Homework 4 Exercise 1

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1 Homework 4 Exercise 1

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In this excercise we attempt to apply the Expectation-Maximization algorithm to adapt the means of a 2D Gaussian Mixture Model with fixed covariance matrices. This notebook uses functions from the gmmlib library which I have implemented and included.

```
In [1]: import csv, copy, gzip, pickle

        import numpy as np
        import matplotlib.pyplot as plt

        from scipy.stats import chi2

        %matplotlib inline
```

1.1 Deriving the EM Equations

We can derive the equations for the Expectation-Maximization algorithm by starting with the multivariate Gaussian distribution:
$p(x|\mu, \sum) = N(x|\mu, \sum) = \frac{exp(-\frac{1}{2}(x-\mu)^T \sum^{-1}(x-\mu))}{(2\pi)^{D/2}|\sum|^{\frac{1}{2}}}$
and taking its log:
$ln(p(x|\mu, \sum)) = -\frac{1}{2}ln(2\pi) - \frac{1}{2}ln|\sum| - \frac{1}{2}(x-\mu)^T \sum^{-1}(x-\mu)$
We can then take the derivative of this log with respect to the parameters μ and $\sum$ and set them to 0 to get their maximum values:
$\frac{d(ln(p(x|\mu,\sum)))}{d\mu} = 0 \rightarrow \mu_k = \sum_n p_{n,k} x^{(n)} / p_k$
$\frac{d(ln(p(x|\mu,\sum)))}{d\sum} = 0 \rightarrow \sum_k = \sum_n p_{n,k}(x^{(n)} - \mu_k)(x^{(n)} - \mu_k)^T / p_k$
This gives us our first two equations from the M-step. The remaining equations follow directly from the model.

And so we arrive at our final EM Equations:
E-step: We compute $p_{n,k}$ and p_k:
$p_{n,k} = p(c_k|x^{(n)}, \theta_{1:K})$
$p_k = \sum_n p_{n,k}$
M-step: For each class, we compute the updated mean μ_k, covariance $\sum_k$, and class prior $p(c_k)$:
$\mu_k = \sum_n p_{n,k} x^{(n)} / p_k$

$\sum_k = \sum_n p_{n,k}(x^{(n)} - \mu_k)(x^{(n)} - \mu_k)^T / p_k$
$p(c_k) = p_k$

1.2 Loading the Data

We can load the Yellowstone faithful geyser data from the class example to demonstrate the algorithm:

```
In [2]: with open('data/faithful.txt', 'rt') as csvfile:
            dataReader = csv.reader(csvfile, delimiter=' ')
            # initialize an empty array
            data = []
            for row in dataReader:
                data.append(np.array(row).astype(np.float))
            # convert data into a numpy array
            data = np.asarray(data)
```

1.3 Initializing the Mixture Model

We can initialize the mixture model with starting means (μ, mu) and covariance matrices ($\sum$, sigma) and check to make sure the latter's values are legal:

```
In [3]: ngmm = 2 # quantity of Gaussian Mixture Model
        mu = np.asarray([[2, 70],
                         [4, 80]]
                       ).astype('float')

        sigma = np.asarray([[[1, 0],
                             [0, 3]],
                            [[0.5, 0.2],
                             [0.2, 0.6]]]
                          ).astype('float')
        def covmatIsLegal(sigma):
            for covmat in sigma:
                if not(np.allclose(covmat, covmat.T)) or np.any(np.linalg.eigvals(covmat) <= 0
                    return False
            return True

        print("Convariance Matrices are Legal? : %r" % covmatIsLegal(sigma))
        gmm = [{'mean': mu[m], 'covariance': sigma[m], 'prior': 1.0/ngmm} for m in range(ngmm)

Convariance Matrices are Legal? : True
```

1.4 Plotting the Mixture Model

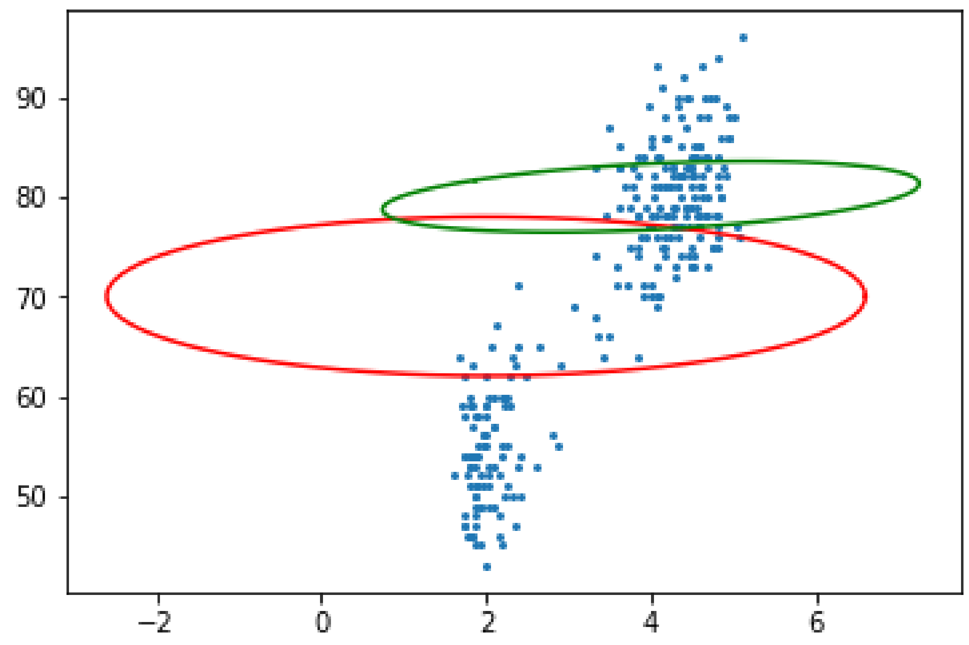
Included is the helper methods from the example for plotting the data and model. Each cluster is represented by an ellipse, with the corresponding mean dictating its center and covariance matrix dictating its distortion along each dimension of the data. Here it outputs the initial model before we run the EM algorithm:

```
In [4]: 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))

        gmmplot(data, gmm)
```



1.5 Optimizing the Mixture Model with the EM Algorithm

We can then iteratively run the expectation and maximization functions to converge on the ideal set of means for our model to fit the data. Expectation computes the posterior probabilities of class k given datapoint x, which is determined by the multivariate normal distribution. Maximization_mean then uses these posteriors to update the means in the mixture model. They correspond to the E and M steps of the EM algorithm, respectively. The results at intermediate steps and the final result are displayed below, and we can observe the representative elipses converging to best fit around the data. However, only their locations can change and not their dimensions, which is the focus of the next section. Note that rather than running for a set number of iterations, I made the algorithm run until the change in value of every dimension of every mean was very small, indicating convergence. As can be seen, this does not take very long even with a very small tolerance for the convergence flag, so the model is very accurate.

```
In [23]: from gmmlib import expectation, maximization, maximization_mean

         # make a true copy of our model
         gmmcp = copy.deepcopy(gmm)

         # create figure
         plt.figure(figsize=(16, 8))
         # improve model with EM-Algorithm
         converged = False
         i = 0
         while(not converged):
             means = [gmmcp[k]['mean'] for k in range(len(gmmcp))]
```

```
        # plot current status
        plt.subplot(231 + i)
        gmmplot(data, gmmcp)
        # excute EM-Algorithm
        for j in range(5):
            posterior = expectation(data, gmmcp)
            gmmcp = maximization_mean(posterior, data, gmmcp)
        converged = True
        for k in range(len(gmmcp)):
            for j in range(len(gmmcp[k]['mean'])):
                if abs(means[k][j] - gmmcp[k]['mean'][j]) >.000000000001:
                    converged = False
                    break
        i+= 1
    # plot final status
    plt.subplot(236)
    gmmplot(data,gmmcp)
```