

# Clustering

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- 1 Overview
- 2 Hierarchical clustering
- 3 K-means
- 4 Cluster validity
- 5 Mixture Models
- 6 Community detection

## 1 Overview

## 2 Hierarchical clustering

## 3 K-means

## 4 Cluster validity

## 5 Mixture Models

## 6 Community detection

- Spectral clustering
- Community detection problems
- Modularity
- BigCLAM

- A catalog of 2 billion “sky objects” represents objects by their radiation in 7 dimensions (frequency bands).
- **Problem:** Cluster into similar objects, e.g., galaxies, nearby stars, quasars, etc.
- **Sloan Digital Sky Survey:**



Finding topics:

- Represent a document by a vector  $(x_1, x_2, \dots, x_k)$ , where  $x_i = 1$  iff the  $i$ -th word (in some order) appears in the document
- Documents with similar sets of words may be about the same topic

# Clustering Problem: Images



# What is a cluster?

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**Goal:** partitioning data in maximally homogeneous, maximally distinguished subsets.

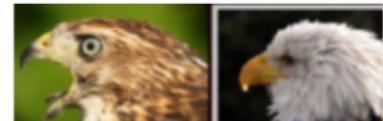
- **Internal criterion:** members of the cluster should be similar to each other (**inter-cluster compactness**).



tigers



whales



raptors

# What is a cluster?

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**Goal:** partitioning data in maximally homogeneous, maximally distinguished subsets.

- **External criterion:** objects outside the cluster should be dissimilar from the objects inside the cluster (**intra-cluster distance**).

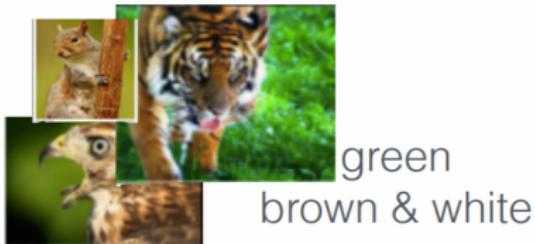


# What is a cluster?

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**Goal:** partitioning data in maximally homogeneous, maximally distinguished subsets.

- **Internal criterion:** members of the cluster should be similar to each other (**inter-cluster compactness**).
- **External criterion:** objects outside the cluster should be dissimilar from the objects inside the cluster (**intra-cluster distance**).



blue  
black  
&  
white



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## 3 K-means

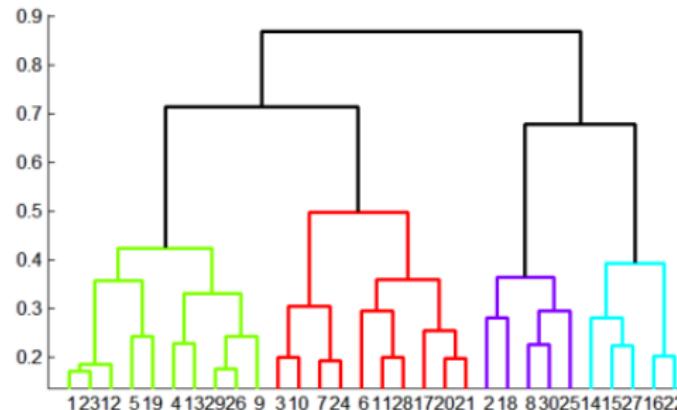
## 4 Cluster validity

## 5 Mixture Models

## 6 Community detection

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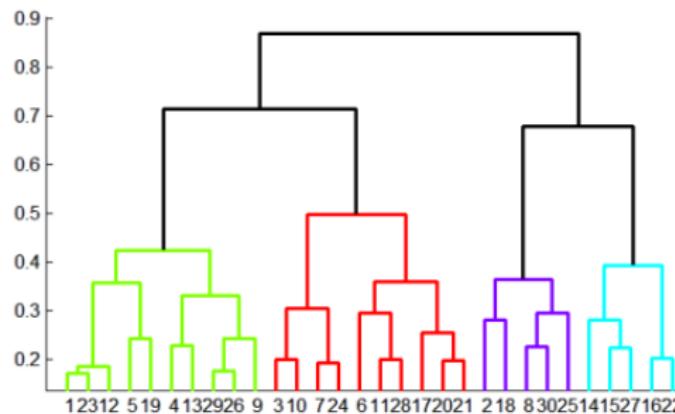
- **Agglomerative (bottom up):**
  - Initially, each point is a cluster;
  - Repeatedly combine the two “nearest” clusters into one.
- **Divisive (top down):**
  - Start with one cluster and recursively split it.



**Key operation:** Repeatedly combine two nearest clusters.

Three important questions:

- ① How do you represent a cluster of more than one point?
- ② How do you determine the “nearness” of clusters?
- ③ When to stop combining clusters?



**Key operation:** Repeatedly combine two nearest clusters

- ① How do you represent a cluster of more than one point?
  - **Key problem:** As you merge clusters, how do you represent the “location” of each cluster, to tell which pair of clusters is closest?
  - **Euclidean case:** each cluster has a centroid = average of its points
- ② How do you determine the “nearness” of clusters?
  - Measure cluster distances by distances of centroids

## Minkowski family of distances:

$$D(x, y) = \sqrt[p]{|x_1 - y_1|^p + |x_2 - y_2|^p + \cdots + |x_n - y_n|^p}.$$

It can be checked that for any  $p \geq 1$ :

- $D(x, y) \geq 0$ ,
- $D(x, x) = 0$ ,
- $D(x, y) = D(y, x)$ ,
- $D(x, y) \leq D(x, z) + D(z, y)$ .

## Minkowski family of distances:

$$D(x, y) = \sqrt[p]{|x_1 - y_1|^p + |x_2 - y_2|^p + \cdots + |x_n - y_n|^p}.$$

In case of  $p = 1$ :

$$D(x, y) = |x_1 - y_1| + |x_2 - y_2| + \cdots + |x_n - y_n|.$$

It is nicknamed **Manhattan distance** (blue):



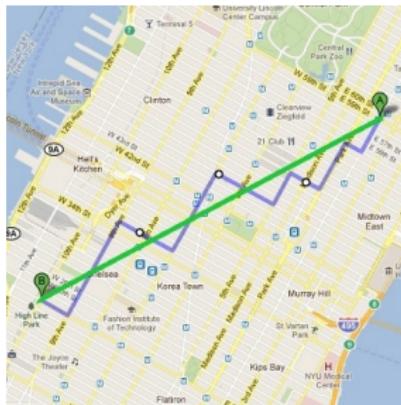
## Minkowski family of distances:

$$D(x, y) = \sqrt[p]{|x_1 - y_1|^p + |x_2 - y_2|^p + \cdots + |x_n - y_n|^p}.$$

In case of  $p = 2$ :

$$\sqrt{|x_1 - y_1|^2 + |x_2 - y_2|^2 + \cdots + |x_n - y_n|^2}.$$

Euclidean distance (green):



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- Randomly **initialize**  $k$  centers:

$$\mu^0 = (\mu_1^0, \dots, \mu_k^0).$$

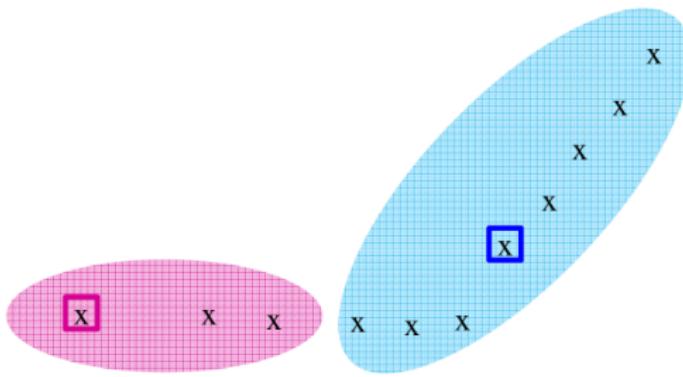
- **Classify:** Assign each point  $j \in \{1, \dots, m\}$  to nearest center:

$$z^j = \arg \min_i \| \mathbf{x}_j - \mu_i^t \|_2^2.$$

- **Recenter:**  $\mu_i$  becomes centroid of its points:

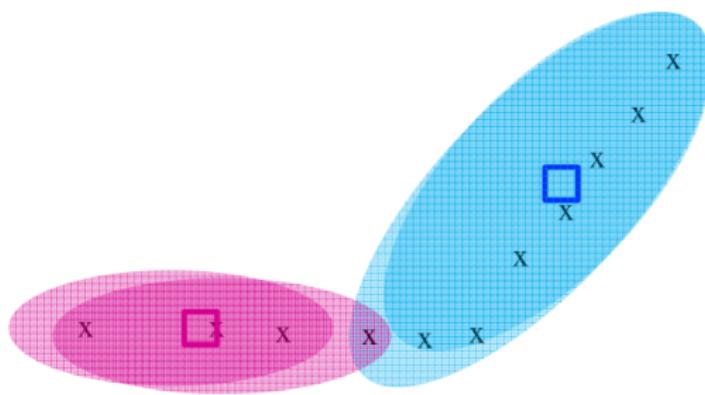
$$\mu_i^{t+1} = \arg \min_{\mu} \sum_{j: z^j = i} \| \mathbf{x}_j - \mu \|_2^2.$$

Equivalent to  $\mu_i$  average of its points!



$\text{x}$  ... data point  
 $\square$  ... centroid

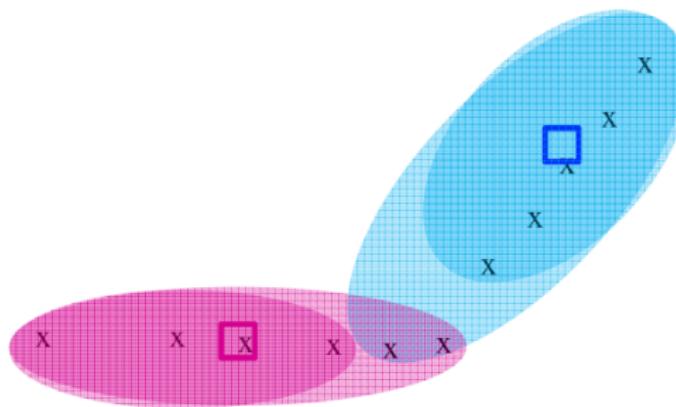
**Clusters after round 1**



X ... data point

□ ... centroid

**Clusters after round 2**



$\text{X}$  ... data point  
 $\square$  ... centroid

**Clusters at the end**

## Assumptions:

- Known number of clusters;
- Clusters of approximately same size and density;
- Spherical form.

1 Overview

2 Hierarchical clustering

3 K-means

4 Cluster validity

5 Mixture Models

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- For supervised classification we have a variety of measures to evaluate how good our model is: accuracy, precision, recall.
- For cluster analysis, the analogous question is how to evaluate the goodness of the resulting clusters?
- We need measures to compare:
  - clustering algorithms;
  - two sets of clusters.

- **External measure:** used to measure the extent to which cluster labels match externally supplied class labels.
  - Example: entropy
- **Internal measure:** used to measure the goodness of a clustering structure without respect to external information.
  - Example: Sum of Squared Errors (SSE)

- Partition obtained:  $P = \{P_1, \dots, P_K\}$ ;
- External (true) partition:  $C = \{C_1, \dots, C_K\}$ ;
- $m_{ij}$  is a number of objects in  $P_i \cap C_j$ ;
- $m_{i\cdot} = \sum_{j=1}^K m_{ij}$ .

- Distribution of objects in  $P_i$ :

$$\frac{m_{i1}}{m_{i\cdot}}, \frac{m_{i2}}{m_{i\cdot}}, \dots, \frac{m_{in}}{m_{i\cdot}}.$$

- Entropy (impurity) of the distribution is

$$\sum_{j=1}^K \frac{m_{ij}}{m_{i\cdot}} \log \frac{m_{ij}}{m_{i\cdot}}.$$

- Overall entropy:

$$E = - \sum_{i=1}^K \frac{m_{i\cdot}}{m} \sum_{j=1}^K \frac{m_{ij}}{m_{i\cdot}} \log \frac{m_{ij}}{m_{i\cdot}}.$$

- The lower the entropy, the better the clustering.

- Given: to which  $P_i$  an object  $x$  belongs
- This fact tells us something about the true class
- The amount information is measured by

$$MI = \sum_{i,j=1}^K p_{ij} \log \frac{p_{ij}}{p_i p_j},$$

where  $p_{ij} = \frac{m_{ij}}{m}$ ,  $p_i = \frac{m_{i\cdot}}{m}$ ,  $p_j = \frac{m_{\cdot j}}{m}$ .

- Higher mutual information implies a higher clustering quality

$$J = \frac{a}{a + b + c},$$

where

- $a$  is the number of pairs of points with the same label in  $C$  and assigned to the same cluster in  $P$ ;
- $b$  is the number of pairs with the same label, but in different clusters;
- $c$  is the number of pairs in the same cluster, but with different class labels.

The index produces a result in the range  $[0, 1]$ , where a value of 1.0 indicates that  $C$  and  $P$  are identical

$$RI = \frac{a + d}{a + b + c + d},$$

where

- $a, b, c$  are as above
- $d$  denotes the number of pairs with a different label in  $C$  that were assigned to a different cluster in  $P$
- The index produces a result in the range  $[0, 1]$ , where a value of 1.0 indicates that  $C$  and  $P$  are identical.
- A high value for this measure generally indicates a high level of agreement between a clustering and the true classes.

Consider an  $i$ -th individual point

- $a(i)$  = average distance of the  $i$ -th point to the points in its cluster.
- $b(i)$  = min (average) distance of the  $i$ -th point to points in other clusters.
- The silhouette coefficient for the point is then given by

$$s(i) = \frac{b(i) - a(i)}{\max\{a(i), b(i)\}}.$$

- Property:  $-1 \leq s(i) \leq 1$ .

$$s(i) = \frac{b(i) - a(i)}{\max\{a(i), b(i)\}}$$

- If  $s(i)$  is close to 1, sample  $i$  is well-clustered and it was assigned to a very appropriate cluster
- If  $s(i)$  is close to zero, sample  $i$  could be assigned to another closest cluster as well, and the sample lies equally far away from both clusters
- If  $s(i)$  is close to  $-1$ , sample  $i$  is misclassified.
- We can consider average  $\frac{\sum_i s(i)}{m}$  of  $s(i)$  for all objects in the whole dataset:
  - the larger it is, the better the clustering is

1 Overview

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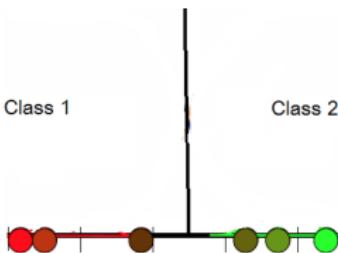
4 Cluster validity

5 Mixture Models

6 Community detection

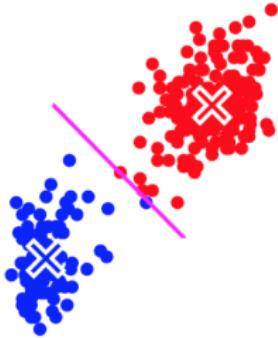
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- K-means performs hard assignment
- Each data point is assigned to one and only one cluster
- Appropriate for points close to cluster centroids
- Not appropriate for points midway between the two cluster centroids

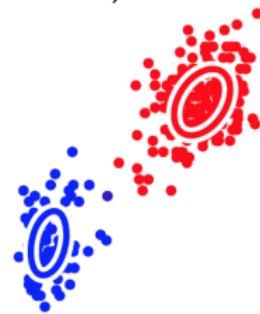


- Each data point is (partially) assigned to clusters with certain probabilities
- One point might be (partially) assigned to multiple clusters
- The midway point is assigned to either cluster with probability 0.5

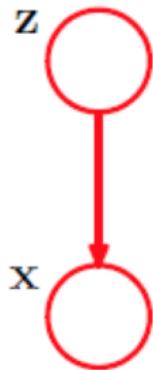




Hard Assignment



Soft Assignment  
(Ellipses: contour of probability functions).



- $K$  clusters:  $1, 2, \dots, K$
- Randomly drawn object
  - $\mathbf{x}$ : attribute values of the object, observed.
  - $z$ : class of the object, latent variable (not observed)
- $P(z)$ : distribution of  $z$ 
  - $\pi_k = P(z = k)$ : probability that the object is from class  $k$
- $p(\mathbf{x}|z)$ : conditional distribution of attribute values
  - $p(\mathbf{x}|z = k)$ : distribution for objects from class  $k$

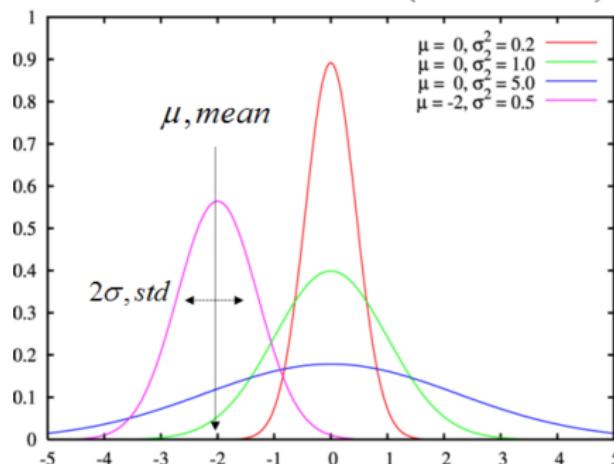
- Distribution of data:

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

- It is a mixture of the distributions for individual classes
- Each  $p(\mathbf{x}|z=k)$  is a component in the mixture
- Gaussian mixtures: each component is a Gaussian distribution

- Gaussian distribution:  $\mathcal{N}(x|\mu, \sigma)$
- Probability density function:

$$p(\mathbf{x}|\mu, \sigma) = \frac{1}{\sigma\sqrt{2\pi}} \exp\left[-\frac{(x - \mu)^2}{2\sigma^2}\right]$$

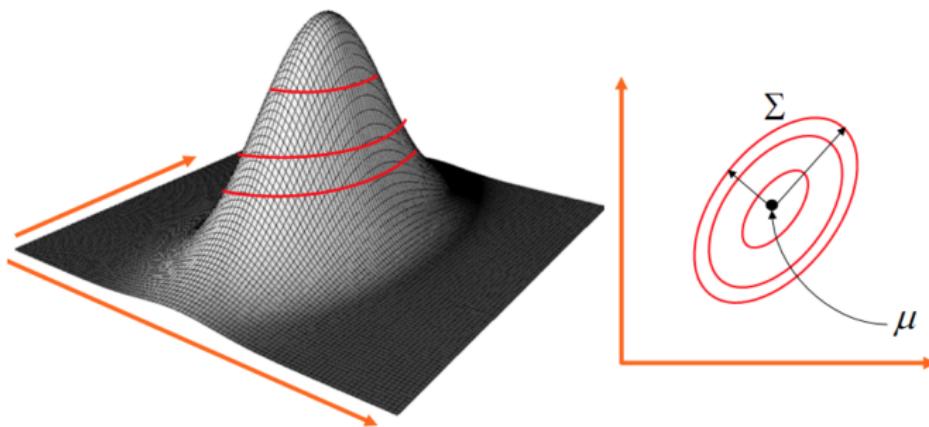


$$p(\mathbf{x}|\boldsymbol{\mu}, \boldsymbol{\Sigma}) = \frac{1}{\sqrt{(2\pi)^d \det(\boldsymbol{\Sigma})}} \exp \left[ -\frac{(\mathbf{x} - \boldsymbol{\mu})^T \boldsymbol{\Sigma}^{-1} (\mathbf{x} - \boldsymbol{\mu})}{2} \right],$$

where

- $d$ : dimension;
- $\mathbf{x}$ : vector of  $d$  random variables, representing data;
- $\boldsymbol{\mu}$ : vector of means;
- $\boldsymbol{\Sigma}$ : covariance matrix.

- $\mu$ : center of contour lines
- $\Sigma$ : orientation and size of contour lines

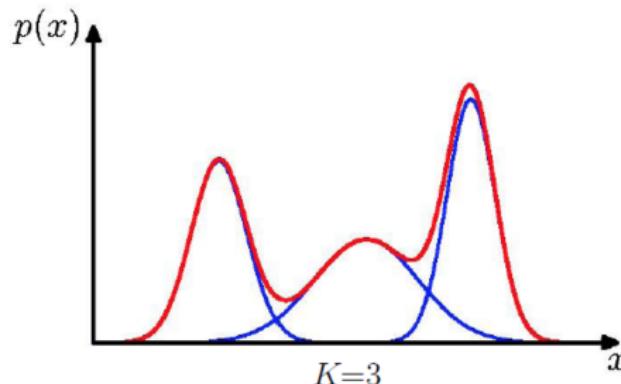


- Mixture distribution:

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

- Each component is a Gaussian distribution:

$$p(\mathbf{x}|z=k) = \mathcal{N}(\mathbf{x}|\boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k).$$

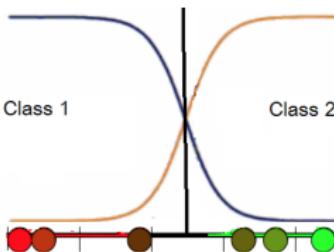


- Given mixture model:

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

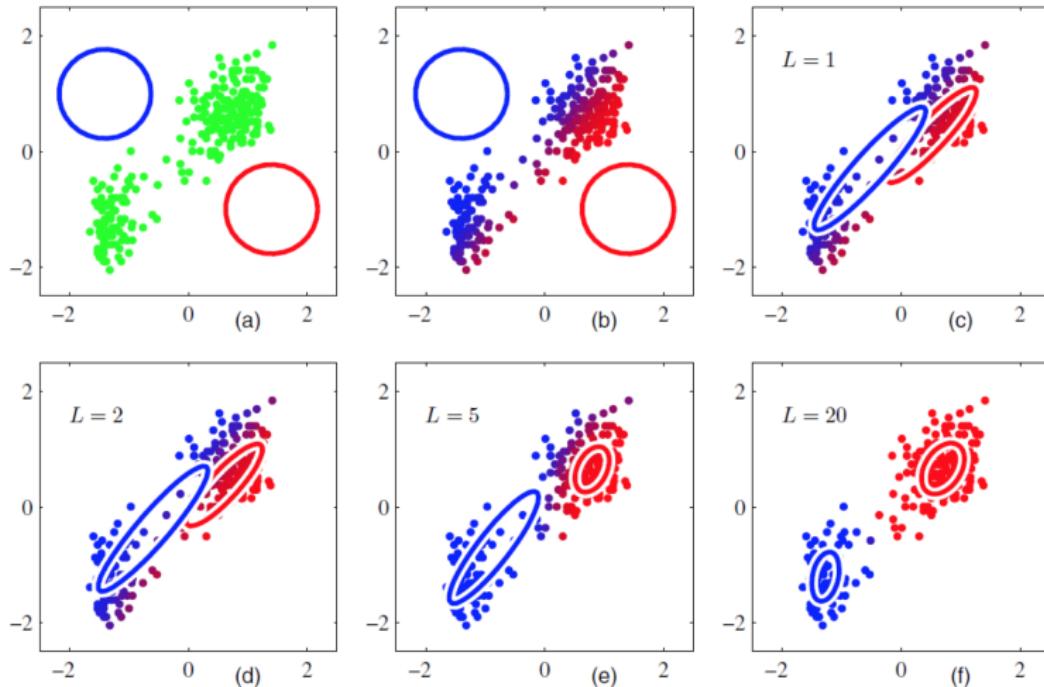
- Object  $\mathbf{x}$  belongs to class  $k$  with probability

$$P(z=k|\mathbf{x}) = \frac{P(z=k)p(\mathbf{x}|z=k)}{p(\mathbf{x})} = \frac{\pi_k p(\mathbf{x}|z=k)}{\sum_{s=1}^K \pi_s p(\mathbf{x}|z=s)}$$



- Given
  - unlabeled data  $\{\mathbf{x}_1, \dots, \mathbf{x}_m\}$ ;
  - number of clusters  $K$
- Find a  $K$ -component Gaussian mixture model:
  - mixing coefficients  $\{\pi_1, \dots, \pi_K\}$ ;
  - components parameters  $\{(\boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)\}_{k=1}^K$by maximizing data likelihood

- Choose initial values for  $\pi_k, \mu_k, \Sigma_k, k = 1, \dots, K$
- repeat:
  - Expectation: for each training example  $\mathbf{x}_n$ 
    - (a) Compute  $r_{nk} = P(z = k | \mathbf{x}_n), k = 1, \dots, K$
    - (b) Break data into  $K$  parts according to the probabilities
$$\mathbf{x}_n[r_{nk}], k = 1, \dots, K$$
    - (c) Assign each part  $\mathbf{x}_n[r_{nk}]$  to the corresponding cluster  $k$
  - Maximization: Re-estimate  $\pi_k, \mu_k, \Sigma_k, k = 1, \dots, K$
- Until convergence



- Main computations are in step (a):

$$\begin{aligned} r_{nk} &= P(z = k | \mathbf{x}_n) \\ &= \frac{P(z = k)p(\mathbf{x}_n | z = k)}{\sum_{k=1}^K P(z = k)p(\mathbf{x}_n | z = k)} \\ &= \frac{\pi_k \mathcal{N}(\mathbf{x}_n | \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)}{\sum_{s=1}^K \pi_s \mathcal{N}(\mathbf{x}_n | \boldsymbol{\mu}_s, \boldsymbol{\Sigma}_s)}. \end{aligned}$$

- $r_{nk}$  are often called responsibilities.

- Total number of examples, assigned to cluster  $k$ :

$$m_k = \sum_{i=1}^m r_{ki}$$

- Re-estimate  $\pi_k, \mu_k, \Sigma_k$ :

$$\pi_k^{new} = \frac{m_k}{m},$$

$$\mu_k^{new} = \frac{1}{m_k} \sum_{i=1}^m r_{ki} \mathbf{x}_i,$$

$$\Sigma_k^{new} = \frac{1}{m_k} \sum_{i=1}^m r_{ki} (\mathbf{x}_i - \mu_k^{new})(\mathbf{x}_i - \mu_k^{new})^T$$

- Choose initial values for  $\pi_k$ ,  $\boldsymbol{\mu}_k$ ,  $\boldsymbol{\Sigma}_k$ .
- Repeat until convergence
  - Expectation: for each training example  $\mathbf{x}_n$  compute

$$r_{nk} = \frac{\pi_k \mathcal{N}(\mathbf{x}_n | \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)}{\sum_{s=1}^K \pi_s \mathcal{N}(\mathbf{x}_n | \boldsymbol{\mu}_s, \boldsymbol{\Sigma}_s)}, \quad k = 1, 2, \dots, K.$$

- Maximization: Re-estimate  $\pi_k$ ,  $\boldsymbol{\mu}_k$ ,  $\boldsymbol{\Sigma}_k$ :

$$\pi_k^{new} = \frac{m_k}{m}, \quad \boldsymbol{\mu}_k^{new} = \frac{1}{m_k} \sum_{i=1}^m r_{ki} \mathbf{x}_i,$$

$$\boldsymbol{\Sigma}_k^{new} = \frac{1}{m_k} \sum_{i=1}^m r_{ki} (\mathbf{x}_i - \boldsymbol{\mu}_k^{new})(\mathbf{x}_i - \boldsymbol{\mu}_k^{new})^T,$$

where  $m_k = \sum_{i=1}^m r_{ki}$

- Let  $\boldsymbol{\pi} = (\pi_1, \dots, \pi_K)$ ,  $\boldsymbol{\mu} = (\boldsymbol{\mu}_1, \dots, \boldsymbol{\mu}_K)$ ,  $\boldsymbol{\Sigma} = (\boldsymbol{\Sigma}_1, \dots, \boldsymbol{\Sigma}_K)$
- Specification of  $\boldsymbol{\pi}, \boldsymbol{\mu}, \boldsymbol{\Sigma}$  defines a probability density functions over features  $\mathbf{x}$ :

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

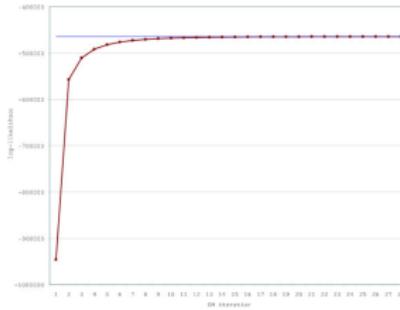
- Data:  $\mathbf{X} = \{\mathbf{x}_1, \dots, \mathbf{x}_m\}$
- Log-Likelihood as function of model parameters:

$$l(\mathbf{X}|\boldsymbol{\pi}, \boldsymbol{\mu}, \boldsymbol{\Sigma}) = \log \prod_{i=1}^m p(\mathbf{x}_i|\boldsymbol{\pi}, \boldsymbol{\mu}, \boldsymbol{\Sigma}) = \sum_{i=1}^m \log p(\mathbf{x}_i|\boldsymbol{\pi}, \boldsymbol{\mu}, \boldsymbol{\Sigma})$$

- EM aims at computing the maximum likelihood estimation (MLE) of the parameters

$$(\boldsymbol{\pi}^*, \boldsymbol{\mu}^*, \boldsymbol{\Sigma}^*) = \arg \max_{\boldsymbol{\pi}, \boldsymbol{\mu}, \boldsymbol{\Sigma}} l(\mathbf{X} | \boldsymbol{\pi}, \boldsymbol{\mu}, \boldsymbol{\Sigma})$$

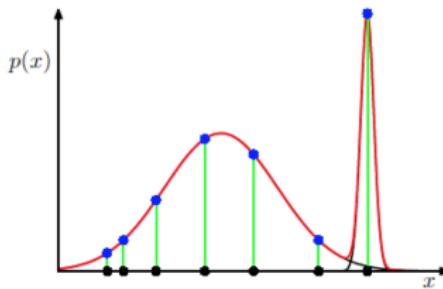
- Let  $l(t)$  be the log-likelihood after iteration  $t$
- The series  $l(1), l(2), \dots$  increases monotonically with  $t$
- Terminate EM when  $l(t+1) - l(t)$  falls below a threshold



- The maximum value of log-likelihood might be infinite:

$$l(\mathbf{X}|\boldsymbol{\pi}, \boldsymbol{\mu}, \boldsymbol{\Sigma}) = \log \prod_{i=1}^m p(\mathbf{x}_i|\boldsymbol{\pi}, \boldsymbol{\mu}, \boldsymbol{\Sigma})$$

- Such singularity in likelihood function happens often in case of outliers and repeated points



- Solution: Bound the eigenvalues of covariance matrix
- To avoid local maximum: multiple restart

## Hard Assignment:

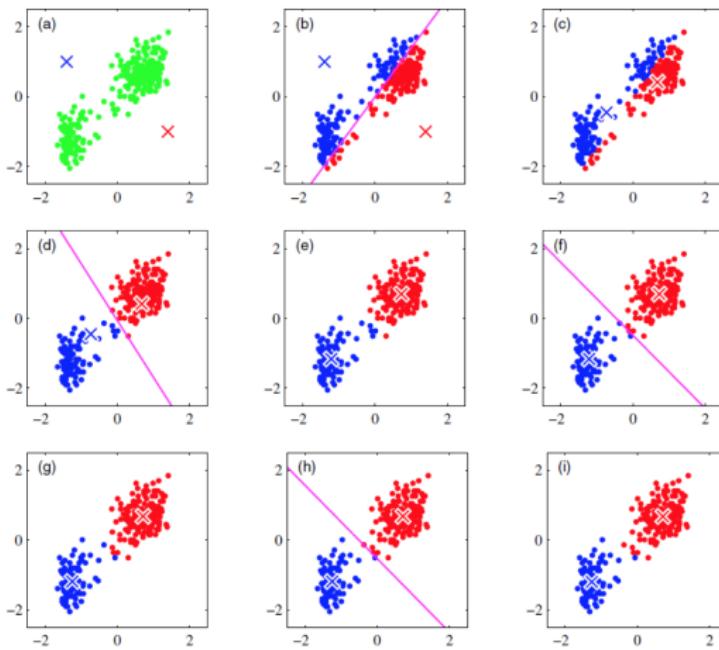
- Select  $K$  points as the initial centroids
- Repeat
  - for  $K$  clusters by assigning all points to the closest centroid;
  - recompute the centroid of each cluster
- until the centroids don't change

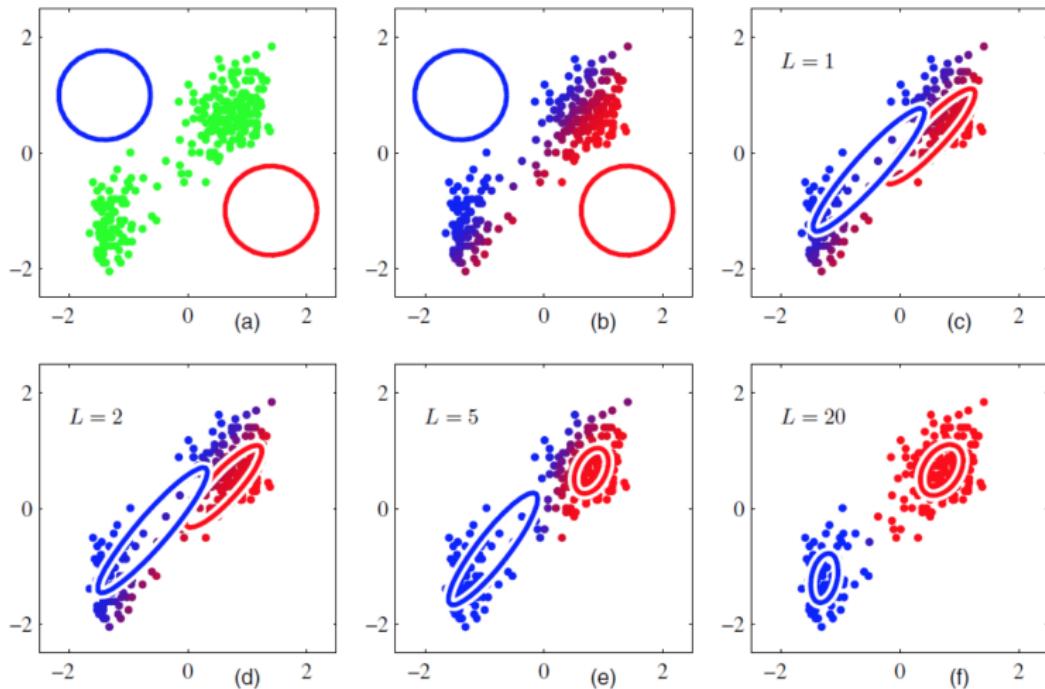
## Soft Assignment:

- Choose initial values for  $\pi_k$ ,  $\mu_k$ ,  $\Sigma_k$
- Repeat
  - Expectation:
    - (a) Compute  $r_{nk} = P(z = k | \mathbf{x}_n)$  for  $k = 1, \dots, K$ ;
    - (b) Break it into  $K$  fractional examples according to the probabilities;
    - (c) Assign each fractional examples to the corresponding cluster  $k$
  - Maximization: Re-estimate  $\pi_k$ ,  $\mu_k$ ,  $\Sigma_k$
- until convergence

# K-means example

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1 Overview

2 Hierarchical clustering

3 K-means

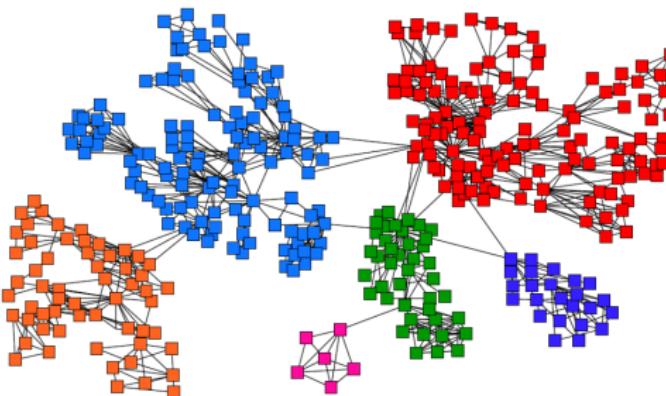
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5 Mixture Models

6 Community detection

- Spectral clustering
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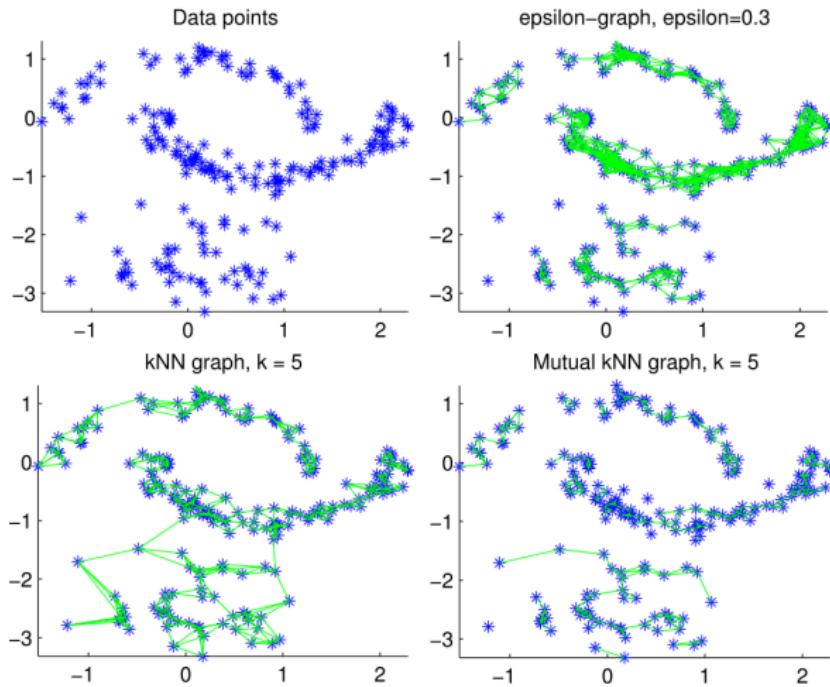
- **Graph**  $G(E, V)$ :
  - Nodes  $v_j$
  - Edge weights  $w_{ij} > 0$
- **Problem:** Want to partition graph such that edges between groups have low weights



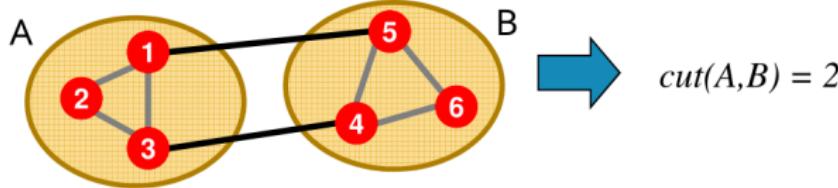
Types of graphs:

- **$\epsilon$ -neighborhood:**
  - Only include edges with distances  $< \epsilon$ ;
  - Treat as unweighted:  $w_{ij} = Const$
- **k-NN:**
  - Connect  $v_i$  and  $v_j$  if  $v_j$  is a k-NN of  $v_i$
  - Weighted by similarity  $w_{ij} = s_{ij}$
  - Directed or undirected
- **Mutual k-NN:**
  - Same as k-NN, but only include mutual k-NN

# Similarity graphs



- **Problem:** Partition graph such that edges between groups have low weights
- **Define:**  $W(A, B) = \sum_{i \in A, j \in B} w_{ij}$
- **MinCut problem:**  $Cut(A_1, \dots, A_k) = \sum_{i=1}^k W(A_i, \overline{A}_i)$
- **Choose:**  $A_1, \dots, A_k = \arg \min_{A_1, \dots, A_k} Cut(A_1, \dots, A_k)$



1 Overview

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3 K-means

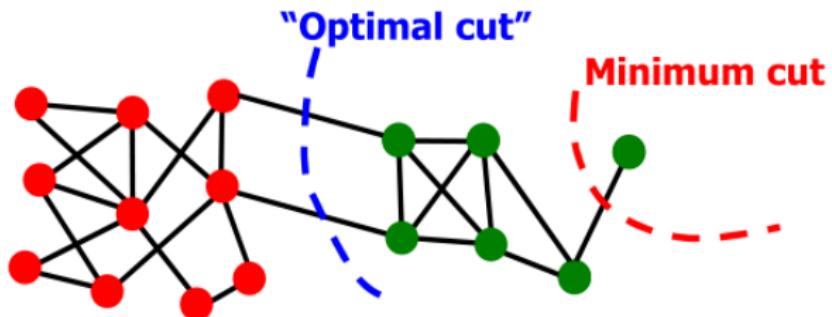
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**Problem:** MinCut favors isolated clusters.



**Solution:**

- Ratio cuts (RatioCut);
- Normalized cuts (Ncut);
- Lead to “balanced” clusters.

Two measures of size of a subset:

- Cardinality:

$$|A| = \# \text{ of vertices in } A$$

- Volume:

$$vol(A) = \sum_{i \in A} \sum_{j=1}^N w_{ij}$$

- Ratio cuts (RatioCut)

- $k = 2$ :  $\text{RatioCut}(A, \bar{A}) = \text{Cut}(A, \bar{A}) \left( \frac{1}{|A|} + \frac{1}{|\bar{A}|} \right).$

- General  $k$ :  $\text{RatioCut}(A_1, \dots, A_k) = \frac{1}{2} \sum_{i=1}^k \frac{\text{Cut}(A_i, \bar{A}_i)}{|A_i|}.$

- Normalized cuts (Ncut)

- $k = 2$ :  $\text{NCut}(A, \bar{A}) = \text{Cut}(A, \bar{A}) \left( \frac{1}{\text{Vol}(A)} + \frac{1}{\text{Vol}(\bar{A})} \right).$

- General  $k$ :  $\text{NCut}(A_1, \dots, A_k) = \frac{1}{2} \sum_{i=1}^k \frac{\text{Cut}(A_i, \bar{A}_i)}{\text{Vol}(A_i)}$

- Problem is NP-hard!

- We need to look at relaxation (solution = Spectral clustering)

# Segmentation of Lena

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Spectral clustering: discretize, 28.62s



1 Overview

2 Hierarchical clustering

3 K-means

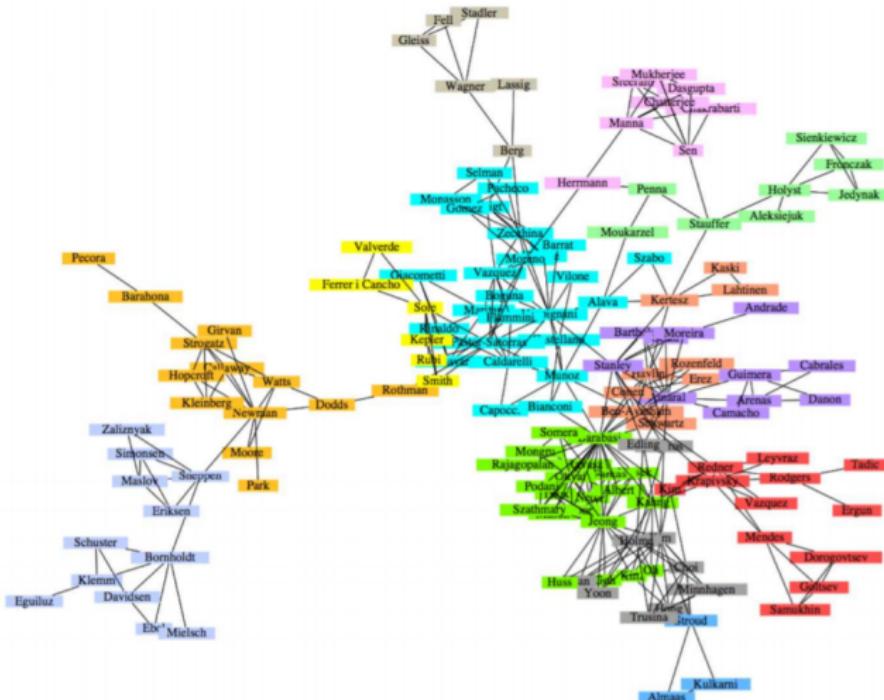
4 Cluster validity

5 Mixture Models

6 Community detection

- Spectral clustering
- Community detection problems
- Modularity
- BigCLAM

# Citation network



Objects of study:

- social networks,
- citation/co-authorship networks,
- designing network protocols,
- biological networks,
- ...

- 1 Overview
- 2 Hierarchical clustering
- 3 K-means
- 4 Cluster validity
- 5 Mixture Models
- 6 Community detection
  - Spectral clustering
  - Community detection problems
  - Modularity
  - BigCLAM

$$Q = \frac{1}{2m} \sum_{(i,j) \in E} \left( w_{ij} - \frac{d_i d_j}{2m} \right) \delta(C_i, C_j),$$

where

- $d_i$  is a degree of node  $i$ ;
- $C_i$  is a community of node  $i$ ;
- $\delta(C_i, C_j)$  is a delta function;
- $m = |E|$  is a total number of edges in a graph

**Interpretation:** difference between the fraction of edges inside the community and its expectation in random graph with fixed node degrees.

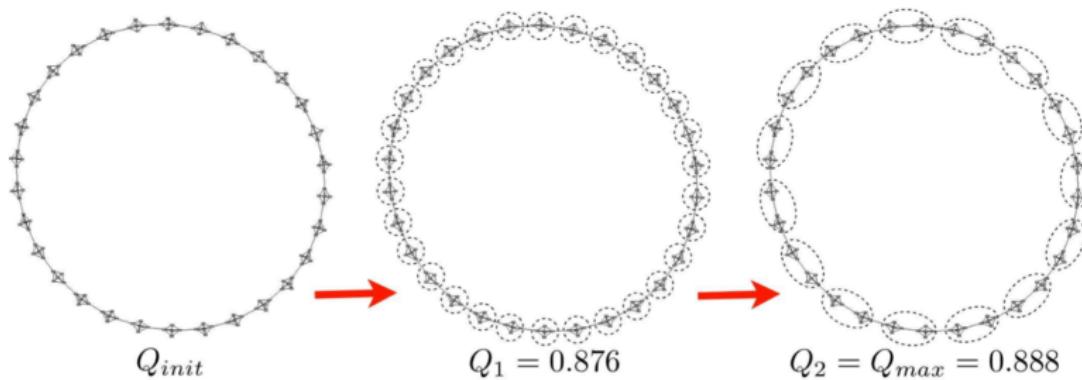
Modularity:

$$Q = \frac{1}{2m} \sum_{(i,j) \in E} \left( w_{ij} - \frac{d_i d_j}{2m} \right) \delta(C_i, C_j),$$

- **Idea:** optimize modularity (discrete optimization problem).
- **Efficient implementation:** Louvain community detection algorithm.
- **Problem:** low resolution.

## Low resolution of modularity

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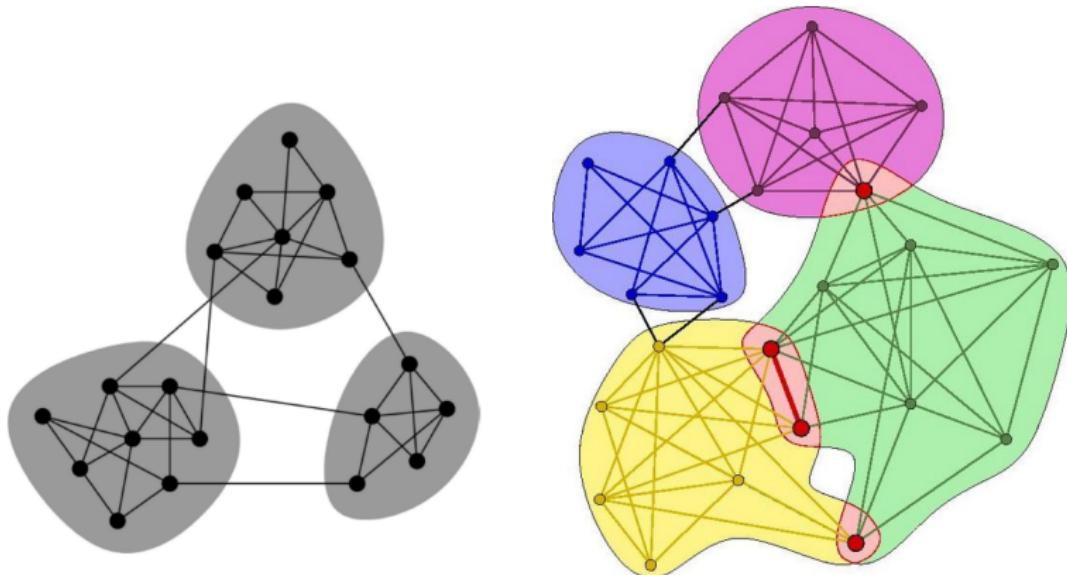
4 Cluster validity

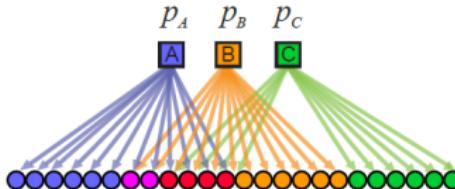
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Non-overlapping vs. overlapping communities





AGM generates the links:

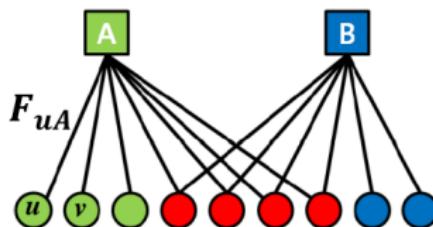
- For each pair of nodes in community  $A$  we connect them with probability  $p_A$ .
- The overall edge probability is:

$$P(u, v) = 1 - \prod_{c \in M_u \cap M_v} (1 - p_c),$$

where  $M_z$  is a set of communities node  $z$  belongs to.

- If  $u, v$  share no communities:  $P(u, v) = \epsilon$ .

**Relaxation:** Memberships have strengths



- $F_{uA}$ : The membership strength of node  $u$  to community  $A$  ( $F_{uA} = 0$ : no membership).
- Each community  $A$  links nodes independently:

$$P_A(u, v) = 1 - \exp\{-F_{uA}F_{vA}\}.$$

- Community membership strength matrix:  $F = (F_{uA}, u \in V, A \in \mathcal{C})$ .
- Community  $A$  links nodes  $u, v$  independently:

$$P_A(u, v) = 1 - \exp\{-F_{uA} \cdot F_{vA}\}.$$

- Then probability at least one common  $C$  links them:

$$P(u, v) = 1 - \prod_{C \in \mathcal{C}} (1 - P_C(u, v)) = 1 - \exp\{-F_u F_v^T\}.$$

**Task:** Given a network  $G(V, E)$ , estimate  $F$ .

- Find  $F$  that maximizes the likelihood:

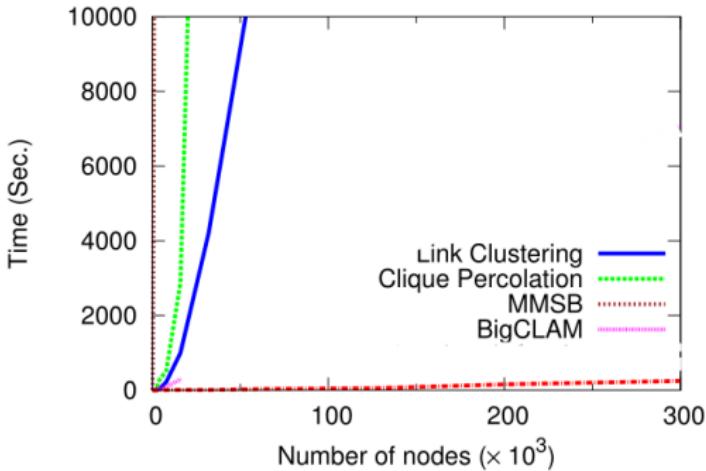
$$\arg \max_F \prod_{(u,v) \in E} P(u,v) \prod_{(u,v) \notin E} (1 - P(u,v)),$$

where  $P(u,v) = 1 - \exp\{-F_u F_v^T\}$ .

**Goal:** Find  $F$  that maximizes log-likelihood:

$$\ell(F) = \sum_{(u,v) \in E} \log(1 - \exp\{-F_u F_v^T\}) - \sum_{(u,v) \notin E} F_u F_v^T.$$

**Note:** Non-convex optimization problem!



- BigCLAM takes 5 minutes for 300k node nets (other methods take 10 days).
- Can process networks with 100M edges!