

哈尔滨工业大学计算机科学与技术学院

实验报告

课程名称：机器学习

课程类型：选修

实验题目：多项式拟合正弦函数

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一、实验目的

实现一个k-means算法和混合高斯模型，并且用EM算法估计模型中的参数。

二、实验要求及实验环境

实验要求：

用高斯分布产生k个高斯分布的数据（不同均值和方差）（其中参数自己设定）。

(1) 用k-means聚类，测试效果；

(2) 用混合高斯模型和你实现的EM算法估计参数，看看每次迭代后似然值变化情况，考察EM算法是否可以获得正确的结果（与你设定的结果比较）。

可以UCI上找一个简单问题数据，用你实现的GMM进行聚类。

实验环境：

Windows 10 专业教育版；python 3.7.4；jupyter notebook 6.0.1

三、设计思想（本程序中的用到的主要算法及数据结构）

1. 算法原理

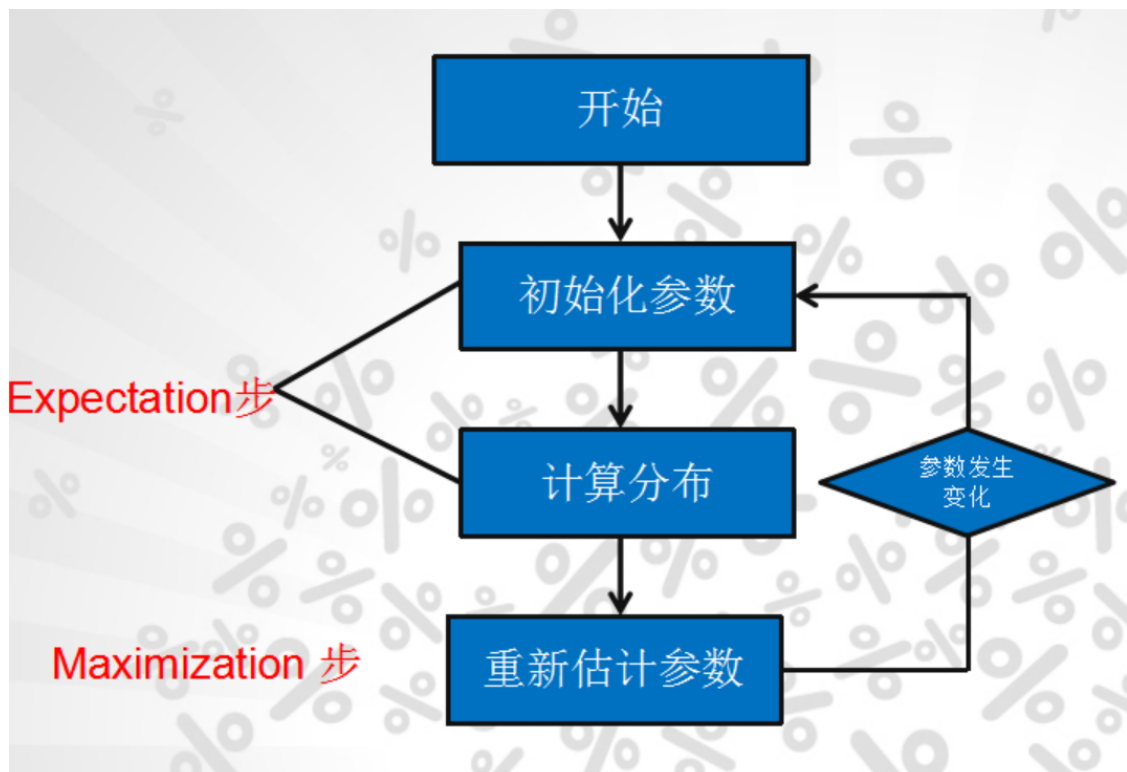
本次实验主要分两部分进行。两个算法K-means和GMM的实现本质上都是EM算法的应用。先介绍EM算法的思想：

EM算法分为两步，

E步：expectation step，求期望步

M步：maximization step，最大化似然步

可以用下图表示



E步是调整分布，M步是根据调整的分佈，求使得目标函数最大化的参数，从而更新了参数，接着参数的更新又可以调整分布，不断循环，直到参数的变化收敛，这一过程目标函数是向更优的方向趋近的，但是在某些情况下会陷入局部最优而非全局最优的问题。

1) K-means算法

K-means算法是EM算法的一个简单体现。伪码如下：

```
1  k ← 输入期望的聚类数
2  centers ← 从样本中初始化k个聚类中心（可以随机选取）
3  while true:
4      E步：遍历所有样本，根据样本到k个聚类中心的距离度量，判断该样本的标签（类别）
        labels[i]
5      M步：根据标签划分结果labels，重新计算k个聚类中心（centers）
6      if k个聚类中心的变化全部小于误差值eps:
7          break
8  return centers, labels
```

假设我们有一组样本 X ，想要把他们分为3类（这个类别数是根据实际情况选择的）。在初始化聚类中心时，一个简单的方法是随机选取 X 中的3个点，作为三个类别的样本中心，因为是随机选取的，所以不能避免初始化的三个中心点之间距离过近的情况，糟糕的初始值选取可能会导致糟糕的分类结果。

然后开始不断迭代，迭代主要分为两步，这两部分别对应着EM算法的E步和M步。其中E步是标签的划分，遍历 X 中的所有点，对任意一个点计算它到3个聚类中心的度量距离（比如欧式距），取距离最小的聚类中心所代表的那一类，作为该点的标签。E步过后，所有样本都更新了标签，然后进入M步，根据E步更新的标签，得到了每一类的样本，然后分别对这三类样本，计算均值（可以分别对每一个维度计算均值，得到均值中心）。得到的均值中心又可以在下一轮迭代中，作为标签更新的参考。

循环过程直到所有的聚类中心收敛。

2) GMM算法

GMM相对K-means是比较复杂的EM算法的应用实现。与K-means不同的是，GMM算法在E步时没有使用“最近距离法”来给每个样本赋类别（hard assignment），而是增加了隐变量 γ 。 γ 是 (N,K) 的矩阵， $\gamma[n,k]$ 表示第 n 个样本是第 k 类的概率，因此， γ 具有归一性。即 γ 的每一行的元素的和值为1。

GMM算法是用混合高斯模型来描述样本的分布，因为在多类情境中，单一高斯分布肯定无法描绘数据分布。多个高斯分布的简单叠加也无法描绘数据分布的。只有混合高斯分布才能较好的描绘一组由多个高斯模型产生的样本。对于样本中的任一个数据点，任一高斯模型能够产生该点的概率，也就是任一高斯模型对该点的生成的贡献（contribution）是不同的，但可以肯定的是，这些贡献的和值是1。

γ 的推导过程如下

$$\begin{aligned}\gamma(z_{nk}) &= p(z_{nk} = 1|x) = \frac{p(x, z_k = 1)}{p(x)} \\ &= \frac{\pi_k N(x|\mu_k, \Sigma_k)}{\sum_{j=1}^K \pi_j N(x|\mu_j, \Sigma_j)}\end{aligned}$$

其中， $\pi_k = p(z_k = 1)$ 为第 k 个高斯模型的权重， N 为概率密度函数

上式中可以看作 π 为先验概率， γ 为后验概率。

而我们的目标函数，即对数极大似然估计为：

$$\ln p(X|\pi, \mu, \Sigma) = \sum_{n=1}^N \ln \sum_{k=1}^K \pi_k N(x|\mu_k, \Sigma_k)$$

令

$$\mu, \Sigma, \pi = \operatorname{argmax}_{\mu, \Sigma, \pi} \ln p(X|\mu, \Sigma, \pi)$$

给定均值、方差和模型权重的初值，便可以从E步开始（计算 γ ），进入EM算法的迭代过程。得到 γ 后，可以对目标函数求导数（参考正态函数求导），令导数为0，得到参数更新：

$$\begin{aligned}\frac{\partial \ln p(X|\pi, \mu, \Sigma)}{\partial \mu_k} &= \sum_n \frac{\pi_k N(x_n|\mu_k, \Sigma_k)}{\sum_j \pi_j N(x_n|\mu_j, \Sigma_j)} \Sigma_k^{-1} (x_n - \mu_k) = 0 \\ \Sigma_k \gamma(z_{nk}) \Sigma_k^{-1} (x_n - \mu_k) &= 0 \\ \sum_n \gamma(z_{nk}) x_n &= \sum_n \gamma(z_{nk}) \mu_k \\ \mu_k &= \frac{1}{N_k} \sum_n \gamma(z_{nk}) x_n, N_k = \sum_n \gamma(z_{nk})\end{aligned}$$

$$\begin{aligned}\frac{\partial \ln p(X|\pi, \mu, \Sigma)}{\partial \Sigma_k} &= \sum_n \frac{1}{\sum_j \pi_j N(x|\mu_j, \Sigma_j)} (\pi_k N(x|\mu_k, \Sigma_k) (\Sigma_k^{-1} - \Sigma_k^{-1} (x_n - \mu_k)(x_n - \mu_k)^T \Sigma_k^{-1})) = 0 \\ \sum_n \gamma(z_{nk}) (\Sigma_k^{-1} - \Sigma_k^{-1} (x_n - \mu_k)(x_n - \mu_k)^T \Sigma_k^{-1}) &= 0 \\ \sum_n \gamma(z_{nk}) \Sigma_k^{-1} &= \sum_n \gamma(z_{nk}) \Sigma_k^{-1} (x_n - \mu_k)(x_n - \mu_k)^T \Sigma_k^{-1} \\ \Sigma_k &= \frac{1}{N_k} \sum_n \gamma(z_{nk}) (x_n - \mu_k)(x_n - \mu_k)^T\end{aligned}$$

至于 π_k 的更新，用 $\sum_k \pi_k = 1$ 约束求导数=0可得

$$\pi_k = \frac{N_k}{N}$$

3) 综述，K-means和GMM都是EM算法的表现。两者的区别在于E步，K-means在E步中计算参数分布时采用hard assignment的方式，即选取距离样本最近的聚类中心的类别，作为该样本的类别。而GMM在E步中计算参数分布时，是评估隐变量 $\gamma(z_{nk})$ ，即每一类样本属于每一类聚类的概率。其实K-means的E步中也是隐变量，只不过在K-means中，在 γ 矩阵中，每一行只有一个元素为1，就是离样本最近的那个类。

此外，K-means还做出了每一类模型对总的贡献相同等比较强的假设。从实际表现来看，GMM的表现更贴近实际，K-means则过于简单。

2. 算法的实现

首先配置好自己生成数据时的高斯分布参数：

```
1 config = {
2     'k':3,
3     'n':200,
4     'dim':2,
5     'mus':np.array([
6         [1,3], [7,8], [8,4]
7     ]),
8     'sigmas':np.array([
9         [[1,0],[0,2]], [[3,0],[0,2]], [[3,0],[0,1]]
10    ])
11 }
```

生成数据时：

data: shape=(k,n, dim)

data_: shape=(k*n, dim)

return data_

kmeans算法数据变量如下：

```

1 classes = np.zeros((N, dim+1)) # classes array
2 center = np.zeros((K, dim)) # center is the cluster center, it has K
  classes
3 distance = np.zeros(K) # in each iterate distance stores the distance
  between each data and the present cluster center
4 num = np.zeros(K) # num stores how many data in each class
5 new_center = np.zeros((K,dim)) # new cluster center

```

GMM算法数据变量如下:

E步中:

```

1 def e_step(data, mus, sigmas, pis, N, K, dim):
2     gammas = np.zeros((N, K))
3     for n in range(N):
4         marginal_prob = 0
5         for j in range(K):
6             marginal_prob += pis[j] * multivariate_normal.pdf(data[n],
  mean=mus[j], cov=sigmas[j])
7         for j in range(K):
8             gammas[n,j] = pis[j] * multivariate_normal.pdf(data[n],
  mean=mus[j], cov=sigmas[j]) / marginal_prob
9     return gammas

```

M步中:

```

1 def m_step(data, gammas, mus, N, K, dim):
2     mus_ = np.zeros((K, dim))
3     sigmas_ = np.zeros((K, dim, dim))
4     pis_ = np.zeros(K)
5     for k in range(K):
6         nk = 0
7         for n in range(N):
8             nk += gammas[n,k]
9         mu_temp = np.zeros(dim)
10        for n in range(N):
11            mu_temp += gammas[n,k] * data[n]
12        mus_[k] = mu_temp / nk
13
14        sigma_temp = np.zeros(dim)
15        for n in range(N):
16            dis = data[n] - mus[k] # one-dimension array can not be
  transposed
17            sigma_temp += dis**2 * gammas[n,k]
18        sigma_temp_ = np.eye(dim)
19        sigma_temp_[0,0] = sigma_temp[0]
20        sigma_temp_[1,1] = sigma_temp[1]
21        sigmas_[k] = sigma_temp_ / nk
22
23        pis_[k] = nk / N
24    return mus_, sigmas_, pis_
25

```

极大似然估计:

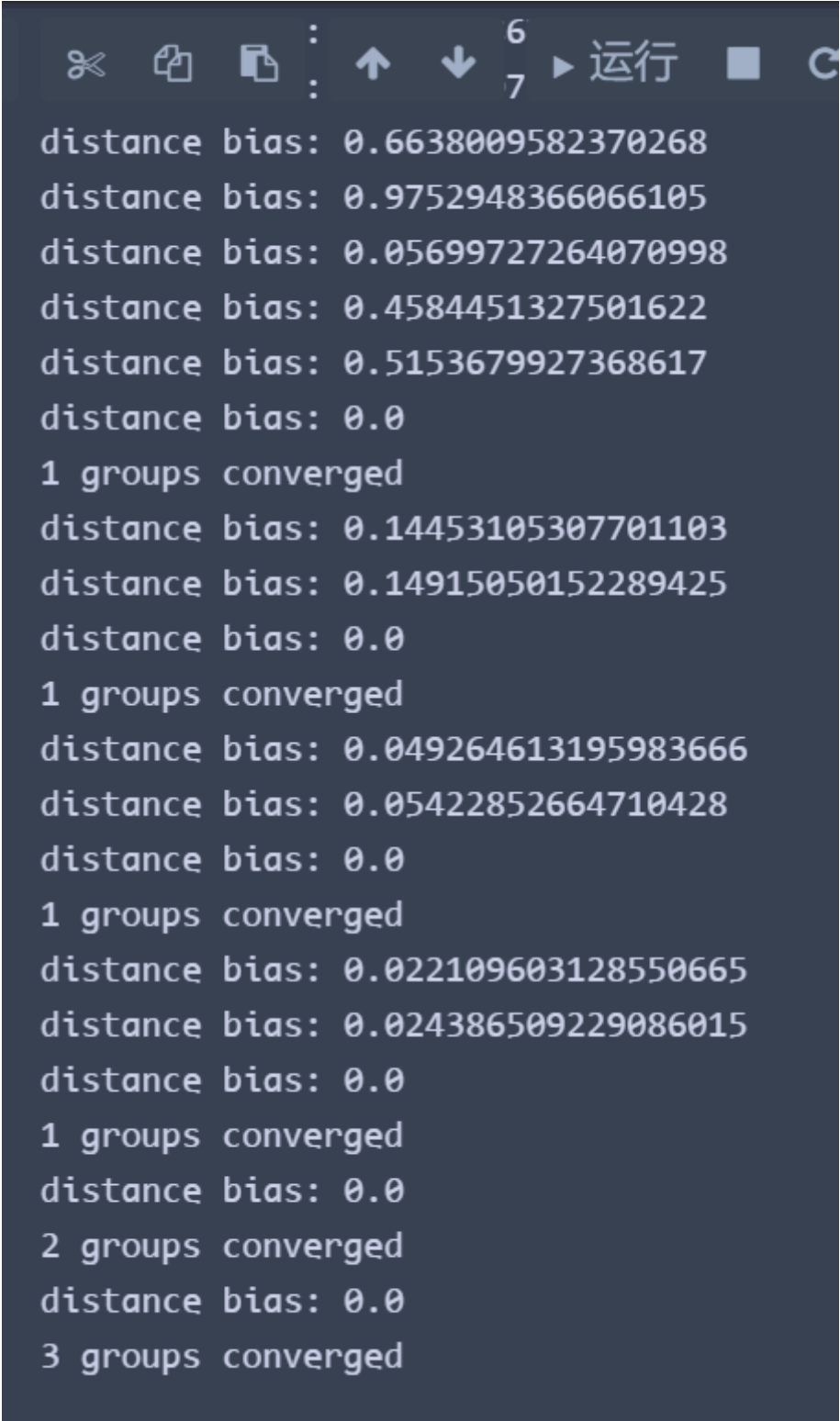
```

1 def log_likelihood(data, mus, sigmas, pis, N, K, dim):
2     l = 0
3     for n in range(N):
4         temp = 0
5         for k in range(K):
6             temp += pis[k] * multivariate_normal.pdf(data[n],
7                 mean=mus[k], cov=sigmas[k])
8         l += math.log(temp)
9     return l

```

四、实验结果与分析

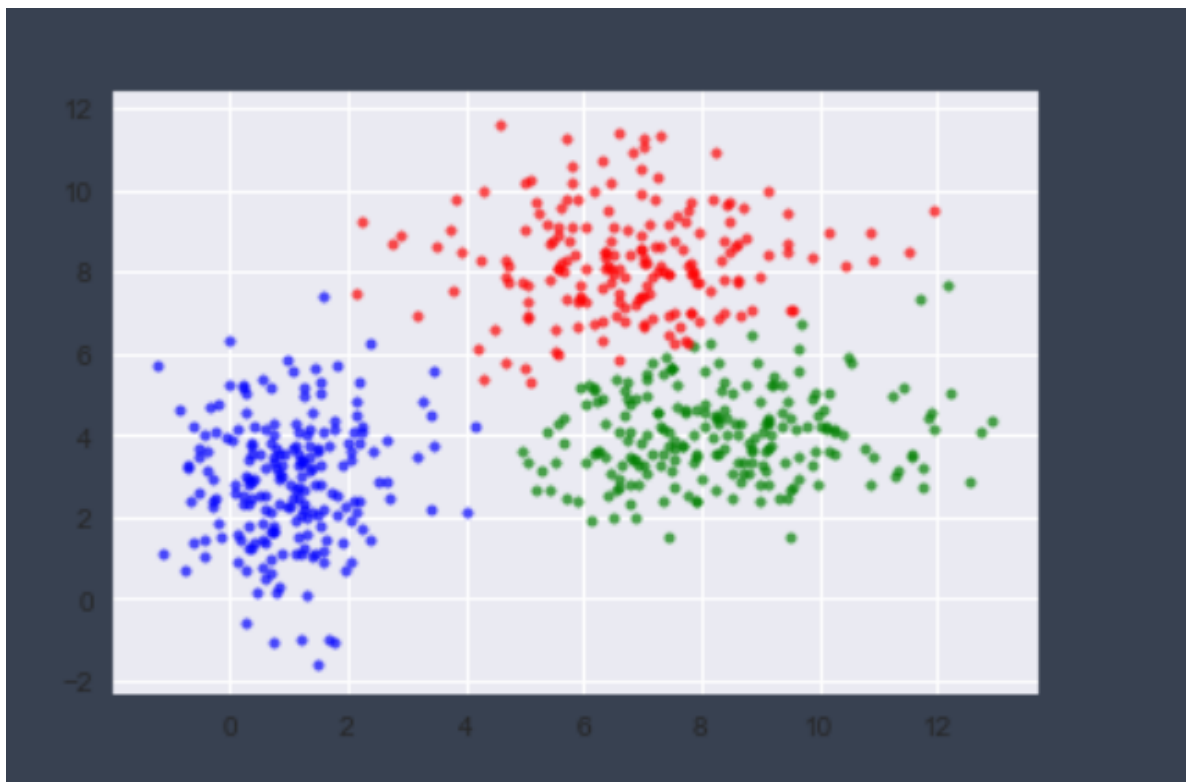
自生成数据, K-means



```

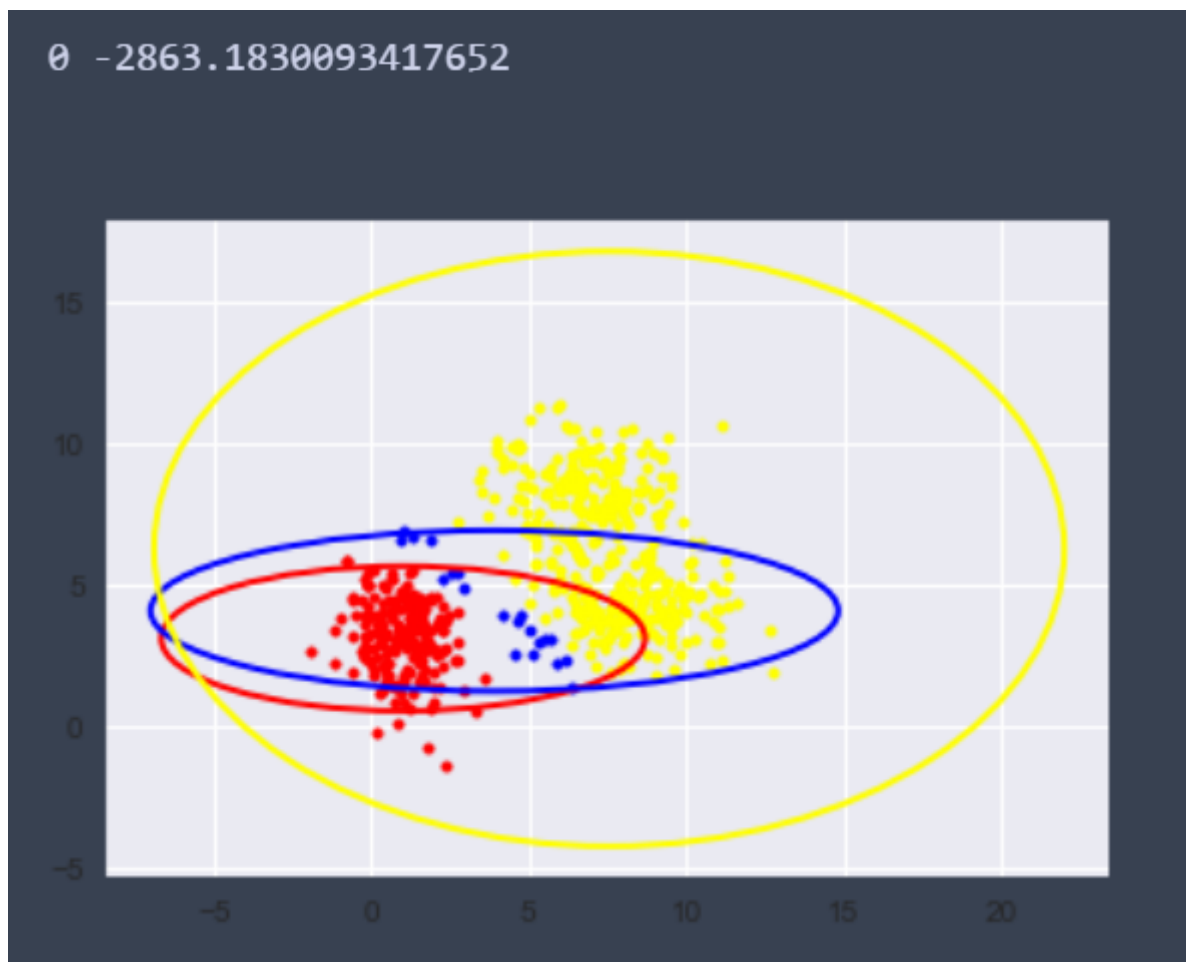
distance bias: 0.6638009582370268
distance bias: 0.9752948366066105
distance bias: 0.05699727264070998
distance bias: 0.4584451327501622
distance bias: 0.5153679927368617
distance bias: 0.0
1 groups converged
distance bias: 0.14453105307701103
distance bias: 0.14915050152289425
distance bias: 0.0
1 groups converged
distance bias: 0.049264613195983666
distance bias: 0.05422852664710428
distance bias: 0.0
1 groups converged
distance bias: 0.022109603128550665
distance bias: 0.024386509229086015
distance bias: 0.0
1 groups converged
distance bias: 0.0
2 groups converged
distance bias: 0.0
3 groups converged

```

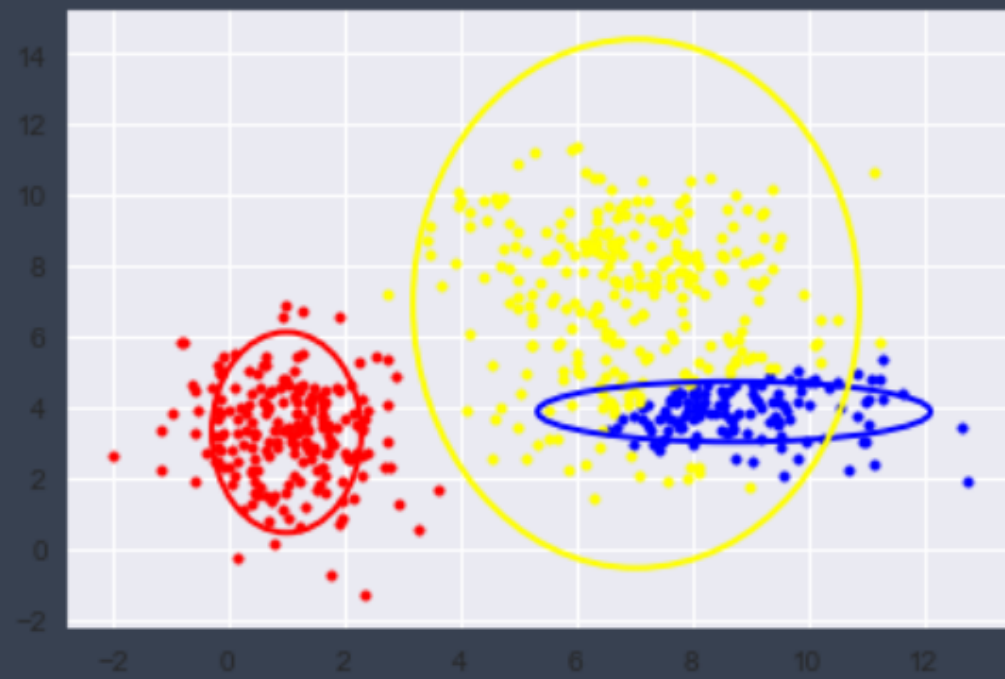


自生成数据，GMM

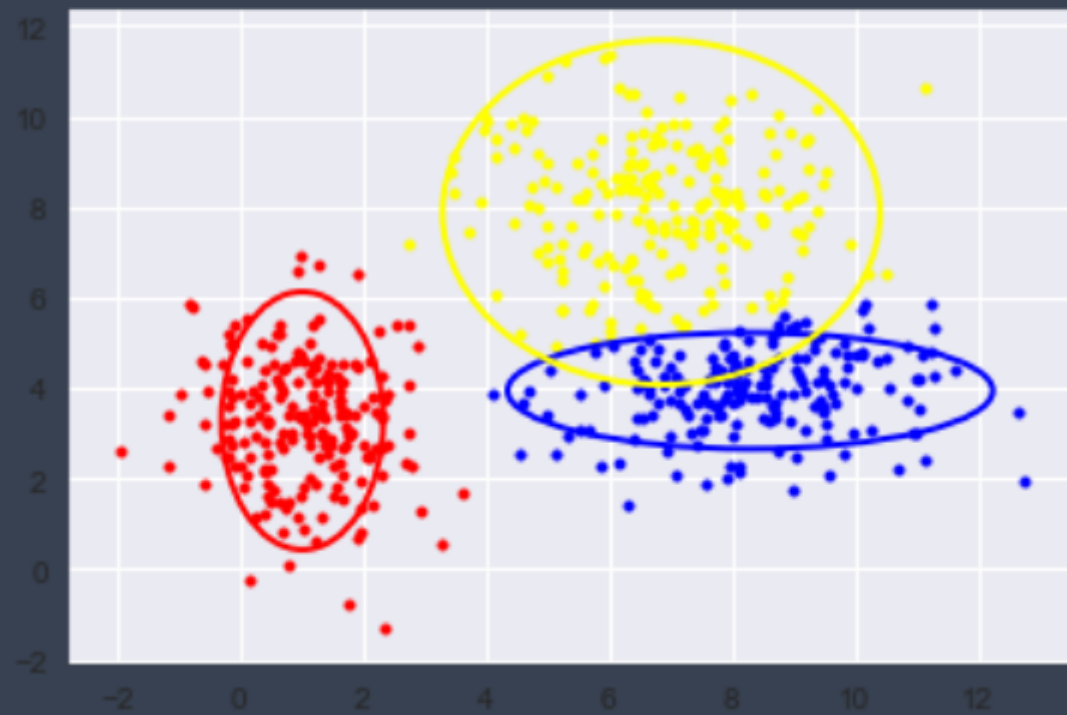
图中给出了每一阶段的样本分类情况和置信椭圆。最后带有填充的透明置信椭圆为生成数据的真实椭圆。



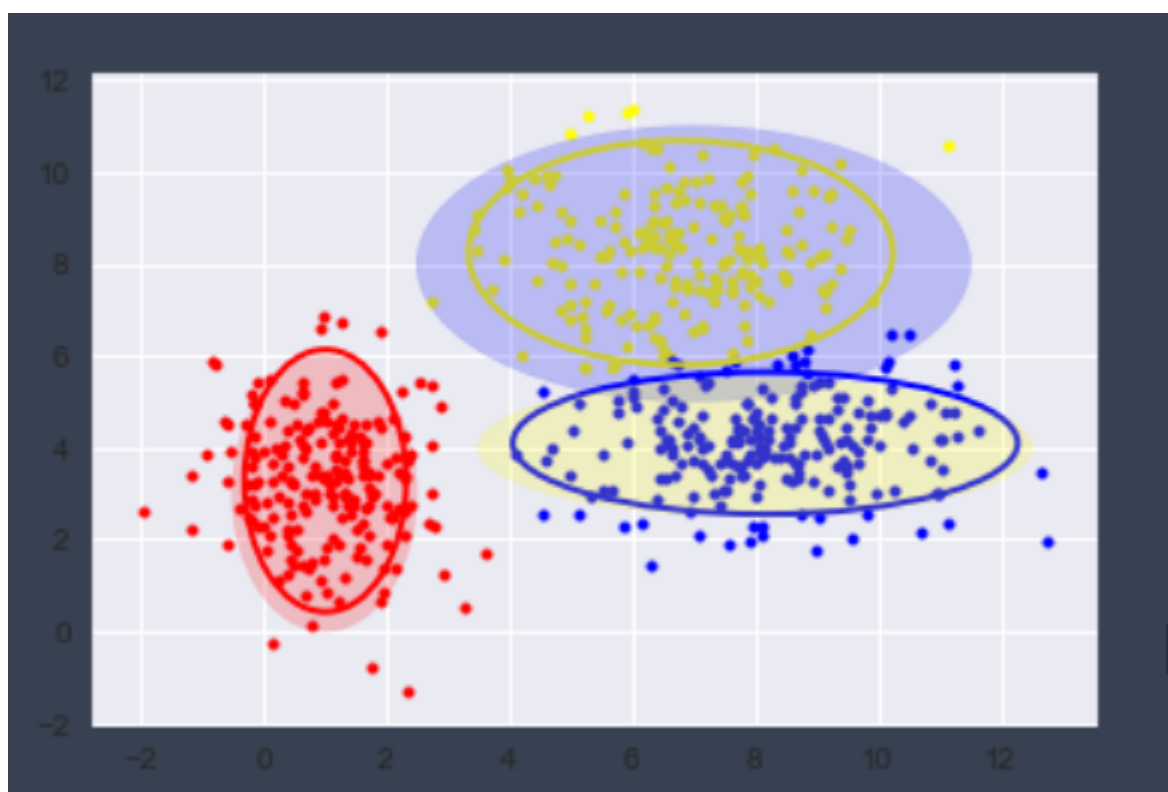
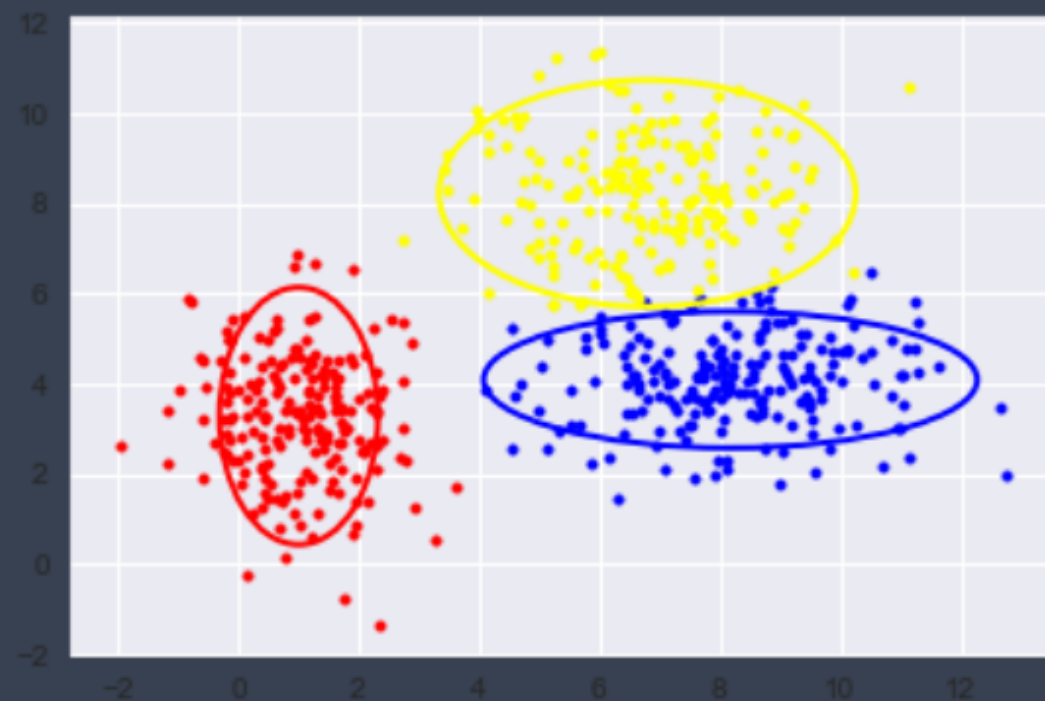
10 -2637.9494669651363



20 -2616.727708794242



30 -2611.366835733978



uci数据, K-means求初值, GMM

```
1 groups converged
distance bias: 0.0
2 groups converged
distance bias: 0.0
3 groups converged
0 -7190.317449853984
10 -9533.006152887352
20 -9147.862208694027
30 -9129.631863621678
[71. 65. 73.]
```

uci种子数据是有标签的，共210组真实数据，分为3类，每类70个样本。

分类结果（丢弃了第一个样本，故总数为209）显示，分为3类的结果中，每类个数分别为71，65和73。打印分类结果，与真实标签情况符合较好。

五、结论

1. K-means和GMM都是EM算法的体现。两者共同之处都有隐变量，遵循EM算法的E步和M步的迭代优化。不同之处在于K-means给出了很多很强的假设，比如假设了所有聚类模型对总的贡献是相等的（平均的），假设一个样本由某一个特定聚类模型产生的概率是1，其他为0。而GMM用混合高斯模型来描述聚类结果。假设多个高斯模型对总模型的贡献是有权重的，且样本属于某一类也是由概率的。两者都能较好的解决简单的分类问题，但存在着可能只取到局部最优的问题。
2. 初值的选取对K-means和GMM的效果影响较大。K-means的初值选取通常是给定聚类个数k和随机选取初始聚类中心。而对于GMM来说，如果初始高斯模型的均值和方差选取不好的话，可能会出现极大似然值为0的情况，即该样本几乎不可能由我们初始的高斯模型生成。另外在实验过程中还会出现协方差矩阵不可逆的情况。

六、参考文献

七、附录：源代码（带注释）

```
1 import numpy as np
2 import matplotlib.pyplot as plt
3 from matplotlib.patches import Ellipse
4 from scipy.stats import multivariate_normal
5 import math
6 import pandas as pd
7 plt.style.use('seaborn')
8 COLOR_LIST = ['red', 'blue', 'yellow', 'green']
9 config = {
10     'k': 3,
11     'n': 200,
12     'dim': 2,
13     'mus': np.array([
14         [1, 3], [7, 8], [8, 4]
15     ]),
16     'sigmas': np.array([
17         [[1, 0], [0, 2]], [[3, 0], [0, 2]], [[3, 0], [0, 1]]
18     ])
```

```

19 }
20 def gen_self_data(k, n, dim, mus, sigmas):
21     data = np.zeros((k, n, dim))
22     for i in range(k):
23         data[i] = np.random.multivariate_normal(mus[i], sigmas[i], n)
24     data_ = np.zeros((k * n, dim))
25     for i in range(k):
26         data_[i * n:(i + 1) * n] = data[i]
27     return data_
28
29 def gen_seeds_data(file_name):
30     df = pd.read_csv(file_name)
31     data = df.values
32     return data

```

```

1 def kmeans(data, K, N, dim):
2     classes = np.zeros((N, dim+1)) # classes array
3     classes[:,0:dim] = data[:,:]
4     # center is the cluster center, it has K classes
5     # use a random value to initialize the K centers
6     center = np.zeros((K, dim))
7     for i in range(K):
8         center[i,:] = data[np.random.randint(0, high=N),:]
9     # K-means
10    while True:
11        distance = np.zeros(K) # in each iterate distance stores the
12        # distance between each data and the present cluster center
13        num = np.zeros(K) # num stores how many data in each class
14        new_center = np.zeros((K,dim)) # new cluster center
15        # classify Expectation
16        for i in range(N):
17            for j in range(K):
18                distance[j] = np.linalg.norm(data[i,:] - center[j,:]) #
19                # calculate the Eculidean distance between data and present center
20            arg = np.argmin(distance) # the index of the min of distance
21            classes[i,dim] = arg; # tag the data with class
22
23        k = 0 # counter
24        # update the new center Maximize
25        for i in range(N):
26            if classes[i,dim] >= K:
27                print('There may be a wrong class: %d'%(K))
28            else:
29                c = int(classes[i,dim])
30                new_center[c,:] = new_center[c,:] + classes[i,:dim]
31                num[c] += 1
32        for i in range(K):
33            if num[i] != 0:
34                new_center[i,:] /= num[i]
35            distance_bias = np.linalg.norm(new_center[i,:] - center[i,:])
36            print('distance bias:', distance_bias)
37            if distance_bias < 1e-9:
38                k += 1
39                print('%d groups converged'%(k))
40        # when K classes all converge then the progress is done
41        if k == K:
42            break

```

```

41         else:
42             center = new_center # update center, next iterate
43         return classes

```

```

1  def kmeans_self():
2      data = gen_self_data(config['k'], config['n'], config['dim'],
3      config['mus'], config['sigmas'])
4      K = 3
5      N = np.size(data, axis=0)
6      dim = 2
7      classes = kmeans(data, K, N, dim)
8      # scatter
9      fig = plt.figure()
10     ax = fig.add_subplot(111)
11     for i in range(N):
12         if classes[i,dim] == 0:
13             ax.scatter(classes[i,0], classes[i,1], alpha=0.7, c='blue',
14             marker='.')
15         elif classes[i,dim] == 1:
16             ax.scatter(classes[i,0], classes[i,1], alpha=0.7, c='green',
17             marker='.')
18         elif classes[i,dim] == 2:
19             ax.scatter(classes[i,0], classes[i,1], alpha=0.7, c='red',
20             marker='.')
21         elif classes[i,dim] == 3:
22             ax.scatter(classes[i,0], classes[i,1], alpha=0.7, c='yellow',
23             marker='.')
24         elif classes[i,dim] == 4:
25             ax.scatter(classes[i,0], classes[i,1], alpha=0.7, c='magenta',
26             marker='.')
27     plt.show()

```

```

1  def e_step(data, mus, sigmas, pis, N, K, dim):
2      gammas = np.zeros((N, K))
3      for n in range(N):
4          marginal_prob = 0
5          for j in range(K):
6              marginal_prob += pis[j] * multivariate_normal.pdf(data[n],
7              mean=mus[j], cov=sigmas[j])
8          for j in range(K):
9              gammas[n,j] = pis[j] * multivariate_normal.pdf(data[n],
10              mean=mus[j], cov=sigmas[j]) / marginal_prob
11     return gammas
12
13 def m_step(data, gammas, mus, N, K, dim):
14     mus_ = np.zeros((K, dim))
15     sigmas_ = np.zeros((K, dim, dim))
16     pis_ = np.zeros(K)
17     for k in range(K):
18         nk = 0
19         for n in range(N):
20             nk += gammas[n,k]
21         mu_temp = np.zeros(dim)
22         for n in range(N):
23             mu_temp += gammas[n,k] * data[n]
24         mus_[k] = mu_temp / nk

```

```

23
24     sigma_temp = np.zeros(dim)
25     for n in range(N):
26         dis = data[n] - mus[k] # one-dimension array can not be
transposed
27         sigma_temp += dis**2 * gammas[n,k]
28         sigma_temp_ = np.eye(dim)
29         sigma_temp_[0,0] = sigma_temp[0]
30         sigma_temp_[1,1] = sigma_temp[1]
31         sigmas_[k] = sigma_temp_ / nk
32
33         pis_[k] = nk / N
34     return mus_, sigmas_, pis_

```

```

1 def log_likelihood(data, mus, sigmas, pis, N, K, dim):
2     l = 0
3     for n in range(N):
4         temp = 0
5         for k in range(K):
6             temp += pis[k] * multivariate_normal.pdf(data[n], mean=mus[k],
cov=sigmas[k])
7         l += math.log(temp)
8     return l

```

```

1 def show_gmm_result(data, mus, sigmas, classes, real_ce):
2     fig = plt.figure()
3     ax = plt.subplot()
4     K = np.size(mus, 0)
5     N = np.size(data, 0)
6     for i in range(K):
7         ellipse = Ellipse(
8             xy=mus[i], width=3*sigmas[i,0,0], height=3*sigmas[i,1,1],
edgecolor=COLOR_LIST[i], lw=2, fill=False)
9         ax.add_patch(ellipse)
10    if real_ce:
11        for i in range(K):
12            ellipse = Ellipse(
13                xy=config['mus'][i], width=3*config['sigmas'][i,0,0],
height=3*config['sigmas'][i,1,1], color=COLOR_LIST[i], alpha=0.2)
14            ax.add_patch(ellipse)
15        for i in range(N):
16            plt.scatter(data[i,0], data[i,1], marker='.',
color=COLOR_LIST[int(classes[i])])
17        # plt.scatter(data[:,0], data[:,1], marker='.',
color=COLOR_LIST[classes])
18    plt.show()

```

```

1 def gmm_self():
2     data = gen_self_data(config['k'], config['n'], config['dim'],
config['mus'], config['sigmas'])
3     # print(data)
4     N = np.size(data, axis=0)
5     K = 3
6     dim = 2
7     mus = np.array([

```

```

8         [3,3], [4,4], [5,5]
9     ])
10    sigmas = np.array([
11        [[1,0],[0,1]]
12    ] * K)
13    pis = np.array([1 / K] * K)
14    epoch = 100
15    eps = 1e-3
16
17    classes = np.zeros(N)
18    for i in range(epoch):
19        old_loss = log_likelihood(data, mus,sigmas, pis, N, K, dim)
20        gammas = e_step(data, mus, sigmas, pis, N, K, dim)
21        mus, sigmas, pis = m_step(data, gammas, mus, N, K, dim)
22        new_loss = log_likelihood(data, mus,sigmas, pis, N, K, dim)
23        if i % 10 == 0:
24            print(i, new_loss)
25            argmaxs = np.argmax(gammas, axis=1)
26            for ii in range(N):
27                classes[ii] = argmaxs[ii]
28            show_gmm_result(data, mus, sigmas, classes, False)
29            if (abs(new_loss - old_loss) < eps):
30                break
31    argmaxs = np.argmax(gammas, axis=1)
32    for ii in range(N):
33        classes[ii] = argmaxs[ii]
34    show_gmm_result(data, mus, sigmas, classes, True)

```

```

1  def uci():
2      # data = frog_gen_data('./Frogs_MFCCs.csv')
3      data = gen_seeds_data('./seeds_dataset.csv')
4      labels = data[:,-1]
5      np.delete(data, -1, axis=1)
6      N = np.size(data, axis=0)
7      dim = np.size(data, axis=1)
8      K = 3
9      classes = kmeans(data, K, N, dim)
10     mus = np.array([
11         [0] * dim
12     ] * K)
13     sigmas = np.array([
14         np.eye(dim)
15     ] * K)
16     temp = np.array([
17         [0] * dim
18     ] * K)
19     temp_counts = np.array([0] * K)
20     for i in range(N):
21         c = int(classes[i,-1])
22         temp_counts[c] += 1
23         for j in range(dim):
24             temp[c,j] += classes[i,j]
25     for i in range(K):
26         for j in range(dim):
27             mus[i,j] = temp[i,j] / temp_counts[i]
28     for i in range(K):
29         # c = int(temp_counts[i])

```

```

30         for j in range(dim):
31             for k in range(N):
32                 if classes[i,-1] == i:
33                     sigmas[i,j,j] += pow((classes[i,j] - mus[i,j]), 2)
34                     sigmas[i,j,j] /= temp_counts[i]
35     pis = np.array([1 / K] * K)
36     epoch = 100
37     eps = 1e-3
38     gmm_classes = np.zeros(N)
39     for i in range(epoch):
40         old_loss = log_likelihood(data, mus,sigmas, pis, N, K, dim)
41         gammas = e_step(data, mus, sigmas, pis, N, K, dim)
42         mus, sigmas, pis = m_step(data, gammas, mus, N, K, dim)
43         new_loss = log_likelihood(data, mus,sigmas, pis, N, K, dim)
44         if i % 10 == 0:
45             print(i, new_loss)
46             argmaxs = np.argmax(gammas, axis=1)
47             for ii in range(N):
48                 classes[ii] = argmaxs[ii]
49             if (abs(new_loss - old_loss) < eps):
50                 break
51     argmaxs = np.argmax(gammas, axis=1)
52     for ii in range(N):
53         gmm_classes[ii] = argmaxs[ii]
54     classes_count = np.zeros(K)
55     for i in range(N):
56         classes_count[int(gmm_classes[i])] += 1
57     print(classes_count)

```

```

1 kmeans_self()
2 gmm_self()
3 uci()

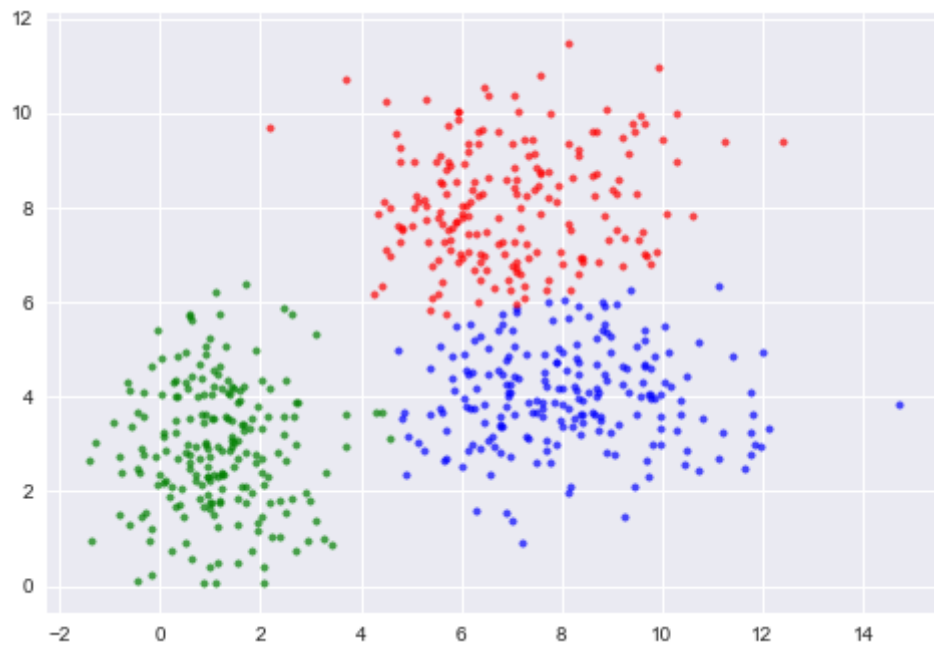
```

```

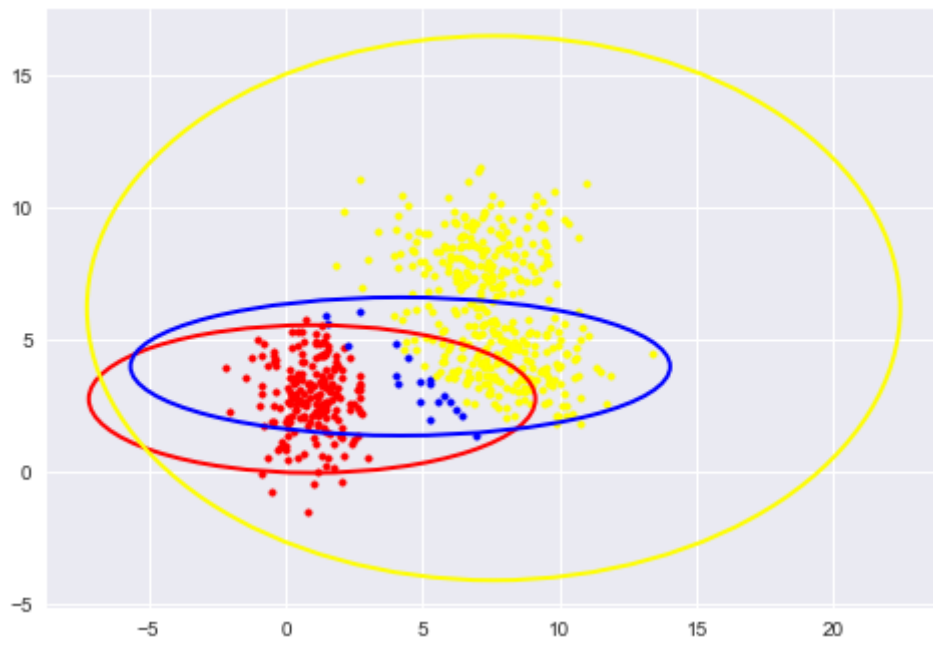
1 distance bias: 3.083324312796322
2 distance bias: 2.972872294784163
3 distance bias: 0.39381867341463334
4 distance bias: 0.9704027729129306
5 distance bias: 1.6252317891992243
6 distance bias: 0.7972332267189581
7 distance bias: 0.6401858744851695
8 distance bias: 1.9718213279065842
9 distance bias: 0.6494934395673909
10 distance bias: 0.6028800089308306
11 distance bias: 0.9922104872872277
12 distance bias: 0.28004531054930387
13 distance bias: 1.1796145340363111
14 distance bias: 0.2886885356230116
15 distance bias: 0.06191595338758368
16 distance bias: 1.1163478530637279
17 distance bias: 0.09693196578158009
18 distance bias: 0.33583719948663376
19 distance bias: 1.1101375155934743
20 distance bias: 0.06308340360750482
21 distance bias: 0.8108652292660083
22 distance bias: 0.4277347404588608
23 distance bias: 0.01617850862080447

```

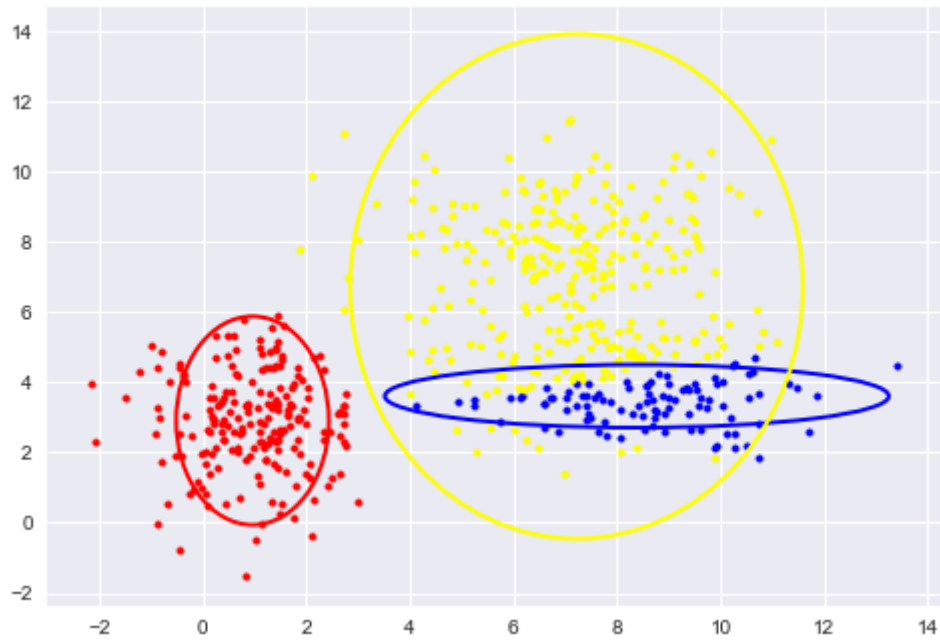
```
24 distance bias: 0.585744619426924
25 distance bias: 0.12618076253570384
26 distance bias: 0.03343857130709641
27 distance bias: 0.1324460281563676
28 distance bias: 0.06425522480472237
29 distance bias: 0.0
30 1 groups converged
31 distance bias: 0.07076655826196006
32 distance bias: 0.010418282879045436
33 distance bias: 0.0
34 1 groups converged
35 distance bias: 0.011771445508246074
36 distance bias: 0.0
37 1 groups converged
38 distance bias: 0.0
39 2 groups converged
40 distance bias: 0.0
41 3 groups converged
```



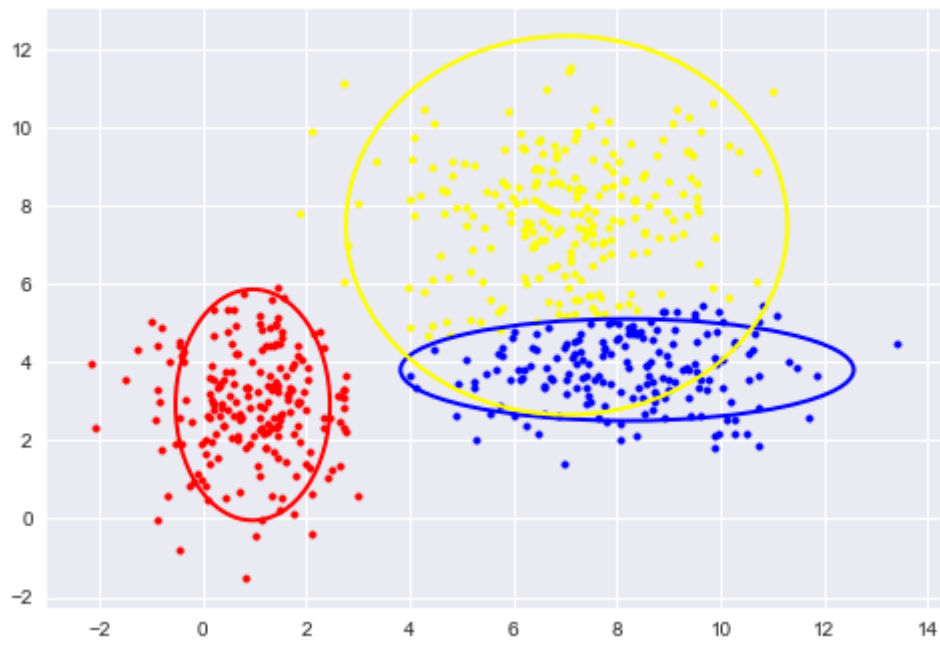
```
1 | 0 -2877.3663996465784
```

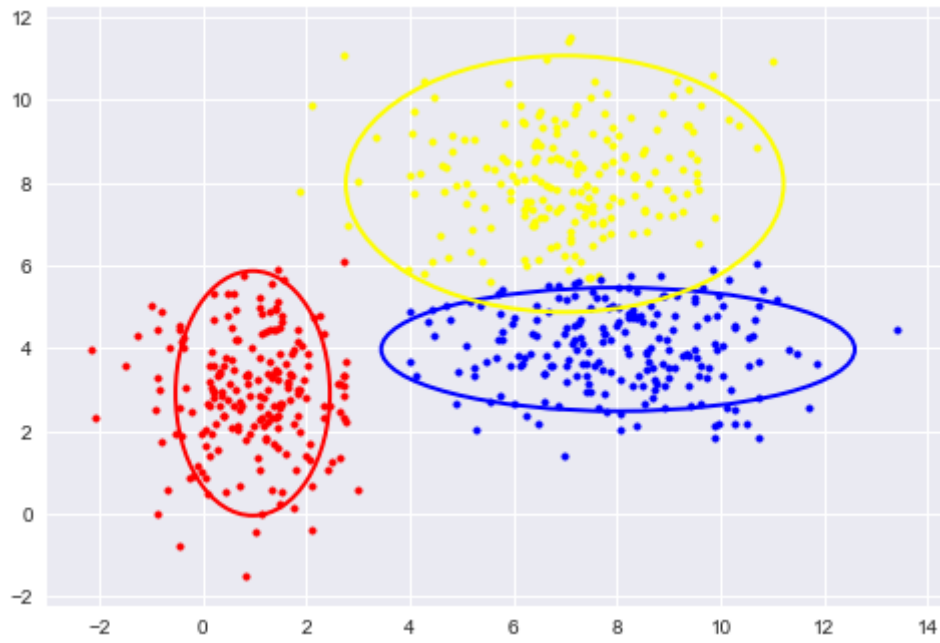
1 | 10 -2682.532886407031



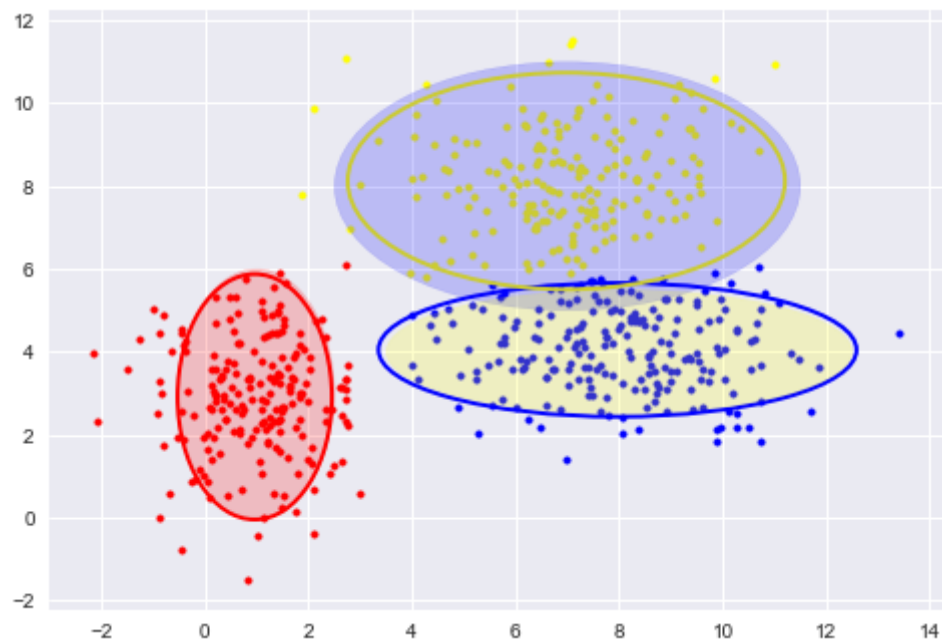
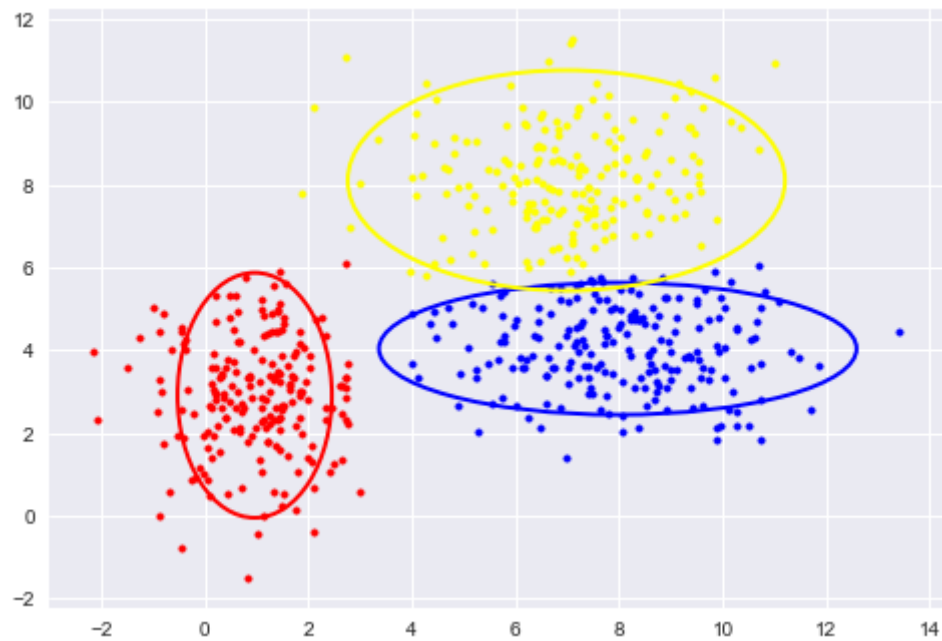
1 | 20 -2667.972207762223



1 | 30 -2661.6199175566203



1 | 40 -2660.8746225441946



```

1 distance bias: 0.8217318680446959
2 distance bias: 0.9308262798579227
3 distance bias: 1.2717002187885862
4 distance bias: 0.8480798919941978
5 distance bias: 0.1637473971976366
6 distance bias: 1.3268732183141505
7 distance bias: 0.45564950396648163
8 distance bias: 0.5566088002629445
9 distance bias: 0.6643525920283189
10 distance bias: 0.12594429368098323
11 distance bias: 0.2026175820387384
12 distance bias: 0.3086453453165971
13 distance bias: 0.07944495115512543
14 distance bias: 0.15647780583361648
15 distance bias: 0.22470875878830027
16 distance bias: 0.0
17 1 groups converged
18 distance bias: 0.06218726955475801
19 distance bias: 0.059648809672817944

```

```
20 distance bias: 0.0
21 1 groups converged
22 distance bias: 0.0
23 2 groups converged
24 distance bias: 0.0
25 3 groups converged
26 0 -7190.317449853984
27 10 -9533.006152887352
28 20 -9147.862208694027
29 30 -9129.631863621678
30 [71. 65. 73.]
```