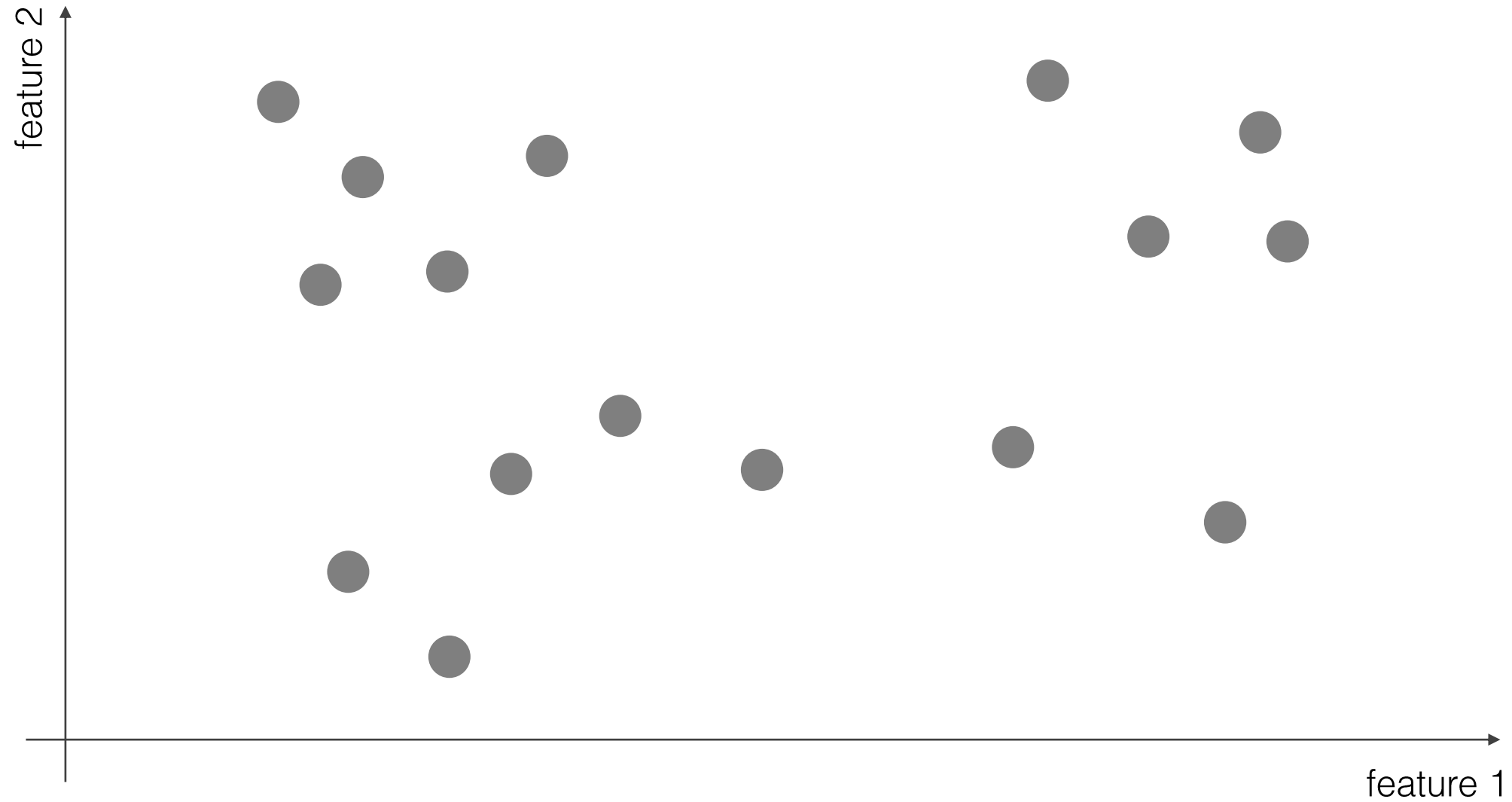


# Clustering I

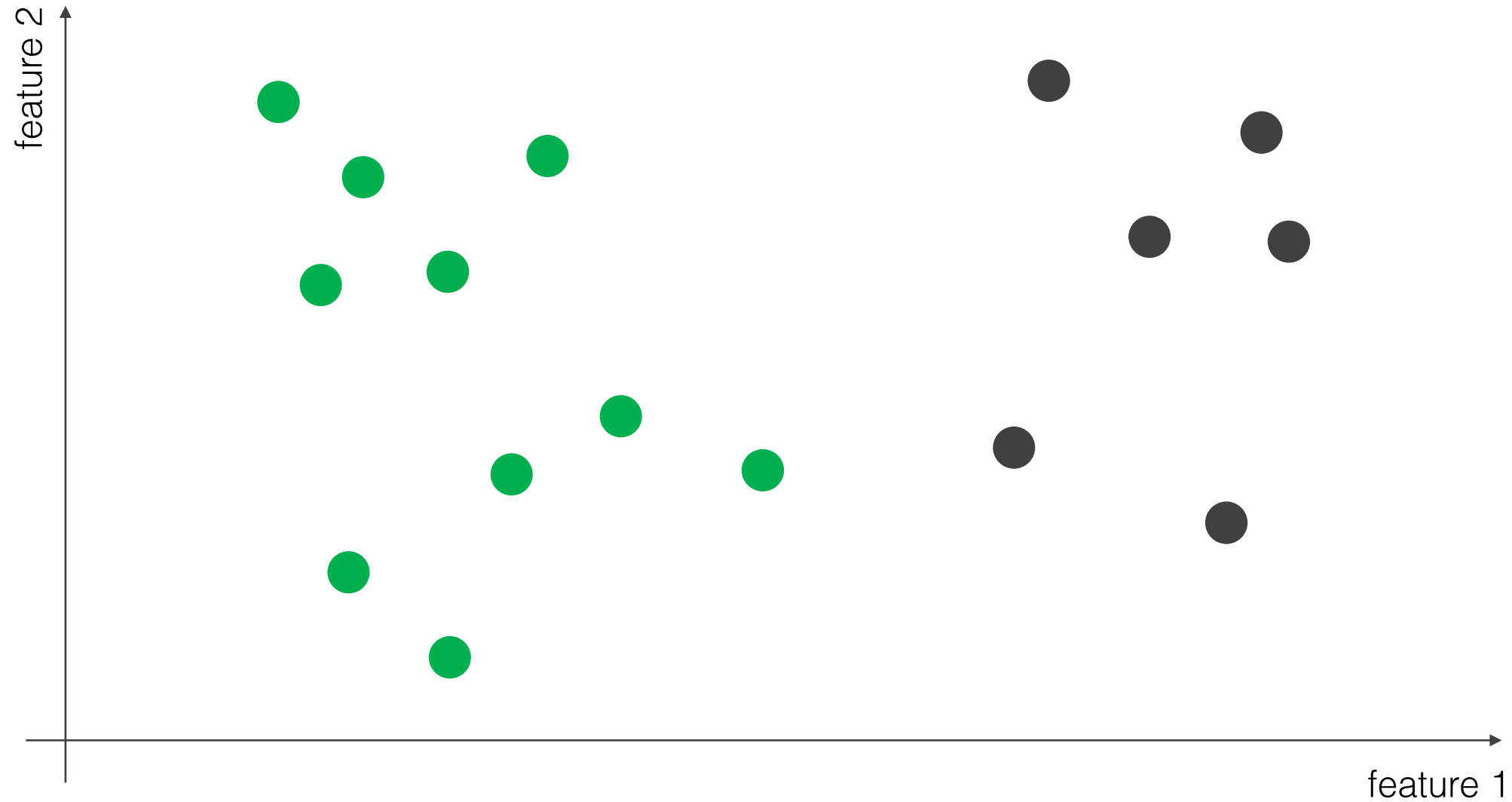
## Lecture 14

# Clustering



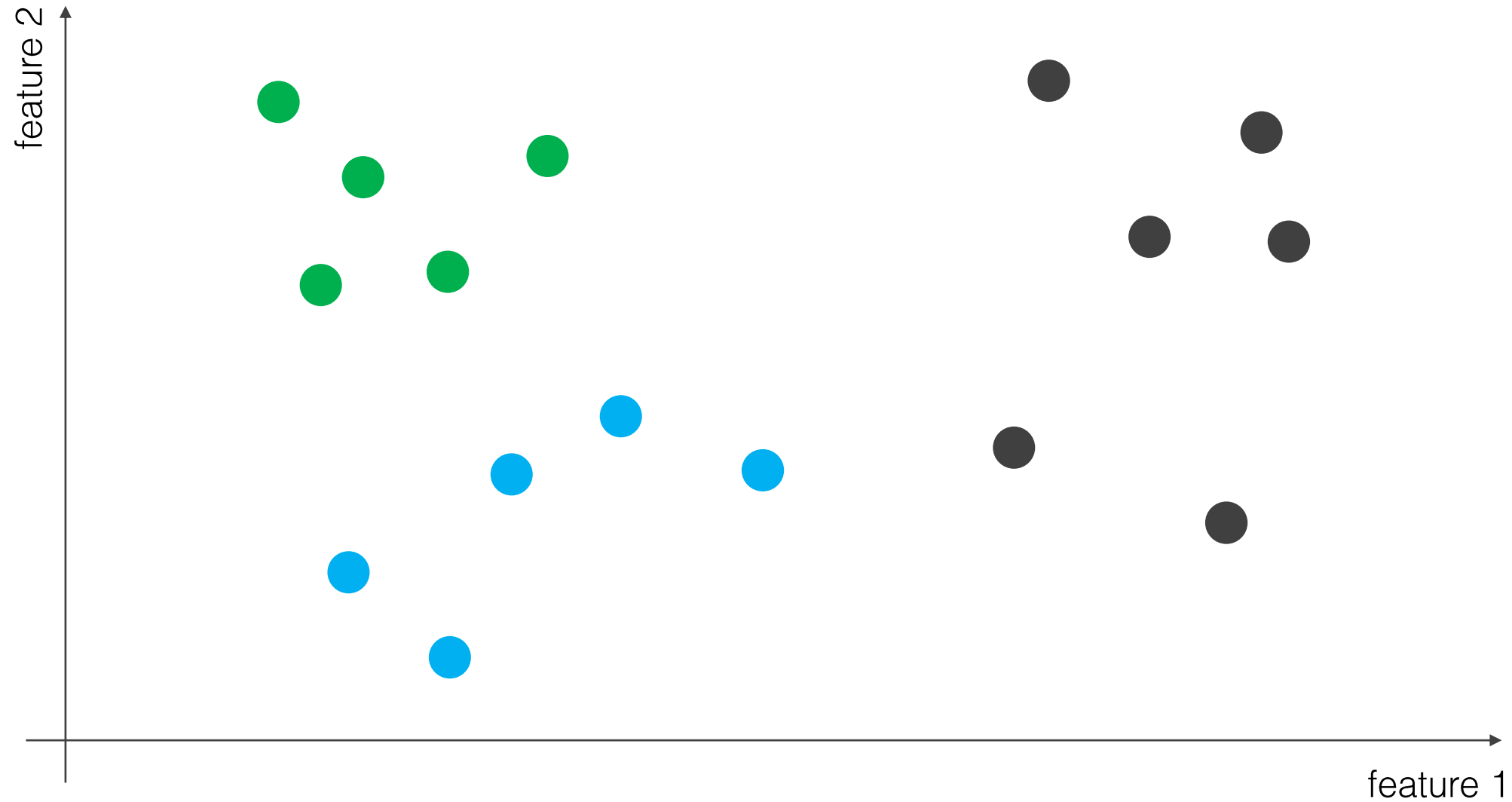
# Clustering

Looks like 2 clusters...



# Clustering

... or maybe 3?



# Applications

Differentiating tissue types in PET scans

Customer segmentation for market research

Social network analysis and identifying communities

Crime tracking to identify hot spots for certain types of crimes

# Types of clustering algorithms

## Methods

Centroid-based clustering (e.g. K-Means)

Distribution-based clustering (e.g. Gaussian mixture model)

Density-based clustering (e.g. DBSCAN)

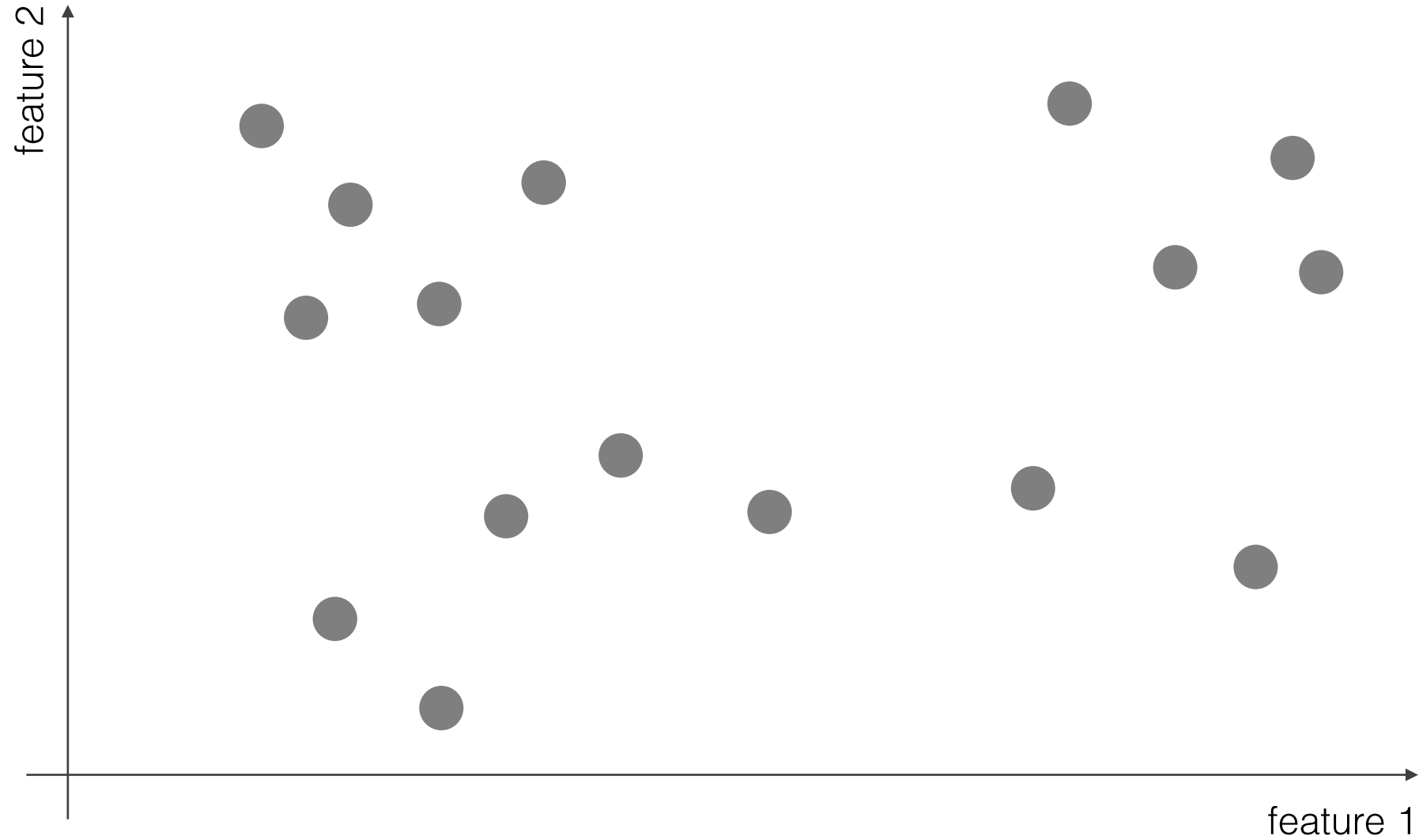
Hierarchical clustering (e.g. agglomerative clustering)  
a.k.a. connectivity-based clustering

## Cluster assignment

Hard clustering

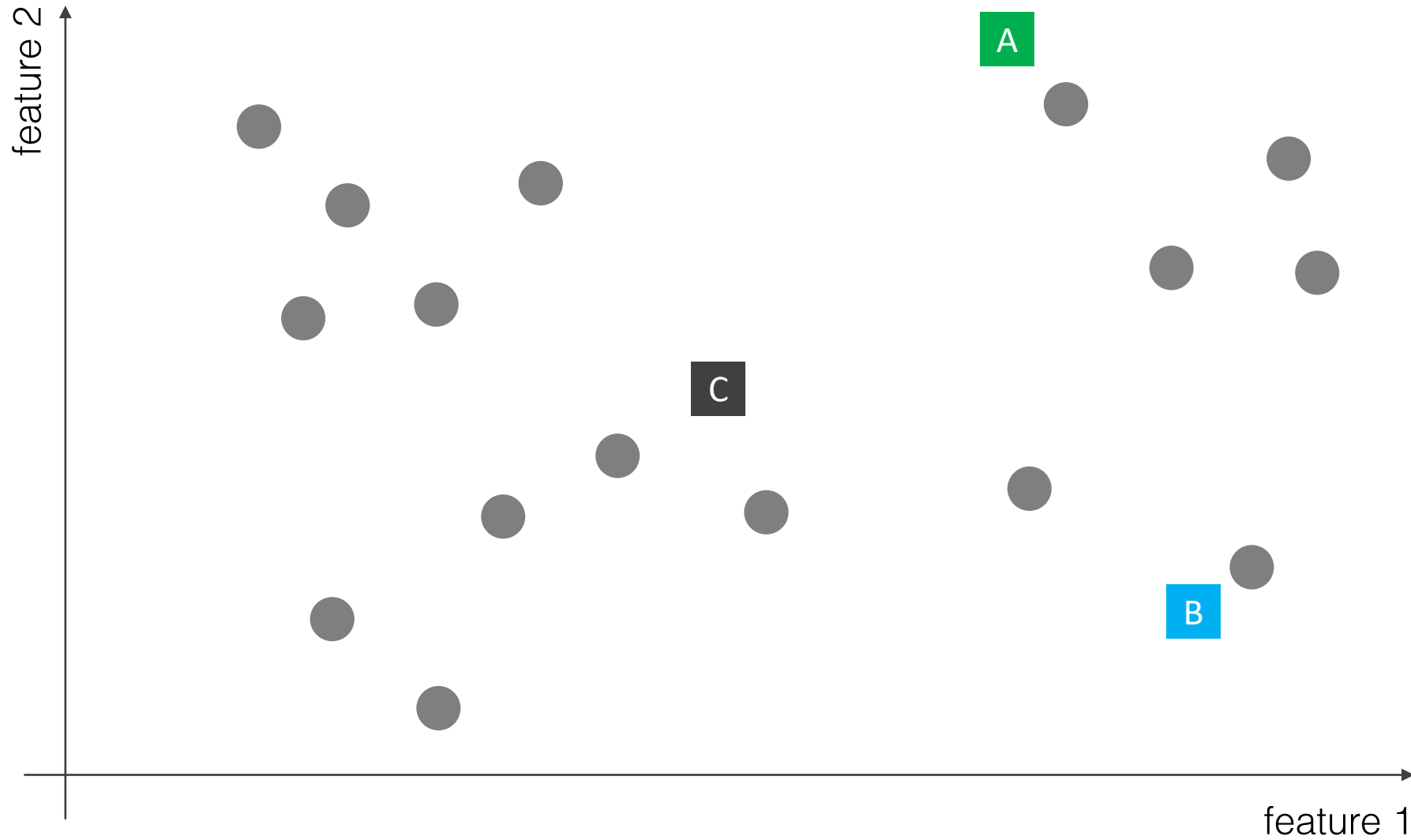
Soft clustering (a.k.a. fuzzy clustering)

# K-means clustering



# K-means clustering

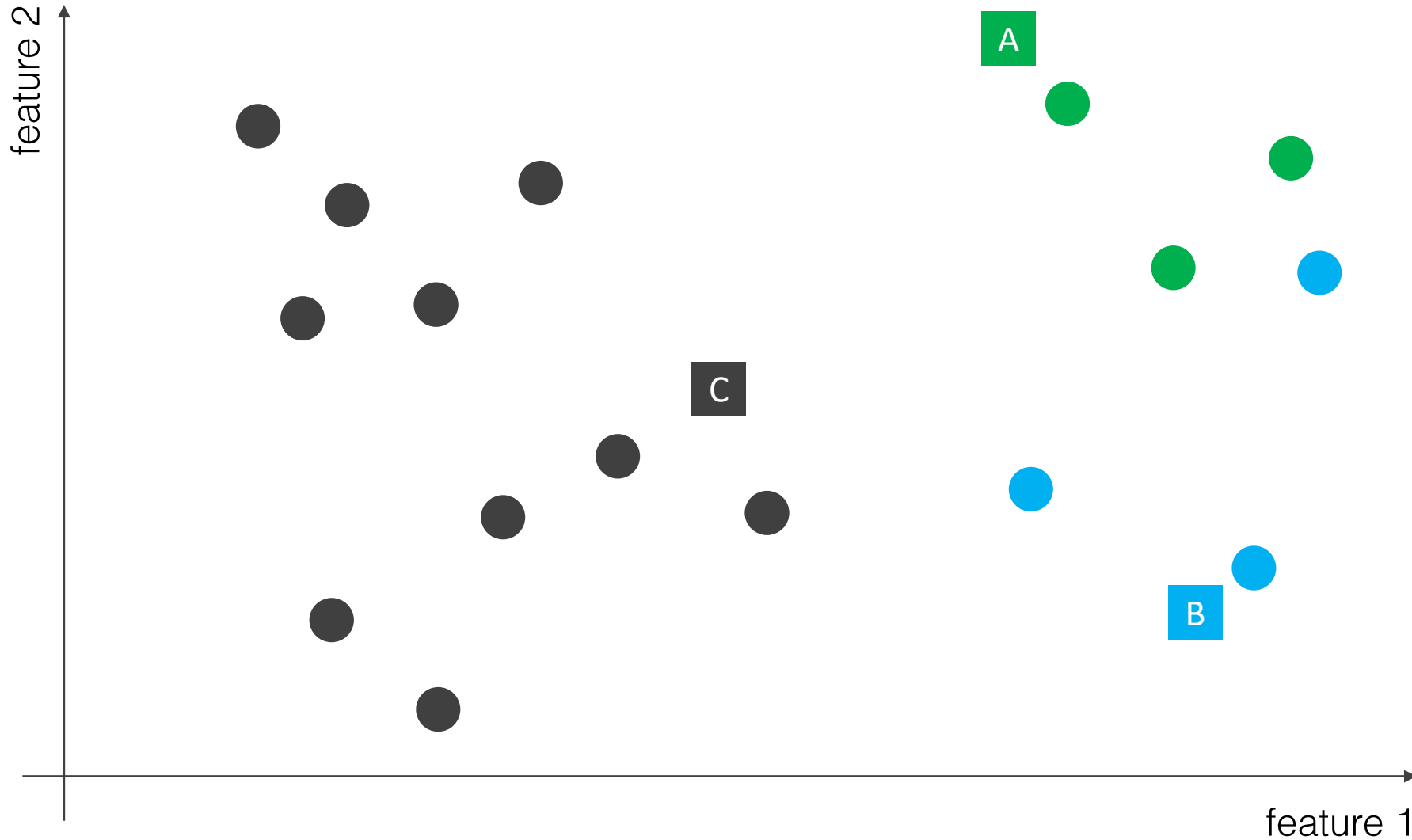
- 1 Select k and randomly initialize k mean values



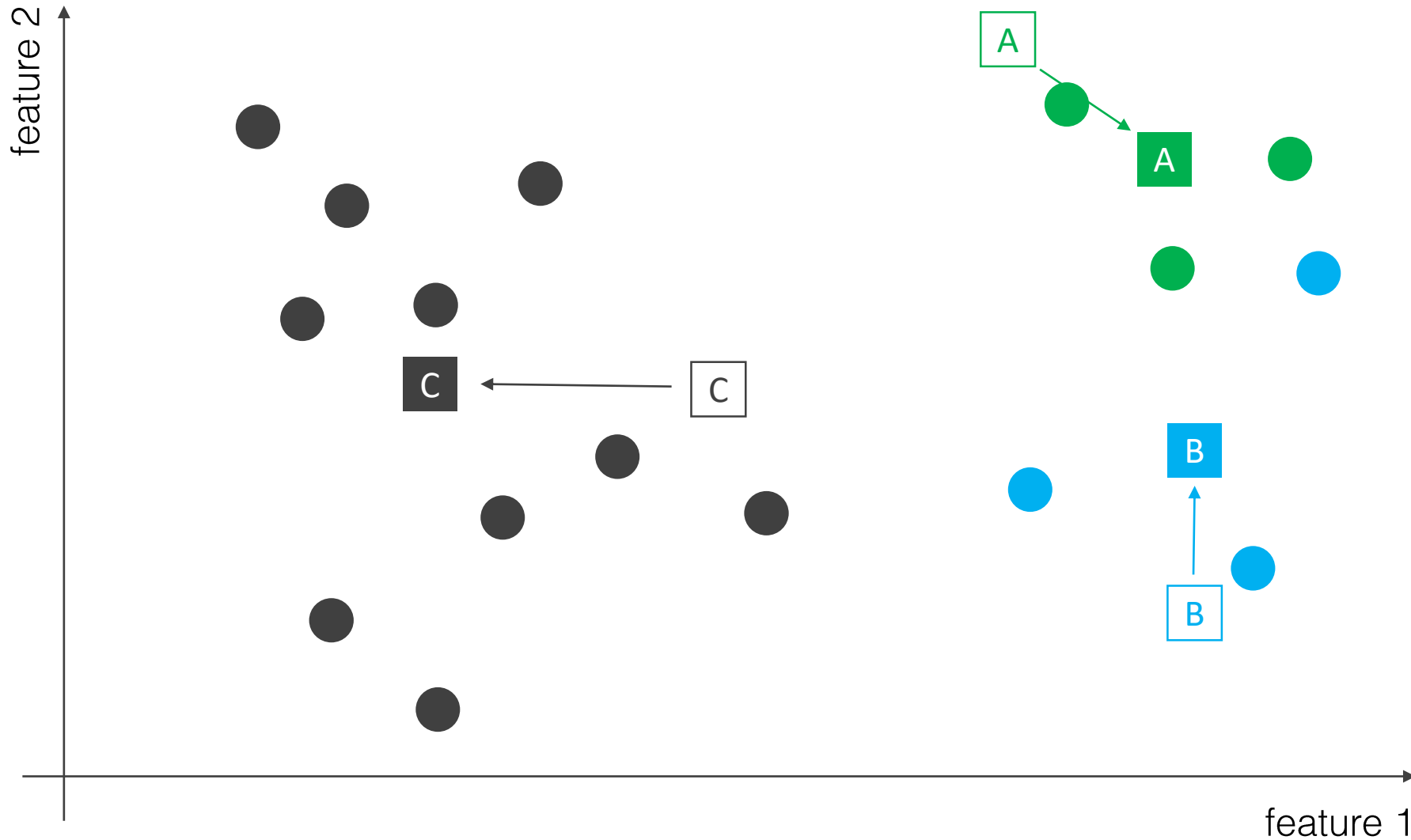


# K-means clustering

- 1 Select  $k$  and randomly initialize  $k$  mean values
- 2 Assign observations to the nearest mean

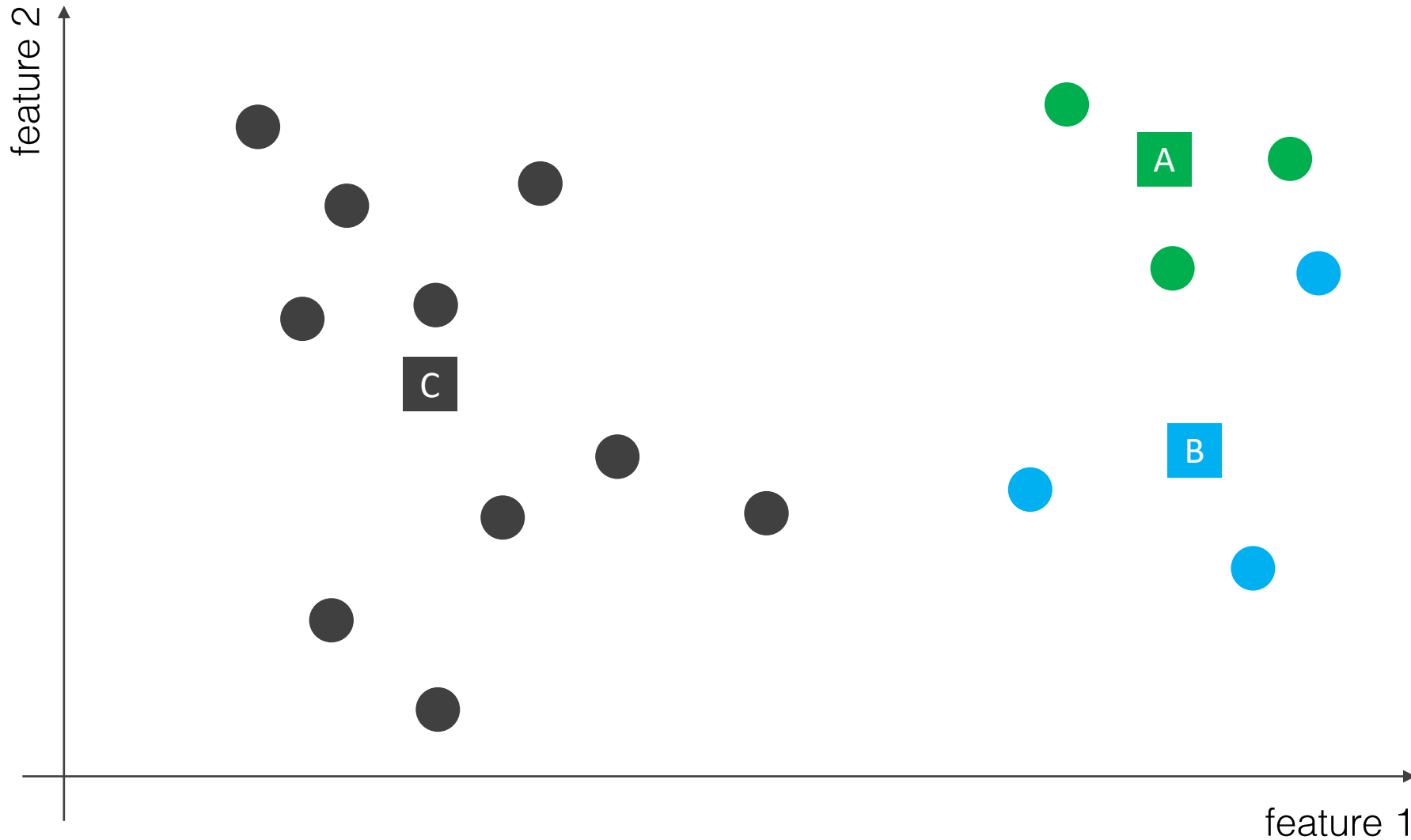


# K-means clustering



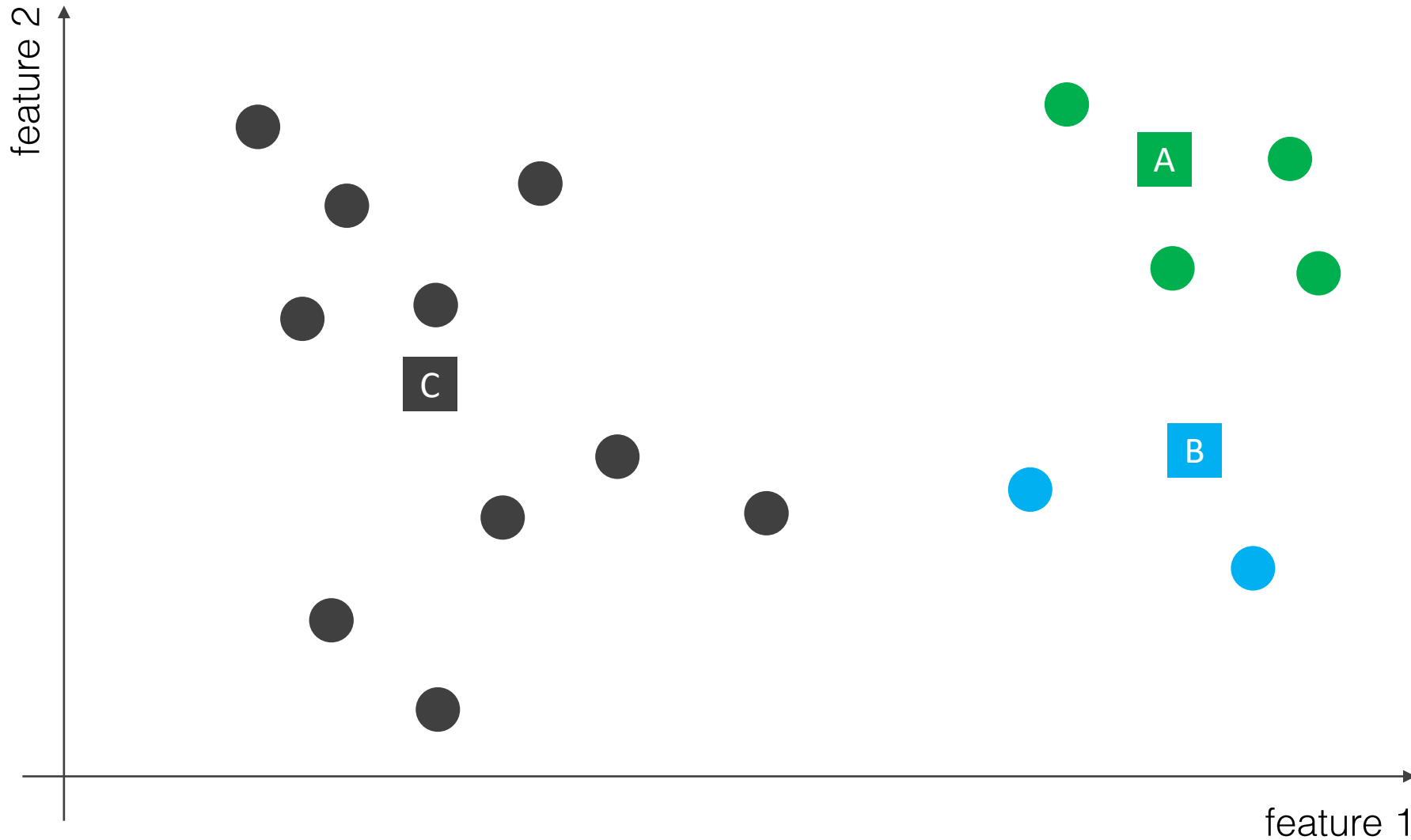
- 1 Select  $k$  and randomly initialize  $k$  mean values
- 2 Assign observations to the nearest mean
- 3 Update the mean to be the centroid of the labeled data

# K-means clustering



- 1 Select  $k$  and randomly initialize  $k$  mean values
- 2 Assign observations to the nearest mean
- 3 Update the mean to be the centroid of the labeled data
- 4 Repeat steps 2 and 3 until convergence

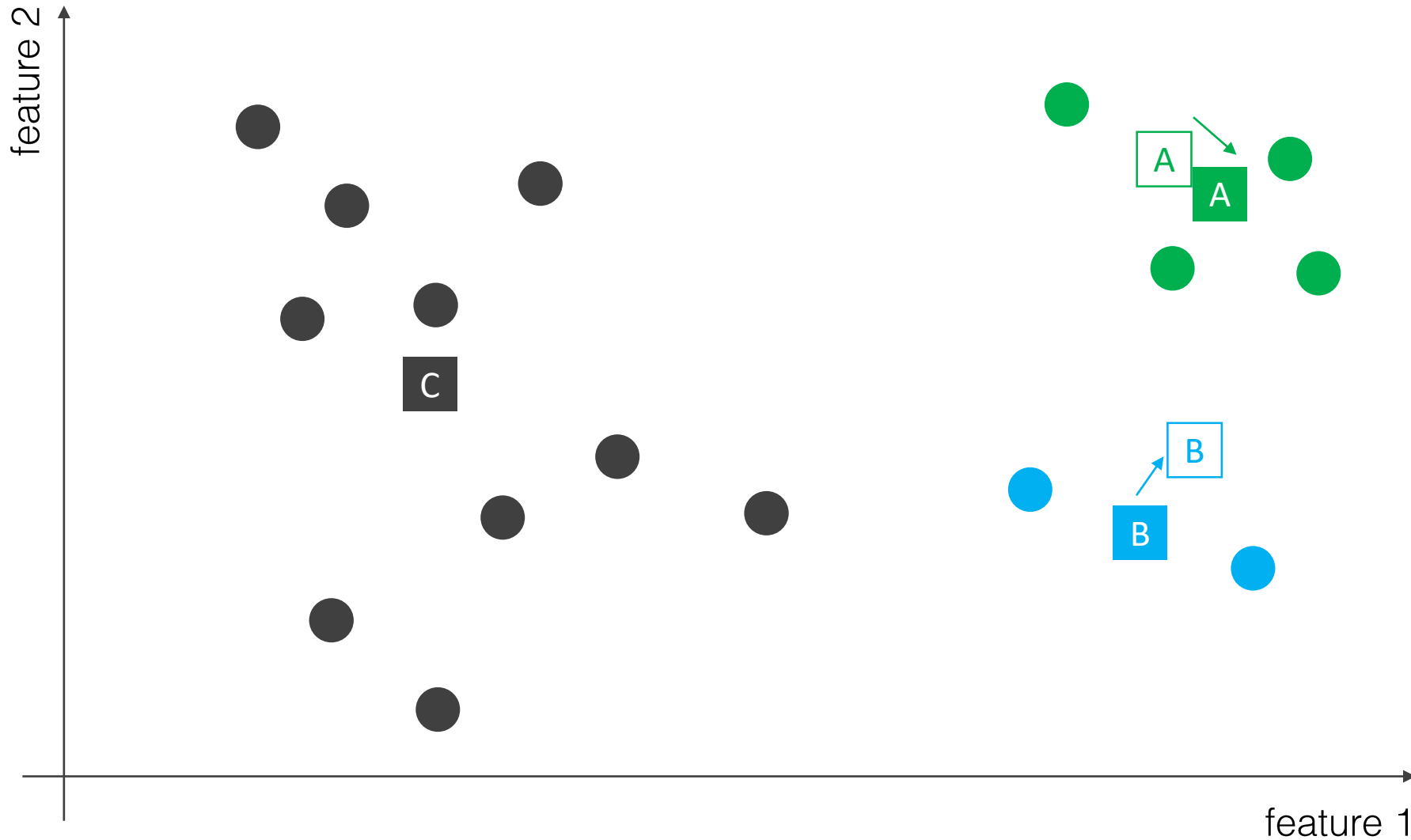
# K-means clustering



- 1 Select  $k$  and randomly initial  $k$  mean values
- 2 Assign observations to the nearest mean
- 3 Update the mean to be the centroid of the labeled data
- 4 Repeat steps 2 and 3 until convergence

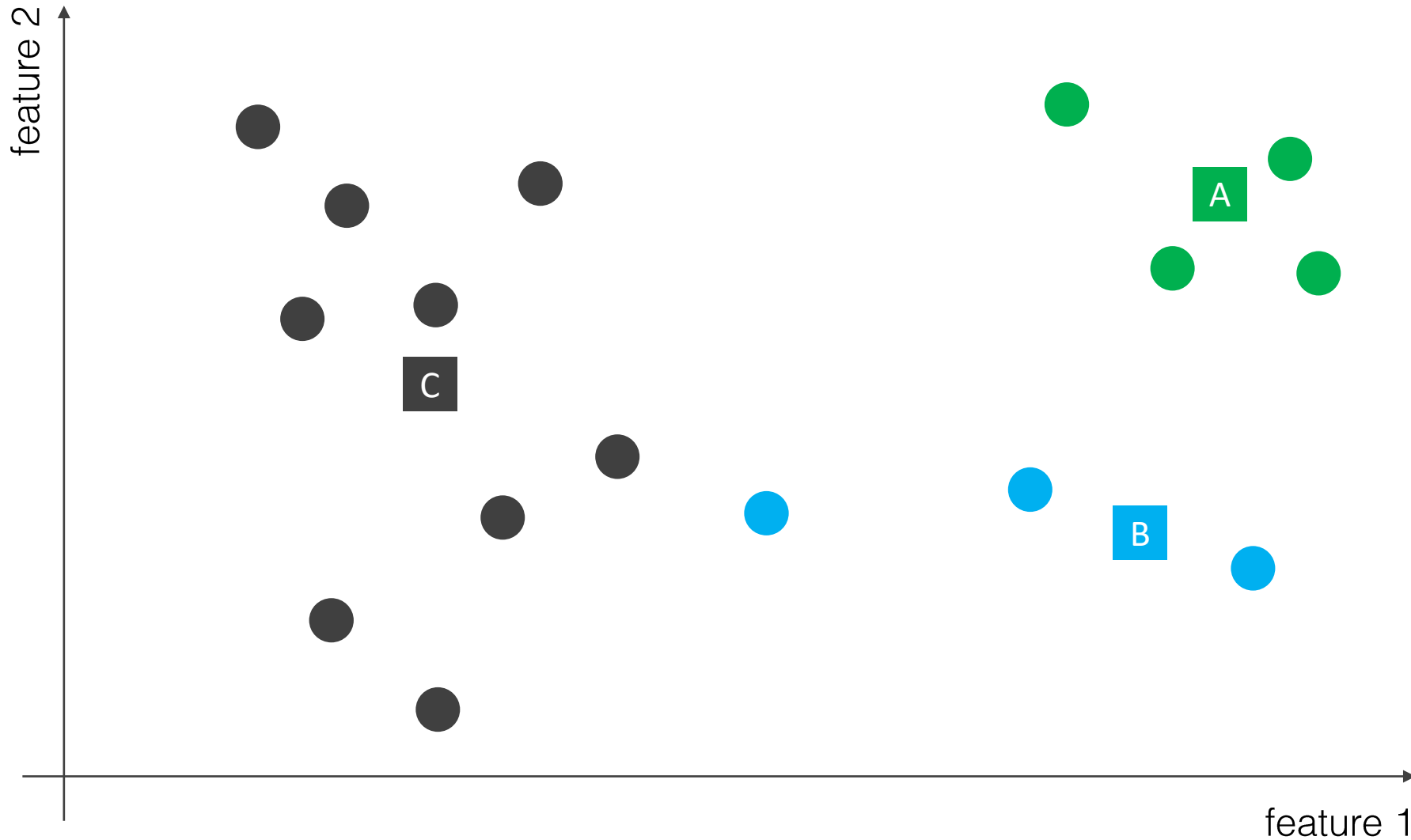
...Iteration 2

# K-means clustering



- 1 Select  $k$  and randomly initialize  $k$  mean values
- 2 Assign observations to the nearest mean
- 3 Update the mean to be the centroid of the labeled data
- 4 Repeat steps 2 and 3 until convergence

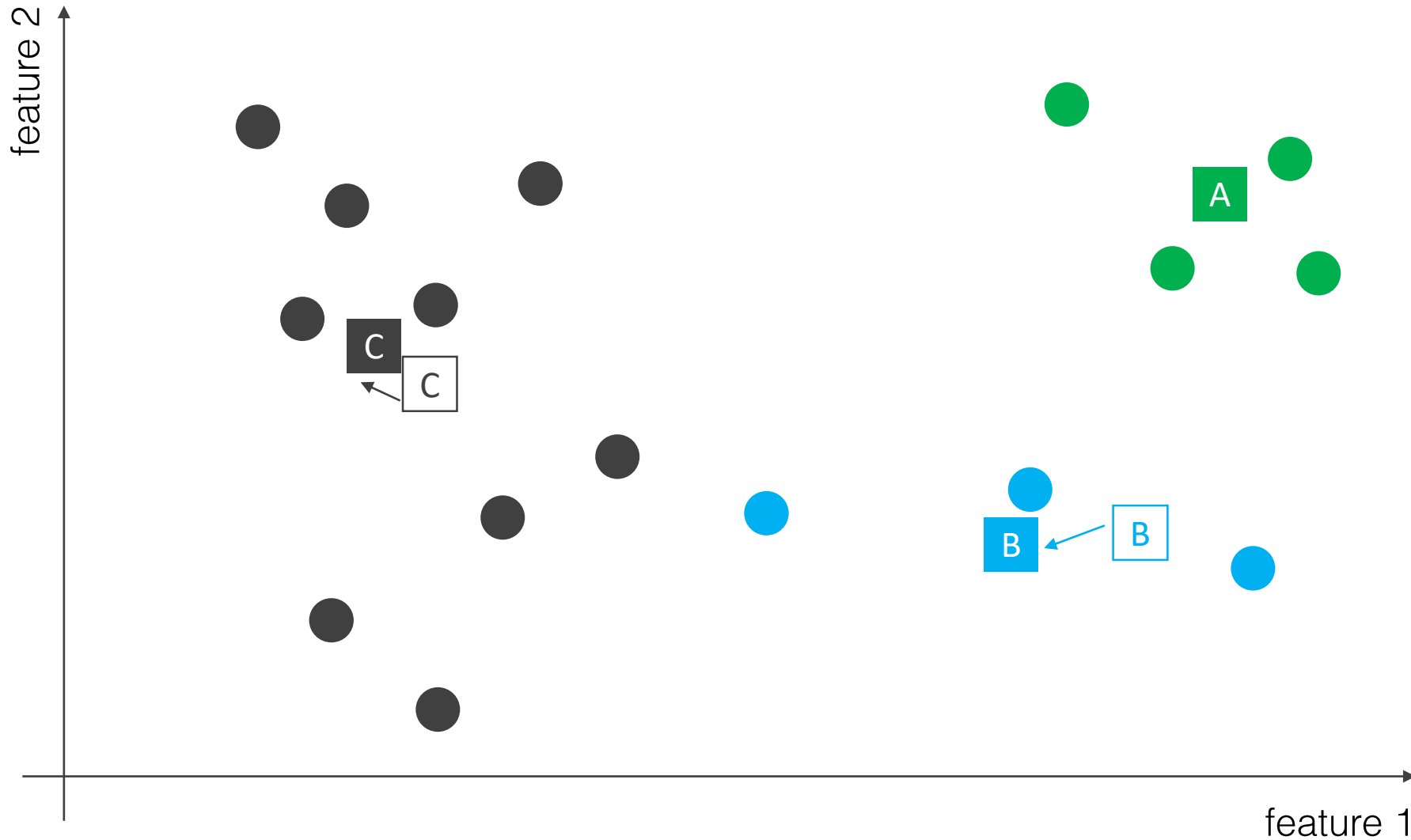
# K-means clustering



- 1 Select  $k$  and randomly initialize  $k$  mean values
- 2 Assign observations to the nearest mean
- 3 Update the mean to be the centroid of the labeled data
- 4 Repeat steps 2 and 3 until convergence

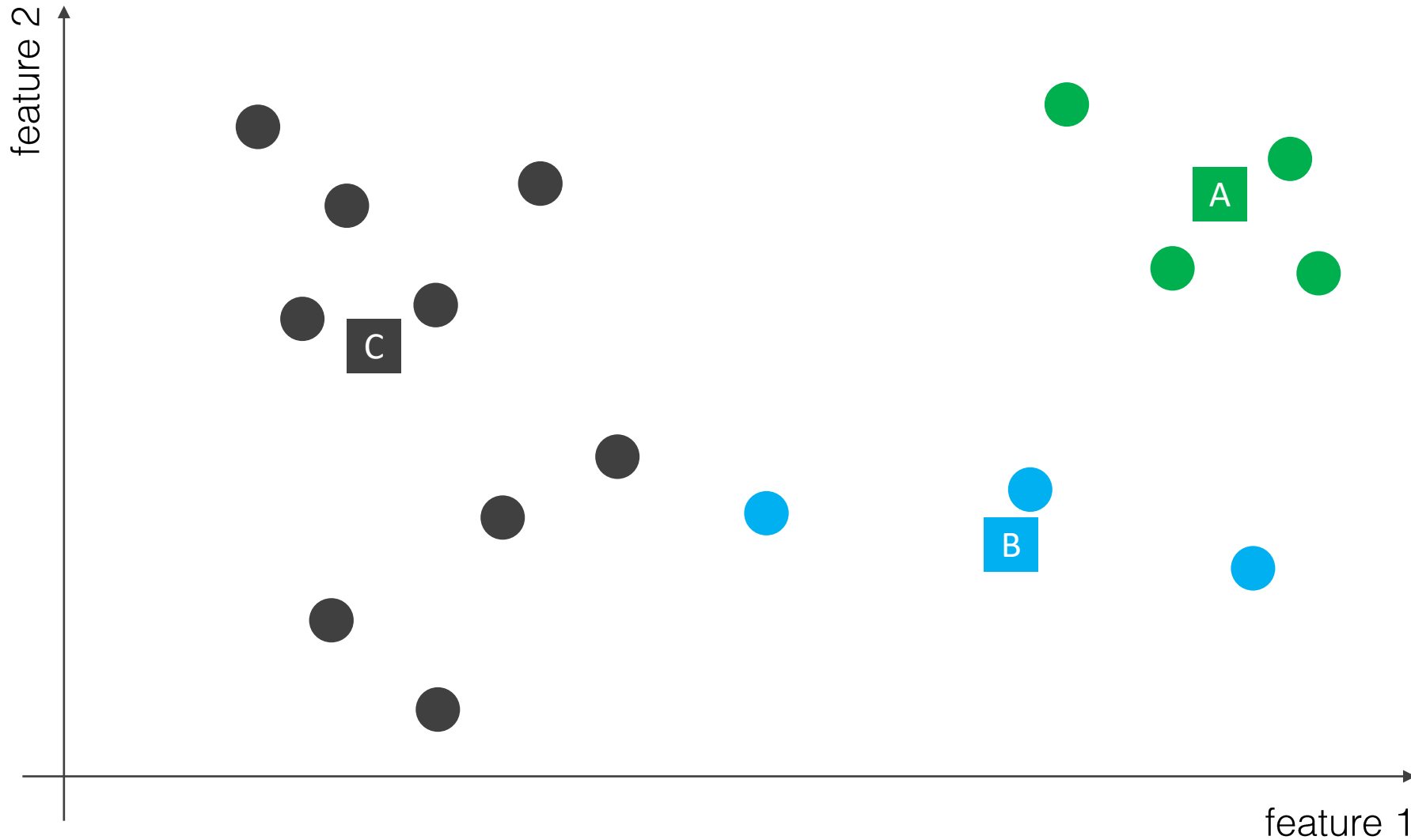
...Iteration 3

# K-means clustering



- 1 Select  $k$  and randomly initialize  $k$  mean values
- 2 Assign observations to the nearest mean
- 3 Update the mean to be the centroid of the labeled data
- 4 Repeat steps 2 and 3 until convergence

# K-means clustering

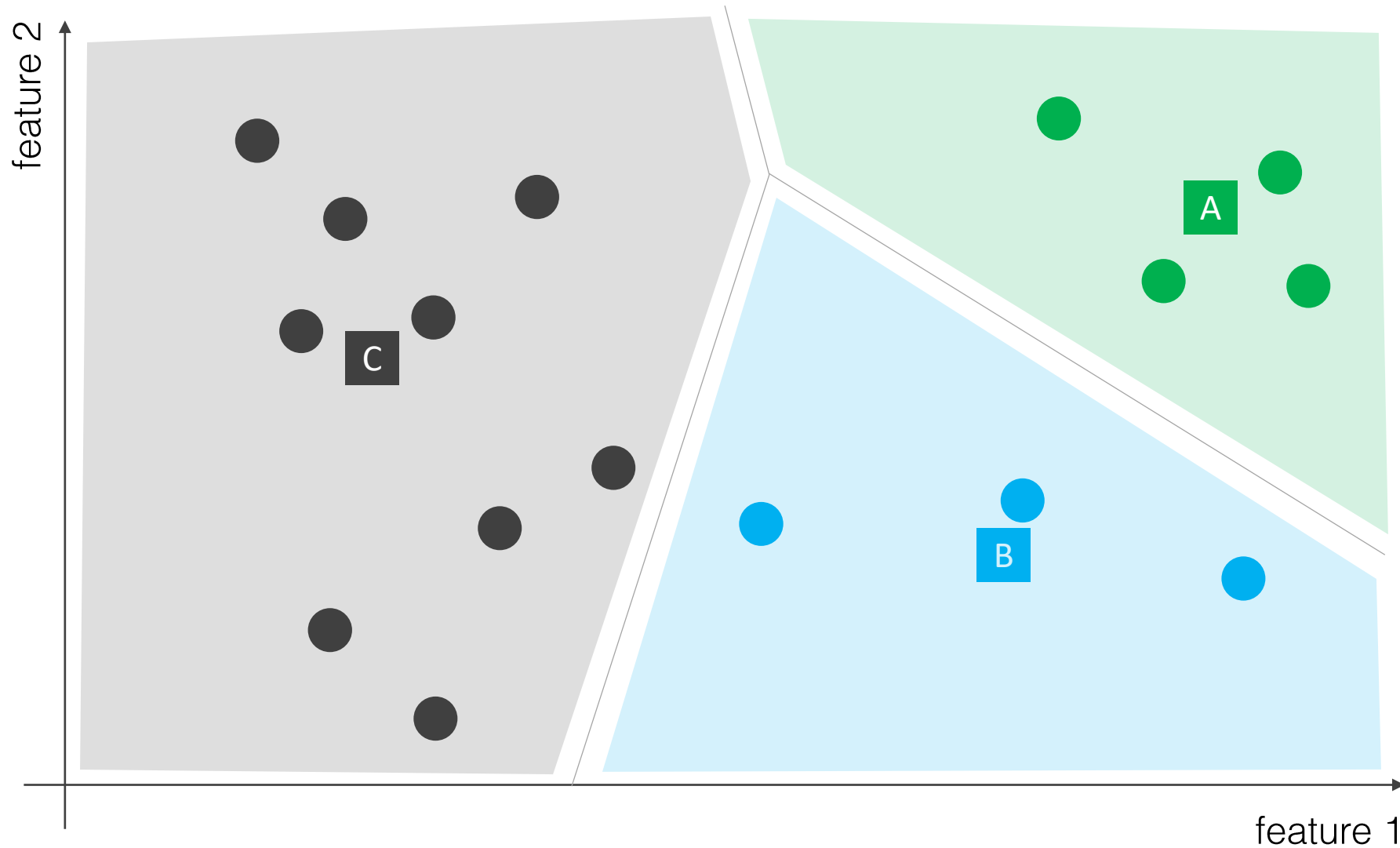


- 1 Select  $k$  and randomly initialize  $k$  mean values
- 2 Assign observations to the nearest mean
- 3 Update the mean to be the centroid of the labeled data
- 4 Repeat steps 2 and 3 until convergence

...converged



# K-means partitions the space into Voronoi cells



# Under the hood, we minimize a cost function

**Objective:** identify  $K$  means,  $\mu_k$ , such that the set of closest points in feature space are the minimum distance away.

$$r_{ik} = \begin{cases} 1 & \text{if } \mathbf{x}_j \text{ is closest to the } k\text{th mean } \mu_k \\ 0 & \text{else} \end{cases}$$

$$C(\mathbf{x}_i, \mu_1, \mu_2, \dots, \mu_K) = \sum_{i=1}^N \sum_{k=1}^K r_{ik} \|\mathbf{x}_i - \mu_k\|_2^2$$

L<sub>2</sub> norm  
↓

## 1. E-step

Re-evaluate  $r_{ik}$

$$r_{ik} = \begin{cases} 1 & \text{if } \mathbf{x}_j \text{ is closest to the } k\text{th mean } \mu_i \\ 0 & \text{else} \end{cases}$$

Assign new “expected” cluster labels

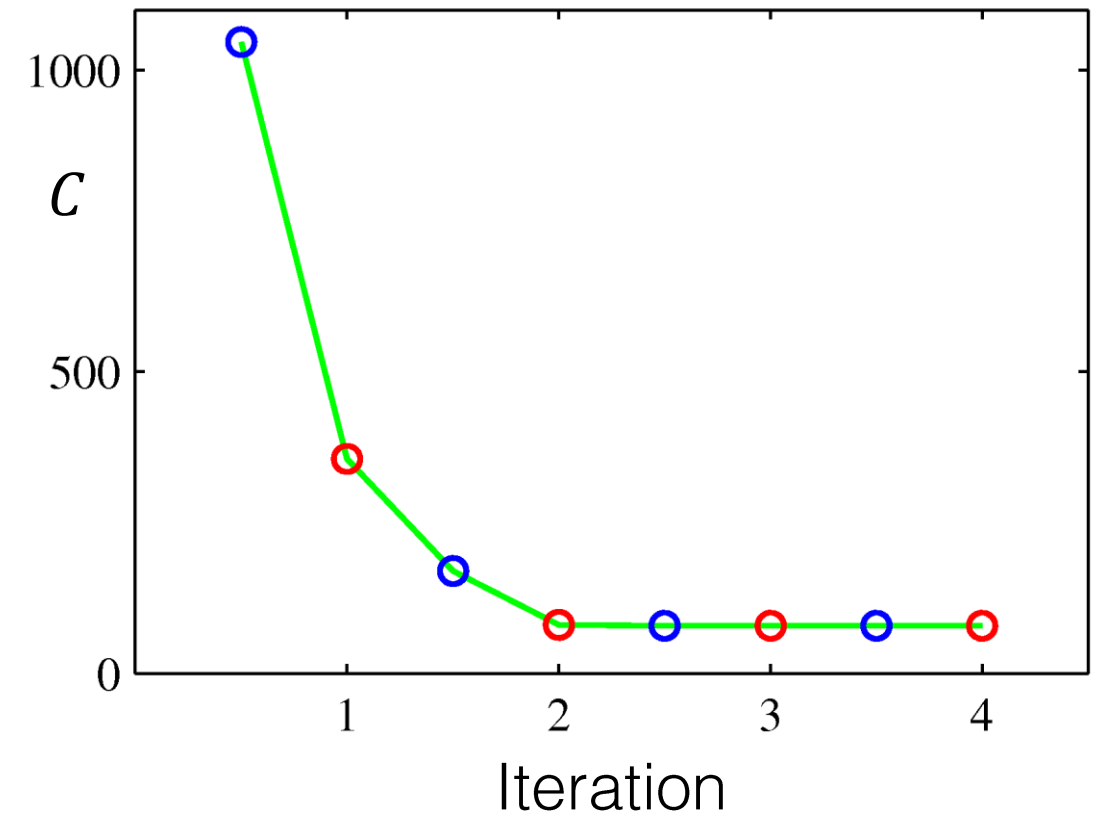
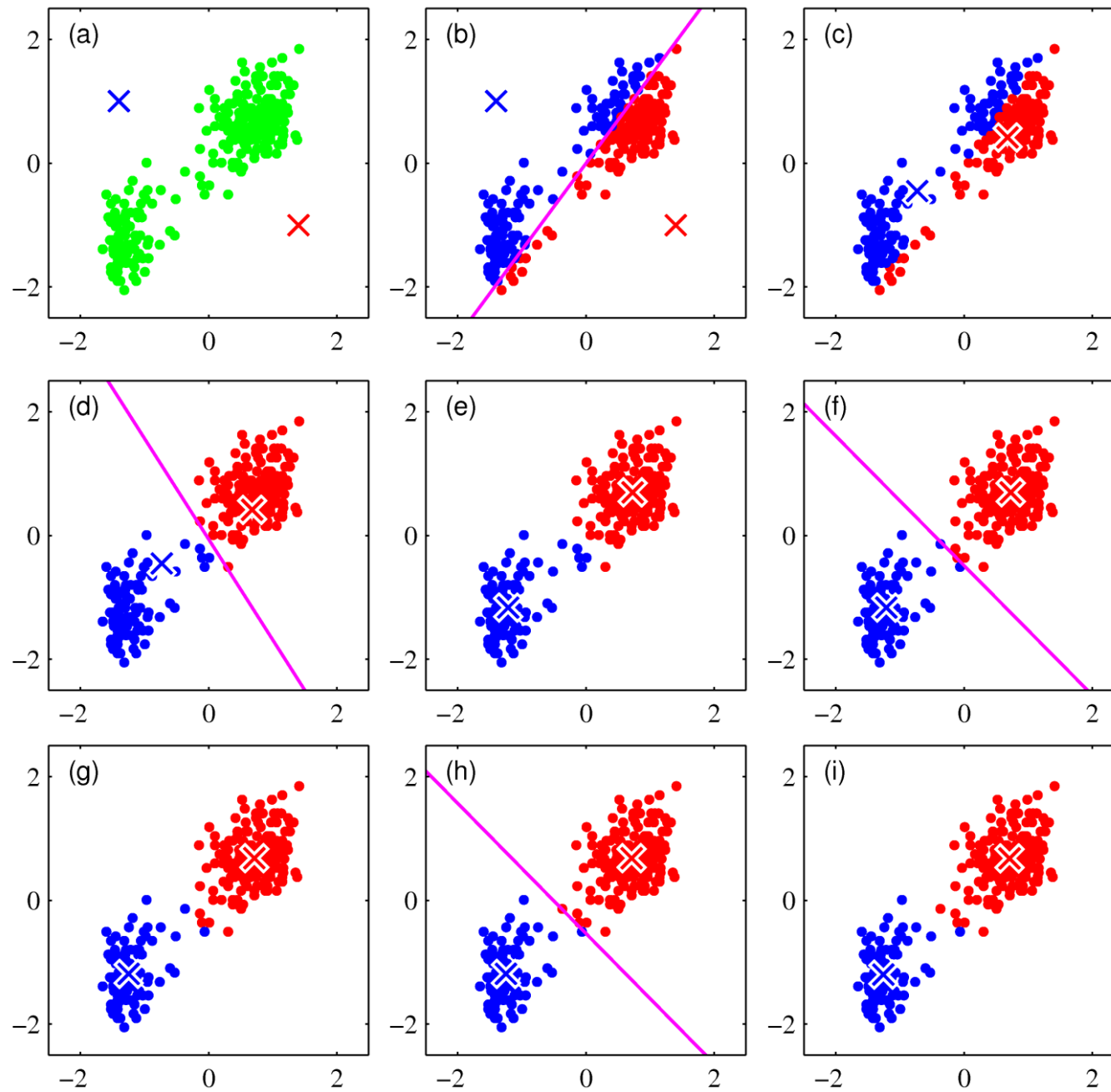
## 2. M-step

Minimize  $C$  wrt  $\mu_i$

$$\mu_k = \frac{\sum_i r_{ik} \mathbf{x}_i}{\sum_i r_{ik}}$$

Update the cluster means to maximize the likelihood

# Convergence



Bishop, Pattern Recognition, 2006

# How to choose k: Elbow method

Run k-means for various k

Choose the value of k at the “elbow” of the curve

Increasing k will improve the fit, but at the cost of potentially overfitting the data

**Other approaches:** silhouette (graphical approach to evaluating cluster fit), Akaike information criterion (AIC) and Bayesian information criterion (BIC) measure relative quality of models and factors in the number of parameters

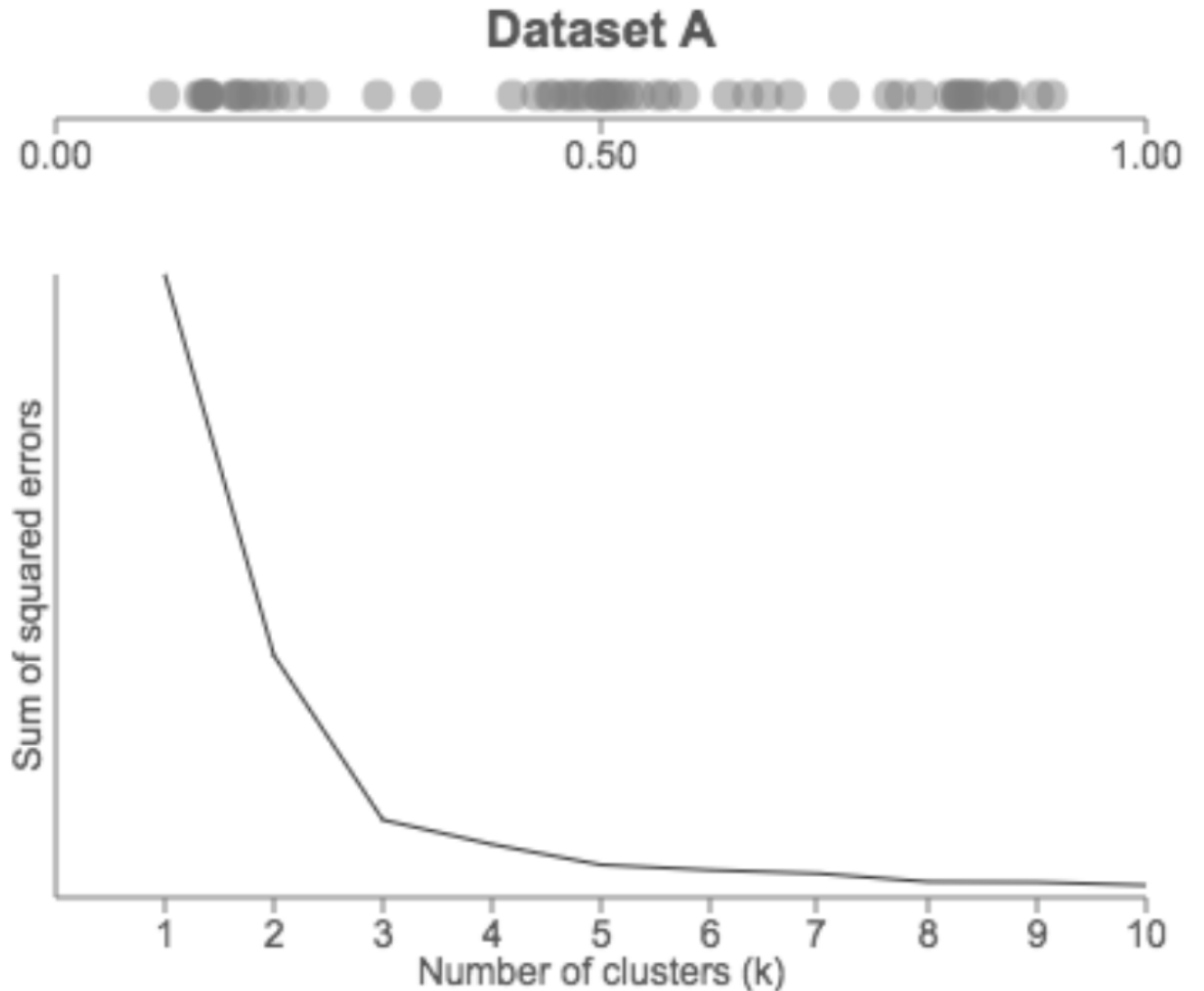


Image by Robert Gove: <https://bl.ocks.org/rpgove/0060ff3b656618e9136b>

# Distance / dissimilarity measure

$$C(\mu_1, \mu_2, \dots, \mu_K) = \sum_{i=1}^N \sum_{k=1}^K r_{ik} D(\mathbf{x}_i, \mu_k)$$

Distance / dissimilarity measure

Distance measure (for distance from the mean):

Name of method:

$L_2$  norm

$$D(\mathbf{x}_i, \mu_k) = \|\mathbf{x}_i - \mu_k\|_2^2 = \sum_{i=1}^n (\mathbf{x}_i - \mu_k)^2$$

K-means

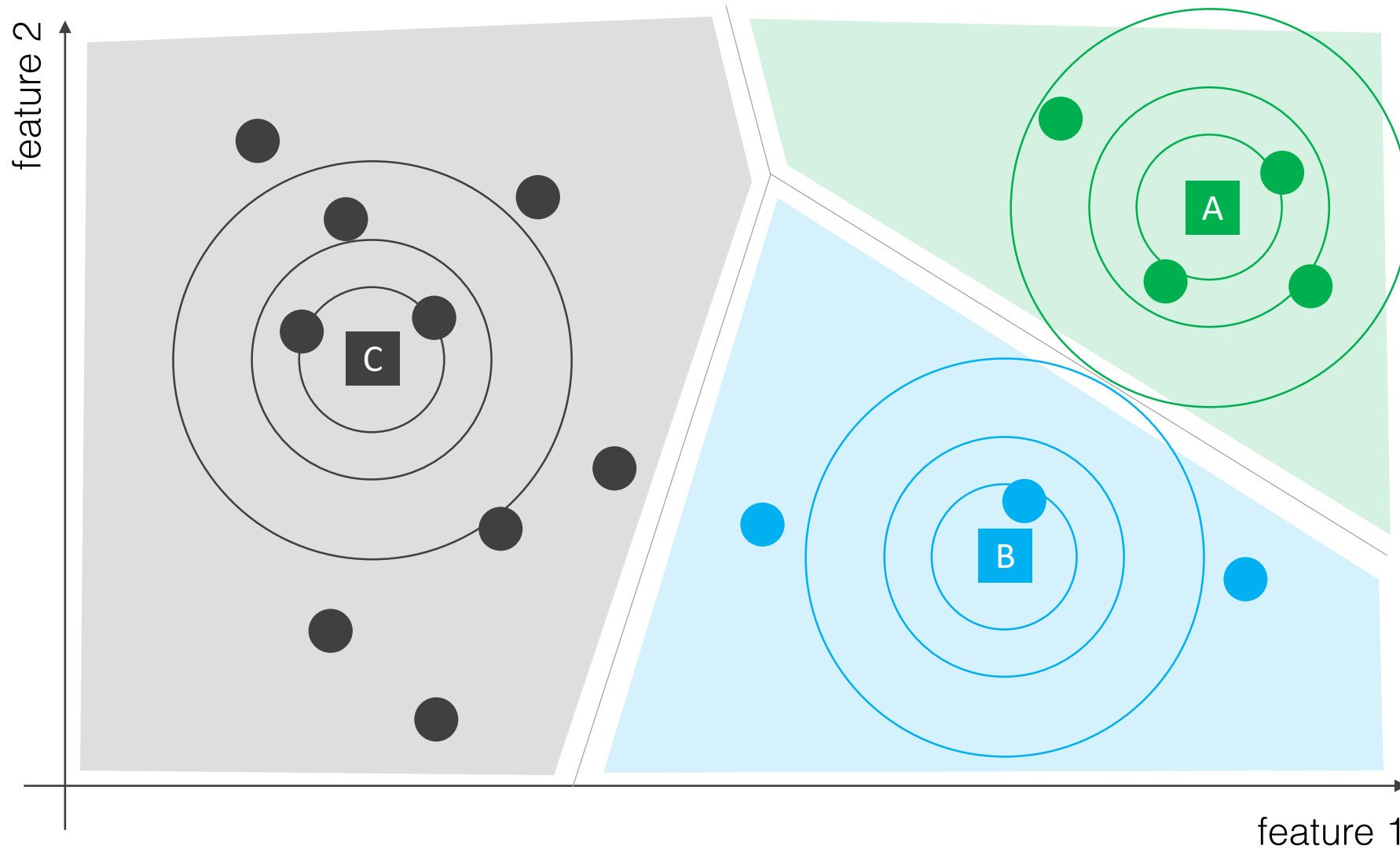
Generalization to **other distance measures**, e.g.:

K-medoids

$L_1$  norm

$$D(\mathbf{x}_i, \mu_k) = \|\mathbf{x}_i - \mu_k\|_1 = \sum_{i=1}^n |\mathbf{x}_i - \mu_k|$$

# Relationship to Gaussian distributions



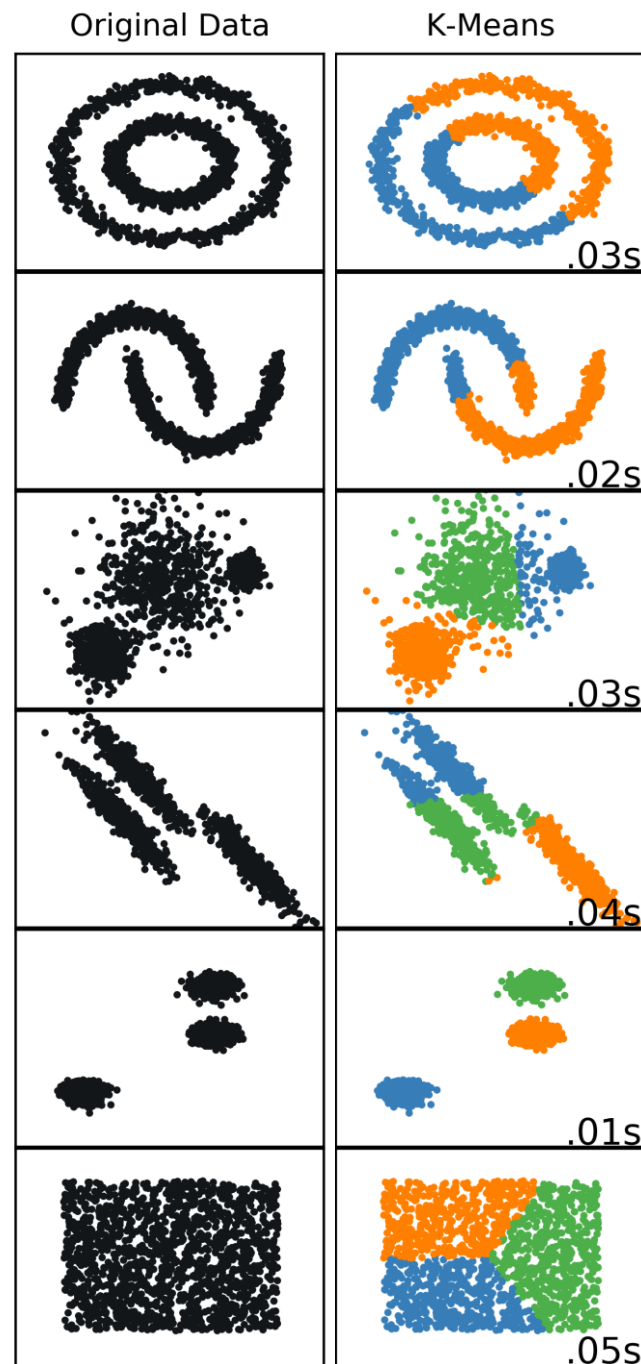
Assumes the clusters are **Gaussians** centered at the mean, each with **identical covariance matrices**, where all the features are independent:

$$\Sigma_k = \sigma^2 I = \begin{bmatrix} \sigma^2 & 0 \\ 0 & \sigma^2 \end{bmatrix}$$

# Examples: K-Means

Converges very quickly

Sensitive to initialization  
of means



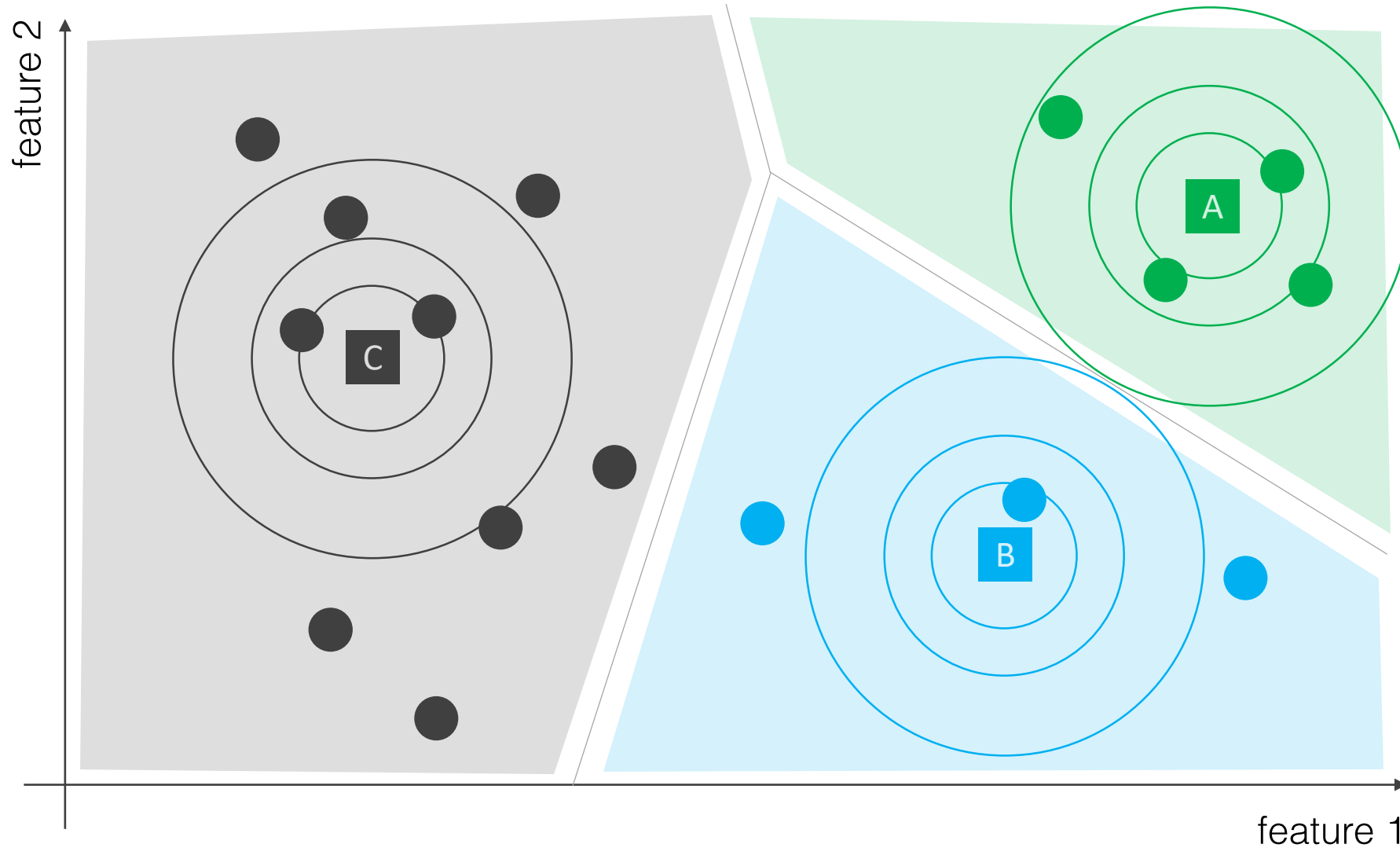
Struggles when there are **nonlinear** boundaries between clusters

Struggles in situations with **variation in cluster variance** and **correlation between features**

Excels with clusters of **equal variance**

Will divide into k clusters even when there are not k

# Relaxing our assumptions on covariance...



What if we **don't** assume the clusters are **Gaussians** centered at the mean, each with **identical covariance matrices**, where all the features are independent:

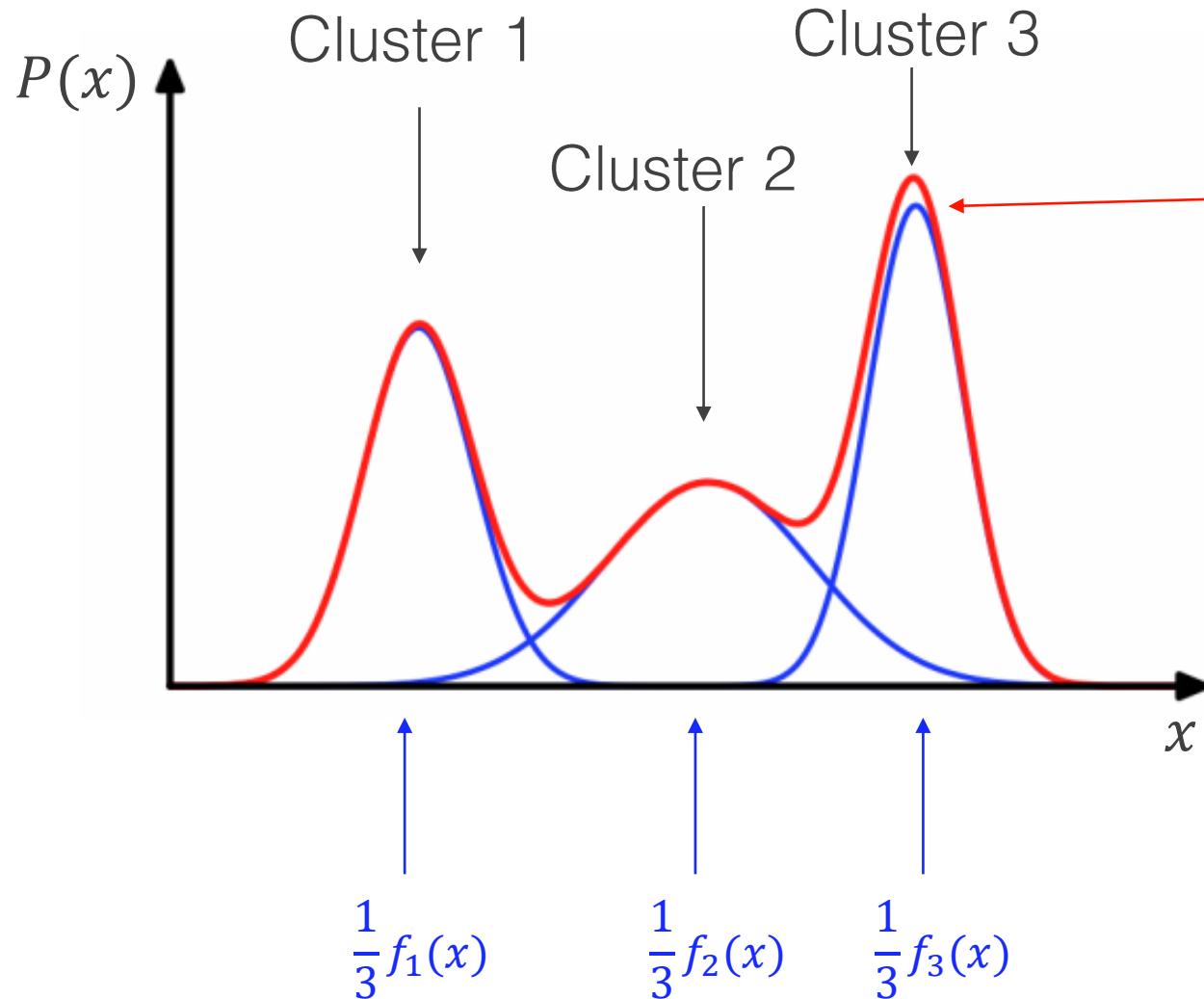
$$\Sigma_k = \sigma^2 I = \begin{bmatrix} \sigma^2 & 0 \\ 0 & \sigma^2 \end{bmatrix}$$



# Gaussian Mixture Models

For clustering and density estimation

# Mixture model



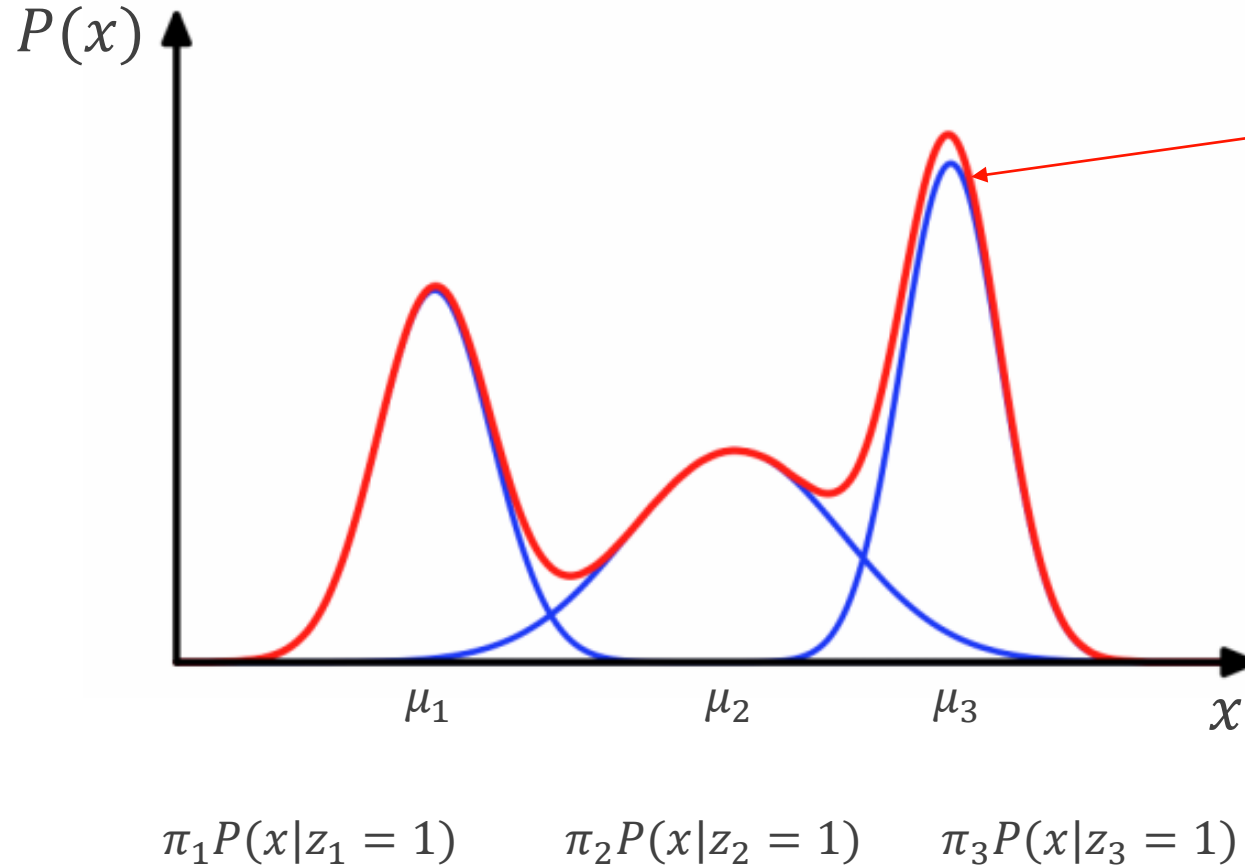
**A weighted average of density functions**

$$P(x) = \frac{1}{3} f_1(x) + \frac{1}{3} f_2(x) + \frac{1}{3} f_3(x)$$

- 1** Fit the model to the data
- 2** Use the model to assign clusters

Image from Shaun Dowling

# Gaussian mixture model



A mixture model is represented as:

$$P(x) = \sum_{k=1}^K P(z_k = 1) P(x|z_k = 1)$$

↑  
If we assume this is Gaussian,  
it becomes a Gaussian mixture  
model (GMM)

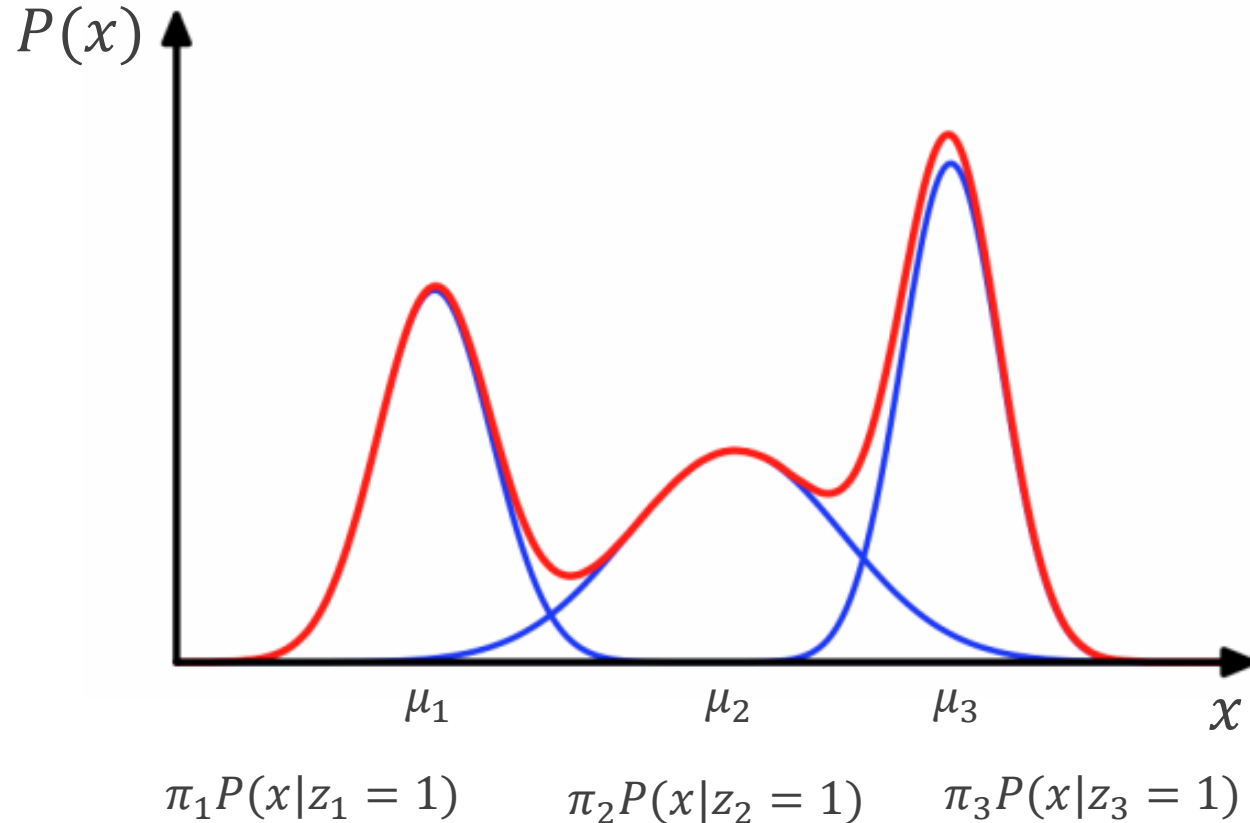
The mixing coefficients  $\pi_k = P(z_k =$

$$\sum_{k=1}^K \pi_k = 1$$

$z_k$  = binary variable that represents cluster membership

Image from Shaun Dowling

# Gaussian mixture model



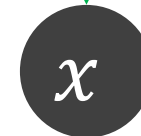
$$P(x) = \sum_{k=1}^K P(z_k = 1)P(x|z_k = 1)$$

Here we assume  $z$  is a **latent** (hidden / unobservable) variable



## Hidden

This variable controls which of the  $k$  mixture components a sample is drawn from



## Observable

Given  $z$ , a sample is drawn from  $P(x|z_k = 1)$

Image from Shaun Dowling

# Gaussian Mixture Model Latent Variables

Complete data with latent  
variable labels  $z$

Incomplete data without latent  
variable labels

Posterior probabilities,  
a.k.a. responsibilities

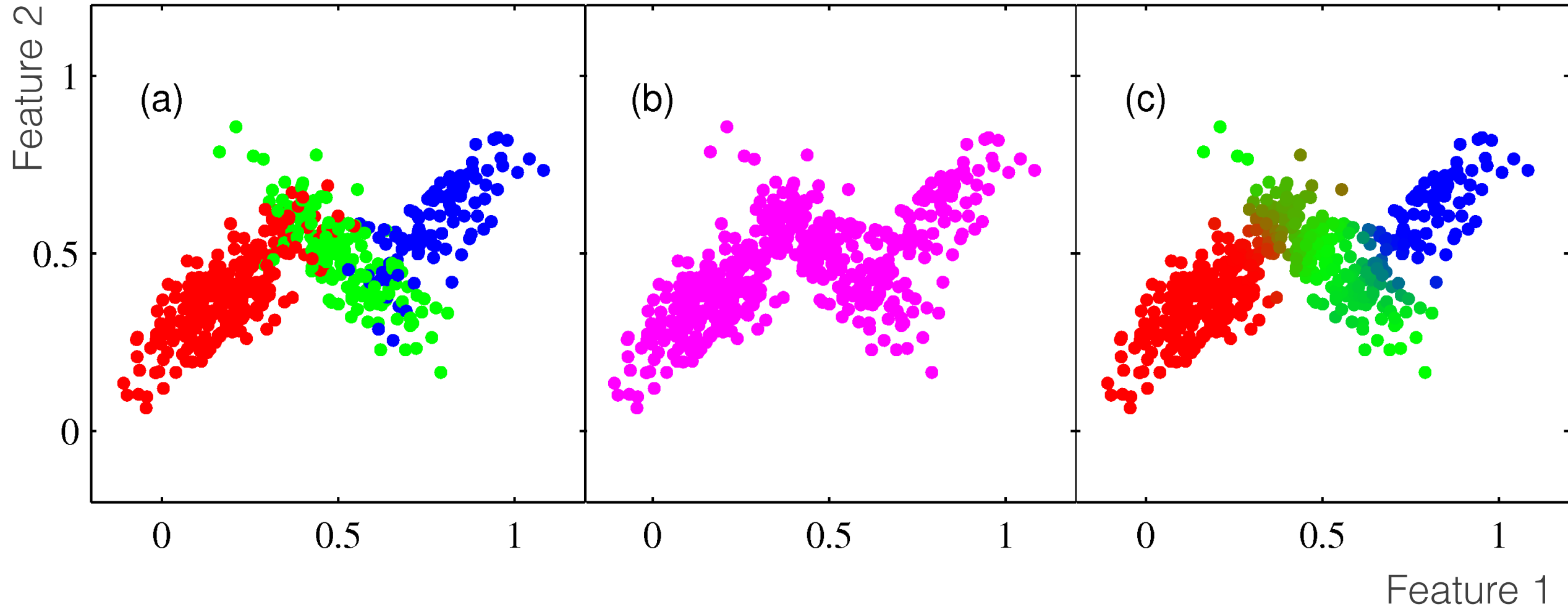
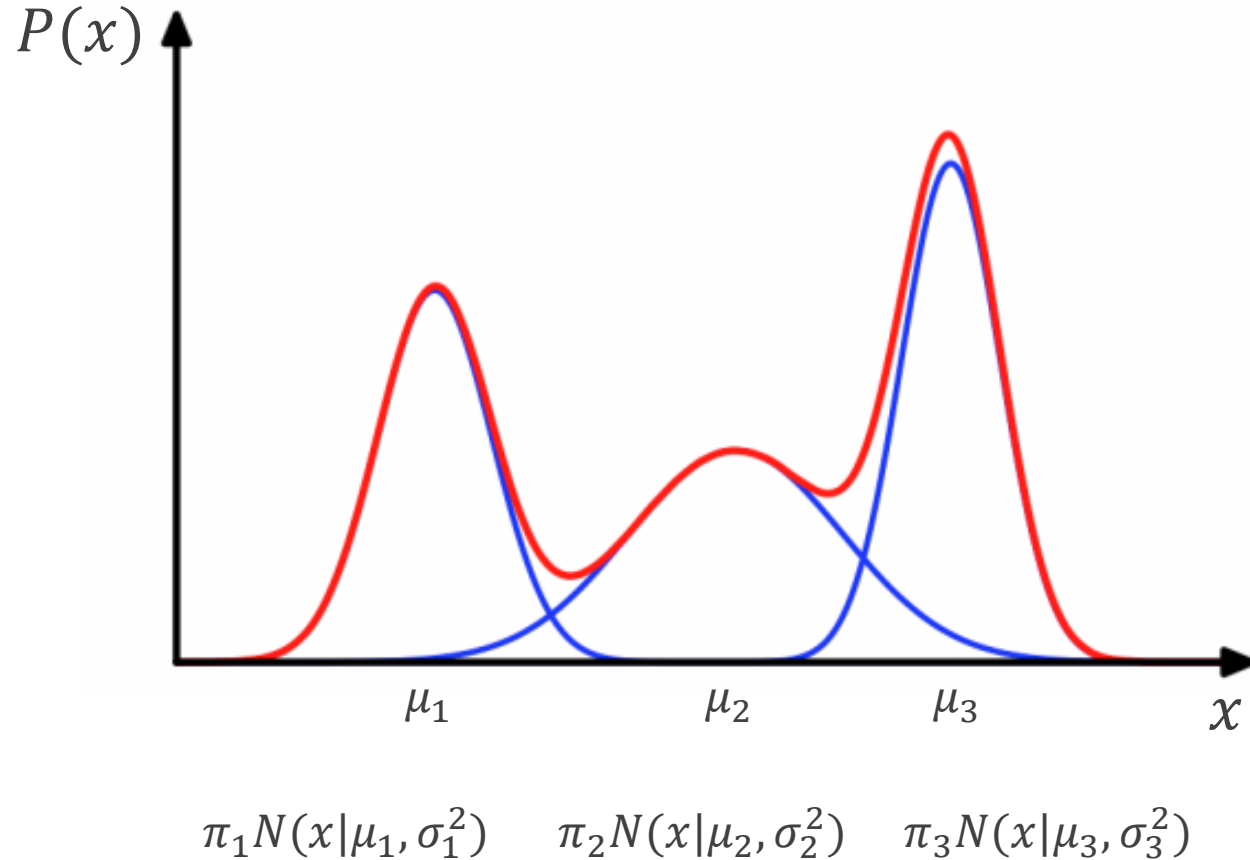


Image from Bishop, Pattern Recognition, 2006

# Gaussian mixture model



The Gaussian mixture model is represented as:

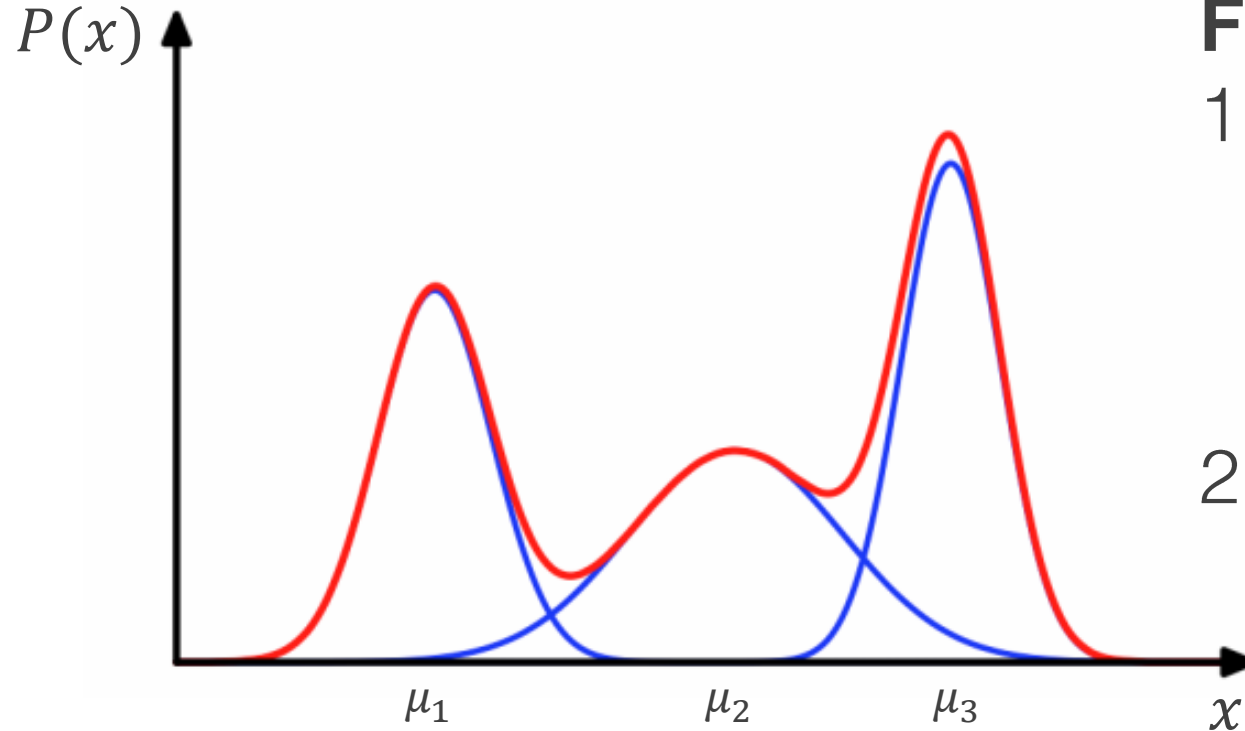
$$P(x) = \sum_{k=1}^K \pi_k N(x|\mu_k, \sigma_k^2)$$

where

$$\sum_{k=1}^K \pi_k = 1$$

Image from Shaun Dowling

# Gaussian mixture model



$$P(x|z_1 = 1) \quad P(x|z_2 = 1) \quad P(x|z_3 = 1)$$

## For clustering:

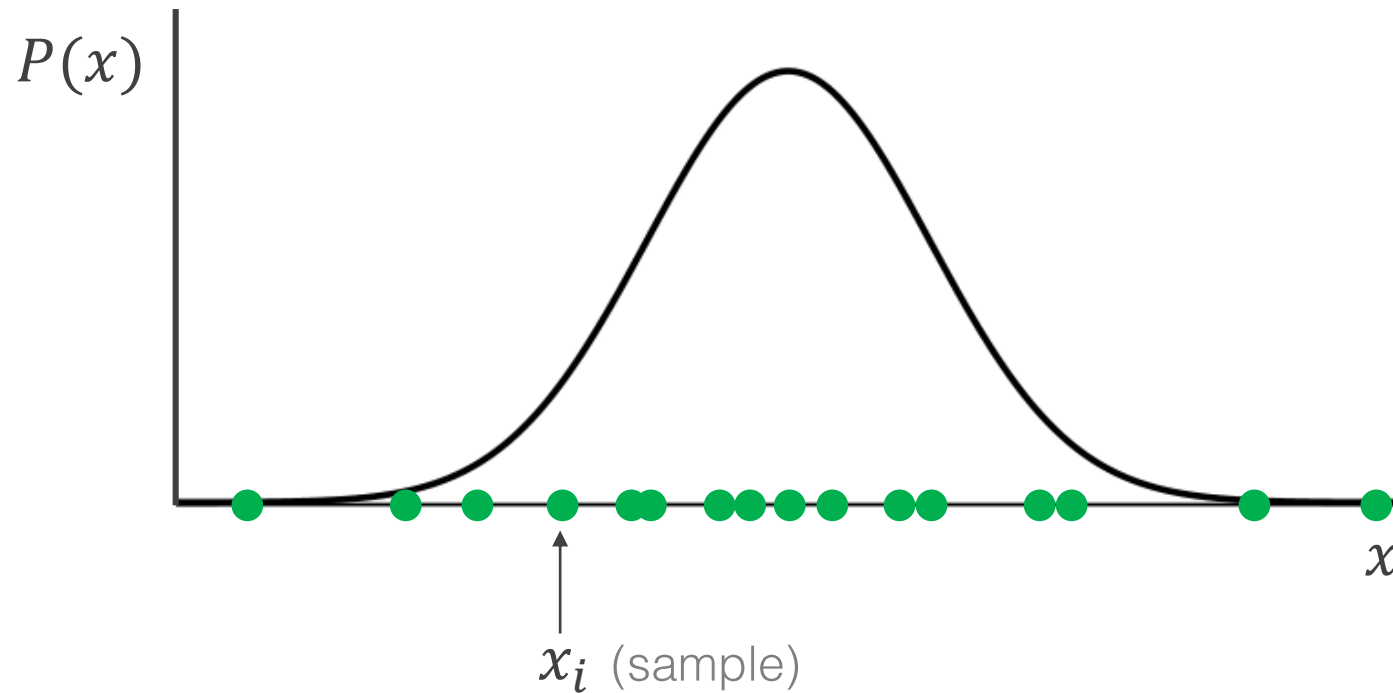
1. Fit a GMM to the data  
(estimate  $\pi_k, \mu_k, \sigma_k^2$  for  $k = 1, \dots, K$  to maximize the likelihood of the data given the model)
2. Pick the cluster,  $z_k$ , that each data point was most likely to come from

Image from Shaun Dowling

# Density estimation for a single mixture component

a.k.a. model fitting

Likelihood of one sample given the model



$$P(x_i|\mu, \sigma^2) = N(x_i|\mu, \sigma^2)$$

$$= \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x_i-\mu)^2}{2\sigma^2}}$$

Assuming independent samples, the likelihood of the data given the model is:

$$P(\mathbf{x}|\mu, \sigma^2)$$

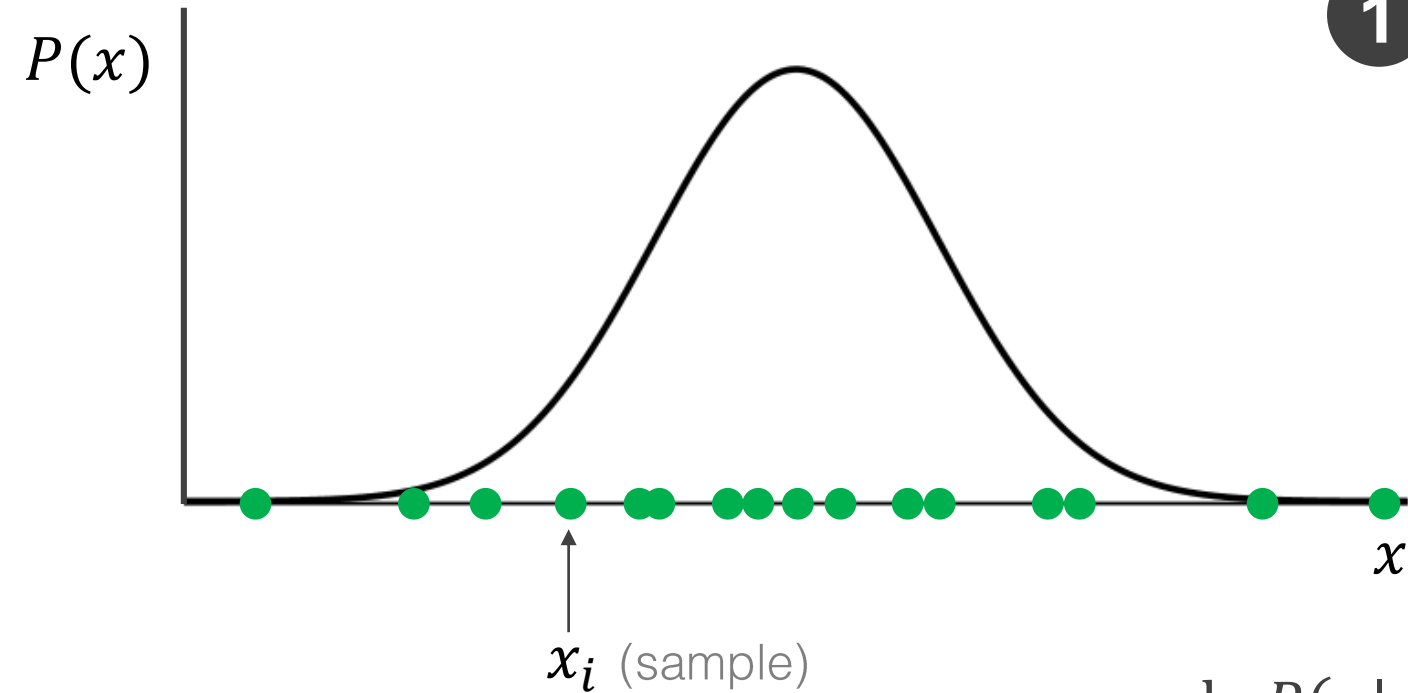
$$= \prod_{i=1}^N P(x_i|\mu, \sigma^2)$$

$$= \prod_{i=1}^N \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x_i-\mu)^2}{2\sigma^2}}$$



# Density estimation for a single mixture component

a.k.a. model fitting



- 1 We follow our familiar pattern: maximize the likelihood of the data by choosing our model parameters:  $\mu, \sigma^2$

$$P(\mathbf{x}|\mu, \sigma^2) = \prod_{i=1}^N \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x_i - \mu)^2}{2\sigma^2}}$$

- 2 Calculate the log likelihood:

$$\ln P(\mathbf{x}|\mu, \sigma^2) = -\frac{N}{2} \ln 2\pi\sigma^2 - \frac{1}{2\sigma^2} \sum_{i=1}^N (x_i - \mu)^2$$

- 3 Take the derivative of the log likelihood w.r.t. each parameter ( $\mu, \sigma^2$ ), set equal to zero, solve for  $\mu, \sigma^2$

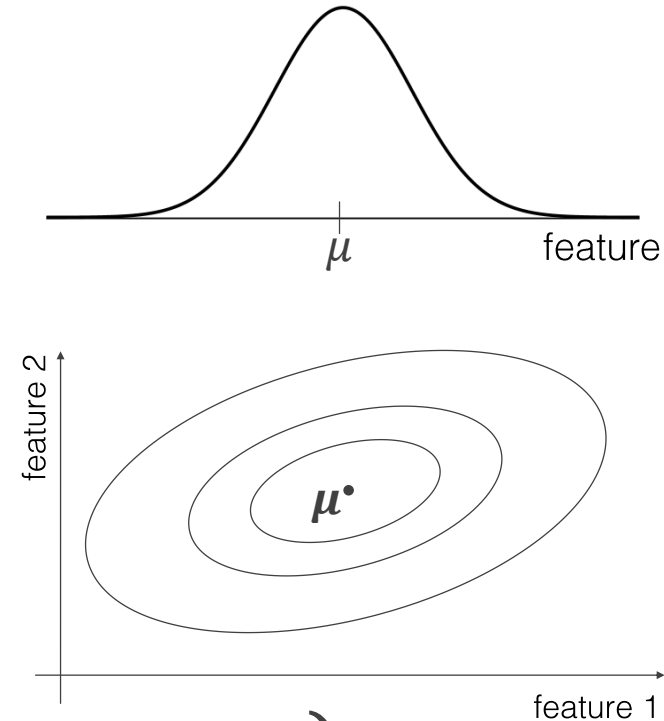
$$\hat{\mu} = \frac{1}{N} \sum_{i=1}^N x_i$$

$$\hat{\sigma}^2 = \frac{1}{N} \sum_{i=1}^N (x_i - \hat{\mu})^2$$

# From a univariate to a multivariate Gaussian

**Univariate Normal** density

$$N(x|\mu, \sigma^2) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp \left\{ -\frac{(x_i - \mu)^2}{2\sigma^2} \right\}$$



**Multivariate Normal** density

$$N(\mathbf{x}|\boldsymbol{\mu}, \boldsymbol{\Sigma}) = \frac{1}{\sqrt{2\pi|\boldsymbol{\Sigma}|}} \exp \left\{ -\frac{1}{2} (\mathbf{x} - \boldsymbol{\mu})^T \boldsymbol{\Sigma}^{-1} (\mathbf{x} - \boldsymbol{\mu}) \right\}$$

# From a univariate to a multivariate Gaussian

**Univariate Normal** MLE parameter estimates:

$$\hat{\mu} = \frac{1}{N} \sum_{i=1}^N x_i \qquad \hat{\sigma}^2 = \frac{1}{N} \sum_{i=1}^N (x_i - \hat{\mu})^2$$

**Multivariate Normal** MLE parameter estimates:

$$\hat{\boldsymbol{\mu}} = \frac{1}{N} \sum_{i=1}^N \mathbf{x}_i \qquad \hat{\boldsymbol{\Sigma}} = \frac{1}{N} \sum_{i=1}^N (\mathbf{x}_i - \hat{\boldsymbol{\mu}})(\mathbf{x}_i - \hat{\boldsymbol{\mu}})^T$$

# Density estimation for a Gaussian mixture model

- 0 We define the likelihood of one observation given our model with parameters  $\boldsymbol{\pi}_k, \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k$  for  $k = 1, \dots, K$

$$P(\mathbf{x}_i | \boldsymbol{\pi}, \boldsymbol{\mu}, \boldsymbol{\Sigma}) = \sum_{k=1}^K \pi_k N(\mathbf{x}_i | \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)$$

- 1 We assume the observations are independent and calculate the likelihood for all our data

$$P(\mathbf{X} | \boldsymbol{\pi}, \boldsymbol{\mu}, \boldsymbol{\Sigma}) = \prod_{i=1}^N \sum_{k=1}^K \pi_k N(\mathbf{x}_i | \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)$$

- 2 Calculate the log likelihood:

$$\ln P(\mathbf{X} | \boldsymbol{\pi}, \boldsymbol{\mu}, \boldsymbol{\Sigma}) = \sum_{i=1}^N \ln \left[ \sum_{k=1}^K \pi_k N(\mathbf{x}_i | \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k) \right]$$

- 3 Take the derivative of the log likelihood w.r.t. each parameter ( $\boldsymbol{\pi}_k, \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k$  for  $k = 1, \dots, K$ ), set equal to zero, solve for the parameters

# Density estimation for a Gaussian mixture model

Log likelihood of the data given the model parameters

$$\ln P(\mathbf{X}|\boldsymbol{\pi}, \boldsymbol{\mu}, \boldsymbol{\Sigma}) = \sum_{i=1}^N \ln \left[ \sum_{k=1}^K \pi_k N(\mathbf{x}_i | \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k) \right]$$

There is no **closed-form solution** that maximizes this.

We could use gradient descent BUT this approach can suffer from **severe overfitting**

Example:  $k = 2$  mixture components

$$\ln P(\mathbf{X}|\boldsymbol{\pi}, \boldsymbol{\mu}, \boldsymbol{\Sigma}) =$$

$$\sum_{i=1}^N \ln [\pi_1 N(\mathbf{x}_i | \boldsymbol{\mu}_1, \boldsymbol{\Sigma}_1) + \pi_2 N(\mathbf{x}_i | \boldsymbol{\mu}_2, \boldsymbol{\Sigma}_2)]$$

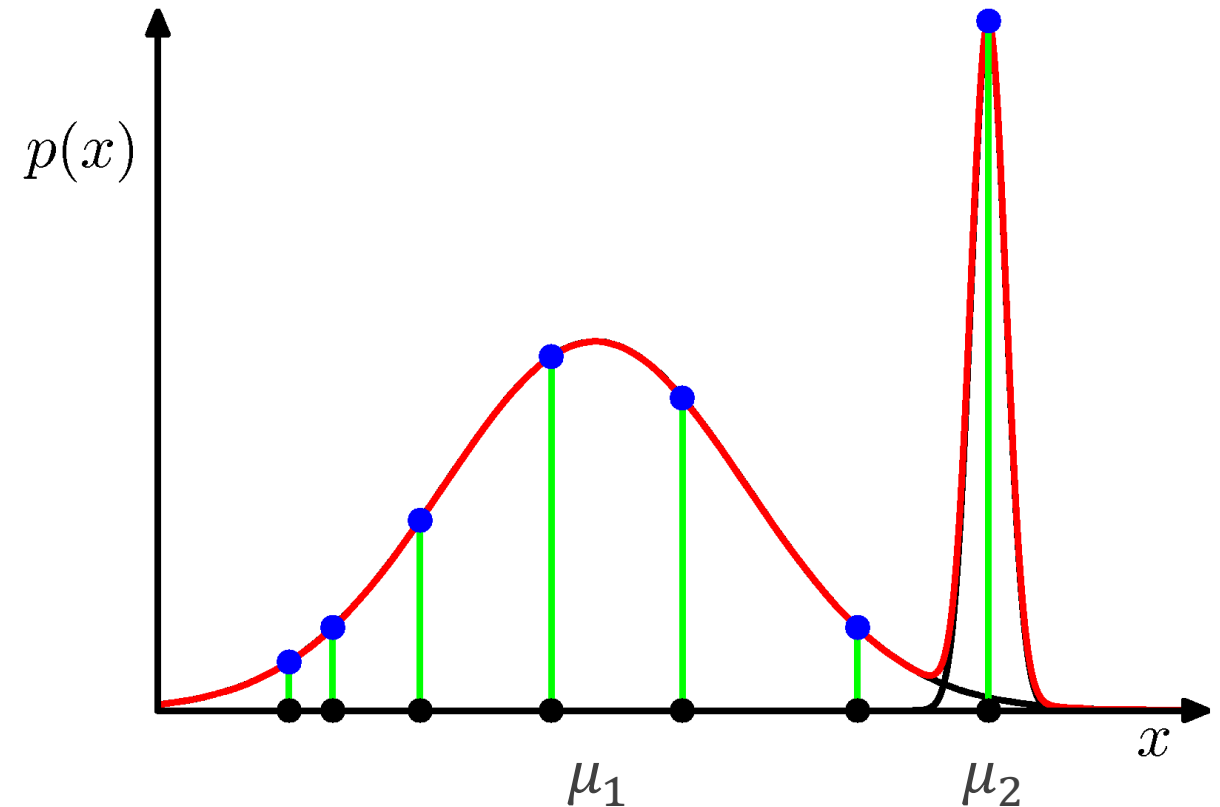
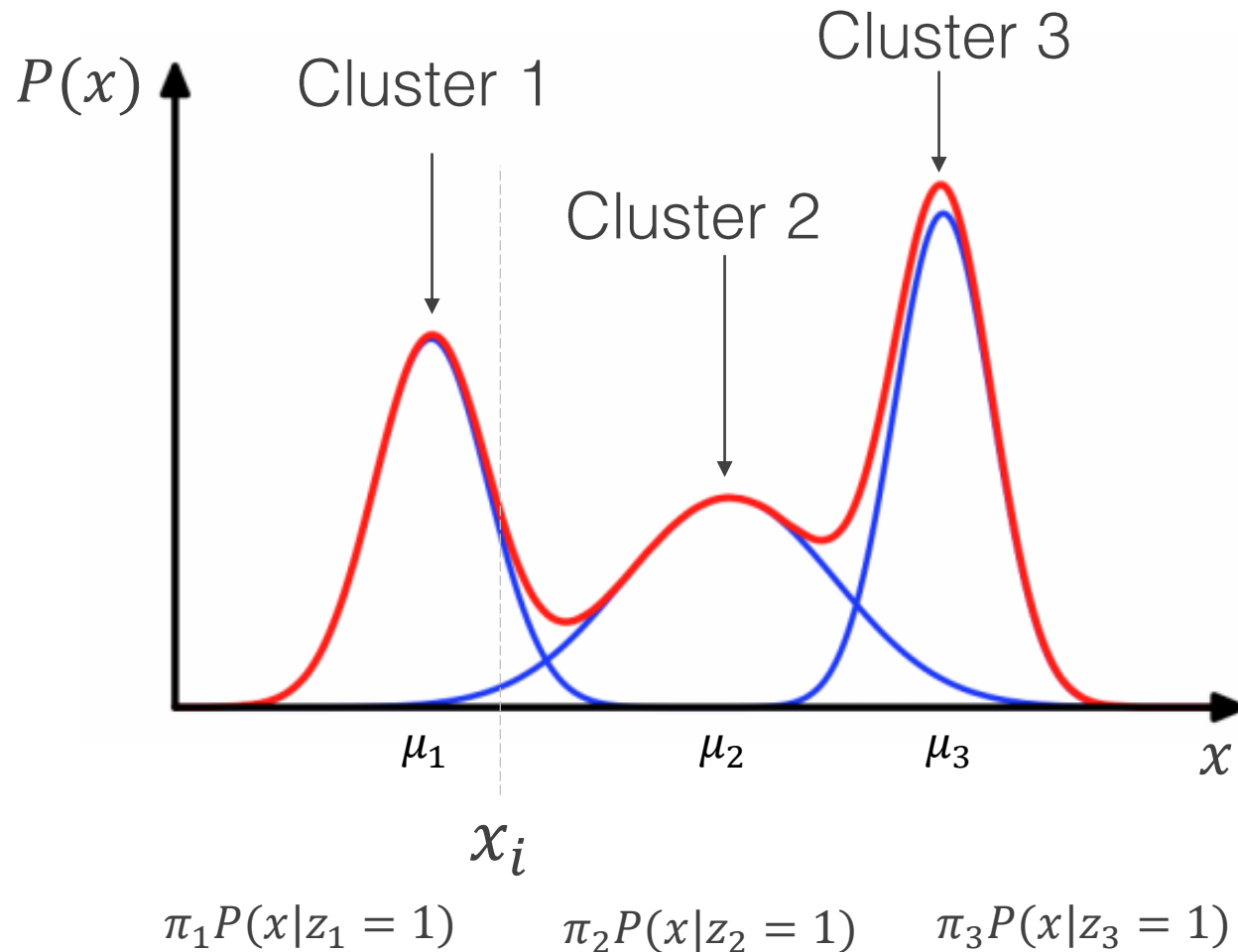


Image from Bishop, Pattern Recognition, 2006

# How do we assign a cluster?

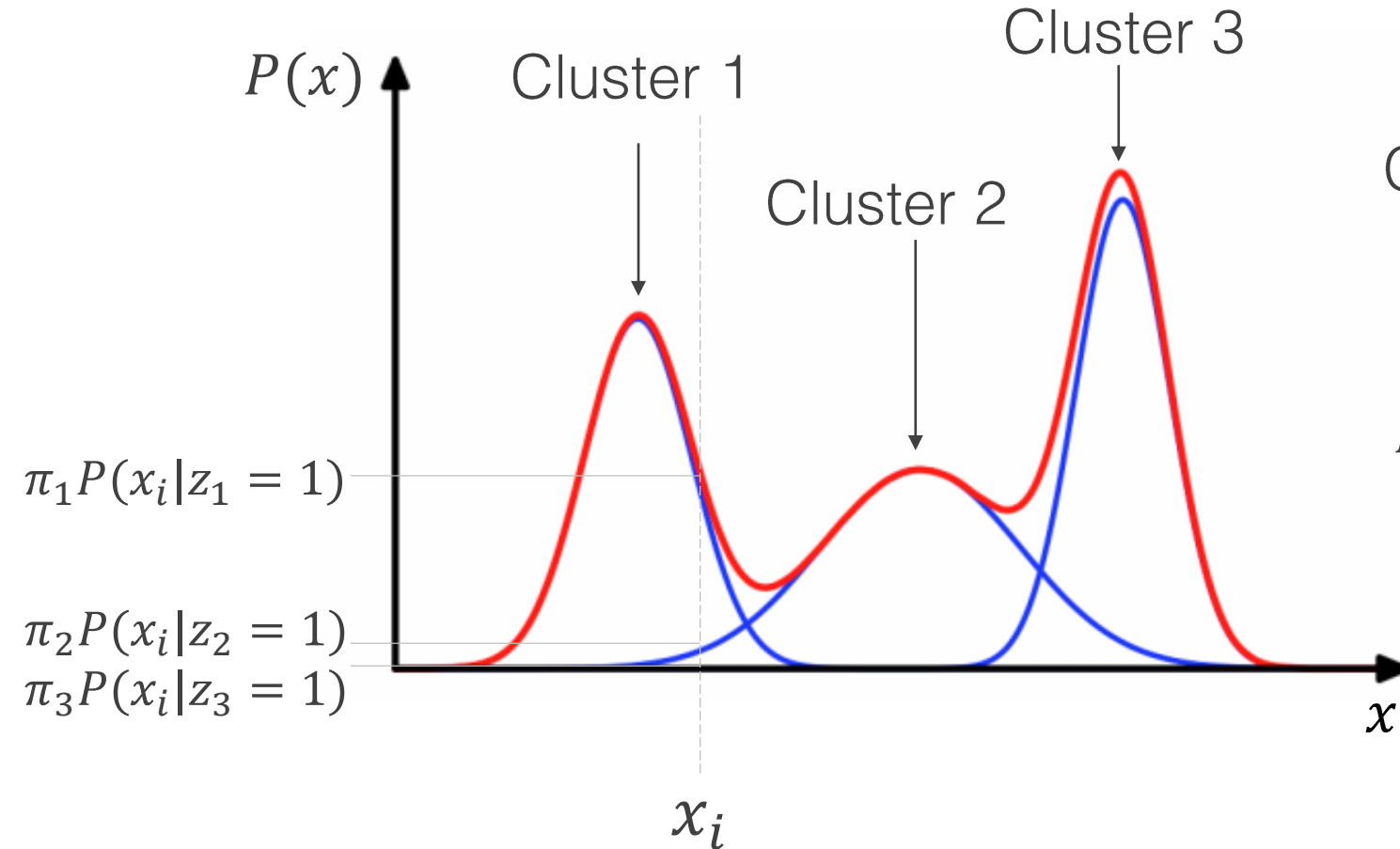


The probability of  $x_i$  is “explained” most by cluster 1, a little by cluster 2, and very little by cluster 3

We assign the cluster,  $z_k$  so that  $P(z_k = 1|x)$  is the largest for all the  $k$ 's

We need an expression for:  $P(z_k = 1|x)$

# How do we assign a cluster?



Consider observation  $x_i$

normal distribution  
for the  $k$ th cluster  $\pi_k$

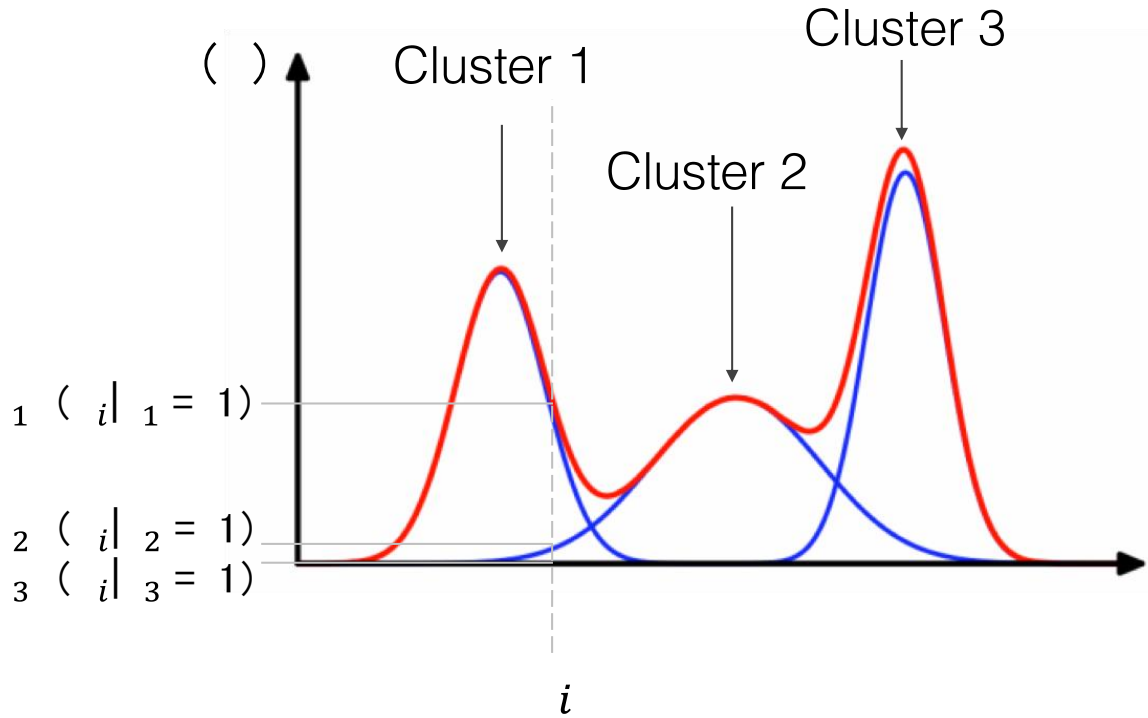
$$P(z_k = 1 | x_i) = \frac{P(x_i | z_k = 1) P(z_k = 1)}{P(x_i)}$$

by Bayes' Rule

$$P(x_i) = \pi_1 P(x_i | z_1 = 1) + \pi_2 P(x_i | z_2 = 1) + \pi_3 P(x_i | z_3 = 1)$$

normalizes the probability,  $P(z_k = 1 | x_i)$ , to add to one when summed over  $k$

# Posterior probabilities / “responsibilities”



Another interpretation of this quantity is what “fraction” of an observation is assigned to this cluster (“fuzzy” or “soft” clustering)

$$N(\mathbf{x}_i | \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k) \quad \pi_k$$

$$\gamma(z_{ik}) \triangleq P(z_k = 1 | x_i) = \frac{P(x_i | z_k = 1) P(z_k = 1)}{\sum_{k=1}^K P(x_i | z_k = 1) P(z_k = 1)}$$

Define  $N_k = \sum_{i=1}^N \gamma(z_{ik})$

Expected number of samples per cluster

$$= \frac{\pi_k N(\mathbf{x}_i | \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)}{\sum_{k=1}^K \pi_k N(\mathbf{x}_i | \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)}$$



# Expectation Maximization for a GMM

Goal: maximize the log likelihood of the data given the model parameters:

$$\ln P(X|\boldsymbol{\pi}, \boldsymbol{\mu}, \boldsymbol{\Sigma}) = \sum_{i=1}^N \ln \left[ \sum_{k=1}^K \pi_k N(\mathbf{x}_i | \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k) \right]$$

## 0. Initialization

Initialize all the parameters  
(often K-means is used for this purpose)

## 1. Expectation-step

Calculate the “responsibilities” based on the model parameters

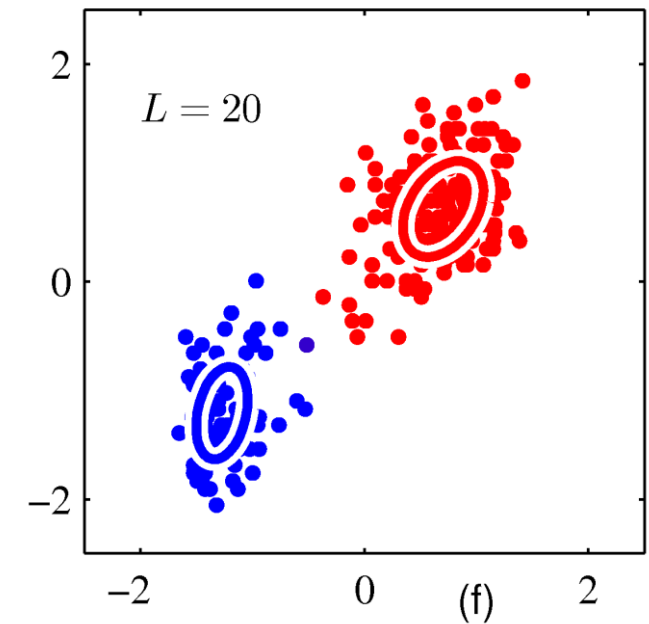
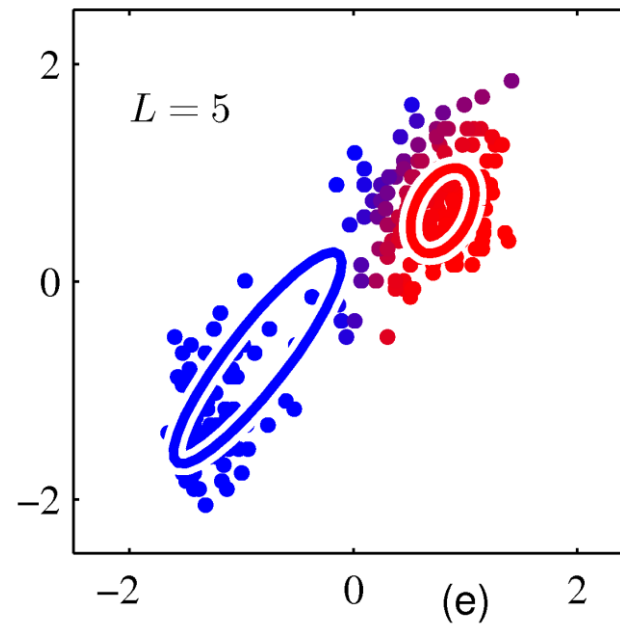
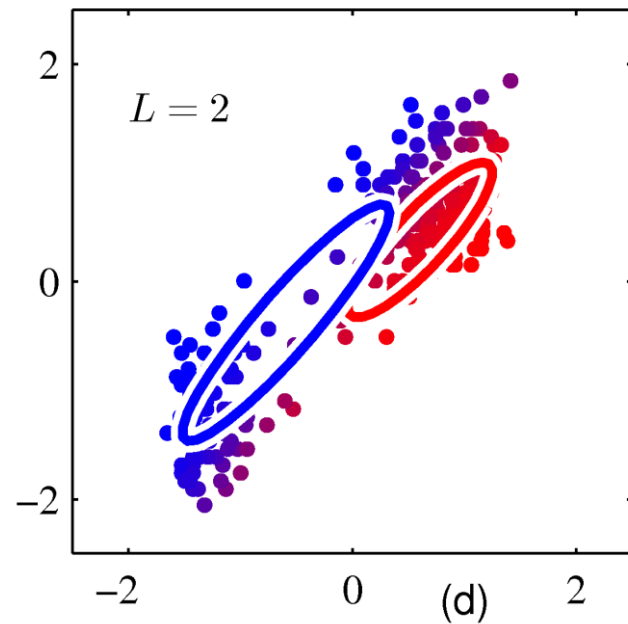
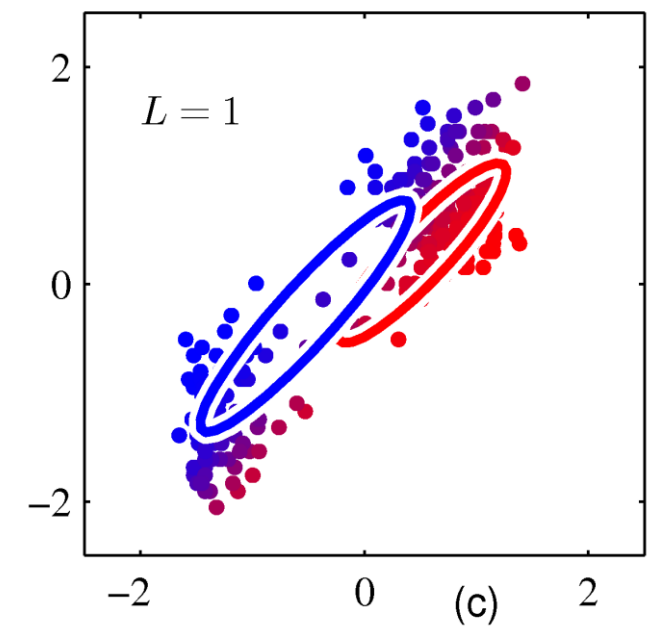
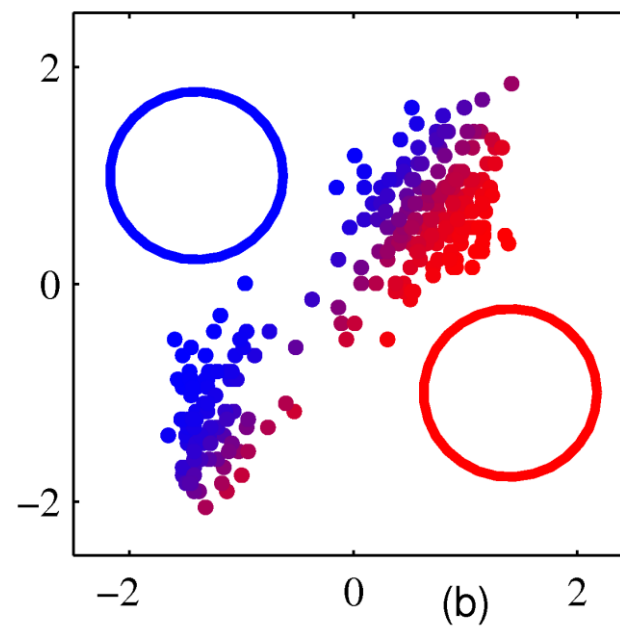
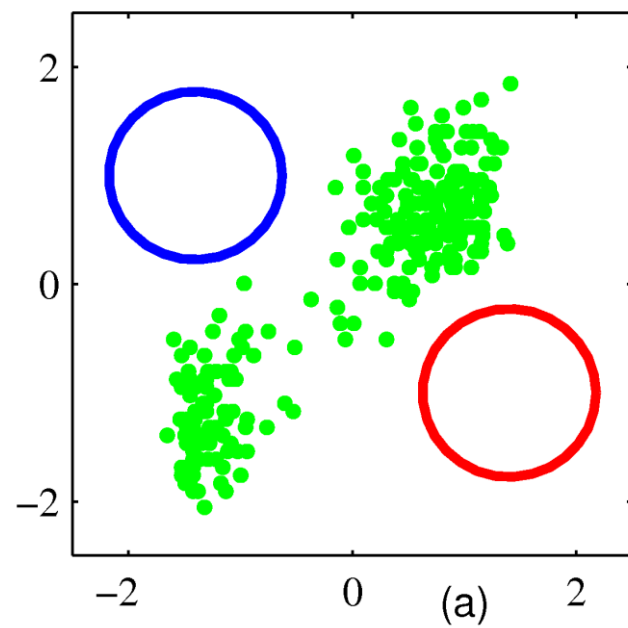
$$\begin{aligned} \gamma(z_{ik}) &\triangleq P(z_k = 1 | \mathbf{x}_i) \\ &= \frac{\pi_k N(\mathbf{x}_i | \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)}{\sum_{k=1}^K \pi_k N(\mathbf{x}_i | \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)} \end{aligned}$$

## 2. Maximization-step

Use the “responsibilities” to update the model parameters to maximize the log likelihood

$$\begin{aligned} \boldsymbol{\mu}_k^{new} &= \frac{1}{N_k} \sum_{i=1}^N \gamma(z_{ik}) \mathbf{x}_i \\ \boldsymbol{\Sigma}_k^{new} &= \frac{1}{N_k} \sum_{i=1}^N \gamma(z_{ik}) (\mathbf{x}_i - \boldsymbol{\mu}_k^{new})(\mathbf{x}_i - \boldsymbol{\mu}_k^{new})^T \\ \pi_k^{new} &= \frac{N_k}{N} \end{aligned} \quad \text{Where } N_k = \sum_{i=1}^N \gamma(z_{ik})$$

# Expectation Maximization for GMM Example



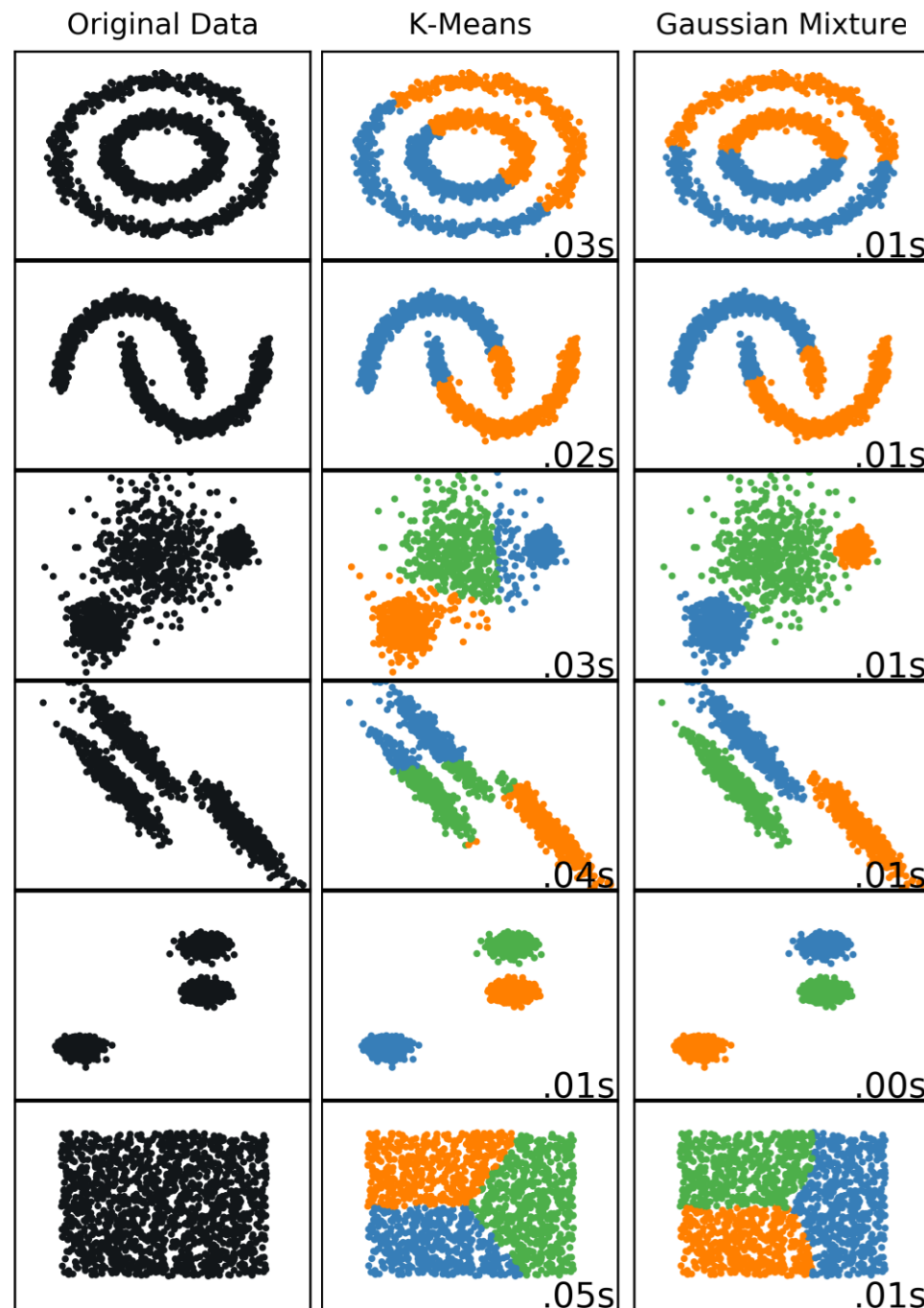
$L$  = number of  
EM cycles

Image from Bishop, Pattern Recognition, 2006

# Examples: GMM

Can produce soft  
clustering

Estimates the density /  
distribution of the data



Struggles when the  
clusters are not  
approximately Gaussian

Excels in situations with  
**variation in cluster  
variance** and **correlation  
between features**

Excels with clusters of  
**equal variance**

Will divide into k clusters  
even when there are not k

# Gaussian Mixture Models

Generative models: model  $P(\mathbf{X}|\boldsymbol{\theta})$ , where  $\boldsymbol{\theta}$  are the model parameters

Very useful for density estimation

Produce hard or soft (fuzzy) clustering

When you restrict the covariance matrix to be diagonal and equal for all clusters, the GMM and K-means algorithm become the same

# Expectation Maximization

**Iterative method** to find maximum likelihood parameter estimates when the model depends on unobserved latent variables, when this can't be solved directly

The E-step updates the latent variable distribution estimates, so that we can calculate the likelihood function given the current parameter values

The M-step identifies the parameters that maximize the likelihood

# Types of clustering algorithms

## Methods

Centroid-based clustering (e.g. **K-Means**)

Distribution-based clustering (e.g. **Gaussian mixture model**)

Density-based clustering (e.g. DBSCAN)

Hierarchical clustering (e.g. agglomerative clustering)  
a.k.a. connectivity-based clustering

## Cluster assignment

**Hard clustering**

**Soft clustering** (a.k.a. fuzzy clustering)