STAT 215A Fall 2020 Week 6

James Duncan, OH: M, Th 2-4pm

Announcements

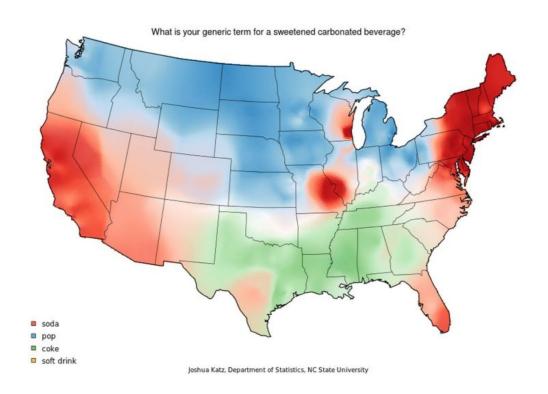
- Lab 2 due in one week **10/08 at 11:59pm**
- Please respond to the <u>discussion section feedback survey!</u>
- Hoping to have grading done this weekend



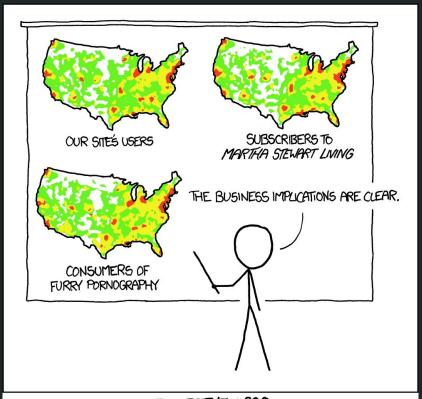
Outline for today

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

Questions on HW2 or Lab 2?



https://www.businessinsider.com/22-maps-that-show-the-deepest-linguistic-conflicts-in-america-2013-6#ok-th is-one-is-crazy-everyone-pronounces-pecan-pie-differently-10 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, for .bib files or other things necessary to reproduce your lab (but don't over do it!).
```

Be careful when using section headers '#'

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)

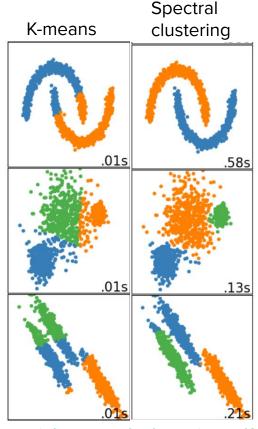
Spectral clustering: a "good" method

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

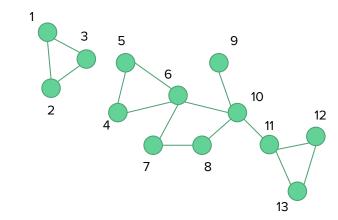


More details: http://people.csail.mit.edu/dsontag/courses/ml14/notes/Luxburg07 tutorial spectral clustering.pdf

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

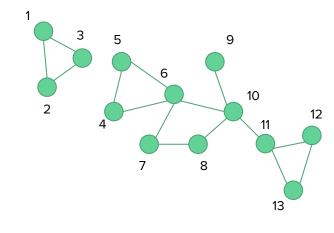
Setup

- Graph: G = (E,V)
- Weighted adjacency matrix: $W = (w_{ij})_{i,j=1,...,n}$
 - o 0 on the diagonal
 - $v_{ij} = 0$ 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 $Lx=\lambda x$

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

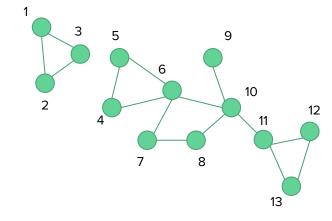


Let's try to find eigenvectors

$$Lx = \lambda x$$

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

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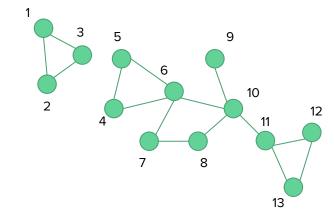


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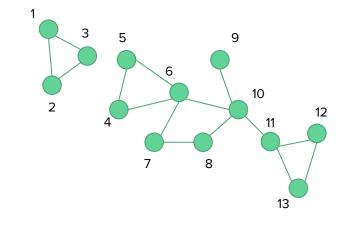
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Let's try to find eigenvectors $Lx=\lambda x$

1, the vector with all entries equal to 1

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



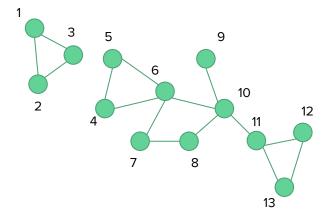
 $(1 \quad 1 \quad 1 \quad 0 \cdots 0)^{\top}$ and also $(0 \quad 0 \quad 0 \quad 1 \cdots 1)^{\top}$

Let's try to find eigenvectors

$$Lx = \lambda x$$

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

• Consider $x^{\top}Lx$

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

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

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• Consider
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• 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^*

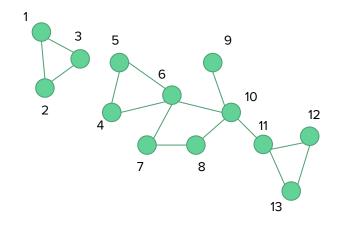
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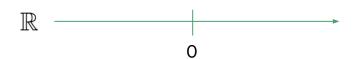
- Call the minimizer x^*
- Another Fact: The eigenvectors with distinct eigenvalues of a real symmetric matrix are orthogonal. $\sum_{i=1}^{n} x_i^* = 0$

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

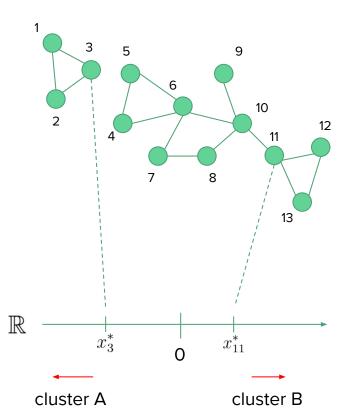
$$\sum_{i=1}^{n} x_i^* = 0$$





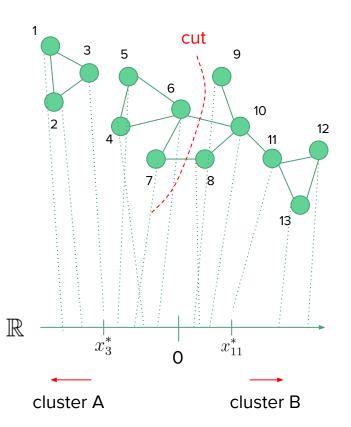
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- Look at where the values of $\,x^*$ fall on the real line.



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- 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^*



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:

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

- Leads to an approximate solution of the **Ncut** objective
- This is advised in practice (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

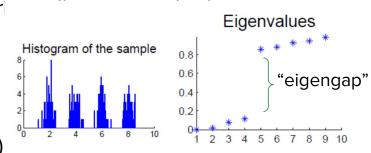
For a given choice of number of clusters K:

- 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 \mathcal{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...



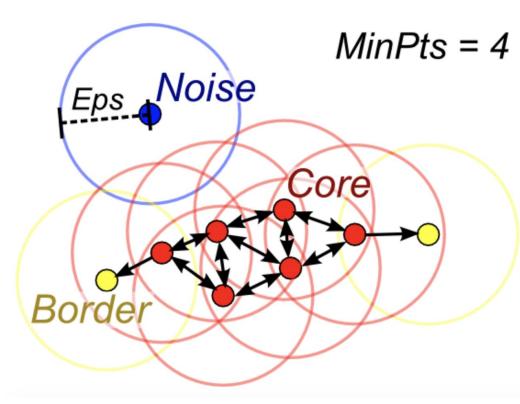
But what if we didn't have to choose K!?

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:
 - 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

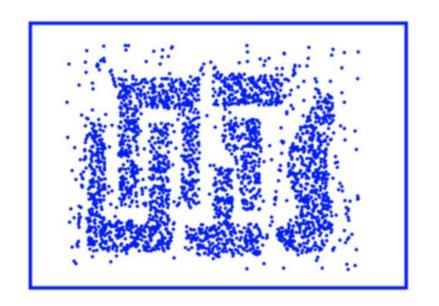


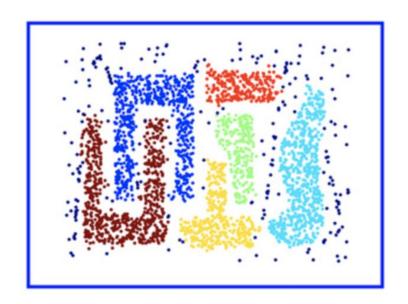
Red: Core Points

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()

Presidential speech dataset

See quick example in clustering_demo.Rin the week6 folder



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

In-class labs

- **Week 1**: tidyverse basics
- **Week 2**: ggplot + Rmd tips and tricks
- **Week 3**: more ggplot + additional plotting tools (pair plots, heatmaps, etc.)
- Week 4: PCA
- Week 5: K-means, hierarchical clustering NMF