# 732A99/TDDE01 Machine Learning Lecture 1b Block 2: Mixture Models

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#### Contents

- Mixture Models
- Maximum Likelihood
- Expectation Maximization Algorithm
- Number of Mixture Components
- Model-Based Clustering
- K-Means Algorithm
- Summary

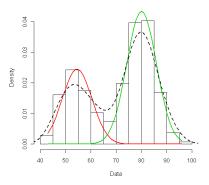
#### Literature

- Main source
  - Bishop, C. M. Pattern Recognition and Machine Learning. Springer, 2006. Sections 2.3.9, 9.1-9.3.3 and 14.5.3.
- Additional source
  - Hastie, T., Tibshirani, R. and Friedman, J. The Elements of Statistical Learning. Springer, 2009. Section 8.5.

 Sometimes the data do not follow any known probability distribution but a mixture of known distributions such as

$$p(\mathbf{x}) = \sum_{k=1}^{K} p(k)p(\mathbf{x}|k)$$

where  $p(\mathbf{x}|k)$  are called mixture components and p(k) are called mixing coefficients, which are usually denoted by  $\pi_k$  and  $0 \le \pi_k \le 1$  and  $\sum_k \pi_k = 1$ .



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- We can also see a mixture model as an ensemble model of a population with subpopulations:
  - 1. Choose a subpopulation according to  $Multinomial(k|\pi_1,\ldots,\pi_K)$ .
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$$p(\boldsymbol{x}) = \sum_{k} \pi_{k} \mathcal{N}(\boldsymbol{x} | \boldsymbol{\mu}_{k}, \boldsymbol{\Sigma}_{k}) \text{ and } \mathcal{N}(\boldsymbol{x} | \boldsymbol{\mu}_{k}, \boldsymbol{\Sigma}_{k}) = \frac{1}{2\pi^{D/2}} \frac{1}{|\boldsymbol{\Sigma}_{k}|^{1/2}} e^{-\frac{1}{2}(\boldsymbol{x} - \boldsymbol{\mu}_{k})^{T} \boldsymbol{\Sigma}_{k}^{-1}(\boldsymbol{x} - \boldsymbol{\mu}_{k})}$$

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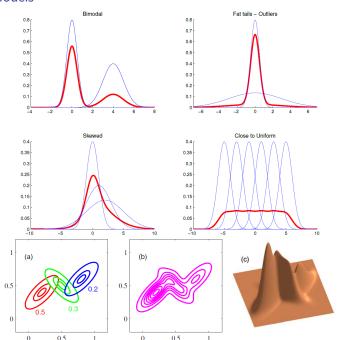


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Note that a mixture model defines a proper probability distribution:

$$0 \le p(x) \le 1$$
 and  $\int p(x)dx = 1$ 



Mixture of multivariate Bernoulli distributions:

$$p(\mathbf{x}) = \sum_{k} \pi_{k} Bernoulli(\mathbf{x}|\boldsymbol{\mu}_{k})$$

where we assume that

$$Bernoulli(\mathbf{x}|\boldsymbol{\mu}_k) = \prod_i Bernoulli(x_i|\mu_{ki}) = \prod_i \mu_{ki}^{x_i} (1 - \mu_{ki})^{(1 - x_i)}$$

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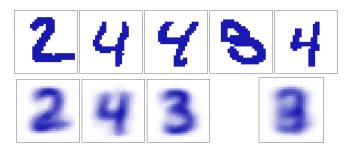


Figure 9.10 Illustration of the Bernoulli mixture model in which the top row shows examples from the digits data set after converting the pixel values from grey scale to binary using a threshold of 0.5. On the bottom row the first three images show the parameters  $\mu_{kl}$  for each of the three components in the mixture model. As a comparison, we also fit the same data set using a single multivariate Bernoulli distribution, again using maximum likelihood. This amounts to simply averaging the counts in each pixel and is shown by the right-most image on the bottom row.

• Given a sample  $\{x_n, k_n\}$  of size N from a mixture of multivariate Bernoulli distributions, rewrite it as  $\{x_n, z_n\}$  where  $z_n$  is a K-dimensional binary vector having only the  $k_n$ -th element equal to 1.

<sup>&</sup>lt;sup>1</sup>Any stationary point of the Lagrangian function is a stationary point of the original function subject to the constraints. Unfortunately, the log likelihood function is typically not concave.

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Let  $x'_{ni} = 1 - x_{ni}$  and  $\mu'_{ki} = 1 - \mu_{ki}$ . To maximize the log likelihood function subject to the constraints  $\sum_k \pi_k = 1$  and  $\mu_{ki} + \mu'_{ki} = 1$ , we maximize

$$\sum_{n} \sum_{k} z_{nk} \left[ \log \pi_{k} + \sum_{i} \left[ x_{ni} \log \mu_{ki} + x'_{ni} \log \mu'_{ki} \right] \right] + \lambda \left( \sum_{k} \pi_{k} - 1 \right) + \sum_{k} \sum_{i} \lambda_{ki} \left( \mu_{ki} + \mu'_{ki} - 1 \right)$$

where  $\lambda$  and  $\lambda_{ki}$  are called Lagrange multipliers.<sup>1</sup>

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• Setting to zero the derivatives with respect to  $\pi_k$ ,  $\mu_{ki}$  and  $\mu'_{ki}$  gives

$$\pi_k = -\sum_n z_{nk}/\lambda$$
 and  $\mu_{ki} = -\sum_n z_{nk} x_{ni}/\lambda_{ki}$  and  $\mu'_{ki} = -\sum_n z_{nk} x'_{ni}/\lambda_{ki}$ 

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• Replacing this into the constraint gives  $\lambda = -N$  and  $\lambda_{ki} = -\sum_n z_{nk}$  and, thus,

$$\pi_k^{ML} = \frac{\sum_n z_{nk}}{N}$$
 and  $\mu_{ki}^{ML} = \frac{\sum_n z_{nk} x_{ni}}{\sum_n z_{nk}}$ 

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$$\mathbb{E}_{Z}[\log p(\{\boldsymbol{x}_{n},\boldsymbol{z}_{n}\}|\boldsymbol{\mu},\boldsymbol{\pi})] = \sum_{n} \sum_{\boldsymbol{z}_{n}} p(\boldsymbol{z}_{n}|\boldsymbol{x}_{n},\boldsymbol{\mu},\boldsymbol{\pi}) \log p(\boldsymbol{x}_{n},\boldsymbol{z}_{n}|\boldsymbol{\mu},\boldsymbol{\pi})$$

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Following a reasoning analogous to the complete-data case, we obtain that

$$\pi_k^{ML} = \frac{\sum_n p(z_{nk}|\mathbf{x}_n, \boldsymbol{\mu}, \boldsymbol{\pi})}{N}$$

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This is not a closed form solution because

$$p(z_{nk}|\mathbf{x}_n,\boldsymbol{\mu},\boldsymbol{\pi}) = \frac{p(z_{nk},\mathbf{x}_n|\boldsymbol{\mu},\boldsymbol{\pi})}{\sum_k p(z_{nk},\mathbf{x}_n|\boldsymbol{\mu},\boldsymbol{\pi})} = \frac{\pi_k p(\mathbf{x}_n|\boldsymbol{\mu}_k)}{\sum_k \pi_k p(\mathbf{x}_n|\boldsymbol{\mu}_k)}$$

but it suggests the following algorithm.

### EM algorithm

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Set \pi and \mu to some initial values Repeat until \pi and \mu do not change Compute p(z_{nk}|\mathbf{x}_n, \mu, \pi) for all k and n /* E step */ Set \pi_k to \pi_k^{ML}, and \mu_{ki} to \mu_{ki}^{ML} for all k and i /* M step */
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- ▶ The EM algorithm can also be obtained by maximizing  $\log p(\{x_n\}|\mu,\pi)$ .
- The EM algorithm is guaranteed to increase  $\log p(\{x_n\}|\mu,\pi)$  in each iteration until a local maximum is reached. So, the algorithm aims for the ML estimates.

 We can derive the EM algorithm for mixtures of multivariate Gaussian distributions in much the same way. Simply,

$$\pi_k^{ML} = \frac{\sum_n p(z_{nk}|\mathbf{x}_n, \boldsymbol{\mu}, \boldsymbol{\pi})}{N}$$

$$\mu_k^{ML} = \frac{\sum_n \mathbf{x}_n p(z_{nk}|\mathbf{x}_n, \boldsymbol{\mu}, \boldsymbol{\pi})}{\sum_n p(z_{nk}|\mathbf{x}_n, \boldsymbol{\mu}, \boldsymbol{\pi})}$$

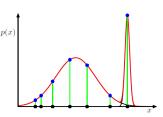
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Unlike in the case of mixture of multivariate Bernoulli distributions, there
can be singularities, i.e. the log likelihood function goes to infinity when a
component of the mixture collapses onto a single data point.

Figure 9.7 Illustration of how singularities in the likelihood function arise with mixtures of Gaussians. This should be compared with the case of a single Gaussian shown in Figure 1.14 for which no singularities arise.

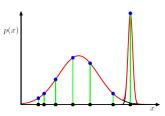


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 Solution: Reset the mean and covariance of the component to random and large values, respectively. Or adopt a Bayesian approach.

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- We can perform a search over the number of components by scoring each number with, for instance, the Bayesian information criterion (BIC):

$$\log p(\{\boldsymbol{x}_n\}|\boldsymbol{\mu}^{ML},\boldsymbol{\pi}^{ML}) - \frac{M}{2}\log N$$

where M is the number of free parameters in the mixture model. Note that the EM algorithm has to be run for each candidate number.

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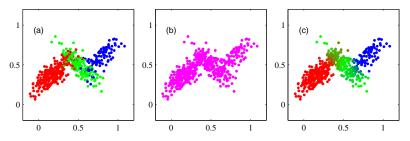
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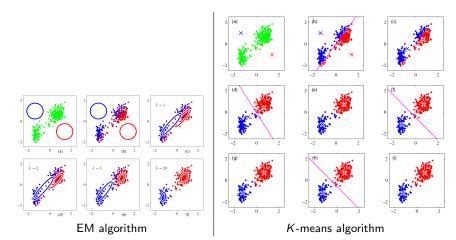
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(a) Sample with cluster labels, (b) initial clustering, and (c) final clustering.

- Assign each point to a cluster (a.k.a subpopulation) at random
- 2 Compute the cluster centroids as the averages of the points assigned to each cluster
- 3 Repeat until the centroids do not change
- 4 Assign each point to the cluster with the closest centroid
- Update the cluster centroids as the averages of the points assigned to each cluster



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- ▶ The K-means algorithm can be used to initialize the EM algorithm.

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- The EM algorithm can be used to estimate the ML parameters from data with any pattern of missing (at random) entries, i.e. not only one latent variable.