Gaussian Mixture Models (GMM)

A GMM is a probability density distribution composed of multiple Gaussians (components). An observation \mathbf{x} is generated by the kth of K components according to some probability π_k . Hence the density of \mathbf{x} is given by:

$$f_{\mathbf{X}|\mathbf{\Theta}}(\mathbf{x}|\mathbf{\Theta}) = \sum_{k=1}^K \pi_k g_k(\mathbf{x}| heta_k)$$

where $g_k(\mathbf{x}|\theta_k)$ is a Gaussian distribution with parameters $\theta_k = (\mu, \Sigma)_k$, and all parameters are in $\Theta = ((\pi, \mu, \Sigma)_k : k \in \{1, K\})$.

Illustration

A recipe for generating a dataset:

- Observations $\mathbf{x} \in \mathbb{R}^2$.
- Most of the time we make an observation, it is generated by one multivariate Gaussian
- The rest of the time it is generated by another multivariate Gaussian
- Define π_1, π_2 in proportion to frequency
- Define parameters of each multivariate Gaussian
- Sample!

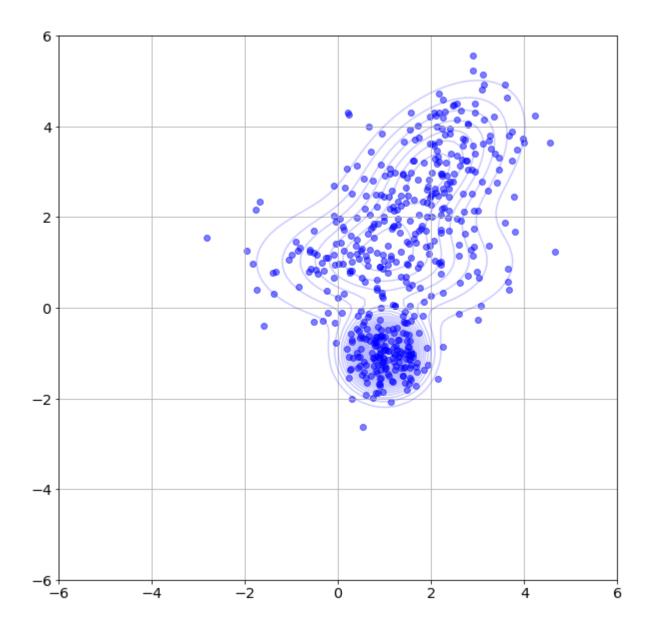
```
In [14]:
```

```
Import numpy as np
N = 580
pi = [0.33,0.33,0.34]
K = len(pi)
param_muA1 = [2,3]; param_muA2 = [1,1]; param_muA3 = [1,-1];
param_CA1 = np.array([[1,0.5],[0.5,1]]); param_CA2 = np.array([[2,0],[0,0.5]])
param_CA3 = np.array([[1,0],[0,1]])/5

from sklearn import mixture
import scipy

GMMA = mixture.GaussianMixture(K)
GMMA.fit(np.random.uniform(size=[N,2])) # this is just to instantiate the object in R2
GMMA.weights_ = pi
GMMA.weights_ = pi
GMMA.means_ = np.array([param_muA1, param_muA2.param_muA3])
GMMA.covariances_ = np.array([param_CA1, param_CA2.param_CA3])
ZA = GMMA.sample(N)
```

```
xx, yy = np.meshgrid(np.linspace(-6,6,100), np.linspace(-6,6,100))
points = np.stack((xx, yy), axis=-1)
pdfA1_true = scipy.stats.multivariate_normal.pdf(points, param_muA1,
param_CA1)
pdfA2 true = scipy stats multivariate normal pdf(points, param muA2,
param_CA2)
pdfA3_true = scipy.stats.multivariate_normal.pdf(points, param_muA3,
param_CA3)
import matplotlib.pyplot as plt
params = {'legend.fontsize': 'x-large','figure.figsize': (10, 10),
plt.rcParams.update(params)
fig = plt.figure(); ax = fig.add_subplot(111)
ax.scatter(ZA[0][:,0],ZA[0][:,1],alpha=0.5,c='blue')
ax.contour(xx, yy,
GMMA.weights [0]*pdfA1 true+GMMA.weights [1]*pdfA2 true+GMMA.weights [2]*pdfA
           levels=40, colors='blue', alpha=0.2)
plt.grid()
plt.show()
```



Illustration

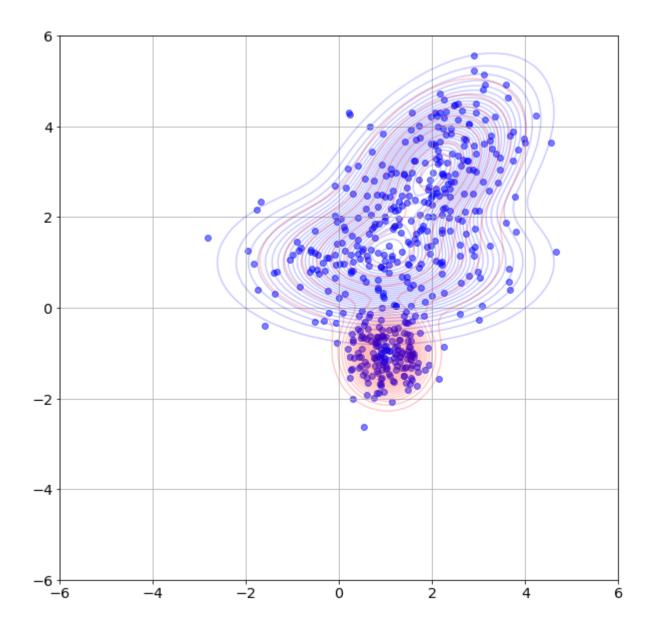
Now we want to fit a GMM to a given dataset:

- Select number of components K.
- Run expectation maximization (EM) on the dataset.
- Results are not deterministic, so run several times with random initializations.
- ullet Possibility of failure, e.g., K too large.

See sklearn.mixture

```
fig = plt.figure(); ax = fig.add subplot(111)
ax.scatter(ZA[0][:,0],ZA[0][:,1],alpha=0.5,c='blue')
xx, yy = np.meshgrid(np.linspace(-6,6,100), np.linspace(-6,6,100))
points = np.stack((xx, yy), axis=-1)
ax.contour(xx, yy, GMMA.weights_[0]*pdfA1_true+GMMA.weights_[1]*pdfA2_true,
           levels=40, colors='blue', alpha=0.2)
pdf_hat = []
for kk in range(K):
    if len(GMMA hat.covariances .shape) == 2:
        pdf_hat.append(GMMA_hat.weights_[kk]*
                       scipy.stats.multivariate normal.pdf(points,
GMMA_hat.means_[kk], GMMA_hat.covariances_[0]))
        pdf_hat.append(GMMA_hat.weights_[kk]*
                       scipy.stats.multivariate normal.pdf(points,
GMMA_hat.means_[kk], GMMA_hat.covariances_[kk]))
sumpdf_hat = np.array(pdf_hat).sum(axis=8)
ax.contour(xx, yy, sumpdf_hat,
           levels=40, colors='red', alpha=0.2)
plt.grid(); plt.show()
```

```
Initialization 0
Initialization converged: True
Initialization 1
Initialization converged: True
Initialization 2
Initialization converged: True
Initialization 3
   Iteration 10
Initialization converged: True
Initialization converged: True
Initialization 4
Initialization converged: True
Mixture weights: [0.34740544 0.3402191 0.31237547] True: [0.33, 0.33, 0.34]
```



How do we judge model fit? How do we choose K?

A GMM allows us to compute a density for each point in the dataset.

We can compute the negative log likelihood of the training set given Θ .

$$L_{\mathcal{D}}(\Theta) = -\log P[\mathcal{D}|\Theta] = -\log \prod_{n=1}^{N} f_{\mathbf{X}|\Theta}(\mathbf{x}_{n}|\Theta)$$

$$= -\sum_{n=1}^{N} \log f_{\mathbf{X}|\Theta}(\mathbf{x}_{n}|\Theta)$$
(1)

$$= -\sum_{n=1}^{N} \log f_{\mathbf{X}|\mathbf{\Theta}}(\mathbf{x}_n|\mathbf{\Theta})$$
 (2)

assuming all observations are iid.

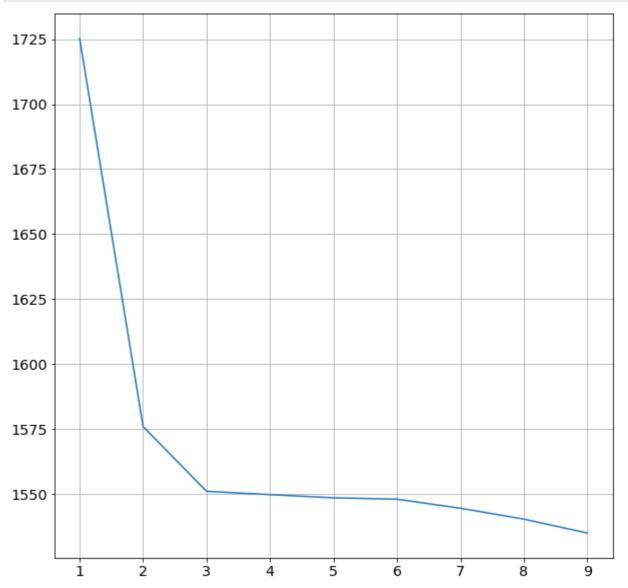
If our model is quite far from our data, we expect this value to be large.

Thus, we can compute $L_{\mathcal{D}}(\Theta)$ for several K and select the order based on this.

```
KK = range(1,10)
for kk in KK:
    GMMA_hat = mixture.GaussianMixture(kk,covariance_type='full',verbose=0,

n_init=5,init_params='kmeans',warm_start=false)
    GMMA_hat.fit(ZA[0])
    llvals.append(-np.sum(GMMA_hat.score_samples(ZA[0])))

fig = plt.figure(); ax = fig.add_subplot(111)
plt.plot(KK,llvals,label='LL')
plt.grid(); plt.draw()
```



How do we judge model fit? How do we choose K?

Another measure is the Akaike information criterion (AIC), which considers the number of model parameters M:

$$AIC(M) = 2M - 2\log\prod_{n=1}^{N}f_{\mathbf{X}|\mathbf{\Theta}}(\mathbf{x}_n|\mathbf{\Theta})$$

Yet another measure is the Bayes information criterion (BIC), which also considers the number of observations N:

$$BIC(M) = M\log(N) - 2\log\prod_{n=1}^N f_{\mathbf{X}| heta_i}(\mathbf{x}_n| heta_i)$$

```
In [7]:
        llvals = []
        aic = []
        bic = []
        KK = range(1,10)
         for kk in KK:
            GMMA_hat = mixture.GaussianMixture(kk,covariance_type='full',verbose=0,
        n_init=5,init_params='kmeans',warm_start=False)
            GMMA hat.fit(ZA[0])
            11vals.append(-np.sum(GMMA_hat.score_samples(ZA[0])))
            aic.append(GMMA_hat.aic(ZA[0]))
            bic.append(GMMA hat.bic(ZA[0]))
        fig = plt.figure(); ax = fig.add_subplot(111)
        plt.plot(KK,llvals/np.max(llvals),label='LL')
        plt.plot(KK,aic/np.max(aic),label='AIC')
        plt.plot(KK,bic/np.max(bic),label='BIC')
        plt.legend()
        plt.grid(); plt.draw()
```

