EECS491 - A4 - E2 - tdm47

May 5, 2018

0.1 EECS491 A4 E2

0.1.1 Tristan Maidment (tdm47)

Goal The goal for this exerise is to implement the covariance portion of the EM algorithm. Since the previous exercise provided a majority of the functionality needed for this exercise, I will not provide redundant comments, and only comment on added functionality.

Implementation

```
In [1]: %matplotlib inline
        import numpy as np
        import matplotlib.pyplot as plt
        import mnist
        import copy
        from scipy.stats import chi2, multivariate_normal

        ngmm = 2

In [2]: mu = np.asarray([[1,60],
                         [3, 80]]
                        ).astype('float')

        sigma = np.asarray([[[1, 0],
                             [0, 42]],
                            [[0.5, 0],
                             [0, 3]]]
                           ).astype('float')

        truth_mu = np.asarray([[2, 70],
                               [4, 80]]
                              ).astype('float')

        truth_sigma = np.asarray([[[1, 0],
                                   [0, 3]],
                                  [[0.5, 0.2],
                                   [0.2, 0.6]]]
                                 ).astype('float')
```

```
In [3]: mu_dist_1 = np.random.multivariate_normal(truth_mu[0], truth_sigma[0], 50)
        mu_dist_2 = np.random.multivariate_normal(truth_mu[1], truth_sigma[1], 50)
```

```
In [4]: ## functions used from the example code provided in class for plotting the distributio
        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
            for index, model in enumerate(gmm):
                plotGaussianModel2D(model['mean'], model['covariance'], colorPicker(index))
```

```
In [5]: gmm = [{'mean': mu[m], 'covariance': sigma[m], 'prior': 1.0/ngmm} for m in range(ngmm)]
```

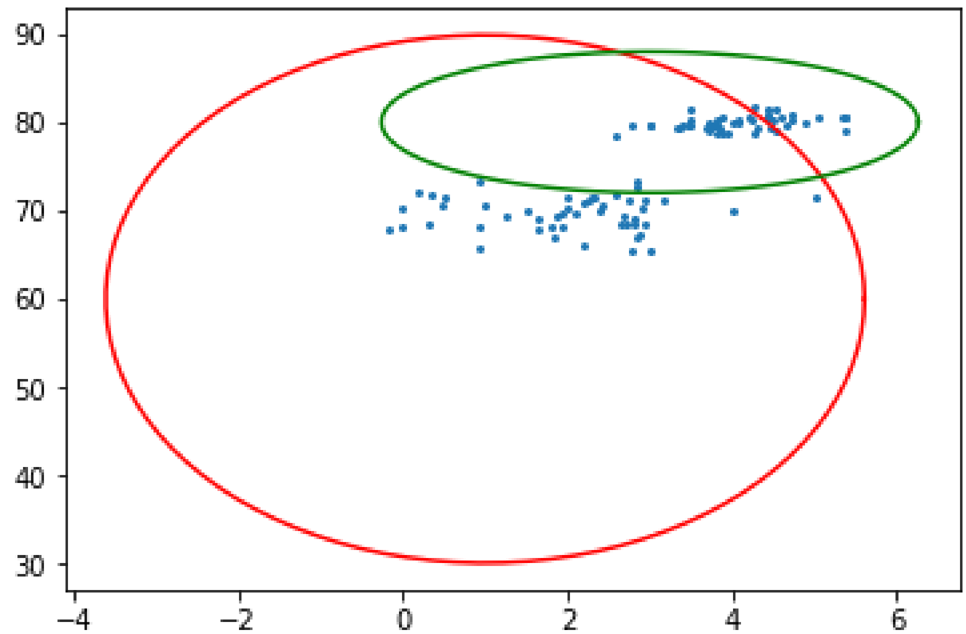
The only change from the previous exercise is the inclusion of the covariance maximiation step. This step is similar to the maximization of the mean, but it adds the weighted (by the `posterior`) covariance of each data point in the domain. The covariance of each point is found by doing an outer product `np.outer`, of the distance of the datapoint from the mean, and it's transpose.

```
In [6]: def expectation(data, gmmcp):
            num = np.zeros((len(gmmcp), data.shape[0]))
            den = np.zeros((len(gmmcp), data.shape[0]))
            for k in range(len(gmmcp)):
                #print(gmmcp[k]["mean"], gmmcp[k]["covariance"])
                num[k] = gmmcp[k]["prior"] * multivariate_normal.pdf(data, gmmcp[k]["mean"], g
                for l in range(len(gmmcp)):
                    den[k] += gmmcp[l]["prior"] * multivariate_normal.pdf(data, gmmcp[l]["mean"
            return np.divide(num, den)

        def maximization(posterior, data, gmmcp):
```

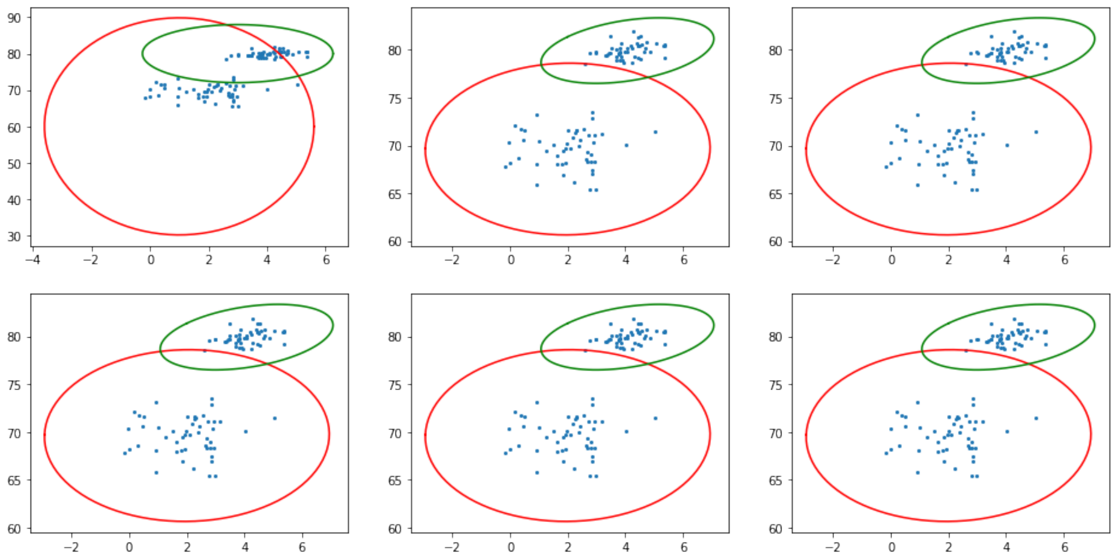
```
        # calculate Nk
        N = np.zeros(len(gmmcp))
        for k in range(N.shape[0]):
            N[k] = np.sum(posterior[k])

        mu = np.zeros((len(gmmcp), len(gmmcp[0]["mean"])))
        for k in range(mu.shape[0]):
            for n in range(data.shape[0]):
                mu[k] += posterior[k, n] * data[n]
            gmmcp[k]["mean"] = 1/N[k] * mu[k]

        sigma = np.zeros((len(gmmcp), data.shape[1], len(gmmcp[0]["covariance"])))
        for k in range(sigma.shape[0]):
            for n in range(data.shape[0]):
                sigma[k] += posterior[k, n] * np.outer((data[n] - gmmcp[k]["mean"]), (data
            gmmcp[k]["covariance"] = 1/N[k] * sigma[k]

        prior = np.zeros(len(gmmcp))
        for k in range(prior.shape[0]):
            prior[k] = np.divide(N[k],N.sum())
            gmmcp[k]["prior"] = prior[k]

        return gmmcp
```

```
In [9]: data = np.concatenate((mu_dist_1, mu_dist_2), axis=0)
        print("Cluster 0", gmm[0], "Cluster 1", gmm[1])
        gmmplot(data, gmm)
```

```
Cluster 0 {'mean': array([ 1., 60.]), 'covariance': array([[ 1.,  0.],
       [ 0., 42.]]), 'prior': 0.5} Cluster 1 {'mean': array([ 3., 80.]), 'covariance': array([
       [0.  , 3. ]]), 'prior': 0.5}
```




```
In [10]: # make a true copy of our model
         gmmcp = copy.deepcopy(gmm)

         pi = np.array([0.5, 0.5])
         # create figure
         plt.figure(figsize=(16, 8))
         # improve model with EM-Algorithm
         for i in range(5):
             # plot current status
             plt.subplot(231 + i)
             gmmplot(data, gmmcp)
             #plt.show()
             # excute EM-Algorithm
             for j in range(5):
                 #print((gmmcp[0]["covariance"]).shape)
                 posterior = expectation(data, gmmcp)
                 #print("Posterior:", posterior)
                 gmmcp = maximization(posterior, data, gmmcp)
         # plot final status
         plt.subplot(236)
         gmmplot(data,gmmcp)
```



0.1.2 Conclusion

As we can see, the elipses depicting the clusters “tighten” up around the data, providing a more accurate representation than just the mean maximization from the previous exercise.