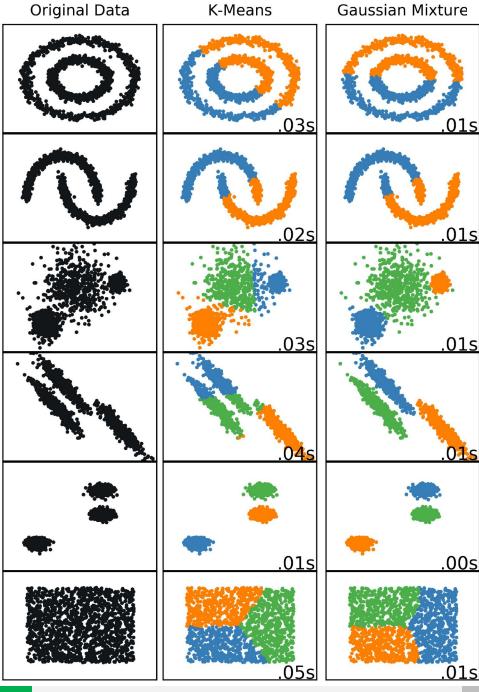
Clustering and Density Estimation

K-Means Gaussian **Mixture** Models (GMMS)

Clustering and Density Estimation (GMMS)

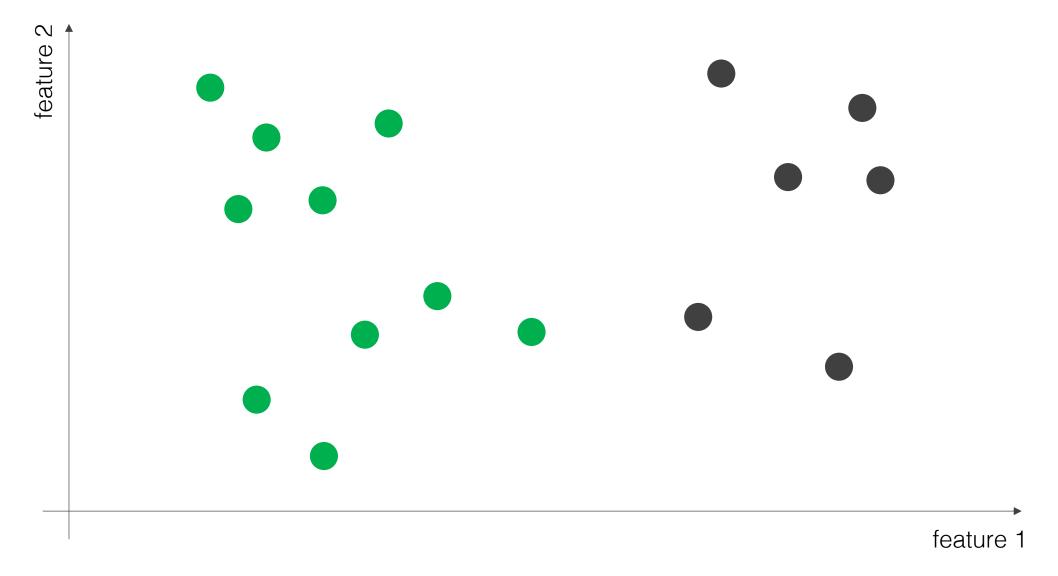


Clustering

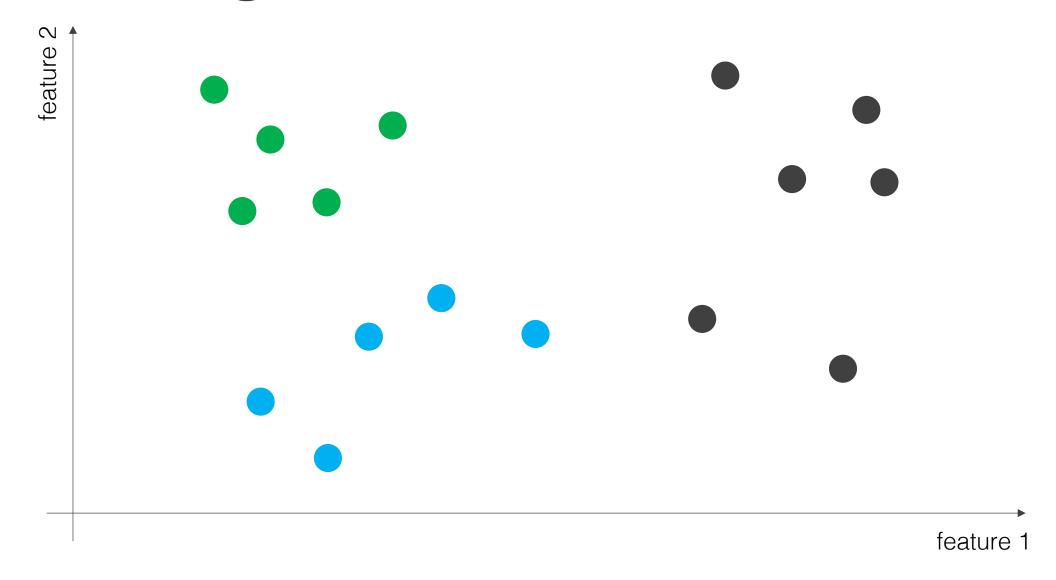




Looks like 2 clusters...



... 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)

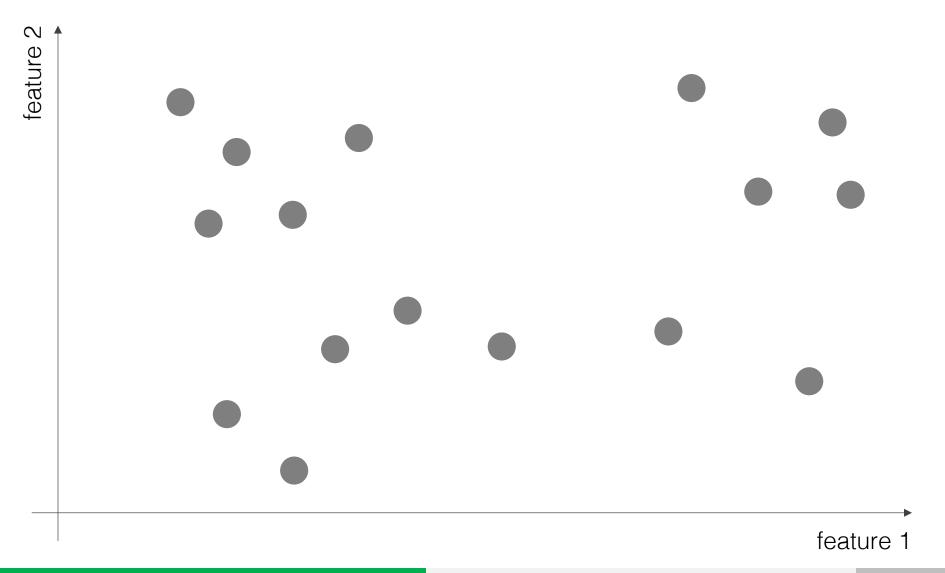
Hierarchical clustering (e.g. agglomerative clustering)

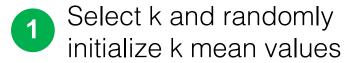
a.k.a. connectivity-based clustering

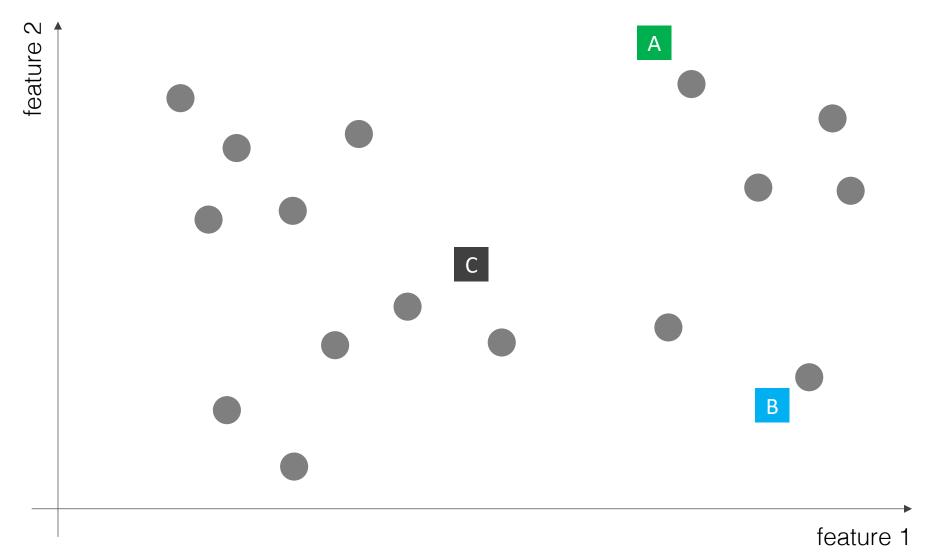
Cluster assignment

Hard clustering

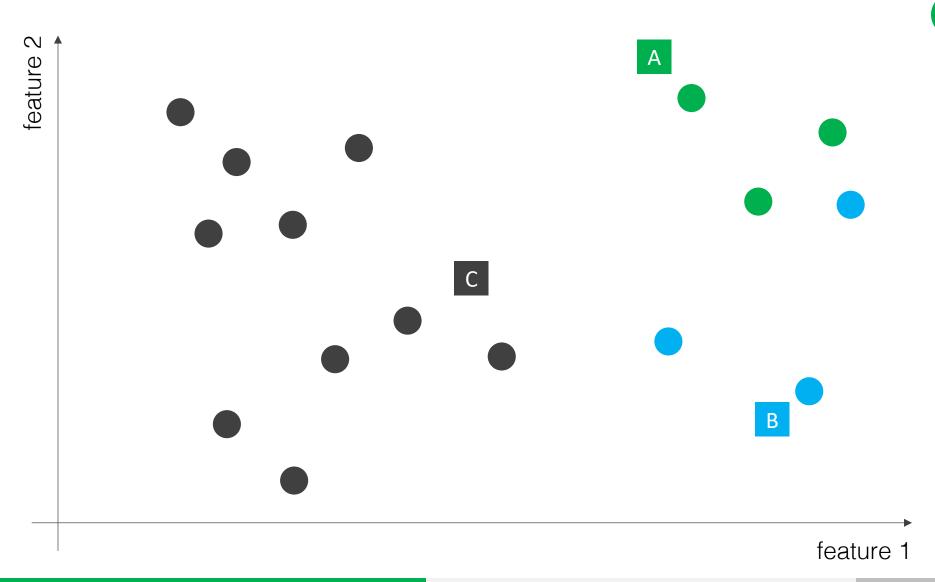
Soft clustering (a.k.a. fuzzy clustering)



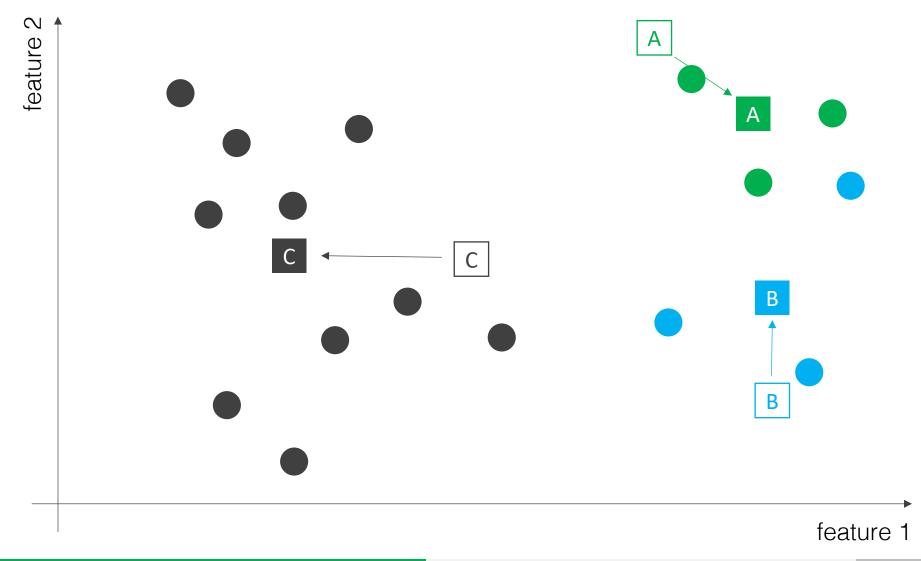




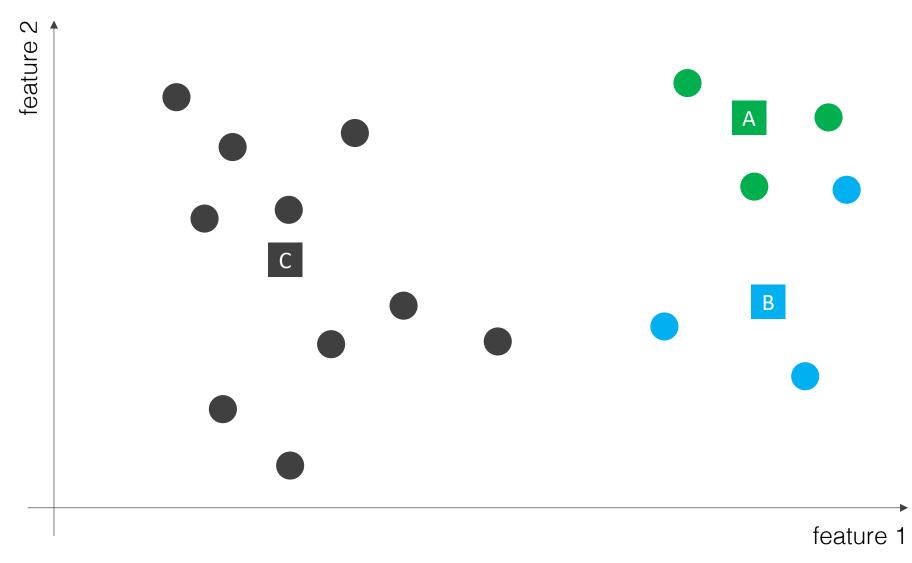
Clustering I Lecture 18



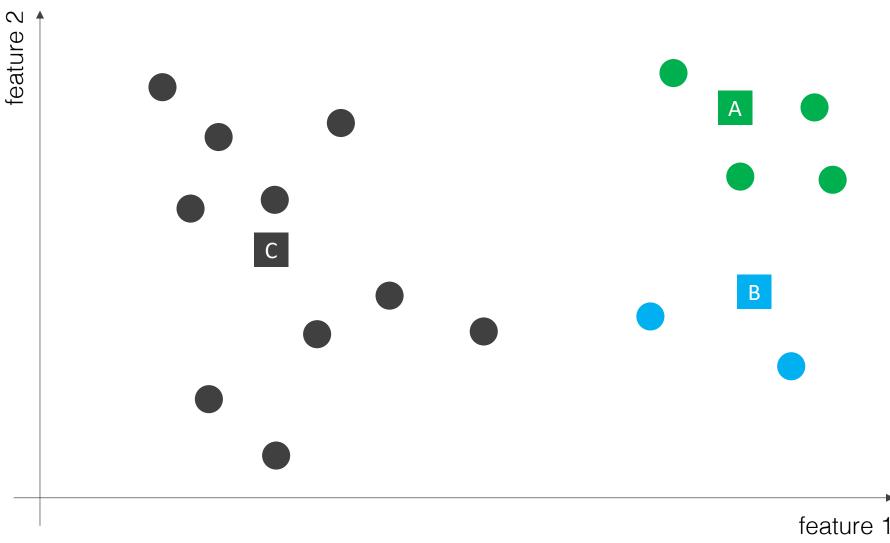
- Select k and randomly initialize k mean values
- Assign observations to the nearest mean



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

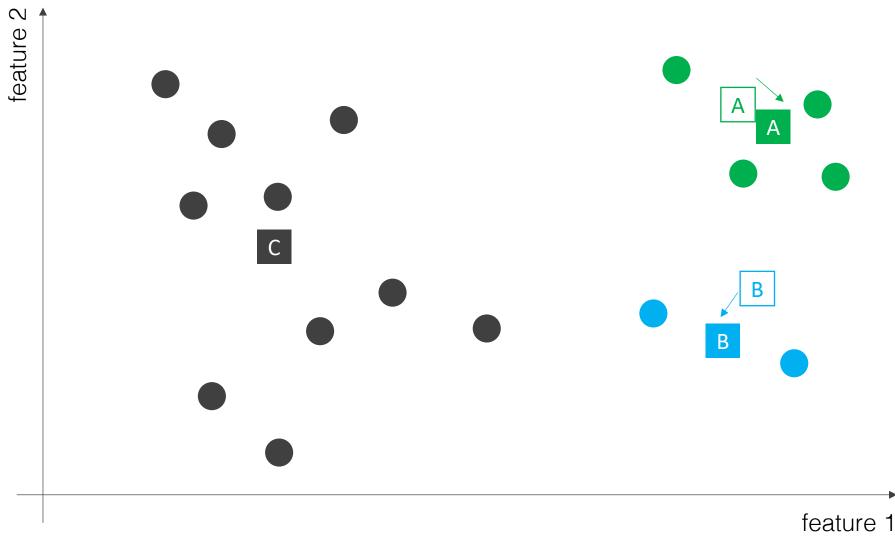


- Select k and randomly initialize k mean values
- Assign observations to the nearest mean
- Update the mean to be the centroid of the labeled data
- Repeat steps 2 and 3 until convergence



- Select k and randomly initial k mean values
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- Repeat steps 2 and 3 until convergence

...Iteration 2

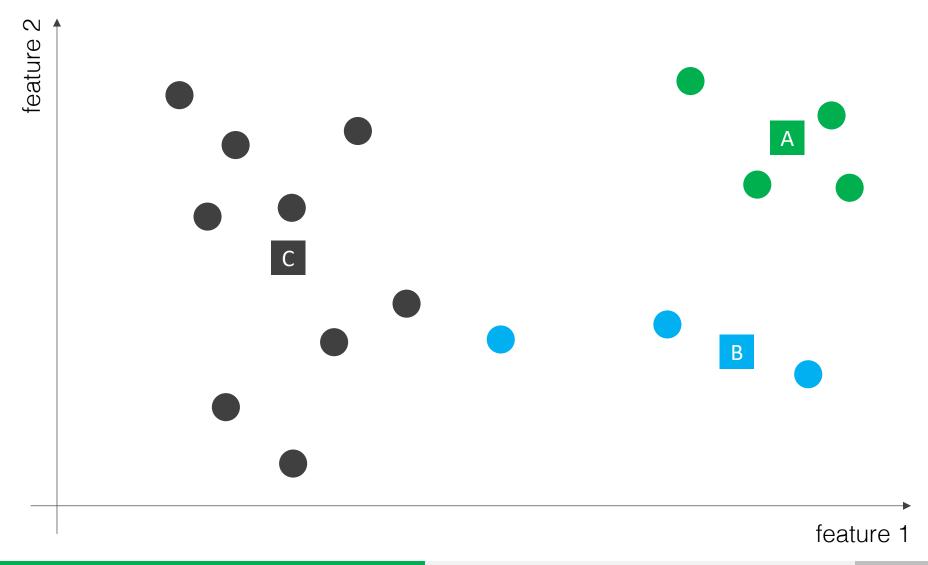


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- Repeat steps 2 and 3 until convergence

...Iteration 2

eature i

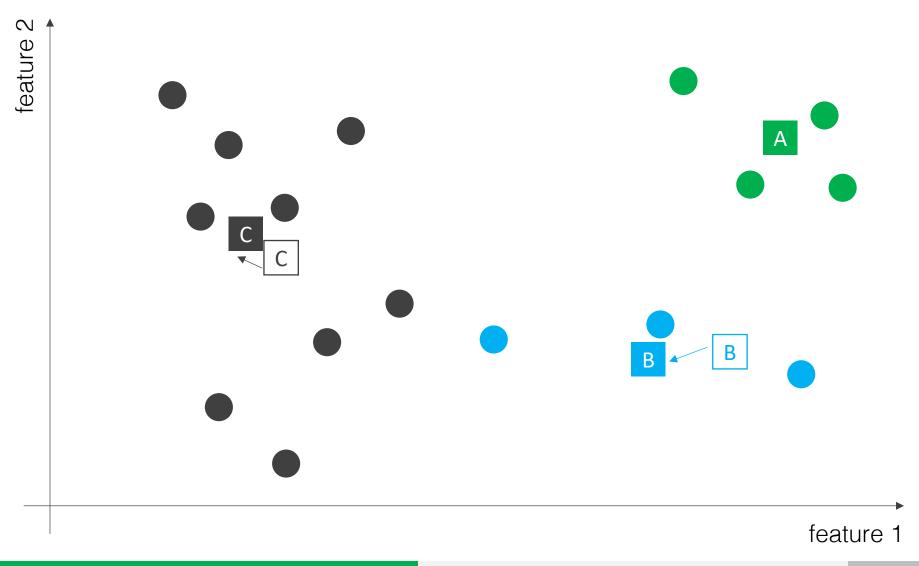
Kyle Bradbury



- Select k and randomly initialize k mean values
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- Repeat steps 2 and 3 until convergence

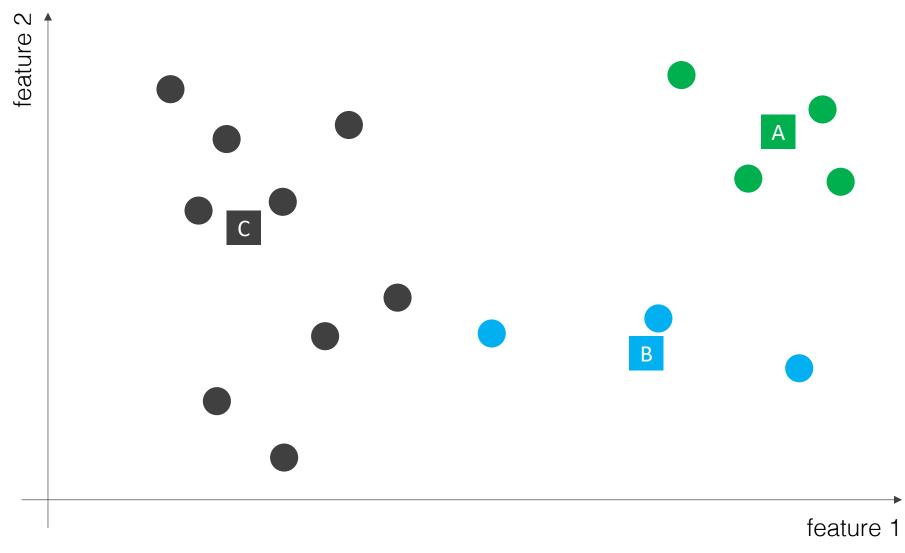
...Iteration 3

Lecture 18 15



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

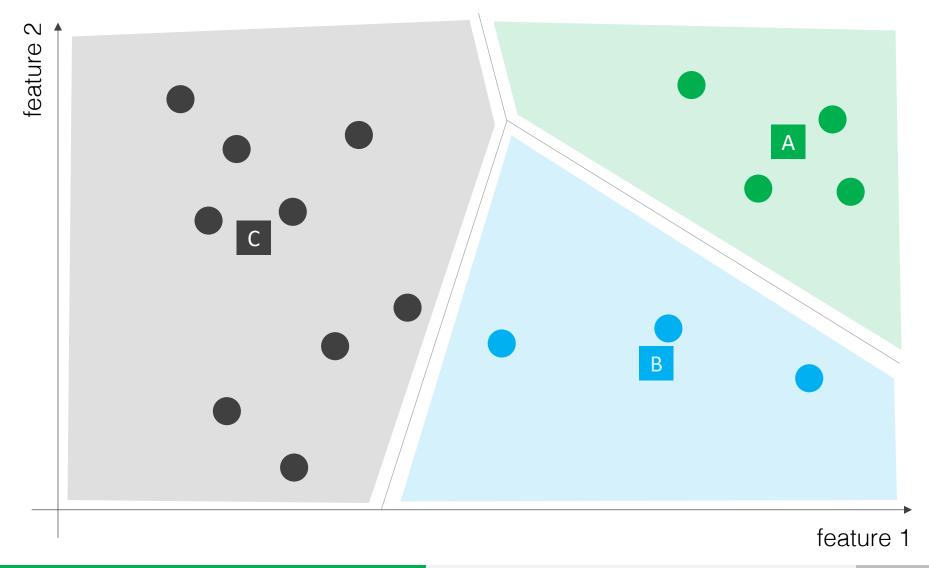
...Iteration 3



- Select k and randomly initialize k mean values
- Assign observations to the nearest mean
- Update the mean to be the centroid of the labeled data
- 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: For our N samples, identify K means, μ_k , such that the set of closest points in feature space are the minimum distance away.

$$r_{ik} = \left\{egin{array}{ll} 1 & ext{ if } oldsymbol{x}_i & ext{ is closest to the kth mean } oldsymbol{\mu}_k \\ 0 & ext{ else} \end{array}
ight. \quad \left. \begin{array}{ll} L_2 & ext{ norm} \\ \downarrow \\ C(oldsymbol{x}_i, oldsymbol{\mu}_1, oldsymbol{\mu}_2, \dots, oldsymbol{\mu}_K) = \sum_{i=1}^N \sum_{k=1}^K r_{ik} \|oldsymbol{x}_i - oldsymbol{\mu}_k \|_2^2 \end{array}
ight.$$

1. E-step

Re-evaluate r_{ik}

$$r_{ik} = \left\{ egin{array}{ll} 1 & ext{if } oldsymbol{x}_i & ext{is closest to the kth mean } oldsymbol{\mu}_i \ 0 & ext{else} \end{array}
ight.$$

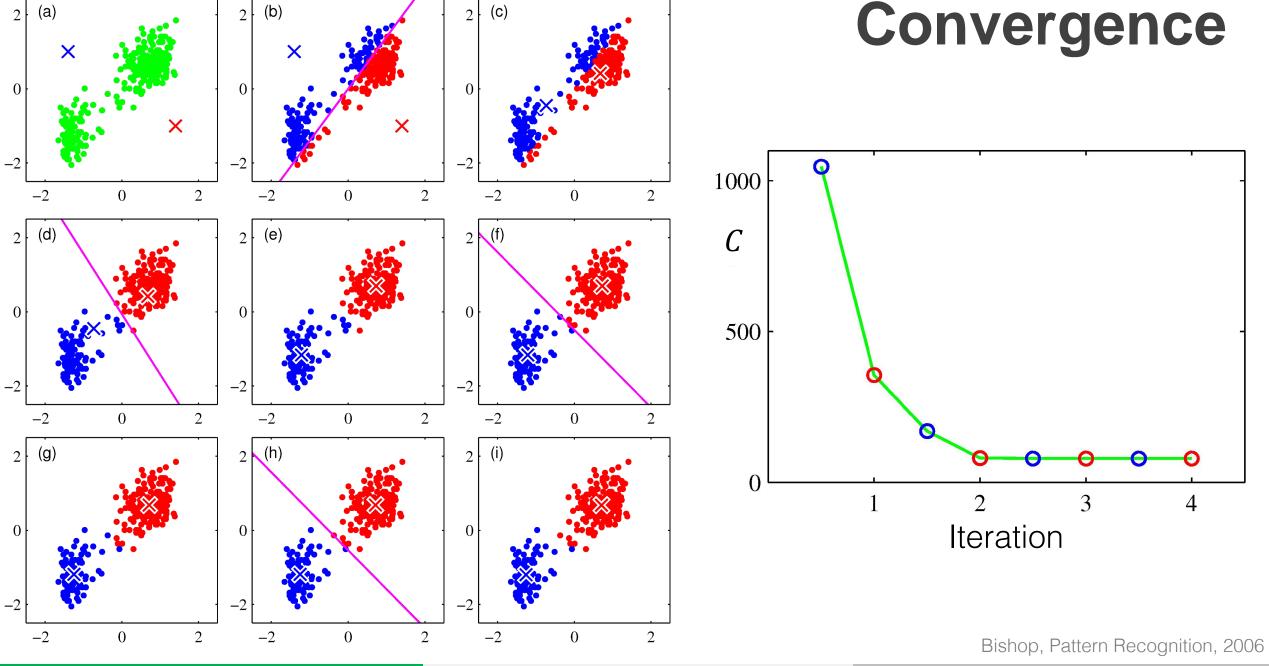
Assign new "expected" cluster assignments

2. M-step

Minimize C wrt μ_i

$$\mu_k = \frac{\sum_i r_{ik} \, x_i}{\sum_i r_{ik}}$$

Update the cluster means to maximize the likelihood



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 approach: silhouette (graphical approach to evaluating cluster fit)

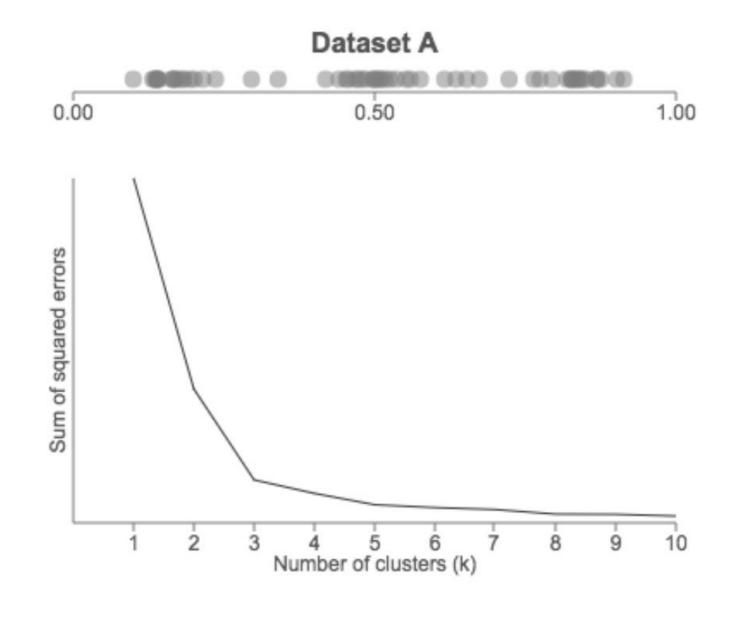


Image by Robert Gove: https://bl.ocks.org/rpgove/0060ff3b656618e9136b

Distance / dissimilarity measure

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

Distance measure (for distance from the mean):

Name of method:

$$L_2$$
 norm

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

K-means

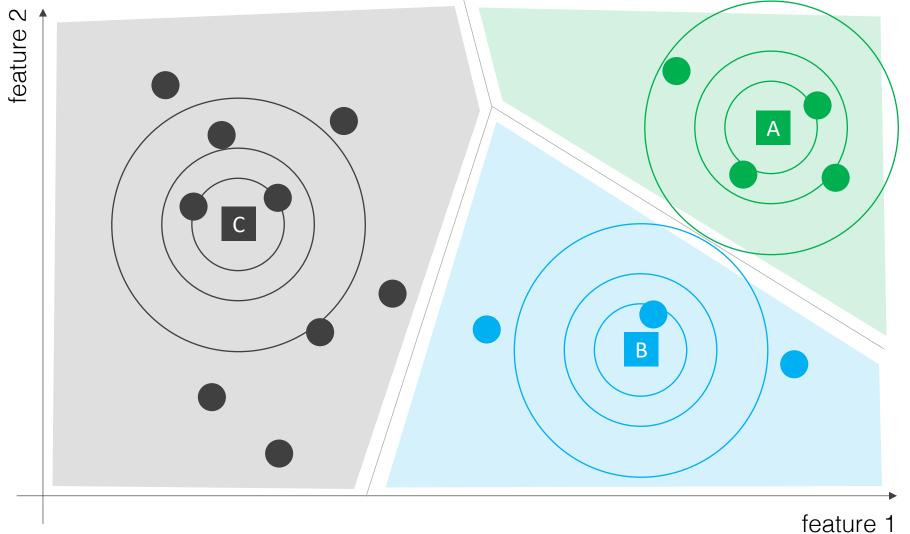
Generalization to other distance measures, e.g.:

K-mediods

$$L_1$$
 norm

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

Relationship to Gaussian distributions



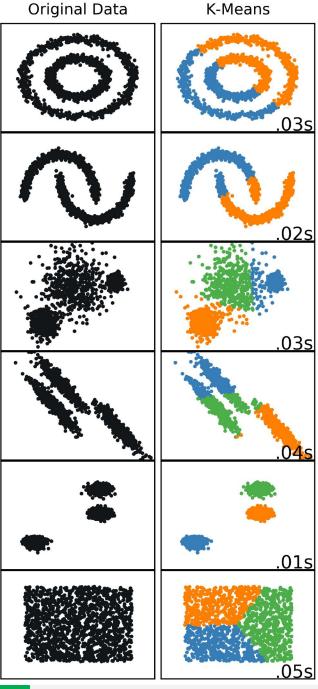
Assumes the clusters are **Gaussians** centered at the mean, each with identical covariance matrices, where all the features are independent:

$$\mathbf{\Sigma}_{\mathbf{k}} = \sigma^2 \mathbf{I} = \begin{bmatrix} \sigma^2 & 0 \\ 0 & \sigma^2 \end{bmatrix}$$

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

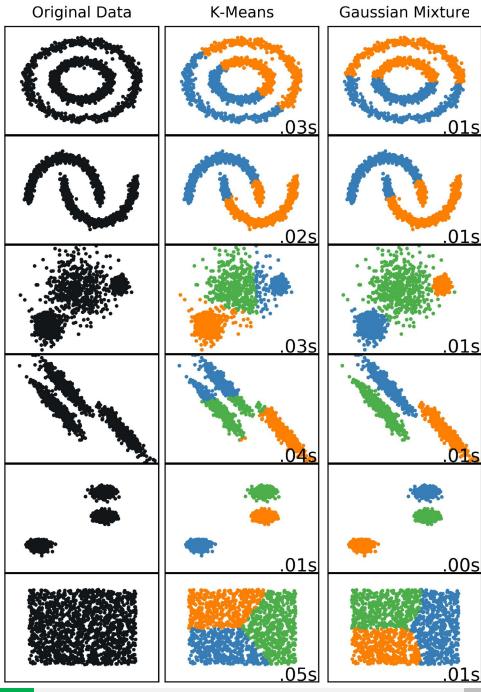
K-Means

Gaussian Mixture

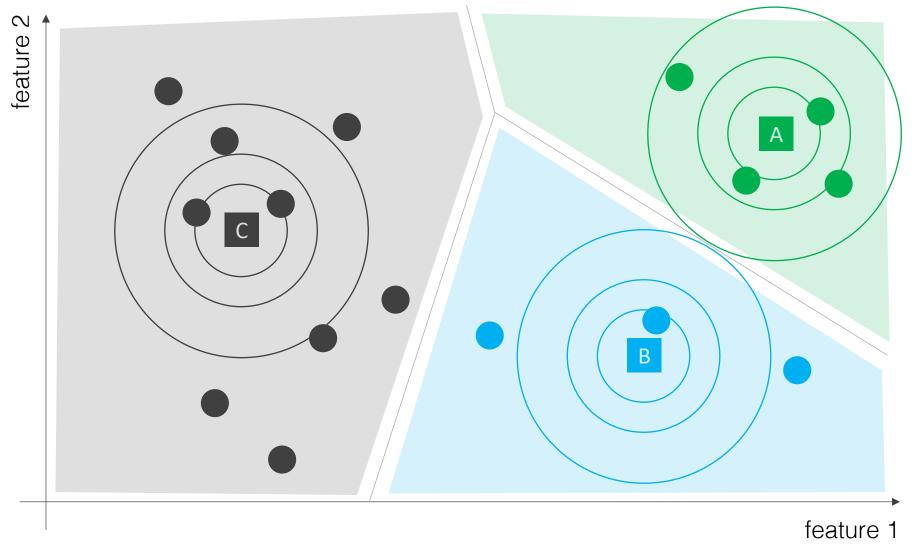
Models

(GMMS)

Clustering and Density Estimation (GMMS)



Relaxing our assumptions on covariance...



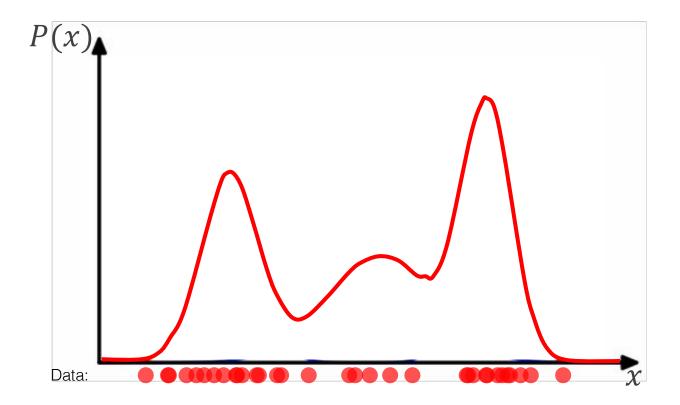
What if we don't assume the Gaussian clusters have identical, diagonal covariance matrices?

Lecture 18 26

Gaussian Mixture Models

For clustering and density estimation

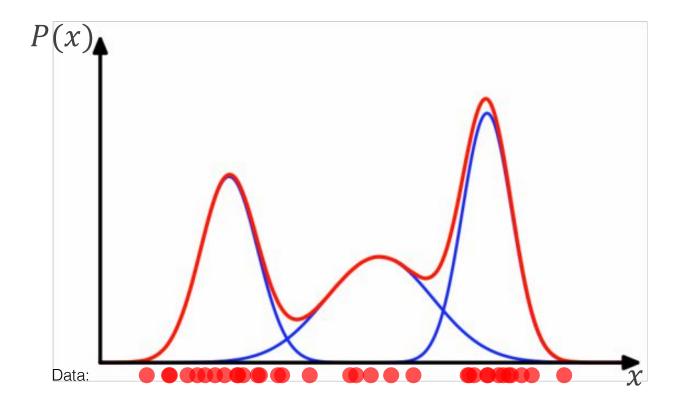
Mixture model



We can estimate the distribution density of our data...

Image from Shaun Dowling

Mixture model

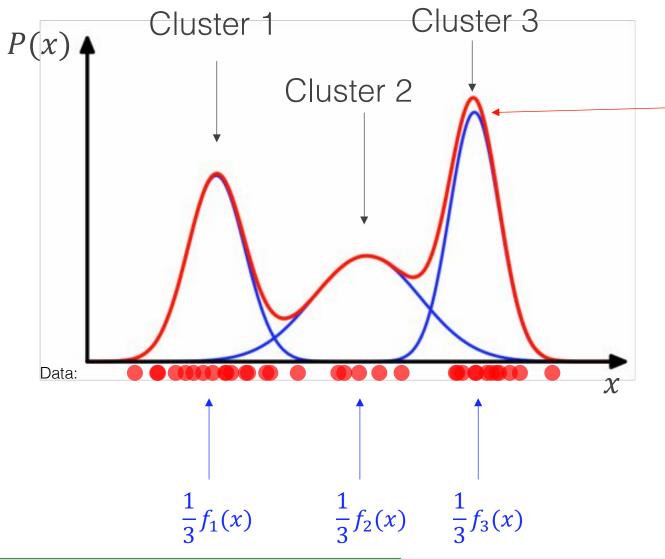


We can estimate the distribution density of our data...

...using a mixture of distributions

Image from Shaun Dowling

Mixture model



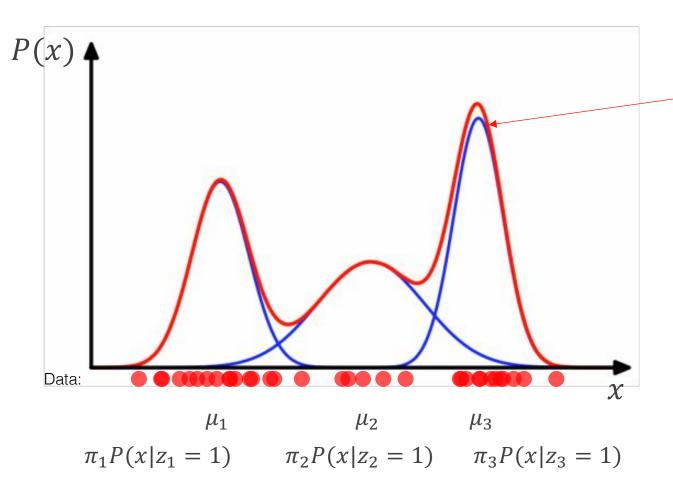
A weighted average of density functions

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

- 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)

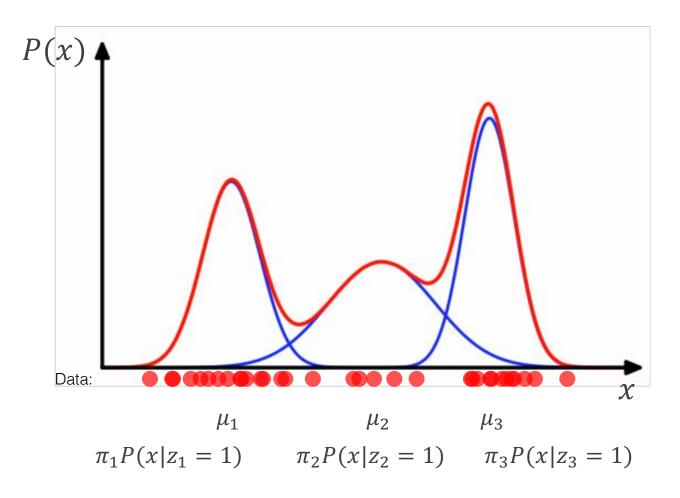
Image from Shaun Dowling

The mixing coefficients

 $\pi_k = P(z_k = 1)$ need to sum to 1 for a valid distribution K

 z_k = binary variable that represents cluster membership

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. We don't DIRECTLY see this.
- Observable
 Given z, we assume a sample is drawn from $P(x|z_k=1)$

Note: We can use these terms to compute the posterior probability $P(z_k|x)$

Kyle Bradbury

Image from Shaun Dowling

Gaussian Mixture Model Latent Variables

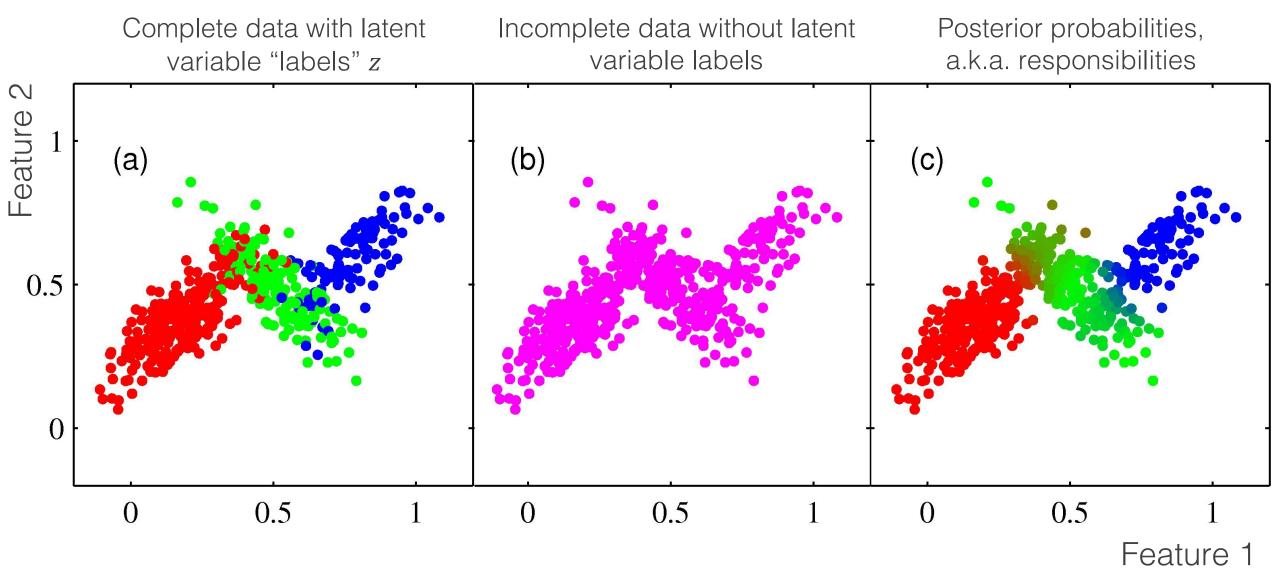
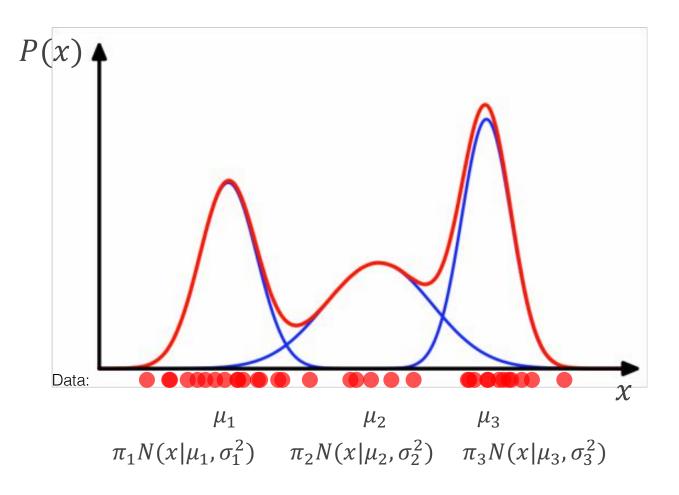


Image from Bishop, Pattern Recognition, 2006

Gaussian mixture model



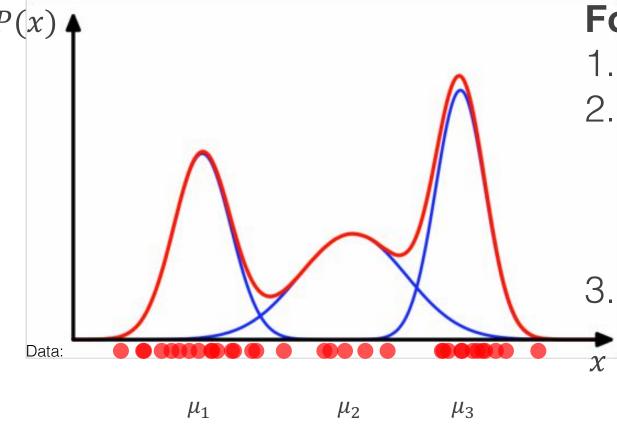
The Gaussian mixture model is represented as:

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

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

Image from Shaun Dowling

Gaussian mixture model



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

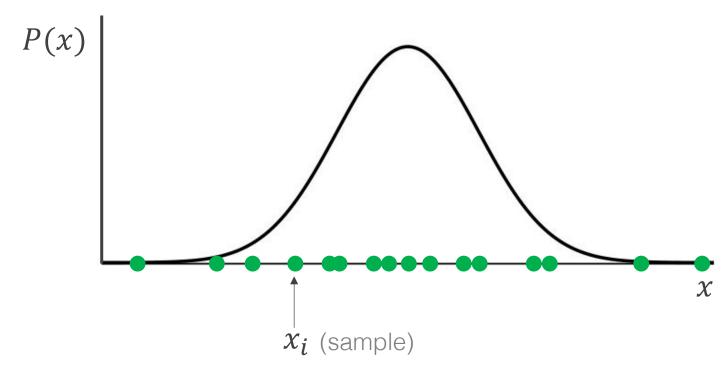
For clustering:

- 1. Pick a number of clusters, K
- 2. Fit a GMM to the data (estimate π_k , μ_k , σ_k^2 for $k=1,\ldots,K$ to maximize the likelihood of the data given the model)
- 3. 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:

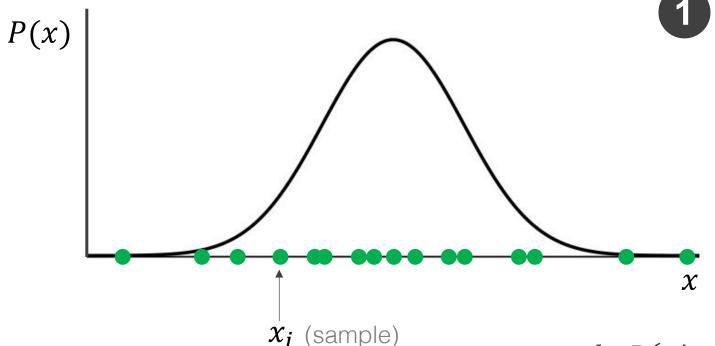
$$P(x|\mu, \sigma^{2})$$

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

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

Density estimation for a single mixture component

a.k.a. model fitting



We follow our familiar pattern: maximize the likelihood of the data by choosing our model parameters: μ , σ^2

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

Calculate the log likelihood:

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

Take the derivative of the log likelihood w.r.t. each parameter (μ, σ^2) , set equal to zero, solve for μ , σ^2

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

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

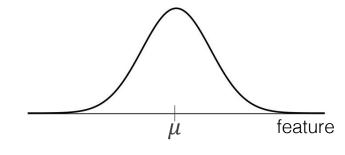
From a univariate to a multivariate Gaussian

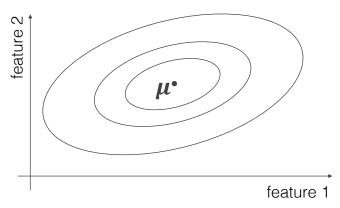
Univariate Normal density

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

Multivariate Normal density

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





From a univariate to a multivariate Gaussian

Univariate Normal MLE parameter estimates:

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

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

Multivariate Normal MLE parameter estimates:

$$\widehat{\boldsymbol{\mu}} = \frac{1}{N} \sum_{i=1}^{N} \boldsymbol{x}_i$$

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

Moving from a single Gaussian to a mixture of Gaussians

Density estimation for a Gaussian mixture model

We define the likelihood of one observation given our model with parameters π_k , μ_k , Σ_k for $k=1,\ldots,K$

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

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

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

2 Calculate the log likelihood:

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

Take the derivative of the log likelihood w.r.t. each parameter (π_k, μ_k, Σ_k) for k = 1, ..., 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

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

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 $\ln P(X|\pi,\mu,\Sigma) =$

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

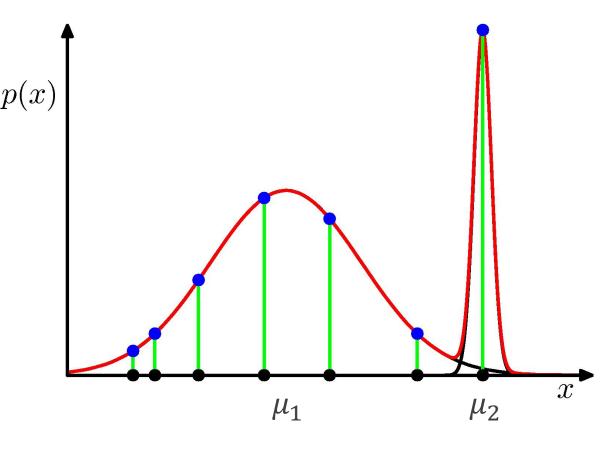
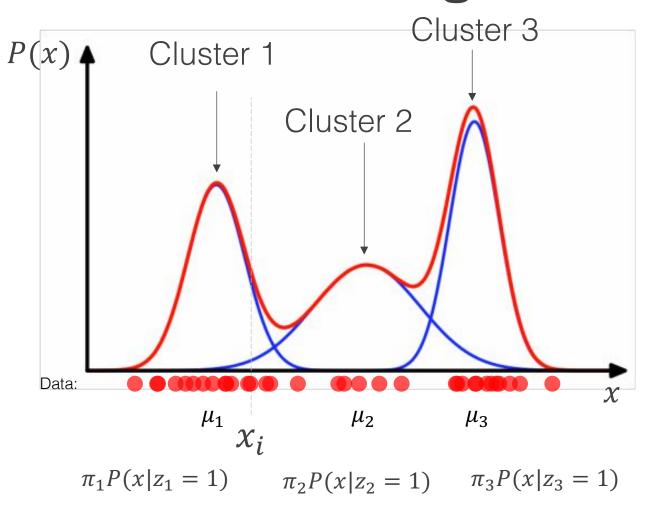


Image from Bishop, Pattern Recognition, 2006

How do we assign a cluster?

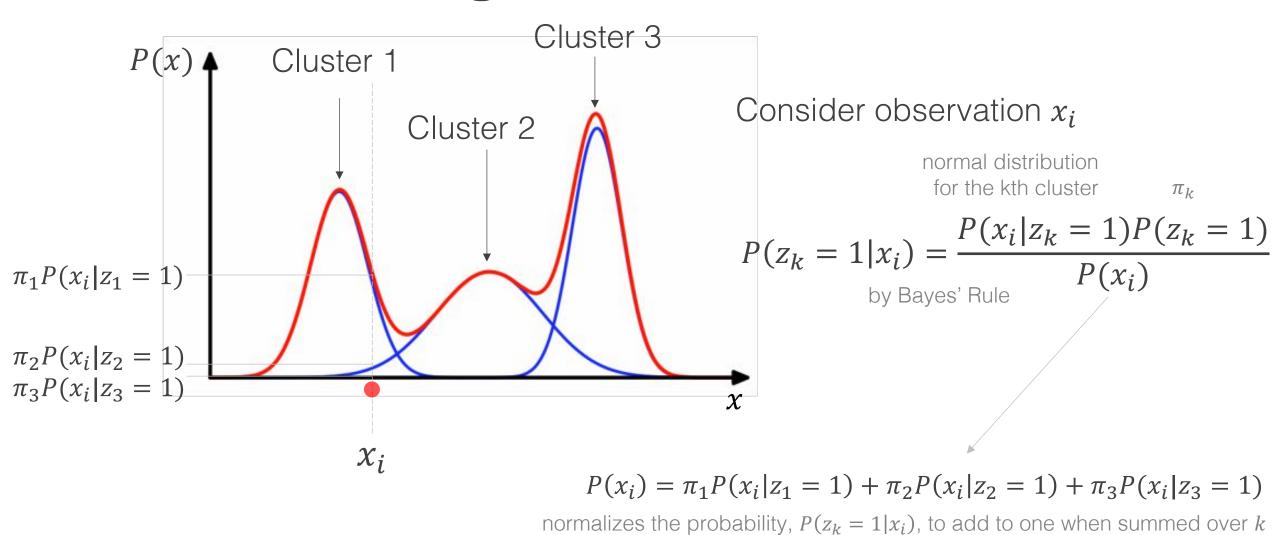


The probability of x_i is "explained" most by cluster 1, a little by cluster 2, and very little by cluster 3

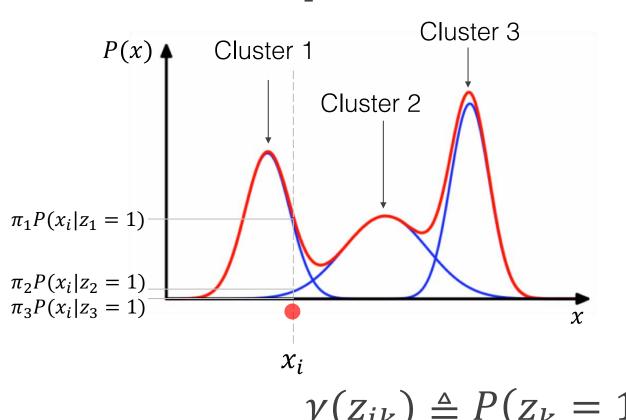
We assign the cluster, z_k so that $P(z_k = 1|x)$ is the largest for all the k's

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

How do we assign a cluster?



Posterior probabilities / "responsibilities"



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

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

 π_k

Define
$$N_k = \sum_{i=1}^N \gamma(z_{ik})$$
 = $\frac{\pi_k N(\boldsymbol{x}_i | \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)}{\sum_{k=1}^K \pi_k N(\boldsymbol{x}_i | \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)}$ Expected number of samples per cluster

Clustering I **Kyle Bradbury** Lecture 18

Expectation Maximization for a GMM

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

Note: EM is a general technique for finding maximum likelihood solutions for models with latent variables

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

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

$$\gamma(z_{ik}) \triangleq P(z_k = 1 | x_i)$$

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

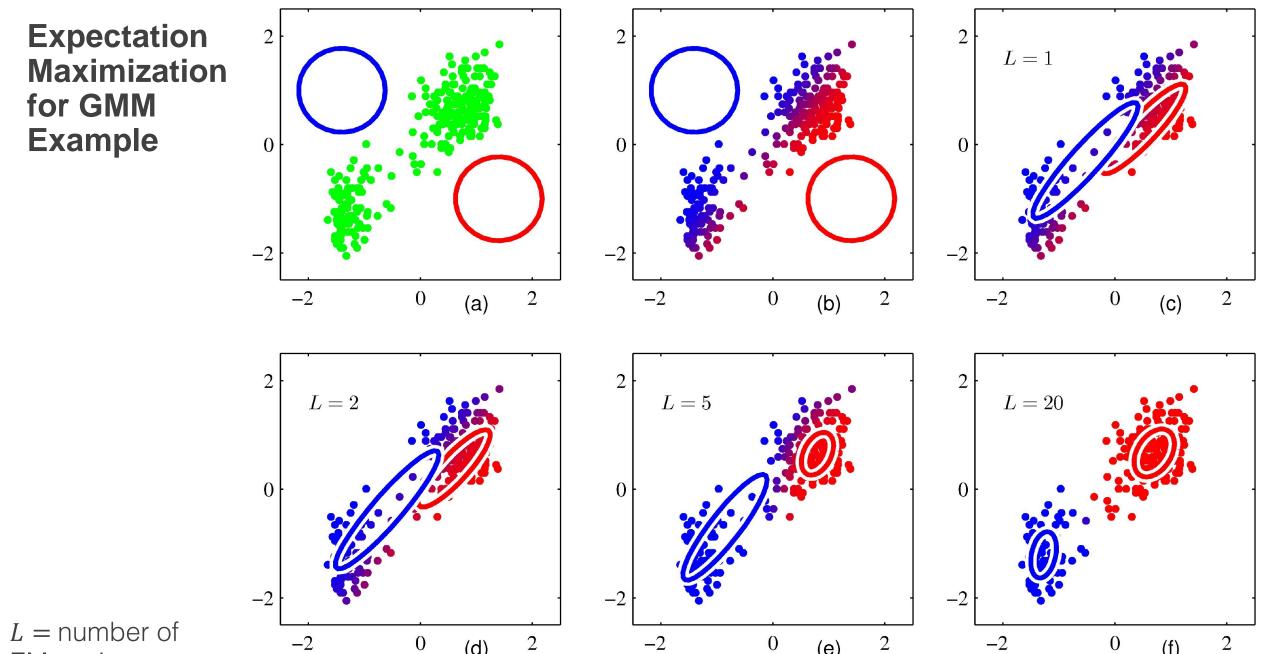
2. Maximization-step

Use the "responsibilities" to update the model parameters to maximize the log likelihood

$$\boldsymbol{\mu}_{k}^{new} = \frac{1}{N_{k}} \sum_{i=1}^{N} \gamma(z_{ik}) \boldsymbol{x}_{i}$$

$$\Sigma_k^{new} = \frac{1}{N_k} \sum_{i=1}^N \gamma(z_{ik}) (\boldsymbol{x}_i - \boldsymbol{\mu}_k^{new}) (\boldsymbol{x}_i - \boldsymbol{\mu}_k^{new})^T$$

$$\pi_k^{new} = \frac{N_k}{N}$$
 Where $N_k = \sum_{i=1}^N \gamma(z_{ik})$



-2

0

(e)

L = number ofEM cycles

Image from Bishop, Pattern Recognition, 2006

0

(d)

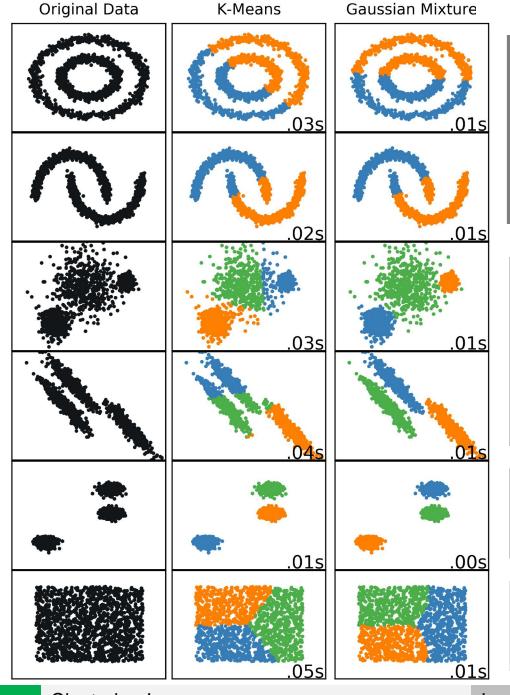
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-2

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 $P(X|\theta)$, where θ 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)