1 Homework 3

1.1 Applied Machine Learning - CS 5785

1.2 Due: October 25, 2022

1.3 Submitted: October 27, 2022 (+2 late days)

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1.4 Part 1. Eigenface for face recognition. (40 pts)

In this assignment you will implement the Eigenface method for recognizing human faces. You will use face images from The Yale Face Database B, where there are 64 images under different lighting conditions per each of 10 distinct subjects, 640 face images in total.

Read more (optional): - Eigenface onWikipedia: https://en.wikipedia.org/wiki/Eigenface - Eigenface on Scholarpedia: http://www.scholarpedia.org/article/Eigenfaces

(a) (2 pts) Download The Face Dataset and unzip faces.zip, You will find a folder called images which contains all the training and test images; train.txt and test.txt specifies the training set and test (validation) set split respectively, each line gives an image path and the corresponding label.

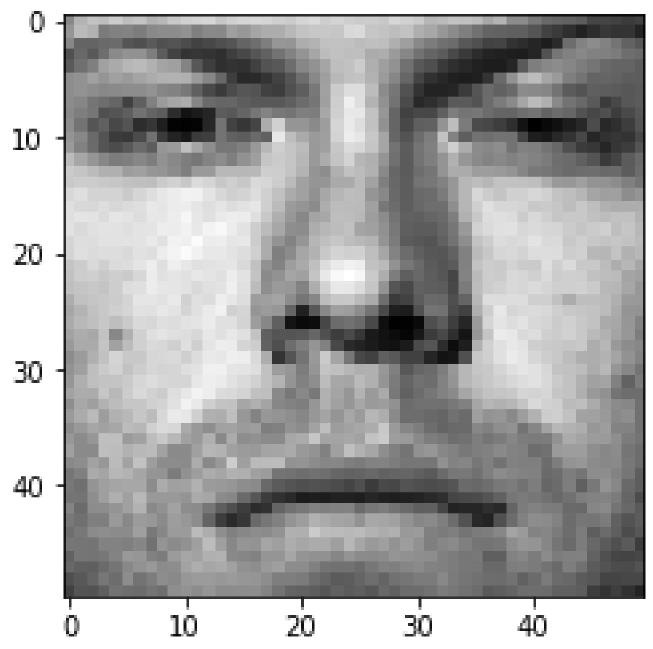
COMPLETE

(b) (2 pts) Load the training set into a matrix X: there are 540 training images in total, each has 50 $\times$ 50 pixels that need to be concatenated into a 2500-dimensional vector. So the size of X should be 540 $\times$ 2500, where each row is a flattened face image. Pick a face image from X and display that image in grayscale. Do the same thing for the test set. The size of matrix Xtest for the test set should be 100\$$\times$\$2500.

```
[1]: # importing dependecies
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from matplotlib.pyplot import figure
import imageio
import matplotlib.cm as cm
%matplotlib inline
```

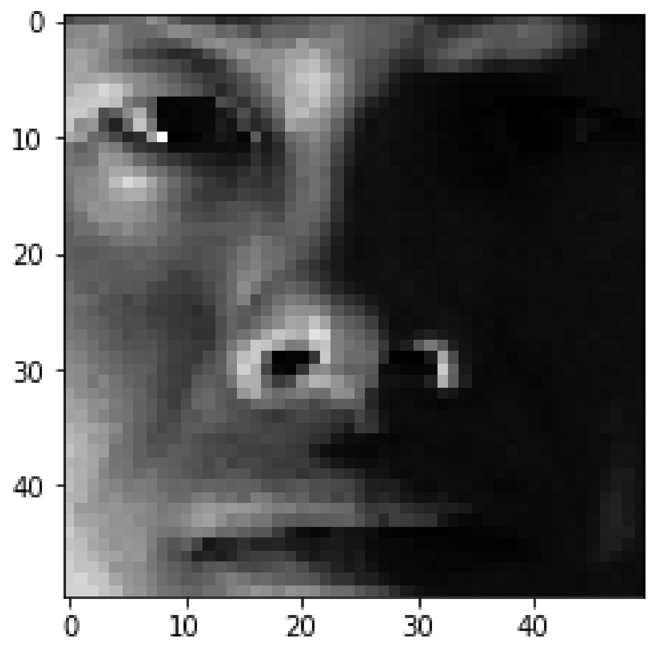
```
[2]: # importing train data
train_labels, train_data = [], []
missing_images = 0


for line in open('faces/train.txt'):
    try:
        im = imageio.imread(line.strip().split()[0])
        train_data.append(im.reshape(2500,))
        train_labels.append(line.strip().split()[1])
    except:
        missing_images += 1
train_data, train_labels = np.array(train_data, dtype=float), np.
 ↪array(train_labels, dtype=int)

print("No. Train Images not Available: " + str(missing_images))
print(train_data.shape, train_labels.shape)
plt.imshow(train_data[10, :].reshape(50,50), cmap = cm.Greys_r)
plt.show()
```

```
No. Train Images not Available: 0
(540, 2500) (540,)
```



[3]:
```python
# importing test data
test_data, test_labels = [], []
missing_images = 0


for line in open('faces/test.txt'):
    try:
        im = imageio.imread(line.strip().split()[0])
        test_data.append(im.reshape(2500,))
        test_labels.append(line.strip().split()[1])
    except:
        missing_images += 1
test_data, test_labels = np.array(test_data, dtype=float), np.array(test_labels,␣
 ↪dtype=int)

print("No. Test Images not Available: " + str(missing_images))
print(test_data.shape, test_labels.shape)
plt.imshow(test_data[10, :].reshape(50,50), cmap = cm.Greys_r)
plt.show()
```

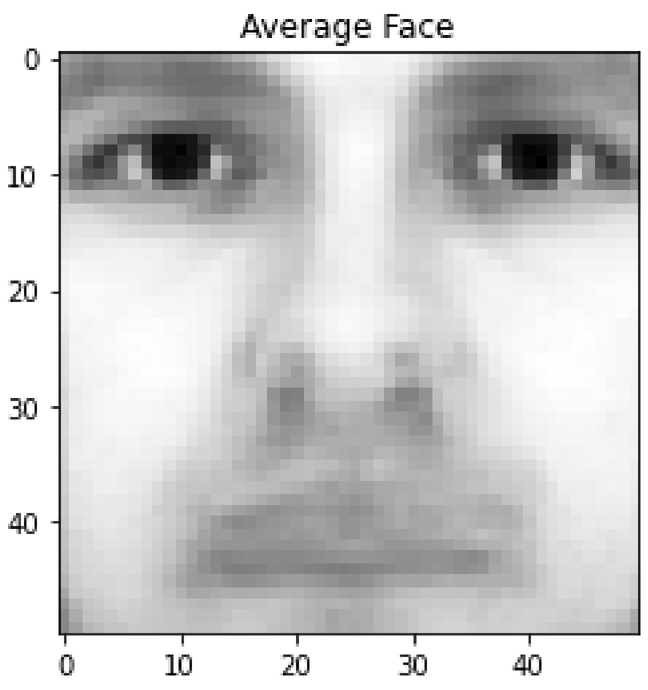
```
No. Test Images not Available: 0
(100, 2500) (100,)
```



(c) (3 pts) Average Face. Compute the average face μ from the whole training set by summing up every row in X then dividing by the number of faces. Display the average face as a grayscale image.

```
[4]: # Average Face sum
     average_face = (train_data.sum(axis = 0) / train_data.shape[0])
     plt.imshow(average_face.reshape(50,50),
                cmap = cm.Greys_r)
     plt.title("Average Face")
```

```
[4]: Text(0.5, 1.0, 'Average Face')
```

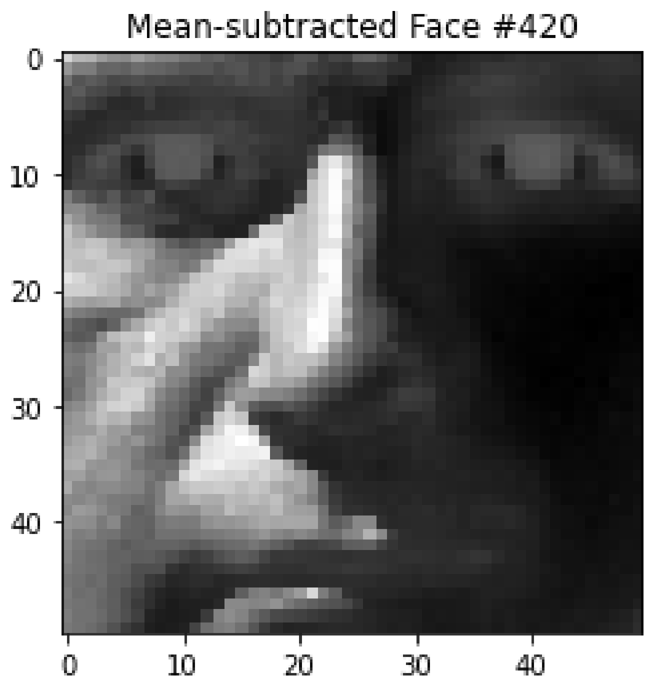


(d) (3 pts) Mean Subtraction. Subtract average face from every row in X. That is, $x_i := x_i \mu$, where x_i is the i-th row of X. Pick a face image after mean subtraction from the new X and display that image in grayscale. Do the same thing for the test set Xtest using the pre-computed average face μ in **(c)**.

```
[5]: import copy
     mean_subtracted = copy.copy(train_data)

     for x in range(0, train_data.shape[0]):
         mean_subtracted[x,:] = mean_subtracted[x, :] - average_face
```

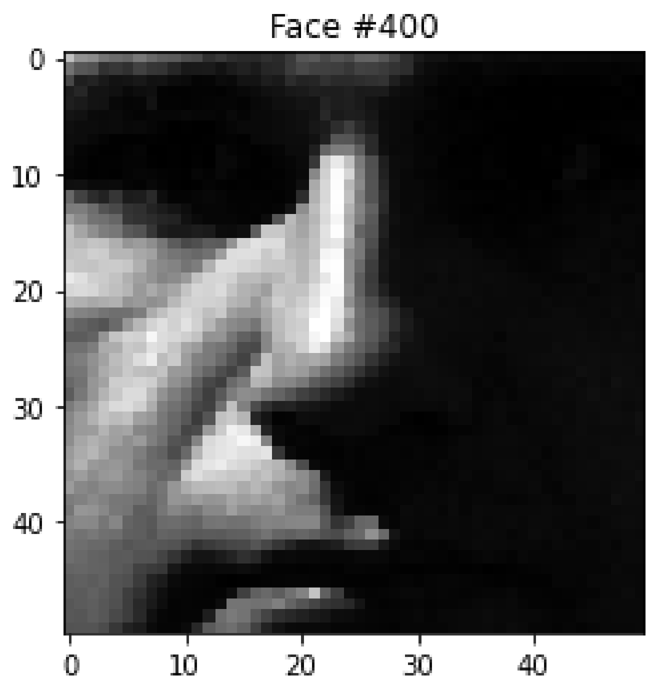
```
[6]: plt.imshow(mean_subtracted[420, :].reshape(50,50), cmap = cm.Greys_r)
     plt.title("Mean-subtracted Face #420")
```

```
[6]: Text(0.5, 1.0, 'Mean-subtracted Face #420')
```



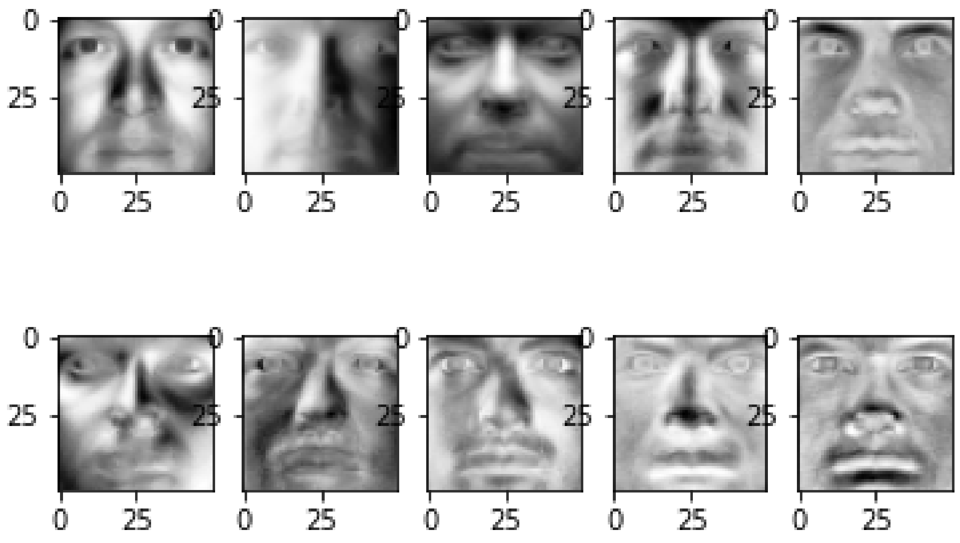
```
[7]: # reference to mean-subtracted image #420
     plt.imshow(train_data[420, :].reshape(50,50), cmap = cm.Greys_r)
     plt.title("Face #400")
```

```
[7]: Text(0.5, 1.0, 'Face #400')
```



(e) (10 pts) Eigenface. Perform eigendecomposition on $X^T X = V \lambda V^T$ to get eigenvectors V^T , where each row of VT has the same dimension as the face image. We refer to v_i, the i^{th} row of V^T , as i^{th} eigenface. Display the first 10 eigenfaces as 10 images in grayscale.

[8]:
```
# All of the images are already in vector form

# calculating covariance matrix
cov_matrix = np.cov(mean_subtracted.T)

# calculate eigenvalues and eigenvectors
eigen_values, eigen_vectors = np.linalg.eig(cov_matrix)

# consider only real part of complex numbers
eigen_vectors = np.real(eigen_vectors)

# eigenfaces
eigenfaces = eigen_vectors.T

# plot first 10 eigenfaces
f = plt.figure()
for i in range(10):
    f.add_subplot(2, 5, i + 1)
    plt.imshow(eigenfaces[i].reshape(50,50), cmap = cm.Greys_r)

plt.show(block=True)
```



(f) (10 pts) Eigenface Feature.

The top r eigenfaces $V^T[: r, :] = v1, v2, ..., vr^T$ span an r-dimensional linear subspace of the original image space called face space, whose origin is the average face μ, and whose axes are the eigenfaces $v1, v2, ..., vr$. Therefore, using the top r eigenfaces $v1, v2, ..., vr$, we can represent a 2500-dimensional face image z as an r-dimensional feature vector f : $f = V^T[: r, :]z = [v1, v2, ..., vr]^T z$.

Write a function to generate r-dimensional feature matrix F and F_{test} for training images X and test images X_{test}, respectively (to get F, multiply X to the transpose of first r rows of V^T , F should have same number of rows as X and r columns; similarly for X_{test}).

[9]:
```python
def eigenface_feature(V, r, x):
    """
    Eigenface Feature

    Description:
    This function represents images in the 2500 dimensional face
    in the r-dimensional space.

    Parameters:
    V - Eigenfaces
    r - Number of eigenfaces to consider
    z - Face to represent in r-dimensional space
    """
    return x @ V.T[:r, :].T
```

[10]:
```python
# determine number of eigenfaces vectors to consider
r = 347

# Calculating Eigenface features for train and test
```

```
train_eigenface_347 = eigenface_feature(eigenfaces, r, train_data)
test_eigenface_347 = eigenface_feature(eigenfaces, r, test_data)
```

(g) (10 pts) Face Recognition. For this problem, you are welcome to use libraries such as scikit learn to perform logistic regression. Extract training and test features for $r = 10$. Train a Logistic Regression model using F and test on F_{test}. Report the classification accuracy on the test set. Plot the classification accuracy on the test set as a function of r when $r = 1, 2, ..., 200$. Use "one-vs-rest" logistic regression, where a classifier is trained for each possible output label. Each classifier is trained on faces with that label as positive data and all faces with other labels as negative data. sklearn calls this the `ovr` mode.

[11]:
```
# import sklearn modules
from sklearn.linear_model import LogisticRegression

# intialize series r
r = np.arange(1, 201)

# store accuracy metrics
accuracy = pd.DataFrame(columns = ["r", "IS", "OOS"])

# get accuracy for all r models
for i in r:
    # Calculate Eigenface features for i eigenface vectors
    train_eigenface_i = eigenface_feature(eigenfaces.T, i, train_data)
    test_eigenface_i = eigenface_feature(eigenfaces.T, i, test_data)

    # fit model
    clf = LogisticRegression(multi_class = "ovr",
                             max_iter = 1000).fit(train_eigenface_i,
                                                  train_labels)
    # calculate accuracy metric
    in_sample_acc_i = clf.score(train_eigenface_i, train_labels)
    oos_acc_i = clf.score(test_eigenface_i, test_labels)

    # update accuracy
    accuracy = accuracy.append({"r" : i,
                                "IS" : in_sample_acc_i,
                                "OOS" : oos_acc_i},
                               ignore_index=True)


accuracy
```

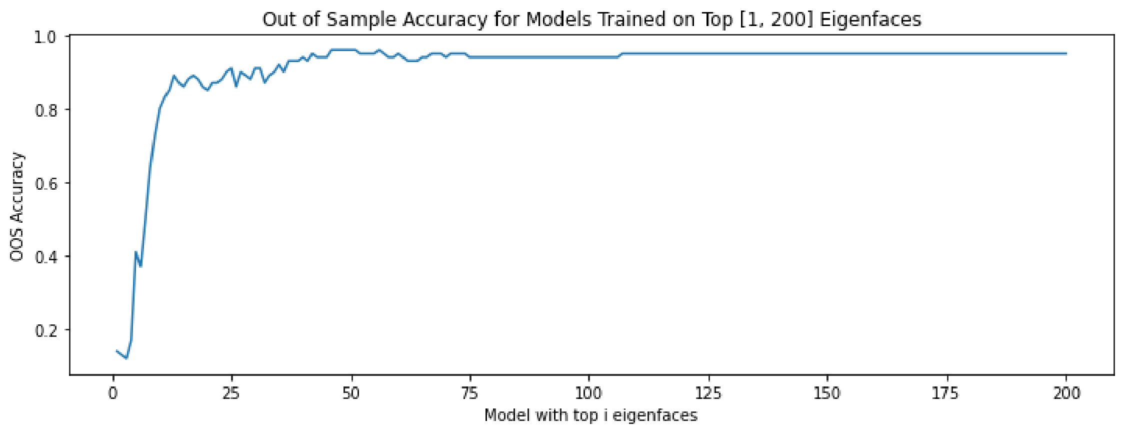
```
C:\Users\amira\anaconda3\lib\site-
packages\sklearn\linear_model\_logistic.py:763: ConvergenceWarning: lbfgs failed
to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.
```

```
Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-
regression
  n_iter_i = _check_optimize_result(
```

[11]:
```
         r        IS   OOS
0      1.0  0.129630  0.14
1      2.0  0.120370  0.13
2      3.0  0.151852  0.12
3      4.0  0.187037  0.17
4      5.0  0.472222  0.41
..     ...       ...   ...
195  196.0  1.000000  0.95
196  197.0  1.000000  0.95
197  198.0  1.000000  0.95
198  199.0  1.000000  0.95
199  200.0  1.000000  0.95

[200 rows x 3 columns]
```

[12]:
```
# plot accuracy scores across all 200 models
plt.rcParams['figure.figsize'] = [12, 4]
plt.plot(accuracy["r"], accuracy["OOS"])
plt.title("Out of Sample Accuracy for Models Trained on Top [1, 200] Eigenfaces")
plt.xlabel("Model with top i eigenfaces")
plt.ylabel("OOS Accuracy")
```

[12]:
```
Text(0, 0.5, 'OOS Accuracy')
```



[13]:
```
accuracy.describe()
```

```
[13]:                r           IS          OOS
      count  200.000000  200.000000  200.000000
      mean   100.500000    0.967722    0.911200
      std     57.879185    0.137429    0.131934
      min      1.000000    0.120370    0.120000
      25%     50.750000    1.000000    0.940000
      50%    100.500000    1.000000    0.950000
      75%    150.250000    1.000000    0.950000
      max    200.000000    1.000000    0.960000
```

1.5 2. Implement EM algorithm. (40 pts)

In this problem, you will implement a bimodal GMM model fit using the EM algorithm. Bimodal means that the distribution has two peaks, or that the data is a mixture of two groups. If you want, you can assume the covariance matrix is diagonal (i.e. it has the form $diag(\sigma_1^2, \sigma_2^2, ..., \sigma_d^2)$ for scalars σ_i) and you can randomly initialize the parameters of the model.

You will need to use the Old Faithful Geyser Dataset. The data file contains 272 observations of the waiting time between eruptions and the duration of each eruption for the Old Faithful geyser in Yellowstone National Park.

You should do this without calling the Gaussian Mixture library in scikit learn. You can use numpy or scipy for matrix calculation or generating Gaussian distributions.

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

```
[14]: # import dataset
      faithful_df = pd.read_excel("Old_Faithful_Geyser_Data.xlsx")

      # snapshot
      faithful_df.head()
```

```
[14]:    eruptions  waiting
      0      3.600       79
      1      1.800       54
      2      3.333       74
      3      2.283       62
      4      4.533       85
```

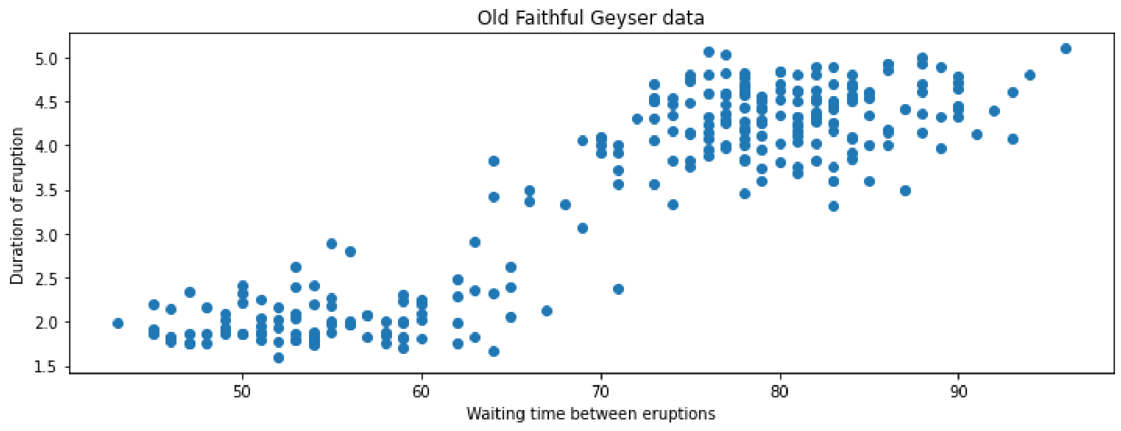
```
[15]: # descriptive statistics
      faithful_df.describe()
```

```
[15]:         eruptions     waiting
      count  272.000000  272.000000
      mean     3.487783   70.897059
      std      1.141371   13.594974
      min      1.600000   43.000000
      25%      2.162750   58.000000
```

```
50%       4.000000   76.000000
75%       4.454250   82.000000
max       5.100000   96.000000
```

[16]:
```
# plot Old Faithful Geyser data
plt.rcParams['figure.figsize'] = [12, 4]
plt.scatter(faithful_df["waiting"], faithful_df["eruptions"])
plt.title("Old Faithful Geyser data")
plt.xlabel("Waiting time between eruptions")
plt.ylabel("Duration of eruption")
```

[16]:
```
Text(0, 0.5, 'Duration of eruption')
```



(b) (3 pts) Recall that EM learns the parameter θ of a Gaussian mixture model $P_\theta(x, z)$ over a dataset $D = \{x^{(i)}|i = 1, 2, ...n\}$ by performing the E-step and the M-step for $t = 0, 1, 2, ...$ We repeat the E-step and and M-step until convergence.

In the E-step, for each $x^{(i)} \in D$, we compute a vector of probabilities $P_{\theta t}(z = k|x)$ for the event that each $x^{(i)}$ originates from a cluster k given the current set of parameters θ_t.

Write the expression for $P_{\theta t}(z = k|x)$, which is the posterior of each data point $x^{(i)}$. Recall that by Bayes' rule,

$$P_{\theta t}(z = k|x) = \frac{P_{\theta t}(z = k, x)}{P_{\theta t}(x)} = \frac{P_{\theta t}(z = k, x)}{\Sigma_{l=1}^{k} P_{\theta t}(x|z = l) P_{\theta t}(x = l)}$$

Note that we have seen this formula in class. We are asking you to write it down and try to understand and it before implementing it in part (e).

Let's define the variables.

$x^{(i)} \in \mathbb{R}$ represents the datapoints we look to cluster.

$z^{(i)} \in 1, 2$ are the cluster ID's.

We are looking to fit a gausian mixture model and we are told that there are two clusters in the data. We can observe these clusters in the visualization above. The first cluster is denoted $z^{(1)}$ and the second cluster is denoted $z^{(2)}$. $x \in \mathbb{R}$ is continuous, and conditioned on $z = k$, we have a normal distribution $P_\theta(x|z = k) = \mathcal{N}(\mu_k, \Sigma_k)$.

The paramter θ_k defines μ_k, Σ_k, ϕ_k for all \$ k $\in \{1, 2\}$\$.

This is the intuition behind the GMM model. We will look to sample realizations from the RV $P_\theta(x|z = k) = \mathcal{N}(\mu_k, \Sigma_k)$. To do this we will utilize the EM (Expectation Maximization) algorithm. The EM algorithm learns the parameters θ of a latent variable model $P_\theta(x, z)$ over the dataset $\mathcal{D} = \{x^{(i)}|i = 1, 2, ..., n\}$ over two steps.

1. Expectation-step: For each $x^{(i)} \in \mathcal{D}$ compute $P_{\theta_t}(z|x^{(i)})$. This means that we calculate the expected values for these clusters of θ_t.
2. Maximization-step: This consists of maximatizing the expectations calculated in the E-step with respect to the model parameters. This step updates the values of μ_k, Σ_k, ϕ_k for all k. Compute new weights θ_{t+1} as

$$\theta_{t+1} = \max_\theta \Sigma_{i=1}^n \left(\mathbb{E}_{z^{(i)} \sim P_{\theta_t}(z|x^{(i)})} log P_\theta(x^{(i)}, z^{(i)}) \right)$$

$$= \max_\theta \left(\Sigma_{k=1}^K \Sigma_{x \in \mathcal{D}} P_{\theta_t}(z_k|x) log P_\theta(x|z_k) + \Sigma_{k=1}^K \Sigma_{x \in \mathcal{D}} P_{\theta_t}(z_k|x) log P_\theta(z_k) \right)$$

We repeat this for $t = 1, 2, ...,$ until convergence, ultimately returning the maximum likelihood estimate of the data with k clusters. The algoirhtm works because knowing the cluster assignment for each $x^{(i)}$ makes solving for μ_k, Σ_k, ϕ_k easy, and knowing μ_k, Σ_k, ϕ_k makes inferring $P(z|x^{(i)})$ easy. Alternating between which values are assumed known, the MLE of the non-fixed values can be calculated efficiently.

EM is a technique commonly used to estimate a model's parameters, and these are learned the MLE (maximum likelihood estimation) techniques. Unfortunately, finding the MLE solution for mixture models by differentiating the log likelihood and solving for 0 is usually analytically impossible. The EM algorithm is a numeric technique for the MLE, and is used when closed form expressions for updating model parameters can be calculated. EM is an iterative algorithm and has the convenient property that the maximum likelihood of the data strictly increased with each subsequent iteration, it is guarenteed to converge to a local maximum.

So we have the following equation for the posterior of the E-step in each iteration of the EM algorithm.

$$P_{\theta_t}(z_k|x) = \frac{P_{\theta_t}(z = k, x)}{P_{\theta_t}(x)} = \frac{P_{\theta_t}(x|z_k) P_{\theta_t}(z_k)}{\Sigma_{l=1}^k P_{\theta_t}(x|z_l) P_{\theta_t}(z_l)}$$

Let's look at each component of the equation.

- $P_{\theta t}(x|z_k) = \prod_{j=1}^d P_\theta(x_j|y = k)$
  This is the probability of the data coming from a cluster z_k. This is the product of the occurance probabilities of each $x^{(i)}$.

- $P_{\theta_t}(z_k) = \phi_k$
  This is the probability of cluster z_k. It is determined as the average likelihood of all the data points for distribution/cluster z_k.
- $\Sigma_{l=1}^{k} P_{\theta_t}(x_l) P_{\theta_t}(z_l)$
  This is the law of total probability. In our case, it is the sum of all probabilities of all data-points appearing in a cluster for all clusters.

(c) (5 pts) In the M-step, we compute new parameters θ_{t+1}. Our goal is to find μ_k, Σ_k and ϕ_k that optimize

$$\max_{\theta} \left(\Sigma_{k=1}^{K} \Sigma_{x \in D} P_{\theta_t}(z_k|x) log P_\theta(x|z_k) + \Sigma_{k=1}^{K} \Sigma_{x \in D} P_{\theta_t}(z_k|x) log P_\theta(z_k) \right)$$

Write down the formula for μ_k, Σ_k, and for the parameters ϕ_k at the M-step (we have also seen these formulas in class).

Let γ be the likelihood of one data point being realized from cluster/distribution z_k. Intuitively, this represents the likelihood of a point being part of a cluster. The liklihood calculated using the gausian probability density function, and takes μ_k, Σ_k as input. I use z_k for $z = k$.

One Dimensional Model:

$$\gamma_i = \mathcal{N}(x|\mu_i, \sigma_i) = P(z_k|x^{(i)}) = \frac{1}{\Sigma_k \sqrt{2\pi}} e^{\frac{-(x^{(i)} - \mu_k)^2}{2\Sigma^2}}$$

Multi-Dimensional Model:

$$\gamma_i = \mathcal{N}(\vec{x}|\vec{\mu}_i, \Sigma_i) = P(z_k|x^{(i)}) = \frac{1}{\sqrt{(2\pi)^K |\Sigma_i|}} e^{-\frac{1}{2}(\vec{x} - \vec{\mu}_i)^T \Sigma_i^{-1} (\vec{x} - \vec{\mu}_i)}$$

As a result we can calculate the closed form solution μ_k, Σ_k, ϕ_k by taking the derivative of the objective function, setting it to 0 and solving for these parameters. Inquitively, the optimal mean and covariance are the emperical mean and covariance of the dataset $\mathcal{D}$ when each element $x^{(i)}$ has weight γ_i.

Given that this data has weights, the best guess of the mean μ of each cluster k is then calculated as the mean of the data where each data point $x^{(i)}$ is scaled by γ_i, that is its likelihood (or probability kinda) of appearing in cluster z_k.

$$\mu_k = \frac{\Sigma_{i=1}^{n} \gamma_i x^{(i)}}{n_k}$$

Similarly, we take the weighted averages of the covariances to calculate Σ_k.

$$\Sigma_k = \frac{\Sigma_{i=1}^{n} \gamma (x^{(i)} - \mu_k)(x^{(i)} - \mu_k)^T}{n_k}$$

The normalizing parameter here n_k is the sum of the probabilities that all x_i belong to cluster z_k for all $x \in \mathcal{D}$.

$$n_k = \Sigma_{i=1}^{n} \gamma_i$$

The best estimate for the proportion of each class, denoted ϕ_k is the average of the probabilities that the datapoints belong to cluster z_k, where n is of course the number of datapoints.

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

(d) (25 pts) Implement and run the E Malgorithm. Specifically:

```
i. (10 pts) Implement the EM algorithm from scratch (e.g., in Python and numpy).
```

The implementation programed below is the best we could do. The shapes of the variables are good, I believe the problem has to do with how the variables are being updated. We understand the intuition behind the GMM and EM algorithms.

```
ii. (5 pts) Choose a termination criterion for when the algorithm stops repeating the E-step and
```

A logical termination criterion for then the algorithm stops repeating the E-step and the M-step would be when none of the conditional probabilities computed during the previous E-step changes in a meaningful way as compared to the previous iteration. In other words, if continuing to run the E-step yields infinitely small changes in the conditional probability then it would make sense to terminate. The threshold in which termination occurs may vary but a standard number to implement could be 1e-6.

```
iii. (10 pts) Plot the trajectories of the two mean vectors (1 and 2) in two dimensions as they
```

To plot the trajectories of the vectors μ_1 and μ_2 across iterations one simply has to save them to a variable, and the plot the difference between every consecutive set of μs over the final distributions $\mathcal{N}(\mu_{t1}, \Sigma_{t1})$ and $\mathcal{N}(\mu_{t2}, \Sigma_{t2})$.

[17]:
```
# helper functions
from scipy.stats import multivariate_normal

def random_sample(arr, n = 1):
    """
    Selects n many random items from a list.
    This is used to initialize mus.
    """
    return arr[np.random.choice(len(arr), size=n, replace=False)]

def covariance(x, y):
    """
    Return covariance of two vectors x, y
    """
    # get means of each vec
    mean_x = sum(x)/float(len(x))
    mean_y = sum(x)/float(len(x))

    # distance between point and mean of vec
    dist_x = [i - mean_x for i in x]
    dist_y = [i - mean_y for i in y]

    # solve covariance
    cov = (sum([dist_x[i] * dist_y[i] for i in range(len(dist_x))])) / (len(x) -␣
 ↪1)
    return np.cov(x, y)

def solve_mu_k(gamma_k, x_k, n_k):
    """
    Solves for mean of cluster k given hilucinated x assigned data points
    """
    return np.sum(gamma_k * x_k) / n_k


def solve_Sigma_k(gamma_k, x_k, n_k):
    """
    Solves for covariance of cluster k given hilucinated x assigned data points
    """
    mu_k = solve_mu_k(gamma_k, x_k, n_k)
    var_part = np.array([x_k[i] - mu_k for i in range(len(x_k))])
    return np.sum(gamma_k.reshape(-1, 1, 1) * (var_part @ var_part)) / n_k


def solve_phi_k(gamma_k, n_k):
    """
    Solve for probability of cluster
    This is the average of the likelihoods of all x given cluster gamma_k
    """
    x_len = len(x)
    return np.sum(gamma_k) / n_k


def likelihood(x, mu, Sigma):
    """
    Likelihood Function for p(x|z_k)
    Multivariate Gaussian PDF given point x
    """
    return multivariate_normal(mean = mu, cov = Sigma).pdf(x)

def log_likelihood(x, mu, Sigma):
    """
    Log of the Multivariate Gaussian PDF given point x
    """
    return np.log(likelihood(x, mu, Sigma))

def hallucinate_x_assignments(gamma, x):
    """
    Assume cluster index label for values in x given posterior probabilities
    """
    # store labels
    hallucinated_labels = np.zeros(len(x))

    # assign label per gamma
    for i in range(len(x)):
        if gamma[i, 0] > gamma[i, 1]:
            hallucinated_labels[i] = 0
        else:
            hallucinated_labels[i] = 1

    return hallucinated_labels
```

[18]:
```
# Now that we have all the parts, let's put everything together

################
### GMM Model ###
################

def GMM_implementation(x, termination_criteria = 100):
    """
    Gausian Mixture Model

    Assumes there are K = 2 clusters.
    """
    # step counter
    iteration = 0

    ### getting initial mu's, Sigma's, and phi's

    # initial component means will be set to random data points x_i in D
    mu_prior = np.zeros([2, 2])

    for k in range(2):
        # get random index
        index = np.random.randint(len(x))

        # get two mu's for both columns of x
        mu_0 = x[index, 0]
        mu_1 = x[index, 1]
        mu_prior[k] = np.array([mu_0, mu_1])

    # intitial component variances will be set to the sample covariance
    cov_initial = covariance(x[:, 0], x[:, 1])
    Sigma_0 = np.cov(x[:, 0], x[:, 1])
    Sigma_1 = np.cov(x[:, 0], x[:, 1])
    Sigma_prior = np.array([Sigma_0, Sigma_1])

    # initial component distribution prior estimates are
    # set to the uniform distribution
    phi_0 = 1.0 / 2.0
    phi_1 = 1.0 / 2.0
    phi_prior = np.array([phi_0, phi_1])

    print(mu_prior)
    print(Sigma_prior)
    print(phi_prior)

    # initialize prior likelihood
    prior_log_likelihood = 0

    # EM Algorithm
    while True:
        # E-step
        gamma = np.zeros((len(x), 2))
        law_of_total_prob = 0
        print(x.shape, mu_prior.shape, Sigma_prior.shape, phi_prior.shape)
        for k in range(2):
            law_of_total_prob += np.sum(log_likelihood(x, mu_prior[k],␣
↪Sigma_prior[k])) * phi_prior[k]


        for k in range(2):
            for i in range(len(x)):
                gamma[i, k] = log_likelihood(x[i], mu_prior[k], Sigma_prior[k])␣
↪* phi_prior[k] / law_of_total_prob

        #print(gamma)


        # test for convergence
        #post_log_likelihood = posterior
        if (iteration > termination_criteria):
            print(f"Model Converged at {iteration} iterations.")
            return mu_prior, Sigma_prior

        # M-step
        # assume assignments
        x_hallucinations = hallucinate_x_assignments(gamma = gamma, x = x)

        mu_post = np.zeros(2)
        Sigma_post = np.zeros(2)
        phi_post = np.zeros(2)

        for k in range(2):
            # calculate means and probabilities of clusters
            n_k = np.sum(x_hallucinations == k)
            x_in_k = [x_hallucinations == k]
            x_k = x[x_in_k]
            likelihood_k_i = multivariate_normal.pdf(x_k, mu_prior[k],␣
↪Sigma_prior[k]).reshape(-1, 1)
            phi_post[k] += solve_phi_k(likelihood_k_i, n_k)
            mu_post[k] += solve_mu_k(likelihood_k_i, x_k, n_k) + 1e-10

            # calculate sum of log likelihoods
            gamma_k_prior = np.sum(gamma[k])

            # with the mean of the clusters we can calculate the covariances
            for i in range(len(x)):
                if x_hallucinations[i] == k:
                    Sigma_post[k] += solve_Sigma_k(gamma_k =  gamma_k_prior, x_k␣
↪= x_hallucinations, n_k = n_k) + 1e-10

            # final calculations
            mu_prior[k] = mu_post
            Sigma_prior[k] = Sigma_post
            phi_prior[k] = phi_post[k] / len(x)


        Sigma_prior = np.array(Sigma_prior)

        print(mu_prior)
        print(np.array(Sigma_prior))
        print(np.array(phi_prior))



        iteration += 1
        print(iteration)
```

[19]:
```
# casting x as array
x = np.array(faithful_df)

# GMM
GMM_implementation(x)
```

```
[[ 4.333 82.   ]
 [ 2.017 52.   ]]
[[[  1.30272833  13.97780785]
  [ 13.97780785 184.82331235]]
 [[  1.30272833  13.97780785]
  [ 13.97780785 184.82331235]]]
[0.5 0.5]
(272, 2) (2, 2) (2, 2, 2) (2,)
[[0.14109569 0.        ]
 [0.14109569 0.17360483]]
[[[0.60443981 0.        ]
  [0.60443981 0.        ]]

 [[0.60443981 0.59670647]
  [0.60443981 0.59670647]]]
[8.6271671e-06 7.8664628e-06]
1
(272, 2) (2, 2) (2, 2, 2) (2,)
```

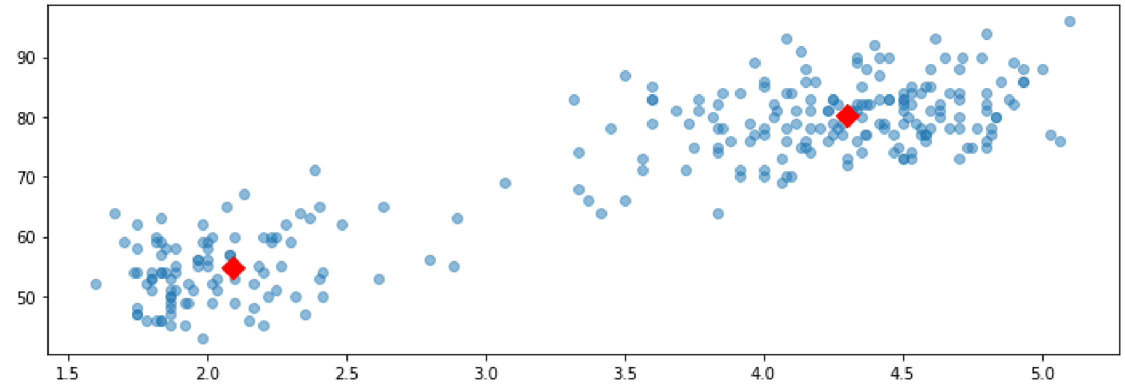
```
C:\Users\amira\AppData\Local\Temp/ipykernel_17684/650328186.py:84:
FutureWarning: Using a non-tuple sequence for multidimensional indexing is
deprecated; use `arr[tuple(seq)]` instead of `arr[seq]`. In the future this will
be interpreted as an array index, `arr[np.array(seq)]`, which will result either
in an error or a different result.
  x_k = x[x_in_k]
```

```
---------------------------------------------------------------------------
ValueError                                Traceback (most recent call last)
~\AppData\Local\Temp/ipykernel_17684/3763853887.py in <module>
      3
      4 # GMM
----> 5 GMM_implementation(x)

~\AppData\Local\Temp/ipykernel_17684/650328186.py in GMM_implementation(x,␣
 ↪termination_criteria)
     54         print(x.shape, mu_prior.shape, Sigma_prior.shape, phi_prior.shape
     55         for k in range(2):
---> 56             law_of_total_prob += np.sum(log_likelihood(x, mu_prior[k],␣
 ↪Sigma_prior[k])) * phi_prior[k]
     57
     58

~\AppData\Local\Temp/ipykernel_17684/226600434.py in log_likelihood(x, mu, Sigma)
     61     Log of the Multivariate Gaussian PDF given point x
     62     """
---> 63     return np.log(likelihood(x, mu, Sigma))
     64
     65 def hallucinate_x_assignments(gamma, x):

~\AppData\Local\Temp/ipykernel_17684/226600434.py in likelihood(x, mu, Sigma)
     55     Multivariate Gaussian PDF given point x
     56     """
---> 57     return multivariate_normal(mean = mu, cov = Sigma).pdf(x)
     58
     59 def log_likelihood(x, mu, Sigma):

~\anaconda3\lib\site-packages\scipy\stats\_multivariate.py in __call__(self, mean,␣
 ↪cov, allow_singular, seed)
    358         See `multivariate_normal_frozen` for more information.
    359         """
--> 360         return multivariate_normal_frozen(mean, cov,

    361                                           allow_singular=allow_singular,
    362                                           seed=seed)

~\anaconda3\lib\site-packages\scipy\stats\_multivariate.py in __init__(self, mean,␣
 ↪cov, allow_singular, seed, maxpts, abseps, releps)
    728         self.dim, self.mean, self.cov = self._dist._process_parameters(
    729                                                     None, mean,␣
 ↪cov)
--> 730         self.cov_info = _PSD(self.cov, allow_singular=allow_singular)
    731         if not maxpts:
    732             maxpts = 1000000 * self.dim

~\anaconda3\lib\site-packages\scipy\stats\_multivariate.py in __init__(self, M,␣
 ↪cond, rcond, lower, check_finite, allow_singular)
    160         eps = _eigvalsh_to_eps(s, cond, rcond)
    161         if np.min(s) < -eps:
--> 162             raise ValueError('the input matrix must be positive␣
 ↪semidefinite')
    163         d = s[s > eps]
    164         if len(d) < len(s) and not allow_singular:

ValueError: the input matrix must be positive semidefinite
```

(e) (5 pts) If you were to run K-means clustering instead of the EM algorithm you just implemented, do you think you will get different clusters? You are welcome to experiment with K-means clustering on the same dataset with $K = 2$. (The KNN library from scikit learn is a good way to try). Comment on why do you think the results will or will not change.

[20]:
```
from sklearn.cluster import KMeans

kmeans = KMeans(n_clusters=2, random_state=0).fit(x)

# display the clusters in 2D
plt.scatter(x[:,0], x[:,1], alpha=0.5)
plt.scatter(kmeans.cluster_centers_[:,0], kmeans.cluster_centers_[:,1],␣
 ↪marker='D', c='r', s=100)
```

```
[20]: <matplotlib.collections.PathCollection at 0x1f8fb510460>
```



If I were to run K-means clustering instead of the EM algorithm, I do think slightly different clusters will appear. The K-means algorithm may perform non-trivially worse if there are recognized outliers that don't obviously belong to a cluster within the data. Another reason why I believe the results may subtly change is that K-means locates and places points based on means which assumes a certain shape to the data whereas in EM, we assume that data points are gaussian distributed. This makes K-means biased towards spherical clusters. Additionally, we can assume that results may differ due to the difference of how EM assigns points to a given set of clusters. EM assigns points based on the likelihood of a point belonging to a particular cluster and does not depend on the L2 norm like K-means does.