

# Clustering

Emma Yu and Jaya Zenchenko

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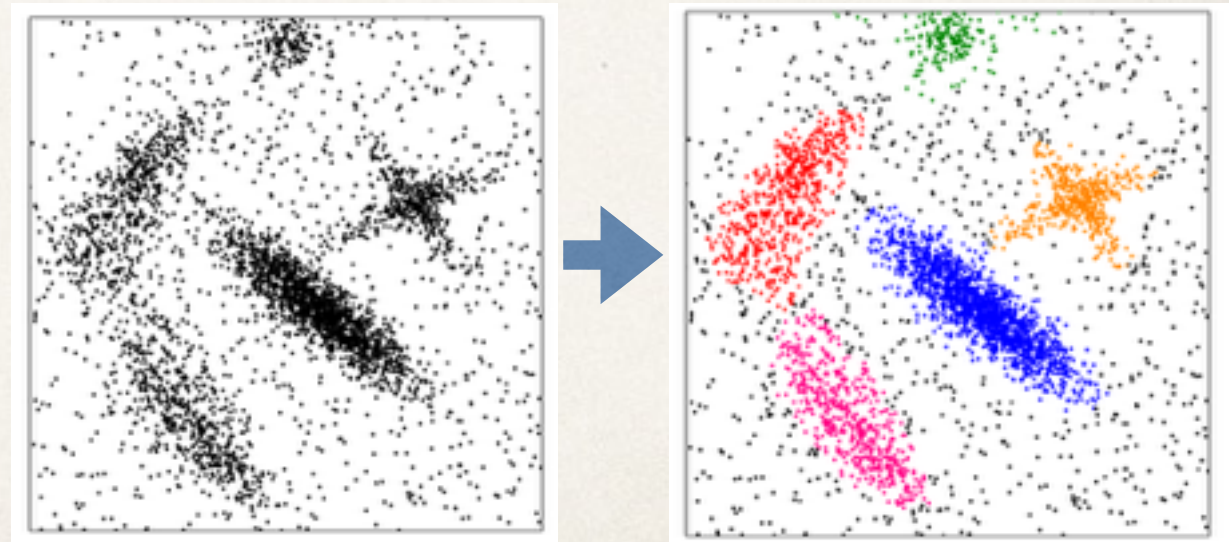
Slides adapted from David Blei, David Sontag, Piyush Rai, Jure Leskove, Anand Rajaraman, Shimon Ullman and Elena Marchiori

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# What is clustering?

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- ❖ Given a set of data points, group them into clusters so that:
  - points within each cluster are similar to each other
  - points from different clusters are dissimilar
- ❖ Requires data, but no labels





# Why would we want to do this?

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- ❖ Group customers according to purchase histories
- ❖ Group search results according to topics
- ❖ Detect regions of images
- ❖ Clustering gene expression data

K=2



K=3



K=10



Original



4%



8%



17%





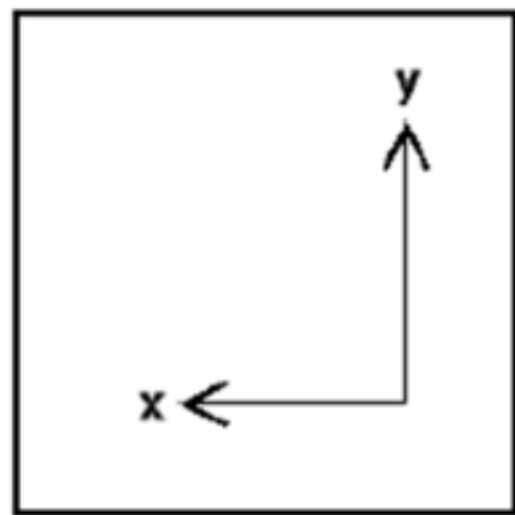
# what does similar mean, exactly?

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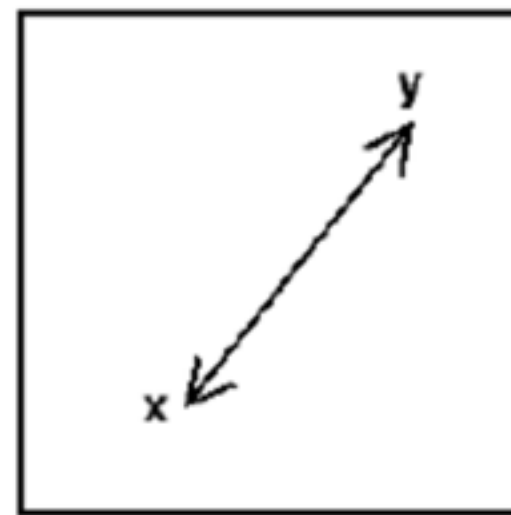
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- ❖ It depends on how we define the distance / similarity
- ❖ Euclidean distance, Manhattan (L1) distance



**Manhattan**

$$\sum_{i=1}^d |a_i - b_i|.$$



**Euclidean**

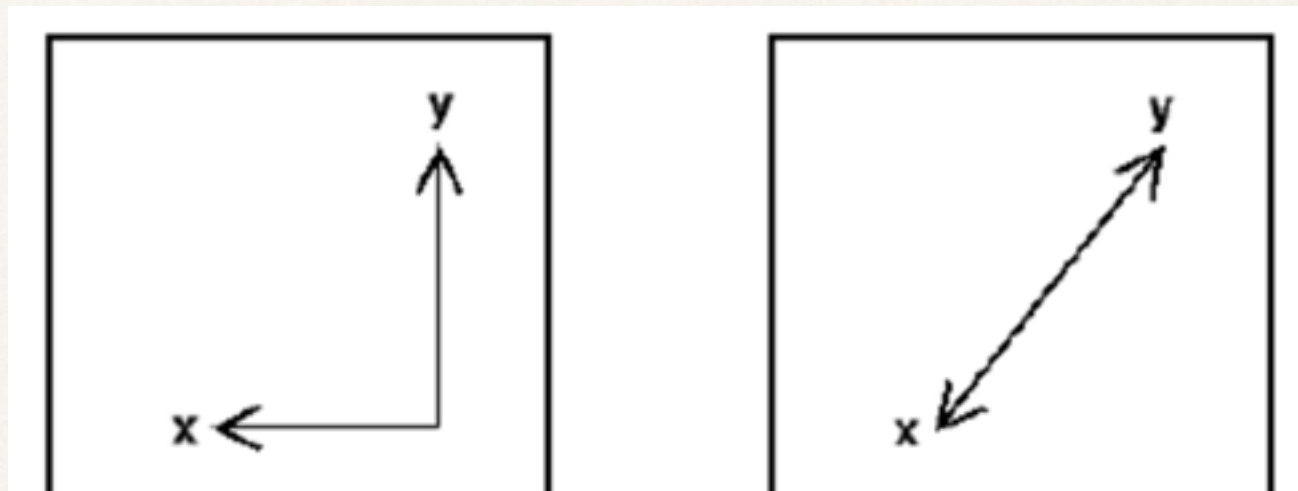
$$\sqrt{\sum_{i=1}^d (a_i - b_i)^2}.$$



# what does similar mean, exactly?

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They are special cases of **Minkowski distance**:

$$d_p(\mathbf{x}_i, \mathbf{x}_j) = \left( \sum_{k=1}^m |x_{ik} - x_{jk}|^p \right)^{\frac{1}{p}}$$

❖ Jaccard distance

$$\mathbf{d}_J(A, B) = 1 - \mathbf{JS}(A, B) = 1 - \frac{|A \cap B|}{|A \cup B|},$$

❖ Cosine distance

$$\mathbf{d}_{\cos}(a, b) = 1 - \frac{\langle a, b \rangle}{\|a\| \|b\|} = 1 - \frac{\sum_{i=1}^d a_i b_i}{\|a\| \|b\|}$$



# How do we do it?

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- ❖ Partition algorithms: determine all clusters at once.
- ❖ Hierarchical algorithms (agglomerative): find successive clusters using previously established clusters.
  - Do not need the number of clusters as an input, and can be viewed at different levels of granularities with different  $k$

# K-means

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- ❖ A partition algorithm
- ❖ Basic idea: to describe each cluster by its mean value
- ❖ Goal: find the assignment of  $k$  clusters that minimizes the sum of square distance of cluster members to their cluster centers.



## ① Initialization

- Data are  $\mathbf{x}_{1:N}$
- Choose initial cluster means  $\mathbf{m}_{1:k}$  (same dimension as data).

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## ② Repeat

- ① Assign each data point to its closest mean

$$z_n = \arg \min_{i \in \{1, \dots, k\}} d(\mathbf{x}_n, \mathbf{m}_i)$$



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## 2 Repeat

- 1 Assign each data point to its closest mean

$$z_n = \arg \min_{i \in \{1, \dots, k\}} d(\mathbf{x}_n, \mathbf{m}_i)$$

- 2 Compute each cluster mean to be the coordinate-wise average over data points assigned to that cluster,

$$\mathbf{m}_k = \frac{1}{N_k} \sum_{\{n : z_n = k\}} \mathbf{x}_n$$

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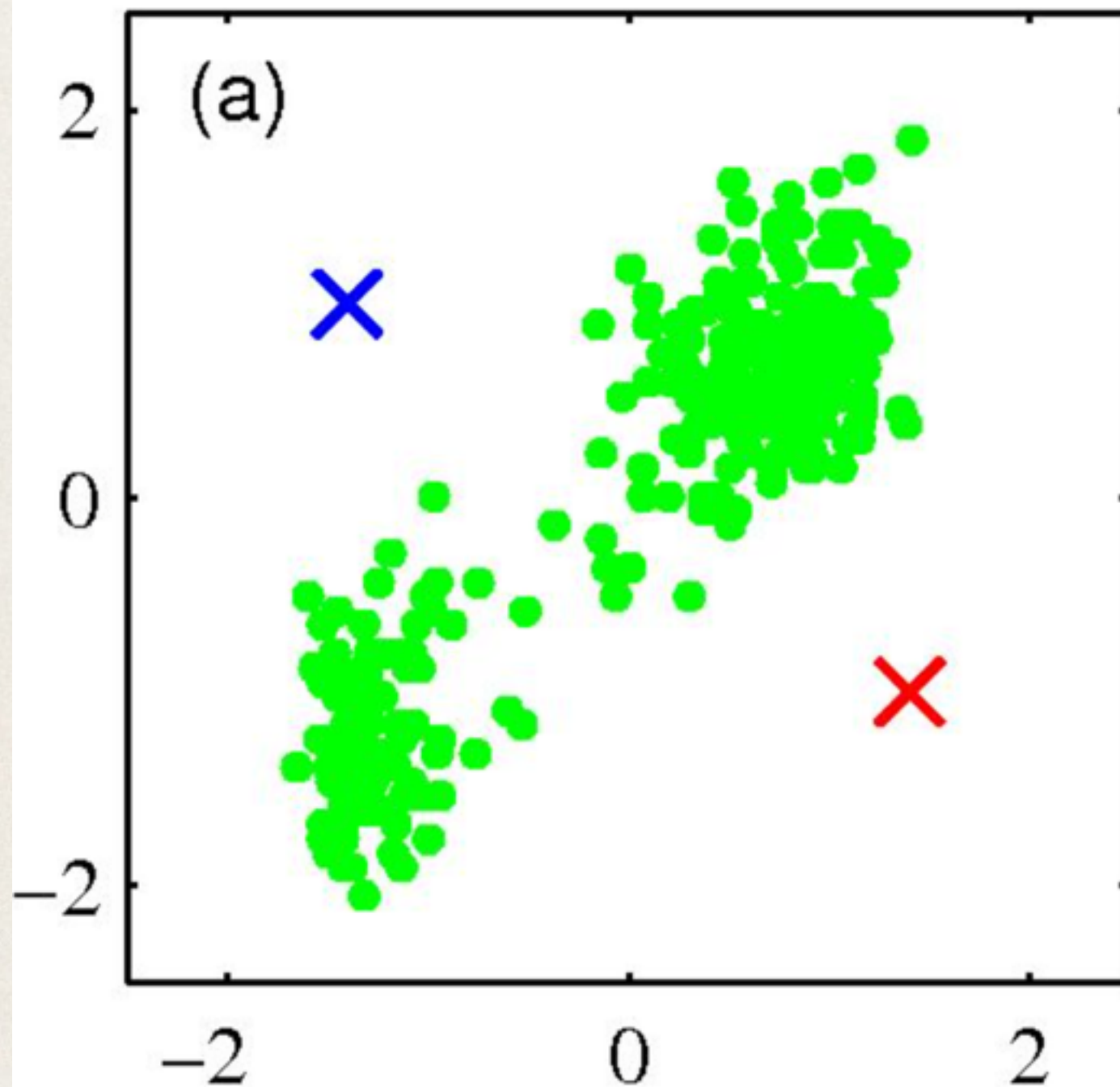
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- 3 Until assignments  $\mathbf{z}_{1:N}$  do not change



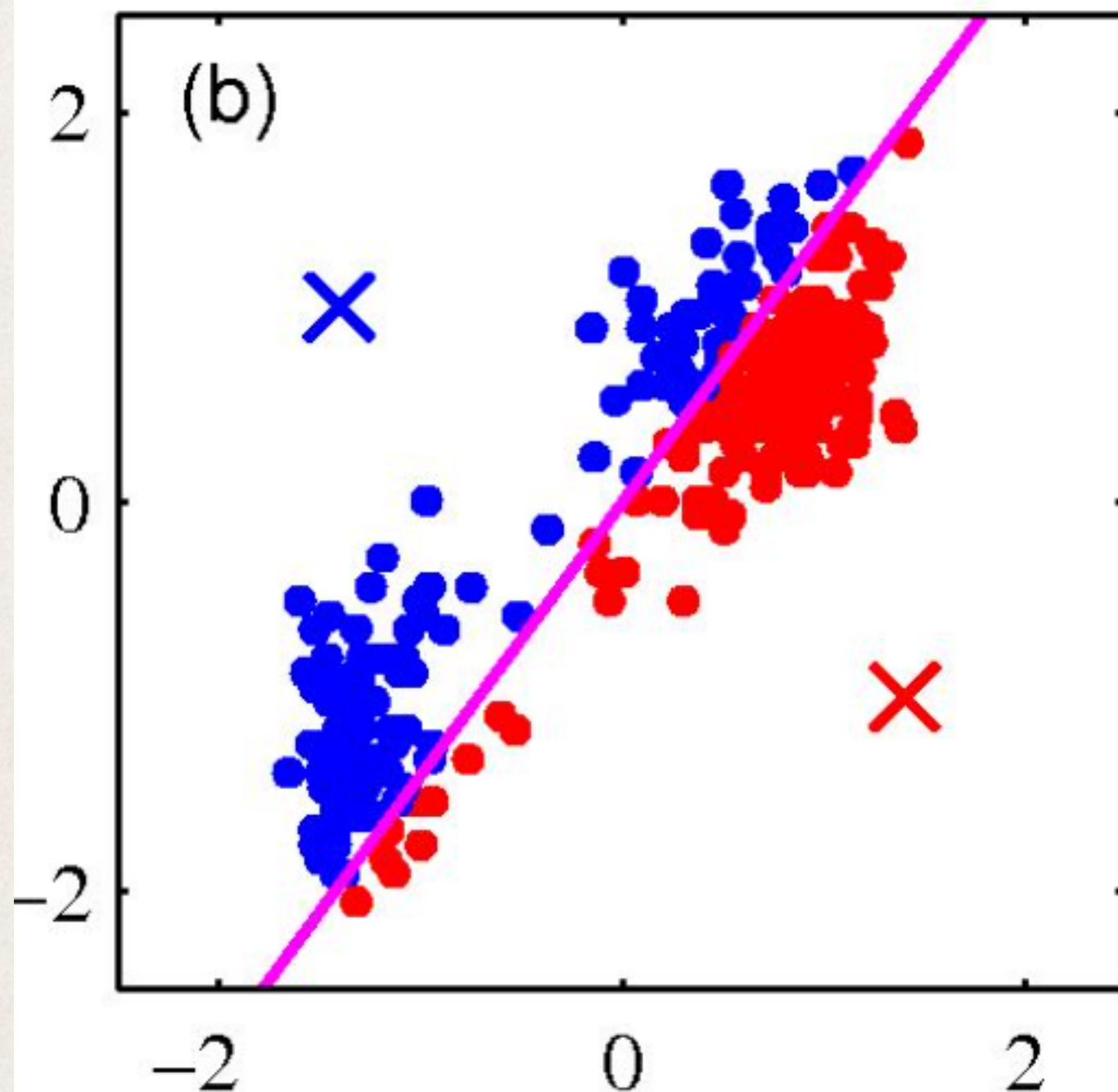
# K-means — an example



- Pick  $K$  random points as cluster centers (means)

Shown here for  $K=2$

# K-means — an example

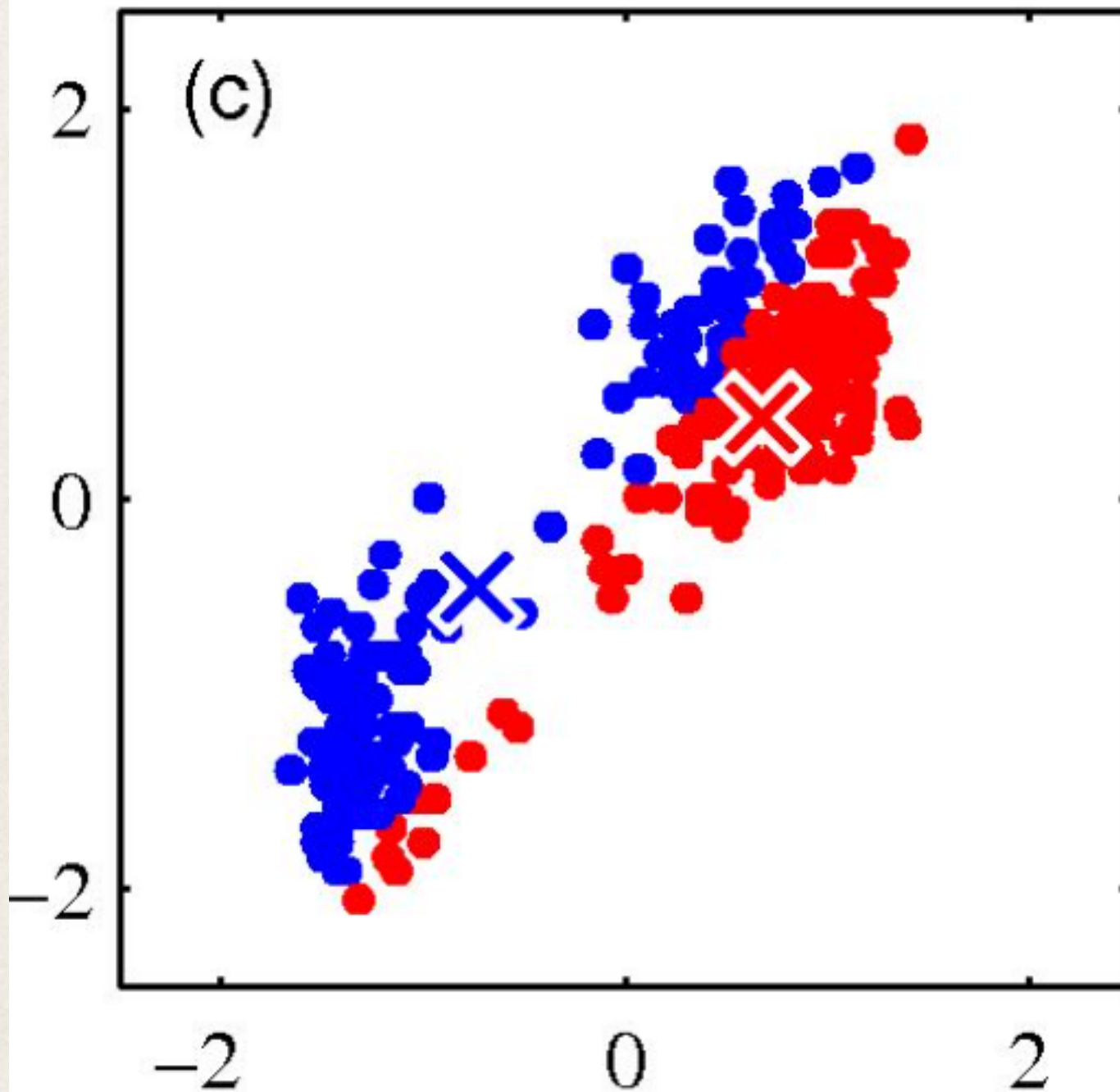


## Iterative Step 1

- Assign data points to closest cluster center



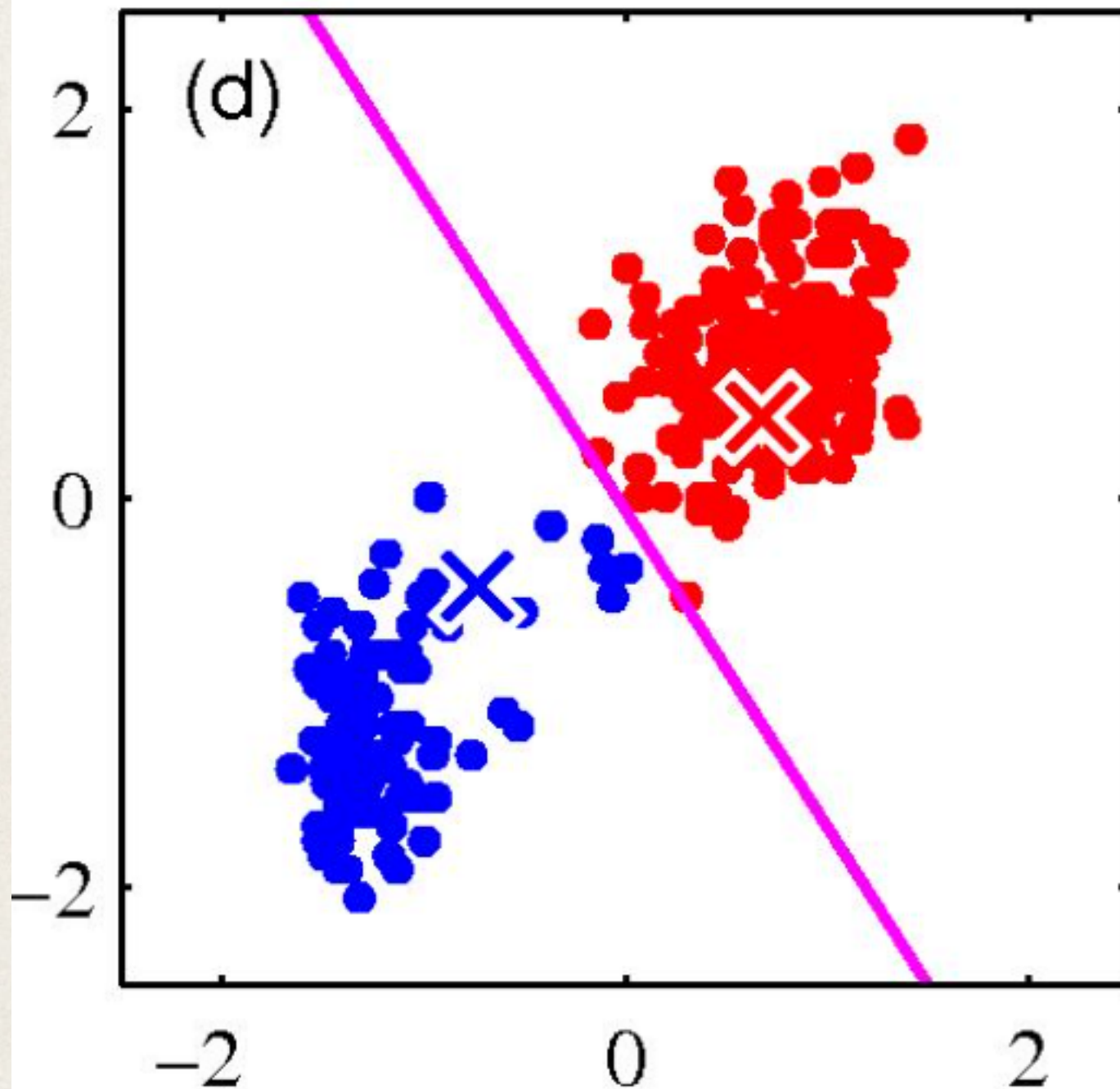
# K-means — an example



## Iterative Step 2

- Change the cluster center to the average of the assigned points

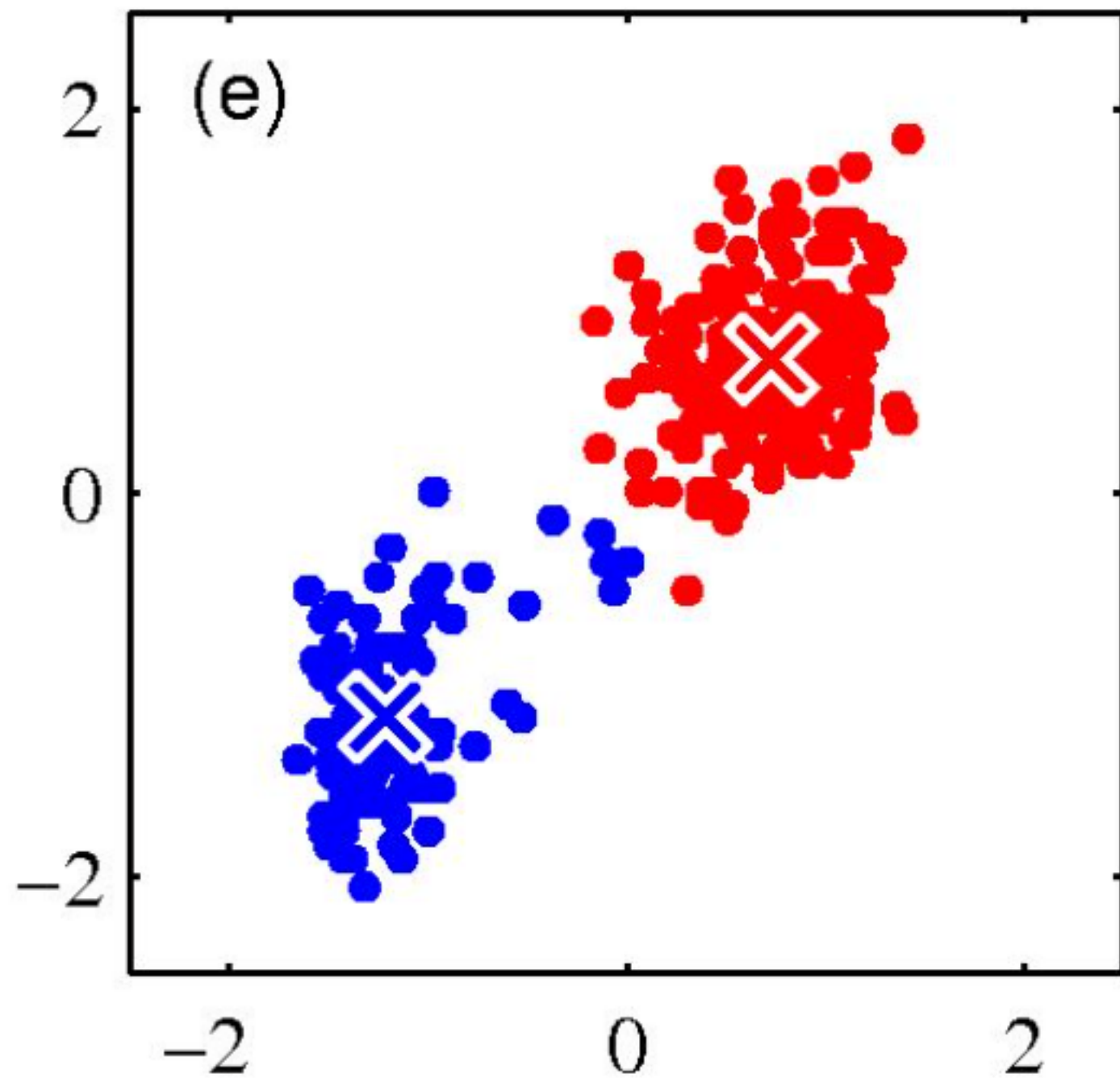
# K-means — an example



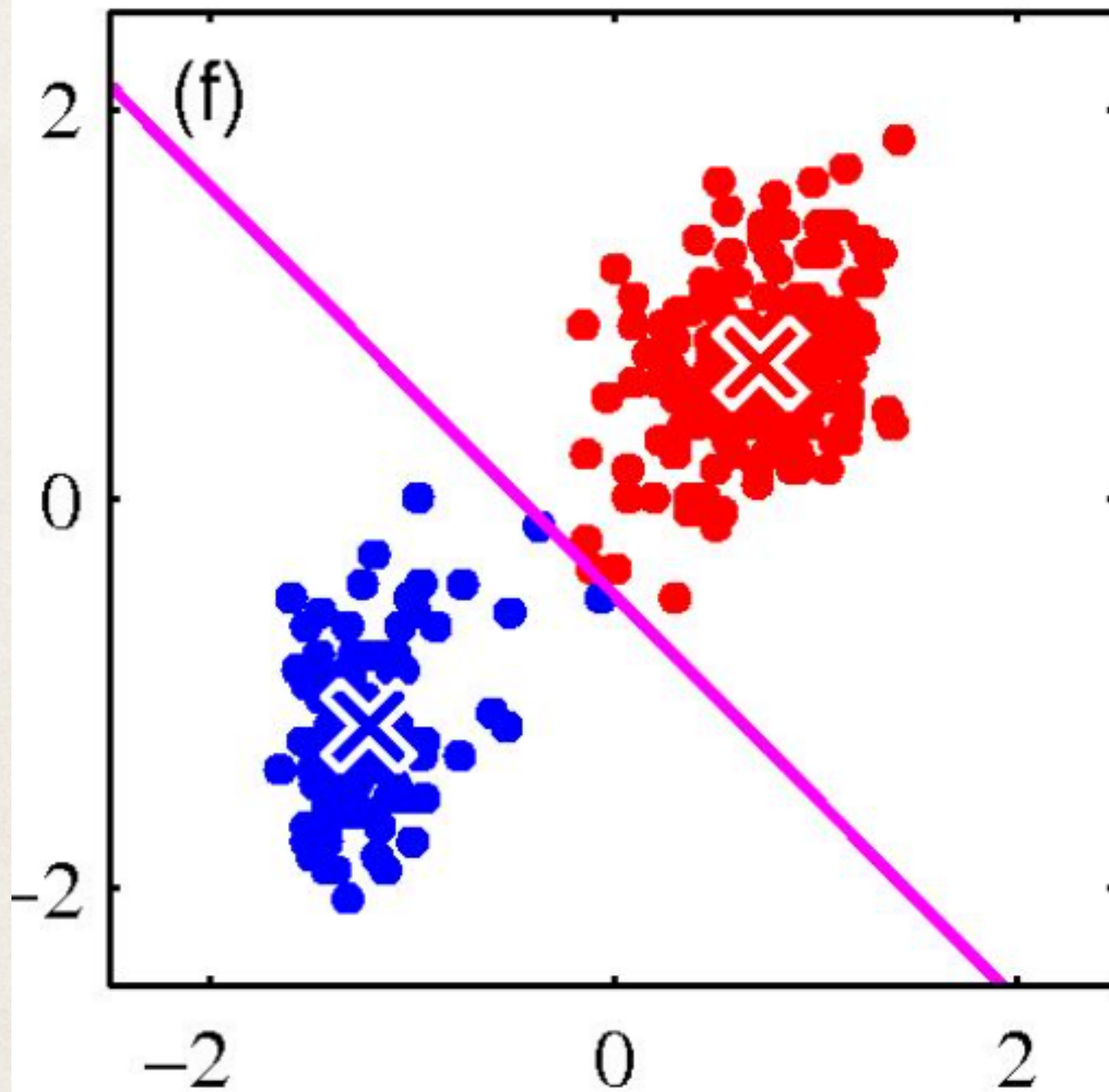
- Repeat until convergence



# K-means — an example



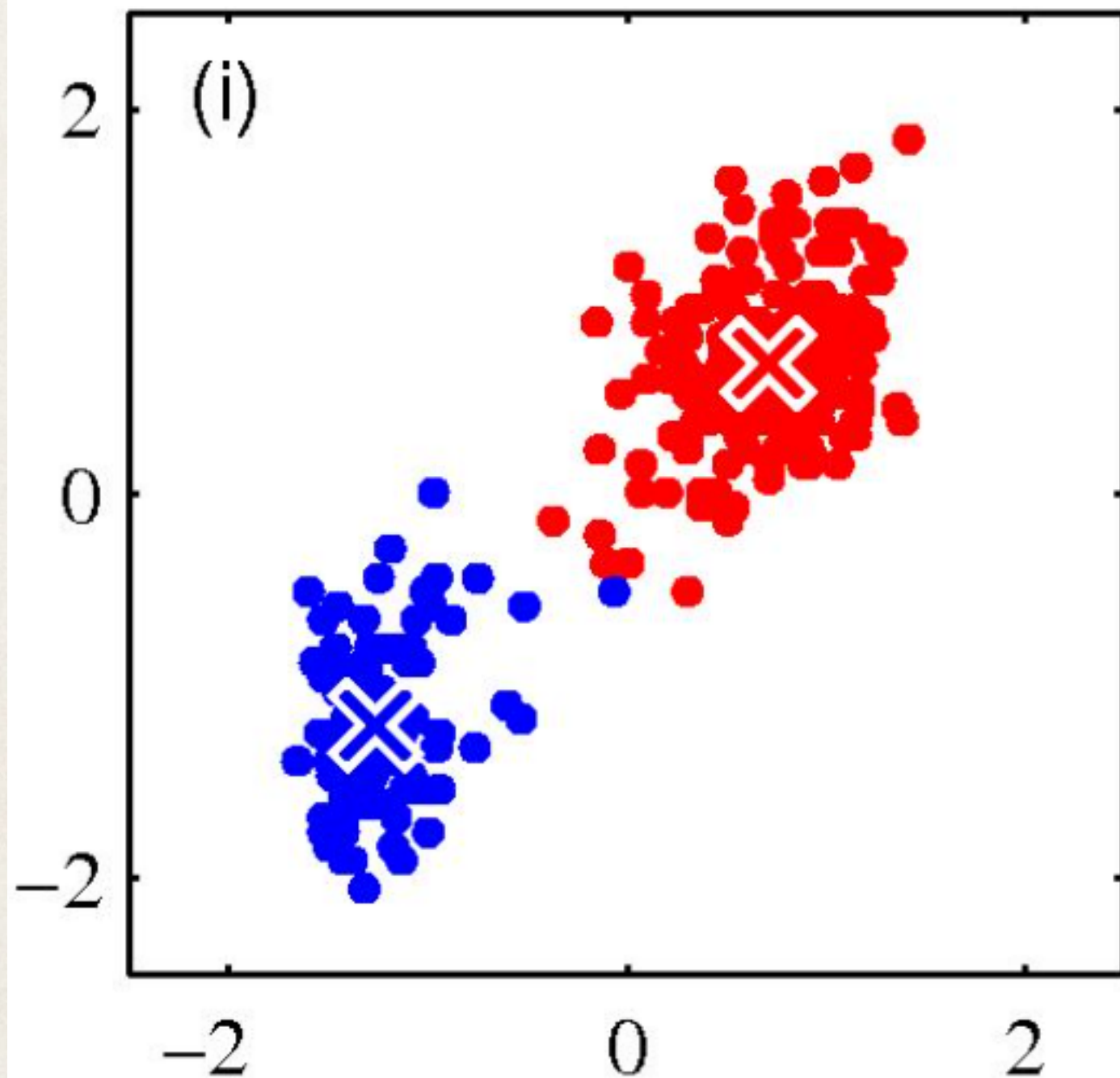
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# K-means — an example

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# Coordinate descent

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$$F(z_{1:N}, \mathbf{m}_{1:k}) = \frac{1}{2} \sum_{n=1}^N \|\mathbf{x}_n - \mathbf{m}_{z_n}\|^2$$

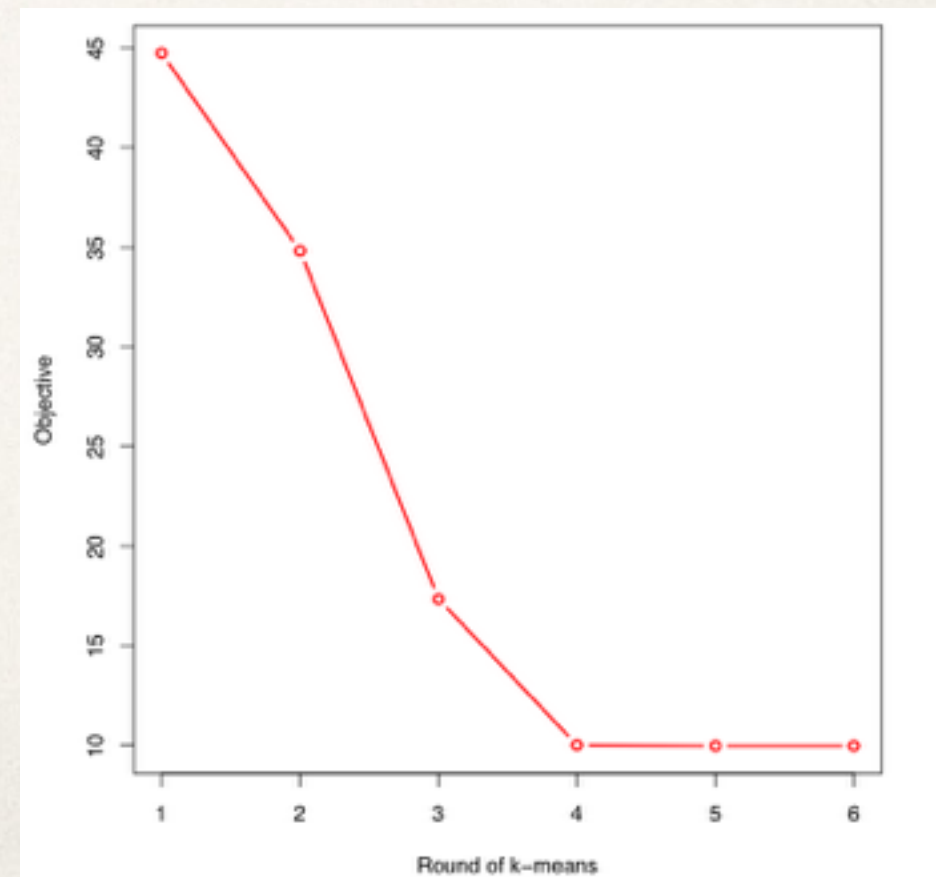
- Holding the means fixed, assigning each point to its closest mean minimizes  $F$  with respect to  $z_{1:N}$ .
- Holding the assignments fixed, computing the centroids of each cluster minimizes  $F$  with respect to  $\mathbf{m}_{1:k}$ .



# When to stop?

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- ❖ No (or minimum) re-assignment of data points to different clusters, or
- ❖ no (or minimum) change of centroids, or
- ❖ minimum decrease in the sum of squared error



# Knobs to turn:

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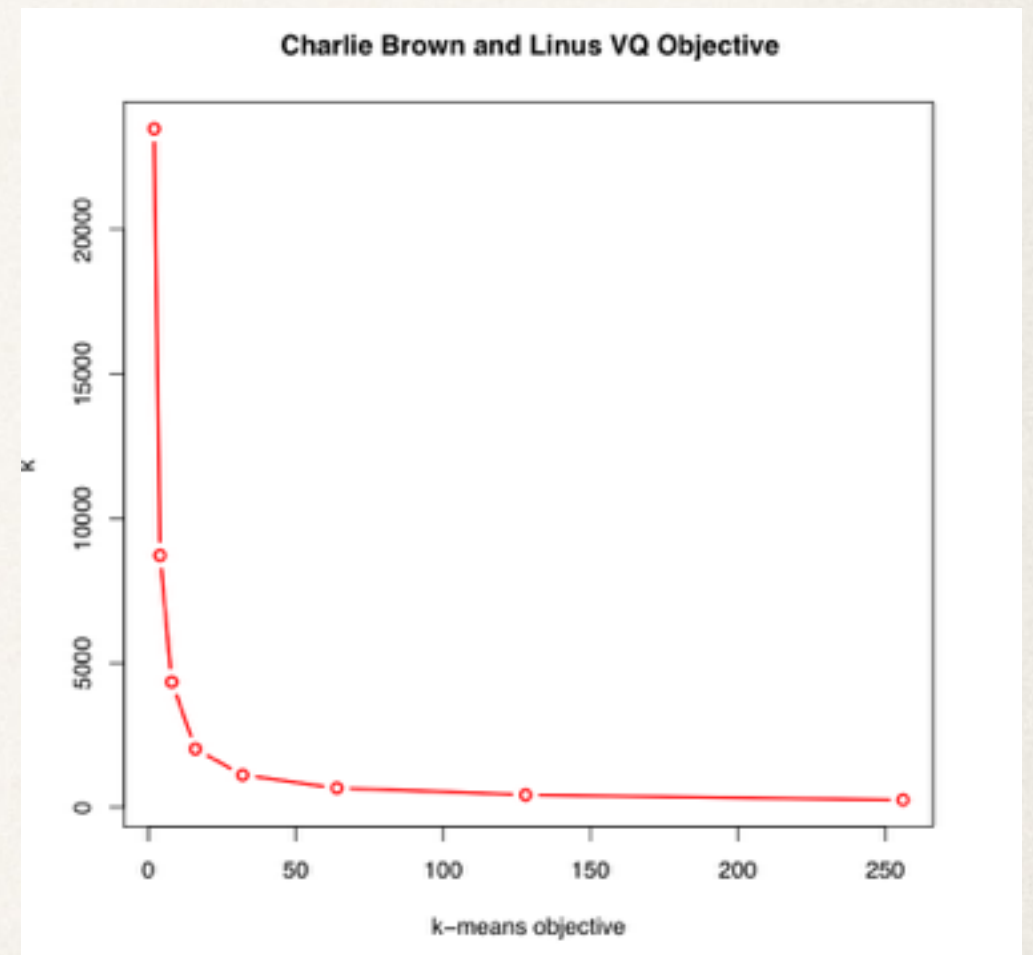
- ❖ a distance measure between data points
- ❖ number of clusters  $k$
- ❖ initial assignment of data to clusters



# How to choose K?

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- ❖ Base on the required quality in the image compressing case
- ❖ Base on limits in real life applications
- ❖ Heuristic: a kink in the objective function



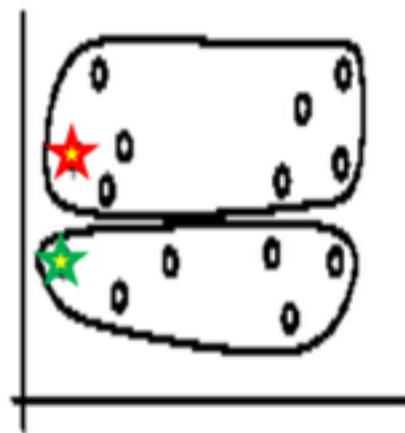
- ❖ K-mean algorithm finds the local minimum and is sensitive to initialization



Random selection of seeds (centroids)



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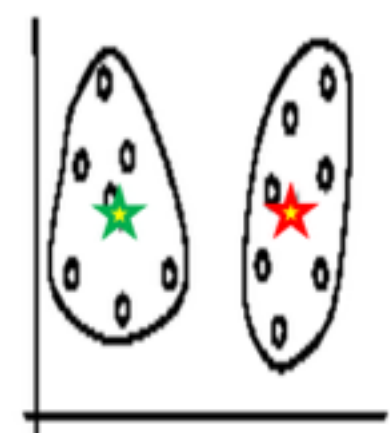
Iteration 1



Iteration 2



Iteration 1



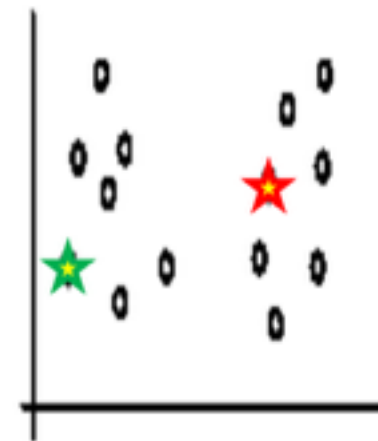
Iteration 2



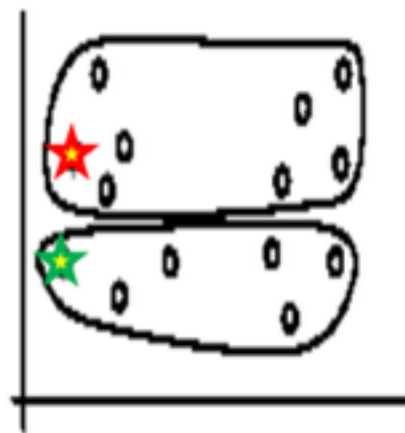
- ❖ K-mean algorithm finds the local minimum and is sensitive to initialization
  - ❖ Try multiple initiations and choose the best result



Random selection of seeds (centroids)



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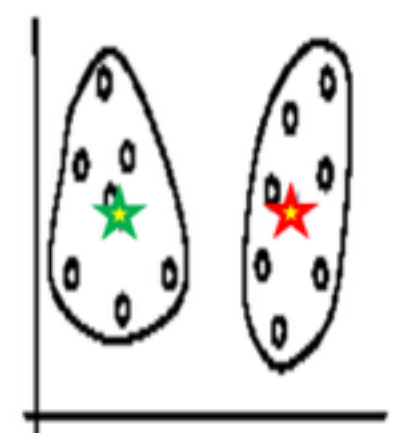
Iteration 1



Iteration 2

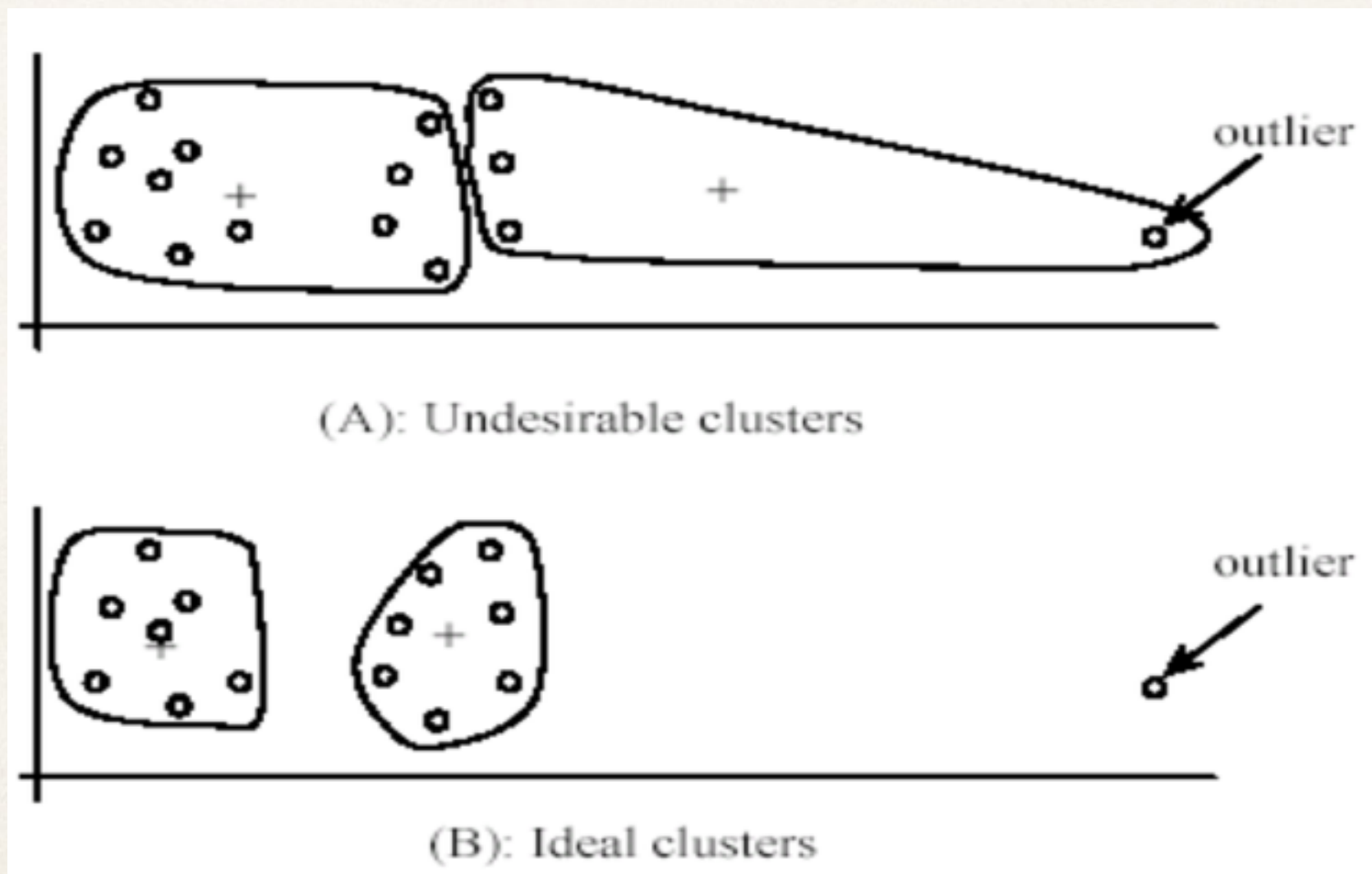


Iteration 1



Iteration 2

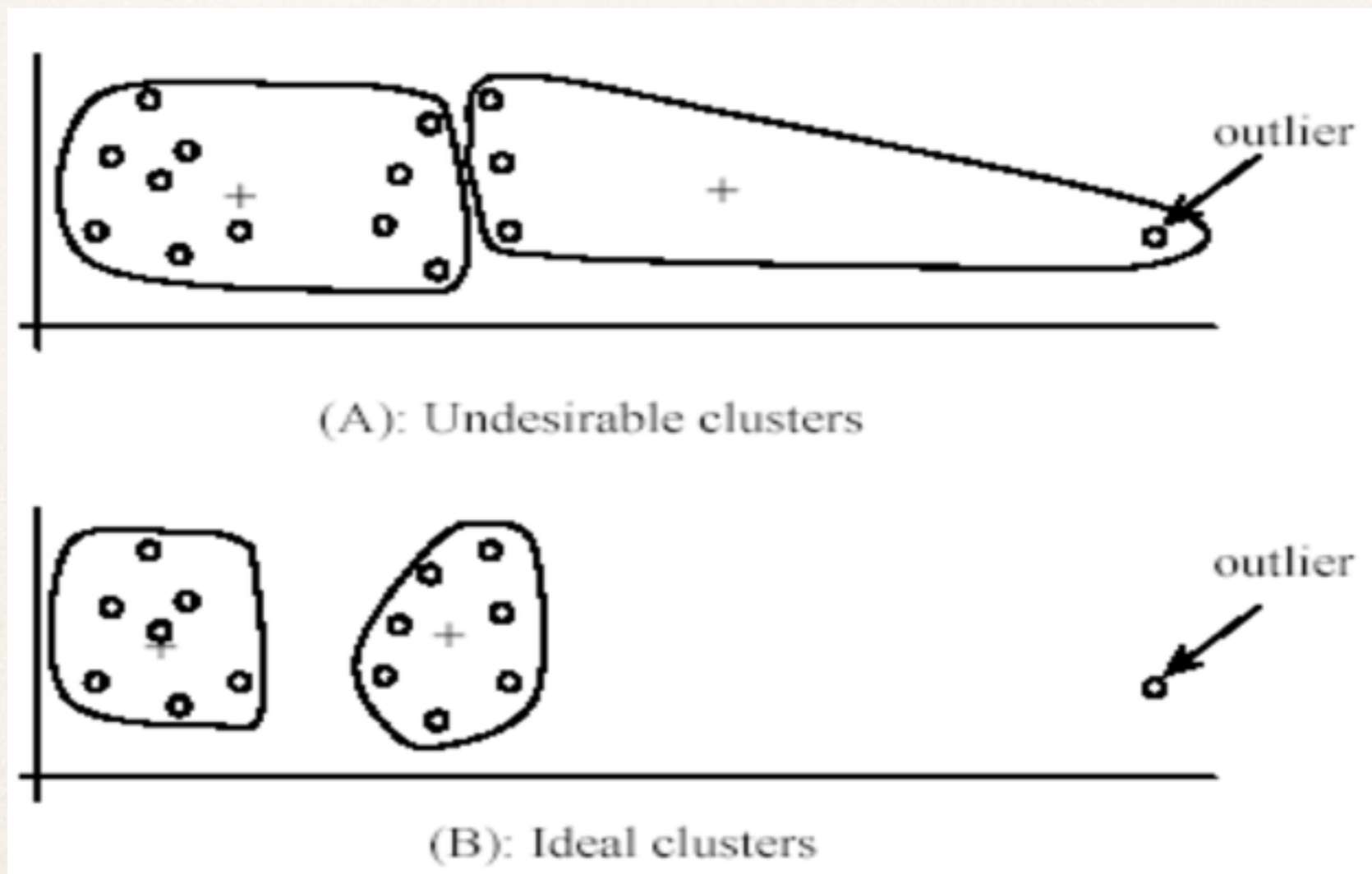
- ❖ k-mean algorithm is sensitive to outliers



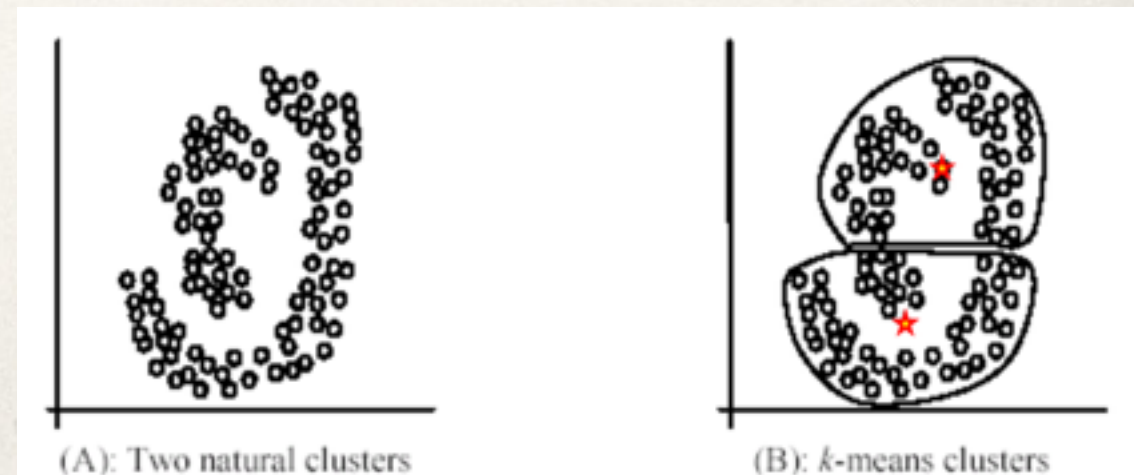


- ❖ k-mean algorithm is sensitive to outliers

- ❖ Remove outliers, resample, or use medians



- ❖ K-means is efficient to compute -  $O(tkn)$  (t is the number of iteration)
- ❖ K-means requires hard assignment - a point either belongs to a cluster or not. Other methods such as gaussian mixture models and fuzzy k-means allow one to assign a point to multiple clusters with certain probabilities
- ❖ K-means works well with round shaped clusters of roughly equal sizes and densities





# Hierarchical clustering

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- ❖ Basic idea: Initially, each point is a cluster by itself. Repeatedly combine the two “nearest” clusters into one.
- ❖ It only requires a measure of similarity between groups of data points
- ❖ It's up to the user to choose a “natural” clustering from the merging sequence

# How to define “closest” for clusters?

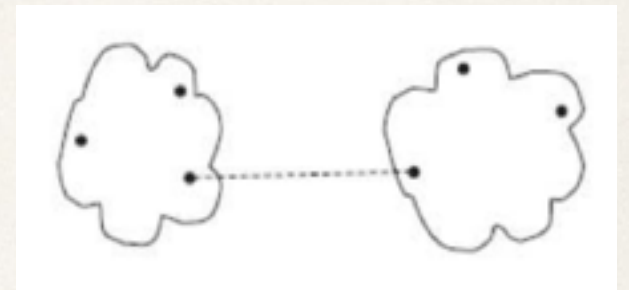
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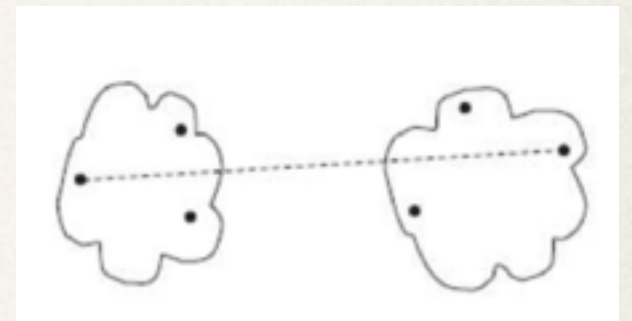
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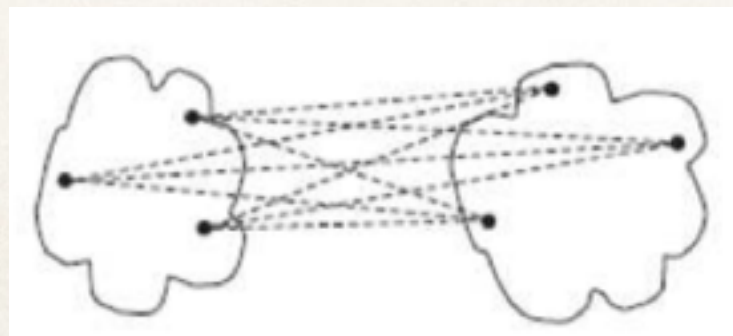
- ❖ Closest pair: single - link clustering



- ❖ Farthest pair: complete-link clustering



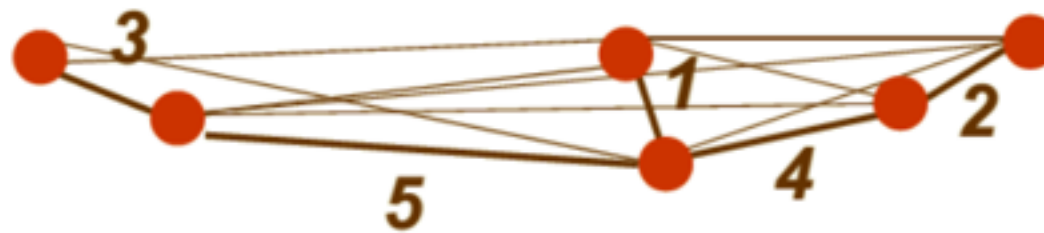
- ❖ Average similarity between groups: group average clustering



# Single linkage

- Agglomerative clustering with minimum distance

$$d_{\min}(D_i, D_j) = \min_{x \in D_i, y \in D_j} \|x - y\|$$



- generates minimum spanning tree
- encourages growth of elongated clusters
- disadvantage: very sensitive to noise

*what we want at level with  $c=3$*



*noisy sample*

*what we get at level with  $c=3$*



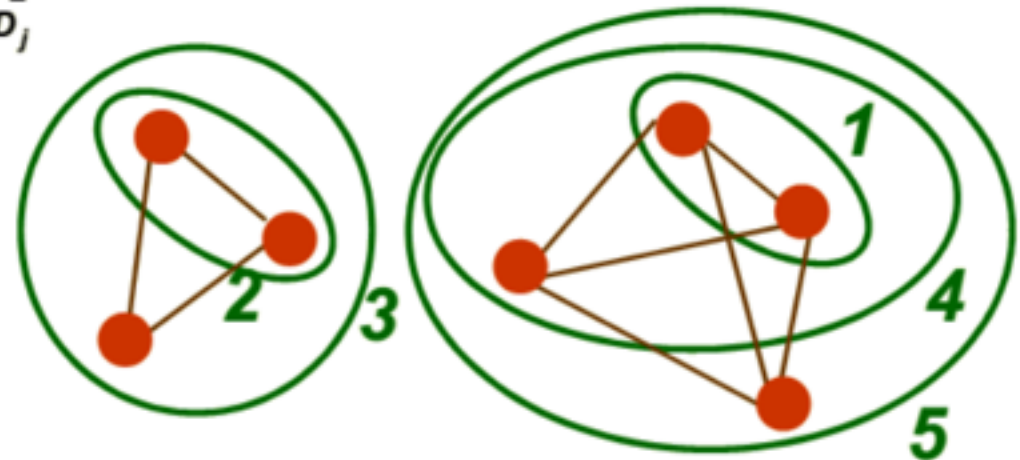


# Complete linkage

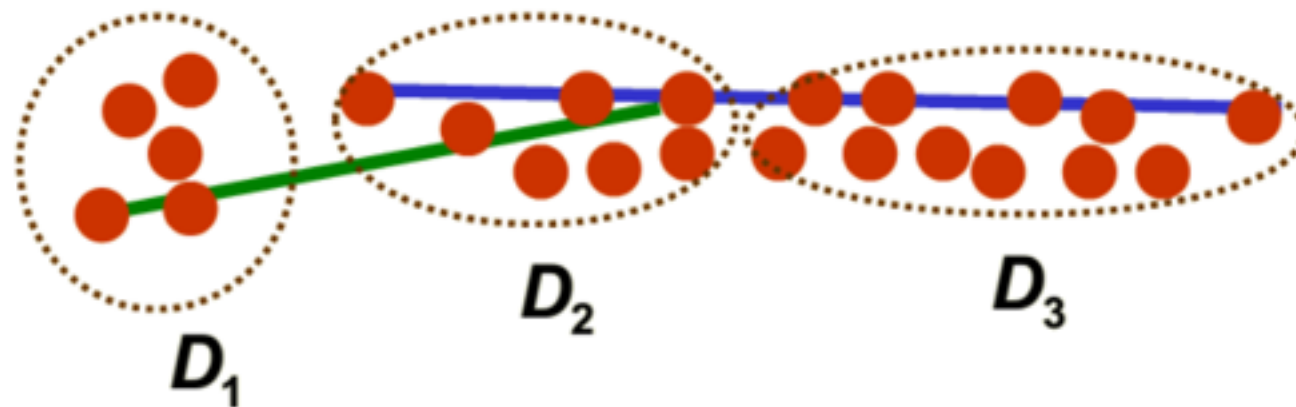
- Agglomerative clustering with maximum distance

$$d_{\max}(D_i, D_j) = \max_{x \in D_i, y \in D_j} \|x - y\|$$

- encourages compact clusters



- Does not work well if elongated clusters present



- $d_{\max}(D_1, D_2) < d_{\max}(D_2, D_3)$
- thus  $D_1$  and  $D_2$  are merged instead of  $D_2$  and  $D_3$

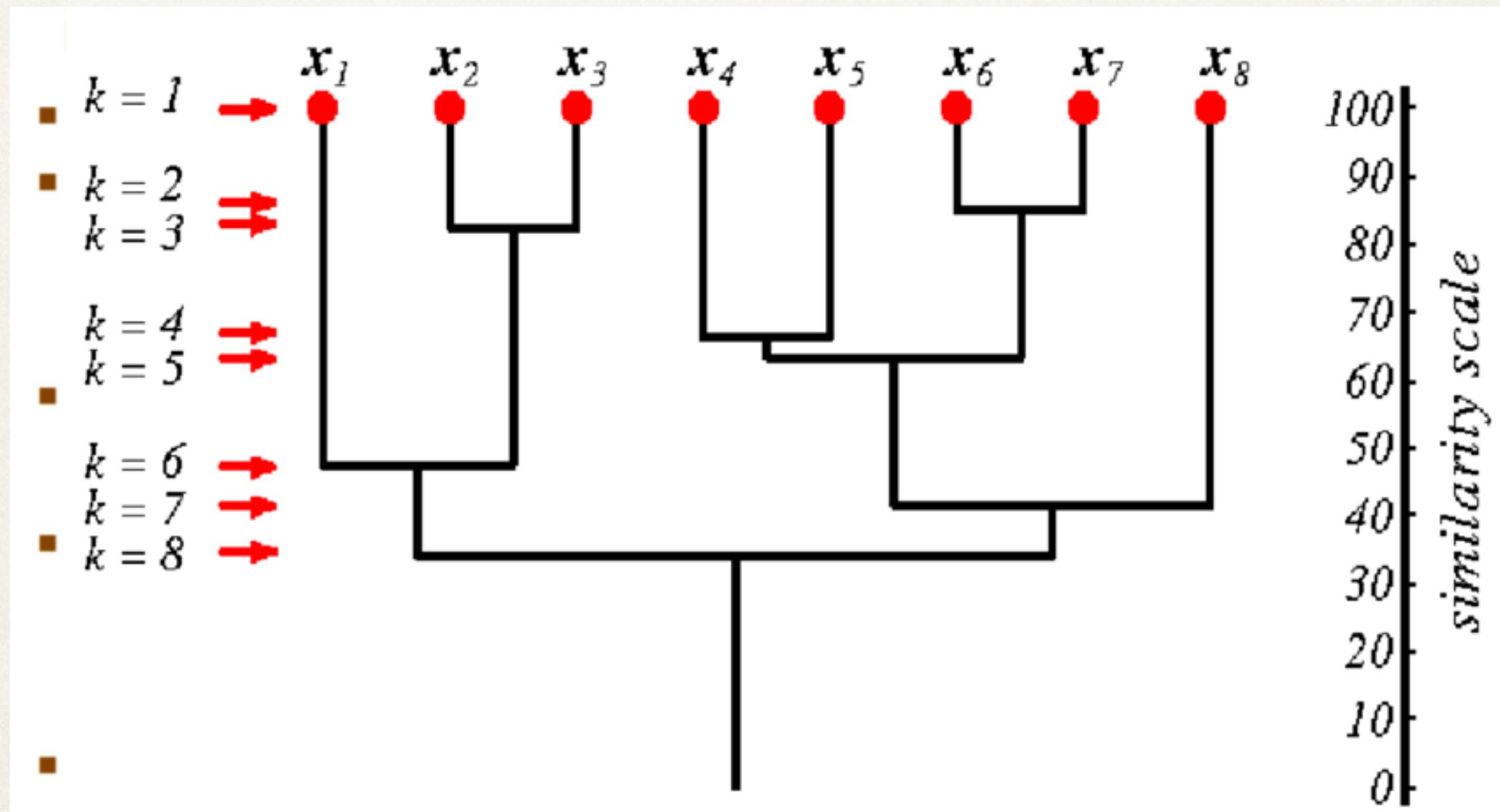
# When to stop?

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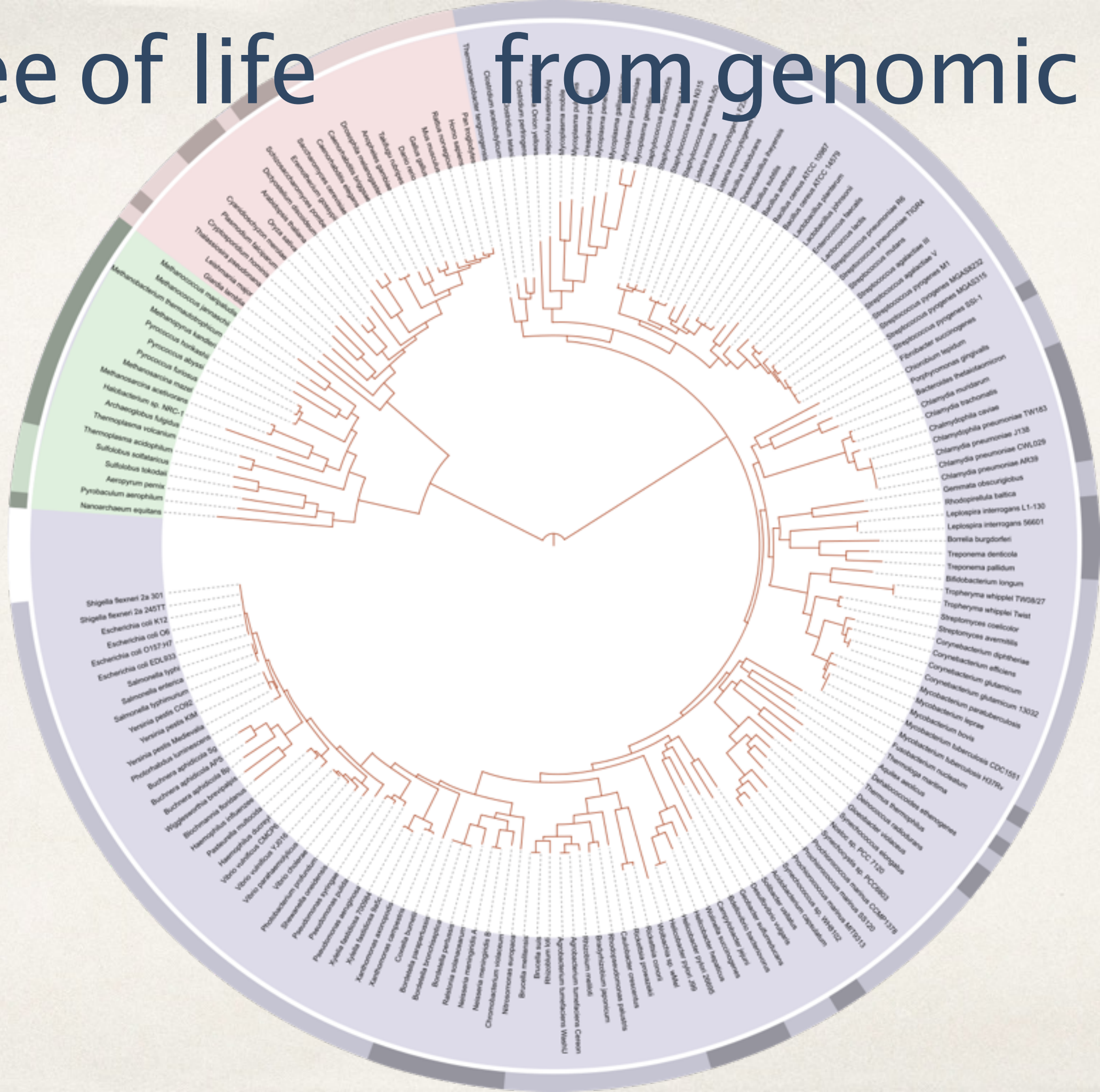
- ❖ Stop when we have  $k$  clusters
- ❖ Stop when cohesion of the cluster resulting from the best merger falls below a threshold
- ❖ Stop when there is a sudden jump in the cohesion value



# Visualizing with a dendrogram



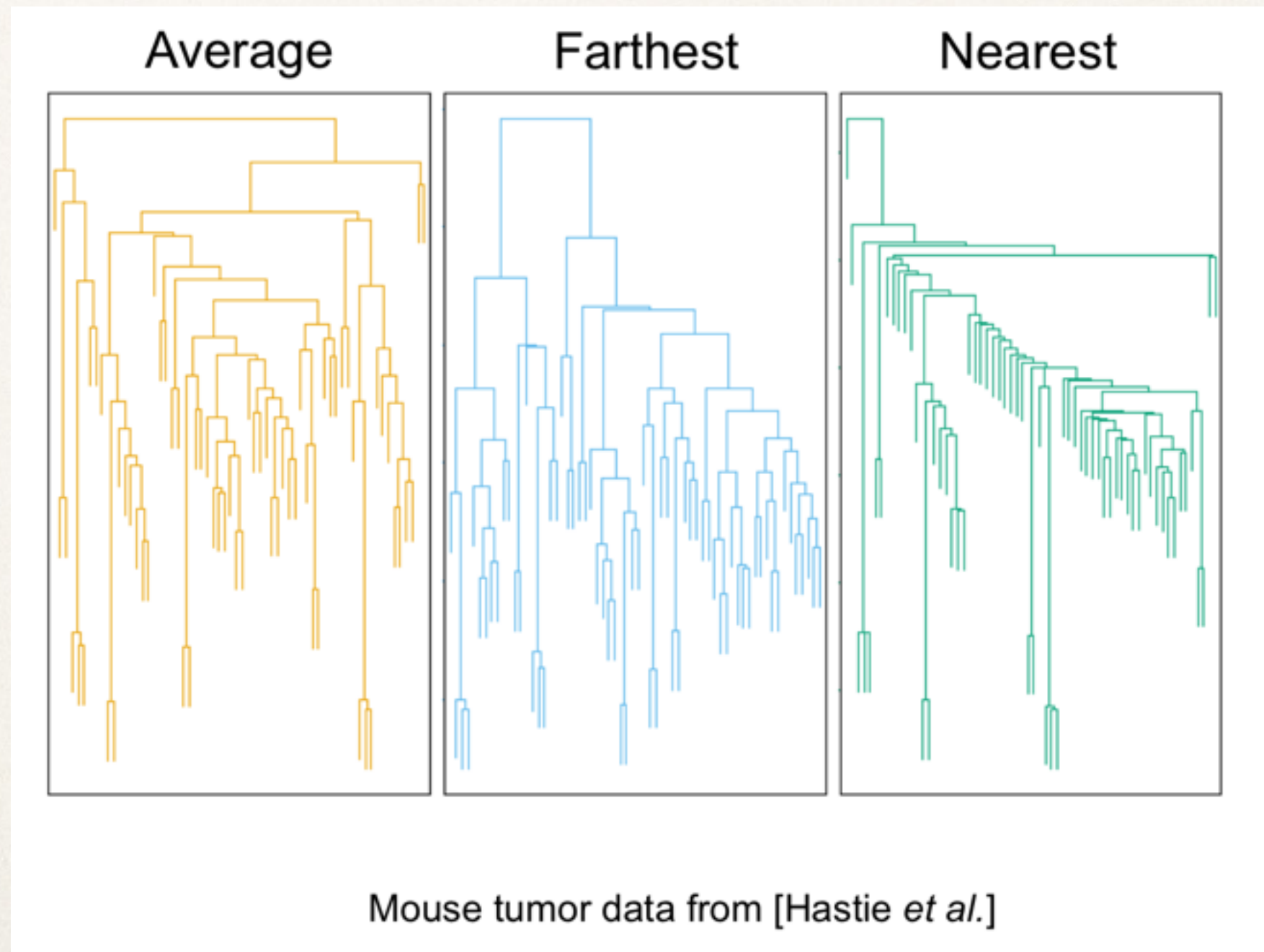
# Tree of life from genomic data





# Caveats

- ❖ Different decisions about group similarities can lead to vastly different dendrograms



- ❖ Be cautious! The algorithm imposes a hierarchical structure on the data, even when it's not appropriate
- ❖ It's quite expensive to compute pairwise distances between each pair of cluster (naive implementation  $O(N^3)$ , with a priority queue  $O(N^2 \log N)$ )



Demo time!

# Useful materials

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- ❖ Distance metrics:
- ❖ [http://www.improvedoutcomes.com/docs/WebSiteDocs/Clustering/Clustering\\_Parameters/Distance\\_Metrics\\_Overview.htm](http://www.improvedoutcomes.com/docs/WebSiteDocs/Clustering/Clustering_Parameters/Distance_Metrics_Overview.htm)
- ❖ <http://scikit-learn.org/stable/modules/generated/sklearn.neighbors.DistanceMetric.html>
- ❖ <https://www.cs.utah.edu/~jeffp/teaching/cs5955/L7-Distances.pdf>