

STAT 215A Fall 2020

Week 6

Theo Saarinen

Announcements

- Lab 2 released, due in two weeks **10/09 at 11:59pm**
- Will send out peer reviews today, these are due **10/09 at 11:59pm**
 - Each student will get the blinded version of 2 labs, then will need to fill out Google form with feedback: <https://forms.gle/2iVwgvXV7tkrT4Nb8>

Announcements

Reminders when submitting the homework + lab

- Submit the HW 2 by pushing *homework2.pdf* **inside** your lab2 folder.
- Please **do not** push the raw data with your submission, this slows down the grading process.
- Please submit your lab within a folder called lab2 within the github repo, if you are uploading through the desktop and don't know how to create a folder, see: <https://stackoverflow.com/questions/12258399/how-do-i-create-a-folder-in-a-github-repository>

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 \mathbf{X} , NMF solves

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

- You can modify this to work for \mathbf{X} with missing data (in R:

`NNLM::nnmf()`¹):

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

1. NNLM was archived on CRAN, so to install you need to use `devtools::install_github("linxihui/NNLM")`

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 \mathbf{X}
- For each potential choice of K:
 1. Apply NMF to the data with missing values: \mathbf{W}_M and \mathbf{H}_M
 2. Impute the missing values of \mathbf{X} using corresponding entries of $\mathbf{W}_M \mathbf{H}_M$
 3. 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)

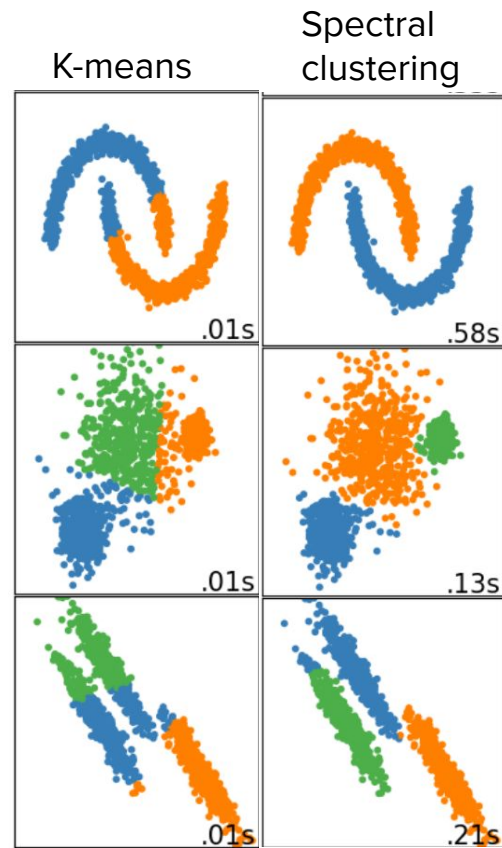
Spectral clustering: a “good” method

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

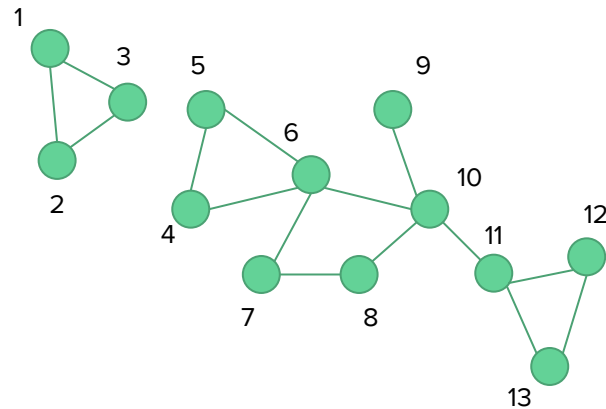


More details: http://people.csail.mit.edu/dsontag/courses/ml14/notes/Luxburg07_tutorial_spectral_clustering.pdf

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

Setup

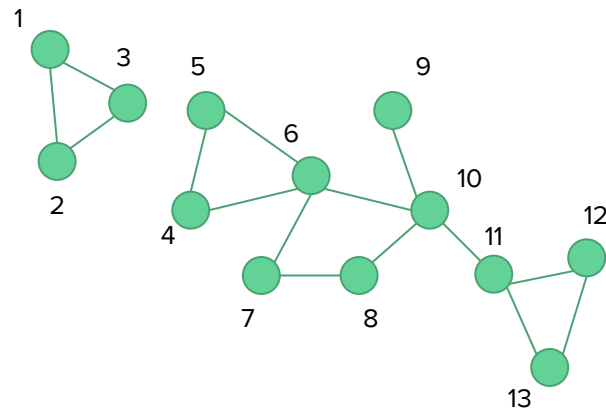
- Graph: $G = (E, V)$
- Weighted adjacency matrix: $W = (w_{ij})_{i,j=1,\dots,n}$
 - 0 on the diagonal
 - $w_{ij} = 0$ if there is no edge between v_i and v_j
- Diagonal degree matrix $D : D_{ii} = \sum_j W_{ij}$
- (Unnormalized) graph Laplacian: $L = D - W$



What can the graph Laplacian tell us?

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

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

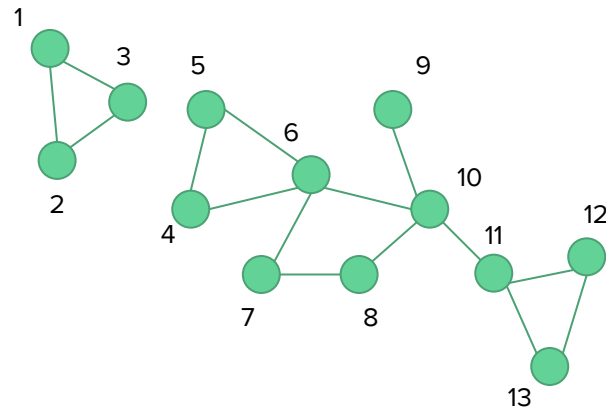


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$\mathbf{1}$, the vector with all entries equal to 1

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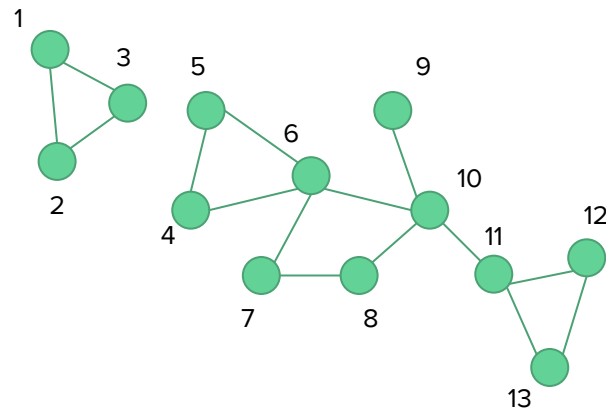


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$$(1 \quad 1 \quad 1 \quad 0 \dots 0)^\top$$



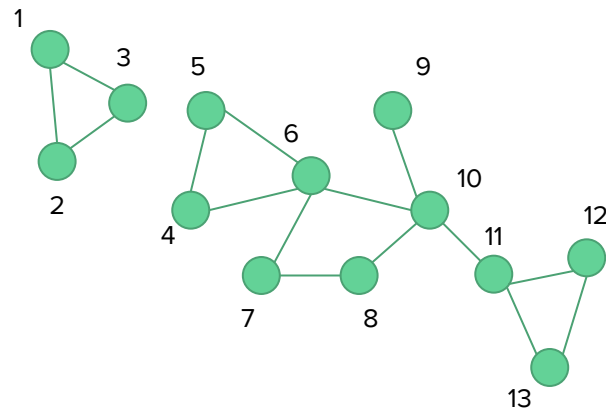
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$$(1 \ 1 \ 1 \ 0 \cdots 0)^\top \text{ and also } (0 \ 0 \ 0 \ 1 \cdots 1)^\top$$



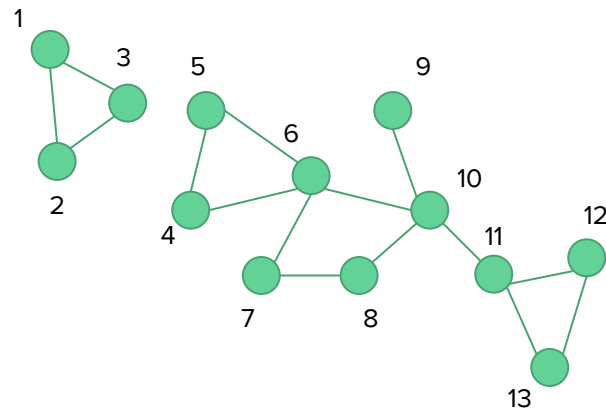
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$\lambda_1 = 0$ in these cases, so the multiplicity of the eigenvalue 0 tells us about the number of **connected components** in the graph.

What about the other eigenvectors of L ?

- Fact¹: $\lambda_2 = \min_{x: \|x\|=1} x^\top M x$

Second smallest eigenvalue

M symmetric

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

¹ See <https://math.stackexchange.com/questions/1403920/second-smallest-eigenvalue-as-min-x-frac{tx}{x}x> for a proof

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Second smallest eigenvalue

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- Consider $x^\top L x$

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What about the other eigenvectors of L ?

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

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

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Second smallest eigenvalue

M symmetric

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

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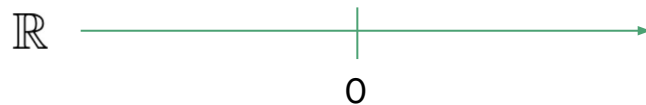
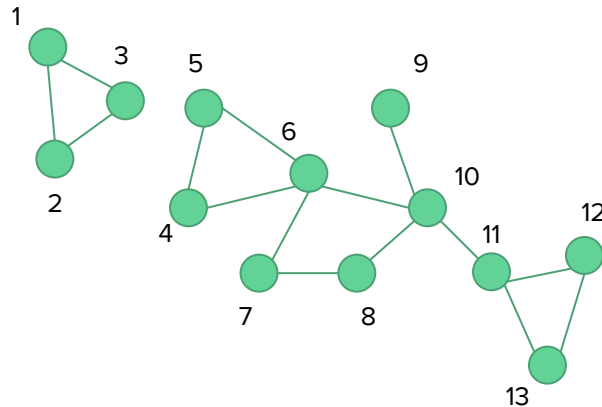
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- Another Fact: The eigenvectors with distinct eigenvalues of a real symmetric matrix are orthogonal. $\sum_{i=1}^n x_i^* = 0$

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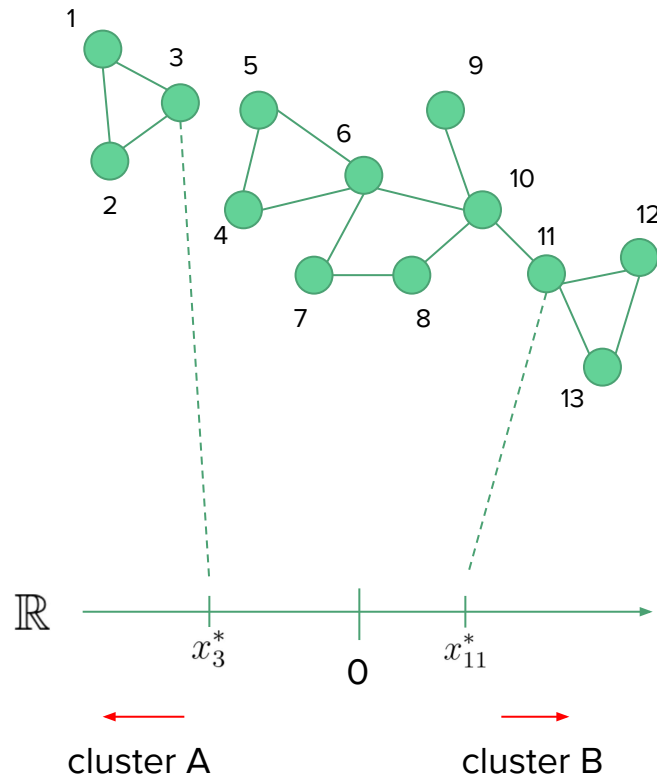
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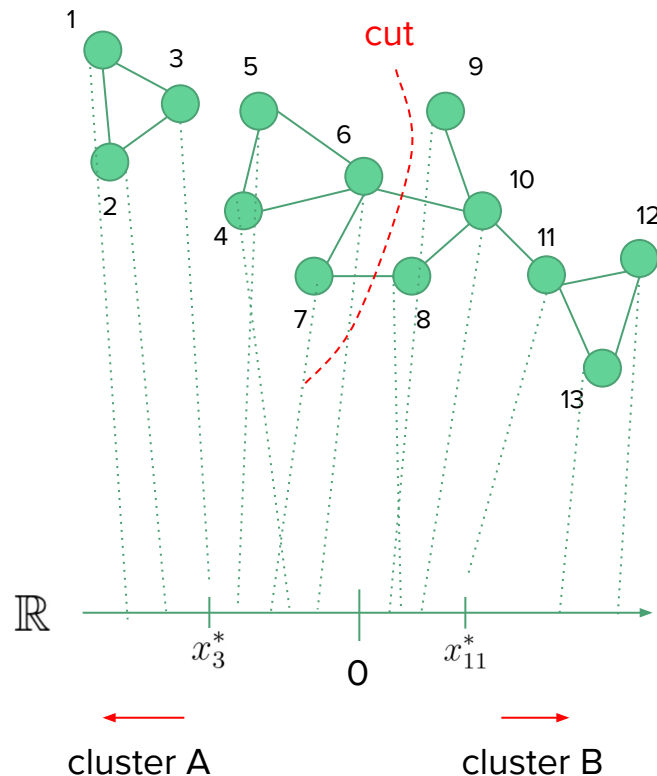
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- Look at where the values of x^* fall on the real line.



What about the other eigenvectors of L ?

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

- Call the minimizer x^*
- Another Fact: The eigenvectors with distinct eigenvalues of a real 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 \bar{A} for the complement of A . For a given number k of subsets, the mincut approach simply consists in choosing a partition A_1, \dots, A_k which minimizes

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

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

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

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

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:

- Remember D is the diagonal degree matrix: $D : D_{ii} = \sum_j W_{ij}$

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

- 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
 - Example: Gaussian similarity $\exp\{-\|x_i - x_j\|^2/2\sigma^2\}$

Spectral clustering algorithm

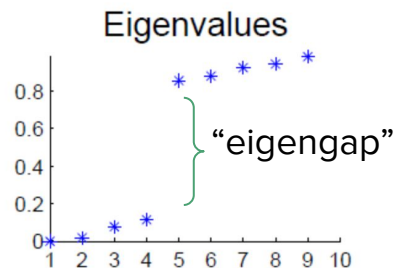
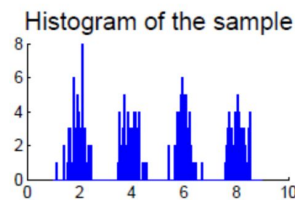
For a given choice of number of clusters K :

1. Construct a similarity graph and its weighted adjacency matrix 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!?

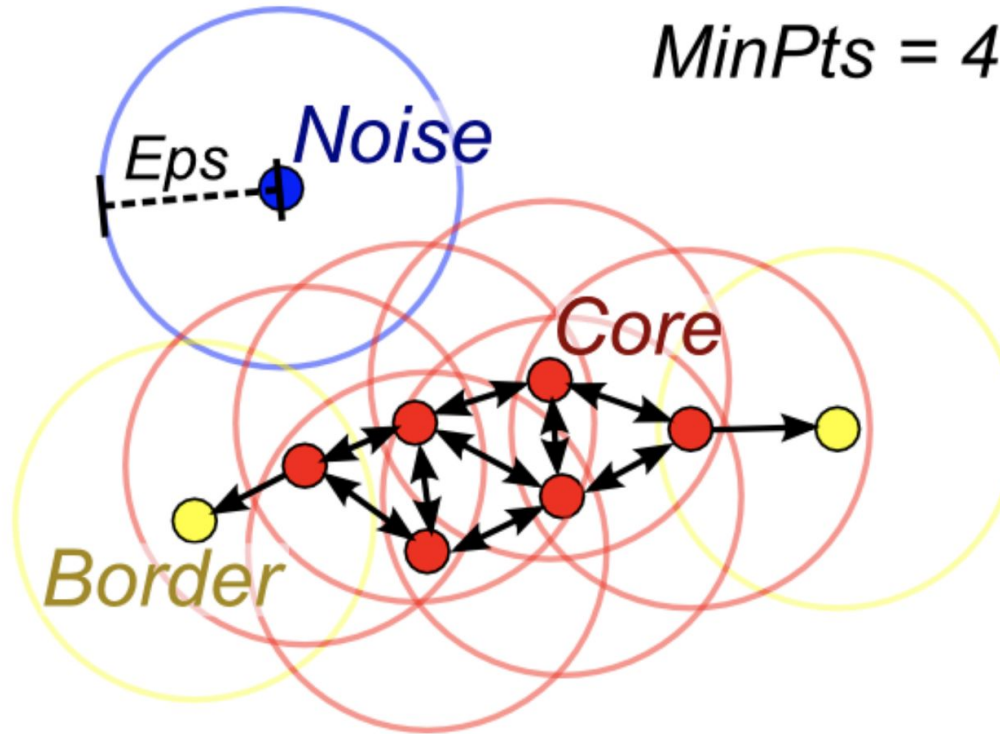
DBSCAN (Ester, Martin, et al. 1996)

- 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:
 - ϵ : how close points should be to each other to be in the same cluster (so we need a distance metric)
 - 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>

The slides on DBSCAN thanks to Tiffany Tang

DBSCAN

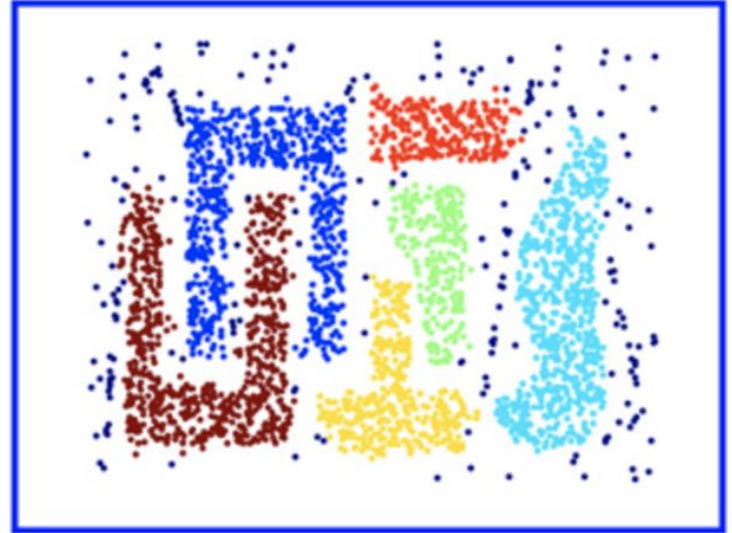


Red: Core Points

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::dbscan()`

Presidential speech dataset

See quick example in `clustering_demo.R` in the week6 folder



DBSCAN

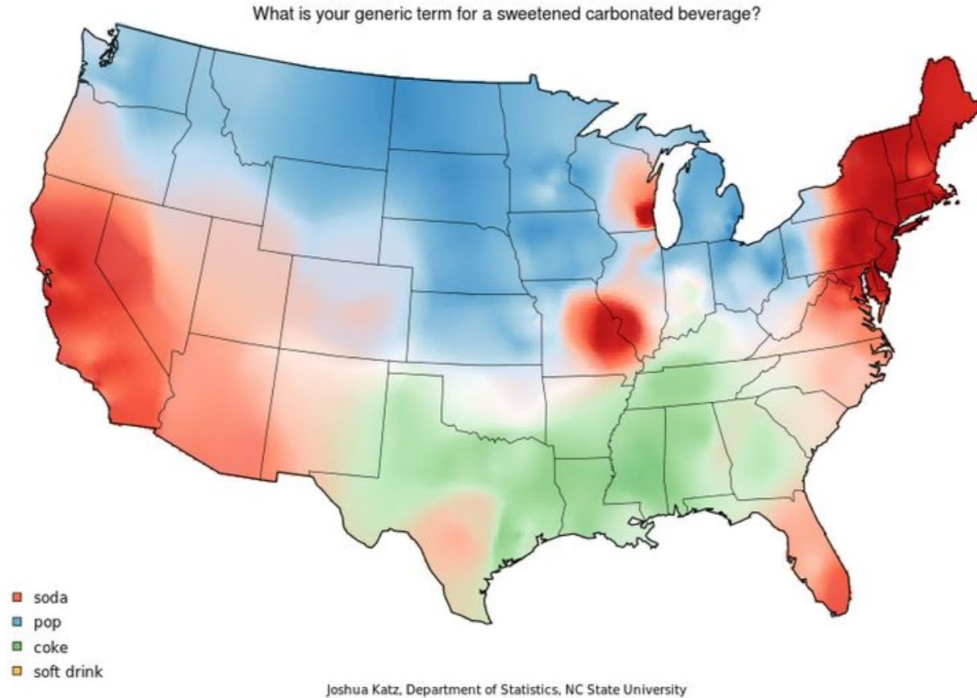
Advantages:

- 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

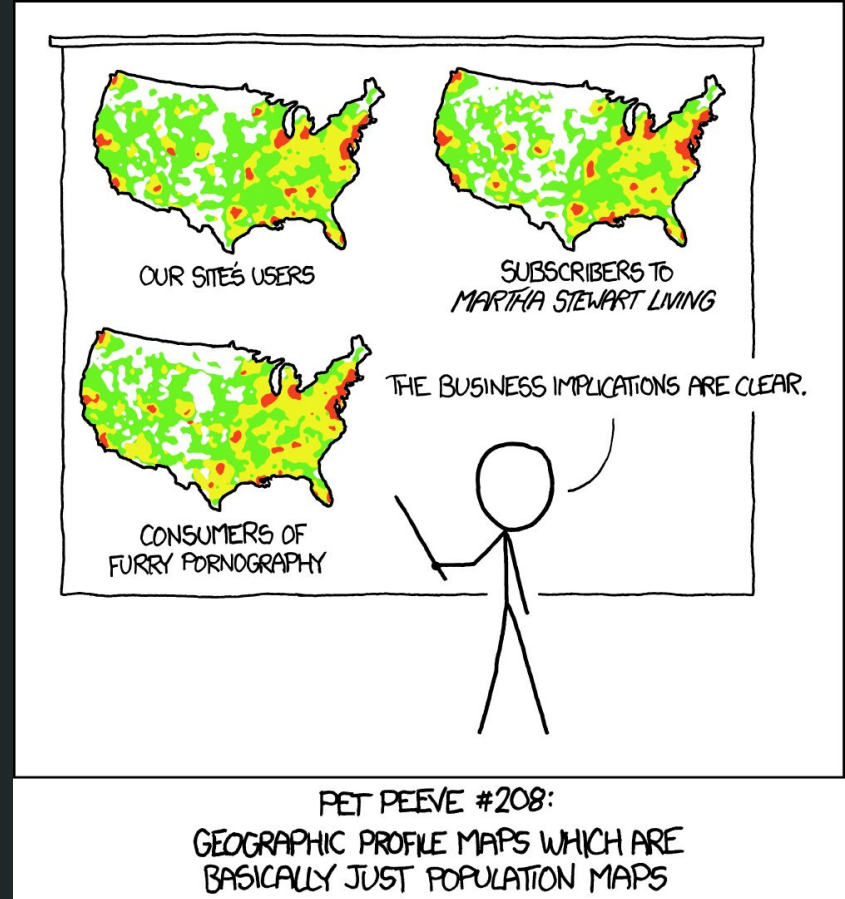
- If the data and scale are not well understood, choosing a meaningful distance threshold ϵ and minPts can be difficult
- Struggles when clusters are of varying densities since (ϵ , minPts) cannot be chosen appropriately for all clusters
- Curse of dimensionality when distance metric is Euclidean distance
- 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

Questions on HW2 or Lab 2?




<https://www.businessinsider.com/22-maps-that-show-the-deepest-linguistic-conflicts-in-america-2013-6#ok-this-one-is-crazy-everyone-pronounces-pecan-pie-differently-10>

Is your map more than a
map of population density?



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/`
 - `other/`  Optional, for .bib files or other things necessary to reproduce your lab (but don't over do it!).
- Be careful when using section headers `#`

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