## Multivariate Gaussian mixture model

We use multivariate Gaussian mixture model to describe the expression of genes. The joint probability of gene expression value is

$$p(\mathbf{g}_1, \cdots, \mathbf{g}_D) = \sum_{k=1}^K \pi_k N(\boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)$$

where  $\{g_1, \dots, g_D\}$  are genes,  $\pi_k$  is the weight of the kth component and  $\sum_{k=1}^K \pi_k = 1$ ,  $\mu_k$  and  $\Sigma_k$  are the mean vector and the covariance matrix of the kth component respectively.

## Parameter estimation

Suppose we have a set of genes  $\{g_1, \dots, g_D\}$  in one module and there are N expression data points  $\{e_1, \dots, e_N\}$ , this data set can be represented as an  $N \times D$  matrix E. We assume the N data points are independent from the same multivariate Gaussian mixture distribution. The log-likelihood of the observed data is:

$$\ln p(\boldsymbol{E}|\boldsymbol{\pi}, \boldsymbol{\mu}, \boldsymbol{\Sigma}) = \sum_{n=1}^{N} \ln \left\{ \sum_{k=1}^{K} \pi_k N(\boldsymbol{e}_n | \boldsymbol{u}_k, \boldsymbol{\Sigma}_k) \right\}$$

The training process is to find the maximum likelihood estimate of  $(\pi, \mu, \Sigma)$ . An elegant and powerful method for handling this task is the Expectation - Maximization (EM) algorithms.

E step: Evaluate the responsibilities using the current parameter values

$$\gamma(z_{nk}) = \frac{\pi_k N(\mathbf{e}_n | \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)}{\sum_{j=1}^K \pi_j N(\mathbf{e}_n | \boldsymbol{\mu}_j, \boldsymbol{\Sigma}_j)}$$

 $\gamma(z_{nk})$  is the posterior probability that component k is responsible for generating  $e_n$ .

M step: Re-estimate the parameters using the current responsibilities

$$m{\mu}_k^{ ext{new}} = rac{1}{N_k} \sum_{n=1}^N \gamma(z_{nk}) m{e}_n$$
 $m{\Sigma}_k^{ ext{new}} = rac{1}{N_k} \sum_{n=1}^N \gamma(z_{nk}) (m{e}_n - m{\mu}_k^{ ext{new}}) (m{e}_n - m{\mu}_k^{ ext{new}})^{ ext{T}}$ 
 $m{\pi}_k^{ ext{new}} = rac{N_k}{N}$ 

where

$$N_k = \sum_{n=1}^{N} \gamma(z_{nk})$$