HW5_edgarsp2

October 28, 2019

1 STAT 542 / CS 598: Homework 5

Fall 2019, by Edgar Pino

Due: Monday, Oct 28 by 11:59 PM Pacific Time

```
[151]: import pandas as pd
      import numpy as np
      import matplotlib.pyplot as plt
      from matplotlib.patches import Ellipse
      import matplotlib.transforms as transforms
      import math, random
      from functools import partial, reduce
      from sklearn.metrics import accuracy_score
      from collections import Counter
      from sklearn.decomposition import PCA
      from sklearn.cluster import KMeans as SKMeans
      from sklearn.preprocessing import StandardScaler
      import time
[152]: def get_images_and_labels():
          data = pd.read_csv('zip.train.csv')
          labels = data.V1.to_numpy()
          images = data.drop(columns=['Unnamed: 0', 'V1']).to_numpy()
          return images, labels
[153]: images, labels = get_images_and_labels()
```

2 Question 1 [50 Points] K-Means Clustering

```
[154]: def showImage(pixels):
    img_pixels = pixels.reshape((16,16))
    plt.imshow(img_pixels, cmap='gray')
    plt.show()
[155]: def euclidean_distance(a, b):
    return np.linalg.norm(a-b)
```

2.1 [15 Points] Write your own code of k-means that iterates between two steps, and stop when the cluster membership does not change.

```
[156]: class KMeans:
          def __init__(self, k):
              self.k = k
              self.means = None
              self.labels = None
          def get_item_label(self, x):
              distances = np.zeros(self.k)
              for i in range(self.k):
                  centroid = self.means[i]
                  distances[i] = euclidean_distance(centroid, x)
              return np.argmin(distances)
          def get_cluster_labels(self, data):
              cluster_labels = [None] * data.shape[0]
              for index in range(len(data)):
                  item = data[index]
                  label = self.get_item_label(item)
                  cluster_labels[index] = label
              return np.array(cluster_labels)
          def get_initial_centroids(self, data):
              return data[np.random.choice(data.shape[0], self.k, replace=False)]
          def train(self, data):
              self.means = self.get_initial_centroids(data)
              while True:
                  new_labels = self.get_cluster_labels(data)
                  if np.array_equal(self.labels, new_labels):
                      return
                  self.labels = new_labels
                  for i in range(self.k):
                      i_points = [p for p, a in zip(data, self.labels) if a == i]
                      if i_points:
                          self.means[i] = np.mean(i_points, axis=0)
```

2.2 [10 Points] Perform your algorithm with one random initialization with

```
[157]: np.random.seed(0)
[158]: model = KMeans(5)
[159]: model.train(images)
```

2.2.1 For this question, compare your cluster membership to the true digits

```
[160]: accuracy_score(y_true=labels, y_pred=model.labels)
[160]: 0.07145796187079961
```

2.2.2 What are the most prevalent digits in each of your clusters?

```
[161]: clusters = {}
[162]: for i in range(len(model.labels)):
    label = model.labels[i]

    if label in clusters:
        clusters[label].append(labels[i])
    else:
        clusters[label] = [labels[i]]

[163]: for i in clusters:
    counts = Counter(clusters[i])
    print(f"Cluster {i+1} top 2 most common numbers: {counts.most_common(2)}")

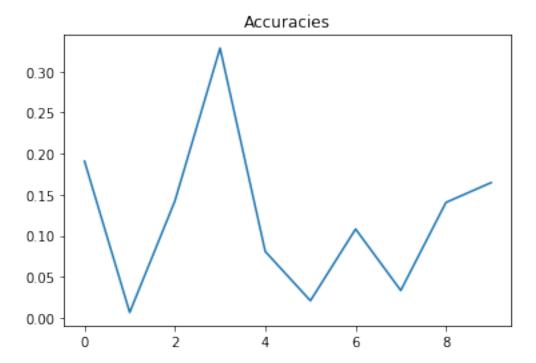
Cluster 2 top 2 most common numbers: [(6, 578), (2, 563)]
    Cluster 4 top 2 most common numbers: [(0, 881), (6, 68)]
    Cluster 5 top 2 most common numbers: [(7, 629), (9, 609)]
    Cluster 1 top 2 most common numbers: [(3, 615), (5, 383)]
    Cluster 3 top 2 most common numbers: [(1, 1003), (4, 57)]
```

2.3 [10 Points] Perform your algorithm with 10 independent initiations with k = 5 and record the best

```
[164]: accuracies = []
    pred_labels = []

[165]: for i in range(10):
        model = KMeans(5)
        model.train(images)
        pred_labels.append(model.labels)
        accuracies.append(accuracy_score(y_true=labels, y_pred=model.labels))
```

```
[166]: plt.plot(range(10), accuracies)
    plt.title('Accuracies')
    plt.show()
```

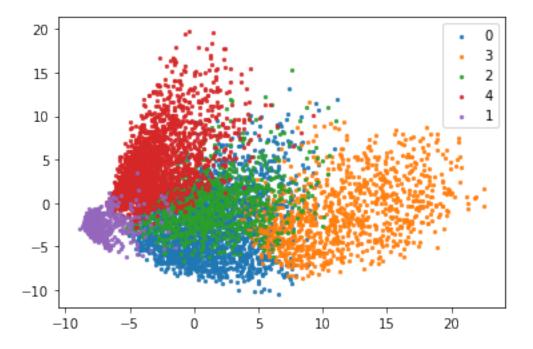


2.3.1 For this question, plot your clustering results on a two-dimensional plot, where the two axis are the first two principle components of your data

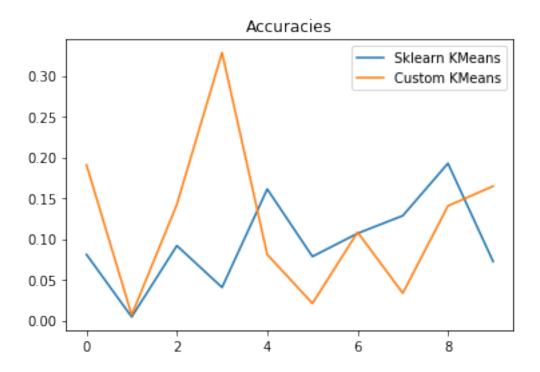
```
[167]: scaler = StandardScaler()
[168]: scaled_images = scaler.fit_transform(images)
[169]: pca = PCA(n_components=2)
    images_pca = pca.fit_transform(scaled_images)
[170]: image_clusters = {}
    best_model = pred_labels[3]
    for i in range(len(best_model)):
        label = best_model[i]

        if label in image_clusters:
            image_clusters[label].append(images_pca[i])
        else:
            image_clusters[label] = [images_pca[i]]
[171]: for i in image_clusters:
        cluster = np.array(image_clusters[i])
```

```
plt.scatter(cluster[:, 0], cluster[:, 1], alpha=.9, s=5, label=i)
plt.legend()
plt.show()
```



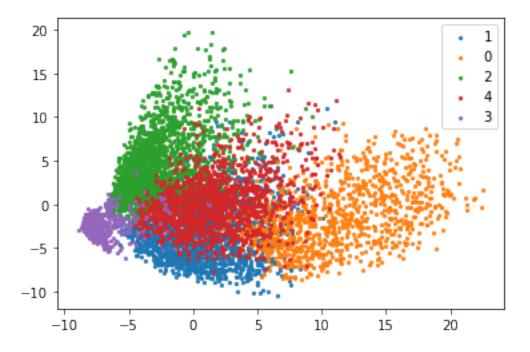
2.4 [15 Points] Compare the clustering results from the above two questions with the built-in kmeans() function in R. Use tables/figures to demonstrate your results and comment on your findings.



```
[176]: b_image_clusters = {}
best_model = b_pred_labels[7]
for i in range(len(best_model)):
    label = best_model[i]

    if label in b_image_clusters:
        b_image_clusters[label].append(images_pca[i])
else:
        b_image_clusters[label] = [images_pca[i]]

[177]: for i in b_image_clusters:
        cluster = np.array(b_image_clusters[i])
        plt.scatter(cluster[:, 0], cluster[:, 1], alpha=.9, s=5, label=i)
    plt.legend()
    plt.show()
```



It appears that my custom KMeans algorithm performs about the same as the one from Sklearn. It starts about the same, my kmeans performs better at the 3rd iteration and then the Sklearn model performs better. This is most likely do to the random centroids being selected every time. There can also be a problem of high dimensions but that's not very likely.

3 Question 2 [50 Points] Two-dimensional Gaussian Mixture Model

```
[178]: import numpy as np
      import random
      import math
[179]: faithful = pd.read_csv('./faithful.csv').drop(columns=['row']).to_numpy()
[180]: class MyGMM:
          def __init__(self, K, data, mu, sigma, likelihood_threshold=1e-3):
              self.K = K
              self.data = np.array(data)
              self.N = len(data)
              self.mu = np.array(mu)
              self.sigma = np.array(sigma)
              self.likelihood_threshold = likelihood_threshold
              self.p = np.array([0.5, 0.5])
              self.gammas = np.zeros([K, len(data)])
              self.likelihood = None
          def get_normal_prob_distribution(self, Xi, Uk, Sk, d):
```

```
first = 1 / pow((2 * math.pi), -d / 2)
       exp = pow(abs(np.linalg.det(Sk)), -1 / 2) * np.exp(
           -1 / 2 * np.dot(np.dot((Xi - Uk).T, np.linalg.inv(Sk)), (Xi - Uk))
      return first * exp
  def calculate m likelihood(self):
      new_likelihood = 0
      for i in range(self.N):
          temp = 0
           for k in range(self.K):
               temp += self.p[k] * self.get_normal_prob_distribution(
                   self.data[i].T, self.mu[k].T, self.sigma[k], self.data.
⇒shape[1]
          new_likelihood += np.log(temp)
      return new_likelihood
  def e_step(self):
       s = np.zeros(self.N)
      for i in range(self.N):
           temp_array = np.zeros(self.K)
           for c_k in range(self.K):
               temp_array[c_k] = float(
                   self.p[c_k]
               ) * self.get_normal_prob_distribution(
                   self.data[i].T, self.mu[c_k].T, self.sigma[c_k], self.data.
⇒shape[1]
               s[i] += temp_array[c_k]
           for c_k in range(self.K):
               self.gammas[c_k][i] = temp_array[c_k] / s[i]
  def m_step(self):
      for c_k in range(self.K):
           self.p[c_k] = np.sum(self.gammas[c_k]) / self.N
          total = np.zeros(self.mu.shape[1])
          for i in range(self.N):
               total += self.gammas[c_k][i] * self.data[i]
           self.mu[c_k] = total / np.sum(self.gammas[c_k])
           summ = np.zeros([self.data.shape[1], self.data.shape[1]])
           for i in range(self.N):
```

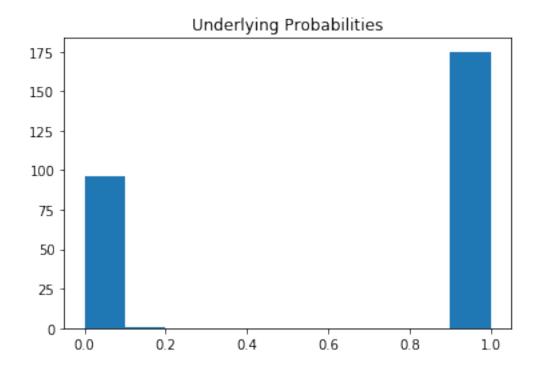
```
if self.data[i].ndim == 1:
                          data_temp = self.data[i].reshape(self.data.shape[1], 1)
                          mu_temp = self.mu[c_k].reshape(self.mu.shape[1], 1)
                          diff_temp = data_temp - mu_temp
                          summ += self.gammas[c_k][i] * np.dot(diff_temp, diff_temp.T)
                      else:
                          summ += self.gammas[c_k][i] * np.dot(
                              self.data[i] - self.mu[i], (self.data[i] - self.mu[i]).T
                          )
                  self.sigma[c_k] = summ / np.sum(self.gammas[c_k])
          def fit(self):
              start = time.time()
              new_likelihood = self.calculate_m_likelihood()
              recursion = 0
              while (recursion == 0) or (new_likelihood - self.likelihood > self.
       →likelihood_threshold):
                  self.likelihood = new_likelihood
                  self.e step()
                  self.m_step()
                  new_likelihood = self.calculate_m_likelihood()
                  recursion += 1
              end = time.time()
              print("Recursions:", recursion)
              print("Recursions time:", end - start)
[181]: Sigma1 = [[0.1, 0], [0, 10]]
      Sigma2 = [[0.1, 0], [0, 50]]
      Sigmas = np.array([Sigma1, Sigma2])
      Mu1 = [3, 80]
      Mu2 = [3.5, 60]
      Mus = np.array([Mu1, Mu2])
[182]: gmm = MyGMM(2, faithful, mu=Mus, sigma=Sigmas)
[183]: gmm.fit()
     Recursions: 17
     Recursions time: 0.6636650562286377
     3.0.1 The distribution parameters p, 1, 1, 2, and 2
```

```
[184]: print('p:', gmm.p)
p: [0.64411726 0.35588274]
```

```
[185]: print('Mu 1:', gmm.mu[0])
    Mu 1: [ 4.28968326 79.96837252]
[186]: print('Mu 2:', gmm.mu[1])
    Mu 2: [ 2.03641252 54.47875856]
[187]: print('Sigma 1:', gmm.sigma[0])
    Sigma 1: [[ 0.16994142  0.9402658 ]
    [ 0.9402658  36.04234529]]
[188]: print('Sigma 2:', gmm.sigma[1])
    Sigma 2: [[ 0.06918678  0.43536718]
    [ 0.43536718  33.69864512]]
```

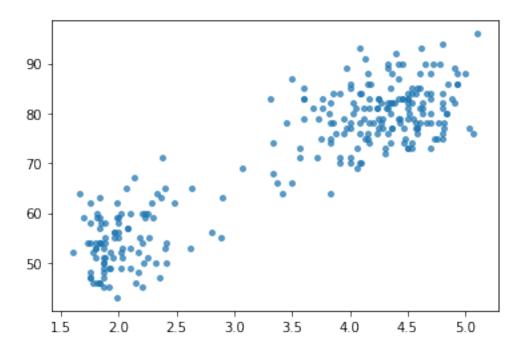
3.0.2 A histogram of the underlying probabilities of the latent variables

```
[192]: plt.hist(gmm.gammas[0])
    plt.title('Underlying Probabilities')
    plt.show()
```



3.0.3 Plot the normal densities at the 2nd, 3rd, 4th and the final iteration of your algorithm

```
[190]: plt.scatter(faithful[:,0], faithful[:,1], alpha=.7, s=15) plt.show()
```



3.1 Now, experiment a very different initial value of the parameters and rerun the algorithm. Comment on the efficiency and convergence speed of this algorithm.

```
[214]: Sigma1 = np.array([[5, 0], [5, 20]])
    Sigma2 = np.array([[1.9, 0], [4, 15]])
    Sigmas = np.array([Sigma1, Sigma2])
    Mu1 = np.array([30, 80])
    Mu2 = np.array([3.5, 60])
    Mus = np.array([Mu1, Mu2])

[215]: gmm = MyGMM(2, faithful, mu=Mus, sigma=Sigmas)

[216]: gmm.fit()
```

Recursions: 2

Recursions time: 0.1022791862487793

```
[217]: print('p:', gmm.p)
```

p: [1.05624275e-19 1.00000000e+00]

```
[218]: print('likelihood:', gmm.likelihood)
```

likelihood: -289.99162092592945

I changed the sigmas and mus to random number I though of. The recursions went down along with the time but the likelihood is definetly not good. It seems like it jump a little higher and it was the best it could find.

```
[219]: Sigma1 = [[0.2, 0], [1, 15]]
    Sigma2 = [[0.4, 0], [2, 45]]
    Sigmas = np.array([Sigma1, Sigma2])
    Mu1 = [3, 78]
    Mu2 = [2.5, 64]
    Mus = np.array([Mu1, Mu2])

[220]: gmm = MyGMM(2, faithful, mu=Mus, sigma=Sigmas)

[221]: gmm.fit()
```

Recursions: 11

Recursions time: 0.43671321868896484

```
[222]: print('p:', gmm.p)
```

p: [0.64408922 0.35591078]

```
[223]: print('likelihood:', gmm.likelihood)
```

likelihood: -130.45973615430552

This time I changed the sigmas and mus by a little bit only, some went higher and others lower. The recursions are lower compared to the original parameters along with the time. The overall likelihood and p are about the same as the one with the original values.