

COMP4121 Advanced Algorithms

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Clustering algorithms





• Fundamentally important for data science

- Making sense of data on its own
- Data preprocessing for other algorithms
- It is a type of *unsupervised learning*.

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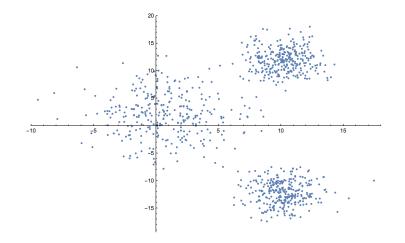
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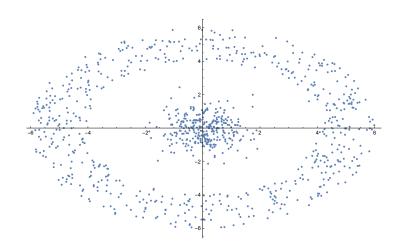
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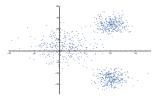
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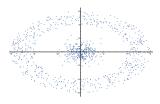
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What are clusters?

- Two kinds of clusters:
 - center based clusters



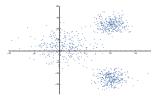
2 high density clusters



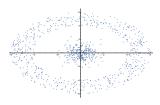
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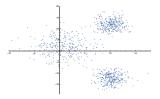
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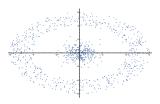
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• A good clustering algorithm should be able to handle both kinds.

• We have to make sure that the data is adequately represented.

- In general, there are two most common representations:
 -] as vectors in \mathbb{R}^{c}
 - This is suitable when you have several numerical measurements of each object, such as the red blood cell count, white blood cell count, haemoglobin content, etc for each patient in a group of patients.
 - Another example might be the relative frequencies of the key words in each document from a collection.
 - Note that *d* can be extremely large, corresponding to thousands or more of possible keywords.
 - This can be a problem due to complexities of storing and handling such high dimensional data. (this is where Johnson - Lindenstrauss Theorem come to play)
 - as a weighted graph
 - Data points are represented as vertices of the graph;
 - The weights of the edges reflect the degree of similarity (or dissimilarity) of the data points.
 - Data represented as vectors in \mathbb{R}^d can be represented as a weighted graph where the weights of edges reflect dissimilarity of the end points as measured by some form of distance between the end points.

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• The distance between two data points $x, y \in \mathbb{R}^d$ can be defined as either

$$d(x,y) = \sum_{i=1}^{d} |x_i - y_i|$$
 or as $d(x,y) = \sqrt{\sum_{i=1}^{d} (x_i - y_i)^2}$

- Such a distance d(x, y) is then taken as a measure of dissimilarity of x and y.
- If the scales of the i^{th} and j^{th} coordinates x_i and x_j differ significantly, or if they are not of equal importance, we might consider instead

$$d(x,y)^2 = \sum_{i=1}^d w_i (x_i - y_i)^2$$

- The weights w_i are chosen to normalise different variances of x_i and x_j or to encode their relative significances.
- Graph representation of data is often much a more compact representation than as vectors in \mathbb{R}^d , which does not suffer from problems of high dimensionality.
- Note that in the graph representation of data the geometry of the data points is lost, so the clustering is based only on mutual distances of pairs of points, which is good when clustering is not center based. < = > = ->~

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We assume data points are represented as vectors in \mathbb{R}^d .

• k-center clustering: Find a partition $C = \{C_1, \ldots, C_k\}$ of a set of data points $A = \{a_1, \ldots, a_n\}$ into k clusters, with the corresponding centers c_1, \ldots, c_k , which minimize the maximum distance between any data point and the center of its cluster.

• That is, we want to minimize

$$\Phi(\mathcal{C}) = \max_{j=1}^{k} \max_{a \in \mathcal{C}_j} d(\mathbf{a}, \mathbf{c}_j)$$

- This is the "fire-station location problem" since one can think of it as the problem of building k fire-stations in a city so as to minimise the maximum distance a fire-truck needs to travel to put out a fire.
- The *radius* of a clustering $A = \bigcup_{m=1}^{k} A_m$ is the largest distance of a point from A to its associated cluster centre.
- Thus, center-based clustering algorithms try to minimise the radius of the resulting clustering.

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Center-based clustering

k-median clustering: Find a partition C = {C₁,...C_k} of a set of data points A = {a₁,..., a_n} into k clusters, with the corresponding centers c₁,..., c_k, which minimizes the sum of distances between data points and their corresponding cluster centres.

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- Note that $d(\mathbf{a}, \mathbf{c}_j)$ can be any distance metric, such as ℓ^1 metric $d_1(\mathbf{a}, \mathbf{c}_j) = \sum_{k=1}^d |(\mathbf{a})_k (\mathbf{c}_j)_k|$ or ℓ^2 metric $d_2(\mathbf{a}, \mathbf{c}_j) = \sqrt{\sum_{k=1}^d ((\mathbf{a})_k (\mathbf{c}_j)_k)^2}.$
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- If the distance is the ℓ_1 distance, one can show that the coordinates of the optimal centers are the coordinate-wise medians of points in each cluster.

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The most frequently used center-based clustering algorithm is the $k\mbox{-means}$ algorithm.

- **k-means clustering problem:** Find a partition C = {C₁,...C_k} of a set of data points A = {a₁,..., a_n} into k clusters, with the corresponding centers c₁,..., c_k, which minimize the sum of the squares of distances between data points and their corresponding cluster centers.
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Keep in mind that each a_i is a vector in R^d, so

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• Let
$$\mathbf{c} = (c_1, \ldots, c_d)$$
 with for all $1 \le k \le d$,

$$c_k = (a_{1k} + \ldots + a_{nk})/n$$

i.e., c_k is the arithmetic mean of the k^{th} coordinates of all of the points $\mathbf{a}_1, \ldots, \mathbf{a}_n$.

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is minimised when **x** is the centroid $\mathbf{c} = \frac{1}{n} \sum_{i=1}^{n} \mathbf{x}_{i}$. • **Proof:** By the previous theorem.

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 $\bullet\,$ This is easy to see just by replacing c by its definition plus doing some obvious algebra.

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• Let $A = {\mathbf{a}_1, \dots, \mathbf{a}_n}$ be a set of points in \mathbb{R}^d and let \mathbf{c} be the centroid of A. Then

$$\frac{1}{2n}\sum_{i,j=1}^{n} \|\mathbf{a}_{i} - \mathbf{a}_{j}\|^{2} = \sum_{m=1}^{n} \|\mathbf{a}_{m} - \mathbf{c}\|^{2}$$

 $\bullet\,$ This is easy to see just by replacing c by its definition plus doing some obvious algebra.

• Thus, if we are given a set of points $A = \{\mathbf{a}_1, \dots, \mathbf{a}_n\}$ in \mathbb{R}^d and the problem is to find a partition of A into k disjoint components $A = \bigcup_{i=1}^k A_i$ and k points $\mathbf{x}_1, \dots, \mathbf{x}_k$ such that the sum

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• Thus, finding disjoint components $A = \bigcup_{m=1}^{k} A_m$ which minimises

$$\sum_{m=1}^k \sum_{\mathbf{a}_j \in A_m} \|\mathbf{a}_j - \mathbf{c}_m\|^2$$

is equivalent to minimising

$$\sum_{m=1}^{k} \frac{1}{2|A_m|} \sum_{\mathbf{a}_i, \mathbf{a}_j \in A_m} \|\mathbf{a}_i - \mathbf{a}_j\|^2$$

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• **Claim:** At every round *p* of its loop, Lloyd's algorithm reduces the size of

$$\sum_{m=1}^{k} \sum_{\mathbf{a}_j \in A_m^{(p)}} \|\mathbf{a}_j - \mathbf{c}_m^{(p)}\|^2$$

where $A_m^{(p)}$ are the "temporary" clusters and $\mathbf{c}_m^{(p)}$ is the "temporary" centre of cluster $A_m^{(p)}$ at round p of the loop.

- This is obvious, because both steps of the loop have this property: replacing the cluster centres with the centroid of the cluster recuses every summand $\sum_{\mathbf{a}_j \in A_m^{(p)}} \|\mathbf{a}_j \mathbf{c}_m^{(p)}\|^2$ and so does associating every point with the nearest cluster centre.
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- In lots of applications this local minimum provides a good clustering.
- However, sometimes better results are obtained by running the algorithm several times with different initial set of cluster centres and picking the solution from the run for which the sum

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- One good option is to pick a random point \mathbf{a}_q from A as the first centre $\mathbf{c}_1^{(0)} = \mathbf{a}_q$.
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- Continue in this manner to get all k cluster centres, always picking as the next centre a point from A which has the largest minimal distance to all previously picked centres.

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- In fact, such a procedure for finding the initial centres $\mathbf{c}_m^{(0)}$ of initial clusters is used as a simple clustering algorithm in itself. You first choose cluster centers as described and then simply clustering points from A according to which is the closest centre $\mathbf{c}_m^{(0)}$ to that point.
- $\bullet\,$ This algorithm is usually called The Farthest Traversal k-clustering algorithm.
- The Farthest Traversal k-clustering algorithm, despite its simplicity, provides a reasonably good approximate clustering in the following sense.
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- **Theorem:** If A has a k-clustering of radius r, then the Farthest Traversal k-clustering algorithm produces a clustering of radius at most 2r.
- **Proof:** Suppose opposite, that there is $\mathbf{a} \in A$ at a distance to its cluster larger that 2r. This would mean that the distance of \mathbf{a} to all cluster centres is larger than 2r.
- But this implies that also the distances between all pairs of cluster centres must also be larger than 2r because otherwise a would have been chosen as one of the cluster centres.
- Thus, we would have at least k + 1 points (a plus the k cluster centres) which are all on pairwise distances larger than 2r.
- Since we have k + 1 points in k clusters, two such points must be in the same cluster.
- But no such two points can be in the same cluster of radius r, because their distance would be at most the diameter of the circle which is 2r.
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- Loyd's algorithm has been recently randomized by instead of picking always the furthest point, by picking a point with probability proportional to the shortest distance to one of already picked points.
- Let A_m be a cluster with its centroid \mathbf{c}_m as its centre; let us set

$$\operatorname{cost}(A_m) = \sum_{\mathbf{a}_i \in A_m} \|\mathbf{a}_i - \mathbf{c}_m\|^2$$

- The k-means clustering algorithms are trying to minimise the sum $\sum_{m=1}^{k} \operatorname{cost}(A_m).$
- Note that if we have two clusters A_m and A_l and take their union $B = A_m \cup A_l$ and the centroid of B as the cluster centre of B, then

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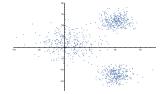
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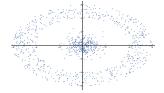
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• How do we cluster data when clusters are not centre based??



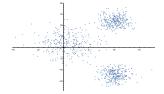


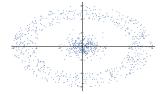
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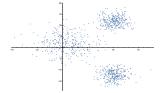


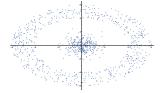
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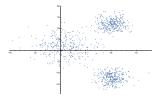


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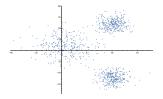


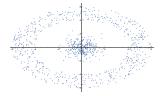
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- We represent a set of data points $A = \{\mathbf{a}_1, \dots, \mathbf{a}_n\}$ as the set of vertices $\{v_1, \dots, v_n\}$ of an undirected weighted graph G = (V, E).
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- So graph G is a compact summary of the set of data points $A = \{\mathbf{a}_1, \dots, \mathbf{a}_n\}.$
- The geometry of A is completely lost, and only pairwise similarities between the data points are preserved.
- This is actually good because it will allow us to handle clustering of points which is not centre based, but is based on "local similarity" of data points, as we will see later.
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- Given a subset $S \subset V$ of vertices, we denote by $\mathbb{1}_S$ the indicator vector $\mathbb{1}_S = (f_1, \ldots, f_n) \in \mathbb{R}^n$ where

$$f_i = \begin{cases} 1 & \text{if } v_i \in S \\ 0 & \text{if } v_i \notin S \end{cases}$$

• For simplicity, we abbreviate $v_i \in S$ as $i \in S$.

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- The *degree* matrix D is defined as a diagonal matrix with degree d_i of vertex v_i on the i^{th} entry of the diagonal of D and zeros everywhere off diagonal.
- So graph G is a compact summary of the set of data points $A = \{\mathbf{a}_1, \dots, \mathbf{a}_n\}.$
- The geometry of A is completely lost, and only pairwise similarities between the data points are preserved.
- This is actually good because it will allow us to handle clustering of points which is not centre based, but is based on "local similarity" of data points, as we will see later.
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$$W(S,B) = \sum_{i \in S, j \in B} w_{ij}$$

and for any set S we define two types of measurements of the "size" of S:

- |S| is the number of elements in S;
 vol(S) = ∑_{i∈S} d_i
- Recall that $d_i = \sum_{j=1}^n w_{ij}$ is the degree of vertex v_i .
- A natural partition of vertices of a graph G = (V, E) is into its connected components.

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- Given a set of data points $A = \{\mathbf{a}_1, \dots, \mathbf{a}_n\}$ we associate vertices $\{v_1, \dots, v_n\}$ of a similarity graph G, but there are many ways how we can associate weights w_{ij} which measure the similarity of data points \mathbf{a}_i and \mathbf{a}_j that correspond to vertices v_i and v_j .
 - (1) The ε -neighbourhood graph:
 - We connect all pairs of vertices v_i, v_j such that the distances between the associated data points a_i, a_j are smaller than ε.
 - The distance is usually the Euclidean distance

 $\|\mathbf{a}_i - \mathbf{a}_j\| = \sqrt{\sum_{p=1}^d (a_{ip} - a_{jp})^2},$ where $\mathbf{a}_i = (a_{i1}, \dots, a_{id}) \in \mathbb{R}^d$.



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- There are two flavours of k-nearest neighbour graphs:
 - Unidirectional k-nearest neighbour graph. We connect v_i with v_j if either v_j is among k nearest neighbours of v_i or vice versa, v_i is among k nearest neighbours of v_j .
 - **2** Mutual k-nearest neighbour graph. We connect v_i with v_j if both v_j is among k nearest neighbours of v_i and v_i is also among k closest neighbours of v_j .
- In both cases the edge is then weighted with the degree of similarity of the vertices v_i and v_j .

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(3) The fully connected graphs:

- We simply connect all pairs of vertices v_i and v_j for which the corresponding data points \mathbf{a}_i and \mathbf{a}_j have a strictly positive similarity, or similarity higher than some prescribed threshold ε .
- To ensure that such a graph represents local neighbourhood relationships, the similarity measure must be chosen to respect such localisation condition.
- Often we take weights which reflect such local similarities by the following formula:

$$\mathbf{W}_{ij} = e^{-\frac{\|\mathbf{a}_i - \mathbf{a}_j\|^2}{2\sigma^2}}$$

• Here σ is a parameter which determines "the size" of the neighbourhood, namely how fast the similarity decreases as distance increases.

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- Recall that the $n \times n$ diagonal matrix D has the degrees d_i of vertices v_i on its diagonal, where $d_i = \sum_{j=1}^n w_{ij}$.
- The (unnormalised) graph Laplacian matrix L is defined as

$$L = D - W$$

where $W = (w_{ij})_{i,j=1}^n$.

- Clearly, L is symmetric and it does not depend on w_{ii} , $1 \le i \le n$.
- Graph Laplacians are crucial for spectral clustering.
- A matrix M of size $n \times n$ is *positive semi-definite* if for all vectors $f \in \mathbb{R}^n$ we have

$$f^{\mathsf{T}}Mf \geq 0$$

- From linear algebra we know that a symmetric matrix is positive semi-definite iff all of its eigenvalues are real and non-negative.
- The next theorem summarises their main properties important for spectral clustering.

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• **Theorem:** The matrix L = D - W has the following properties: (1) For every vector $f \in \mathbb{R}^n$,

$$f^{\mathsf{T}}Lf = \frac{1}{2} \sum_{i,j=1}^{n} w_{ij} (f_i - f_j)^2$$

- (2) L is a symmetric positive semi-definite matrix.
- (3) The smallest eigenvalue of L is 0 and its corresponding eigenvector is $\mathbb{1} = (1, 1, \dots, 1)$.
- Proof:

(1)
$$f^{\mathsf{T}}Lf = f^{\mathsf{T}}Df - f^{\mathsf{T}}Wf = \sum_{i=1}^{n} d_i f_i^2 - \sum_{i,j=1}^{n} w_{ij} f_i f_j$$

$$= \frac{1}{2} \left(\sum_{i=1}^{n} \left(\sum_{j=1}^{n} w_{ij} \right) f_i^2 - 2 \sum_{i,j=1}^{n} w_{ij} f_i f_j + \sum_{j=1}^{n} \left(\sum_{i=1}^{n} w_{ij} \right) f_j^2 \right)$$
$$= \frac{1}{2} \sum_{i=1}^{n} w_{ij} (f_i - f_j)^2.$$

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$$= \frac{1}{2} \left(\sum_{i=1}^{n} \left(\sum_{j=1}^{n} w_{ij} \right) f_i^2 - 2 \sum_{i,j=1}^{n} w_{ij} f_i f_j + \sum_{j=1}^{n} \left(\sum_{i=1}^{n} w_{ij} \right) f_j^2 \right)$$
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$$= \frac{1}{2} \left(\sum_{i=1}^{n} \left(\sum_{j=1}^{n} w_{ij} \right) f_i^2 - 2 \sum_{i,j=1}^{n} w_{ij} f_i f_j + \sum_{j=1}^{n} \left(\sum_{i=1}^{n} w_{ij} \right) f_j^2 \right)$$
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- (3) Note that L1 = D1 W1. However, it is easy to see that both D1 and W1 produce the same vector with the *ith* coordinate equal to the degree d_i of vertex v_i. Thus, L1 = D1 W1 = 0 = 0 ⋅ 1. So, since L1 = 0 ⋅ 1, 0 is the smallest eigenvalue of L (because all eigenvalues are non-negative) and 1 is the corresponding eigenvector.
 - Let M be an $n \times n$ matrix. Then an eigenvalue λ of this matrix has:
 - An algebraic multiplicity k if the characteristic polynomial $P_n(x)$ has a form $P_n(x) = (x \lambda)^k Q(x)$ where Q(x) is a polynomial of degree n k.
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Thus, if two vertices v_i and v_j are connected by an edge, then $w_{ij} > 0$ and consequently $f_i = f_j$. Going along any path we get that the coordinates of f must be constant at all vertices along that path. Since G is connected, obviously all coordinates of f must be constant. Thus, $\mathbb{1}_V = (1, 1, \ldots, 1)$ is an eigenvector. (Note that we do not normalise eigenvectors).

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• **Proof (continued):** Assume now that *G* has *k* connected components. We can assume that the vertices of the connected components are listed in order of the component they belong to. Thus, matrix *W* is a block matrix of the form

$$W = \begin{pmatrix} W_1 & & & 0 \\ & W_2 & & \\ & & \ddots & \\ 0 & & & W_k \end{pmatrix}$$

where the block W_i corresponds to the connected component A_i and with 0's outside the blocks W_i .

• But then L = D - W also has the same structure:

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- Assume now that a graph G has k connected components which we would like to find.
- After forming the Laplacian matrix L we would use a standard software to find its eigenvalues.
- Such a software would output that 0 is an eigenvalue of L with multiplicity k and it would output k eigenvectors corresponding to eigenvalue 0.
- However, generally, these vectors would not be the indicators $\mathbb{1}_{A_i}$ of the connected components but k (mutually orthogonal) linear combinations of these indicator vectors, because any k orthogonal vectors in the eigensubspace corresponding to the eigenvalue 0 are equally good candidates.
- Thus, we will obtain k vectors from \mathbb{R}^n which look like this:

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- Note that for every two vertices v_i, v_j which belongs to the same connected component A_m the corresponding vectors \mathbf{y}_i and \mathbf{y}_j are identical and equal $(\alpha_m^1, \alpha_m^2, \ldots, \alpha_m^k)$ because only $\mathbb{1}_{A_m}$ has 1's at positions *i* and *j*; all other $\mathbb{1}_{A_i}$ for $l \neq m$ have zeros at these positions, given that v_i, v_j belong to the connected component A_m and that the components are disjoint.
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- When we cluster points into disjoint clusters we want any two vertices v_i, v_j with high similarity (i.e., with high weight w_{ij} of the corresponding edge (v_i, v_j)) to be in the same cluster, and any two vertices from different clusters either not to be connected with an edge (i.e., $w_{ij} = 0$) to be connected with an edge with a weight w_{ij} as small as possible.
- Thus, the clusters should be, in a sense, "approximate connected components" of tightly connected vertices with weak edges between such "approximate components".
- We can take k eigenvectors $\mathbf{e}_1, \ldots, \mathbf{e}_k$ corresponding to the k smallest eigenvalues (in place of eigenvalue 0 of multiplicity k) and form the corresponding matrix E with these eigenvectors as columns.
- We again consider the row vectors $\mathbf{y}_1, \mathbf{y}_2, \ldots, \mathbf{y}_n$. If the graph G had k connected components, then for every two points v_i and v_j from the same components we saw that the corresponding vectors \mathbf{y}_i and \mathbf{y}_j would be identical.
- For clustering this is no longer the case, but since within each optimal cluster the weights of edges are high and the weights of edges between different clusters are low, we can hope that the points v_i and v_j from the same optimal cluster will have similar vectors \mathbf{y}_i and \mathbf{y}_j and points v_i and v_j from different optimal clusters will have substantially different vectors \mathbf{y}_i and \mathbf{y}_j .

- When we cluster points into disjoint clusters we want any two vertices v_i, v_j with high similarity (i.e., with high weight w_{ij} of the corresponding edge (v_i, v_j)) to be in the same cluster, and any two vertices from different clusters either not to be connected with an edge (i.e., $w_{ij} = 0$) to be connected with an edge with a weight w_{ij} as small as possible.
- Thus, the clusters should be, in a sense, "approximate connected components" of tightly connected vertices with weak edges between such "approximate components".
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- The previous heuristic analysis suggests the following clustering algorithm which can produce clusters of similar points that are not centre based.
- Spectral Clustering Algorithm.

Input: a set of data points $A = \{\mathbf{a}_1, \dots, \mathbf{a}_n\}$, number k of clusters to construct.

- Construct a similarity graph G by one of the ways described; let $W = \{w_{ij} : 1 \le i, j \le n\}$ be its weighted adjacency matrix.
- 2 Compute the Laplacian L = D W.
- 3 Compute the k eigenvectors $\mathbf{e}_1, \ldots, \mathbf{e}_k$ of L which correspond to k smallest eigenvalues.
- (a) Let *E* be the matrix of size $n \times k$ containing the eigenvectors $\mathbf{e}_1, \ldots, \mathbf{e}_k$ as columns.
- So For i = 1,...,n, let y_i be the vector corresponding to the ith row of E.
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Output: Clusters A_1, \ldots, A_k with A_i defined as $A_{i_k} \equiv \{v_{j_k}; y_{j_k}; C_i\}$.

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Output: Clusters A_1, \ldots, A_k with A_i defined as $A_i = \{v_j : y_j \in C_i\}$.

• For a given number k of subsets, the MinCut approach to graph partitioning simply consists in choosing a partition A_1, \ldots, A_k which minimises

$$\operatorname{cut}(A_1, \dots, A_k) = \frac{1}{2} \sum_{i=1}^n W(A_i, \overline{A_i}) \tag{1}$$

- (Note that if k = 2 this is just the standard MinCut problem like we had for Karger's algorithm).
- Recall that for any two sets A and B, we have $W(A, B) = \sum_{i \in A, j \in B} w_{ij}$, and that \overline{A} denotes the complement of set A.
- Note that the factor $\frac{1}{2}$ in (2) is present because every edge is counted twice.
- Unfortunately, minimising (2) is not a good idea.
- The reason is that minimising (2) often produces clusters some of which contain only a single vertex or just a few vertices.

• A better idea is to find a partition A_1, \ldots, A_k which minimises

$$\operatorname{RatioCut}(A_1, \dots, A_k) = \frac{1}{2} \sum_{i=1}^n \frac{W(A_i, \overline{A_i})}{|A_i|}$$
(2)

- Having $|A_i|'s$ in the denominator encourages the algorithm to find clusters A_i which all have reasonably large number of points, rather than just a few.
- For every partition A_1, \ldots, A_k we can define the corresponding set of orthonormal indicator vectors $\mathbf{h}_j = (h_{1j}, h_{2j}, \ldots, h_{nj})^{\mathsf{T}}$ by setting $\mathbf{h}_j = 1/|A_j| \cdot \mathbb{1}_{A_j}$, i.e., by letting

$$h_{ij} = \begin{cases} \frac{1}{\sqrt{|A_j|}} & \text{if } v_i \in A_j \\ 0 & \text{if } v_i \notin A_j \end{cases}$$

• Note that

$$\|\mathbf{h}_j\|^2 = \sum_{v_i \in A_j} \left(\frac{1}{\sqrt{|A_j|}}\right)^2 = |A_j| \frac{1}{|A_j|} = 1$$

and, since $A'_{j}s$ are pairwise disjoint, $\mathbf{h}_{m} \cdot \mathbf{h}_{l} = 0$ if $m \neq l$.

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• Also, note that we have shown that

$$\mathbf{h}_{j}^{\mathsf{T}} L \mathbf{h}_{j} = \frac{1}{2} \sum_{m,l=1}^{n} w_{ml} (h_{mj} - h_{lj})^{2}$$

$$= \frac{1}{2} \left(\sum_{m \in A_{j}; l \notin A_{j}} w_{ml} (h_{mj} - h_{lj})^{2} + \sum_{l \in A_{j}; m \notin A_{j}} w_{ml} (h_{mj} - h_{lj})^{2} \right)$$

$$= \frac{1}{2} \left(\sum_{m \in A_{j}; l \notin A_{j}} w_{ml} \frac{1}{|A_{j}|} + \sum_{l \in A_{j}; m \notin A_{j}} w_{ml} \frac{1}{|A_{j}|} \right)$$

$$= \frac{\operatorname{cut}(A_{j}, \overline{A_{j}})}{|A_{j}|}$$

Let H be the matrix of size n × k with vectors h_j, 1 ≤ j ≤ k as columns.
Then the above equality implies that the sum of the diagonal elements of H^TLH, i.e. the trace of H^TLH satisfies

$$\operatorname{Tr}(H^{\mathsf{T}}LH) = \sum_{j=1}^{k} \frac{\operatorname{cut}(A_{j}, \overline{A_{j}})}{|A_{j}|}$$
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• Since we have proved that

RatioCut
$$(A_1, \dots, A_k) = \sum_{j=1}^k \frac{\operatorname{cut}(A_j, \overline{A_j})}{|A_j|} = \operatorname{Tr}(H^{\mathsf{T}}LH)$$

we can conclude that to minimise $\operatorname{RatioCut}(A_1, \ldots, A_k)$ we have to find disjoint sets A_1, \ldots, A_k which minimise $\operatorname{Tr}(H^{\mathsf{T}}LH)$ where the columns \mathbf{h}_j of H are of the form $\mathbf{h}_j = 1/|A_j| \cdot \mathbb{1}_{A_j}$.

• This is an NP hard problem, so we find only an approximate solution by solving the following relaxation of it:

Find
$$H \in \mathbb{R}^{n \times k}$$
 which minimises $\operatorname{Tr}(H^{\mathsf{T}}LH)$
subject to the constraint $H^{\mathsf{T}}H = H$

• The Rayleigh-Ritz theorem from linear algebra tells us that such an $H \in \mathbb{R}^{n \times k}$ is obtained as the matrix with k eigenvectors corresponding to the k smallest eigenvalues of L as the k columns of H.

Image: A matrix and a matrix

• Just as before, these eigenvectors might be approximations of linear combinations of the indicator functions $\mathbb{1}_{A_j}$, so we again cluster the n rows of H into k clusters $C_1, \ldots C_k$ to obtain the partition $A_1, \ldots A_k$ defined by

 $v_j \in A_m$ if an only if the j^{th} row of H belongs to C_m

- But notice that this is precisely what our spectral clustering algorithm does.
- Thus, besides the original heuristics with the connected components, we now see that the spectral clustering algorithm finds an approximate solution to the problem of finding A_1, \ldots, A_k which minimise the ratio cut

RatioCut
$$(A_1, \dots, A_k) = \sum_{j=1}^k \frac{\operatorname{cut}(A_j, \overline{A_j})}{|A_j|}$$

• It is possible to normalise the Laplacian so that the solution approximately minimises the so called Neut defined as

$$\operatorname{Ncut}(A_1, \dots, A_k) = \sum_{j=1}^k \frac{\operatorname{cut}(A_j, \overline{A_j})}{\operatorname{vol}(A_j)}$$

where vol(A) is the sum of the degrees of all vertices in A:

$$\operatorname{vol}(A) = \sum_{v_i \in A} d_i = \sum_{v_i \in A} \left(\sum_{j=1}^n w_{ij} \right)$$

- This sometimes produces better clustering, which also has a nice interpretation via random walk on graphs (a random walk seldom switches between different clusters).
- You can find all the details in a wonderfully written tutorial by Ulrike von Luxburg from the Max Planck Institute for Biological Cybernetics, available at http://www.tml.cs.uni-tuebingen.de/team/luxburg/ publications/Luxburg07_tutorial.pdf, which we have followed closely in a part of our presentation. A B A A B A

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