

# K-means and Hierarchical Clustering

Schwartz

August 15, 2017

# Best. Music. EVAR

1. Elliott Smith
2. Sufjan Stevens
3. Iron and Wine
4. Damien Rice

1. Die Antwoord
2. Kendrick Lamar
3. Dan le Sac Vs Scroobius Pip

1. Rufus Wainwright
2. Lyle Lovett
3. Julie Doiron

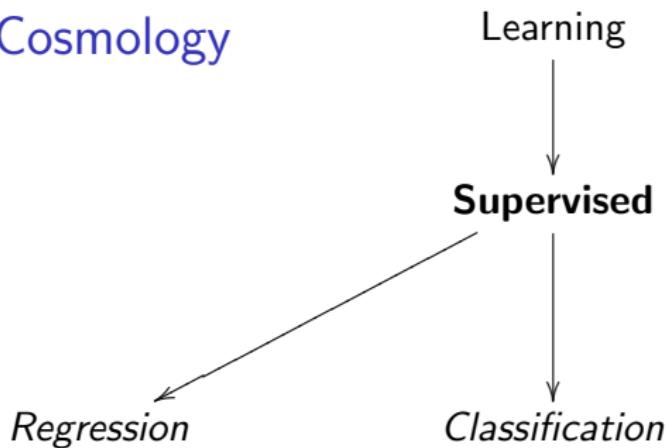
1. D'Gary
2. Kishi Bashi
3. Christine and the Queens
4. Beirut

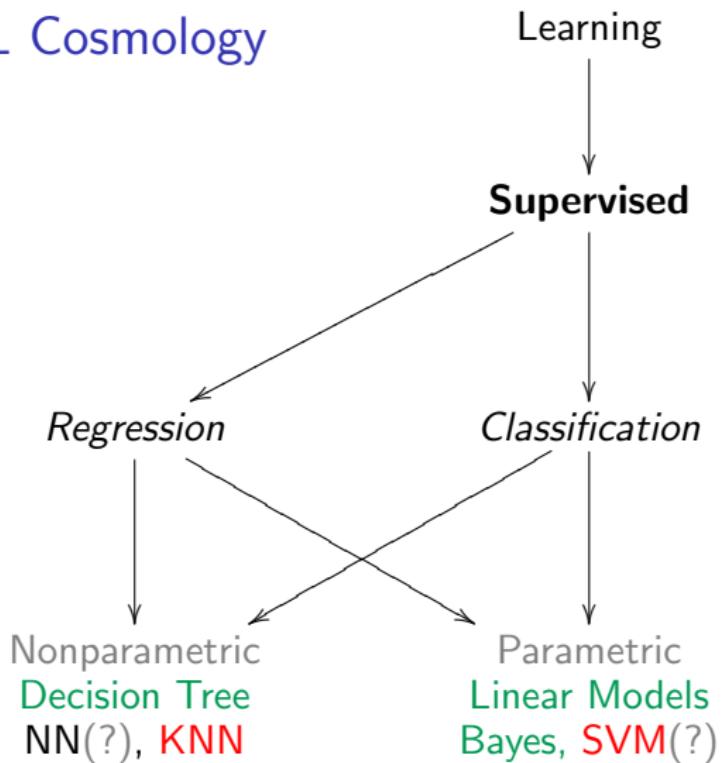
1. Rage Against the Machine
2. System of a Down
3. Smashing Pumpkins

1. Beck
2. Cake
3. Beastie Boys

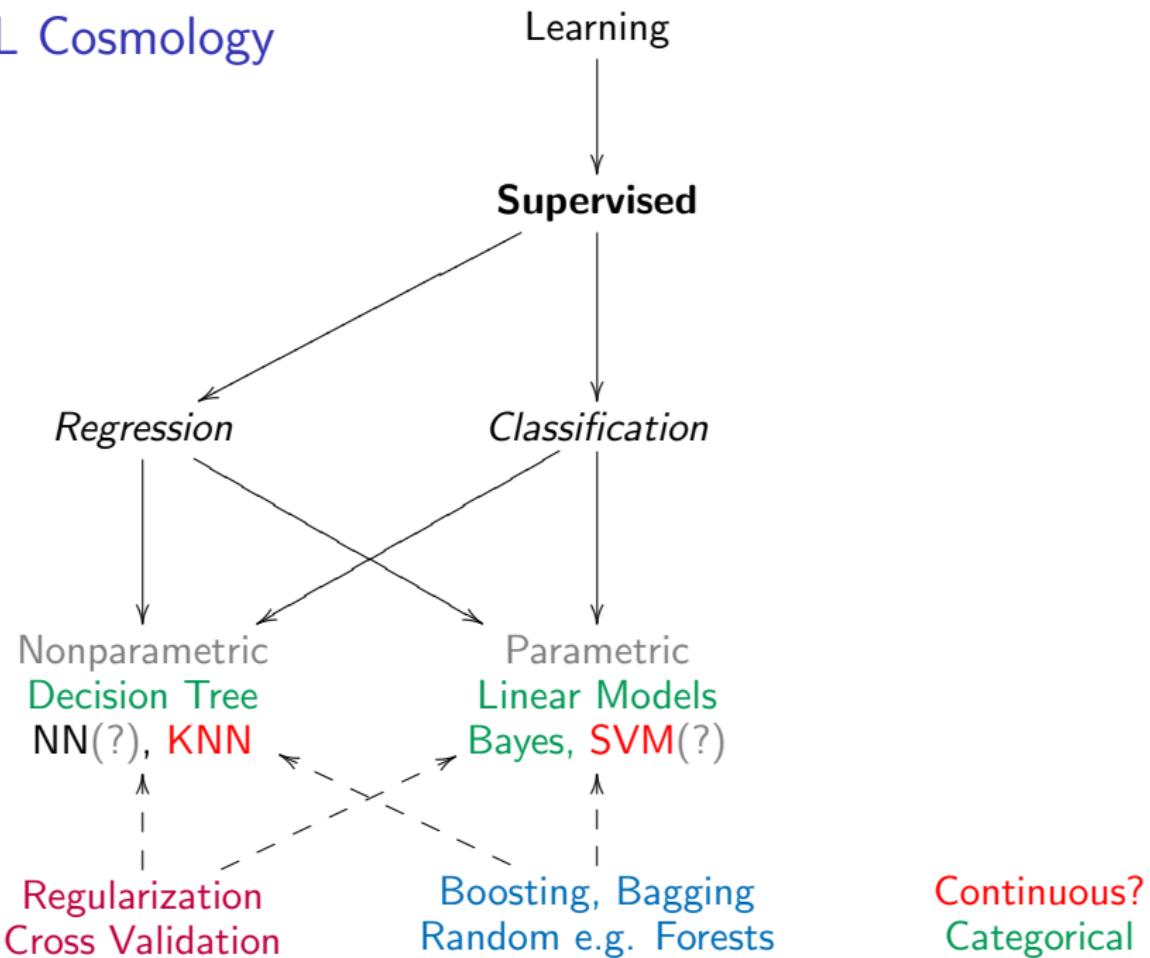
# Objectives

- ▶ Review *Supervised* versus *Unsupervised*
- ▶ *K*-means (not to be confused with *KNN*)
  - ▶ and the curse of dimensionality
  - ▶ *norms* and the curse of dimensionality
  - ▶ more about the curse of dimensionality
- ▶ Choosing *K*
  - ▶ Elbow, Silhouette, and Gap methods
- ▶ Hierarchical clustering
- ▶ DBSCAN
- ▶ Bayesian mixture models
- ▶ Expectation-Maximization (EM) algorithm

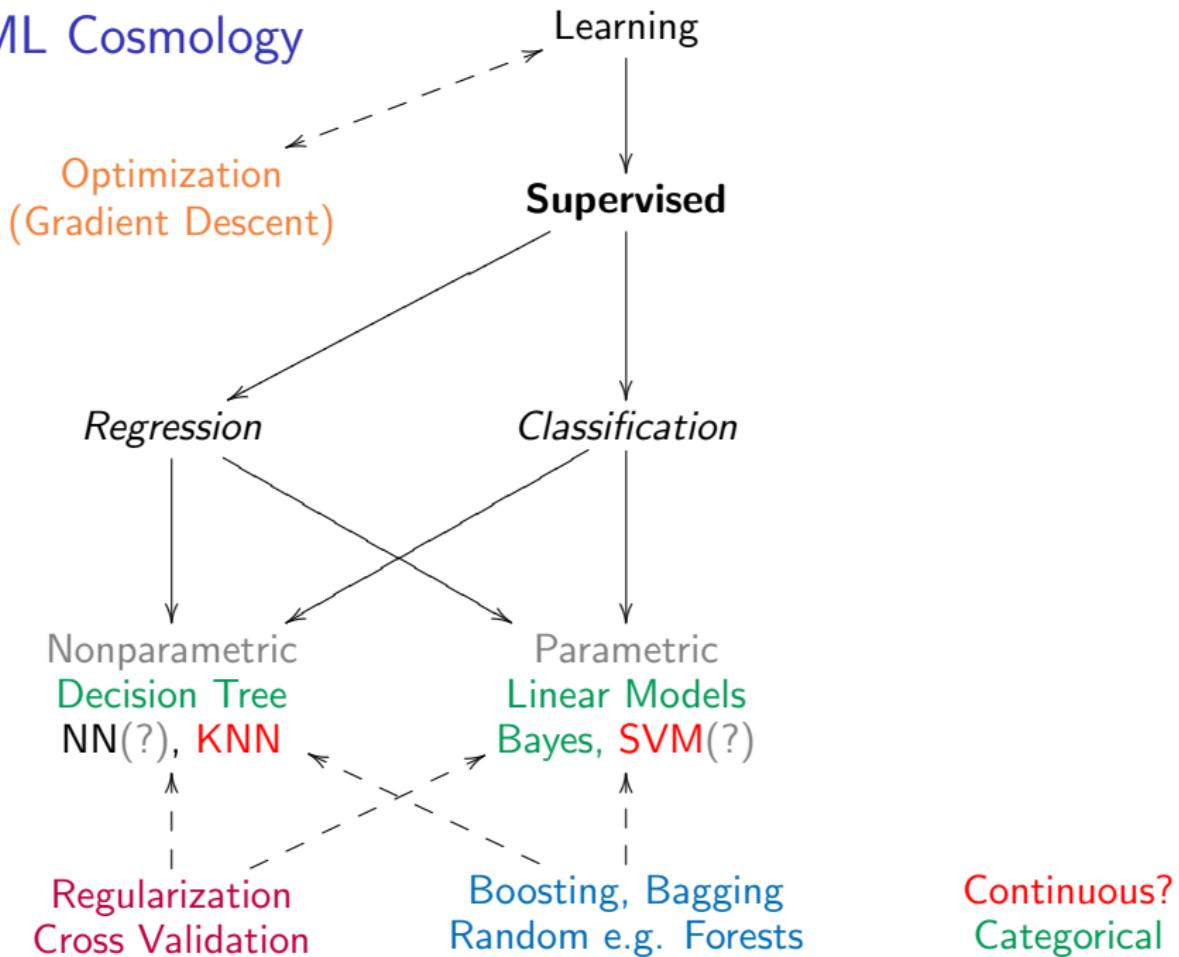




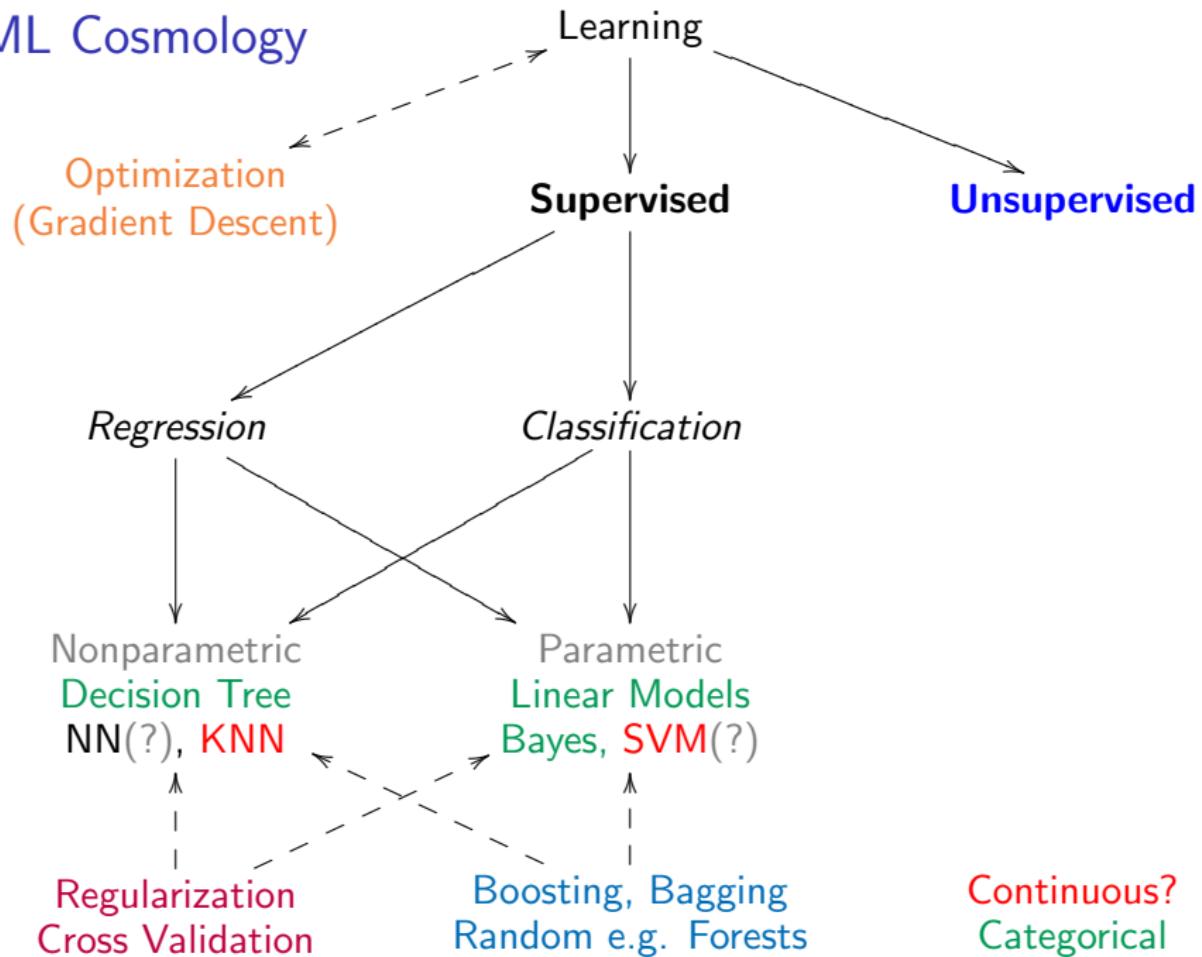
Continuous?  
Categorical



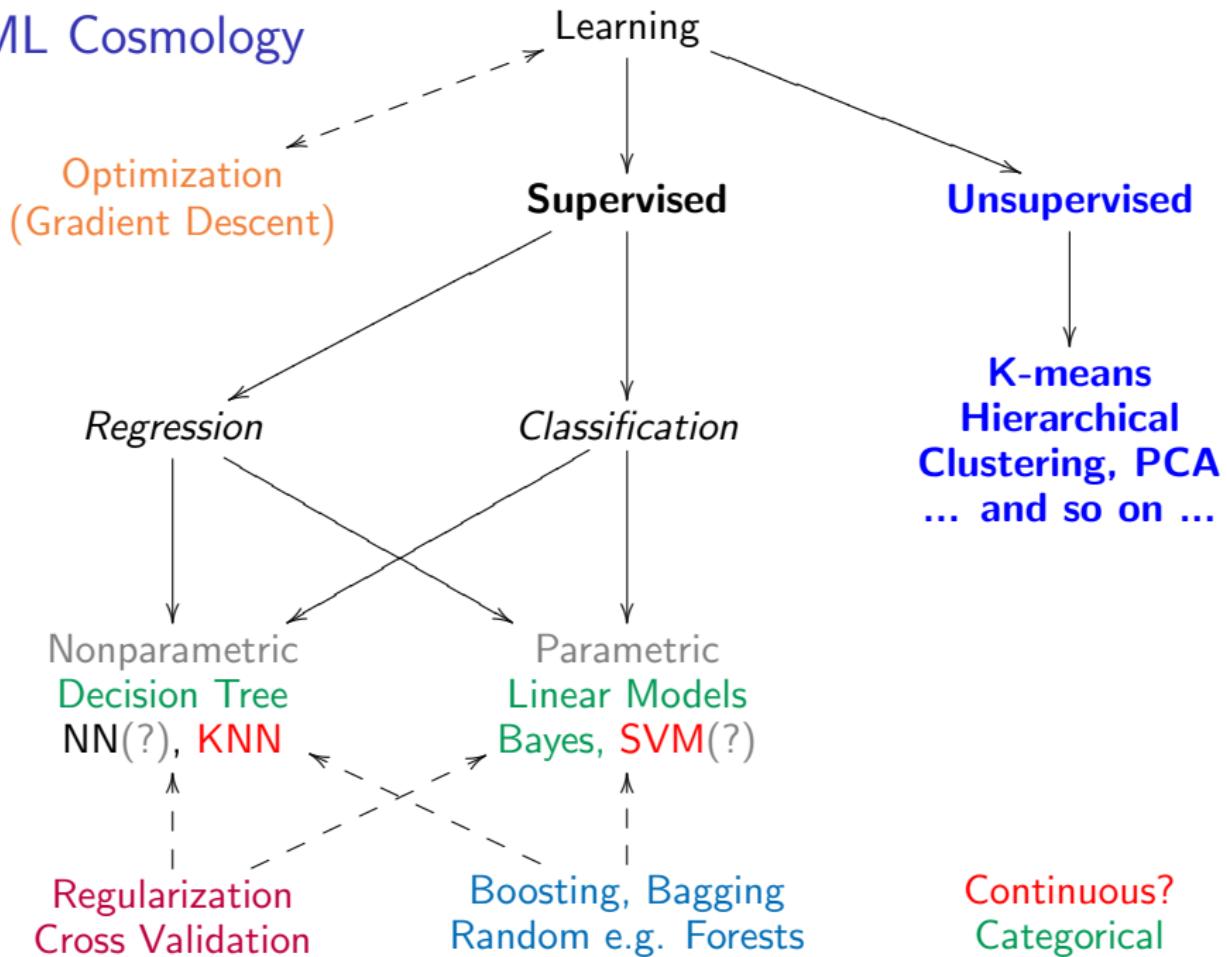
# ML Cosmology



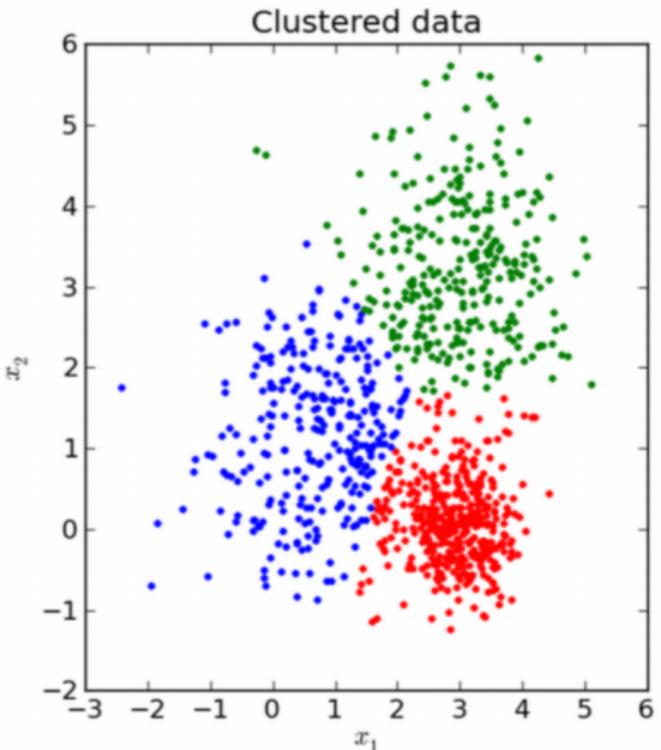
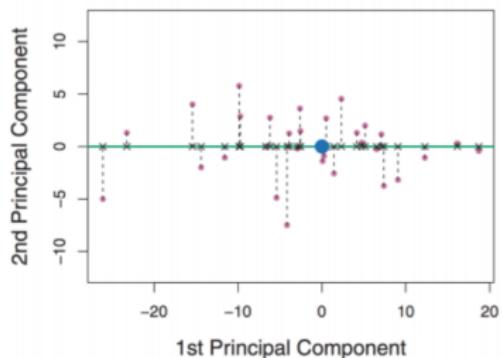
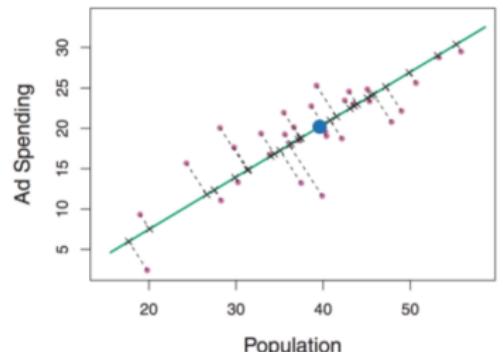
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# Unsupervised learning

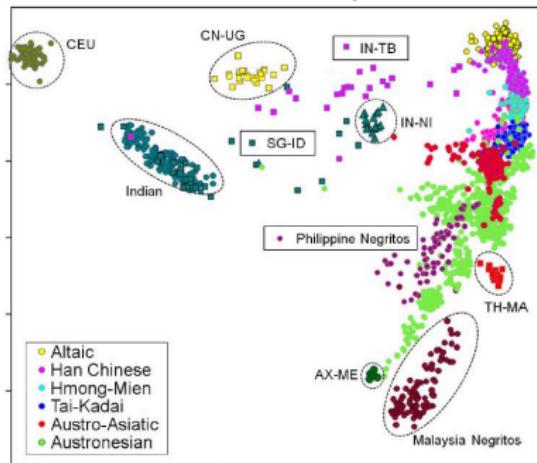


Low dimensional representations  
of data capturing data variation

Homogeneous subgroups  
capturing data substructure

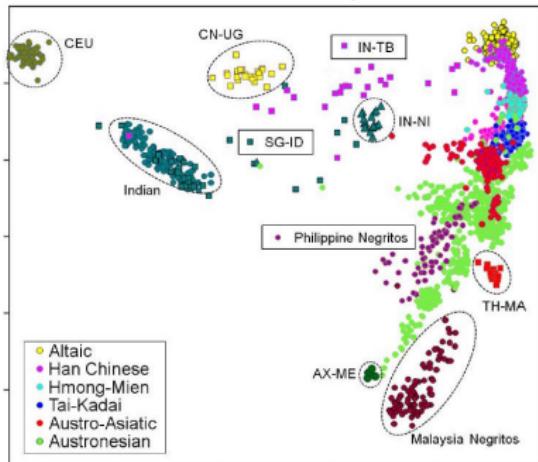
# Supervised versus Unsupervised

## Human Genetic Diversity in Asia Two-Dimensional Representation



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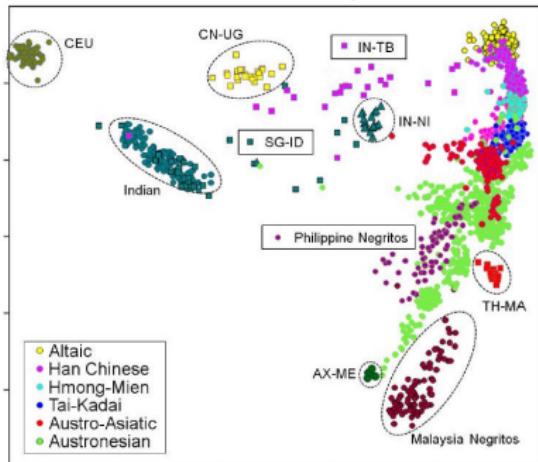
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Unsupervised learning provides

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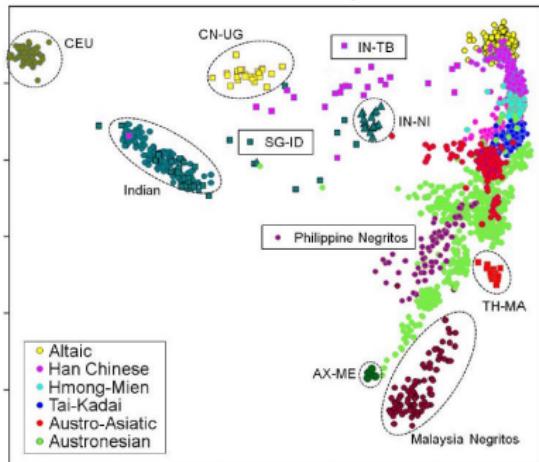


Unsupervised learning provides

- ▶ exploratory data analysis (EDA) to look at/uncover feature structure

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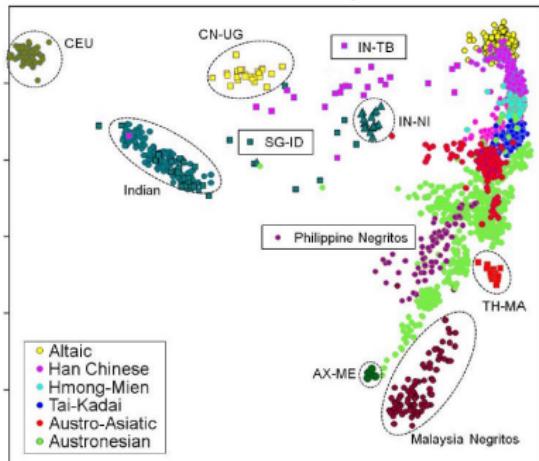


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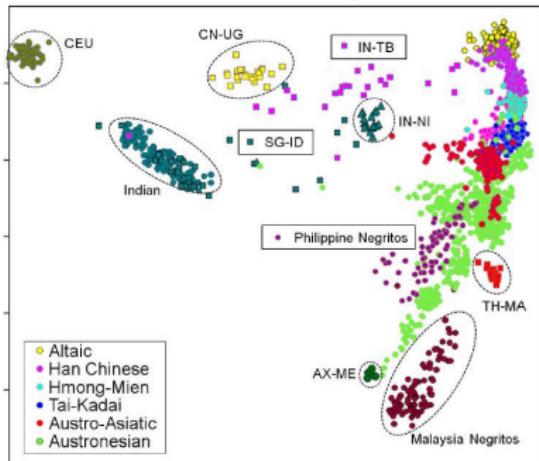


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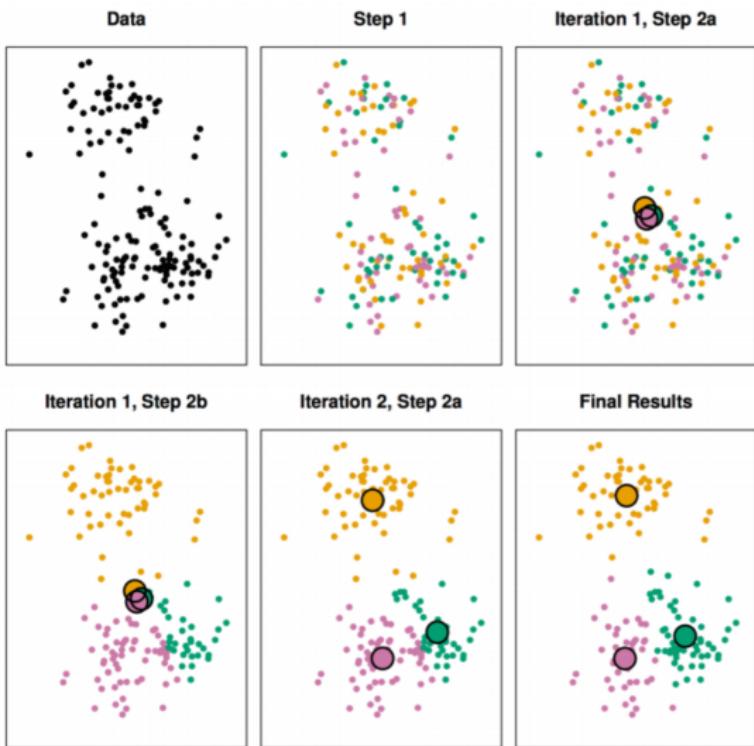
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“Labels” are sometimes used to facilitate these objectives but unlike supervised learning, unsupervised learning is not necessarily immediately concerned with predicting outcomes (labels, targets,  $Y$ , dependent/endogenous variables)

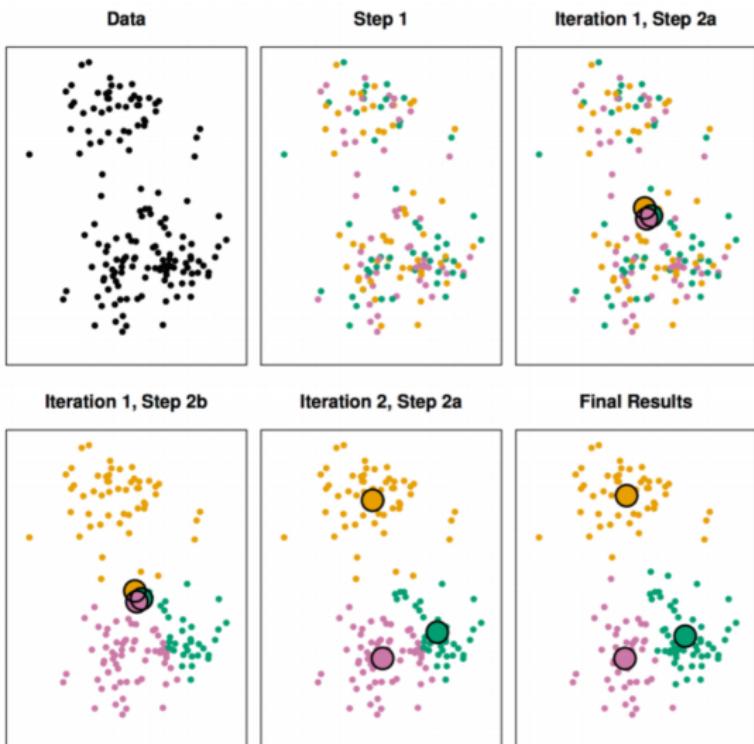
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1. Choose *number of clusters*,  $K$
2. Randomly assign data to each cluster  $k$
3. Compute the centroid for each cluster  $k$
4. Assign data to the cluster with the closest centroid
5. Return to step 3, unless the centroids have stabilized



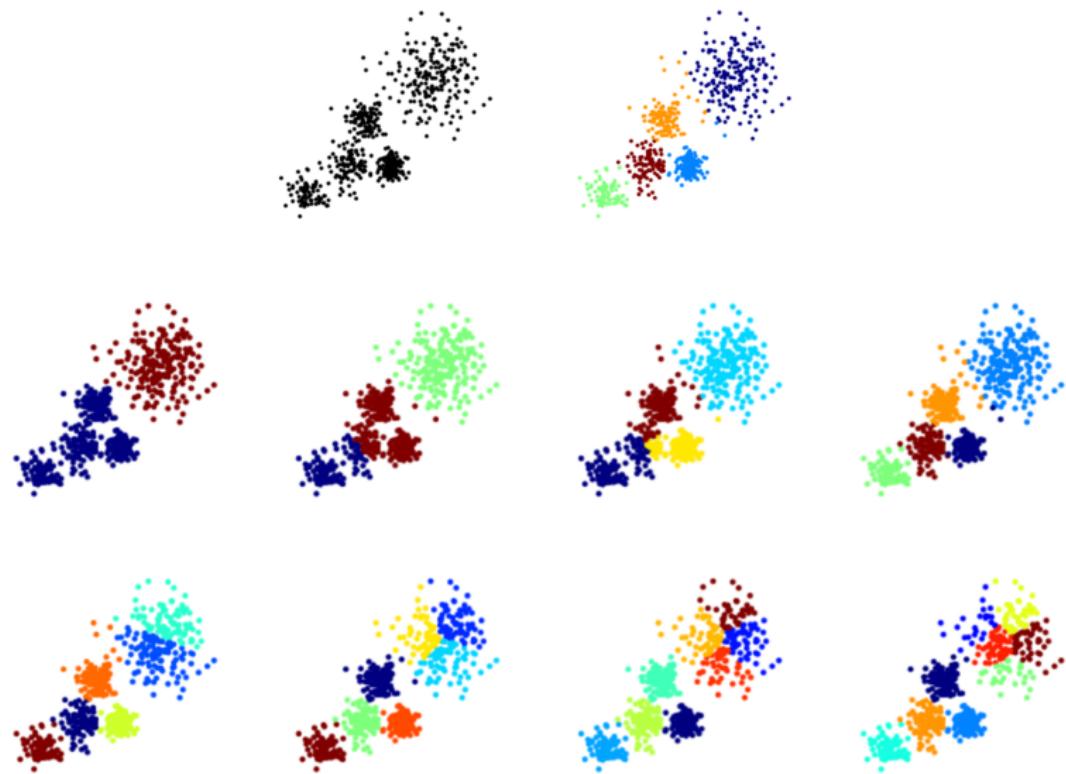
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Other init. ideas?

K?



## Elbow and Silhouette methods

For some clustering

$$C_K(i) \mapsto \{1, 2, \dots, K\}$$

clustering fit can be measured as

$$W(C_K) = \frac{1}{K} \sum_{C_K(i)=C_K(j)=k} \|x_i - x_j\|^2$$

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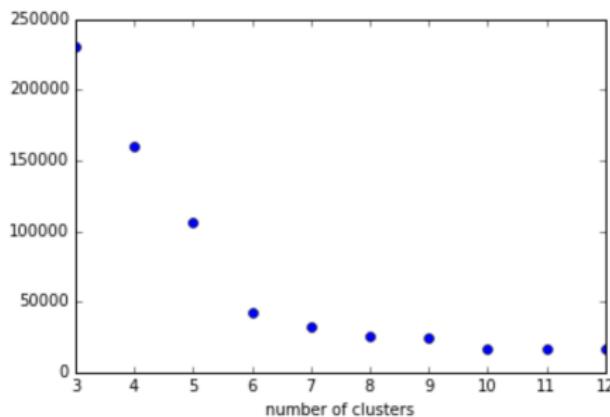
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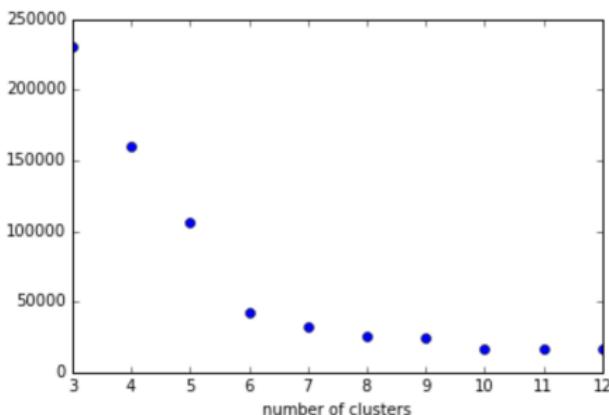
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$\bar{\Delta}_i^k$ :  $x_i$ 's dissimilarity in cluster  $k$

$\bar{\Delta}_i^{k'}$ :  $x_i$ 's dissimilarity to cluster  $k'$   
( $x_i$  in, & closest to clusters  $k, k'$ )

$$\text{Silhouette}(i) = \frac{\bar{\Delta}_i^{k'} - \bar{\Delta}_i^k}{\max(\bar{\Delta}_i^{k'}, \bar{\Delta}_i^k)}$$

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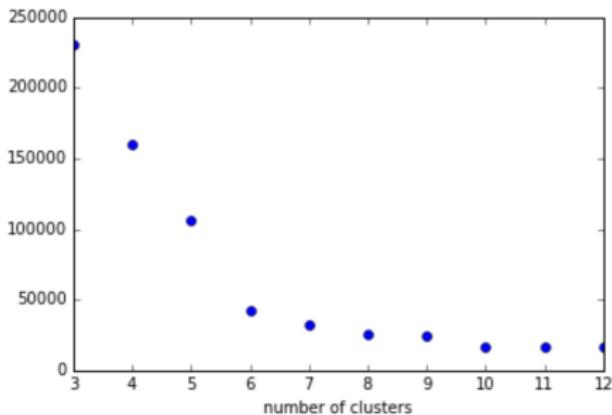
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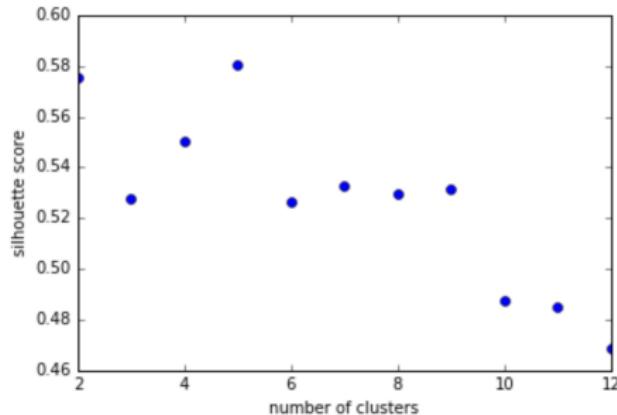
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Compare average silhouette scores



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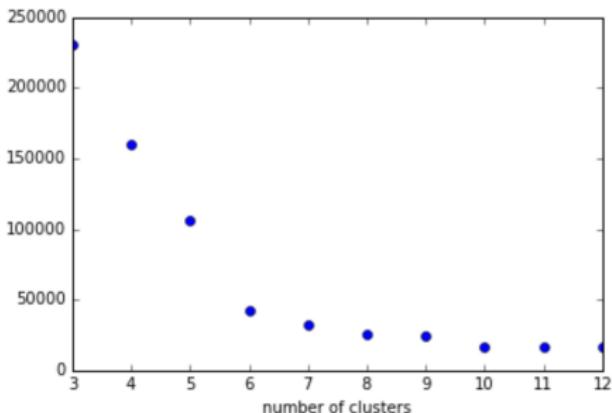
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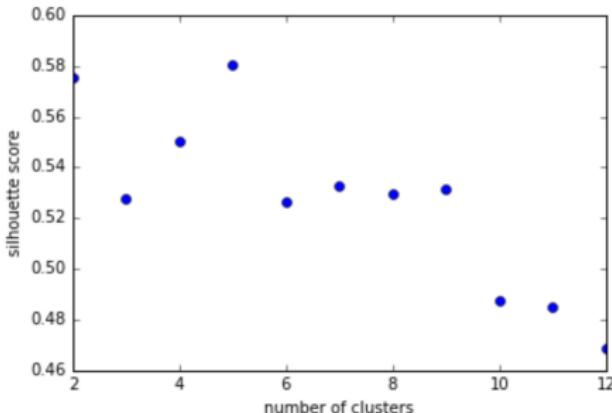
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Interpret silhouette scores?

Select based on diminishing returns



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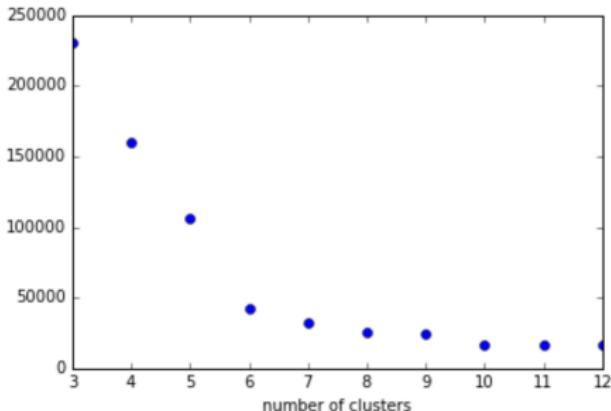
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Does the scaling of the  $x$  matter?

Select based on diminishing returns



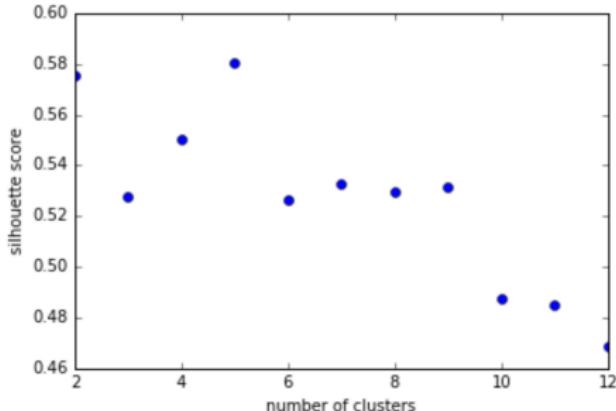
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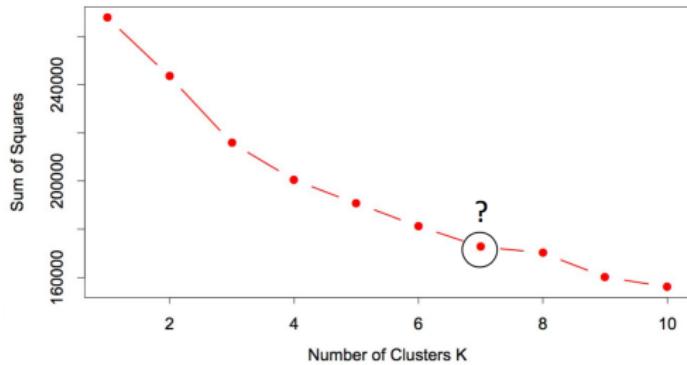
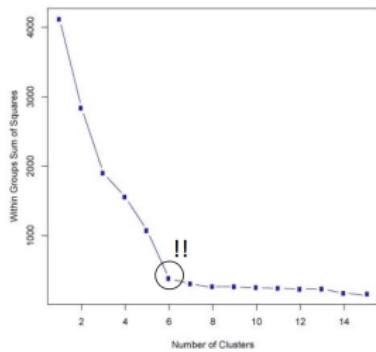
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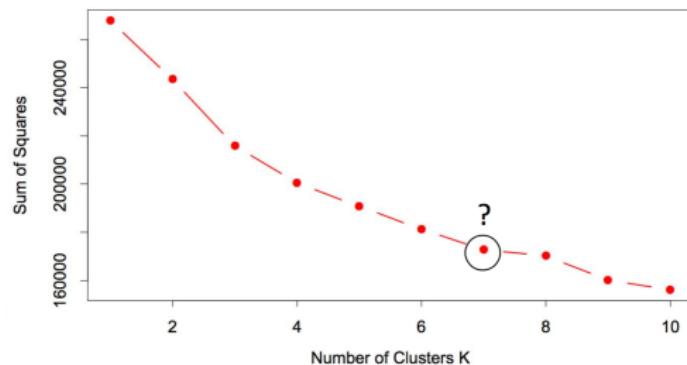
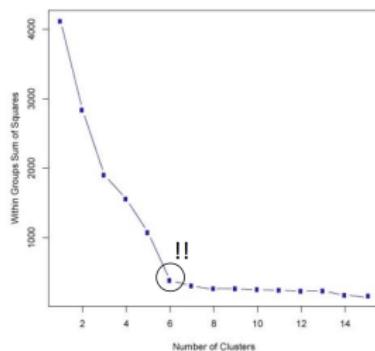
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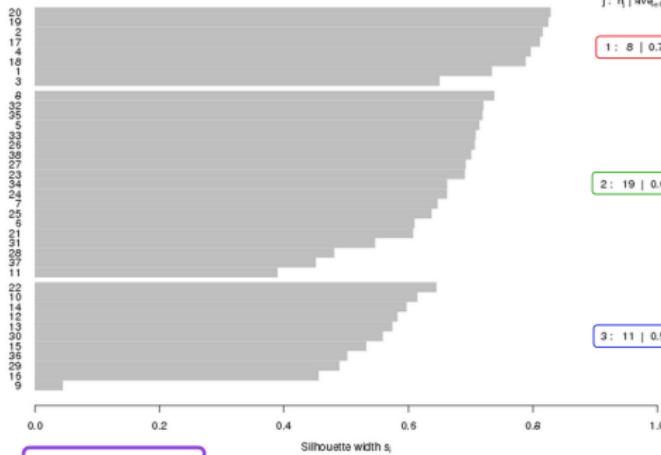
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Silhouette plot of pam(x = cars.dist, k = 3)  
n = 38



3 clusters  $C_1$   
j: 11 | avg $s_{C_1} s_j$

1: 19 | 0.64

3: 11 | 0.51

## Guidelines for Overall Avg Silhouette

Range	Interpretation
0.71 – 1.0	Strong structure found
0.51 – 0.7	Reasonable structure
0.26 – 0.5	Structure weak/artificial
< 0.25	No substantial structure

## The permutation test

- ▶ Students enrolling for a popular class get ids  $i = 1, \dots, n$ . As the class quickly fills, another section of the class is opened and students for that class are given ids  $i = n + 1, \dots, 2n$ .

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How could we test which class is doing better?

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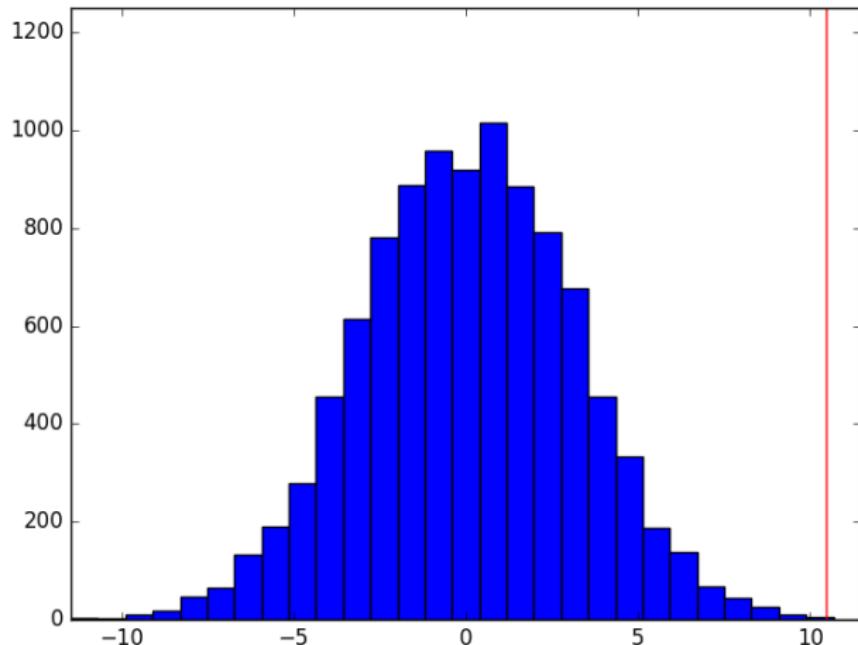
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1. Repeatedly permute the index and recalculating the test statistic each time
2. These samples approximate the test statistic distribution under the null
3. Compare the test statistic to this null distribution  
to suggest how "strange" the actual observed test statistic is if the null is true

## The *permutation test* (*This is my favorite test, btw*)

1. Permute the ids (i.e., believe the null is true: ids don't matter)
2. Recalculate the test statistic each time (under null)
3. See how strange your observed statistic is compared to nulls



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- ▶ What was needed in the permutation test was really the distribution of the test statistic under the null hypothesis
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but that was just a means to an end
- ▶ We can test against ANY null distribution we wish to propose

# The Gap statistic

412 R. Tibshirani, G. Walther and T. Hastie

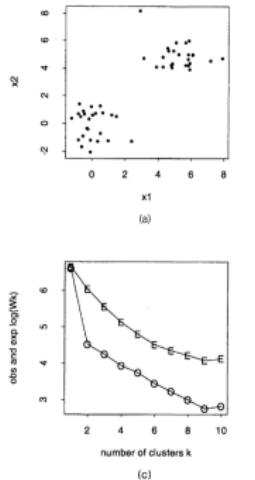


Fig. 1. Results for the two-cluster example: (a) data; (b) within sum of squares function  $W_k$ ; (c) functions  $\log(W_k)$  (O) and  $E_n(\log(W_k))$  (E); (d) gap curve

416 R. Tibshirani, G. Walther and T. Hastie

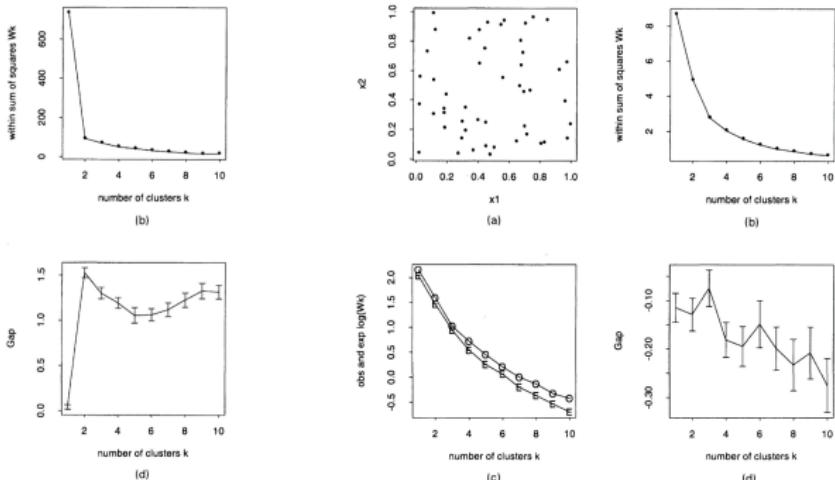


Fig. 2. Results for the uniform data example: (a) data; (b) within sum of squares function  $W_k$ ; (c) functions  $\log(W_k)$  (O) and  $E_n(\log(W_k))$  (E); (d) gap curve

# The Gap statistic

For  $M$  null distribution samples, calculate

$$\text{Gap}(K) = \bar{I} - \log W^{(*)}(C_K) \quad \text{and} \quad s_K = \sqrt{\frac{1}{R} \sum_{j=1}^M (\log W^{(r)}(C_K) - \bar{I})^2}$$

$$\text{where } W^{(r)}(C_K) = \sum_{C_K(i)=C_K(j)=k} \|x_i^{(r)} - x_j^{(r)}\|^2 \quad \text{and} \quad \bar{I} = \frac{1}{R} \sum_{r=1}^R \log W^{(r)}(C_K)$$

Then choose the smallest  $K$  such that  $\text{Gap}(K) \geq \text{Gap}(K+1) - s_{K+1}$

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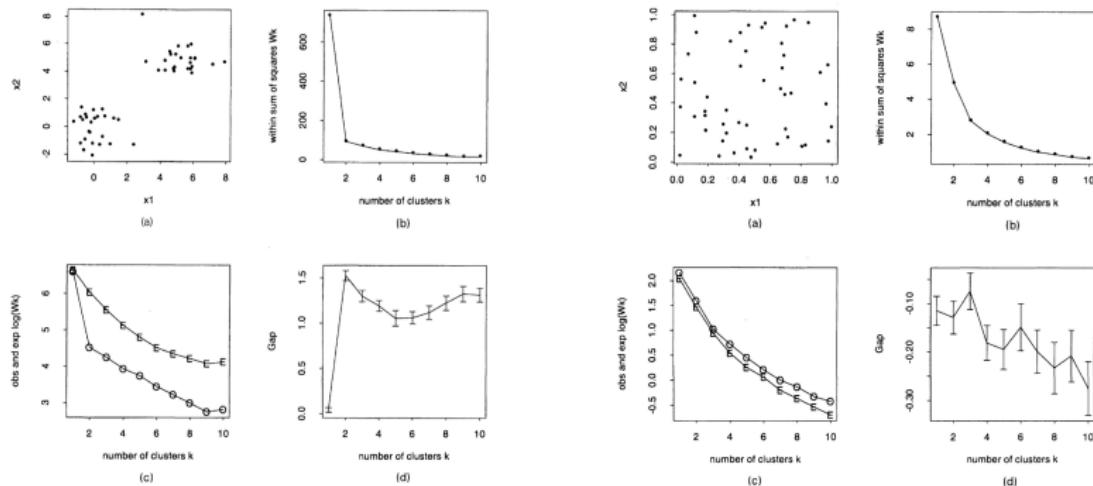


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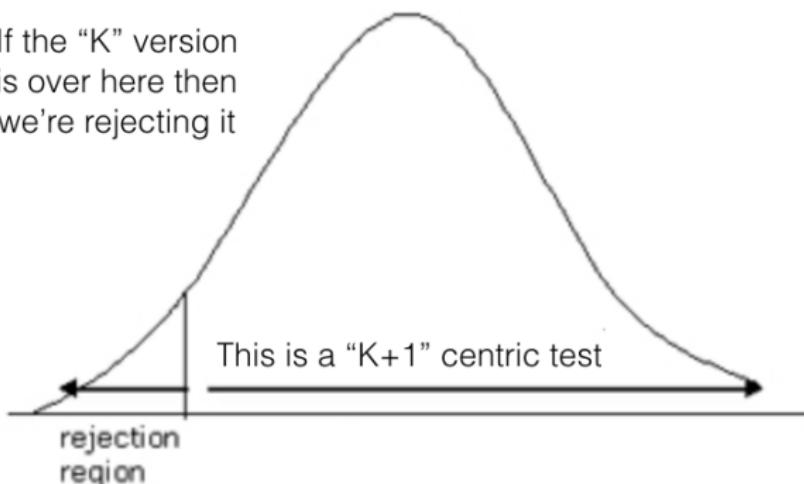
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Then choose the smallest  $K$  such that  $\text{Gap}(K) \geq \text{Gap}(K+1) - s_{K+1}$

If the "K" version  
is over here then  
we're rejecting it



# The Curse of Dimensionality

Just as nearest neighbors breaks down in high dimensional space...  
Distance based clustering breaks down in high dimensional space...

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Go see Ryan's great slides motivating *The Curse of Dimensionality*

They're in the KNN slides

(THIS is the KMEANS lecture, NOT the KNN lecture)

# The Curse of Dimensionality

Just as nearest neighbors breaks down in high dimensional space...

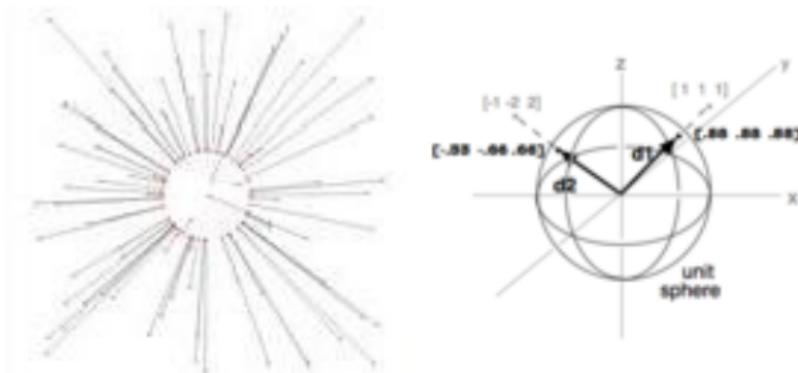
Distance based clustering breaks down in high dimensional space...

Go see Ryan's great slides motivating *The Curse of Dimensionality*

They're in the KNN slides

(THIS is the KMEANS lecture, NOT the KNN lecture)

However, when we normalize a vector (e.g., turn bag-of-words into probabilities, or make it a unit vector) we project all vectors onto a *manifold* where “locality” and “neighborhoods” make sense again.



# The Curse of Dimensionality

So who is effected by *The Curse of Dimensionality* and *why (not)?*

Hint: *Overfitting* and  
*The Curse of Dimensionality* are  
slightly different things...

# Challenge

A

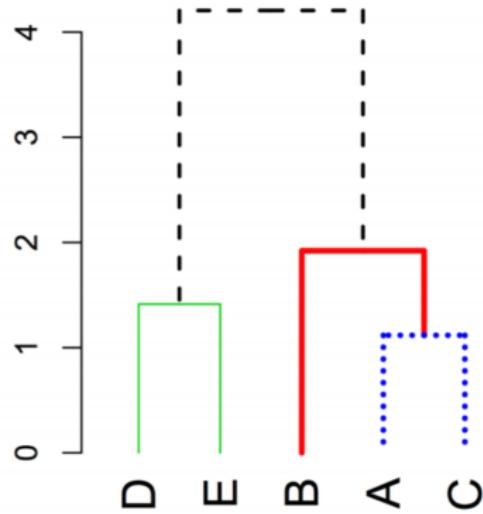
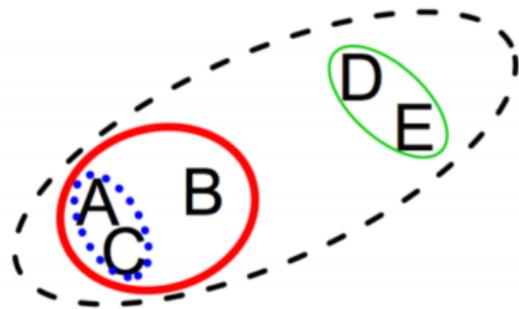
B

C

D

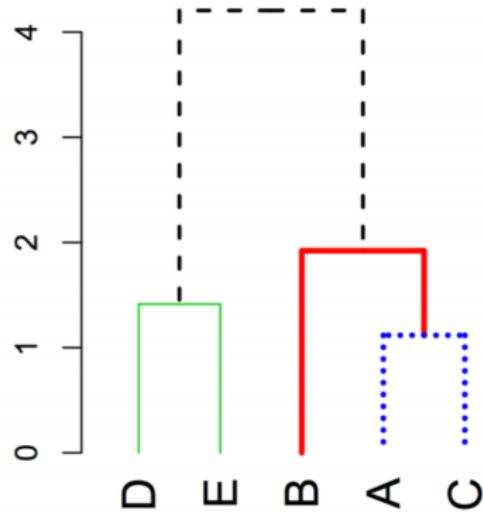
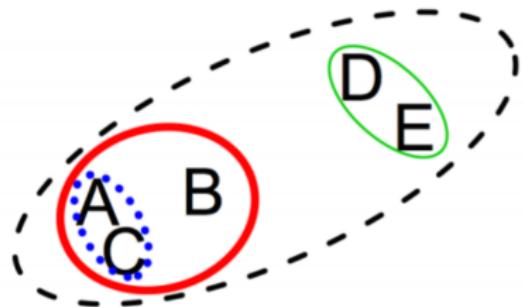
E

# Hierarchical clustering



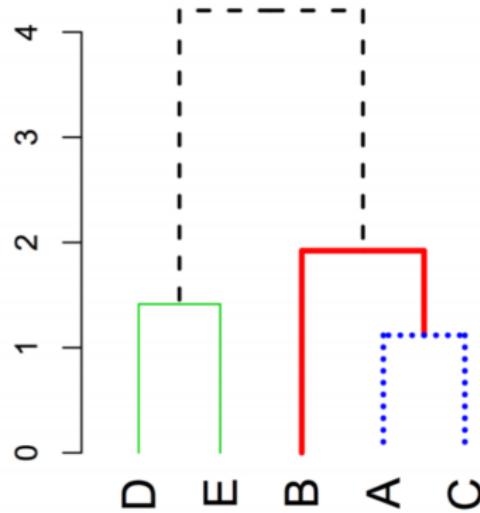
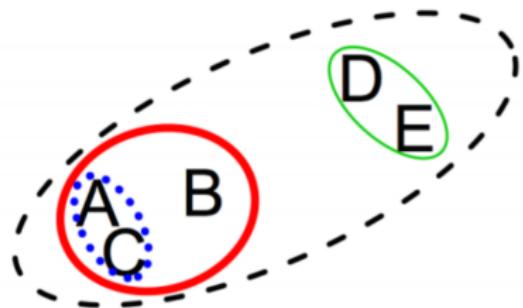
1. Assign each point to its own cluster

# Hierarchical clustering



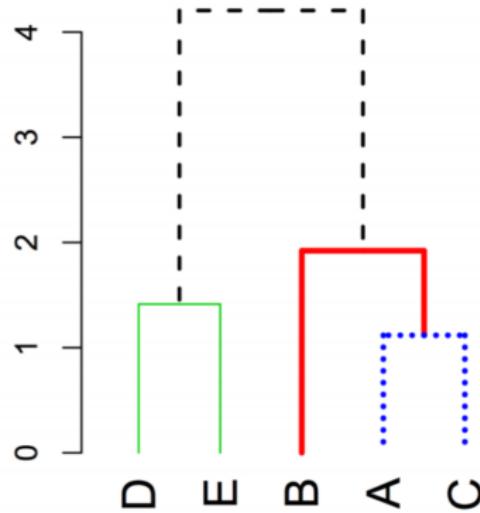
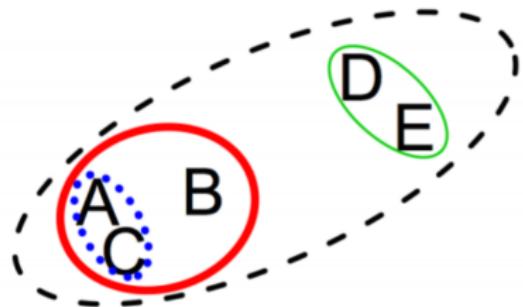
1. Assign each point to its own cluster
2. Computer pairwise cluster distances

# Hierarchical clustering



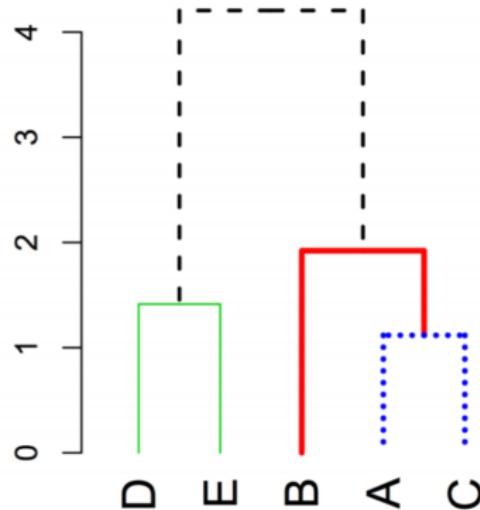
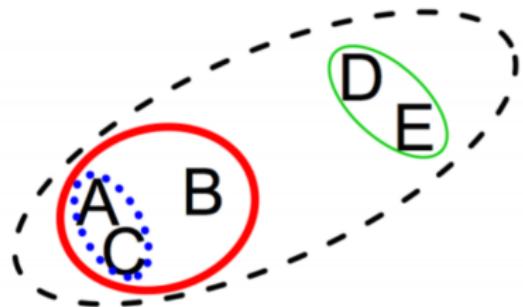
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3. Merge *closest two clusters*

# Hierarchical clustering



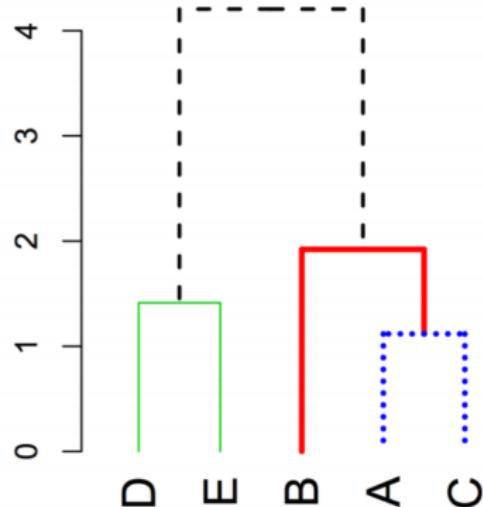
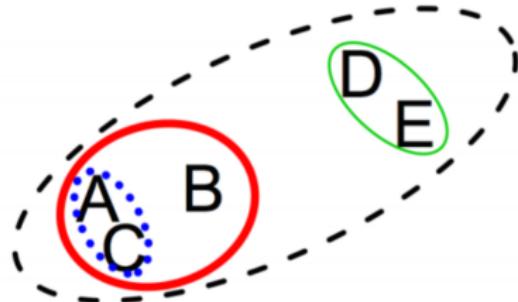
1. Assign each point to its own cluster
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3. Merge *closest two clusters*
4. Return to 2 until all clusters merged

# Hierarchical clustering

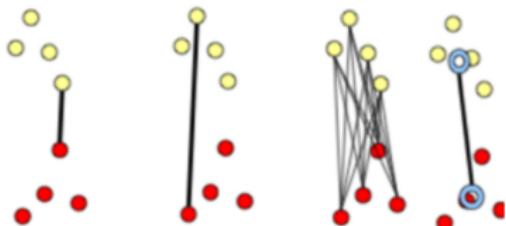


1. Assign each point to its own cluster
  2. Compute pairwise cluster distances
  3. Merge *closest two* clusters
  4. Return to 2 until all clusters merged
- ▶ Single: minimum pairwise point dissimilarity
  - ▶ Complete: maximum pairwise point dissimilarity
  - ▶ Average: average pairwise point dissimilarity
  - ▶ Centroid: centroid dissimilarity

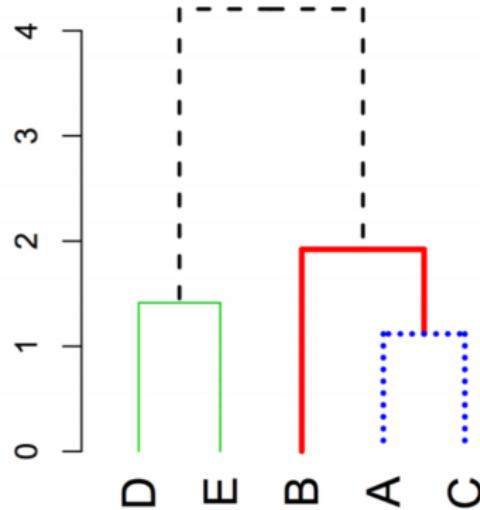
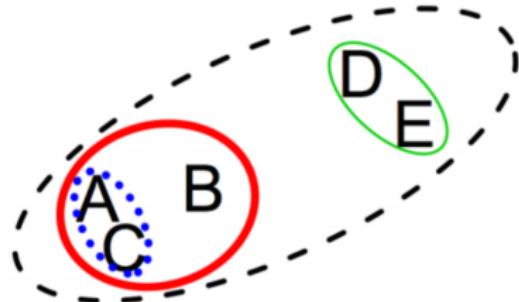
# Hierarchical clustering



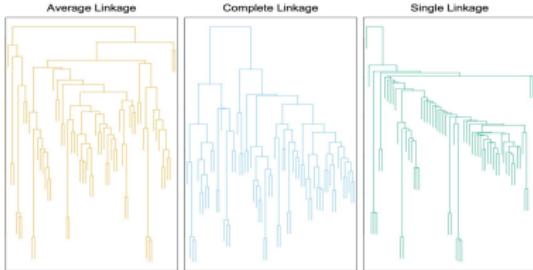
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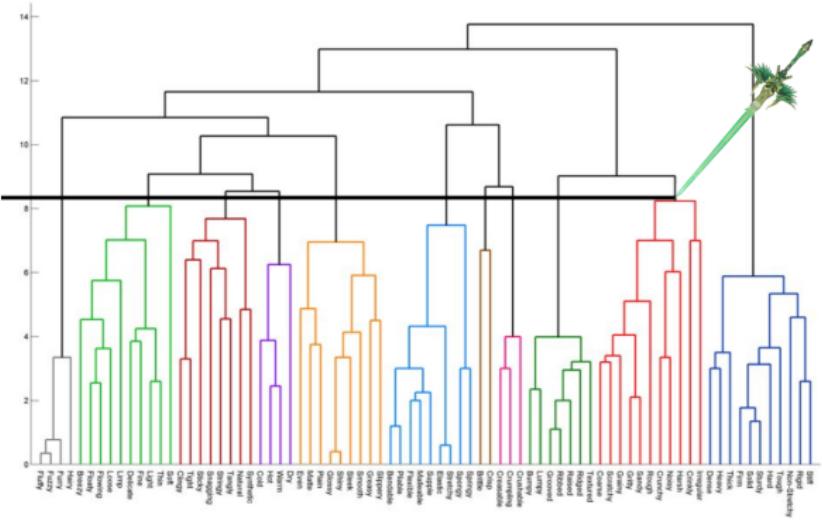
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# Hierarchical clustering

Clusterings are created based on distance between proposed merges

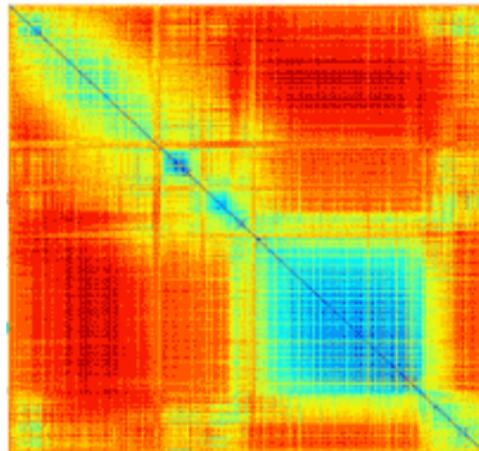
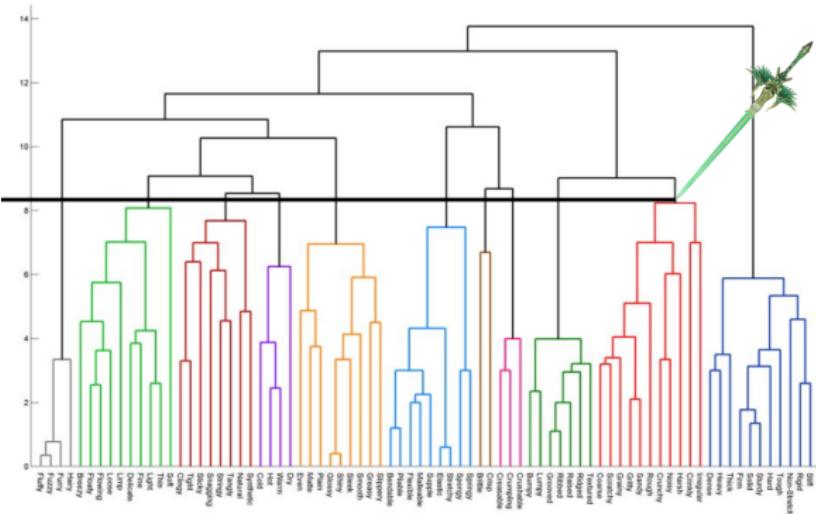
And then the number of clusters can be chosen *just like K-means...*



# Hierarchical clustering

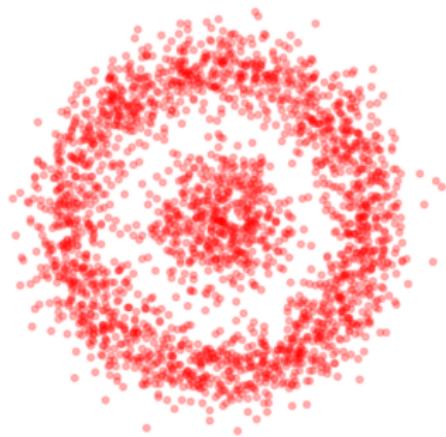
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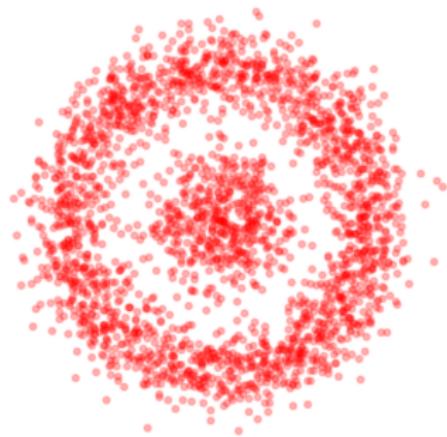


This is super cool, but  
unlike K-means, hierarchical clustering requires all pairwise  
comparisons so it doesn't scale gracefully with increasing data...

# DBSCAN

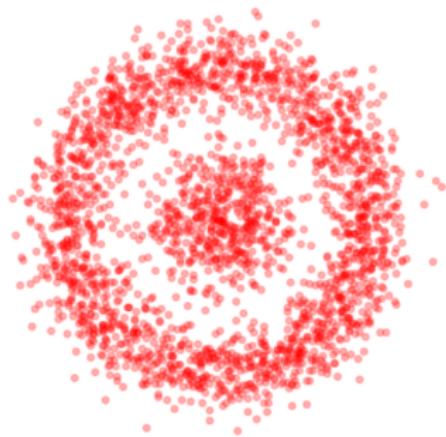


# DBSCAN



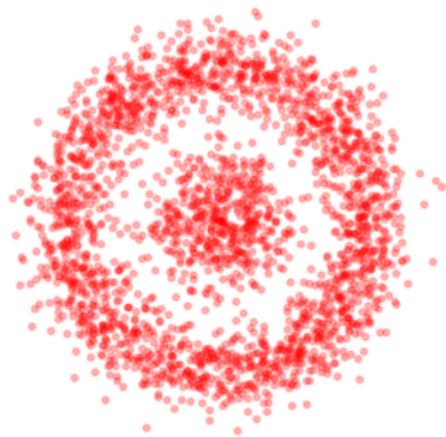
- ▶ Specify connection distance  $\epsilon$  and minimum number of points for core  $m$

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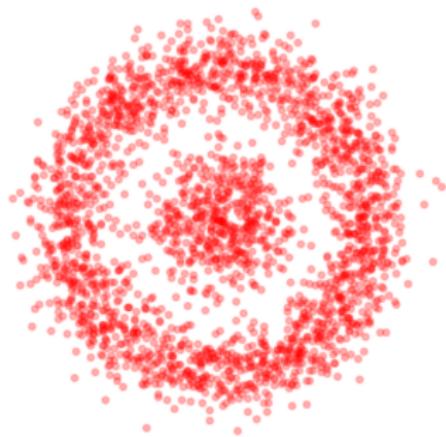
- ▶ Specify connection distance  $\epsilon$  and minimum number of points for core  $m$
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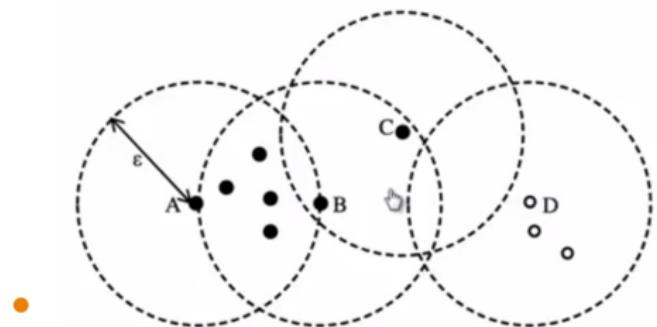


- ▶ Specify connection distance  $\epsilon$  and minimum number of points for core  $m$
- ▶ A cluster is all connected *core points*
- ▶ All other points are *noise*

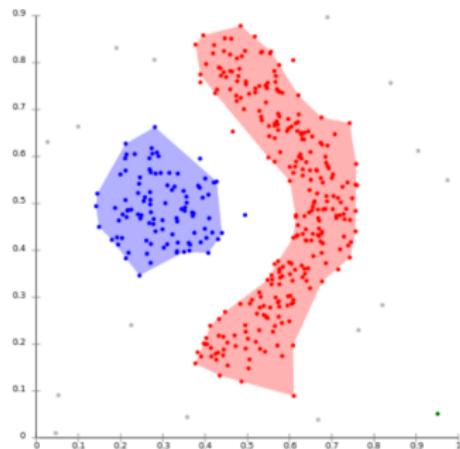
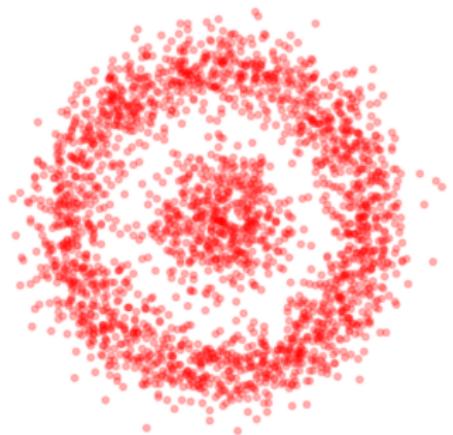
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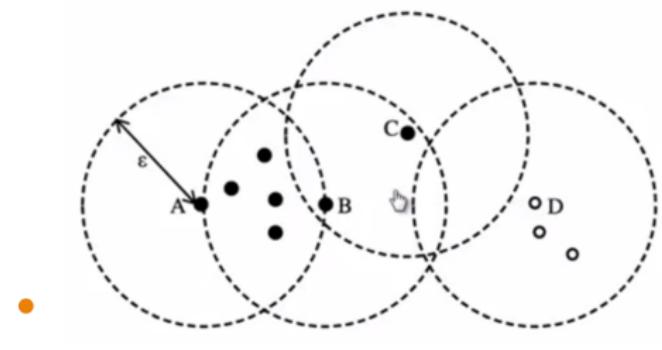
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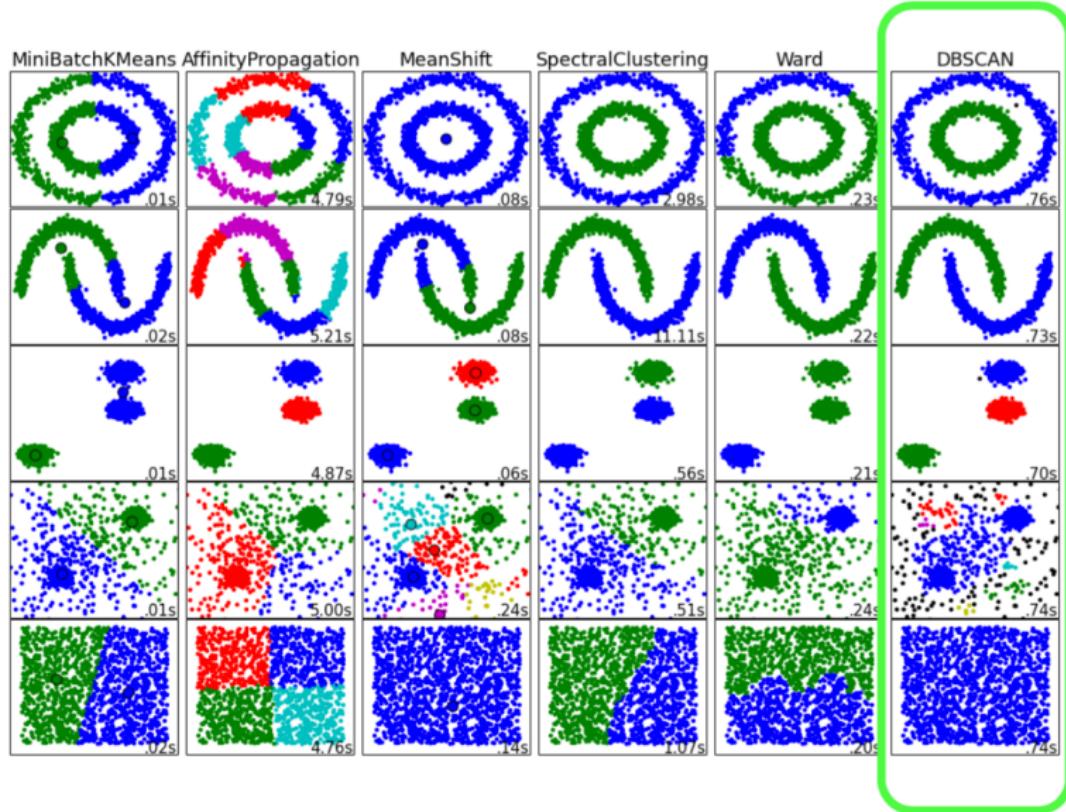
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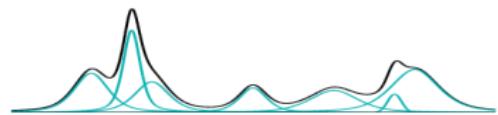


# DBSCAN



# Bayesian Mixture Models (*xtra: my grad school jam*)

$$f(X_i|\mu, \sigma^2, \pi, \pi) = \sum_{k=1}^K \pi_k N(\mu_k, \sigma_k^2)$$



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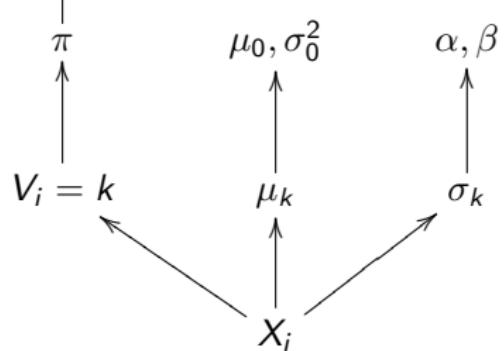
$$f(X_i|V_i, \mu, \sigma^2, \pi) = N(\mu_{V_i}, \sigma_k^2)$$

$$\Pr(V_i) = \text{Multinomial}(\pi, n=1)$$

$$f(\pi) = \text{Dirichlet}(\omega)$$

$$f(\mu_k) = N(\mu_0, \sigma_0^2)$$

$$f(\sigma_k^{-2}) = \text{Gamma}(\alpha, \beta)$$



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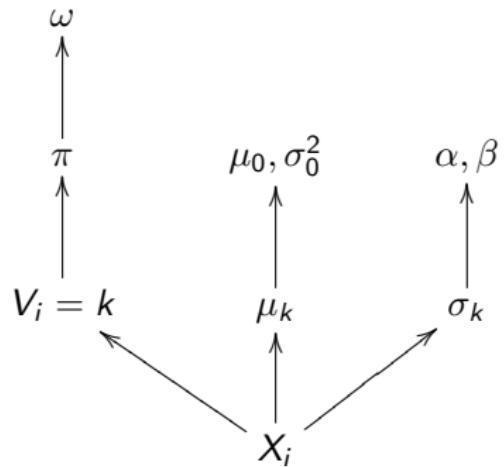
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$$f(\mathbf{X}, \mathbf{V}, \boldsymbol{\mu}, \sigma^2, \boldsymbol{\pi} | \mu_0, \sigma_0^2, \alpha, \beta, \boldsymbol{\omega}) =$$

$$\prod_{i=1}^n \left[ \left( \sum_{k=1}^K \mathbb{1}_{[V_{ik}=1]} \frac{1}{\sqrt{2\pi}\sigma_k} e^{-\frac{1}{2}\left(\frac{X_i - \mu_k}{\sigma_k}\right)^2} \right) \left( \prod_{k=1}^K \pi_k^{V_{ik}} \right) \right] \\ \times \left( \prod_{k=1}^K \frac{1}{\sqrt{2\pi}\sigma_0} e^{-\frac{1}{2}\left(\frac{\mu_k - \mu_0}{\sigma_0}\right)^2} \frac{\beta^\alpha}{\Gamma(\alpha)} \left(\frac{1}{\sigma^2}\right)^{\alpha-1} e^{-\beta\frac{1}{\sigma^2}} \right) \left( \frac{1}{\mathbf{B}(\boldsymbol{\omega})} \prod_{k=1}^K \pi_k^{\omega_k-1} \right)$$

## Markov Chain Monte Carlo (MCMC) posterior sampling

A Gibbs sampler for the posterior

$$f(\mathbf{V}, \boldsymbol{\mu}, \sigma^2, \boldsymbol{\pi} | \mathbf{X}, \mu_0, \sigma_0^2, \alpha, \beta, \boldsymbol{\omega})$$

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Is made by cycling through the *full conditional distributions*

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$$\Pr(V_{ik} = 1 | \mathbf{X}, \boldsymbol{\mu}, \sigma^2, \boldsymbol{\pi}, \mu_0, \sigma_0^2, \alpha, \beta, \boldsymbol{\omega})$$

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$$\propto f(\mathbf{X}, \mathbf{V}, \boldsymbol{\mu}, \sigma^2, \pi | \mu_0, \sigma_0^2, \alpha, \beta, \boldsymbol{\omega}) \quad (\text{which is proportional to the joint distribution})$$

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## Markov Chain Monte Carlo (MCMC) *full conditionals*

$$\Pr(V_{ik} = 1 | \mathbf{X}, \boldsymbol{\mu}, \boldsymbol{\sigma}^2, \boldsymbol{\pi}, \mu_0, \sigma_0^2, \alpha, \beta, \boldsymbol{\omega}) \propto \pi_k \frac{1}{\sqrt{2\pi}\sigma_k} e^{-\frac{1}{2}\left(\frac{X_i - \mu_k}{\sigma_k}\right)^2}$$

$$f(\pi | \mathbf{V}, \mathbf{m}\boldsymbol{\mu}, \boldsymbol{\sigma}^2, \mathbf{X}, \mu_0, \sigma_0^2, \alpha, \beta, \boldsymbol{\omega}) = Dirichlet(\{\omega_k + n_k : k = 1, \dots, K\})$$

$$n_k = \sum_{V_{ik}=1} 1$$

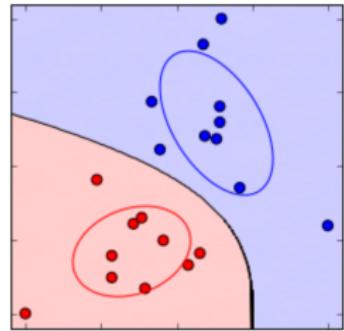
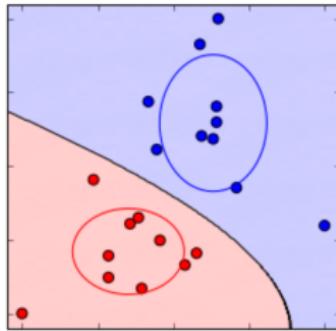
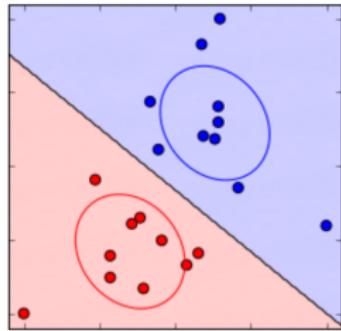
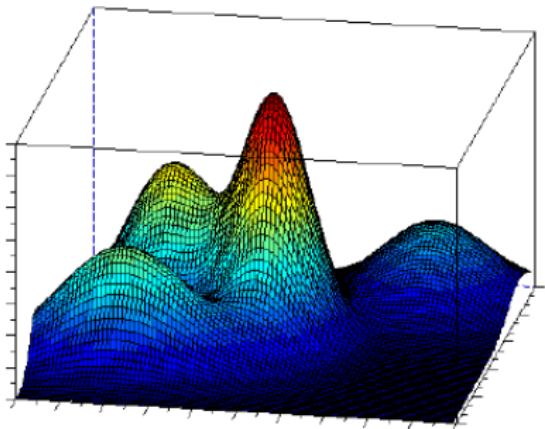
$$f(\sigma_k^2 | \mathbf{V}, \boldsymbol{\mu}, \mathbf{X}, \mu_0, \sigma_0^2, \alpha, \beta, \boldsymbol{\omega}) = Gamma\left(\frac{n_k}{2} + \alpha, \frac{1}{2} \sum_{V_{ik}=1} (X_i - \mu_k)^2 + \beta\right)$$

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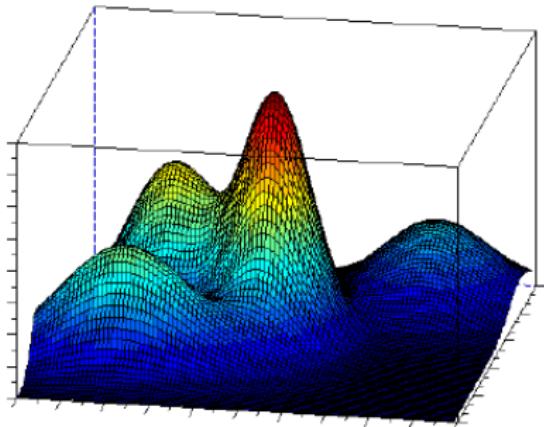
$$N\left(\hat{\sigma}_k^2 \left(\frac{\sum_{V_{ik}=1} X_i}{\sigma_k^2} + \frac{\mu_0}{\sigma_0^2}\right), \hat{\sigma}_k^2 = \left(\frac{n_k}{\sigma_k^2} + \frac{1}{\sigma_0^2}\right)^{-1}\right)$$

# Mixture Models!

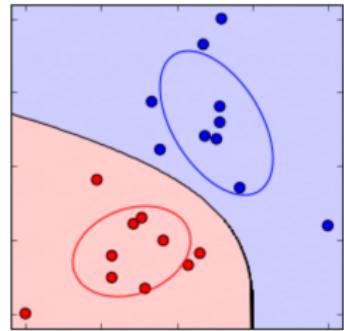
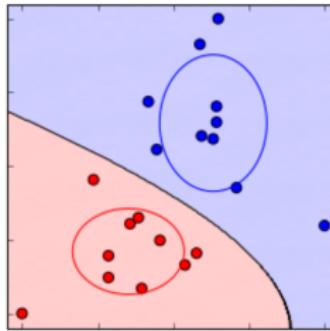
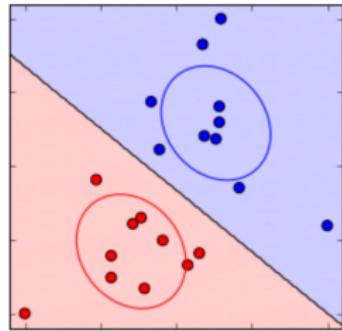
- ▶ Used to model “subpopulations”



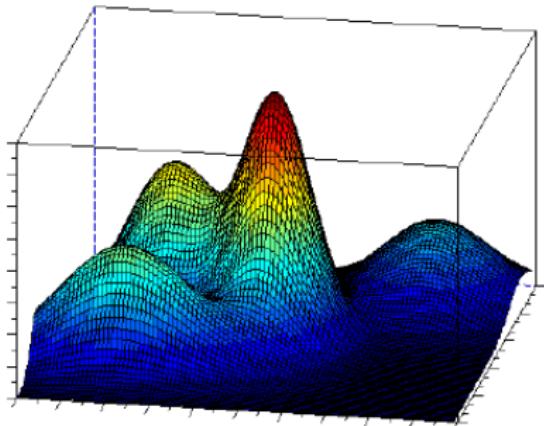
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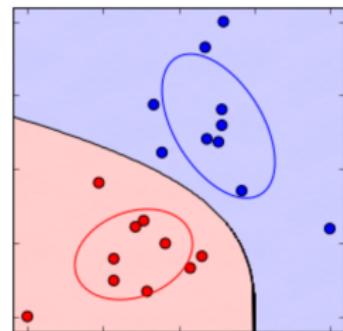
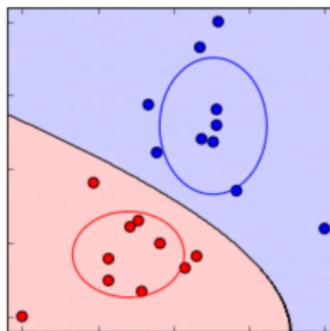
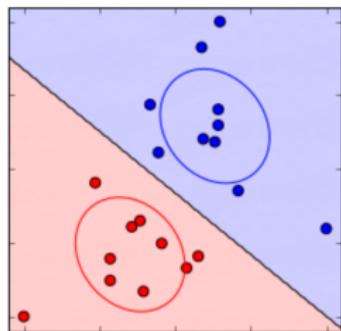
- ▶ Used to model “subpopulations”
- ▶ Or simply complex distributional shapes



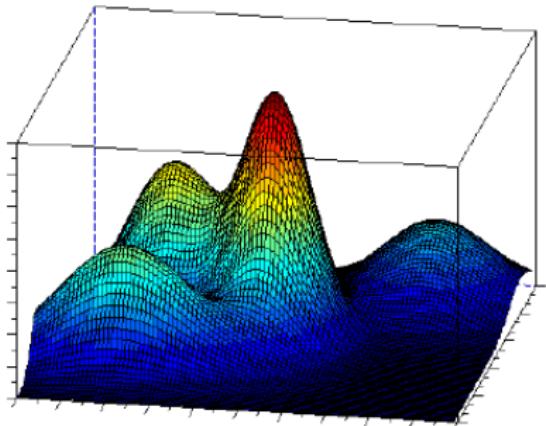
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- ▶ Used to model “subpopulations”
- ▶ Or simply complex distributional shapes
- ▶ It's *almost nonparametric* like kernel density estimation
- ▶ Expectation-Maximization (EM) algorithm is another way to fit mixture models

