# UNSUPERVISED ML

# OBJECTIVE

- Discover information from data without labeled examples
- Extract some hidden organisation, patterns, relation between elements
- Extract a (statistical ?) model of the data ?

# OBJECTIVE

- Typical objectives:
  - <u>Cluster discovery</u>
  - Anomaly Detection
  - Latent variable discovery / Embedding / dimensionality reduction...

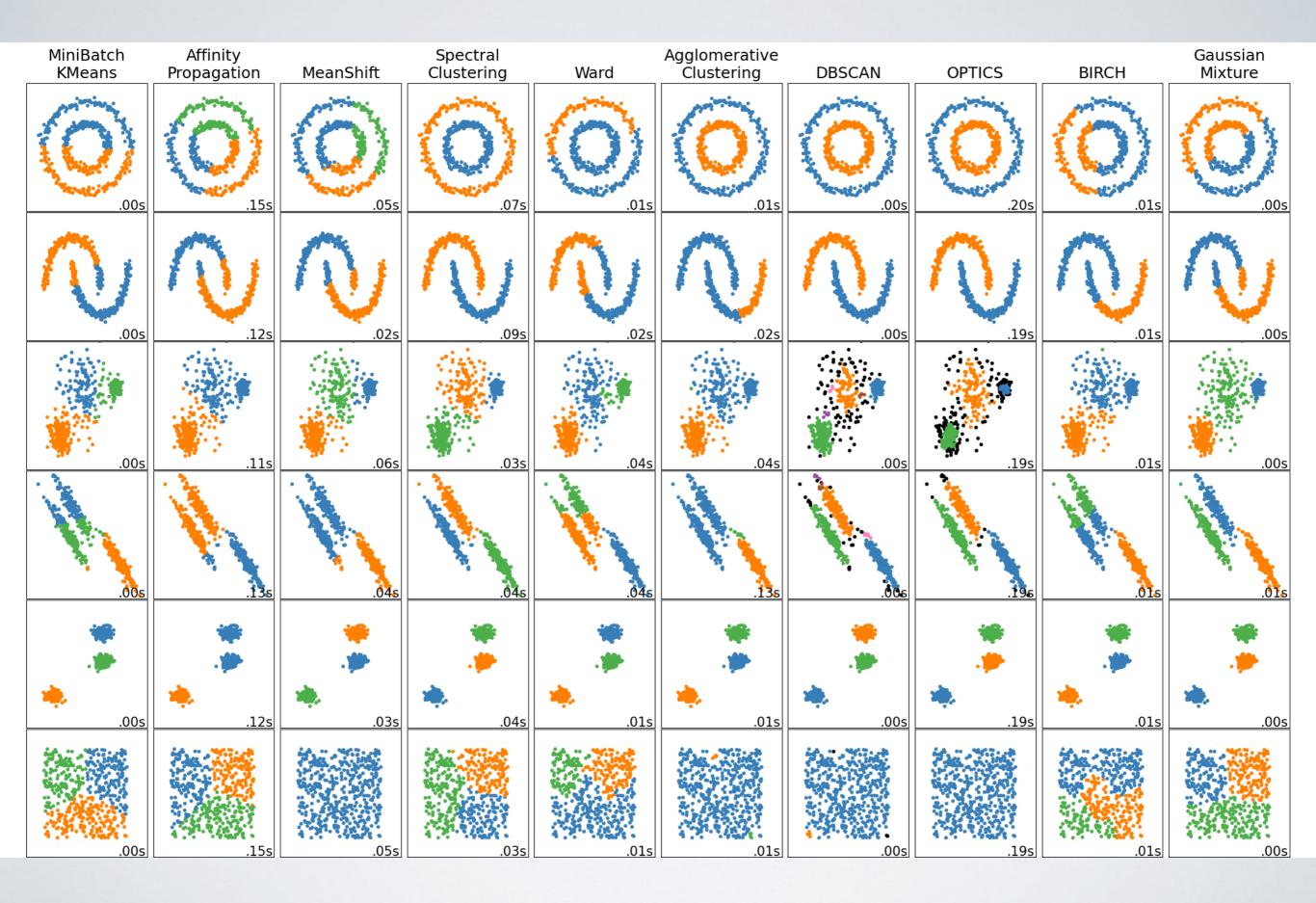
CLUSTERING

## CLUSTERING

- The most famous unsupervised ML problem
- 100+ methods exist
  - Most people use "good old" methods: k-means (1967), DBSCAN (1996)
  - They are often "good enough", well implemented, safe, ...
- Part of the problem: Clustering is not well defined
  - What is "a good cluster"?

## CLUSTERING

- How would you define a good cluster ?
- A good partition in clusters ?



#### K-MEANS

#### • Definition:

- For a target number of clusters k
- Find the item assignment minimizing
  - The inter-cluster variance
  - Equivalently => The squared distance from points to their cluster center
  - Equivalently => The squared distance between cluster elements
- This is only one possible objective !
  - Why this one ?
  - Intuitive, good properties...

#### **K-MEANS**

# $\underset{\mathbf{S}}{\operatorname{arg\,min}} \sum_{i=1}^{k} \sum_{\mathbf{x} \in S_{i}} \| \mathbf{x} - \boldsymbol{\mu}_{i} \|^{2} = \underset{\mathbf{S}}{\operatorname{arg\,min}} \sum_{i=1}^{k} |S_{i}| \operatorname{Var}(S_{i})$

#### with **S** a cluster assignment, x a d dimensional item, and $\mu_i$ the mean of items in cluster $S_i$ .

Note that without fixing k, there is a trivial solution with each item alone in its own cluster.

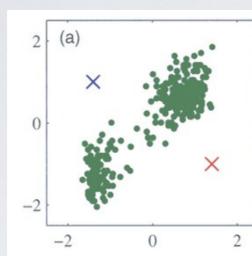
#### K-MEANS

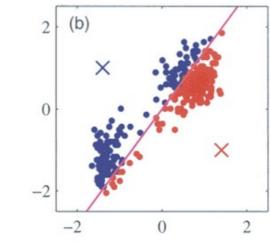
- Discovering the global optimum is NP-hard
- How to find quickly a good solution ?
  - Naive k-means
  - K-means ++ (used in most current implementations)
  - Use optimized data structure (KDtrees...)

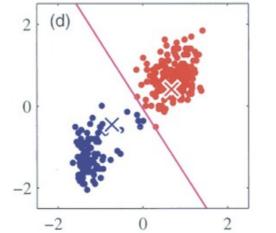
### NAIVE K-MEANS

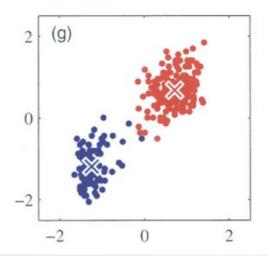
- I)Assigment: Assign each item to its closest cluster center
- 2) Update: Recompute the center of each cluster as the mean (centroid) of items that compose that cluster
- Start with random centroids

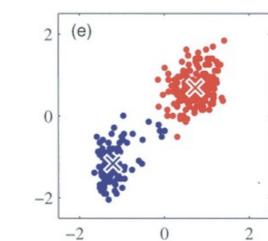
#### NAIVE K-MEANS

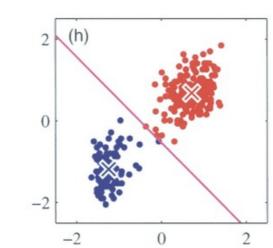


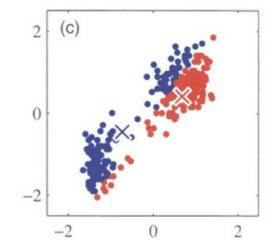


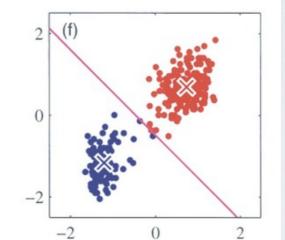


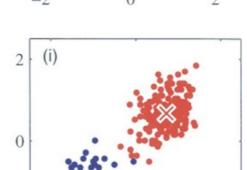


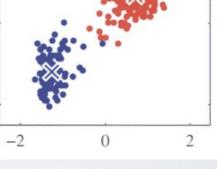






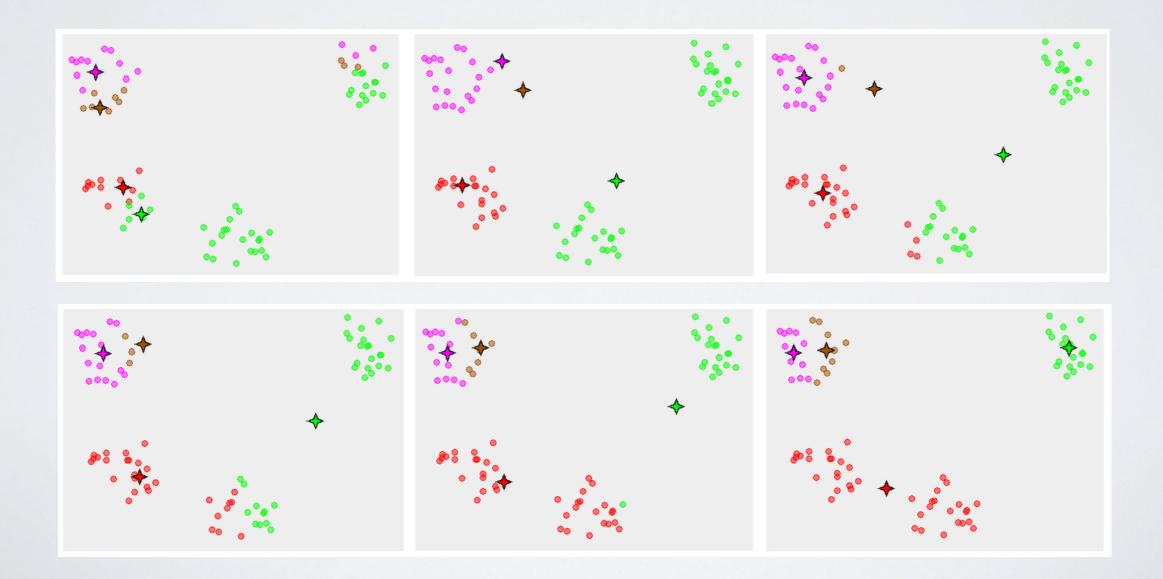






## NAIVE K-MEANS

Known limit: convergence to poor local minimum if poor initial centroids



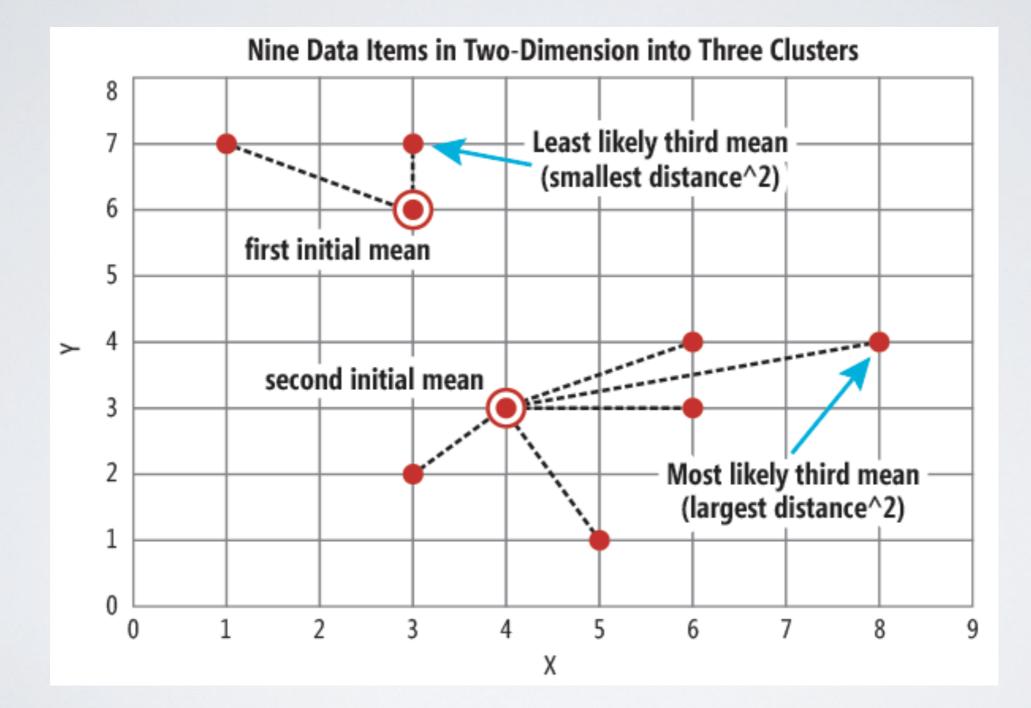
#### K-MEANS++

- Several variants to choose wisely the initial centroids
- K-means++ is proven to improve the results, statistically
  - Not always, but improves more often than deteriorate the results.

K-MEANS++

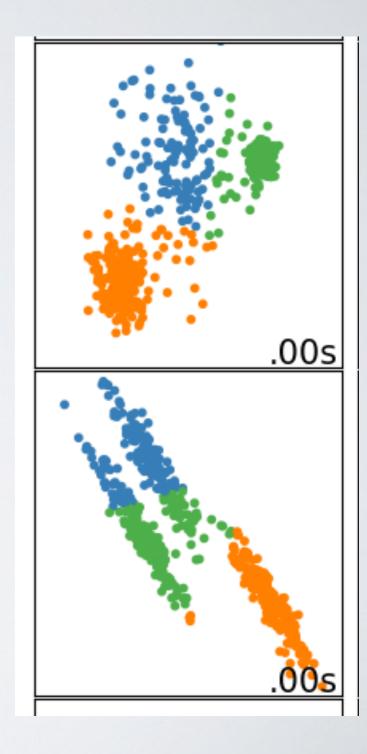
- 1. Choose one center uniformly at random among the data points.
- 2. For each data point x not chosen yet, compute D(x), the distance between x and the nearest center that has already been chosen.
- 3. Choose one new data point at random as a new center, using a weighted probability distribution where a point x is chosen with probability proportional to  $D(x)^2$ .
- 4. Repeat Steps 2 and 3 until k centers have been chosen.

#### K-MEANS++



#### WEAKNESSES

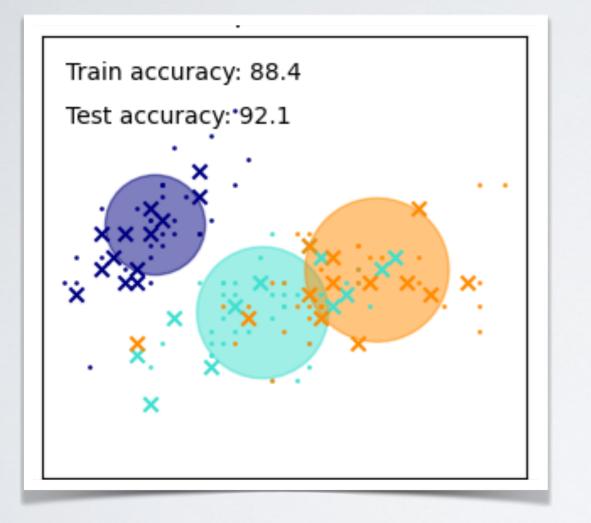
- We can identify some clear weaknesses:
  - K-means has a tendency to search for clusters of equal sizes (minimize overall cluster variance)
  - Clusters tend to be circular, since all directions are worth the same.

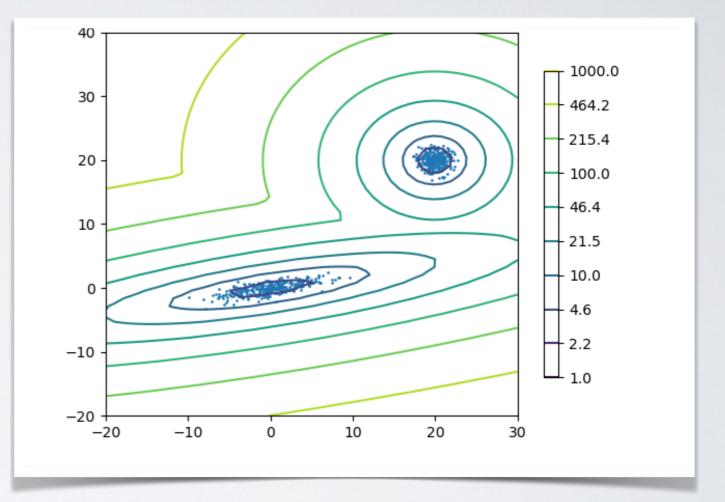


# NORMALIZATION

- Very important point: k-means is based on euclidean distance.
  - We minimize the inter-cluster euclidean distance between points
  - We could adapt the method to other distances
- Data need to be normalized/standardized
  - Clustering based on age in years and revenue in \$.The 'distance' in \$ will dominate
  - Remember: normalization/standardization are not fixing magically problems (outliers..)
    - You need to **think**: is I unit in one dimension *worth* I unit in other dimensions ?

- Generalize k-means concept:
  - Clusters are sets of points that are close in euclidean space
  - Different clusters tend to be far appart
- Translate it statistically:
  - Each cluster can be described using a normal distribution centered on its centroid, with the probability of observing points decreasing with the distance to the centroid.





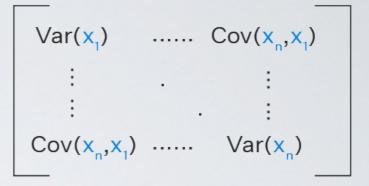
#### • We define a **generative model** for k clusters

- Each cluster corresponds to a gaussian distribution, defined by a center and a *variance*, or *covariance matrix*
- The problem to solve is to find the parameters  $\Theta$  (centers, variances) that maximize the likelihood of the corresponding model to generate the observed items X

0

More formally, we are searching for:  $\arg \max p(X | \Theta)$ 

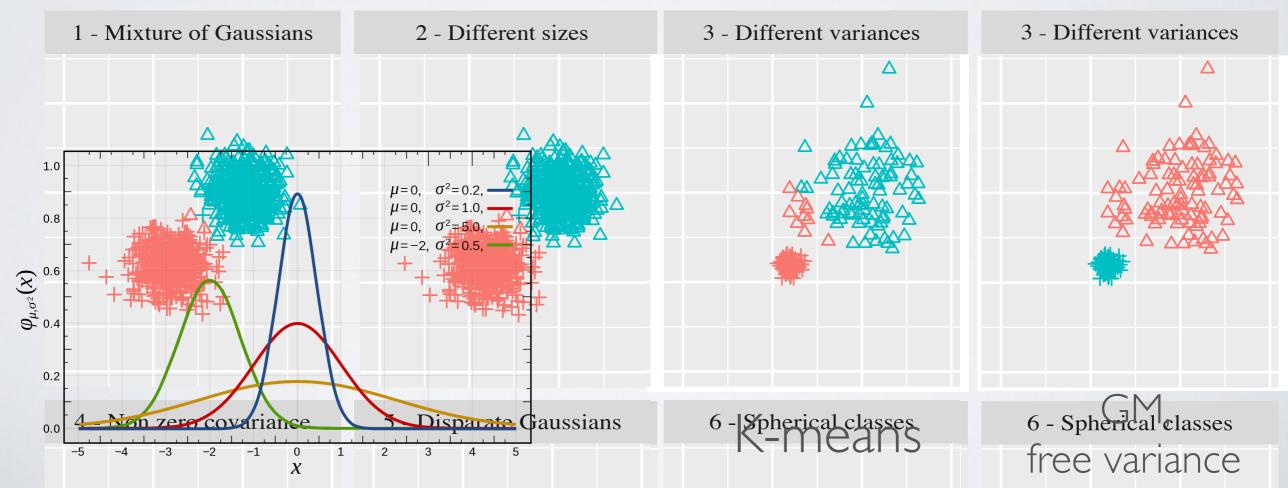
# K-MEANS EQUIVALENCE



- If we assume that:
  - The gaussian distributions are defined only by their variance, not by complete covariance matrices
    - Similar in all directions, "spherical"
  - The variance value is the same for all gaussian distributions
    - Spheres of the same "size"
  - The probability for each item to be generated by each of the gaussian distribution is identical
- Then it can be shown that the objective is equivalent to the kmeans objective !
  - We can relax some of those constraints to get better results

# DENSITY HETEROGENEITY

- Allowing denser/sparser clusters
  - Consider the case in which gaussians are defined by a single value of <u>variance</u> (covariance=0)
  - If they differ for each clusters, some can be denser than others



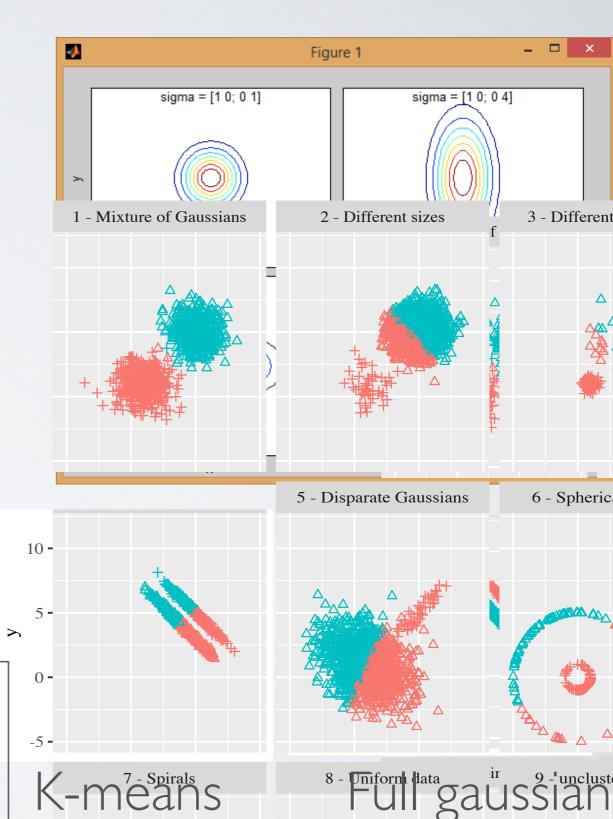
# SHAPEVARIATIONS

- Allowing non-circular shaped clusters
  - If values on the diagonal of the covariance matrix differs, the matrix can have ellipsoidal shape, in the direction of the axes
  - If the full covariance matrix is inferred, any ellipsoidal shape can be obtained

Var(x,)

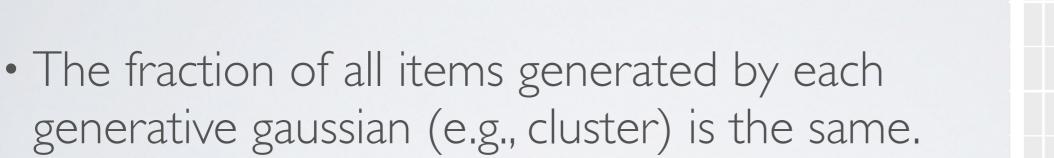
.....  $Cov(x_n, x_1)$ 

 $Cov(x_n, x_1)$  .....  $Var(x_n)$ 



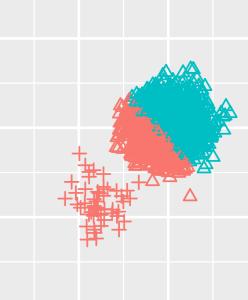
# SIZE HETEROGENEITY

2 - Different sizes

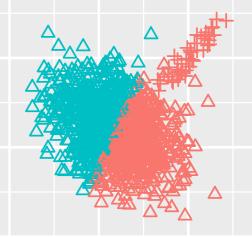


We usually add a strength paramet
4 - Non zero covariance
weight the fraction of items gener;
cluster

$$p(X) = \sum_{k=1}^{K} \pi_k G(X | \mu_k, \sigma_k)$$



5 - Disparate Gaussians



8 - Uniform data

7 - Spirals

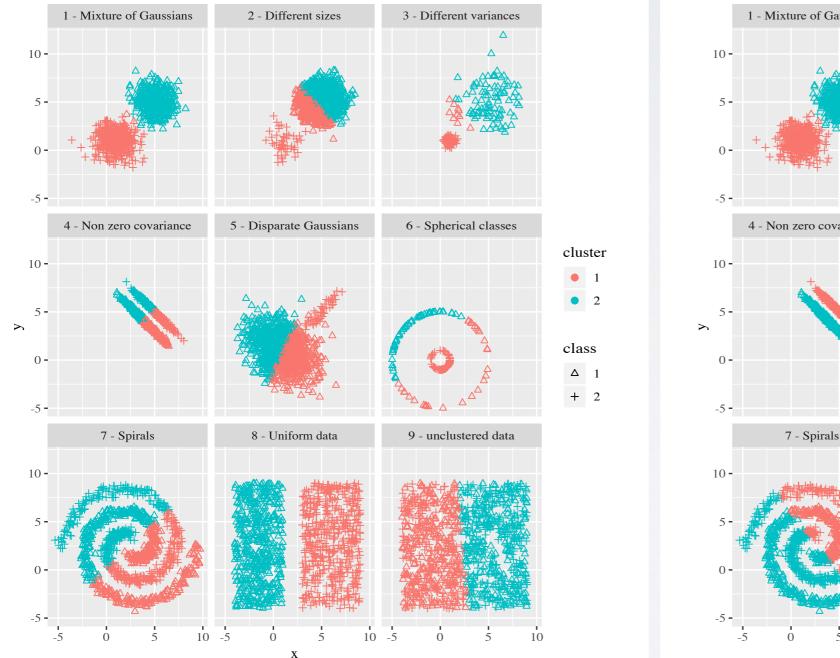
#### ALLTOGETHER

 $p(X) = \sum_{k=1}^{K} \pi_k G(X | \mu_k, \sigma_k)$ k=1

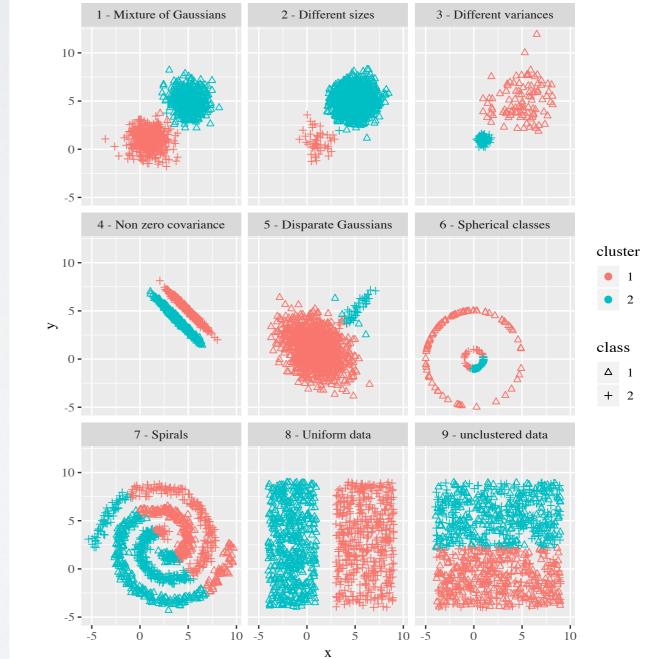
$$\begin{array}{l} \arg\max p(X \mid \Theta) \\ \Theta \end{array} \qquad \qquad \Theta = \mu, \sigma, \pi \end{array}$$

# K-MEANS COMPARISON

#### K-means



#### Full Gaussian Mixture

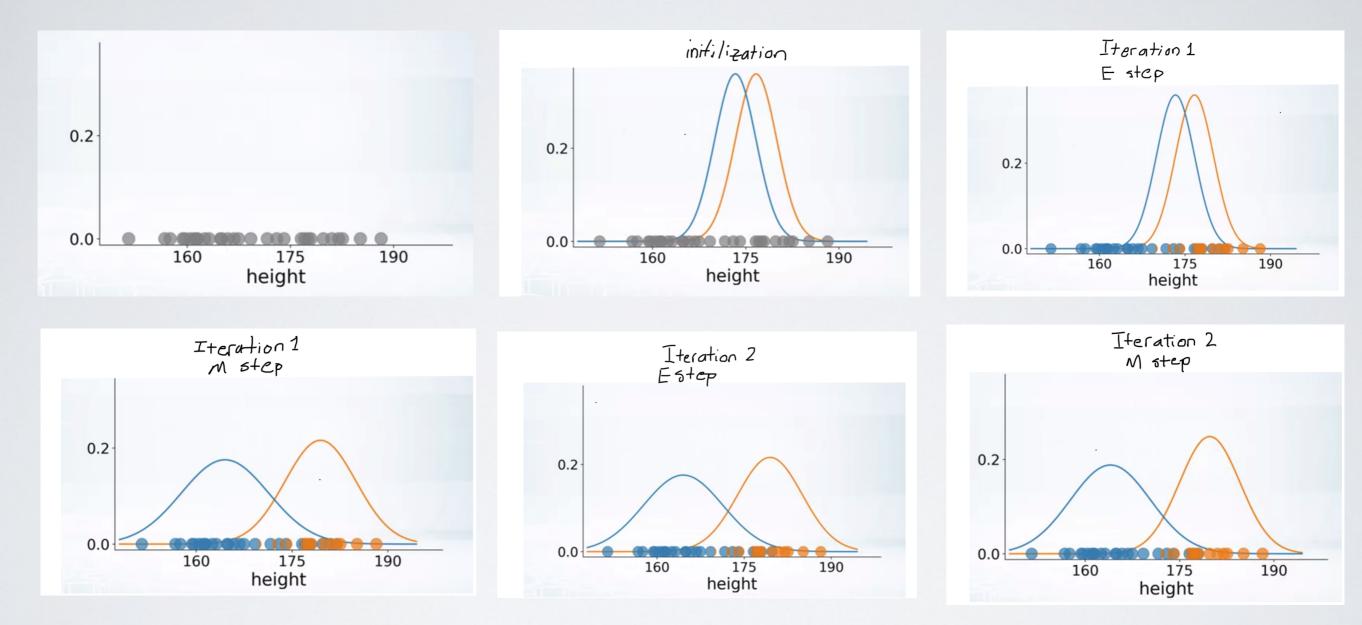


https://smorbieu.gitlab.io/gaussian-mixture-models-k-means-on-steroids/

# EM ALGORITHM

- To search for the parameters, we can use a method similar to naive k-means known as EM (Expectation Maximization)
  - Note Z the cluster assignation of items to their **most likely** clusters
  - I)Initialize parameters  $\Theta$  to random values
  - 2)(E) Compute Z, given  $\Theta$
  - 3)(M) Use assignations in Z to update values of  $\Theta$
  - 4) Iterate steps 2 and 3 until convergence

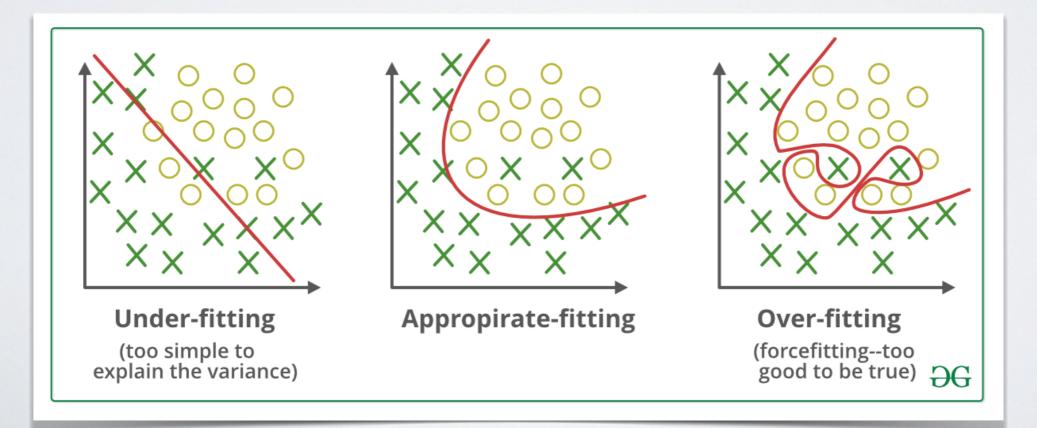
### EM ALGORITHM



https://towardsdatascience.com/gaussian-mixture-models-d13a5e915c8e

# PROS AND CONS

- Gaussian mixture seems an improvement over k-means. Why not always using it?
  - Force of habits
  - Higher computational cost (More parameters => More complex problem)
  - Higher possibility of overfitting (More parameters =>More overfit risk)

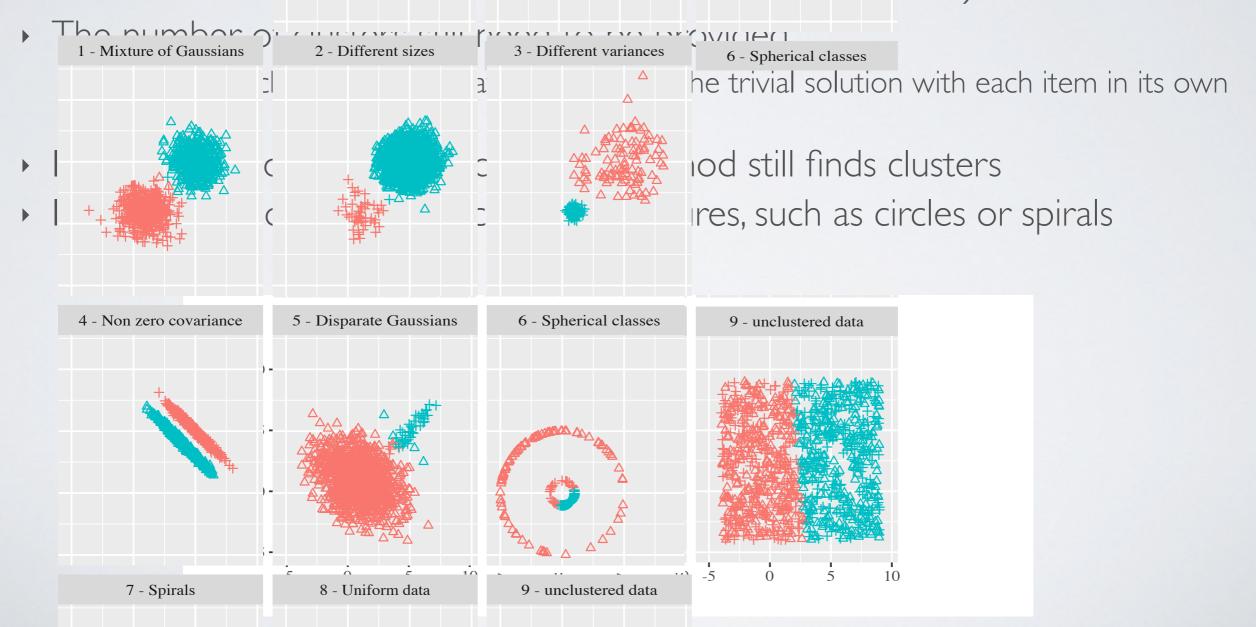


# REMAINING PROBLEMS

3

east)

• We can men

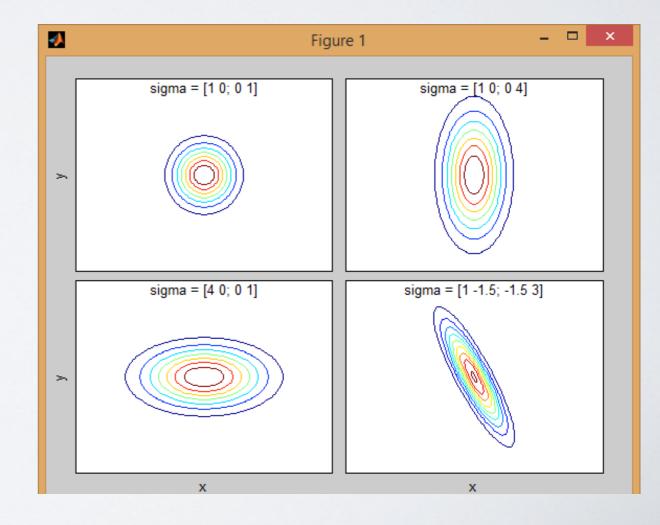


# MDL

- Discovering automatically the number of clusters —and thus finding no clusters in random data— is possible using an MDL approach
- MDL = Minimum Description Length
- The principle is to search a solution maximizing the compression rate, i.e., minimizing the *cost* of the description, e.g., in bits.
- Method introduced later

## NORMALIZATION

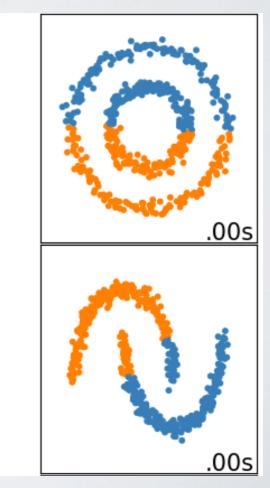
 Is normalization as important for full GM models as for kmeans?



DBSCAN

# K-MEANS/GM LIMITS

 The problem of spiral/Circulal/weird shaped clusters comes from the assumption that items of a cluster should be "normally distributed" around their mean



# LOCAL DEFINITIONS

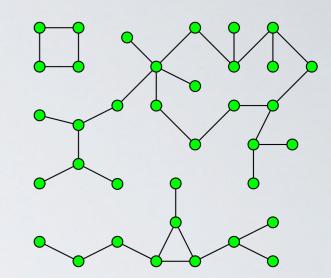
- To overcome this problem, several methods propose local definitions of clusters
  - Does not explicitly optimize a global function
  - Items belong to clusters because they are close enough, locally, to other items in that cluster
  - Clusters exist because there is continuum between all items in it, locally

### DBSCAN

- Define some local parameters:
  - $\epsilon$ , the distance threshold above which items are considered "too different"
  - minPts, a minimal number of reachable points
  - No need to define a number of clusters !
- Define:
  - An item p is a core point if it has at least minPts items at distance less than  $\epsilon$ 
    - Including p itself

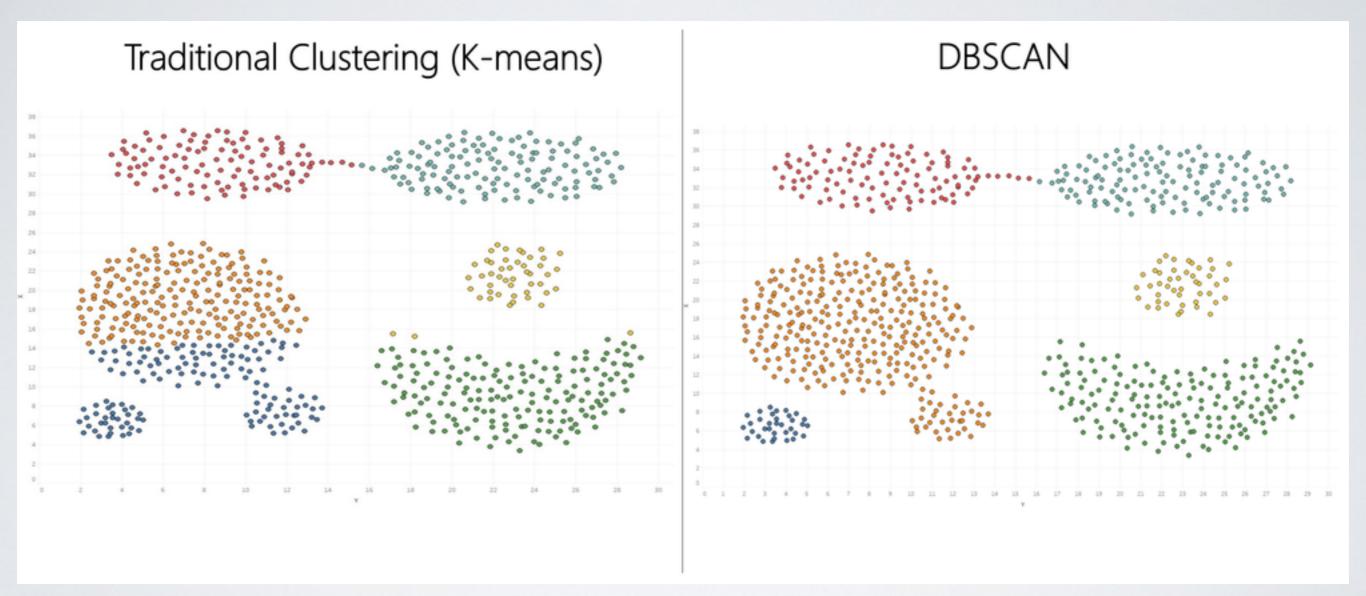
# DBSCAN: GRAPH DEFINITION

- I)Build a graph such as
  - Each core node is a node
  - A link exist between core nodes if they are at d<  $\epsilon$

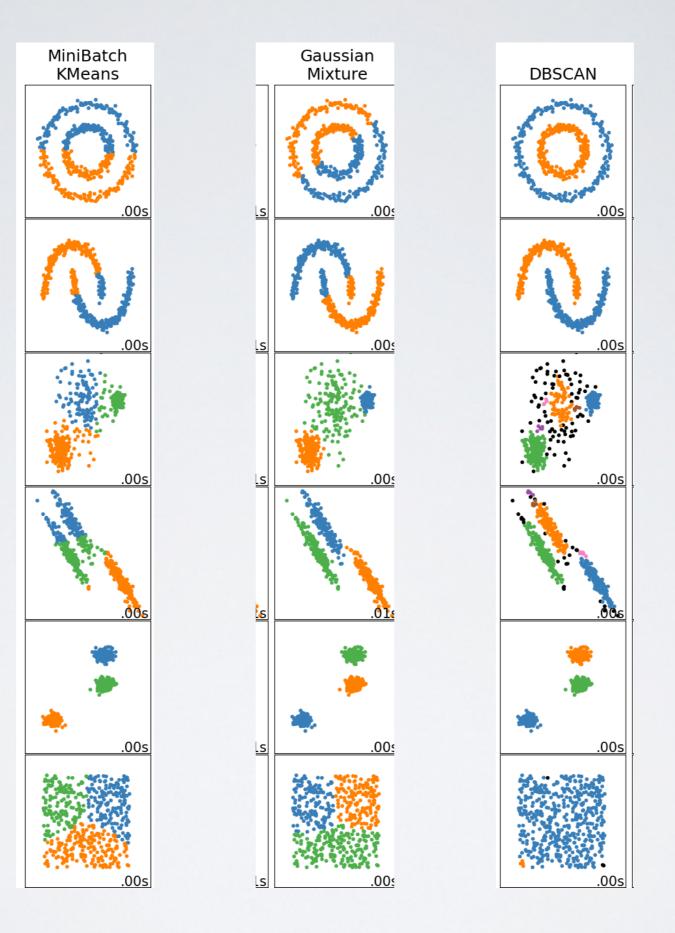


- 2)Detect the connected components of the graph
  - 2 nodes belong to the same connected components if there is a path between them
- 3) For all non-core nodes:
  - If they have no core points directly reachable, discard them as noise
  - Else, attribute them to (one of) the clusters for which one core point is directly reachable
    - Variant DBSCAN\* =>ignore those points as noise

### DBSCAN



https://community.alteryx.com/t5/Data-Science/Partitioning-Spatial-Data-with-DBSCAN/ba-p/446273



### DBSCAN

#### • Strength:

- No need to define the number of clusters
- Can discover arbitrarily-shaped clusters
- A notion of noise
- Weaknesses
  - Defining  $\epsilon$  is extremely difficult
    - Similar to the number of clusters.
    - In fact it determines the number of clusters...
  - Despite safeguards, risk of the stretched clusters effect



### CLUSTERING EVALUATION

### INTERNAL/EXTERNAL

- Two types of evaluation: internal or external
- <u>External</u>: we have a Ground Truth (GT). Like in supervised learning, we compare what we found (predictions) with the ''truth''.
- Internal: No ground truth, we rely only some intrinsic property of our clusters

### INTERNAL/EXTERNAL

- External Evaluation (extrinsic):
  - The ground truth can be exactly the right clustering desired
    - So we are just validating the method, since we already know the answer...
  - The ground truth can be a proxy to what we want
    - e.g., we want to cluster stars based on their characteristics (size, temperature, color...). We already have a manual historic categorization (red dwarf, Brown dwarfs, Red giants...). We assume that the new categories found should be somewhat similar

### EXTERNAL EVALUATION

### EXTERNAL EVALUATION

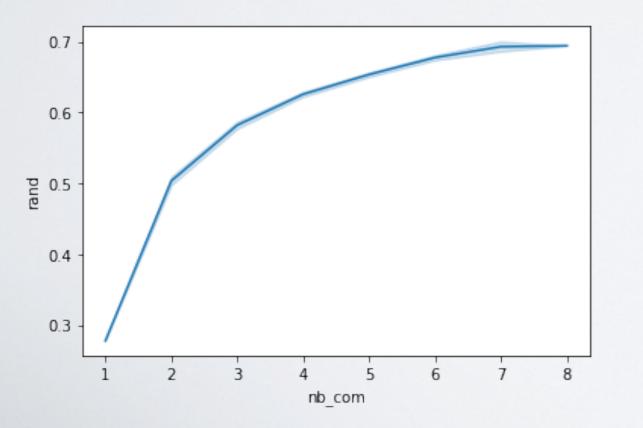
#### • Rand Index = <u>Accuracy</u> over node pairs

# $. RI = \frac{TP + TN}{TP + FP + FN + TN}$

- TP:two nodes in same cluster in both GT and solution
- TN:two nodes in different clusters in both GT and solution
- TP+FP+FN+TN=all possible node pairs
- Problem: complexity. #of pairs=  $\mathcal{O}(n^2)$ 
  - I 00k items: I 0 Billion pairs...

### RAND INDEX

- Rand Index has the same weakness as Accuracy:
  - If the classes are imbalanced, i.e., the size and number of communities vary between GT and clustering, results can be counterintuitive
- In practice:
  - Random communities have different scores depending on their size
  - =>Prefer certain types of communities



Previous example, With random communities

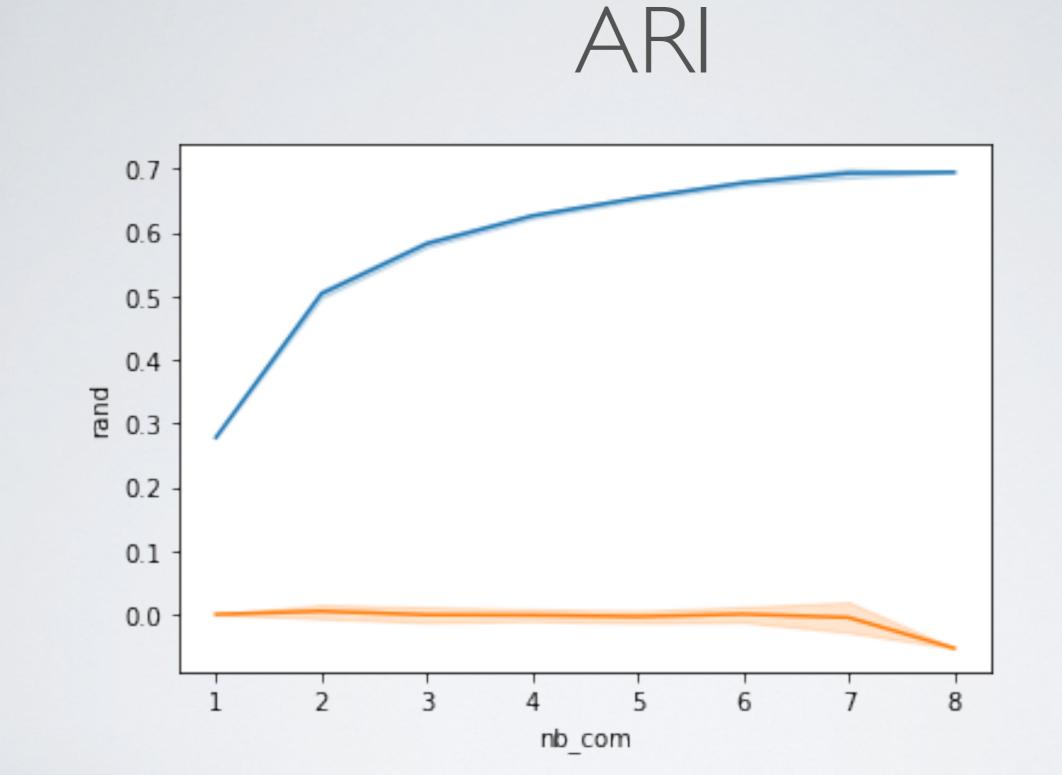


- Solution: Use an adjusted for chance score.
  - Principle: adjust (normalize) such as 0 is the score obtained with a "random" solution, 1 is the highest possible score.
  - Negative solutions are worst than random

Index – Expected index Max index - Expected index

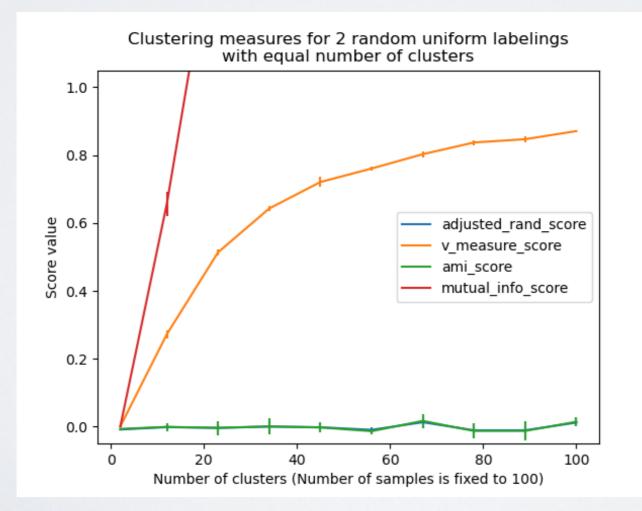
Expected nb of TP

$$E(n_{ij}) = \binom{n_i}{2} \frac{\binom{n_j}{2}}{\binom{n}{2}}$$



### NMI - AMI

- An alternative based on Information Theory is the NMI(Normalized Mutual Information), also called v-score
  - Known to suffer from the exact same problem as Rand Index
  - An adjusted for chance version exist, called AMI (Adjusted Mutual Information)



### INTERNAL EVALUATION

# AD-HOC SCORES

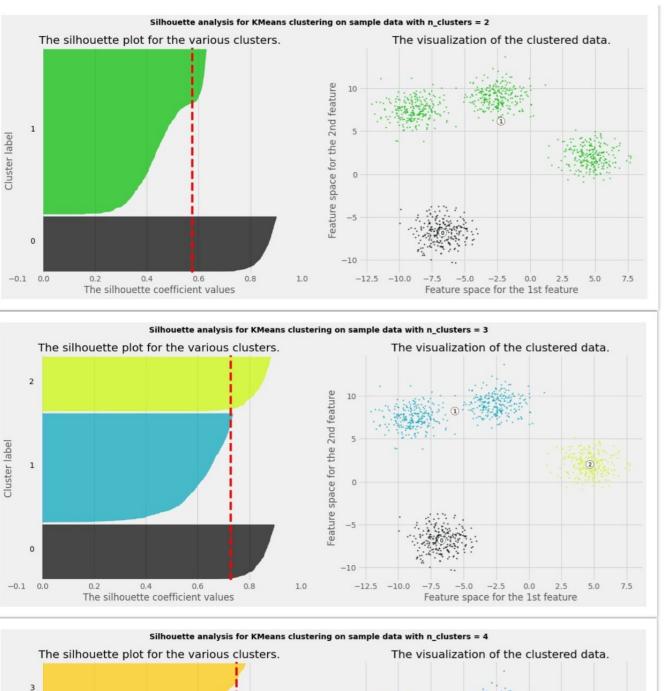
- Several clustering method define their own objective to minimize. This objective can be used as a score for clusters obtained by this method or others
  - k-means minimizes inter-cluster variance
  - Gaussian mixture maximize likelihood
- But can lead to unfair comparison:
  - Using inter-cluster variance to compare k-means and another method such as DBscan is unfair.
    - One explicitly minimizes this objective, the other no...
- As always, the choice of a score is equivalent to choosing a definition of cluster...

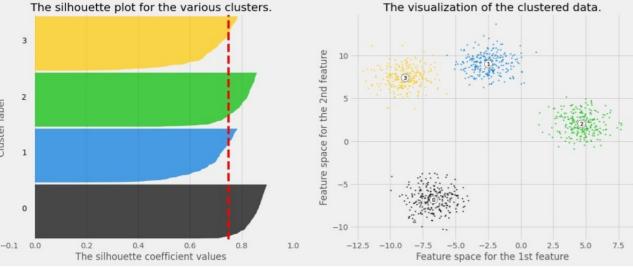
### SILHOUETTE SCORE

- Intrinsic score
- Silhouette score of l item:
  - I)Compute a(i), average distance to all other points of the same cluster
  - 2)Compute b(i), min average distance to all points of another cluster

3) Silhouette:  $s(i) = \begin{cases} 1 - a(i)/b(i), & \text{if } a(i) < b(i) \\ 0, & \text{if } a(i) = b(i) \\ b(i)/a(i) - 1, & \text{if } a(i) > b(i) \end{cases}$ 

- Silhouette coefficient:
  - Average of all individual Silhouette scores.



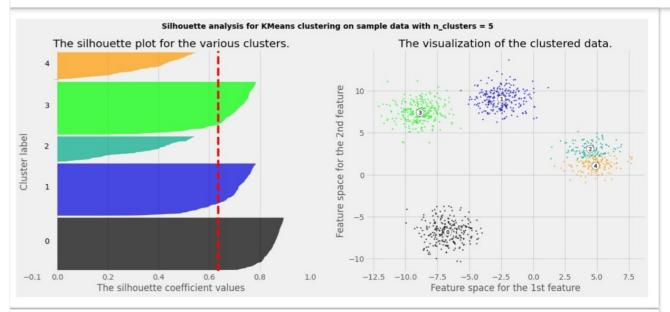


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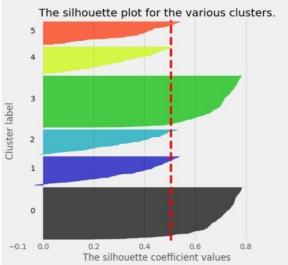
0

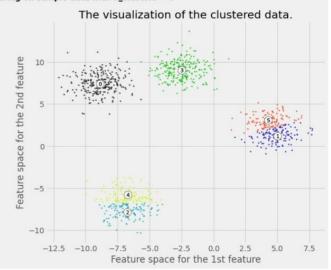
Cluster label



Silhouette analysis for KMeans clustering on sample data with n\_clusters = 6

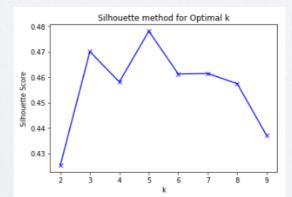
1.0

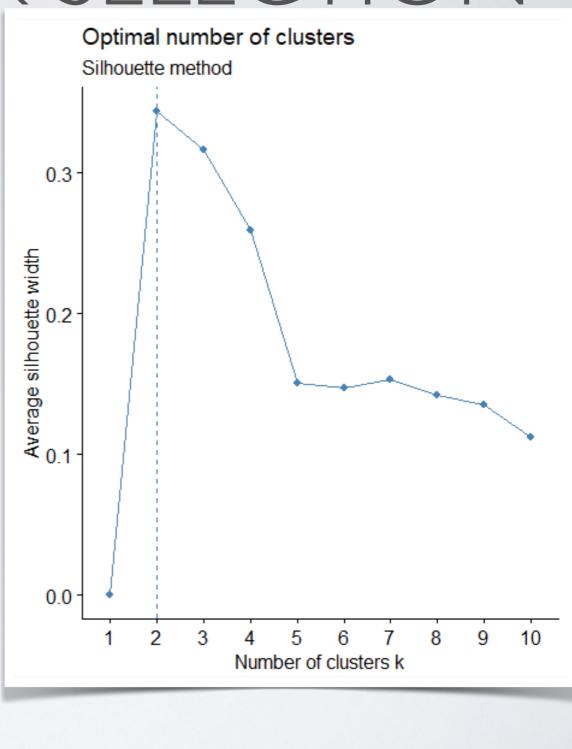




# AUTOMATIC K SELECTION

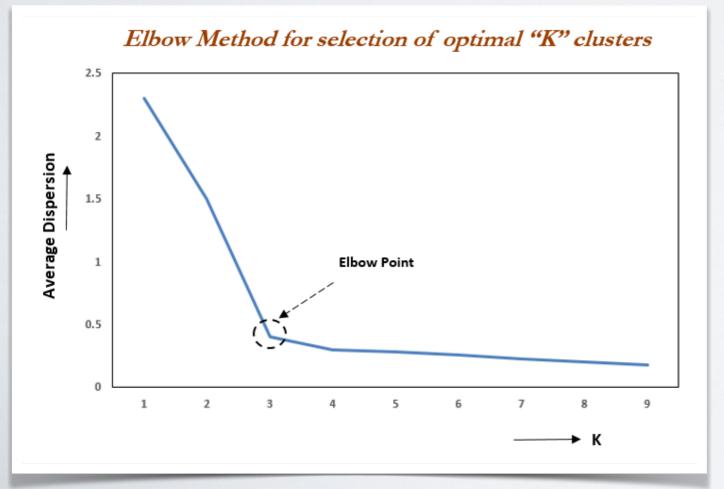
- The Silhouette score can be used to choose automatically the number of clusters:
  - We vary the number of clusters k, and search for the maximum

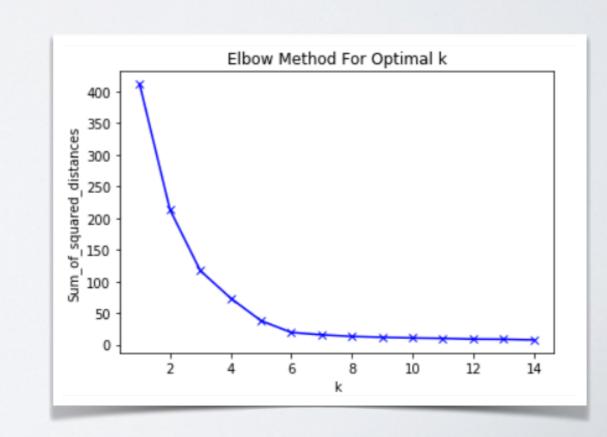




### VARIANT: ELBOW METHOD

- Another well known method to find automatically the number of clusters consists in plotting a measure of quality such as the inter-cluster variance, and cut at an "elbow"
  - Diminishing returns=> less 'worthy' to continue





# NO FREE LUNCH THEOREM

- "Any two optimization algorithms are equivalent when their performance is averaged across all possible problems"
  - Two clustering algorithms with different objective functions are fully comparable, one is not intrinsically better than another.
  - Each is the best for the objective function it defines
  - What is "the best" cluster? Depends on your definition.
- Does not mean that some methods are not more appropriate than other for what most people consider as clusters...