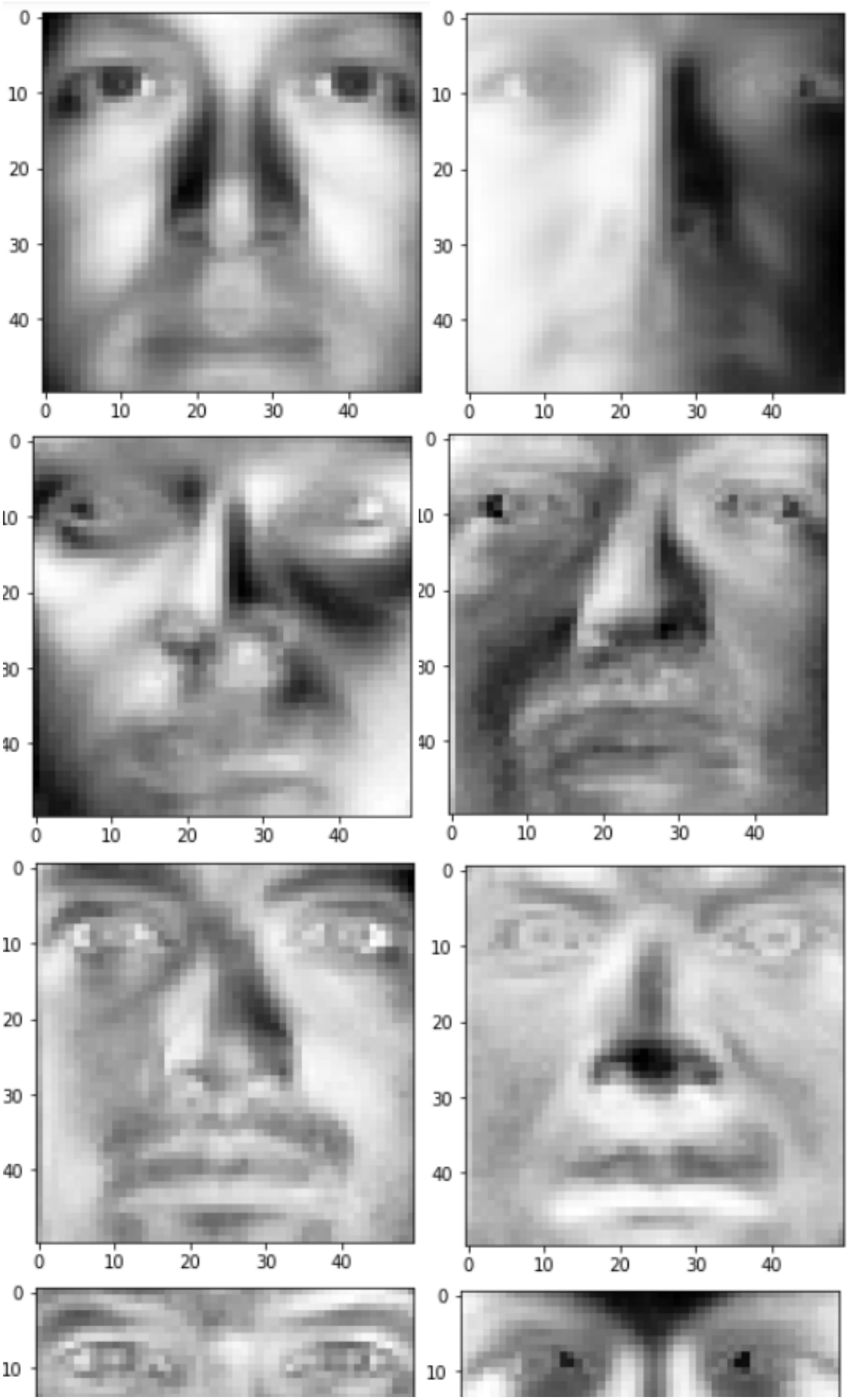


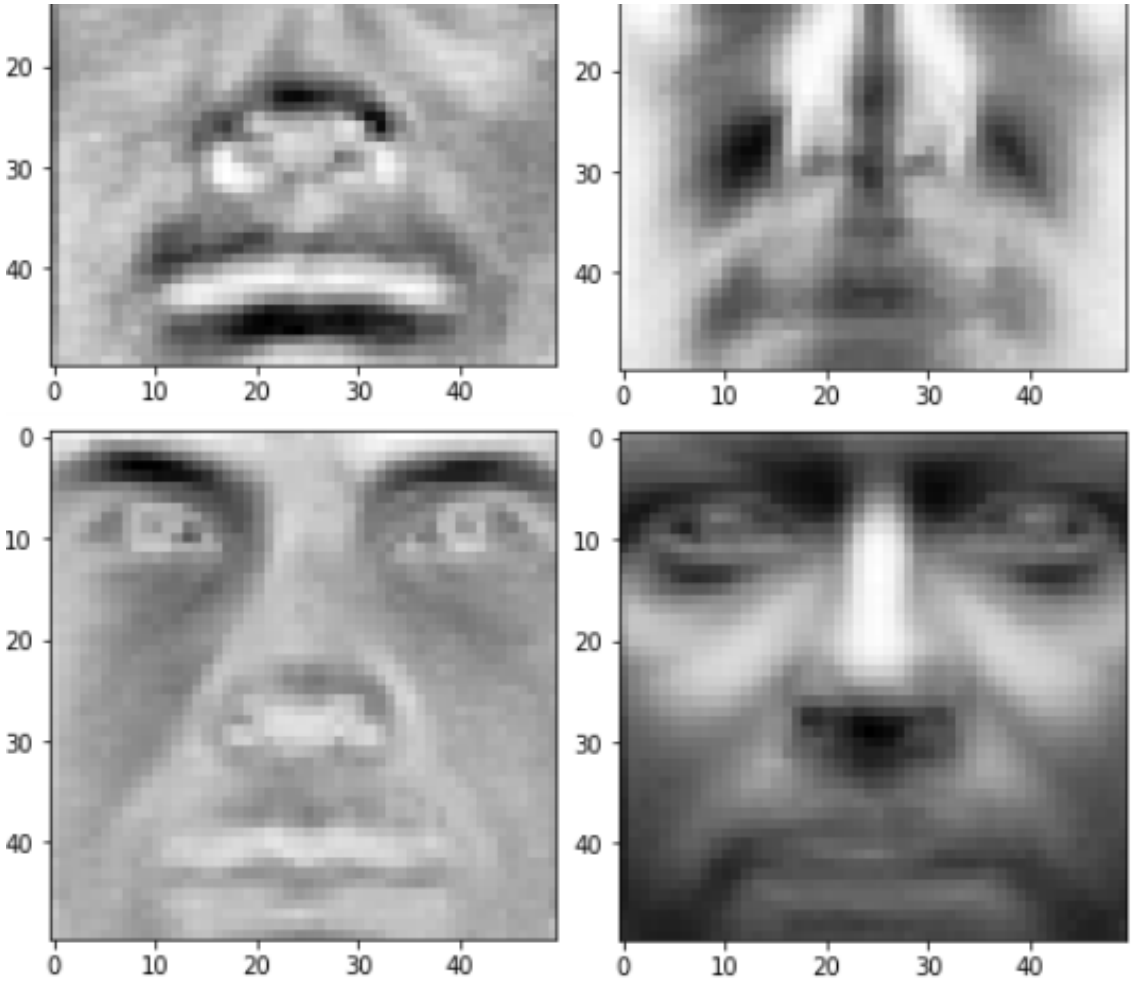
(e) Eigenface

Get eigenvectors VT

```
#eigen = np.dot(np.transpose(train_data),train_data)
def eigen_decomposition(X):
    Sigma = X.T.dot(X) / X.shape[0] # form covariance matrix
    eigen_val, eigen_vec = np.linalg.eig(Sigma) # perform eigendecomposition
    eigen_val = eigen_val.real
    eigen_vec = eigen_vec.real
    return eigen_val, eigen_vec

eigen_val, eigen_vec = eigen_decomposition(train_data)

for i in range(10):
    plt.imshow(np.array([float(x) for x in eigen_vec.T[i]]).reshape(50,50), cmap =
cm.Greys_r)
    plt.show()
```

Display the first 10 eigenfaces as 10 images in grayscale


0
10
20
30
40



(f) Eigenface Feature

Write a function to generate r-dimensional feature matrix F and Ftest for training images X and test images Xtest

```
def feature_matrix_F (x,eigen_vec,r):
    vt = eigen_vec.T
    f = np.dot(x,vt[:r,:].T)

    return f

f = feature_matrix_F(train_data, eigen_vec, 10) #r = 10
f_test = feature_matrix_F(test_data, eigen_vec, 10) #r = 10
```

(g) Face Recognition

Train a Logistic Regression model using F and test on Ftest

Train a Logistic Regression model using F and test on Ftest

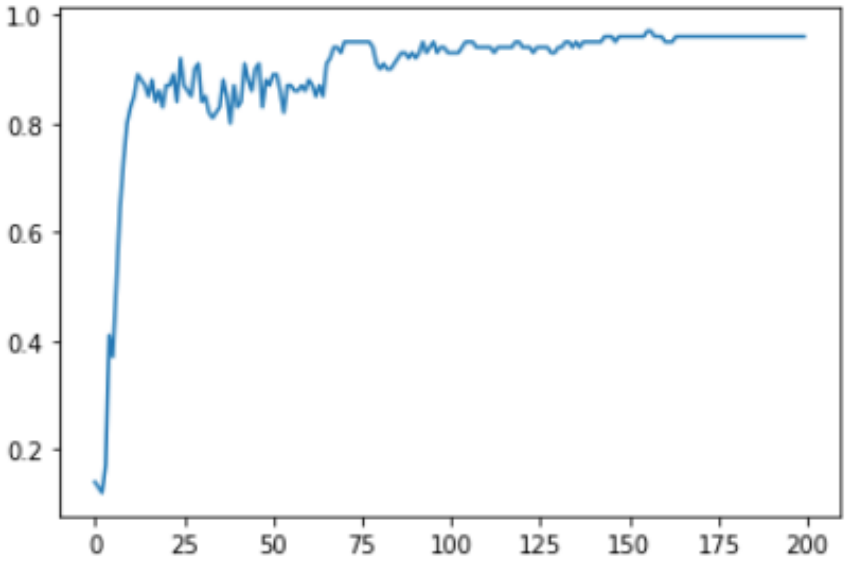
```
logistic = LogisticRegression(multi_class='ovr')
model_ovr = logistic.fit(f,train_labels)
predict = model_ovr.predict(f_test)
print('Accuracy when r=10: ' + str(accuracy_score(predict, test_labels)))

acc_list = []
for i in range(1,201):
    f = feature_matrix_F(train_data, eigen_vec, i)
    f_test = feature_matrix_F(test_data, eigen_vec, i)
    logistic = LogisticRegression(multi_class='ovr')
    model_ovr = logistic.fit(f,train_labels)
    predict = model_ovr.predict(f_test)
    acc_list.append(accuracy_score(predict, test_labels))
```

Report the classification accuracy on the test set

```
Accuracy when r=10: 0.8
```

Plot the classification accuracy on the test set as a function of r when r = 1, 2, . . . , 200

```
plt.plot(acc_list)
```

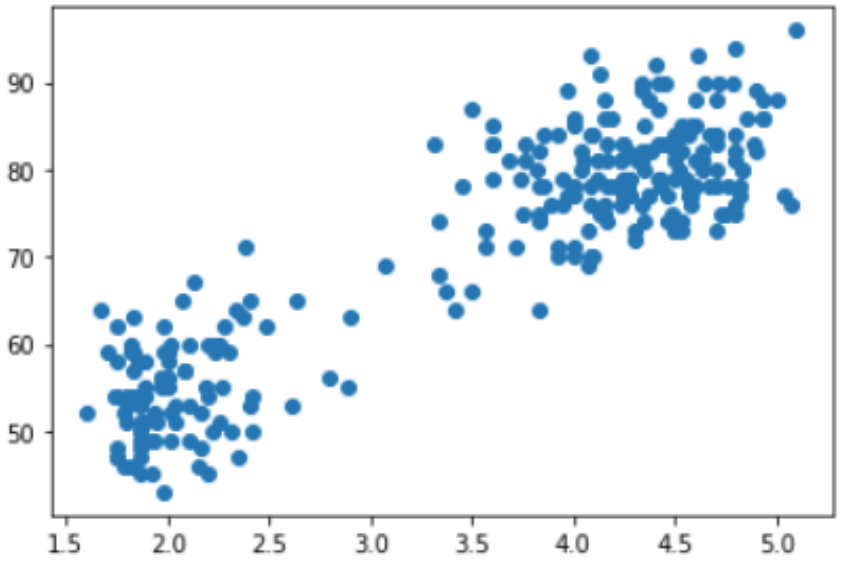


Question 2: Implement EM Algorithm

(a) Treat each data entry as a 2 dimensional feature vector. Parse and plot all data points on 2-D plane

Parse and plot all data points on 2-D plane

```
data = pd.read_csv('data.tsv', sep='\t')
plt.scatter(data.iloc[:,:-1],data.iloc[:,-1:])
```



(b) Write the expression for Pθt (z = k | x)

$$P_\theta(z = k \mid x) = \frac{P_\theta(z = k, x)}{P_\theta(x)} = \frac{P_\theta(x|z = k)P_\theta(z = k)}{\sum_{l=1}^{K} P_\theta(x|z = l)P_\theta(z = l)}$$

(c) Write down the formula for μk , Σk , and for the parameters ϕ at the M-step

$$\mu_k = \frac{\sum_{i=1}^{n} P(z = k|x^{(i)})x^{(i)}}{n_k}$$

$$\Sigma_k = \frac{\sum_{i=1}^{n} P(z = k|x^{(i)})(x^{(i)} - \mu_k)(x^{(i)} - \mu_k)^\top}{n_k}$$

$$n_k = \sum_{i=1}^{n} P(z = k|x^{(i)})$$

$$\phi_k = \frac{n_k}{n}$$

(d)

(a)

i. EM Implementation

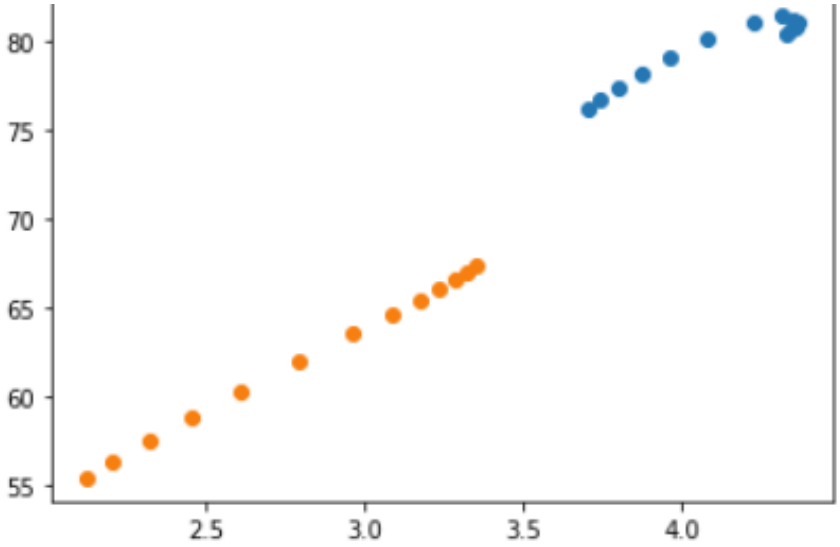
```
class GMM:
    def __init__(self, k, max_iter=9999):
        self.k = k
        self.max_iter = int(max_iter)
        self.mu_list = []

    def initialize(self, X):
        self.shape = X.shape
        self.n, self.m = self.shape

        self.phi = np.full(shape=self.k, fill_value=1/self.k)
        self.posterior = np.full(shape=self.shape, fill_value=1/self.k)

        random_row = np.random.randint(low=0, high=self.n, size=self.k)
        self.mu = [X[row_index,:] for row_index in random_row]
        self.sigma = [np.cov(X.T) for i in range(self.k)]

    def predict_proba(self, X):
        self.likelihood = np.zeros((self.n, self.k))
        for i in range(self.k):
            distribution = multivariate_normal(mean=self.mu[i],cov=self.sigma[i])
            self.likelihood[:,i] = distribution.pdf(X)

        numerator = self.likelihood * self.phi
        denominator = numerator.sum(axis=1)[:, np.newaxis]
        posterior = numerator / denominator
        return posterior

    def e_step(self, X):
        # E-Step
        self.posterior = self.predict_proba(X)
        #Calculating phi
        self.phi = self.posterior.mean(axis=0)

    def m_step(self, X):
        # M-Step
        for i in range(self.k):
            weight = self.posterior[:, [i]]
            total_weight = weight.sum()
            self.mu[i] = (X * weight).sum(axis=0)/total_weight
            #convaraince of the dataset when each element  x(i)  has a weight  P(z=k|x(i))


            self.sigma[i] = np.cov(X.T,aweights=(weight/total_weight).flatten(),
```

```
            self.sigma[i] = np.cov(X.T,aweights=(weight/total_weight).flatten(),
bias=True)
            self.mu_list.append([])
            self.mu_list[i].append(self.mu[i])

    def fit(self, X):
        self.initialize(X)
        self.e_step(X)
        self.m_step(X)
        last_likelihood = self.likelihood
        for iteration in range(1,self.max_iter):
            last_likelihood = self.likelihood
            self.e_step(X)
            self.m_step(X)
            if abs(sum(sum(self.likelihood))-sum(sum(last_likelihood)))<=1E-3:#Stopping
Criterion
                break

        for mu in self.mu_list:
            tmpx = []
            tmpy = []
            for point in mu:
                tmpx.append(point[0])
                tmpy.append(point[1])
            plt.scatter(tmpx,tmpy)

    def predict(self, X):
        posterior = self.predict_proba(X)
        return np.argmax(posterior, axis=1)
```

ii. State your termination criterion and explain the reasoning behind it

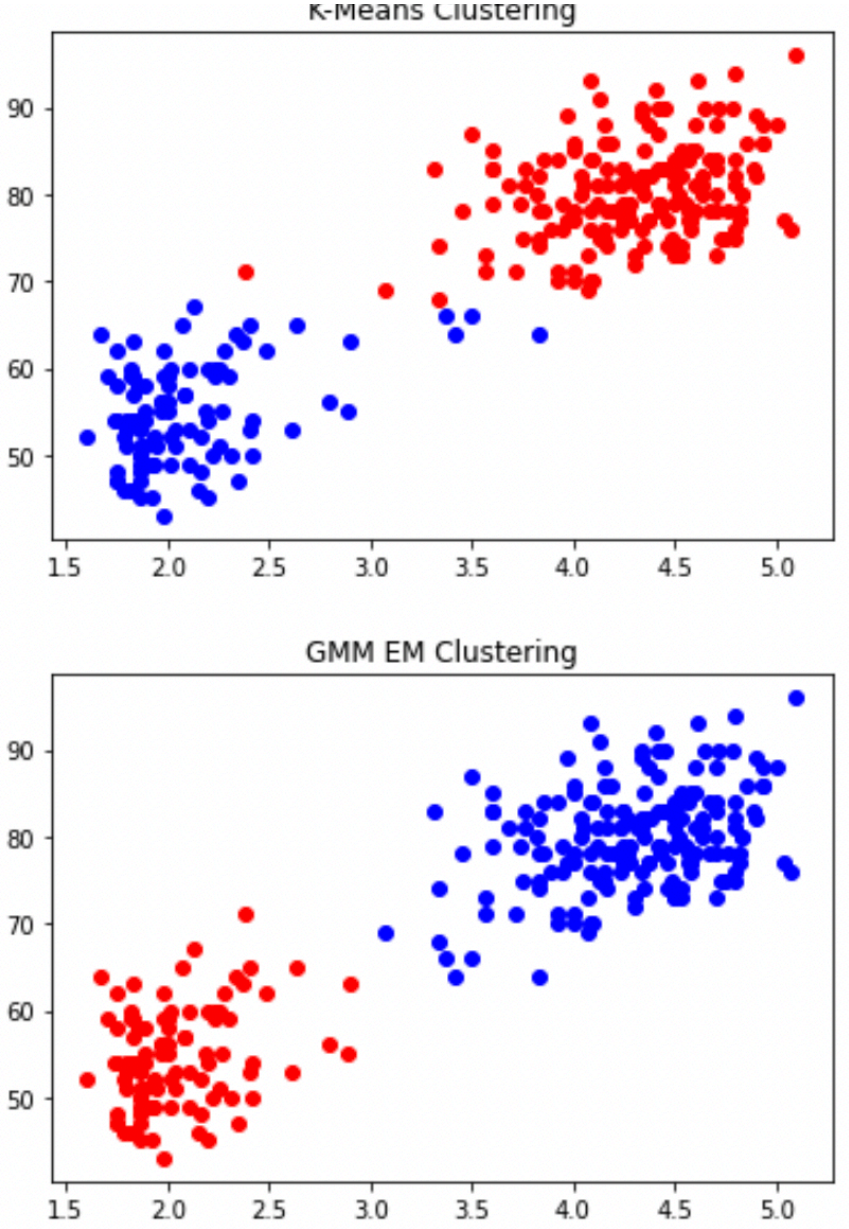
I used the sum of posterior probabilities as termination criterion, if the sum of the probabilities compared to previous clustering is less than 1E-3, then the model probably isn't learning anything new so it will stop iterating in order to preventing converging to local optimum points

iii. Plot the trajectories of the two mean vectors in 2 dimensiosn to show how they change over the course of runnign EM



(e) If you run K-means clustering instead of the EM algorithm you just implemented, do you think you will get different clusters?

```
#Kmeans clusters
kmeans = KMeans(n_clusters=2, random_state=0)
label = kmeans.fit_predict(data)

label0 = data[label == 0]
label1 = data[label == 1]
plt.scatter(label0[:,0] , label0[:,1] , color = 'red')
plt.scatter(label1[:,0] , label1[:,1] , color = 'blue')
plt.title("K-Means Clustering")
plt.show()

#GMM clusters
prediction = model_GMM.predict(data)
data_copy = pd.read_csv('data.tsv', sep='\t')
data_copy.insert(2,'label',prediction,True)

label0 = data_copy.loc[data_copy['label'] == 0]
label1 = data_copy.loc[data_copy['label'] == 1]
plt.scatter(label0.iloc[:,0] , label0.iloc[:,1] , color = 'red')
plt.scatter(label1.iloc[:,0] , label1.iloc[:,1] , color = 'blue')
plt.title("GMM EM Clustering")
plt.show()
```



From the two chart we observe some difference between to two clustering method. Clearly, the EM does a better job at
dividing the two clusters.

Comment on why do you think the results will or will not change

Generally, the clusters will be similar, as the above graph suggests. However, GMM is trying to fit, in this case, two spherical clusters on a 2D plane that is normally distributed while K-Means is trying to fit a line that divides the two clusters (One can easily tell that the K-Means result is divided by a staright line), therefore, there are some differences in how the models handle points on the "boundaries".

Written Exercise

Question 1: SVD and eigendecomposition

$$
\begin{aligned}
X^TX &= (UDV^T)^TUDV^T \\
&= VD^TU^TUDV^T \\
&= VD^TDV^T \\
&= VD^TDV^{-1} \\
&= V\Lambda V^{-1} \text{ ,where } D^TD = \Lambda
\end{aligned}
$$