Clustering

Peng Chen, Jiaqi Xia

School of Management
University of Science and Technology of China

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Outline

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Unsupervised Learning

- In supervised learning, we have training samples $(x_1, y_1), \dots, (x_N, y_N)$ and our interest is to infer the function of x to predict y.
- In unsupervised learning, we have only N p-dimensional observations (x_1, x_2, \dots, x_N) , which is our main interest.
- ightharpoonup The dimension p is sometimes much higher, and the properties of interest are often more complicated.

Example: Human Tumor Microarray Data

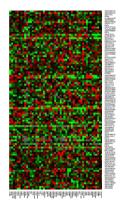
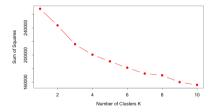


Figure: Human Tumor Microarray Data: a 6830×64 matrix of real numbers, each representing an expression measurement for a gene (row) and sample (column).



Example: Human Tumor Microarray Data

▶ Here we cluster the samples, each of which is a vector of length 6830, corresponding to expression values for the 6830 genes.



Cluster	Breast	CNS	Colon	K562	Leukemia	MCF7
1	3	5	0	0	0	0
2	2	0	0	2	6	2
3	2	0	7	0	0	0
Cluster	Melanoma	NSCLC	Ovarian	Prostate	Renal	Unknown
1	1	7	6	2	9	1
2	7	2	0	0	0	0

ferent choice of the number of clusters K

Figure: The SSE of K-means algorithm with dif- Figure: Number of cancer cases of each type, in each of the three clusters from K-means clustering.

Clustering

- ▶ Cluster analysis or clustering is the task of grouping a set of objects in such a way that objects in the same group (called a cluster) are more similar (in some sense) to each other than to those in other groups (clusters).
- How to group objects, i.e. how to measure the similarities between objects?
- ▶ How to choose the number of clusters *K*?



- Most algorithms presume a matrix \mathbf{D} of dissimilarities with nonnegative entries and zero diagonal elements: $d_{ii} = 0, i = 1, \dots, N$.
- ▶ If the original data were collected as similarities, a suitable monotone-decreasing function can be used to convert them to dissimilarities.
- Most algorithms assume symmetric dissimilarity matrices, so if the original matrix \mathbf{D} is not symmetric it may be replaced by $(\mathbf{D} + \mathbf{D}^{\top})/2$.

Dissimilarities Based on Attributes

- ▶ In order to construct a dissimilarity matrix, we must first construct pairwise dissimilarities between the objects.
- lacktriangle We define a dissimilarity $d_k(x_{ik},x_{jk})$ between values of the kth attribute, and then define

$$d(x_i, x_j) = \sum_{k=1}^{p} d_k(x_{ik}, x_{j_k})$$

as the dissimilarity between objects i and j.



Dissimilarities Based on Attributes

▶ **Quantitative variables** are represented by continuous real-valued numbers. Error between them can be a monotone-increasing function of their absolute difference

$$d(x_i, x_j) = l(|x_i - x_j|).$$

lacktriangle Ordinal variables are often represented as ordered contiguous integers. Error are generally defined by replacing their M original values with

$$\frac{i-1/2}{M}, \quad i=1,\cdots,M.$$

► Categorical variables are unordered categorical variables, the degree-of-difference between pairs of values must be delineated explicitly.



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Clustering

Object Dissimilarity

- Then we can combine the p-individual attribute dissimilarities into a single overall measure of dissimilarity $d(x_i, x_j)$ between two objects (x_i, x_j) .
- ▶ This is nearly always done by means of a weighted average (convex combination)

$$d(x_i, x_j) = \sum_{k=1}^{p} w_k \cdot d_k(x_{ik}, x_{jk}), \quad \sum_{k=1}^{p} w_k = 1.$$

 \blacktriangleright The choice of w_k should be based on subject matter considerations.



- The measure of the similarity between instances x_i and x_j is mainly decided by the distance $d(x_i, x_j)$.
- lacksquare Minkowski Measures (L_r distance): $d(oldsymbol{x}_i,oldsymbol{x}_j) = \left(\sum_{k=1}^p |x_{ik}-x_{jk}|^r
 ight)^{rac{1}{r}}.$
- + The Euclidean (L_2) distance is mostly applied to find similarity between two objects, which are expressed numerically.
- + It is highly sensitive to noise and usually not applied to data with hundreds of attributes also features with high values tend to dominate others.



- ► Cosine Measure: $d(\boldsymbol{x}_i, \boldsymbol{x}_j) = \frac{\langle \boldsymbol{x}_i, \boldsymbol{x}_j \rangle}{||\boldsymbol{x}_i|| \cdot ||\boldsymbol{x}_j||}$.
- + It is popular in in text mining and information retrieval.
- + It is invariant to rotation but not to linear transformations.
- ▶ Pearson Correlation Measure: $d(\boldsymbol{x}_i, \boldsymbol{x}_j) = \frac{(\boldsymbol{x}_i \bar{\boldsymbol{x}}_i)^\top (\boldsymbol{x}_j \bar{\boldsymbol{x}}_j)}{||\boldsymbol{x}_i \bar{\boldsymbol{x}}_i|| \cdot ||\boldsymbol{x}_i \bar{\boldsymbol{x}}_i||}$.
- + It is a measure of linear correlation between two variables.



- **Extended Jaccard Measure**: $d(\boldsymbol{x}_i, \boldsymbol{x}_j) = \frac{\boldsymbol{x}_i^{\top} \boldsymbol{x}_j}{||\boldsymbol{x}_i||^2 + ||\boldsymbol{x}_j||^2 \boldsymbol{x}_i^{\top} \boldsymbol{x}_j}.$
- + The binary Jaccard coefficient measures the degree of overlap between two sets and is computed as the ratio of the number of shared attributes.
- + It is suitable sufficiently to be employed in the documents or word similarity measurement.
- ▶ Dice Coefficient Measure: $d(x_i, x_j) = \frac{2x_i^\top x_j}{||x_i||^2 + ||x_i||^2}$.
- + It is F1 score when applied to binary data.
- Kernel trick.



Choose K

- For data segmentation, the number of clusters K is the part of the problem. For example, a company employ K sales people, and then partition a customer database into K segments, one for each sales person.
- lackbox Often, cluster analysis is used to provide a descriptive statistic for ascertaining the extent to which the observations comprising the data base fall into natural distinct groupings. Here the number of such groups K^* is unknown and need to be estimated from the data.

Choose K

- ▶ Data-based methods for estimating K^* typically examine the within-cluster dissimilarity W_K as a function of the number of clusters K.
- Usually, there will be a sharp decrease in successive differences in criterion value, $W_K W_{K+1}$, at $K = K^*$. That is, $\{W_K W_{K+1} | K < K^*\} \gg \{W_K W_{K+1} | K \ge K^*\}$.
- ▶ An estimate \widehat{K}^* for K^* is then obtained by identifying a "kink" in the plot of W_K as a function of K.

Choose K

- ▶ The recently proposed Gap statistic compares the curve $\log W_K$ to the curve obtained from data uniformly distributed over a rectangle containing the data.
- ▶ It estimates the optimal number of clusters to be the place where the gap between the two curves is largest.

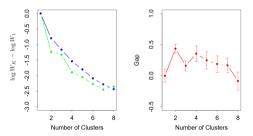


Figure: $K^* = 2$



Hierarchical Clustering Methods

▶ In hierarchical clustering methods, clusters are formed by iteratively dividing the patterns using top-down or bottom up approach.

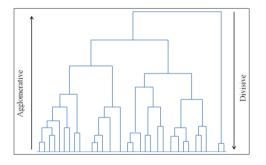


Figure: Hierarchical clustering dendrogram

Agglomerative & Divisive

- ► The agglomerative (bottom-up) approach builds up clusters starting with single object and then merging these atomic clusters into larger and larger clusters, until all of the objects are finally lying in a single cluster.
- ► The divisive (top-down) approach breaks up cluster containing all objects into smaller clusters, until each object forms a cluster on its own.

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Example (Agglomerative)

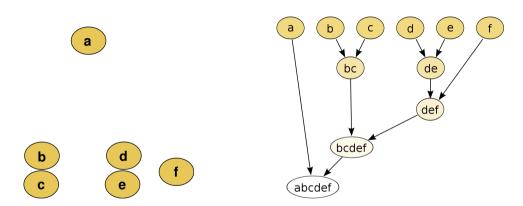


Figure: A simple agglomerative clustering algorithm with single-linkage

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Similarity Measure (Linkage)

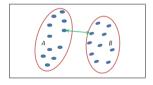


Figure: Single-linkage

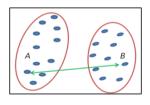


Figure: Complete-linkage

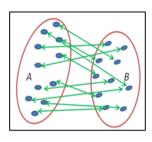


Figure: Average-linkage

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Similarity Measure (Linkage)

Single-linkage:

$$d(A,B) = \min\{d(a,b) : a \in A, b \in B\}.$$

Complete-linkage:

$$d(A,B) = \min\{d(a,b) : a \in A, b \in B\}.$$

Average-linkage:

$$d(A, B) = \frac{1}{|A||B|} \sum_{a \in A} \sum_{b \in B} d(a, b).$$

Criticisms and Enhancement

- ▶ The classic HC algorithms lack robustness and are sensitive to noise and outliers.
- ▶ The computational complexity for most of HC algorithms is $O(N^2)$.

Name	Type of data	Complexity	Ability to handle high dimensional data
BIRCH	Numerical	O(N)	No
CURE	Numerical	$O(N^2 \log N)$	Yes
ROCK	Categorical	$O(N^2 + Nm_m m_a + N^2 \log N)^*$	No
CHEMELEON	Numerical/ Categorical	$O(Nm + N\log N + m^2 \log N)^{**}$	No

Partition Clustering Methods

- ▶ Opposite to hierarchical clustering, here data are assigned into *K* (predefined) clusters without any hierarchical structure by optimizing some criterion (e.g. Minimum Euclidean distance).
- \blacktriangleright Examples: K-means, PAM, CLARA, CLARANS, Fuzzy C-means, DBSCAN etc.

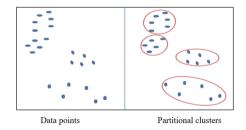


Figure: Partitional clustering approaches

K-means

- ightharpoonup K-means algorithm assign N observations to K clusters in such a way that within each cluster the average dissimilarity of the observations from the cluster mean is minimized.
- ▶ The loss function (within-point scatter) can be written as

$$L = \sum_{k=1}^{K} N_k \sum_{C(i)=k} \|x_i - \bar{x}_k\|^2,$$

where
$$N_k = \sum_{i=1}^N I(C(i) = k)$$
.

▶ Then we need to solve the following optimization problem

$$\min_{C, \{m_k\}_1^K} \sum_{k=1}^K N_k \sum_{C(i)=k} \|x_i - m_k\|^2$$



Iterative Descent Algorithm

Algorithm *K*-means Clustering

- 1. For a given assignment C, minimization with respect to $\{m_1,\ldots,m_K\}$ yielding the means of the currently assigned clusters.
- 2. Given a current set of means $\{m_1,\ldots,m_K\}$, assign each observation to the closest (current) cluster mean

$$C(i) = \underset{1 \le k \le K}{\operatorname{argmin}} ||x_i - m_k||^2.$$

3. Steps 1 and 2 are iterated until the assignments do not change.



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Iterative Descent Algorithm

- ▶ Each of steps 1 and 2 reduces the value of the criterion, so that convergence is assured.
- ▶ We should start the algorithm with many different random choices for the starting means, and choose the solution having smallest loss.

Self-organizing map (SOM) is an unsupervised technique used to produce a low-dimensional (typically two-dimensional) representation of a higher dimensional data set while preserving the topological structure of the data.



Figure: An illustration of the training of a self-organizing map

- \blacktriangleright We consider a SOM with a two-dimensional rectangular grid of K prototypes $m_i \in \mathbb{R}^p$.
- ▶ Each of the K prototypes are parametrized with respect to an integer coordinate pair $l_j \in \mathcal{Q}_1 \times \mathcal{Q}_2$. Here $\mathcal{Q}_1 = \{1, 2, \cdots, q_1\}$, similarly \mathcal{Q}_2 , and $K = q_1 \cdot q_2$.
- ightharpoonup The m_i are initialized and need to be updated iteratively.
- ▶ Once the model is fit, the observations can be mapped down onto the two-dimensional grid.

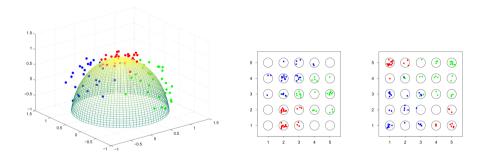


Figure: (Left) Simulated data in three classes. (Right) The 5×5 grid of prototypes.

- ightharpoonup The observations x_i are processed one at a time.
- ▶ We find the closest prototype m_j to x_i in Euclidean distance in \mathbb{R}^p , and then for all neighbors m_k of m_j , move m_k toward x_i via the update

$$m_k \leftarrow m_k + \alpha(x_i - m_k)$$

.

- ▶ The neighbors m_k of m_j are defined with the distance $||l_j l_k||$ and a threshold r.
- ▶ More sophisticated versions modify the update step according to distance:

$$m_k \leftarrow m_k + \alpha h(||l_k - l_j||)(x_i - m_k).$$



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- ▶ Typically α is decreased from say 1.0 to 0.0 over a few thousand iterations (one per observation).
- ▶ If we take the threshold r small enough so that each neighborhood contains only one point, then the SOM algorithm is an online version of K-means clustering.

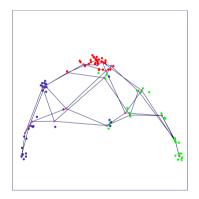


Figure: Wiremesh representation of the fitted SOM model in \mathbb{R}^3 where the purple points are the node centers



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Convex Clustering

- ▶ Lindsten et al. (2011) and Hocking et al (2011). formulate the clustering task as a convex optimization problem.
- ightharpoonup Given n points $\mathbf{x}_1, \dots, \mathbf{x}_n$ in \mathbb{R}^p , they suggest minimizing the convex criterion

$$F_{\gamma}(\mathbf{U}) = \frac{1}{2} \sum_{i=1}^{n} \|\mathbf{x}_{i} - \mathbf{u}_{i}\|_{2}^{2} + \gamma \sum_{i < j} w_{ij} \|\mathbf{u}_{i} - \mathbf{u}_{j}\|_{2}^{2}$$

where γ is a positive tuning constant, w_{ij} is a nonnegative weight, and the i th column \mathbf{u}_i of the matrix \mathbf{U} is the cluster center attached to point \mathbf{x}_i .

▶ Different norm can be used here, e.g. Lindsten et al. consider an ℓ_p norm penalty on the differences $\mathbf{u}_i - \mathbf{u}_j$ while Hocking et al. consider ℓ_1, ℓ_2 , and ℓ_∞ penalties.



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Convex Clustering

- When $\gamma=0$, the minimum is attained when $\mathbf{u}_i=\mathbf{x}_i$, and each point occupies a unique cluster.
- As γ increases, the cluster centers begin to coalesce. Two points \mathbf{x}_i and \mathbf{x}_j with $\mathbf{u}_i = \mathbf{u}_j$ are said to belong to the same cluster.
- ightharpoonup For sufficiently high γ all points coalesce into a single cluster.

Convex Clustering

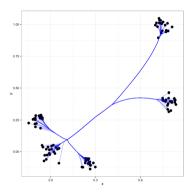


Figure: The blue lines trace the path of the cluster centers as the regularization parameter γ increases.



Convex Clustering

- ▶ The benefits of the formulation of convex relaxation are manifold.
- ▶ The convex relaxation admits a simple and fast iterative algorithm that is guaranteed to converge to the unique global minimizer, e.g. the alternating direction method of multipliers (ADMM) and alternating minimization algorithm (AMA).
- ► The convex relaxation performs continuous clustering which is intuitively appealing, globally optimal, and computationally tractable.

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Introduction

Given a set of observations x_1, \ldots, x_n , suppose we have obtained a similarity matrix:

$$S = (s_{ij})_{n \times n}$$

or a distance matrix

$$D = (d_{ij})_{n \times n},$$

where $s_{ij} = s(x_i, x_j) \ge 0$ and $d_{ij} = d(x_i, x_j) \ge 0$.

Target: clustering the observations based on S or D.

st In the following, we focus on clustering based on S.

Introduction

A Graph Cut Perspective

On the basis of S, we define a similarity graph G=(V,E) and its weighted adjacency matrix $W=(w_{ij})_{n\times n}$, where $V=\{1,\ldots,n\}$ is the vertex set representing x_1,\ldots,x_n , $E\subset V\times V$ and $w_{ij}=s_{ij}I((i,j)\in E)$.

- ▶ ε -neighborhood: $(i,j) \in E$ if $s_{ij} > \varepsilon$ and $(i,j) \notin E$ otherwise.
- ▶ k-nearest neighbor: For each i, only $(i, j_1), \ldots, (i, j_k) \in E$ such that $s_{ij_1} \ge \ldots \ge s_{ij_k} \ge \ldots$
- ▶ Fully connected: $(i, j) \in E$ if $s_{ij} > 0$.

Introduction

Given the number k of clusters, our target translates to obtaining a partition:

$$V = \cup_{i=1}^k A_i,$$

where A_i 's are disjoint.

An intuitive way:

Two nodes in the same group \Rightarrow high similarity;

Two nodes in different groups \Rightarrow low similarity.

Introduction

Cut

For $A, B \subset \{1, \dots, n\}$, define the between-group weight:

$$W(A,B) = \sum_{\substack{i \in A \\ j \in B}} w_{ij}.$$

A straightforward way is to minimize

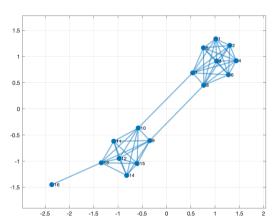
$$cut(A_1, ..., A_k) := \frac{1}{2} \sum_{i=1}^k W(A_i, A_i^c),$$

where $A_i^c = V - A_i$.

Unfortunately, it often yields unsatisfactory partitions in practice.

Introduction

Consider the following unweighted graph. $x_1, \ldots, x_{16} \in \mathbb{R}^2$. E is shown in the figure.



Introduction

Set k = 2. Simple calculation yields

$$A_1 = \{1, \dots, 15\}, \ A_2 = \{16\} \Rightarrow cut(A_1, A_2) = \frac{1}{2};$$

 $A_1 = \{1, \dots, 8\}, \ A_2 = \{9, \dots, 16\} \Rightarrow cut(A_1, A_2) = 1.$

Which indicates that minimizing cut is likely to yield unbalanced clusters.



Derivation

Ratio Cut

An improved method tries to minimize

$$Ratiocut(A_1, ..., A_k) := \frac{1}{2} \sum_{i=1}^k \frac{W(A_i, A_i^c)}{|A_i|}.$$
 (1)

When k = 2, it simplifies to

$$Ratiocut(A_1, A_2) = cut(A_1, A_2) \left(\frac{1}{|A_1|} + \frac{1}{|A_2|} \right).$$

The second term reaches minimum iff $|A_1| = |A_2|$.

* This method minimize the overall between-group similarity, while balancing group sizes.

Derivation

To obtain the minimizor of (1), we introduce two definitions.

▶ Membership matrix: $H = (h_{ij})_{n \times k}$, where

$$h_{ij} = egin{cases} 1/\sqrt{|A_j|}, & i \in A_j \ 0, & ext{otherwise}. \end{cases}$$

▶ Degree matrix: $D = \text{diag}\{d_1, \dots, d_n\}$, where

$$d_i = \sum_{j=1}^n w_{ij}, \quad i = 1, \dots, n.$$

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Derivation

Denote $H = (h_1^T, \dots, h_n^T)^T$ and let L := D - W, we have

$$\frac{W(A_i, A_i^c)}{2|A_i|} = h_i^T L h_i = (H^T L H)_{ii}.$$

Hence, $Ratiocut(A_1, ..., A_k) = tr(H^TLH)$ and we can write the problem as

$$\min_{A_1,\dots,A_k} tr(H^T L H)$$
st $H^T H = I$.

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Derivation

Solving (2) entails searching over $2^{|V|}$ values. For ease of computation, we relax it to

$$\begin{aligned} \min_{H \in \mathbb{R}^{n \times k}} & tr(H^T L H) \\ \text{s.t. } & H^T H = I, \end{aligned}$$

which is exactly an eigenvalue problem.

Derivation

Normalized Cut

For $A \subset \{1, \dots, n\}$, define another measure of the size of A:

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

An alternative method seeks to minimize

$$Ncut(A_1, ..., A_k) := \frac{1}{2} \sum_{i=1}^k \frac{W(A_i, A_i^c)}{vol(A_i)}.$$



Derivation

Let $L_{rw} := D^{-1}L = I - D^{-1}W$. Similar procedure shows that the optimization problem is equivalent to

$$\min_{A_1,\dots,A_k} tr(H^T L_{rw} H)$$
s.t. $H^T H = I$. (3)

Let $L_{sym} := D^{-1/2}LD^{-1/2}$ and substituting in $H = D^{-1/2}T$ transform (3) to

$$\min_{A_1,\dots,A_k} tr(T^T L_{sym}T)$$
st $T^T T = I$

As before, we solve their relaxed form in practice.

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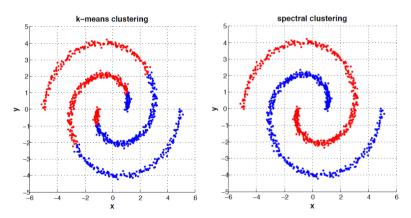
Derivation

To obtain discrete partitions from the resultant membership matrices, we can apply standard algorithms to cluster the rows of them, e.g., the k-means.

* Embedding n-dimensional similarity vectors into a k-dimensional space through Laplacian eigenmap.

Derivation

Compared to k-means, spectral clustering can yield non-convex clusters.



Summary

The Laplacian Matrices

The matrices corresponding to those eigenvalue problems are called the Laplacian matrices in spectral clustering.

► The unnormalized Laplacian matrix

$$L = D - W$$

The normalized Laplacian matrices

$$L_{sym} = D^{-1/2}LD^{-1/2} L_{rw} = D^{-1}L$$



Summary

Properties of L:

- $\forall f \in \mathbb{R}^n, f^T L f = \frac{1}{2} \sum_{i,j=1}^n w_{ij} (f_i f_j)^2.$
- $ightharpoonup L^T = L, L \succ 0.$
- $\lambda_n(L) = 0$ with eigenvector $\mathbf{1} = (1, \dots, 1)^T$.

Properties of L_{sum} and L_{rw} :

- $\blacktriangleright \ \forall f \in \mathbb{R}^n, \ f^T L f = \frac{1}{2} \sum_{i,j=1}^n w_{ij} \left(\frac{f_i}{\sqrt{d_i}} \frac{f_j}{\sqrt{d_j}} \right)^2.$
- lacklart λ is an eigenvalue of L_{rw} with eigenvector $u \Leftrightarrow \lambda$ is an eigenvalue of L_{rw} with eigenvector $D^{1/2}u$.
- $\lambda_n(L_{rw}) = 0$ with eigenvector $\mathbf{1} = (1, \dots, 1)^T$.
- $ightharpoonup L_{rw}, L_{sum} \succeq 0.$



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Summary

Unnormalized Spectral Clustering

Input: similarity matrix S, number k of clusters.

- ightharpoonup Construct a weighted adjacency matrix W.
- ightharpoonup Compute the unnormalized Laplacian L.
- ightharpoonup Compute the first k eigenvectors u_1, \ldots, u_k of L.
- ▶ Let $U := (u_1, ..., u_k) = (y_1^T, ..., y_n^T)^T$.
- ightharpoonup Cluster the points $(y_i)_{i=1,\ldots,n}$ with k-means algorithm into clusters C_1,\ldots,C_k .

Output: Clusters A_1, \ldots, A_k with $A_i = \{j | y_j \in C_i\}$.



Summary

Normalized Spectral Clustering 1

Input: similarity matrix S, number k of clusters.

- ightharpoonup Construct a weighted adjacency matrix W.
- ightharpoonup Compute the unnormalized Laplacian L.
- ightharpoonup Compute the first k eigenvectors u_1, \ldots, u_k of the generalized eigenproblem $Lu = \lambda Du$.
- ▶ Let $U := (u_1, ..., u_k) = (y_1^T, ..., y_n^T)^T$.
- ightharpoonup Cluster the points $(y_i)_{i=1,\ldots,n}$ with k-means algorithm into clusters C_1,\ldots,C_k .

Output: Clusters A_1, \ldots, A_k with $A_i = \{j | y_j \in C_i\}$.



Summary

Normalized Spectral Clustering 2

Input: similarity matrix S, number k of clusters.

- ightharpoonup Construct a weighted adjacency matrix W.
- ightharpoonup Compute the normalized Laplacian L_{sum} .
- ightharpoonup Compute the first k eigenvectors u_1, \ldots, u_k of L_{sum} .
- Let $U := (u_1, \ldots, u_k)$, normalize its rows to norm 1 and obtain T, that is set $t_{ij} = u_{ij}/(\sum_k u_{ik}^2)^{1/2}$.
- ▶ Let $T = (y_1^T, ..., y_n^T)^T$.
- ▶ Cluster the points $(y_i)_{i=1,...,n}$ with k-means algorithm into clusters C_1,\ldots,C_k .

Output: Clusters A_1, \ldots, A_k with $A_i = \{j | y_j \in C_i\}$.



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Practical Details

Number of Clusters

A self-contained method: the eigengap heuristic. Denote the eigenvalues of the Laplacian matrix as

$$\lambda_1 \leq \lambda_2 \leq \cdots \leq \lambda_n$$
.

We choose k that maximize

$$\gamma_k := |\lambda_k - \lambda_{k+1}|, \ k = 1, \dots, n-1.$$



Practical Details

Type of Laplacian Matrix

If all degrees are nearly equal, then three Laplacians are similar. Otherwise, consider the case k=2, recall the objective of clustering:

- ▶ Minimize the between-group similarity \Rightarrow minimize $cut(A, A^c)$.
- Maximize the within-group similarity W(A, A) and $W(A^c, A^c)$.

Practical Details

The within-group similarity is

$$W(A, A) = W(A, V) - W(A, A^{c}) = vol(A) - cut(A, A^{c}).$$

Hence,

Maximize W(A, A)

 $\Rightarrow cut(A, A^c)$ is small and vol(A) is large

 \Rightarrow Minimizing the normalized cut.

On the contrary, the Ratio Cut maximizes |A| and $|A^c|$, which are not necessarily related to W(A,A).

* Theoretical approval for the normalized Laplacians can be found in the literature. To sum up, the normalized Laplacians are prefered.

Practical Details

To select from the two normalized Laplacians:

- ▶ the eigenvectors of L_{rw} are cluster indicators, while the eigenvectors of L_{sym} are additionally multiplied with $D^{1/2}$;
- ▶ Using L_{sym} does not have any computational advantages.

Thus, L_{rw} is prefered.

Outline

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Motivation

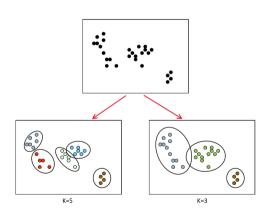
Gaussian mixture (Linear Discriminant Analysis)

Given data $x_1, \ldots, x_n \in \mathbb{R}^2$, we are told that x_i 's are drawn from a mixture of K distinct Gaussian populations, not knowing the value of K. How to fit the mixture model?

We can try different values of K, and run EM algorithm to estimate the corresponding parameters.



Motivation



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Motivation

What if the sample size is large?

- ▶ Sequential fitting plus model selection can be time consuming.
- ▶ Both under and over-fitting are possible due to unobserved heterogeneity.

Motivation

Alternative: infer the number of clusters from the data.

$$x_i | \theta_i \sim F_{\theta_i}, \quad i = 1, \dots, n.$$

 $\theta_i \sim G, \quad i = 1, \dots, n.$

- * $\{F_{\theta}: \theta \in \Theta\}$ is a family of parametric distribution.
- * $\theta_i = \theta_j \Rightarrow x_i$ and x_j belongs to the same cluster.
- * G is the prior for θ .

We introduce the Dirichlet process to define G as the prior distribution of the non-parametric distribution.



Definition

Recall the Dirichlet distribution:

$$\boldsymbol{\theta} = (\theta_1, \dots, \theta_K) \sim \operatorname{Dir}(\alpha_1, \dots, \alpha_K),$$

if

$$P(\boldsymbol{\theta}) = \frac{\Gamma(\sum_{k=1}^{K} \alpha_k)}{\prod\limits_{k=1}^{K} \Gamma(\alpha_k)} \prod_{k=1}^{K} \theta_k^{\alpha_k - 1},$$

where $\alpha_k > 0$, $\theta_k \geq 0$ for $k = 1, \dots, K$ and $\sum\limits_{k=1}^K \theta_k = 1$.

st A distribution of multinomial distributions with K categories.

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Definition

The Dirichlet Process

Definition

Let G_0 be a non-atomic distribution over Θ , $\alpha>0$ is a real number. We say that G is a Dirichlet process, denoted by $G\sim \mathrm{DP}(\alpha,G_0)$, if

$$(G(\Theta_1), \ldots, G(\Theta_k)) \sim \text{Dir}(\alpha G_0(\Theta_1), \ldots, \alpha G_0(\Theta_k))$$

for every finite partition of Θ : $\Theta = \bigcup_{i=1}^k \Theta_i, \ k=1,2,\ldots$

- $* G_0$ is called the base distribution.
- $* \alpha$ is a scaling parameter.



Definition

Properties

For any $\Theta_0 \subset \Theta$, it can be shown that

$$E(G(\Theta_0)) = G_0(\Theta_0).$$

 $Var(G(\Theta_0)) = \frac{G_0(\Theta_0)(1 - G_0(\Theta_0))}{\alpha + 1}.$

* $\alpha \to \infty \Rightarrow G \to G_0$ pointwise.



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Definition

Existence

Consider the hierachical model:

$$\theta_i \sim G,$$

$$G \sim \mathrm{DP}(\alpha, G_0).$$
(1)

It can be shown that the posterior is

$$G|\theta_1,\ldots,\theta_n \sim \mathrm{DP}(\alpha+n,\frac{1}{\alpha+n}(\alpha G_0+\sum_{i=1}^n \delta_{\theta_i}),$$

where δ_{θ} is the dirac measure at $\theta \in \Theta$.



Definition

Since $\theta_1, \ldots, \theta_{n+1}$ are conditional independent given G, we have

$$\theta_{n+1}|G,\theta_1,\ldots,\theta_n\sim G.$$

For any measurable $A \subset \Theta$, we have

$$P(\theta_{n+1} \in A | \theta_1, \dots, \theta_n) = E[G(A) | \theta_1, \dots, \theta_n]$$
$$= \frac{1}{\alpha + n} \left(\alpha G_0(A) + \sum_{i=1}^n \delta_{\theta_i}(A) \right).$$

Definition

Thus,

$$\theta_{n+1}|\theta_1,\dots,\theta_n \sim \frac{1}{\alpha+n} \Big(\alpha G_0 + \sum_{i=1}^n \delta_{\theta_i}\Big).$$
 (5)

It follows from (5) and the chain rule that

$$P(\theta_1, \dots, \theta_n) = P(\theta_{\sigma(1)}, \dots, \theta_{\sigma(n)}),$$

where $(\sigma(1), \ldots, \sigma(n))$ is an arbitary permutation of $(1, \ldots, n)$. So the existence of G follows from de Finetti's theorem.



Definition

Construction

Chinese Restraunt Process

The predictive distribution (5) implies a sequential process of generating $\{\theta_i\}_{i=1}^{\infty}$. Let $\theta_1^*, \dots, \theta_K^*$ be the unique values of $\theta_1, \dots, \theta_n$, then

$$\theta_{n+1}|\theta_1,\dots,\theta_n = \begin{cases} \text{a certain } \theta_k^* & \text{with probability } \frac{\#\{\theta_i:\theta_i=\theta_k^*\}}{n+\alpha} \\ \text{new draw from } G_0 & \text{with probability } \frac{\alpha}{n+\alpha}. \end{cases}$$





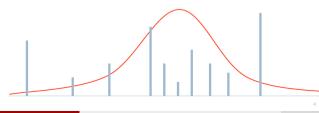




Definition

Stick Breaking

- ightharpoonup Draw $\theta_1^*, \ldots, \theta_k^*, \ldots$ from G_0 .
- ightharpoonup Draw v_1, \ldots, v_k, \ldots from Beta $(1, \alpha)$.
- ► Set $\pi_i = v_i \prod_{j=1}^{i-1} (1 v_j)$.
- ▶ Set $G = \sum_{i=1}^{\infty} \pi_i \delta_{\theta_i^*}$, where δ_x is the dirac measure at x.



Clustering

Dirichlet Process Mixture

The complete model:

$$x_i | \theta_i \sim F_{\theta_i};$$

 $\theta_i | G \sim G;$ (6)
 $G | \alpha, G_0 \sim DP(\alpha, G_0).$

Denote by z_i the cluster indicators:

$$z_i = k$$
 if $\theta_i = \theta_k^*$, $i = 1, \dots, n$.

Denote by $\pi_k = P(z_i = k), k = 1, \dots$



Clustering

With
$$G = \sum\limits_{k=1}^{\infty} \pi_k \delta_{ heta_k^*}$$
, model (6) is equivalent to

$$\pi | \alpha \sim \text{GEM}(\alpha);$$

$$z_{i} | \pi \sim \text{Multinomial}(\pi);$$

$$\theta_{k}^{*} | G_{0} \sim G_{0};$$

$$x_{i} | z_{i}, \theta_{k}^{*} \sim F_{\theta_{k}^{*}}.$$

$$(7)$$

where $GEM(\alpha)$ stands for the distribution of $\pi = (\pi_1, ...)$ constructed from stick breaking.



Inference

Clustering based on (7): Bayesian inference.

- MCMC.
- Variational inference.

* The Dirichlet process specifies a infinite mixture, while only finite components are active, whose number could increase with sample size.

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Peng Chen, Jiaqi Xia (USTC)

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