Clustering in Computer Vision

12 October 2018

CSE473/573 – Autumn 2018

Clustering

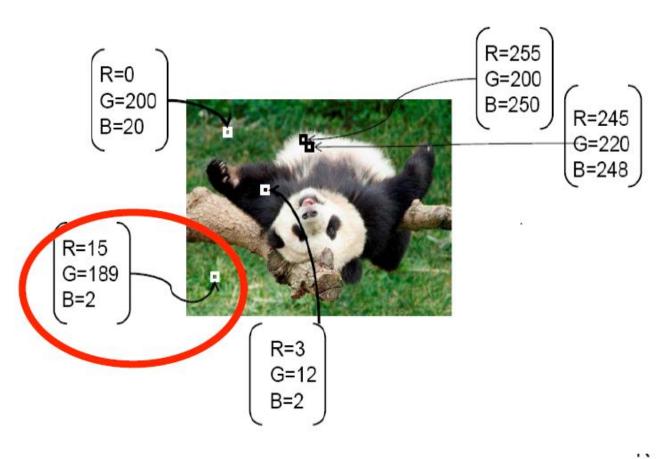
- What is clustering?
 - Grouping of "objects" into meaningful categories
 - Given a representation of N objects, find k clusters based on a suitable measure of similarity.
- Data Clustering is useful in and beyond Computer Vision
 - Segmentation as clustering (today)
 - Texture modeling
 - Quantization
 - Beyond
 - · Data exploration
 - Compression
 - Natural classification

Feature Space

- Every token is identified by a set of salient visual characteristics. For example:
 - Position
 - Color
 - Texture
 - Motion vector
 - Size, orientation (if token is larger than a pixel)

Slide credit: Christopher Rasmussen

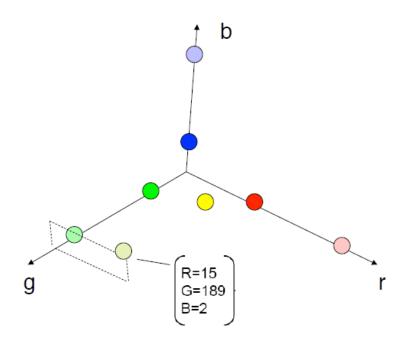
Feature Space - Example



Source: K. Grauman

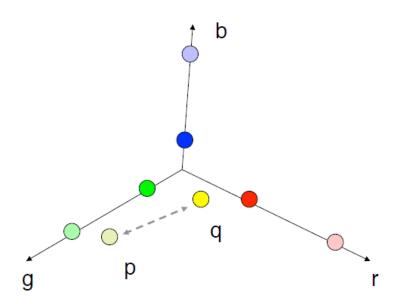
Feature Space - Example

Feature space: each token is represented by a point



Feature Space - Similarity

Token similarity is thus measured by distance between points ("feature vectors") in feature space

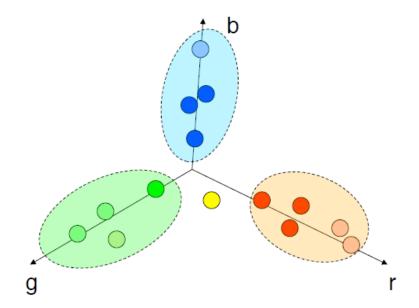


$$\sqrt{(p_1-q_1)^2+(p_2-q_2)^2+\cdots+(p_n-q_n)^2}=\sqrt{\sum_{i=1}^n(p_i-q_i)^2}.$$

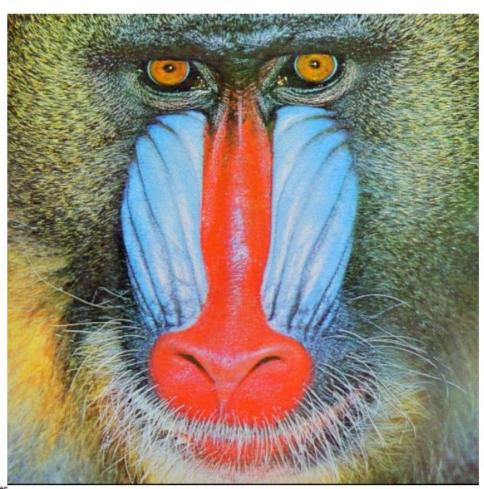
Source: Savarese slides

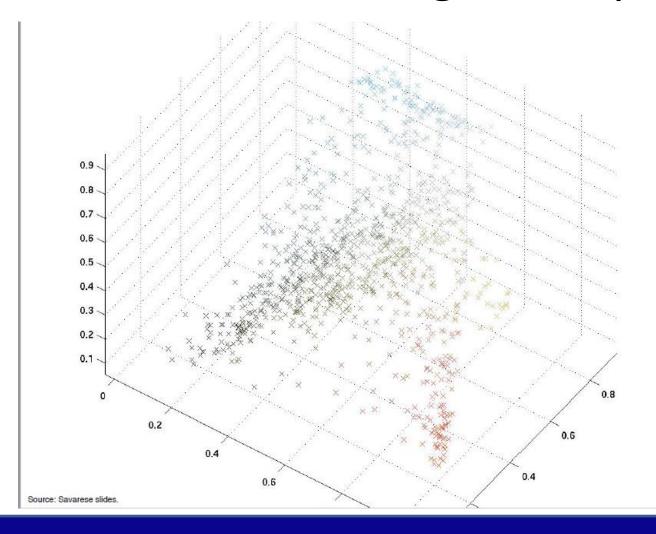
Feature Space - Similarity

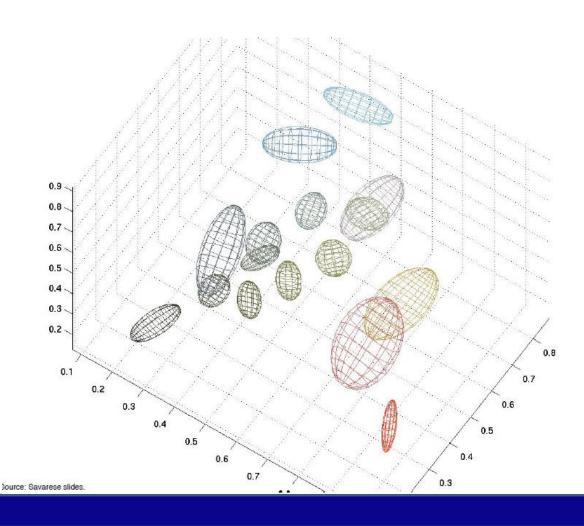
Cluster together tokens with high similarity



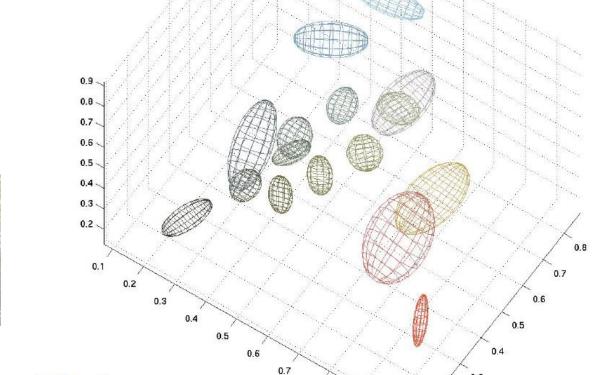
Source: Savarese slides.







Source: Savarese slides.





Clustering – formal definition

• Given a set of N data samples $D=x_1,x_2,\ldots,x_N$ in a d-dimensional feature space, D is partitioned into a number of disjoint subsets D_i :

$$D = \bigcup_{j=1}^{k} D_j$$
 where $D_i \cup D_j = \emptyset$ $\forall i \neq j$

where the points in each subset are similar to each other according to the given similarity function.

A partition is denoted by

$$\pi = (D_1, D_2, \dots, D_k)$$

and clustering is then formulated as

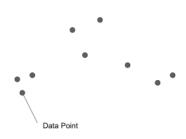
$$\pi^* = \arg\min_{\pi} f(\pi)$$

for $f(\cdot)$ that captures the desired cluster properties.

K-Means Clustering

Iterative process. Takes multiple iterations to converge

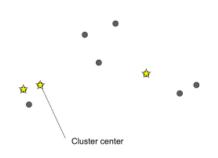
- 1. Randomly initialize $\mu_1, \mu_2, ..., \mu_c$
- 2. Repeat until no change in μ_i :
 - (a) Classify N samples according to nearest μ_i
 - (b) Recompute μ_i



Initialize K centers

K-Means Clustering

- 1. Randomly initialize $\mu_1, \mu_2, ..., \mu_c$
- 2. Repeat until no change in μ_i :
 - (a) Classify N samples according to nearest μ_i
 - (b) Recompute μ_i

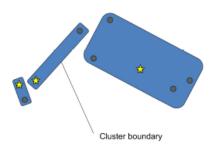


First choose k arbitrary centers

Assign nearest points to clusters

K-Means Clustering

- 1. Randomly initialize $\mu_1, \mu_2, ..., \mu_c$
- 2. Repeat until no change in μ_i :
 - (a) Classify N samples according to nearest μ_i
 - (b) Recompute μ_i

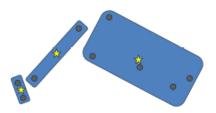


Assign points to closest centers

Re-compute centers of clusters

K-Means Clustering

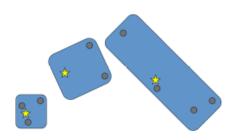
- 1. Randomly initialize $\mu_1, \mu_2, ..., \mu_c$
- 2. Repeat until no change in μ_i :
 - (a) Classify N samples according to nearest μ_i
 - (b) Recompute μ_i



Recompute centers

Re-Assign points to clusters

- 1. Randomly initialize $\mu_1, \mu_2, ..., \mu_c$
- 2. Repeat until no change in μ_i :
 - (a) Classify N samples according to nearest μ_i
 - (b) Recompute μ_i

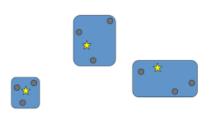


Assign points to closest centers

Iterate....

K-Means Clustering

- 1. Randomly initialize $\mu_1, \mu_2, ..., \mu_c$
- 2. Repeat until no change in μ_i :
 - (a) Classify N samples according to nearest μ_i
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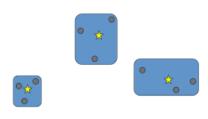


Assign points to closest centers

Iterate....

K-Means Clustering

- 1. Randomly initialize $\mu_1, \mu_2, ..., \mu_c$
- 2. Repeat until no change in μ_i :
 - (a) Classify N samples according to nearest μ_i
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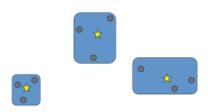


Recompute centers

Stop! When the centers do not move

K-Means Clustering

- 1. Randomly initialize $\mu_1, \mu_2, ..., \mu_c$
- 2. Repeat until no change in μ_i :
 - (a) Classify N samples according to nearest μ_i
 - (b) Recompute μ_i

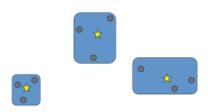


Points already assigned to nearest centers: Algorithm ends

Stop! When the centers do not move

K-Means Clustering

- 1. Randomly initialize $\mu_1, \mu_2, ..., \mu_c$
- 2. Repeat until no change in μ_i :
 - (a) Classify N samples according to nearest μ_i
 - (b) Recompute μ_i



Points already assigned to nearest centers: Algorithm ends

K-Means Clustering Animation

http://shabal.in/visuals/kmeans/1.html

http://simplystatistics.org/2014/02/18/k-means-clustering-in-a-gif/

K-Means Clustering – Pros and Cons

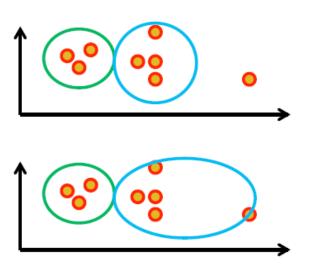
Pros

- Simple and fast

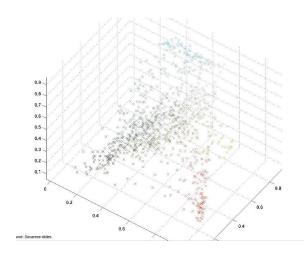
- $\sum_{\text{clusters } i} \sum_{\text{points p in cluster } i} ||p c_i||^2$
- (Always) converges to a local minimum of the error function
- Available implementations (e.g., in Matlab)

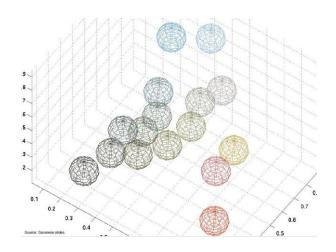
Cons

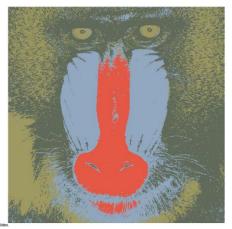
- -Need to pick K
- -Sensitive to initialization
- –Only finds "spherical" clusters
- -Sensitive to outliers



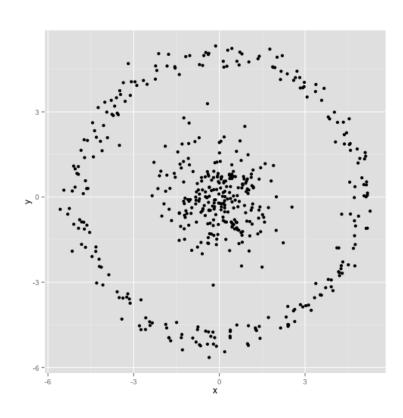
K-Means Clustering – Example



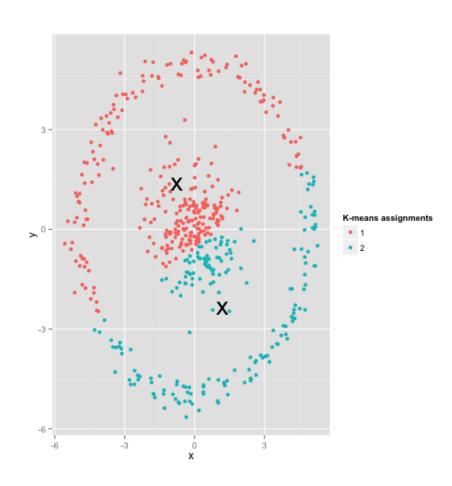




What are the clusters here?



K-Means Clustering fails

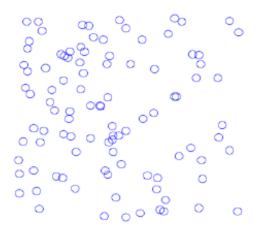


Challenges

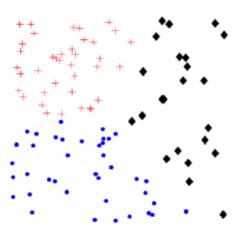
- What is a cluster?
- 2. How to define pair-wise similarity?
- 3. Which features? Which normalizations scheme?
- 4. How many clusters?
- 5. Which clustering method?
- 6. Are the discovered clusters and partitioning valid?
- 7. Does the data have any clustering tendency?

Cluster Validity

 Clustering algorithms find clusters, even if there are no natural clusters in the data.



100 2D uniform data points



k-Means with k=3

Soft vs Hard Clustering

- Kmeans performs Hard clustering:
 - Data point is deterministically assigned to one and only one cluster
 - But in reality clusters may overlap
- Soft-clustering:
 - Data points are assigned to clusters with certain probabilities

Probabilistic Clustering

- Basic questions
 - what's the probability that a point **x** is in cluster m?
 - what's the shape of each cluster?
- K-means doesn't answer these questions
- Basic idea
 - instead of treating the data as a bunch of points, assume that they are all generated by sampling a continuous function
 - This function is called a generative model

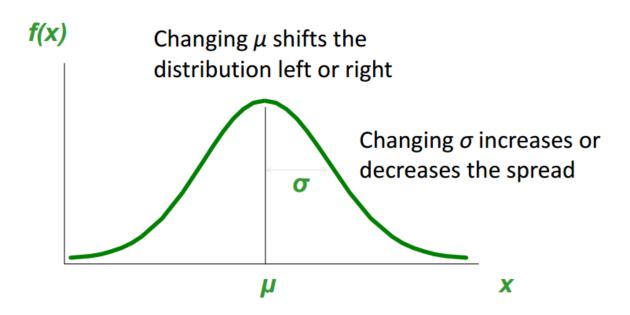
How can we extend K-means to make soft clustering

- Given a set of clusters centers μ₁, μ₂, ..., μ_k, instead of directly assign all data points to their closest clusters, we can assign them partially (probabilistically) based on the distances
- This can be done by
 - assuming a probabilistic distribution (model) for each cluster
 - compute the probability that each point belongs to each cluster
 - Often referred to as Model-based clustering

Gaussian for representing a cluster

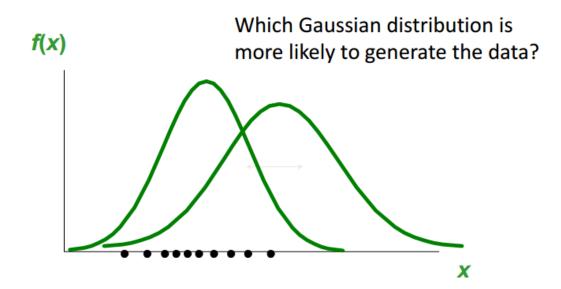
- What exactly is a cluster?
 - Intuitively it is a tightly packed ball-shape like thing
- We can use a Gaussian (normal) distribution to describe it
- Let's first review what is a Gaussian distribution

Gaussian Distribution



Probability density function f(x) is a function of x given μ and σ $N(x \mid \mu, \sigma^2) = \frac{1}{\sigma \sqrt{2\pi}} \exp(-\frac{1}{2} (\frac{x - \mu}{\sigma})^2)$

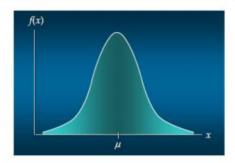
Gaussian Distribution



Define likelihood as a function of μ and σ given $x_1, x_2, ..., x_n$ $\prod_{i=1}^n N(x_i \mid \mu, \sigma^2)$

Multi-variate Gaussian

Univariate Gaussian distribution:

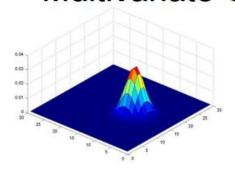


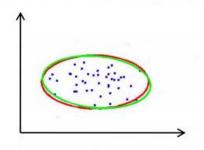
$$N(\mu, \sigma^2)$$

 μ – mean, center of the mass

 σ^2 – standard deviation, spread of the mass

Multivariate Gaussian distribution:





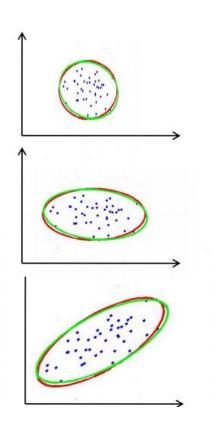
$$N(\mu, \Sigma)$$

$$\mu - (\mu_1, \mu_2)$$

Σ - Covariance matrix

$$\left[\begin{array}{cc} \sigma_1^2 & \sigma_{12} \\ \sigma_{12} & \sigma_{2}^2 \end{array}\right]$$

Different Co-Variance Matrices



Covariance matrix $\Sigma =$

 σ^2 0

 $0 \quad \sigma^2$

Covariance matrix $\Sigma =$

 $\sigma_1^2 0$

 $0 \quad \sigma_2^2$

Covariance matrix $\Sigma =$

 $\sigma_1^2 = \sigma_1$

 $\sigma_{12} \quad \sigma_{2}^{2}$

Log-Likelihood

Multivariate Gaussian

$$\mathcal{N}(x|\mu, \Sigma) = \frac{1}{(2\pi|\Sigma|)^{1/2}} \exp\left\{-\frac{1}{2}(x-\mu)^T \Sigma^{-1}(x-\mu)\right\}$$
mean covariance

Log likelihood

$$L(\mu, \Sigma) = \sum_{i=1}^{n} \ln N(x_i \mid \mu, \Sigma) = \sum_{i=1}^{n} \left(-\frac{1}{2} (x_i - \mu)^T \sum_{i=1}^{-1} (x_i - \mu)\right) - \pi \ln |\Sigma|$$

Gaussian Mixture Models (GMMs)

$$\mathcal{N}(x|\boldsymbol{\mu}, \boldsymbol{\Sigma}) = \frac{1}{(2\pi)^{d/2} |\boldsymbol{\Sigma}|^{1/2}} \exp\left[-\frac{1}{2} (\mathbf{x} - \boldsymbol{\mu})^{\mathsf{T}} \boldsymbol{\Sigma}^{-1} (\mathbf{x} - \boldsymbol{\mu})\right]$$

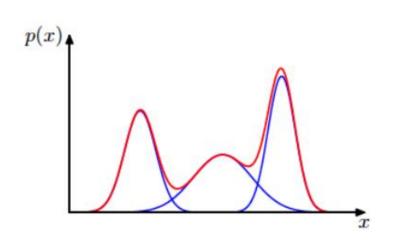
- It forms the basis for the mixture of Gaussians density
- The Gaussian mixture is linear superposition of Gaussians:

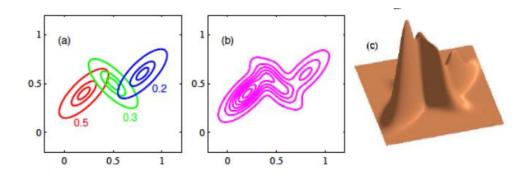
$$p(\mathbf{x}) = \sum_{k=1}^{K} \pi_k \mathcal{N}(\mathbf{x}|\boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)$$

• The π_k are non-negative scalars called mixing coefficients and they govern the relative importance between the various Gaussians in the mixture density. $\sum_k \pi_k = 1$

Gaussian Mixture Models (GMMs)

In below examples – the distribution is a mixture of three gaussians with different means and variances





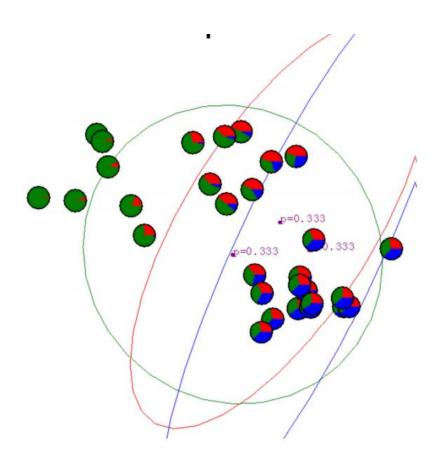
Clustering using GMMs

- Given a set of data points, and assume that we know there are k clusters in the data, we need to:
 - Assign the data points to the k clusters (soft assignment)
 - Learn the gaussian distribution parameters for each cluster: μ and Σ

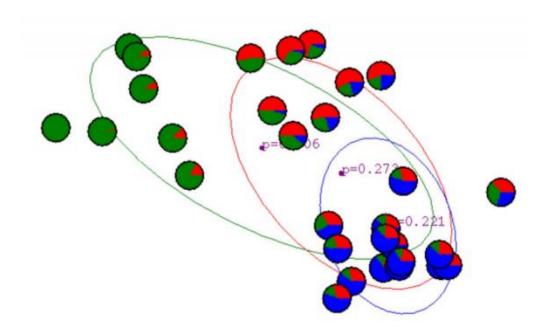
Expectation Maximization (EM)

- Randomly initialize the Gaussian parameters
- Repeat until converge
 - 1. Compute $P(\mathbf{x}^j \in C_i | \mathbf{x}^j)$ for all data points and all clusters
 - This is called the E-step for it computes the expected values of the cluster memberships for each data point
 - Re-compute the parameters of each Gaussian
 This is called the M-step for it performs maximum likelihood estimation of parameters

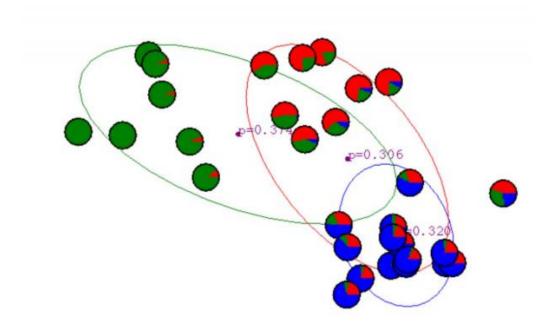
GMM Example - Initialization



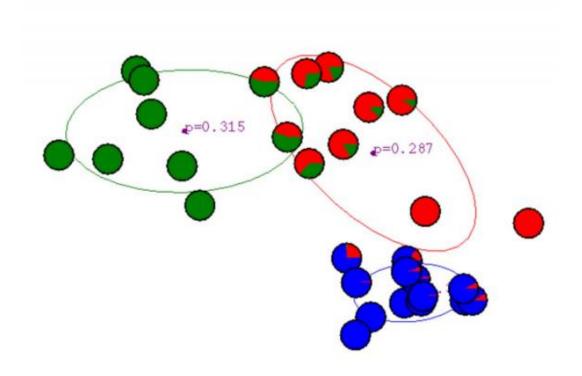
After First Iteration



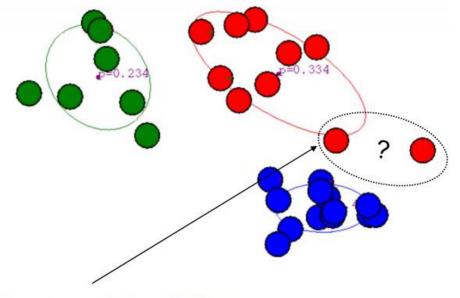
After Second Iteration



After Sixth Iteration



After 20th Iteration



Q: Why are these two points red when they appear to be closer to blue?

K-Means vs GMMs

- Objective function
 - Minimize sum of squared Euclidean distance
- Can be optimized by an EM algorithm
 - E-step: assign points to clusters
 - M-step: optimize clusters
 - Performs hard assignment during E-step
- Assumes spherical clusters with equal probability of a cluster

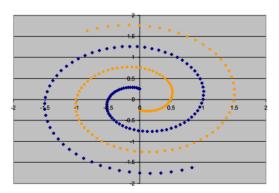
- · Objective function
 - Maximize log-likelihood
- EM algorithm
 - E-step: Compute posterior probability of membership
 - M-step: Optimize parameters
 - Perform soft assignment during E-step
- Can be used for non-spherical clusters
- Can generate clusters with different probabilities

Spectral Clustering

Spectral clustering techniques make use of the spectrum (eigenvalues) of the similarity matrix of the data to perform dimensionality reduction before clustering in fewer dimensions

Spectral approach

- Use similarity graphs to encode local neighborhood information
- Data points are vertices of the graph
- Connect points which are "close"

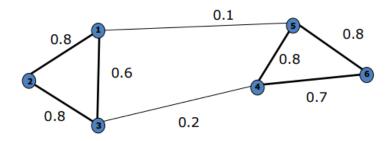


Similarity Graph

- Represent dataset as a weighted graph G(V,E)
- All vertices which can be reached from each other by a path form a connected component
- Only one connected component in the graph—The graph is fully connected

 $V=\{x_i\}$ Set of *n* vertices representing data points

E={W_{ij}} Set of weighted edges indicating pair-wise similarity between points

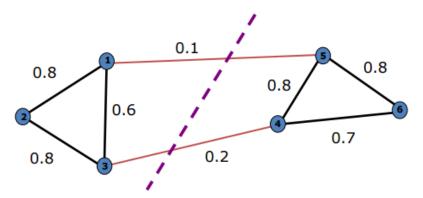


Clustering Objective

Traditional definition of a "good" clustering

- Points assigned to same cluster should be highly similar
- Points assigned to different clusters should be highly dissimilar

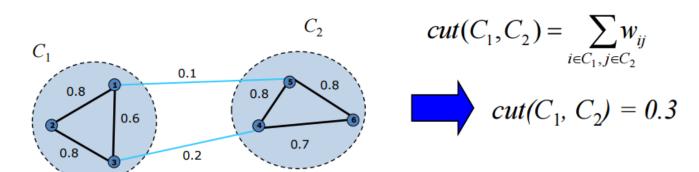
Apply this objective to our graph representation



Minimize weight of between-group connections

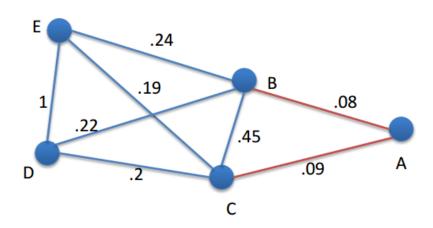
Graph Cut

- Express clustering objective as a function of the edge cut of the partition
- Cut: Sum of weights of edges with only one vertex in each group
- We wants to find the *minimal cut* between groups



Minimum Cut - Example

Minimum Cut



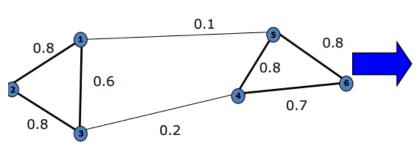
Cut(BCDE, A) = 0.17

Problem

- Identifying a minimum cut is NP-hard
- There are efficient approximations using linear algebra
- Based on the Laplacian Matrix, or graph Laplacian

Similarity Matrix Representation

- Similarity matrix (W)
 - $-n \times n$ matrix
 - $-W = [w_{ij}]$: edge weight between vertex x_i and x_j

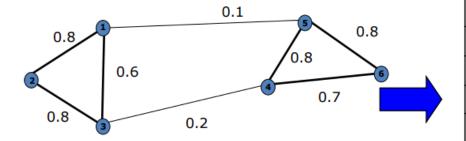


	X _I	x ₂	<i>X</i> ₃	X4	<i>X</i> ₅	<i>X</i> ₆
X _I	0	0.8	0.6	0	0.1	0
X ₂	0.8	0	0.8	0	0	0
<i>X</i> ₃	0.6	0.8	0	0.2	0	0
X4	0	0	0.2	0	0.8	0.7
<i>X</i> ₅	0.1	0	0	0.8	0	0.8
<i>X</i> ₆	0	0	0	0.7	0.8	0

- Important properties
 - Symmetric matrix

Degree Matrix

- Degree matrix (D)
 - -nxn diagonal matrix
 - $D(i,i) = \sum_{j} w_{ij}$: total weight of edges incident to vertex x_i

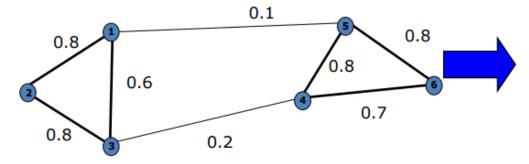


	X ₁	x ₂	<i>X</i> ₃	X4	<i>X</i> ₅	<i>X</i> ₆
X ₁	1.5	0	0	0	0	0
<i>X</i> ₂	0	1.6	0	0	0	0
<i>X</i> ₃	0	0	1.6	0	0	0
X4	0	0	0	1.7	0	0
<i>X</i> ₅	0	0	0	0	1.7	0
<i>X</i> ₆	0	0	0	0	0	1.5

- Used to
 - Normalize adjacency matrix

Laplacian Matrix

- Laplacian matrix (L)
 - $-n \times n$ symmetric matrix



$$L = D - W$$

	X ₁	X ₂	<i>X</i> ₃	<i>X</i> ₄	<i>X</i> ₅	X ₆
X _I	1.5	-0.8	-0.6	0	-0.1	0
<i>X</i> ₂	-0.8	1.6	-0.8	0	0	0
X3	-0.6	-0.8	1.6	-0.2	0	0
X4	0	0	-0.2	1.7	-0.8	-0.7
<i>X</i> ₅	-0.1	0	0	-0.8	1.7	-0.8
<i>X</i> ₆	0	0	0	-0.7	-0.8	1.5

Find an Optimal mincut

• Express a bi-partition (C_1, C_2) as a vector

$$f_i = \begin{cases} 1 & \text{if } x_i \in C_1 \\ -1 & \text{if } x_i \in C_2 \end{cases}$$

 We can minimize the cut of the partition by finding a non-trivial vector f that minimizes the function

$$g(f) = \sum_{i,j \in V} w_{ij} (f_i - f_j)^2 = f^T L f$$
Laplacian matrix

How it works

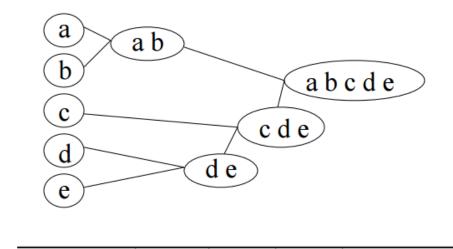
How eigen decomposition of L relates to clustering?

$$L=D-W$$
 $f(x_j)=f_j$ cluster assignment $f^TLf=f^TDf-f^TWf$
$$=\frac{1}{2}\left(\sum_i\left(\sum_jw_{ij}\right)f_i^2-2\sum_{ij}f_if_jw_{ij}+\sum_j\left(\sum_iw_{ij}\right)f_j^2\right)$$

$$=\frac{1}{2}\sum_{ij}w_{ij}(f_i-f_j)^2$$
 --Cluster objective function

Hierarchical Clustering

Agglomerative approach



Step 1

Step 0

Step 2 Step 3

Initialization:

Each object is a cluster

Iteration:

Merge two clusters which are

most similar to each other;

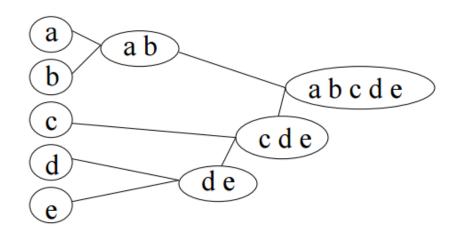
Until all objects are merged

into a single cluster

bottom-up

Hierarchical Clustering

Divisive Approaches

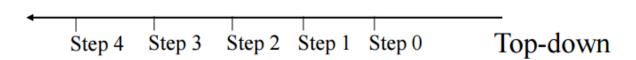


Initialization:

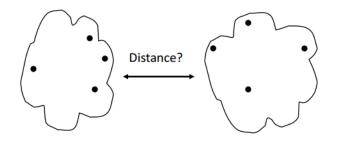
All objects stay in one cluster Iteration:

Select a cluster and split it into two sub clusters

Until each leaf cluster contains only one object



Inter-Cluster Distance



NΛ	IN
IVI	ПV

- MAX
- Group Average
- Distance Between Centroids
-

	p1	p2	рЗ	p4	р5	<u> </u>
p1						
p 2						
<u>p2</u> p3						
<u>p4</u> p5						

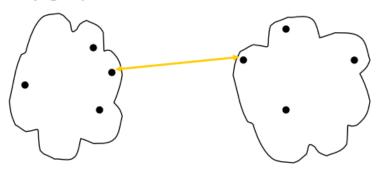
Distance Matrix

.

MIN or Single Link

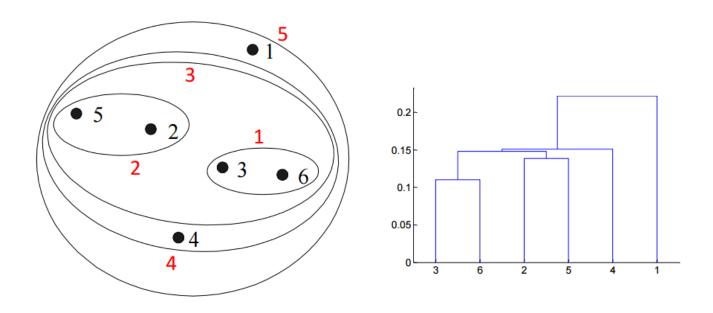
Inter-cluster distance

- The distance between two clusters is represented by the distance of the <u>closest pair of data objects</u> belonging to different clusters.
- Determined by one pair of points, i.e., by one link in the proximity graph



$$d_{\min}(C_i, C_j) = \min_{p \in C_i, q \in C_j} d(p, q)$$

MIN



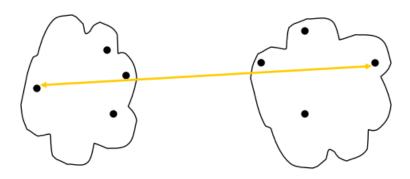
Nested Clusters

Dendrogram

MAX or Complete Link

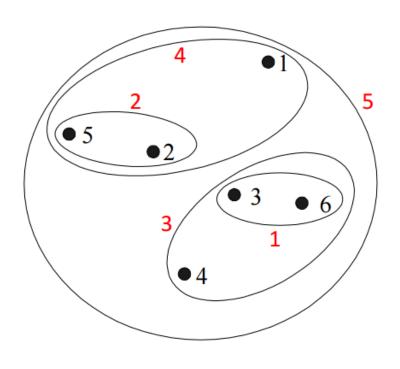
Inter-cluster distance

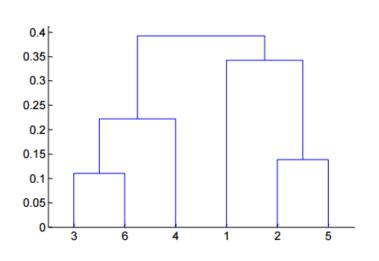
 The distance between two clusters is represented by the distance of the <u>farthest pair of data objects</u> belonging to different clusters



$$d_{\min}(C_i, C_j) = \max_{p \in C_i, q \in C_j} d(p, q)$$

MAX or Complete Link

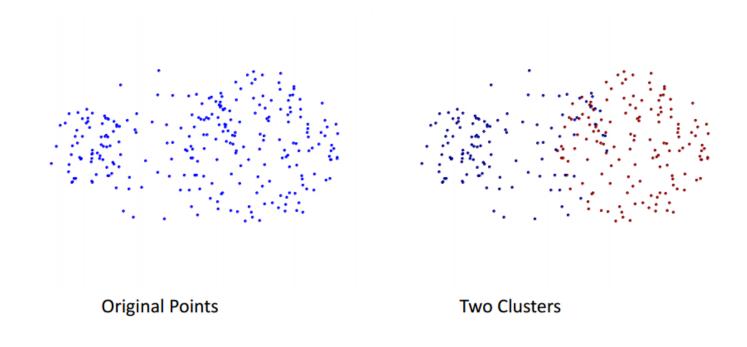




Nested Clusters

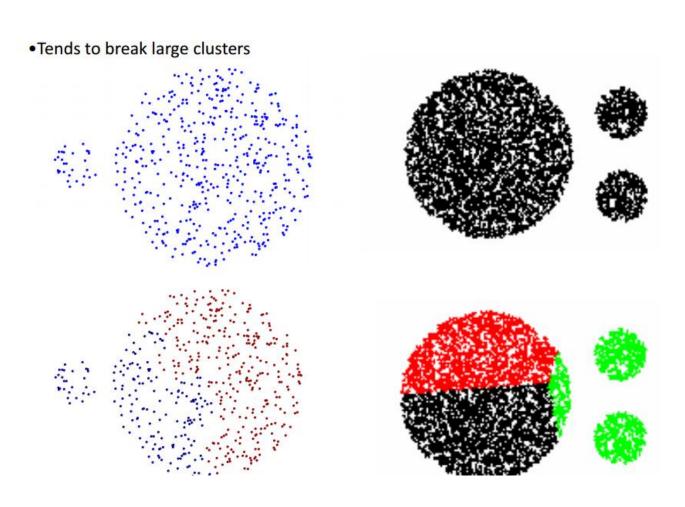
Dendrogram

Limitations of MIN

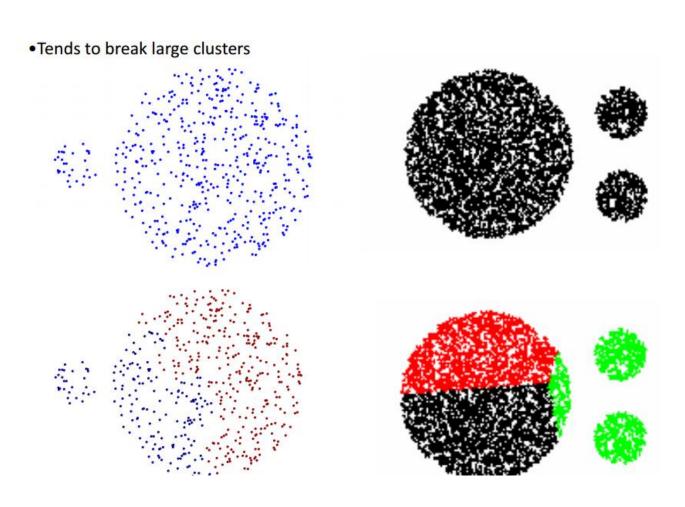


Sensitive to noise and outliers

Limitations of MAX



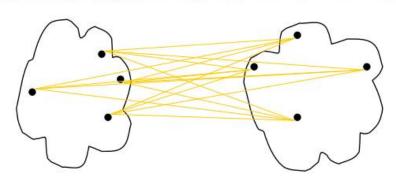
Limitations of MAX



More Techniques with increased complexity

Inter-cluster distance

- The distance between two clusters is represented by the <u>average</u> distance of <u>all pairs of data objects</u> belonging to different clusters
- Determined by all pairs of points in the two clusters



$$d_{\min}(C_i, C_j) = \underset{p \in C_i, q \in C_j}{avg} d(p, q)$$