

<https://github.com/tedinburgh/ads2023>

# Clustering: k-means

Tom Edinburgh  
te269

# Example classes

- There are 2 more small group classes, next week and the following week
- Groups/times will be confirmed very soon
- Next week's class: decision trees
  - Chapter 8 of Introduction to Statistical Learning with Python
  - Questions 4, 5, 9, 10, 12 (ignore BART in Q12)
  - Pdf of the book available at <https://www.statlearning.com/>
  - .csv files are at <https://www.statlearning.com/resources-python>

# Recap recap: do you need to mean-centre for PCA?

- It depends how you define things
- $Q = X^T X / (n - 1)$  is the sample covariance, but only because we'd mean-centred first
- Initially, we defined  $Q$  as the sample covariance for non-centred data
- Sometimes, implementations use  $X^T X$  without subtracting the mean from  $X$  first
- This will lead to the issue with the first component

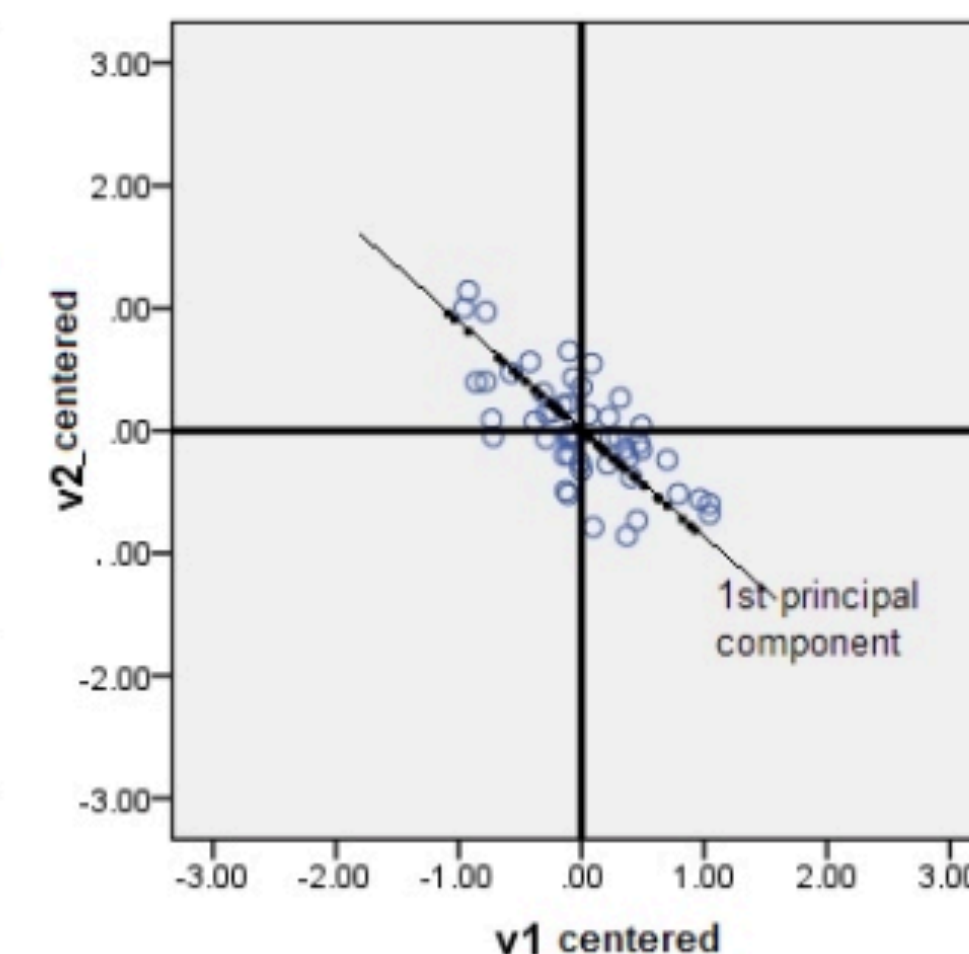
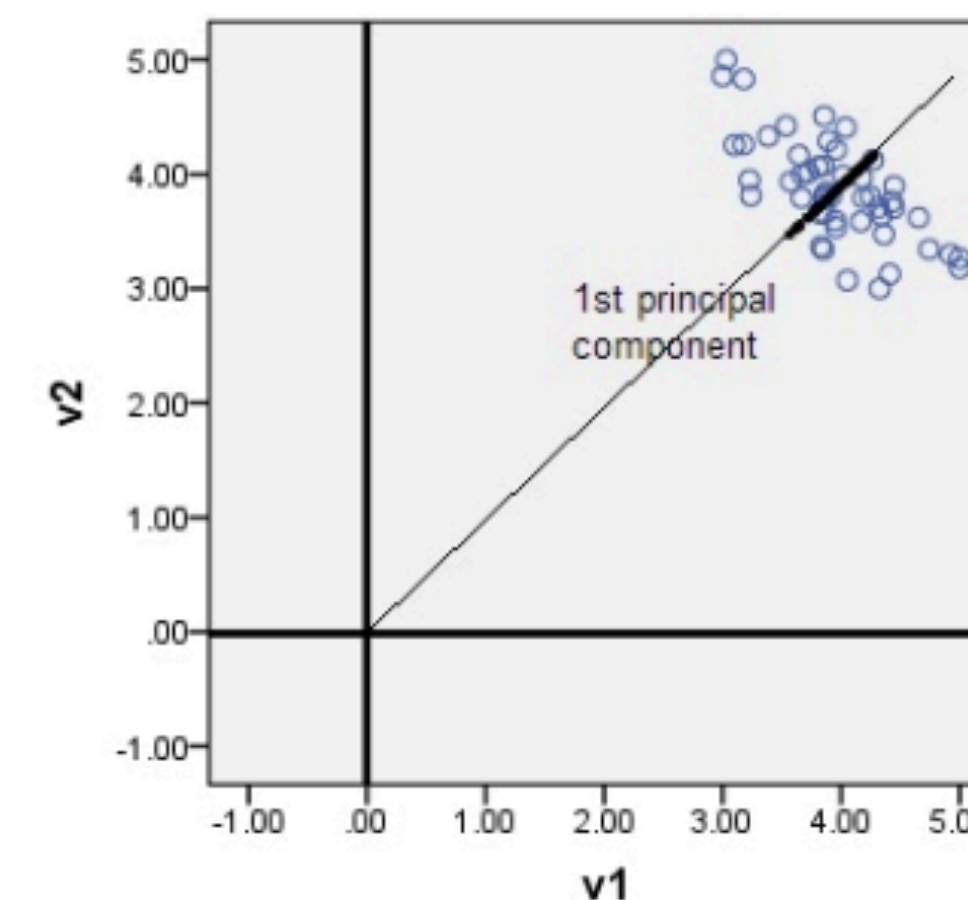
## Maximal variance

- We want to choose a vector  $w$  so that it's as 'informative' as possible i.e. it maximises the variance of the projections of the data onto  $w$ .
- Suppose  $\alpha_i = w \cdot x_i = w^T x_i$  is the projection for observation  $x_i$ , where  $w$  has unit length. We want to maximise the variance of  $\alpha = (\alpha_1, \dots, \alpha_n)$ .

$$\bar{\alpha} = \frac{1}{n} \sum_i \alpha_i = \frac{1}{n} \sum_i w^T x_i = w^T \left( \frac{1}{n} \sum_i x_i \right) = w^T \bar{x}$$

$$\text{var}(\alpha) = \frac{1}{n-1} \sum_i (\alpha_i - \bar{\alpha})^2 = \frac{1}{n-1} \sum_i (w^T x_i - w^T \bar{x})^2 = \frac{1}{n-1} \sum_i w^T (x_i - \bar{x})(x_i - \bar{x})^T w = w^T Q w$$

$$\frac{1}{n-1} \sum_i w^T (x_i - \bar{x})(x_i - \bar{x})^T w = w^T Q w$$

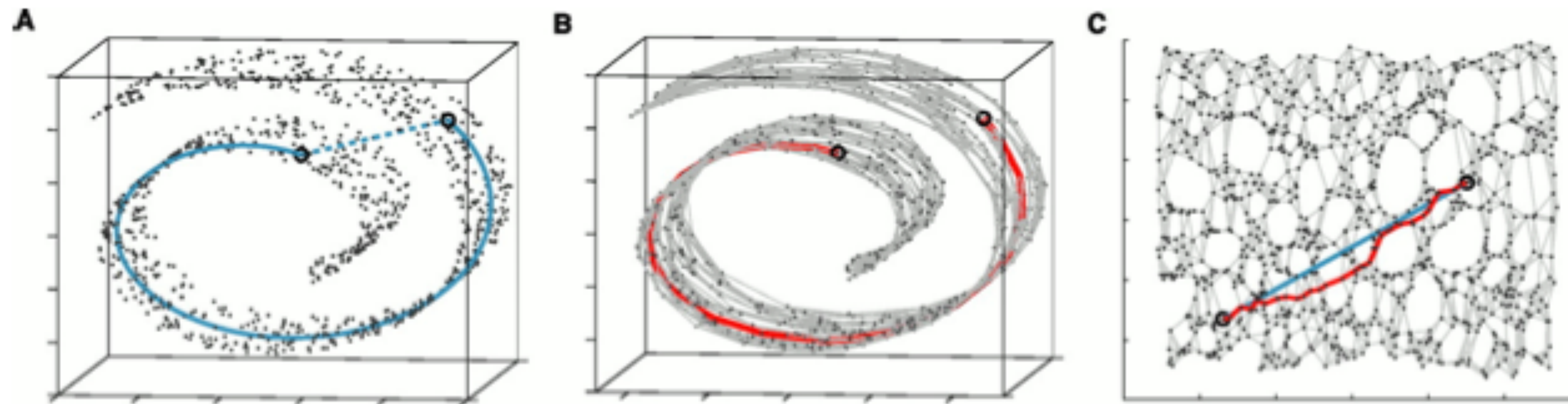


# Recap: MDS vs Sammon mapping

- Metric MDS stress  $S^2(y) = \frac{\sum_{i,j} (d_{ij} - o_{ij})^2}{\sum_{i,j} o_{ij}^2}$  with  $d_{ij} = d(y_i, y_j)$ ,  $o_{ij} = d(x_i, x_j)$
- Sammon's stress  $S^2(y) = \frac{1}{\sum_{i=1}^n \sum_{j=i+1}^n o_{ij}} \sum_{i=1}^n \sum_{j=i+1}^n \frac{1}{o_{ij}} (d_{ij} - o_{ij})^2$
- Sammon mapping gives more weight to small distances, so preserves local structure more than other MDS methods
- I.e. if  $o_{ij}$  is small, then it up-weights the contribution from  $(d_{ij} - o_{ij})^2 / o_{ij}$

# Recap: Isomap

- We need a connected neighbourhood graph, so that it's possible to go from any point to any other point along edges
- Each point connected to  $k$  nearest neighbours,  $k$  is a hyperparameter to specify
- If the neighbourhood graph is disconnected, increase  $k$  (scikit-learn default: 5)
- Approximate geodesic distance (blue) by sum of Euclidean distances between neighbours using e.g. Dijkstra's algorithm (it may have to double back on itself!)





# Today: k-means clustering

- k-means
- Voronoi
- Initialisation
- Extensions (e.g. weighted kernel k-means)
- Fuzzy c-means

Questions: halfway through, at the end, or by email (te269)

# Resources

- Introduction to Statistical Learning with Python, Chapter 12
- Slides adapted from:
  - Prof Stephen Eglen, Cambridge
  - Ethan Fetaya/James Lucas/Emad Andrews, Toronto
  - Ronan Cummins, Cambridge

# Overview: clustering

- Grouping  $n$  observations into  $K$  clusters is one of the common/major problems in unsupervised learning
- We assume the data was generated from a number of different classes, we want to cluster observations (objects) from the same class together (without necessarily describing the classes)
- Objects that are close to each other in high-dimensional space should be in the same cluster (objects in the same cluster should be similar and objects in different clusters should be dissimilar), we want to find a ‘natural’ grouping
- How is this different from classification? What is  $K$ ?



# Types of clustering

- Hard vs soft
  - Do objects belong to only one cluster or can they belong to more than one?
- Hierarchical vs non-hierarchical
  - How are clusters related to each other (i.e. are there parent clusters)?
- Agglomerative vs partitioning/divisive:
  - Do you lump together or split up?
- Centroid vs distribution-based vs density vs graph-based vs spectral

# Motivation and examples

- Pattern recognition
  - Computer vision, e.g. detect moving objects in videos (self-driving cars)
  - Personalised medicine/phenotypes (groups of patients who are similar)
  - Bioinformatics, e.g. gene expression
  - Cosmology
- 
- **Warning:** clustering methods can find structure where there isn't actually any. We should be wary of making strong conclusions about the output of clustering methods!

# Overview: k-means

- Partitioning method: assign each point to one of  $K$  non-nested clusters
- k-means (unsupervised) is similar to k-nearest neighbour classifier (supervised)
- We represent each cluster by a single representative point (the cluster centroid)
- This is an NP-hard problem (finding a global minimum is computationally difficult)
- $K$  is the only parameter, how should we choose  $K$ ?

# Overview: k-means

- Partitioning method: assign each point to one of  $K$  non-nested clusters
- k-means (unsupervised) is similar to k-nearest neighbour classifier (supervised)
- We represent each cluster by a single representative point (the cluster centroid)
- This is an NP-hard problem (there are a lot of possible clusterings and finding a global minimum is computationally difficult)
- $K$  is the only parameter, how should we choose  $K$ ?

# Lloyd's algorithm (naive k-means)

- Observations  $x_i = (x_1, \dots, x_p)$  for  $i = 1, \dots, n$
- $K$  clusters, with centroids  $c_k$  for  $k = 1, \dots, K$
- Cluster membership matrix  $M$  (size  $n \times K$ ) or cluster sets  $C_1, \dots, C_K$ , with  $x_i \in C_k$  and  $m_{ik} = 1$  if  $x_i$  belongs to cluster  $k$  and  $m_{ik} = 0$  otherwise
- Two steps:
  1. Assignment
  2. Centroid update

# Lloyd's algorithm (naïve k-means)

- Initialise clusters or centroids (various approaches, e.g. uniform random)
- Two steps:
  1. Assignment:
    - Assign each observation to the cluster with the nearest\* centroid
  2. Centroid update
    - Recalculate the centroids as the mean of all observations in that cluster
- \*we're using the squared Euclidean distance  $d(x_i, x_j) = \|x_i - x_j\|_2^2$



# Lloyd's algorithm (naïve k-means)

- Initialise clusters or centroids (various approaches, e.g. uniform random)
- Two steps (repeat until  $M$  stops changing):
  1. Assignment:
    - Assign  $x_i$  to cluster  $j$  if  $j = \arg \min_k d(x_i, c_k)$ , i.e.  $m_{ij} = 1, m_{il} = 0 \ \forall l \neq k$
  2. Centroid update
    - New cluster centroids are  $c_k = \frac{\sum_{i=1}^n m_{ik} x_i}{\sum_{i=1}^n m_{ik}}$

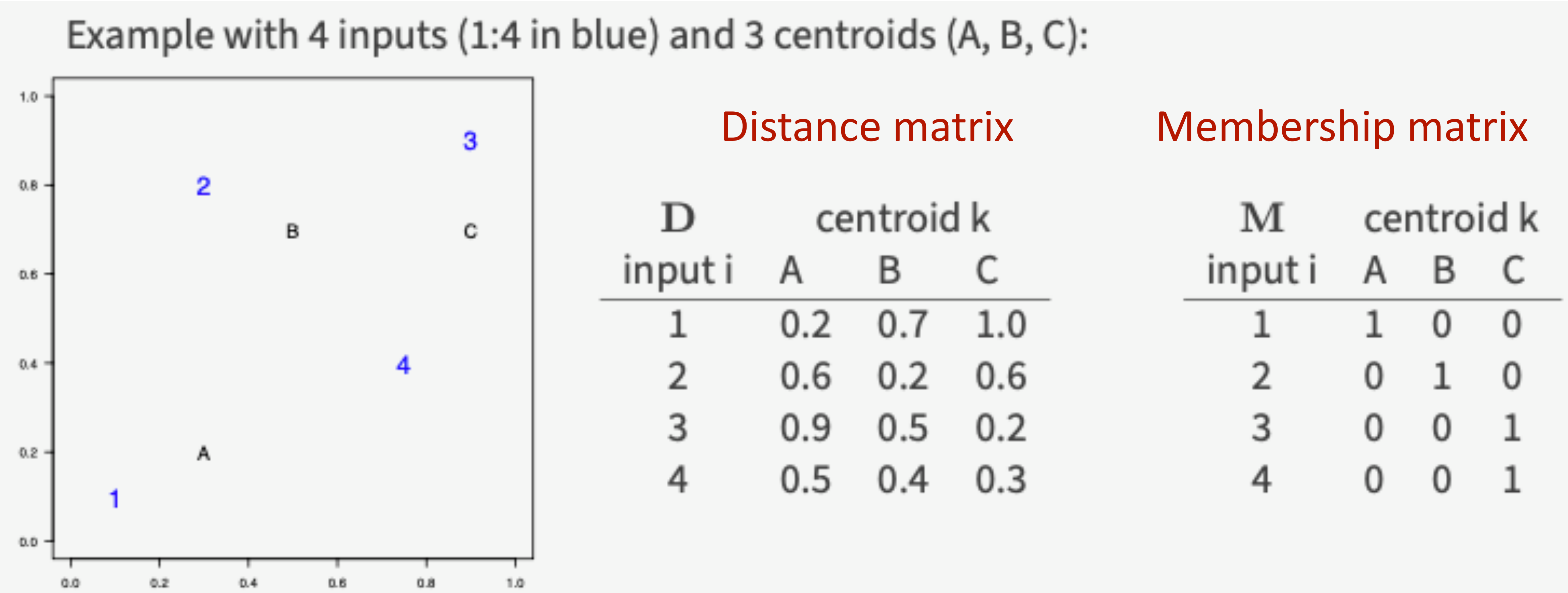
# Lloyd's algorithm (naïve k-means)

- Initialise clusters or centroids (various approaches, e.g. uniform random)
- Two steps (repeat until  $C_k$ 's stop changing):
  1. Assignment:
    - Assign points to cluster set  $C_k = \{x_i : d(x_i, c_k) \leq d(x_i, c_j) \ \forall j = 1, \dots, K\}$
  2. Centroid update
    - New cluster centroids are  $c_k = 1/n_k \sum_{x_i \in C_k} x_i$ , where  $n_k$  is the size of set  $C_k$

# Aside: distance metrics

- In principle, we can use any measure for the distance between  $x_i$  and  $x_j$ , as long as it's a **metric**
- Metrics have a few properties
  - $d(x_i, x_j) = 0 \iff x_i = x_j$  (identity)
  - $d(x_i, x_j) = d(x_j, x_i)$  (symmetry)
  - $d(x_i, x_j) \leq d(x_i, x_k) + d(x_k, x_j)$  (triangle inequality)

# Membership matrix



# Within-cluster sum of squares

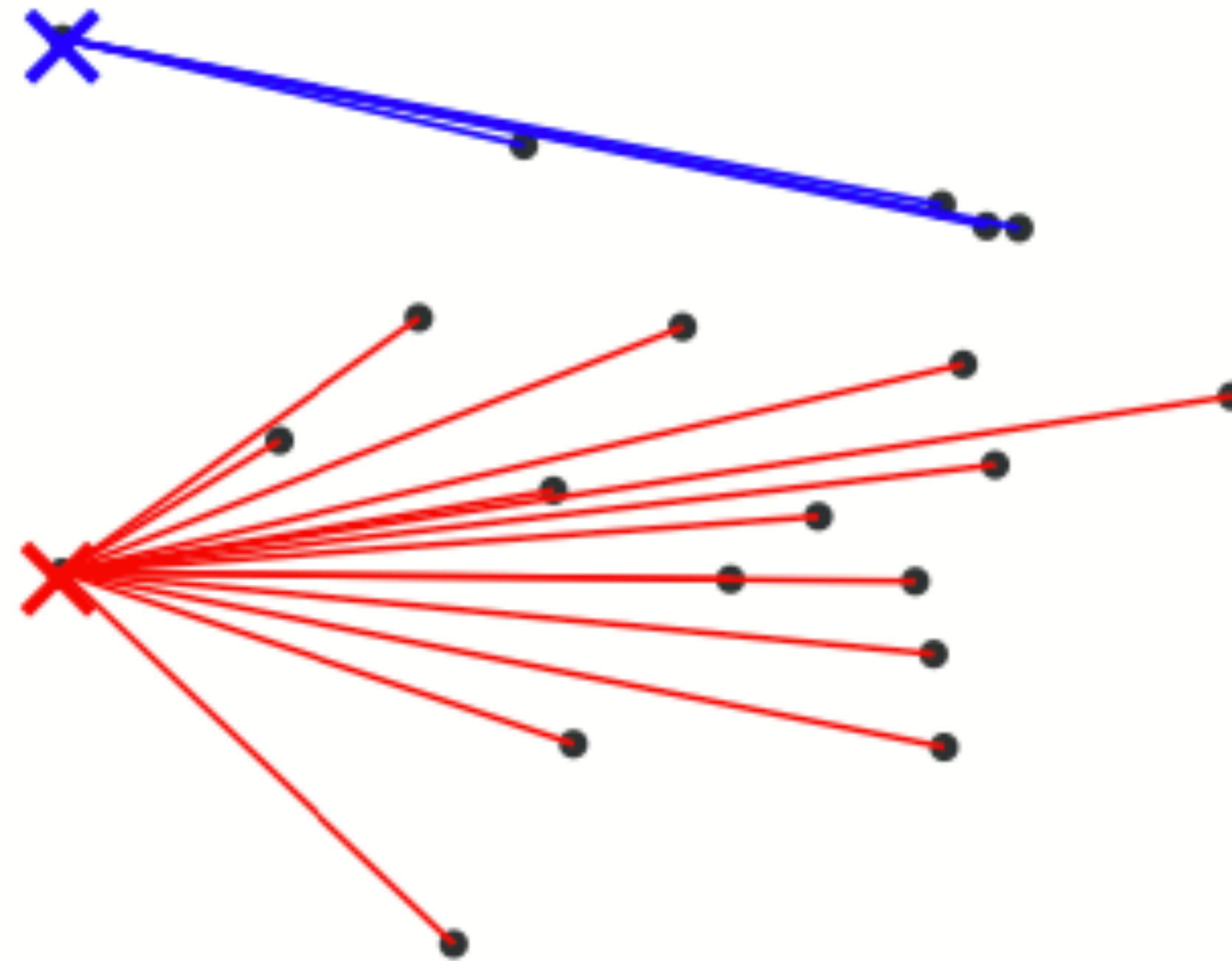
- k-means is really an optimisation problem
- We're rearranging cluster assignments to minimise an error function
- e.g. the within-cluster sum of squares:  $E = \sum_{k=1}^K \sum_{x_i \in C_k} d(x_i, c_k)^2$
- This should decrease every step of Lloyd's algorithm
  - During assignment, each observation  $x_i$  moves to a closer centroid
  - During centroid update, the centroid moves to minimise the average error

# k-means in action (data)

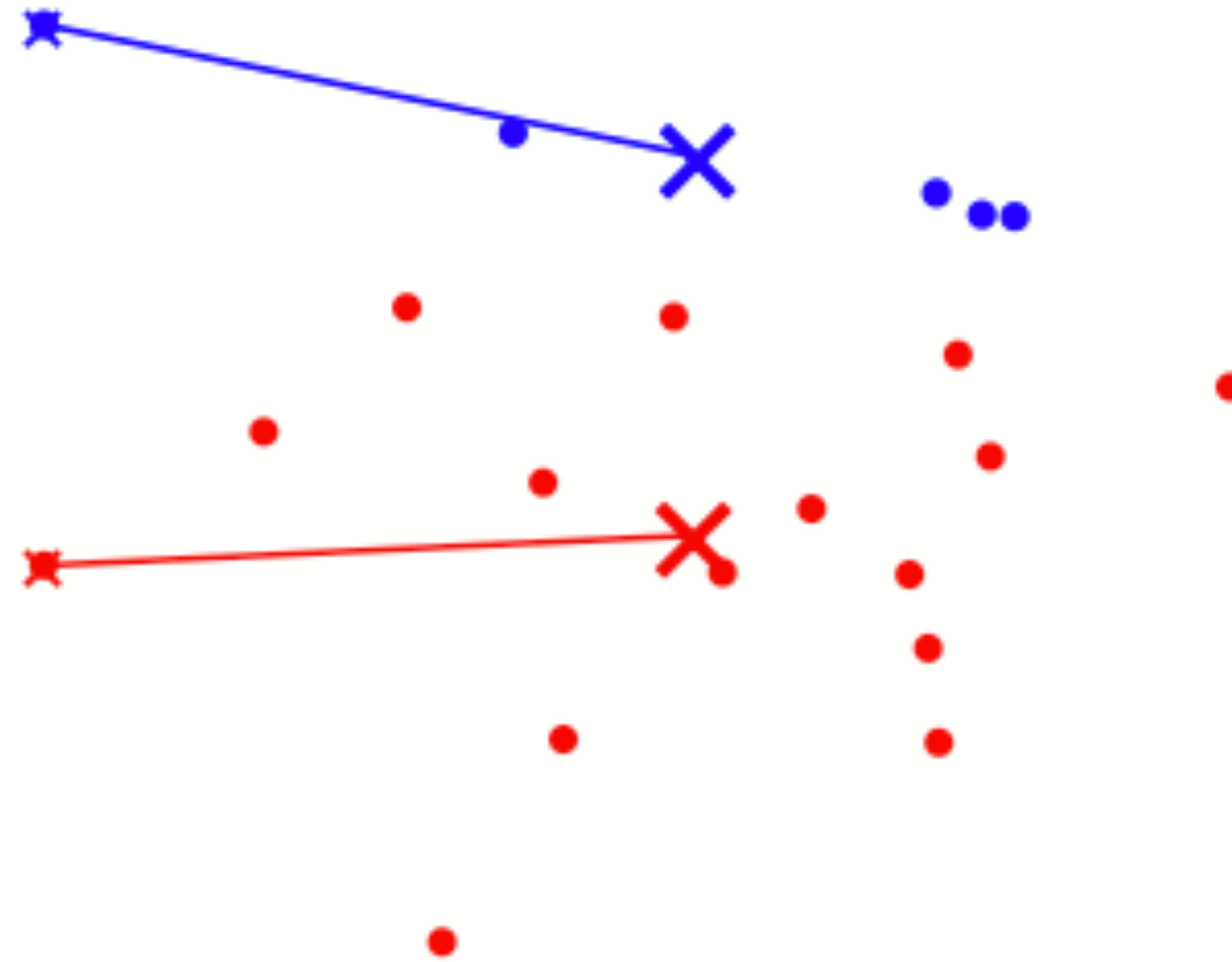




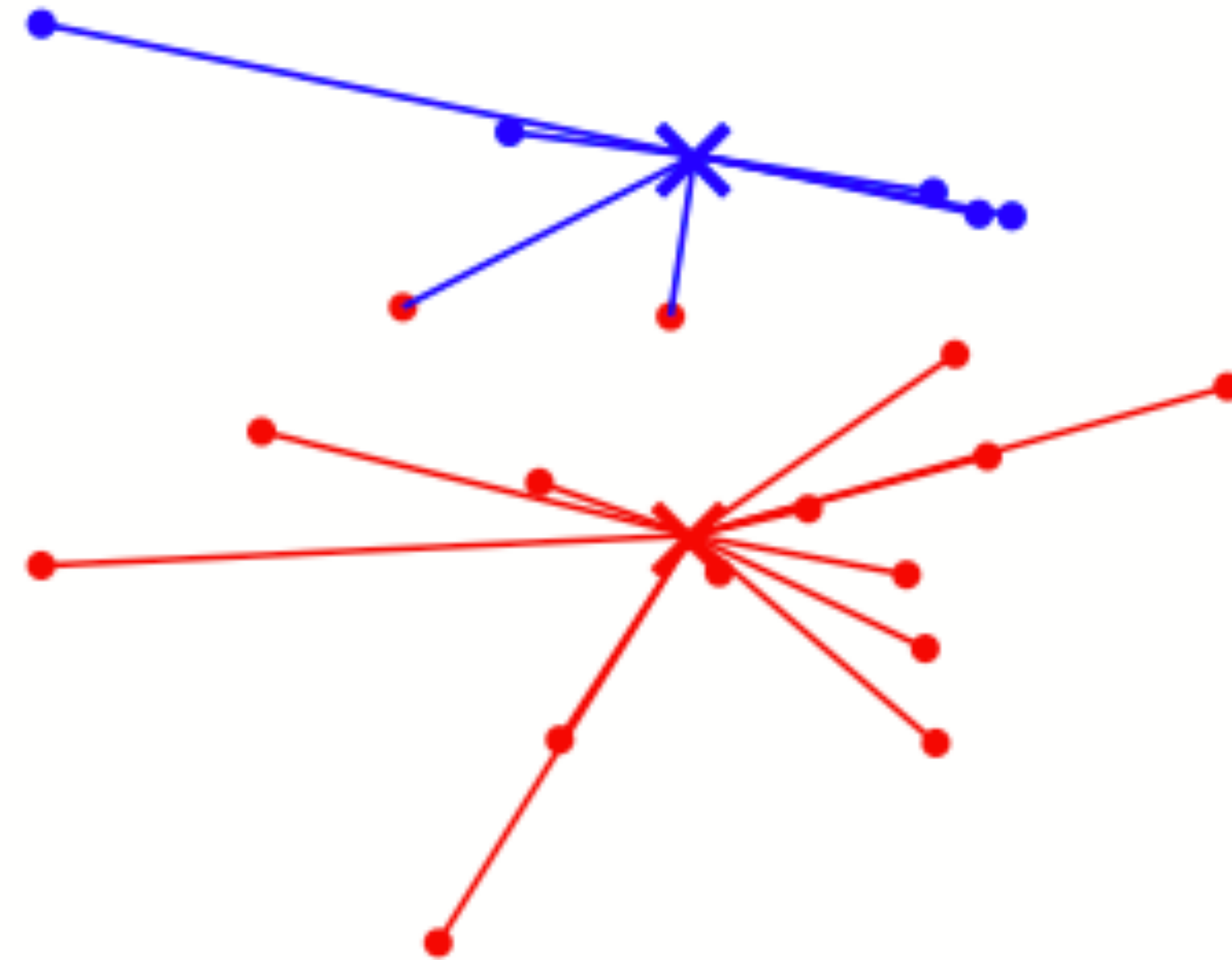
# k-means in action (initialisation + iteration 1 assign)



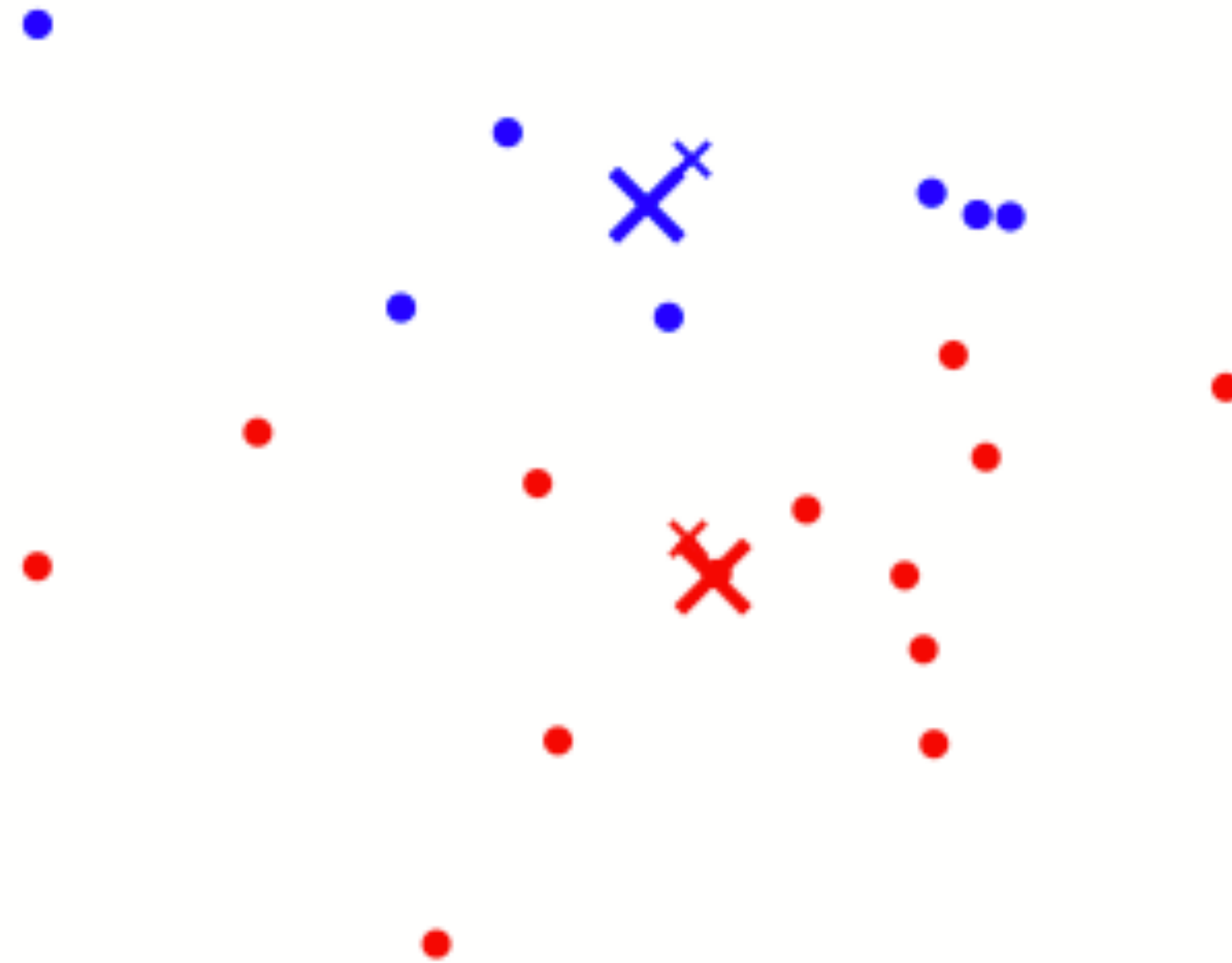
# k-means in action (iteration 1 update centroids)



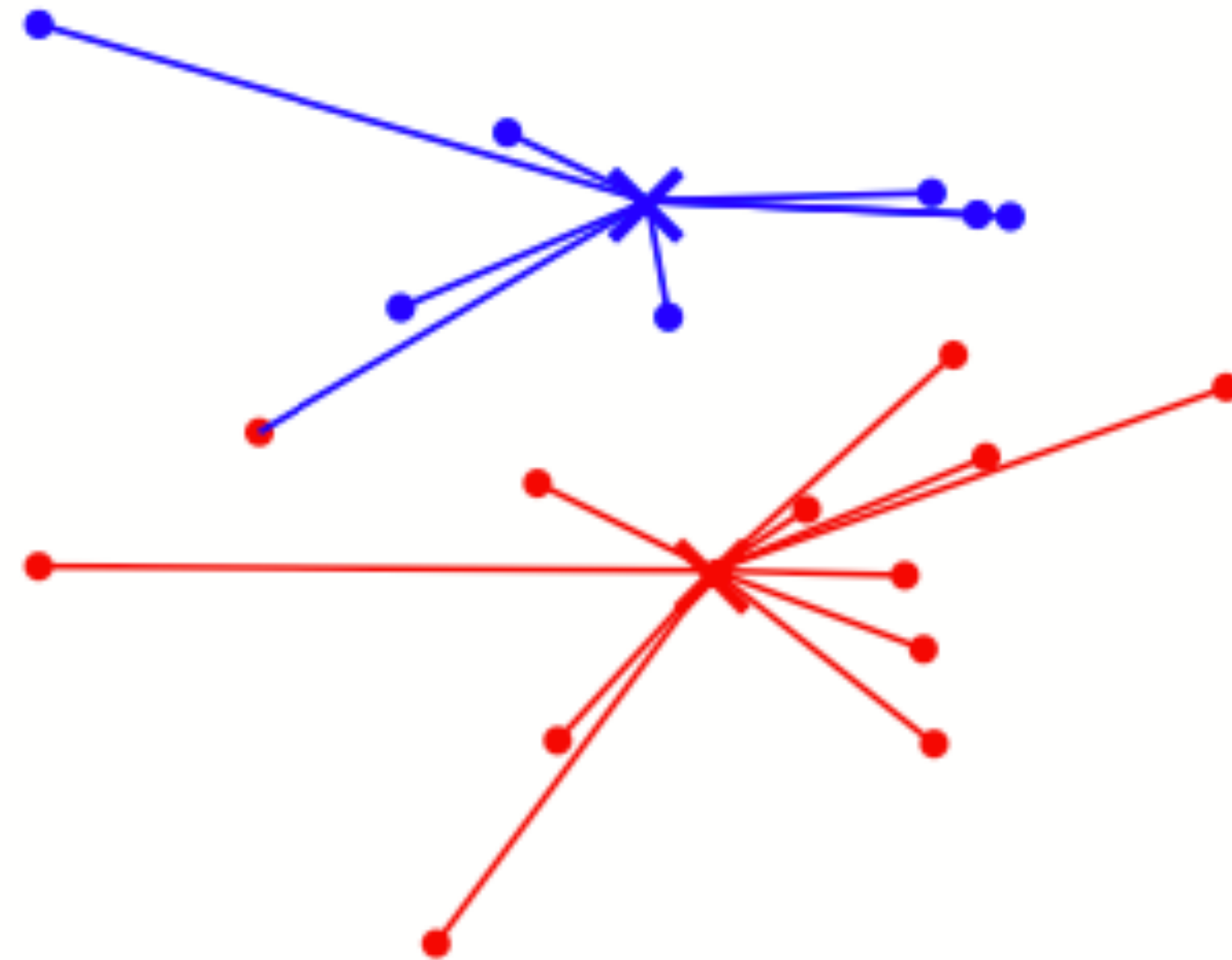
# k-means in action (iteration 2 assignment)



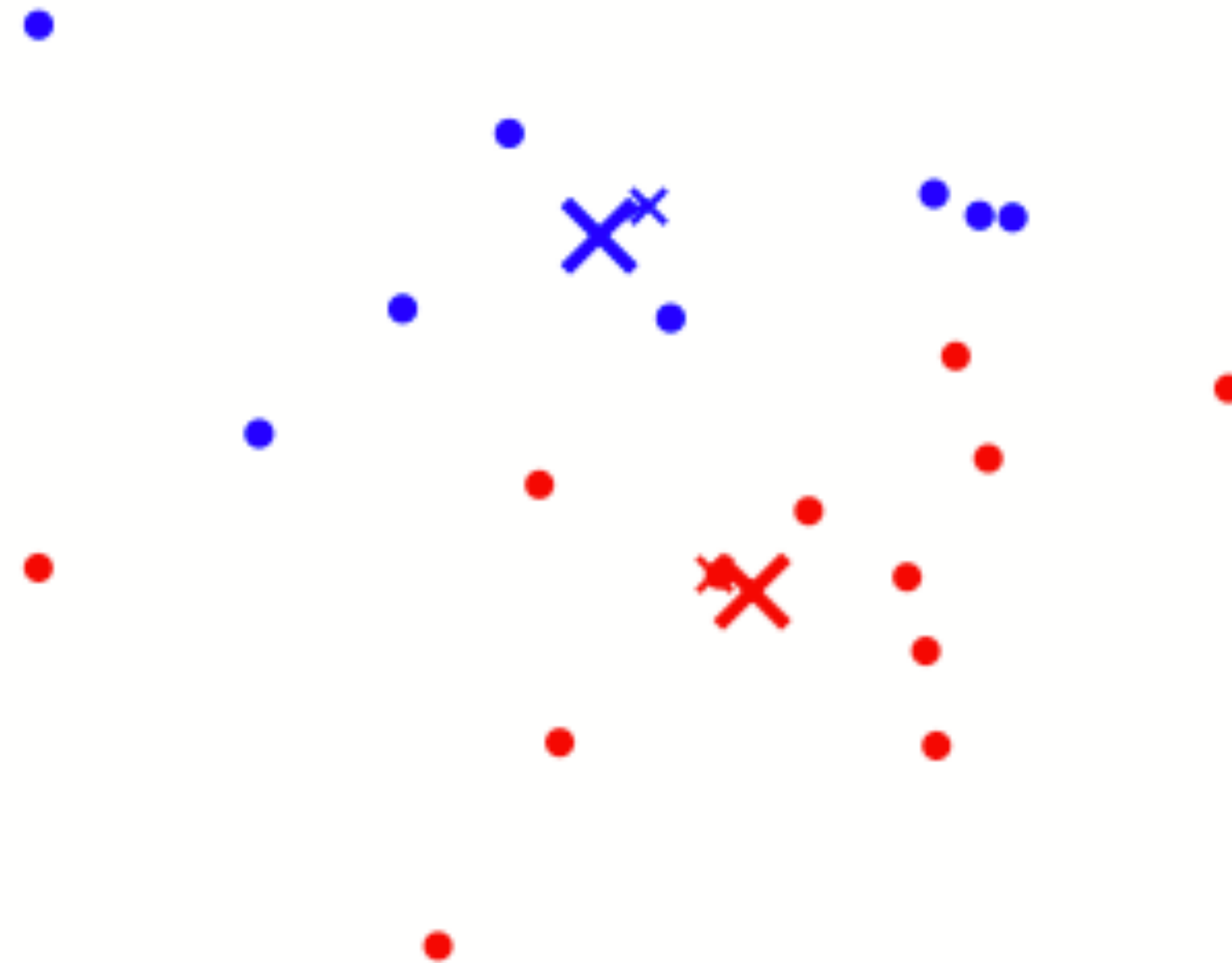
# k-means in action (iteration 2 update centroids)



# k-means in action (iteration 3 assignment)

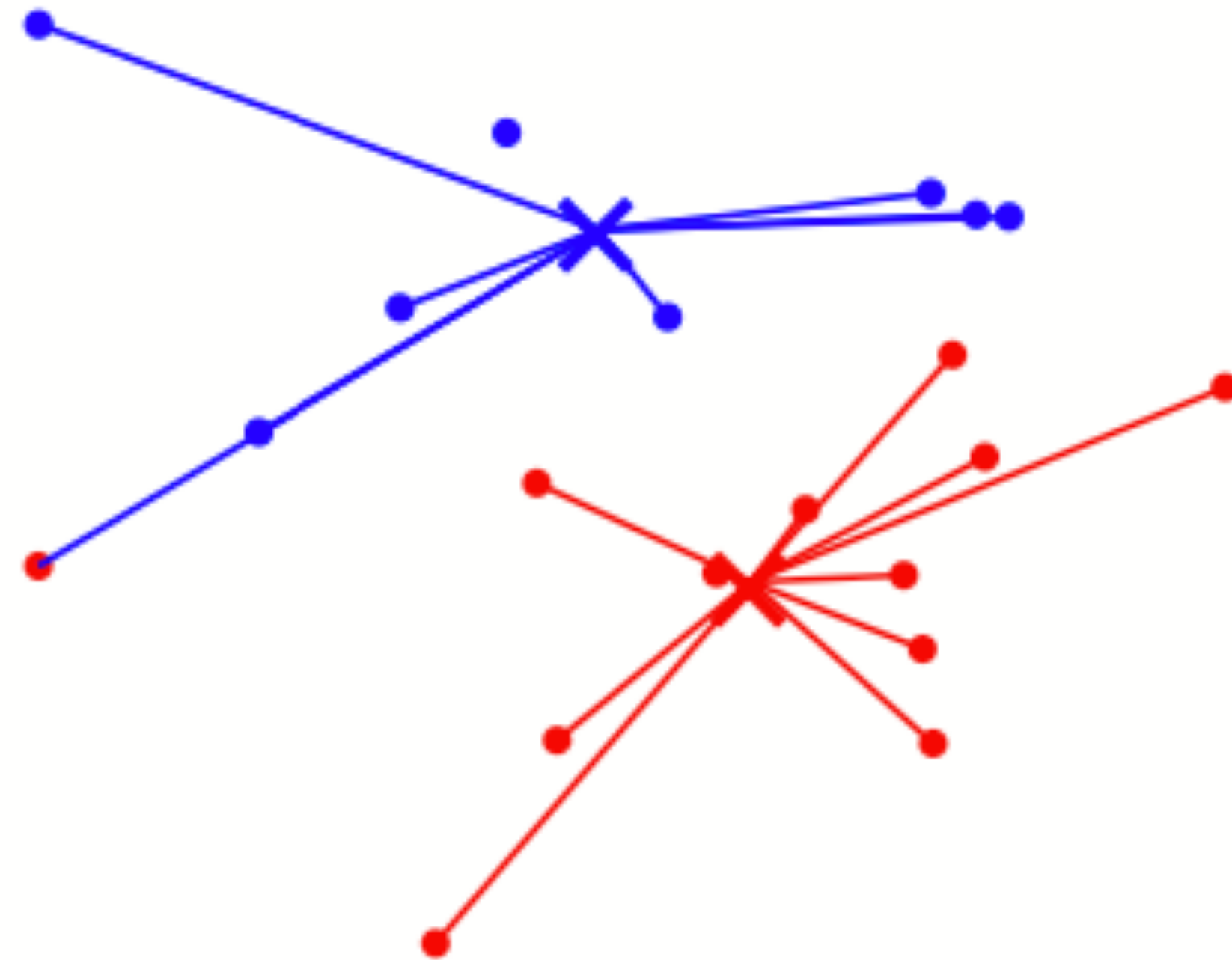


# k-means in action (iteration 3 update centroids)

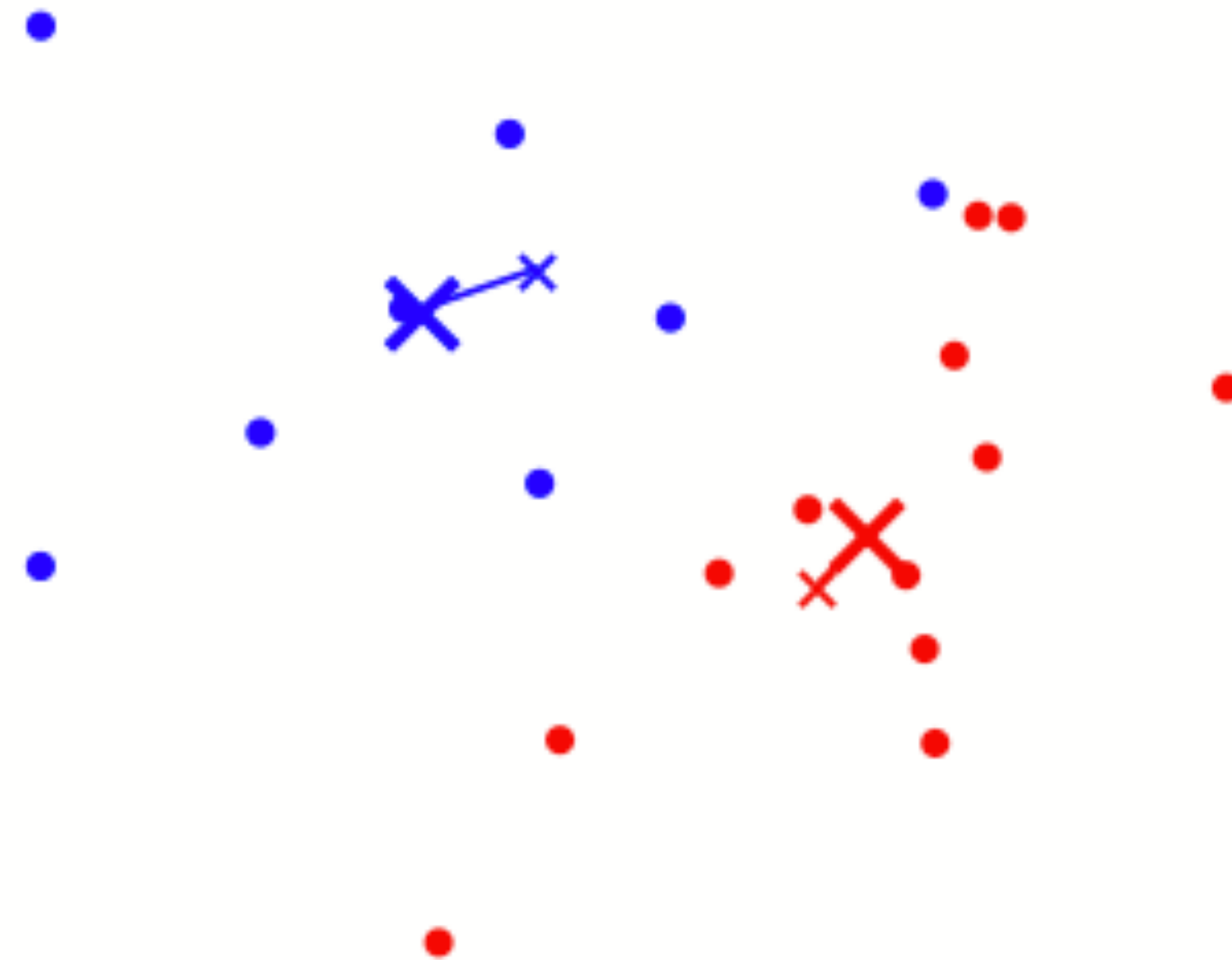




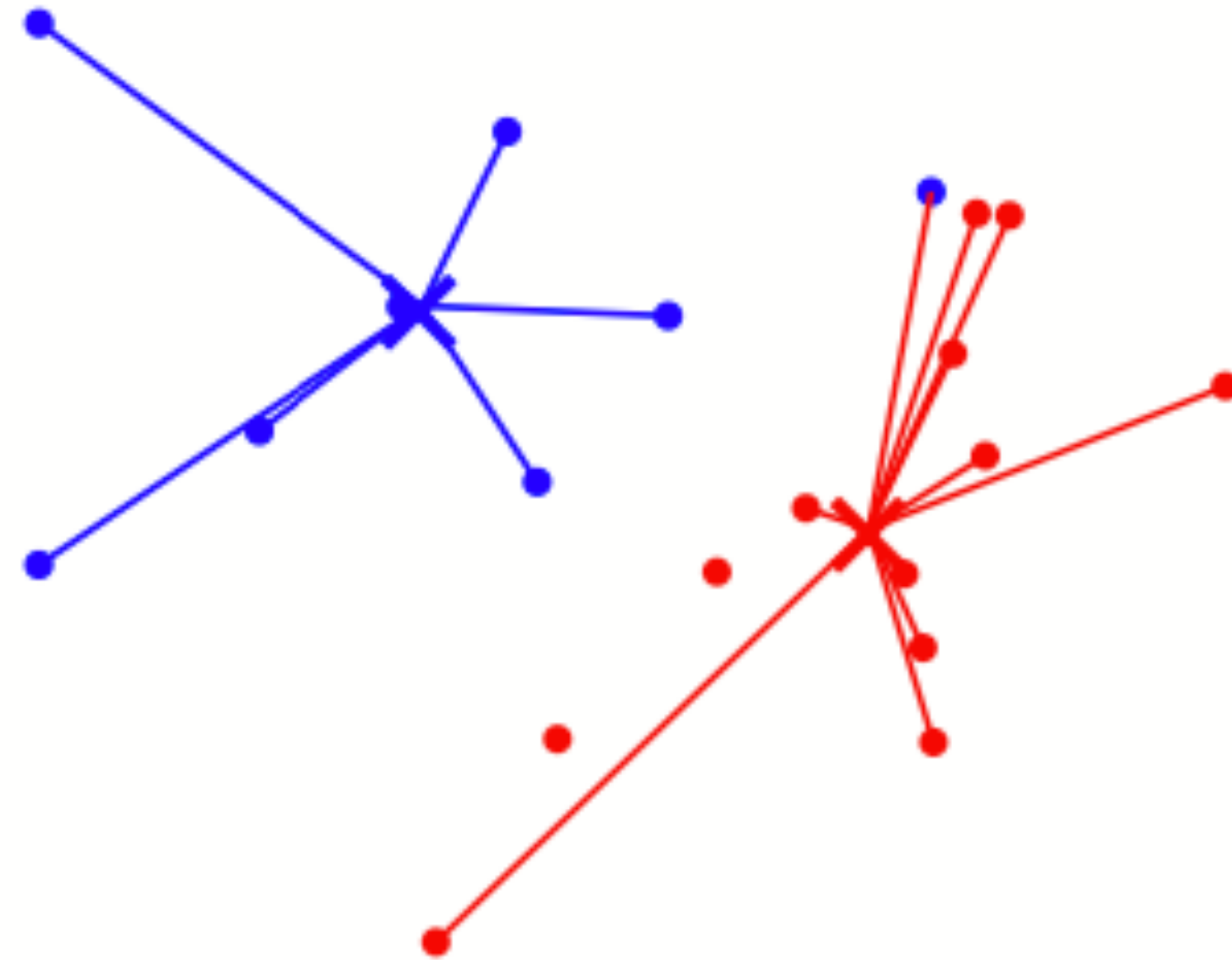
# k-means in action (iteration 4 assignment)



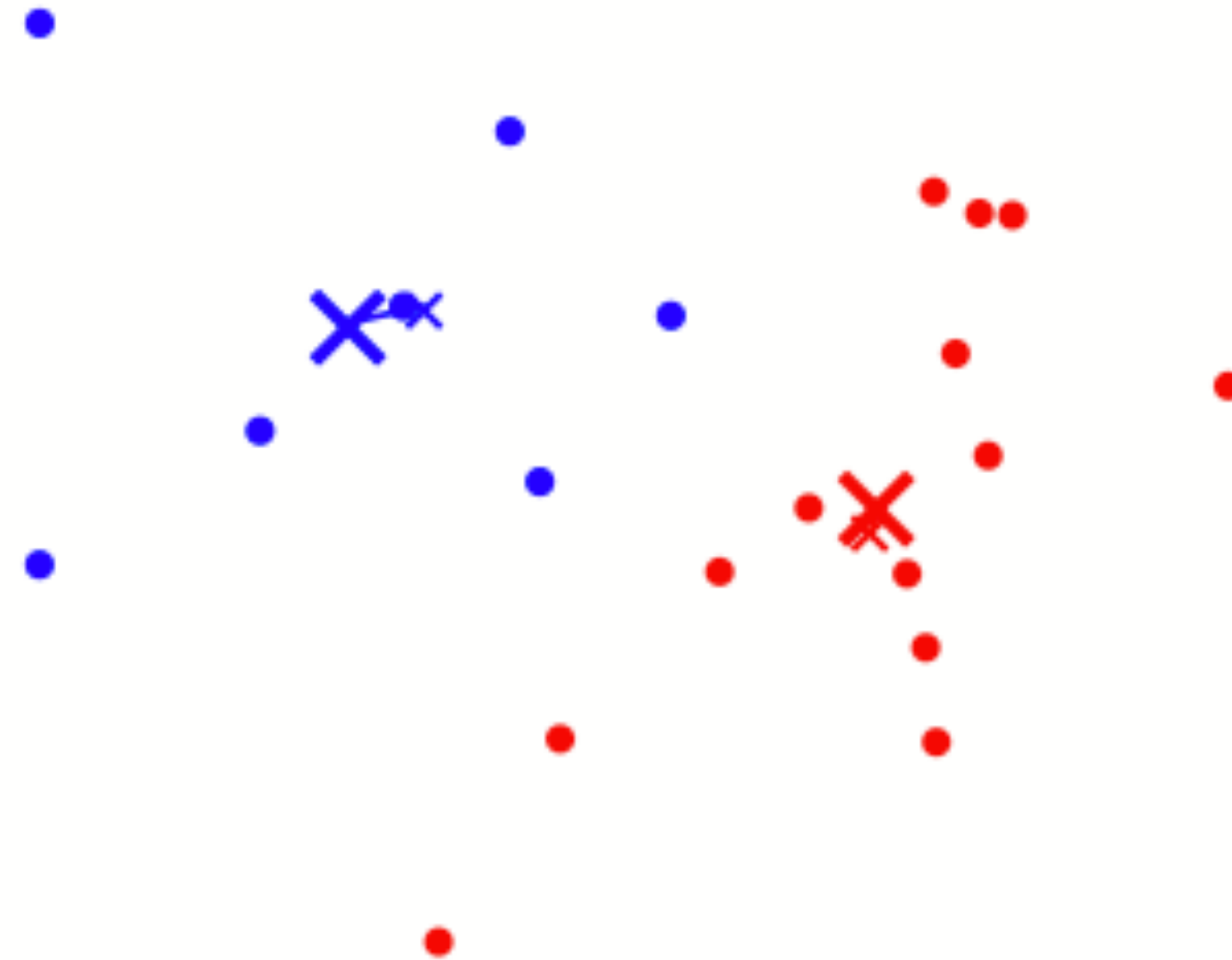
# k-means in action (iteration 4 update centroids)



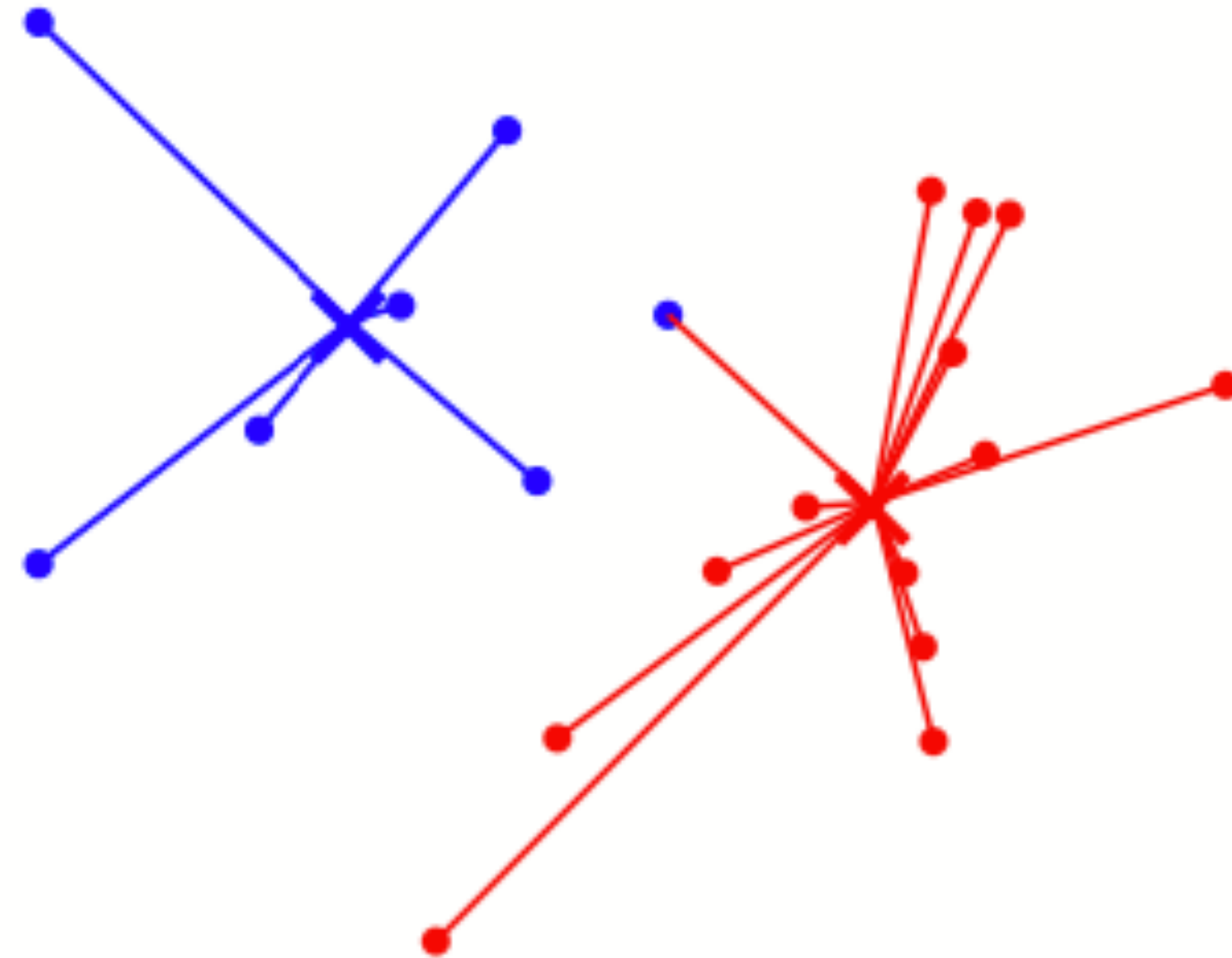
# k-means in action (iteration 5 assignment)



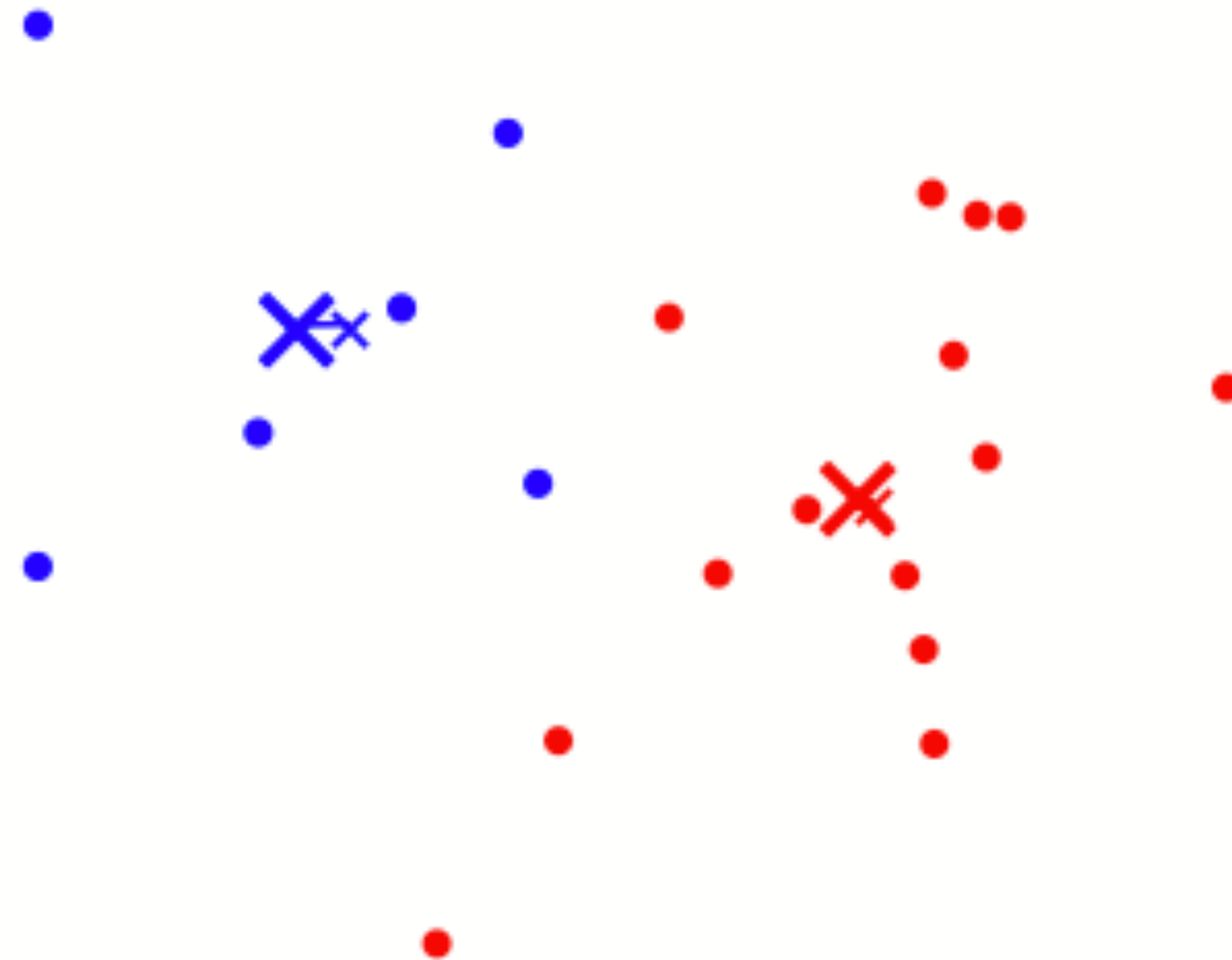
# k-means in action (iteration 5 update centroids)



# k-means in action (iteration 6 assignment)

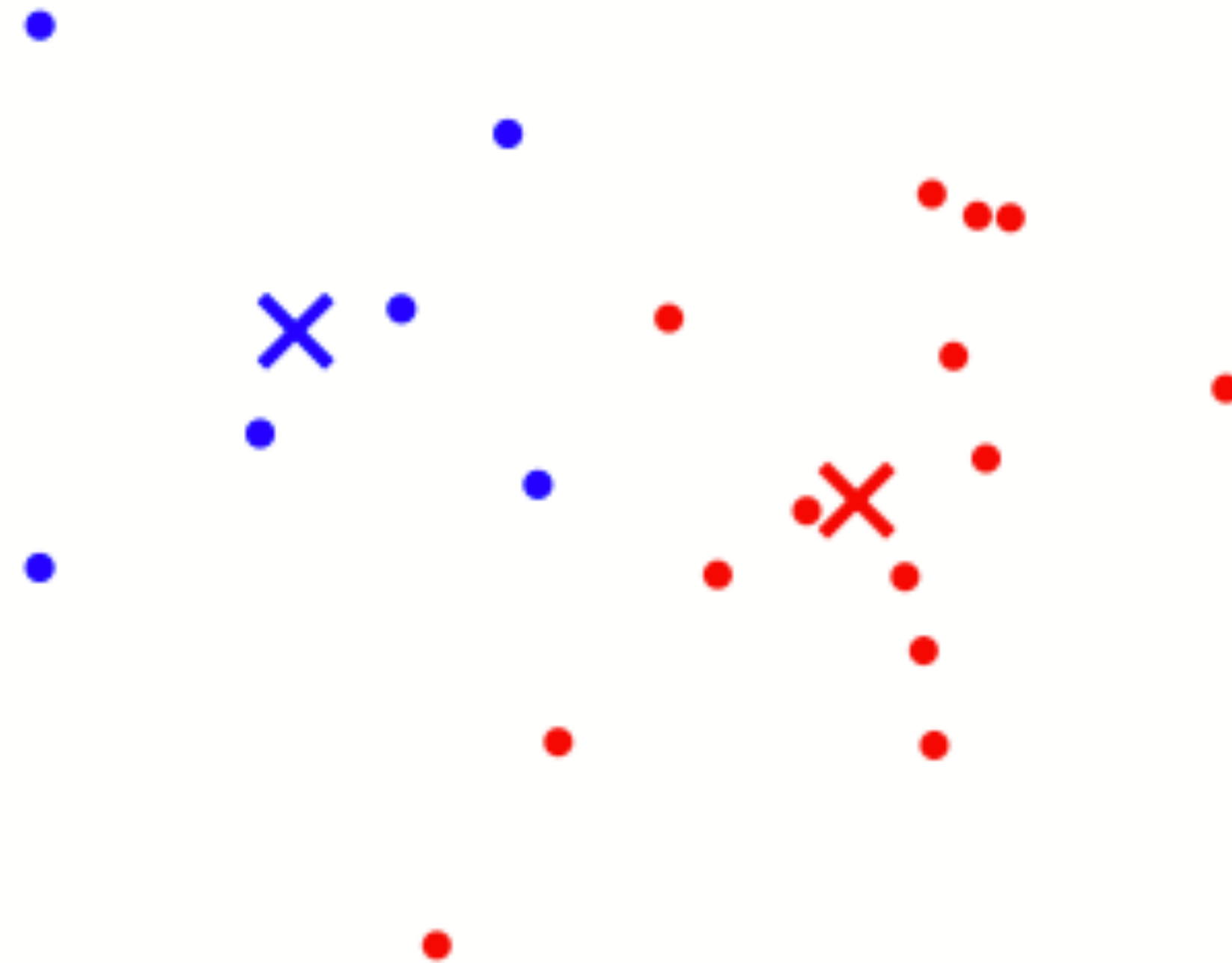


# k-means in action (iteration 6 update centroids)





# k-means in action (convergence)



# Convergence

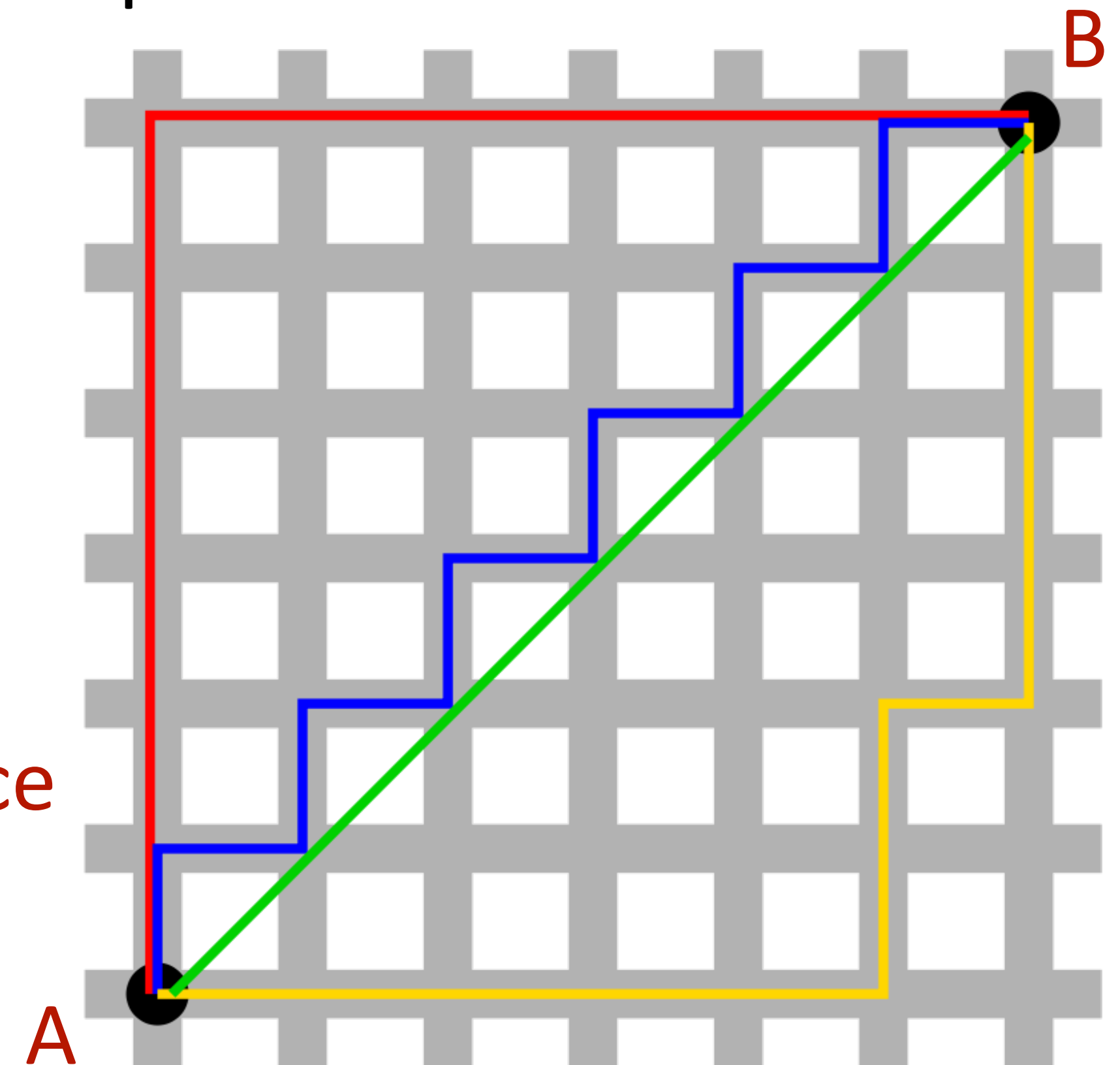
- If WSS decreases at every stage and there are only a finite number of clusterings, then the algorithm must converge to a minimum
- This is almost certainly a local minimum, k-means rarely finds the global optimal solution
- Results often depend on the initialisation and on the number of clusters  $K$

# k-medians

- This uses the median of the observations (independently for each dimension) within each cluster as the centroid, instead of the mean
- Overall, it minimises the error over all clusters with respect to Manhattan distance instead of Euclidean distance
- It uses an alternating update like Lloyd's algorithm
- This sometimes works better than k-means. Why?

Blue, yellow, red are all the minimum Manhattan distance

Green is minimum Euclidean distance



# k-medians

- This uses the median of the observations (independently for each dimension) within each cluster as the centroid, instead of the mean
- Overall, it minimises the error over all clusters with respect to Manhattan distance instead of Euclidean distance
- It uses an alternating update like Lloyd's algorithm
- This sometimes works better than k-means. Why?

# k-medoids

- Also similar to k-means
- The centroids are called medoids, these must be observations i.e.  $\forall k, c_k = x_i$  for some  $i = 1, \dots, n$
- This can make the centroids easier to interpret (exemplar for each cluster)
- k-medoids uses any dissimilarity measure and minimises the sum of pairwise dissimilarities (more general than k-means, also more robust to noise/outliers)

# Initialisation

- k-means final clustering depends on the initial centroids
- There are various methods to find a good initialisation before running Lloyd's algorithm

# Initialisation: Forgy

- Choose  $K$  observations randomly from the observations  $x_i, i = 1, \dots, n$
- These will be the initial centroids  $c_k, k = 1, \dots, K$
- In high-dimensions, this tends to spread the initial centroids out



# Initialisation: Random partition

- Randomly assign each observation to a cluster, then the centroids are the mean of these starting clusters
- In high-dimensions, this tends to put all of the centroids near the mean of the data

# Initialisation: k-means++

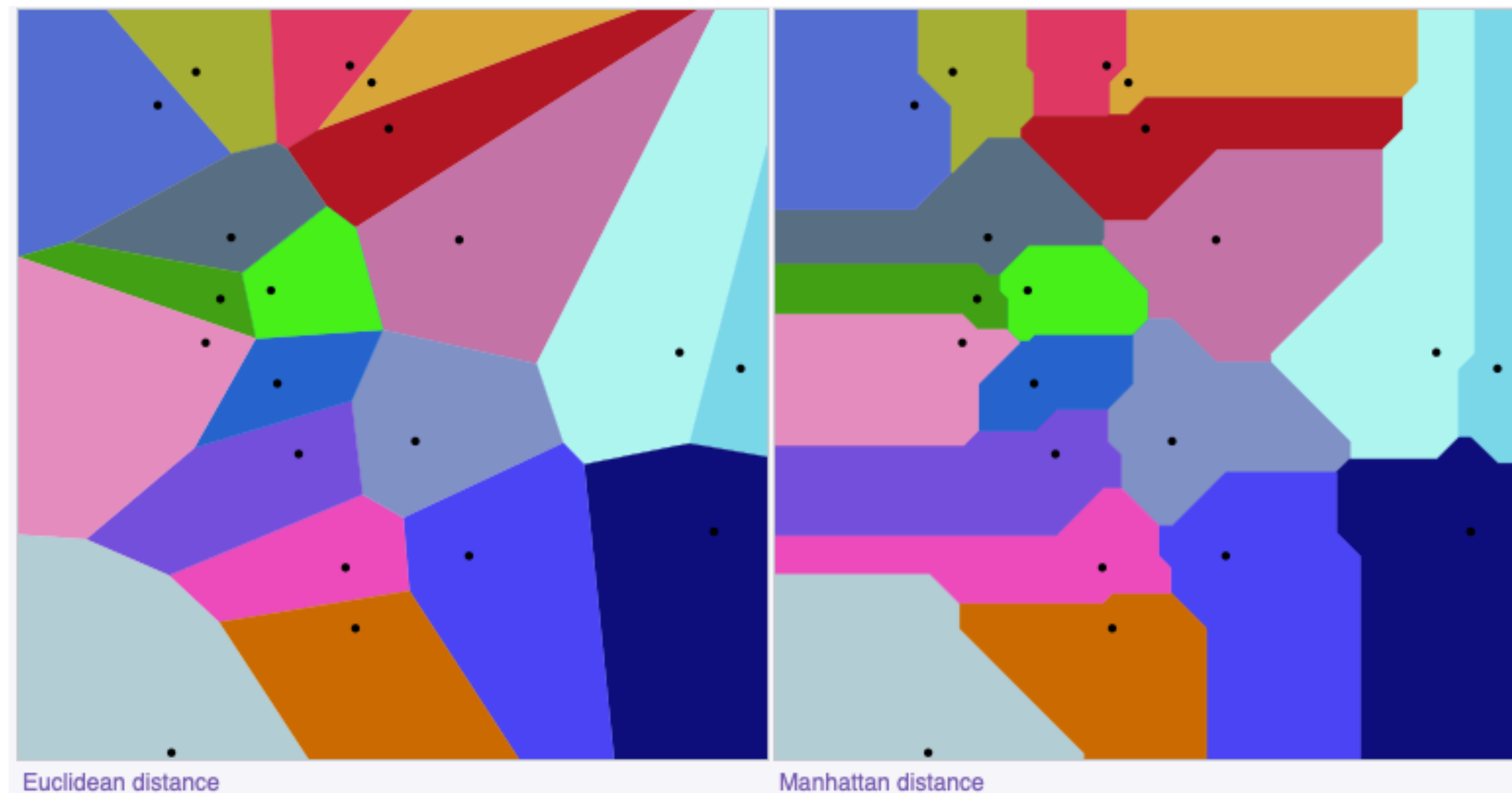
- An initialisation algorithm to ‘seed’ the centroids
- This aims to spread out the initial centroids
  1. Choose one centroid uniformly at random from among the observations
  2. For each observation  $x_i$  that isn't a centroid, compute the distance  $d_i$  between  $x_i$  and the nearest centroid
  3. Choose a new centroid at random, with weighted probability so that  $x_i$  is chosen with probability proportional to  $d_i^2$
  4. Repeat 2. and 3. until there are  $K$  centroids, then run standard k-means

# Other algorithms: Hartigan-Wong method

- A variation of k-means that proposes to move  $x_i$  to move from cluster  $C_k$  to cluster  $C_j$  (for all  $j = 1, \dots, K$ ) with some acceptance strategy
- E.g. cluster cost  $\phi(C_k) = \sum_{x_i \in C_k} \|x_i - c_k\|^2$
- Change in cost  $\Delta(C_k, C_j, x_i) = \phi(C_k) + \phi(C_j) - \phi(C_k \setminus \{x_i\}) - \phi(C_j \cup \{x_i\})$
- Find the  $C_j$  that maximises this, and re-assign  $x_i$  to it

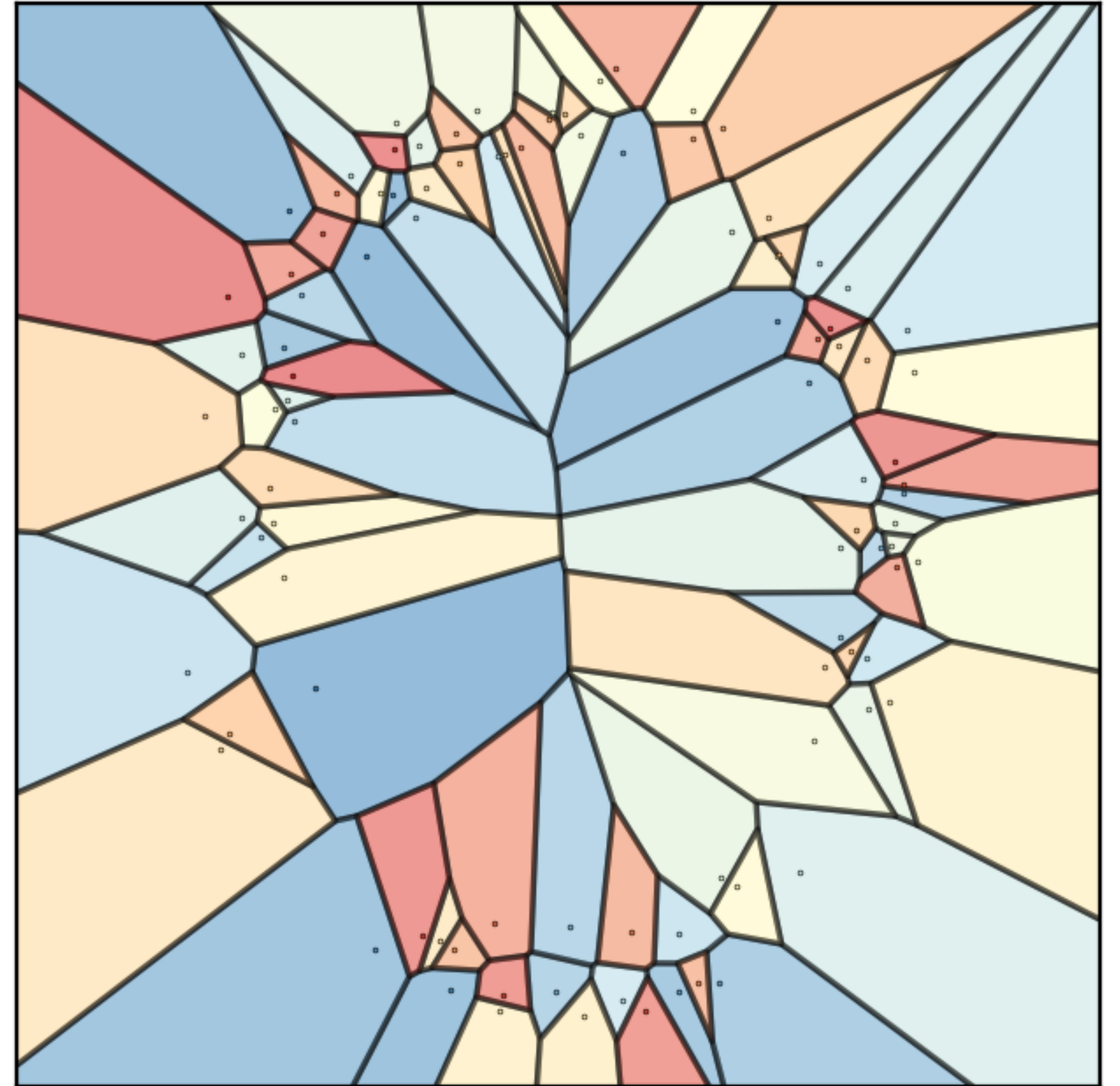
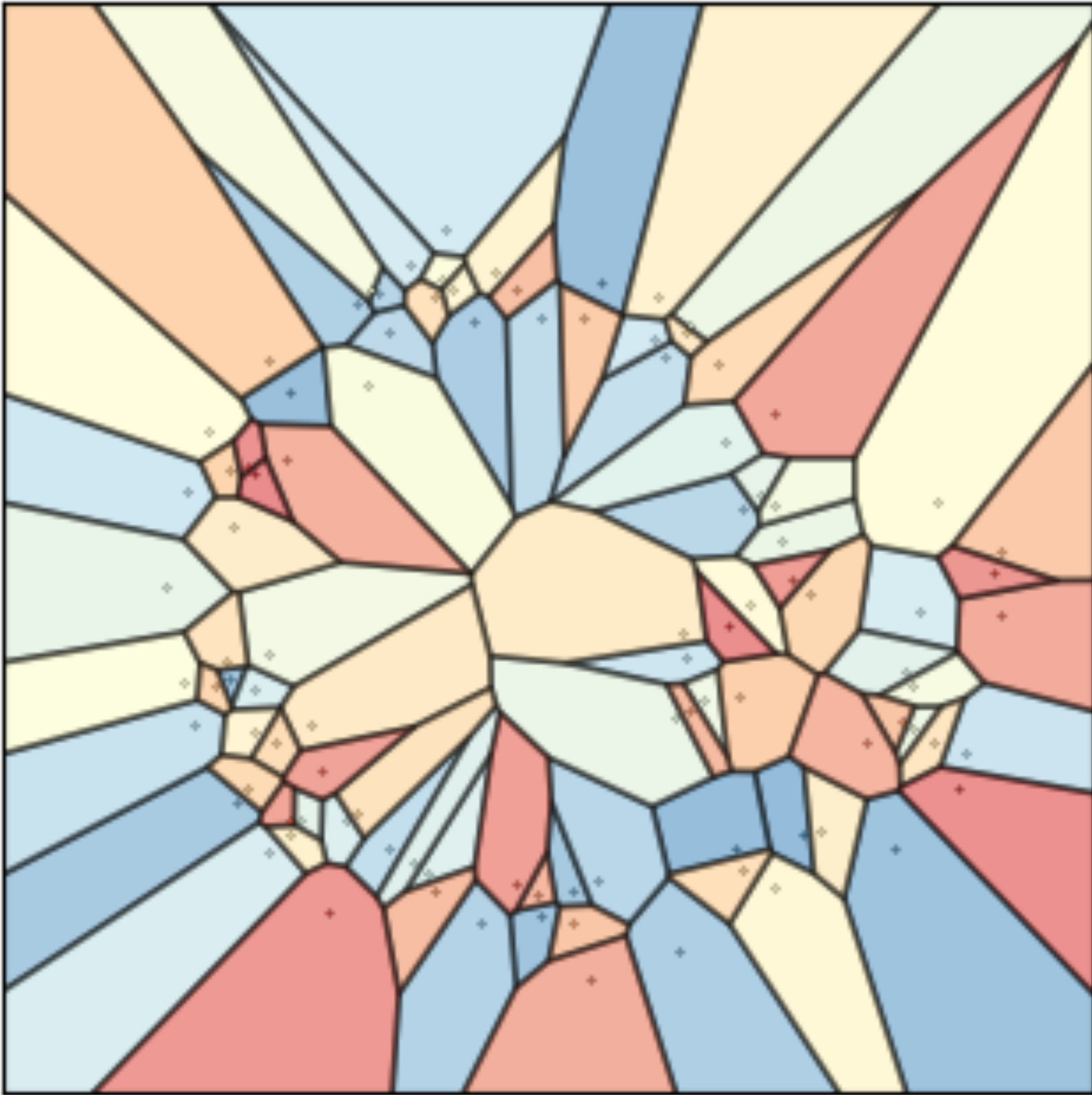
# Voronoi cells look pretty

- A set of points and a distance metric partition the space into regions called Voronoi cells
- The region  $R_k = \{x : d(x, c_k) \leq d(x, c_j), \forall j \neq k\}$ ,  $x_i \in R_k \iff x_i \in C_k$





# Voronoi cells (spiral, 0)



# Fuzzy c-means

- Fuzzy or soft clustering assigns each observation a weight of belonging to each cluster, so it can belong to multiple clusters
- Cluster membership is graded to indicate the degree to which each observation belongs to a cluster (i.e. an observation in the middle of cluster is in the cluster to a greater degree than one at the edge of the cluster)
- Cluster membership matrix  $W$  (size  $n \times K$ ) with  $w_{ik} \in [0,1]$  the degree to which observation  $x_i$  belongs to cluster  $k$

# Fuzzy c-means

- Two steps (as with k-means)

1. Multiple cluster assignment

- $x_i$  has cluster assignment  $w_{ik}$ , with  $w_{ik}^{-1} = \sum_{j=1}^K \left( \frac{\|x_i - c_k\|}{\|x_i - c_j\|} \right)^{\frac{2}{m-1}}$

2. Centroid update

- New cluster centroids are  $c_k = \frac{\sum_{i=1}^n w_{ik}^m x_i}{\sum_{i=1}^n w_{ik}^m}$
- This minimises the weighted mean squared error  $E = \sum_{i=1}^n \sum_{k=1}^K w_{ik}^m \|x_i - c_k\|^2$
- $m$  is a fuzziness hyper parameter



# Questions?

- Feel free to email me at [te269@cam.ac.uk](mailto:te269@cam.ac.uk)

# Next time

- Clustering
  - Hierarchical clustering