STAT 215A Fall 2023 Week 6

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Announcements

 Lab 2: making interactive plots and apps are recommended but not required. To do so, you need to make another .html file or shiny app. The .pdf report won't be compatible with it.

Lab 1 peer review due extended Oct 3 11:59 PM

Outline for today

- Choosing K for NMF
- Spectral clustering
- DBSCAN (time allowing)
- Lab 2 check-in

Nonnegative Matrix Factorization (NMF)

Given a non-negative matrix X, NMF solves

$$\underset{\mathbf{W} \geq 0, \mathbf{H} \geq 0}{\operatorname{argmin}} || \mathbf{X} - \mathbf{W} \mathbf{H} ||_F^2 = \sum_{i,j} (\mathbf{X}_{ij} - \mathbf{W}_i^{\top} \mathbf{H}_j)^2$$

You can modify this to work for X with missing data (in R:

NNLM: nnmf()¹):
$$\underset{\mathbf{W} \geq 0, \mathbf{H} \geq 0}{\operatorname{argmin}} \sum_{\substack{(i,j) \\ \text{not missing}}} (\mathbf{X}_{ij} - \mathbf{W}_i^{\top} \mathbf{H}_j)^2$$

Nonnegative Matrix Factorization (NMF)

Missing Data NMF:
$$\underset{\mathbf{W} \geq 0, \mathbf{H} \geq 0}{\operatorname{argmin}} \sum_{\substack{(i,j) \\ \text{not missing}}} (\mathbf{X}_{ij} - \mathbf{W}_i^{\top} \mathbf{H}_j)^2$$

Idea for choosing K:

- Randomly leave out entries from the data matrix X
- For each potential choice of K:
 - 1. Apply NMF to the data with missing values: W_M and H_M
 - 2. Impute the missing values of ${f X}$ using corresponding entries of ${f W}_M {f H}_M$
 - Compute the imputation error (MSE of difference between imputed and observed values)
 - 4. Repeat many times and compute the mean and SE for this K
- Choose K by taking the minimum or using the 1-SE rule (Breiman, 1984)

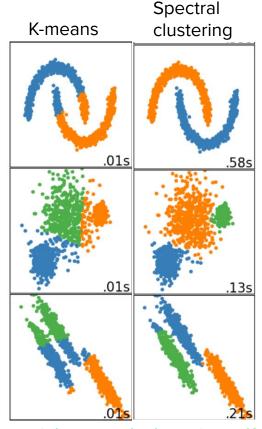
Spectral clustering: a "good" method

Advantages:

- Simple to implement
- Stable to underlying data generation mechanism

Disadvantages

- Need to represent the data as a graph
- Still need to choose K
- Not advised for problems with large numbers of clusters

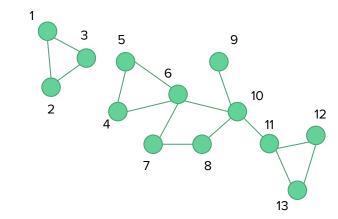


More details: http://people.csail.mit.edu/dsontag/courses/ml14/notes/Luxburg07 tutorial spectral clustering.pdf

Nice summary: https://eric-bunch.github.io/blog/spectral-clustering

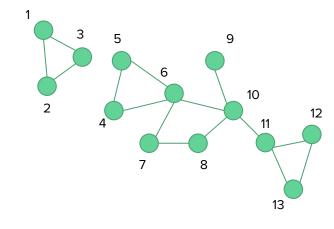
Setup

- Graph: G = (E,V)
- Weighted adjacency matrix: $W = (w_{ij})_{i,j=1,...,n}$
 - 0 on the diagonal
 - $w_{ij} = 0$ if there is no edge between v_i and v_j
- Diagonal degree matrix $D: D_{ii} = \sum_{i} W_{ij}$
- (Unnormalized) graph Laplacian: L=D-W



Let's try to find eigenvectors $Lx=\lambda x$

$$L = \begin{pmatrix} \sum_{j} w_{1j} & -w_{12} & -w_{13} & 0 & \cdots \\ -w_{12} & \sum_{j} w_{2j} & -w_{23} & 0 & \cdots \\ -w_{13} & -w_{23} & \sum_{j} w_{3j} & 0 & \cdots \\ 0 & 0 & 0 & \ddots \\ \vdots & \vdots & \vdots & \vdots \end{pmatrix}$$

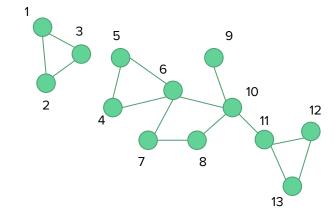


Let's try to find eigenvectors

$$Lx = \lambda x$$

1, the vector with all entries equal to 1

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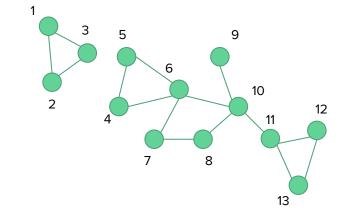


Let's try to find eigenvectors $Lx = \lambda x$

$$Lx = \lambda x$$

 $oldsymbol{1}$, the vector with all entries equal to $oldsymbol{1}$

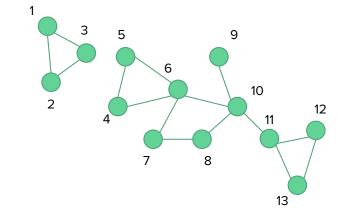
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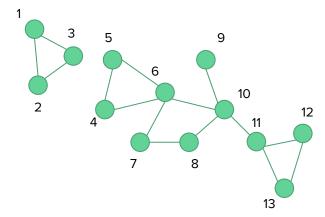
 $(1 \quad 1 \quad 1 \quad 0 \cdots 0)^{ op}$ and also $(0 \quad 0 \quad 0 \quad 1 \cdots 1)^{ op}$

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 $\lambda_1=0$ in these cases, so the multiplicity of the eigenvalue 0 tells us about the number of **connected** components in the graph.

$$(1 \quad 1 \quad 1 \quad 0 \cdots 0)^{\top}$$
 and also $(0 \quad 0 \quad 0 \quad 1 \cdots 1)^{\top}$

• Fact1:
$$\lambda_2 = \min_{x:||x||=1} x^\top M x$$
 Second smallest eigenvalue

Constraint basically ensures this is perpendicular to the eigenvector corresponding to the smallest eigenvalue

• Consider $x^{\top}Lx$

• Consider
$$x^{\top}Lx = \frac{1}{2}\sum_{i,j}w_i(x_i - x_j)^2$$

• Fact1:
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 Second smallest eigenvalue

• Consider
$$x^{\top}Lx = \frac{1}{2}\sum_{i,j}w_i(x_i - x_j)^2$$

• so,
$$\lambda_2 = \min_{x: \|x\|=1} \sum_{i,j} w_{ij} (x_i - x_j)^2$$

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• Call the minimizer x^*

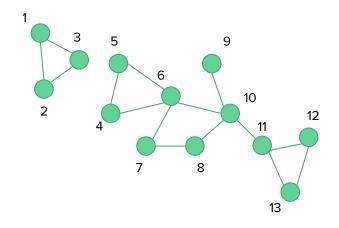
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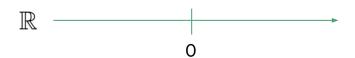
- Call the minimizer x^*
- Another Fact: The eigenvectors with distinct eigenvalues of a real symmetric matrix are orthogonal. $\sum_{i=1}^{n} x_i^* = 0$

$$\lambda_2 = \min_{x:||x||=1} \sum_{i,j} w_{ij} (x_i - x_j)^2$$

- Call the minimizer $\, x^* \,$
- Another Fact: The eigenvectors with distinct eigenvalues of a real $\sum x_i^* = 0$ symmetric matrix are orthogonal. i=1

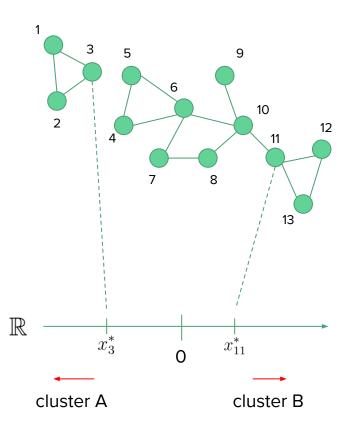
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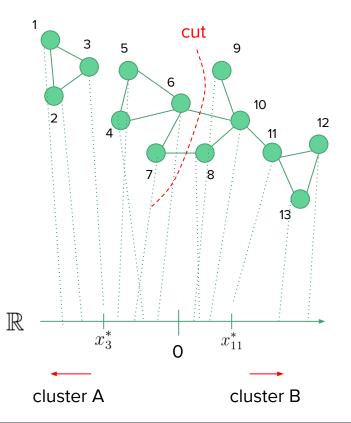
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- Look at where the values of $\,x^*$ fall on the real line.



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- Call the minimizer $\,x^*$
- Another Fact: The eigenvectors with distinct eigenvalues of a real symmetric matrix are orthogonal. $\sum_{i=1}^{n} x_i^* = 0$
- Look at where the values of $\,x^*$ fall on the real line.
- Cut at the point that separates the observations with negative values from those with positive values in x^*



Ratio Cut vs Normalized Cut

Given a similarity graph with adjacency matrix W, the simplest and most direct way to construct a partition of the graph is to solve the mincut problem. To define it, please recall the notation $W(A,B) := \sum_{i \in A, j \in B} w_{ij}$ and \overline{A} for the complement of A. For a given number k of subsets, the mincut approach simply consists in choosing a partition A_1, \ldots, A_k which minimizes

$$\operatorname{cut}(A_1,\ldots,A_k) := \frac{1}{2} \sum_{i=1}^k W(A_i,\overline{A}_i).$$

RatioCut and **NormalizedCut** objectives differ in the factor we use to measure the size of a set of vertices

RatioCut
$$(A_1, \dots, A_k) := \frac{1}{2} \sum_{i=1}^k \frac{W(A_i, \overline{A}_i)}{|A_i|} = \sum_{i=1}^k \frac{\text{cut}(A_i, \overline{A}_i)}{|A_i|}$$

$$\operatorname{Ncut}(A_1,\ldots,A_k) := \frac{1}{2} \sum_{i=1}^k \frac{W(A_i,\overline{A}_i)}{\operatorname{vol}(A_i)} = \sum_{i=1}^k \frac{\operatorname{cut}(A_i,\overline{A}_i)}{\operatorname{vol}(A_i)}.$$

Normalization

- In the simple example above, we used the unnormalized graph Laplacian, which solves an approximation of the RatioCut objective.
- We could instead use the normalized graph Laplacian:
 - \circ Remember D is the diagonal degree matrix: $D:D_{ii}=\sum_{j}W_{ij}$

$$L_{sym} = I - D^{-1/2}AD^{-1/2}$$

- Leads to an approximate solution of the NormalizedCut objective
- Theoretically analyzed (Sarkar and Bickel, 2015)

Representing your data as a graph

- ${\mathcal E}$ **neighborhood graph**: connect all points whose pairwise distances are smaller than ${\mathcal E}$
- k-nearest neighbors graph: connect v_i and v_j if they v_j is one of v_i 's nearest neighbors
 - Variant: only connect if they are mutually nearest neighbors
- Fully connected with similarity function: compute the pairwise similarities or distances between observations
 - \circ Example: Gaussian similarity $\exp\{-\|x_i-x_j\|^2/2\sigma^2\}$

Spectral clustering algorithm

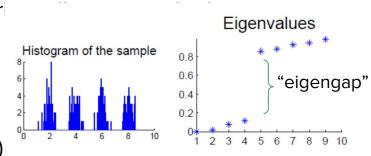
For a given choice of number of clusters K:

- 1. Construct a similarity graph and its weighted adjacency matrix ${\mathcal W}$
- 2. Compute the normalized Laplacian L_{sym}
- 3. Compute the first K eigenvectors of L_{sym} and collect as the columns of a matrix U
- 4. Normalized the rows of U to have norm 1
- 5. Cluster the rows of U using K-means or your preferred "traditional" clustering algorithm

In R: kernlab::specc()

Choice of K

- Open area of research
- Method-specific tools:
 - K-means, hierarchical clustering, spectral clustering
 - NMF: cross-validation / missing data imputation
 - Spectral clustering: Eigengap heuristic
- More general idea/tool: stability
 - Data perturbations (e.g. bootstrap, subsampling)
 - Algorithmic perturbations (e.g., random initialization)
- Still, it's a tough problem...



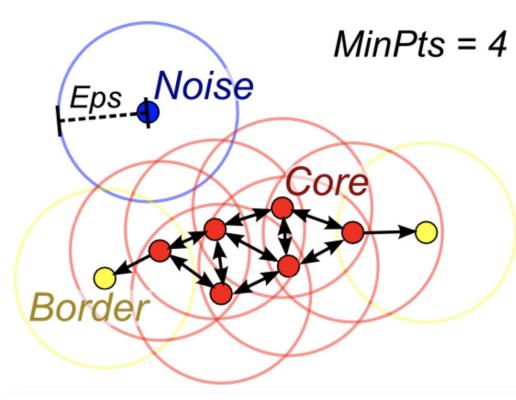
But what if we didn't have to choose K!?

DBSCAN (Ester, Martin, et al. 1996)

- Density-based clustering
- Idea: group together points that are closely packed together (points with many nearby neighbors) while marking points that lie in low-density regions as outliers
- Choose (two?) parameters:
 - \circ ε : how close points should be to each other to be in the same cluster (so we need a distance metric)
 - o minPts = minimum number of points require to form a dense region

Source: https://medium.com/@elutins/dbscan-what-is-it-when-to-use-it-how-to-use-it-8bd506293818

DBSCAN

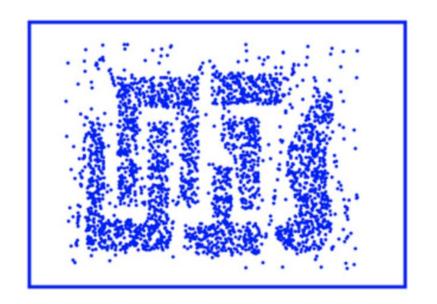


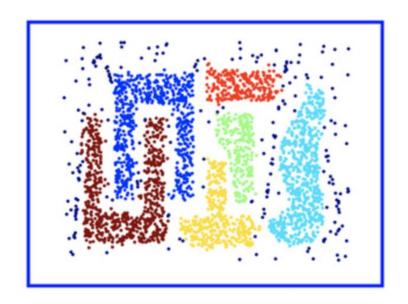
Red: Core Points

Yellow: Border points. Still part of the cluster because it's within epsilon of a core point, but not does not meet the min_points criteria

Blue: Noise point. Not assigned to a cluster

DBSCAN





In R: dbscan()

Source: https://medium.com/@elutins/dbscan-what-is-it-when-to-use-it-how-to-use-it-8bd506293818

DBSCAN

Advantages:

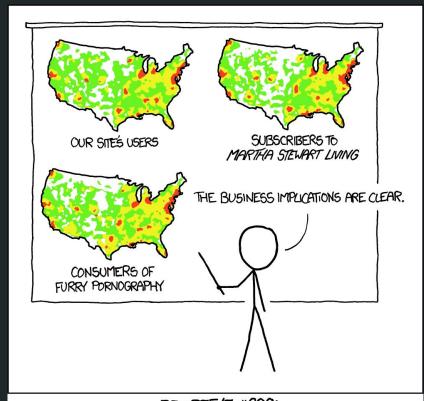
- Don't have to choose K (but depends on choice of ε and minPts)
- Great for spatial data
- Great at separating clusters of similar densities that are well separated
- Robust to outliers
- Flexible to arbitrarily-shaped clusters

Disadvantages

- If the data and scale are not well understood, choosing a meaningful distance threshold arepsilon and minPts can be difficult
- Struggles when clusters are of varying densities since (ε , minPts) cannot be chosen appropriately for all clusters
- Curse of dimensionality when distance metric is Euclidean distance
- Algorithm depends on ordering of points; border points that are reachable from more than one cluster can be part of either cluster, depending on the order the data are processed

Lab 2 caveat

Is your map more than a map of population density?



PET PEEVE #208: GEOGRAPHIC PROFILE MAPS WHICH ARE BASICALLY JUST POPULATION MAPS

Lab 2 reminders

- Use figure captions for cross-referencing: fig.cap="My awesome caption"
- Use png and adjust DPI, e.g.: dev="png", dpi = 300
- Folder structure for submission:

```
stat-215-a/
    lab2/
    lab2.Rmd & .pdf
    lab2_blind.Rmd & .pdf
    R/
    Optional, if you use extra data, etc
```

Be careful when using section headers '#'

Presidential speech dataset

See quick example in clustering_demo.Rin the week6 folder

