Exercise 4

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1 EECS 491: Probabilistic Graphical Models Assignment 4

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2 Exercise 4

In this notebook we will combine the work we have done in the previous exercises to train a Gaussian Mixture Model on the MNIST dataset that has been reduced to two dimensions.

We begin as always by importing the necessary Python packages and importing the needed functions from the previous exercises:

```
In [3]: import csv, copy, gzip, pickle

        import numpy as np
        import matplotlib.pyplot as plt

        from scipy.stats import chi2
        from sklearn.decomposition import PCA

        %matplotlib inline

In [8]: def covmatIsLegal(sigma):
            legal = True
            for covmat in sigma:
                if not(np.allclose(covmat, covmat.T)) or np.any(np.linalg.eigvals(covmat) <= 0
                    legal = False
            print("Convariance Matrices are Legal? : %r" % legal)

In [9]: def plotGaussianModel2D(mu, sigma, pltopt='k'):
            if sigma.any():
                # calculate ellipse constants
                c = chi2.ppf(0.9, 2) # use confidence interval 0.9
                # get eigen vector and eigen values
                eigenValue, eigenVector = np.linalg.eig(sigma)
                # calculate points on ellipse
                t = np.linspace(0, 2*np.pi, 100) # draw 100 points
                u = [np.cos(t), np.sin(t)]
                w = c * eigenVector.dot(np.diag(np.sqrt(eigenValue)).dot(u))
                z = w.T + mu
            else:
                z = mu
            # plot ellipse by connecting sample points on curve
            plt.plot(z[:,0], z[:,1], pltopt)

        def colorPicker(index):
            colors = 'rgbcmyk'
            return colors[np.remainder(index, len(colors))]

        def gmmplot(data, gmm):
            # plot data points
            plt.scatter(data[:, 0], data[:, 1], s=4)
            # plot Gaussian model
            color = 'rgb'
            for index, model in enumerate(gmm):
                plotGaussianModel2D(model['mean'], model['covariance'], colorPicker(index))
```

```
In [10]: def expectation(data, gmmcp):
             rows,dims = data.shape
             cols = len(gmmcp)
             posterior = np.zeros((rows,cols))
             for row in range(rows):
                 for col in range(cols):
                     gmm = gmmcp[col]
                     mean = gmm['mean']
                     covariance = gmm['covariance']
                     prior = gmm['prior']
                     num = multivariate_gaussian(dims, mean, covariance, data[row]) * prior
                     denom = 0
                     for j in range(cols):
                         gmm = gmmcp[j]
                         mean = gmm['mean']
                         covariance = gmm['covariance']
                         prior = gmm['prior']
                         g = multivariate_gaussian(dims, mean, covariance, data[row])
                         denom += g * prior
                     posterior[row, col] = num/denom
             return posterior
```

```
In [11]: def multivariate_gaussian(dims, mean, covariance, example):
             A = 1/((2*np.pi)**(dims/2)*np.linalg.det(covariance)**.5)
             B = np.exp(-.5*(example - mean).T.dot(np.linalg.inv(covariance).dot((example - mea
             return A * B
```

```
In [12]: def maximization(posterior, data, gmmcp):
             update_gmm = gmmcp
```

```
        rows, cols = posterior.shape
        pk = np.zeros(cols)
        for col in range(cols):
            for row in range(rows):
                pk[col] += posterior[row, col]
        for col in range(cols):
            gmm = update_gmm[col]
            # Update the mean
            mean = 0
            for row in range(rows):
                mean += posterior[row,col]*(data[row])/pk[col]
            # Update the covariance
            covariance = 0
            for row in range(rows):
                x = (data[row]-gmm['mean'])[:,None]
                covariance += posterior[row,col]*x.dot(x.T)/pk[col]
            gmm['mean'] = mean
            gmm['covariance'] = covariance
            gmm['prior'] = pk[col]/rows

        return gmmcp
```

```
In [13]: with gzip.open('data/mnist.pkl.gz', 'rb') as f:
             f = pickle._Unpickler(f)
             f.encoding = 'latin1'
             trainSet, validSet, testSet = f.load()
             mnistData = np.concatenate((trainSet[0], validSet[0], testSet[0]), axis=0)
```

```
In [14]: def dimReducePCA(data, dims):
             pca = PCA(n_components=dims)
             reduced_data = pca.fit_transform(data)
             pca = PCA()
             pca.fit(data)
             eigen_vectors = pca.components_.T
             eigen_values = pca.explained_variance_
             return reduced_data, eigen_vectors, eigen_values
```

```
In [16]: mnistData2D, eigenVectors, eigenValues = dimReducePCA(mnistData, 2)
```

We then create functions for randomly initializing a number of means and a number of covariance matrices. The following functions were taken from the demo:

```
In [17]: # randomly pick coordinates as center of Gaussian distribution
         def randinitMean(n, drange):
             mu = []
             for m in range(n):
                 mu.append([np.random.uniform(drange[i]['MIN'], drange[i]['MAX']) for i in rang
             # return inf form of numpy.ndarray
             return np.asarray(mu)
```

```
In [18]: def randinitCovariance(n):
             sigma = []
             for m in range(n):
                 # randomly pick a direction
                 angle = np.random.uniform(0, 2 * np.pi)
                 # create eigen vector with the direction and direction orthogonal to it
                 eigenVector = np.asarray([[np.cos(angle), np.sin(angle)],
                                           [np.cos(angle + np.pi/2), np.sin(angle + np.pi/2)]]
                 # randomly generate eigen values
                 eigenValue = abs(np.random.normal(size=2))
                 # compose covariance matrix
                 sigma.append(eigenVector.T.dot(np.diag(eigenValue).dot(eigenVector)))
             # return in form of numpy.ndarray
             return np.asarray(sigma)
```

We can now test the random covariance matrix generation function to ensure that it produces legal covariance matrices:

```
In [19]: covmatIsLegal(randinitCovariance(10))
```

```
Convariance Matrices are Legal? : True
```

While our algorithm will work just fine on the entirety of the MNIST dataset, it will take a really long time so we'll train on a smaller sample of the dataset:

```
In [20]: ndata = 1000
         # randomly pick a subset of data
         data = mnistData2D[np.random.randint(len(mnistData2D), size=ndata)]
```

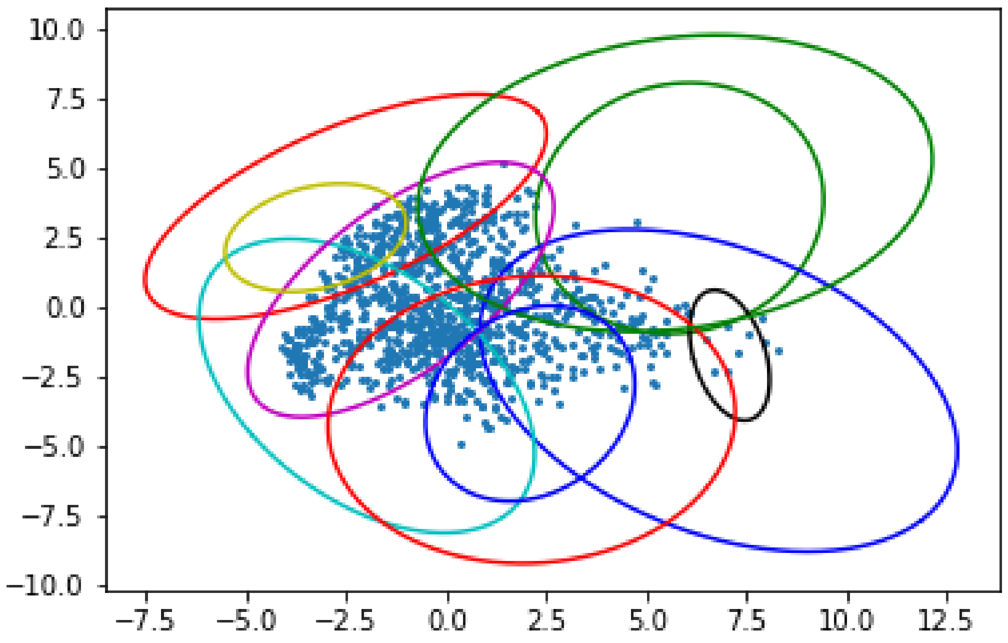
Now let's initialize our Gaussian Mixture Model:

```
In [21]: ngmm = 10

         # get information of range on each dimension
         dataRange = []
         for i in range(data.shape[1]):
             dataRange.append({'MIN': min(data[:,i]), 'MAX': max(data[:,i])})

         # randomly initialize Gaussian mixture model
         mu    = randinitMean(ngmm, dataRange)
         sigma = randinitCovariance(ngmm)
         gmm   = [{'mean': mu[m], 'covariance': sigma[m], 'prior': 1.0/ngmm} for m in range(ng

         # show initial state
         gmmplot(data, gmm)
```



Now let us train our GMM using our Expectation-Maximization algorithm:

```
In [22]: gmmcp = copy.deepcopy(gmm)

         # create figure
         plt.figure(figsize=(16, 16))
         # improve model with EM-Algorithm
         for i in range(8):
             # plot current status
             plt.subplot(331 + i)
             gmmplot(data, gmmcp)
             # excute EM-Algorithm
             for j in range(5):
                 posterior = expectation(data, gmmcp)
                 gmmcp = maximization(posterior, data, gmmcp)
         # plot final status
         plt.subplot(339)
         gmmplot(data,gmmcp)
```