Clustering

MGTF 495

Class Outline

- Representation Learning
  - k-means
  - EM optional
  - Agglomerative hierarchical clustering
  - Hands-On
- Informative Projections
  - PCA
  - SVD optional
  - Latent semantic indexing (LSI)
  - Hands-On

Representation learning

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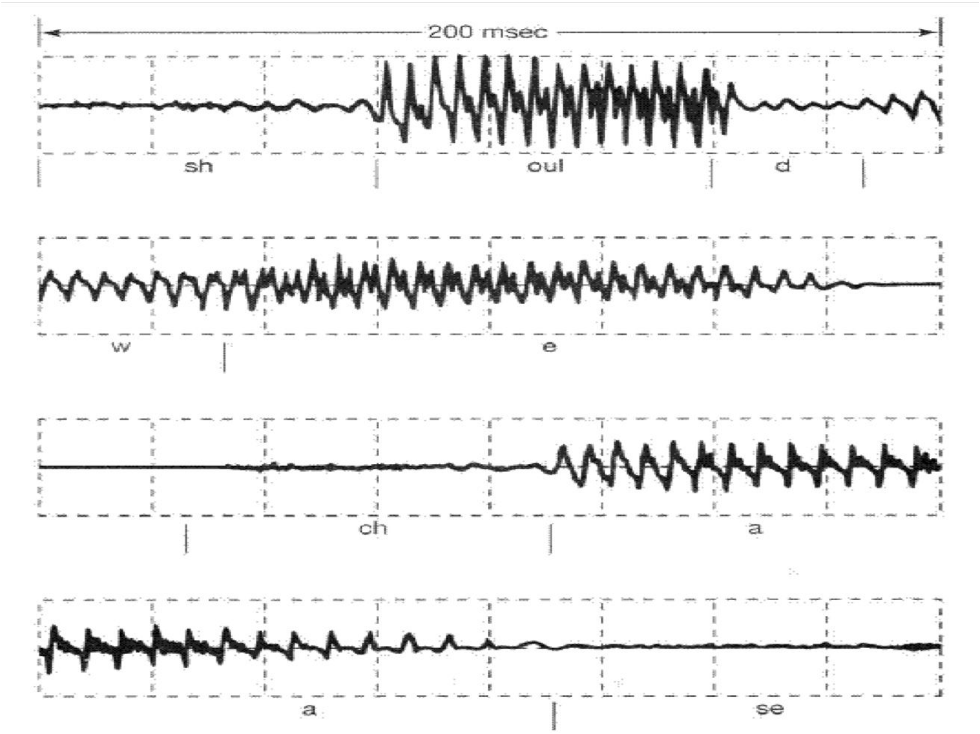
- They bring out the true degrees of freedom in the data.
- They capture relevant structure at multiple scales.
- They screen out noisy or irrelevant structure.

Degrees of freedom



Usual representation of speech:

- Take overlapping windows of the speech signal
- Apply many filters within each window
- More filters ⇒ higher dimensional

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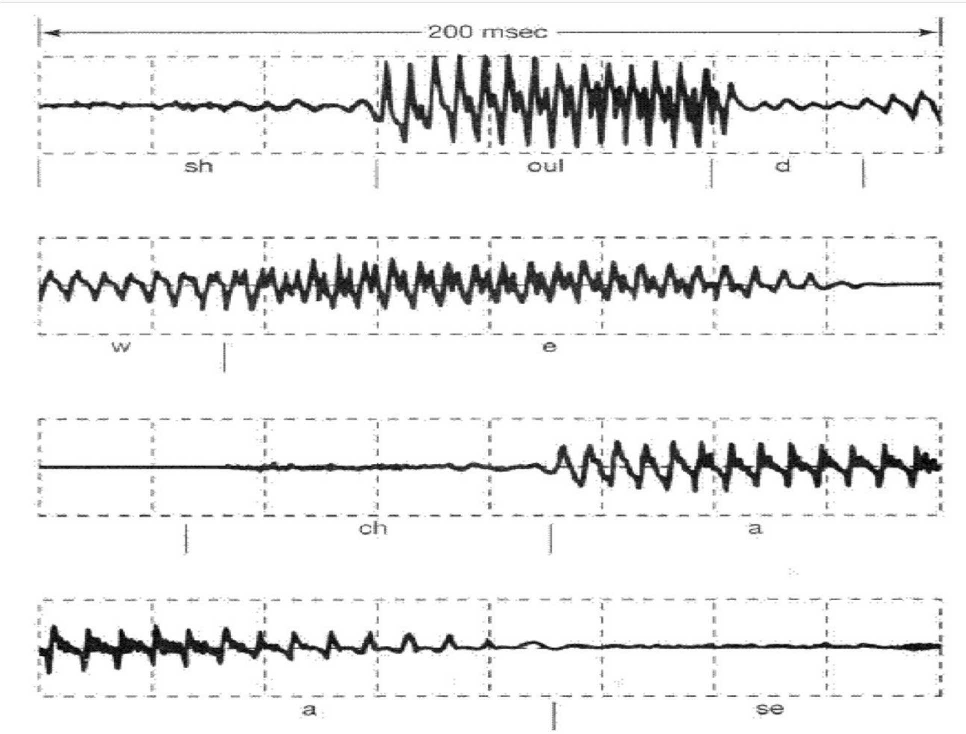

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But the speech is produced by a physical system (vocal tract) with a fixed number of degrees of freedom. And the phoneme being uttered can be characterized by the configuration of this apparatus.

Multiscale structure

Commonly-occurring structure at many levels:

- Low-level: like local edges
- Higher-level: like wheels, windows

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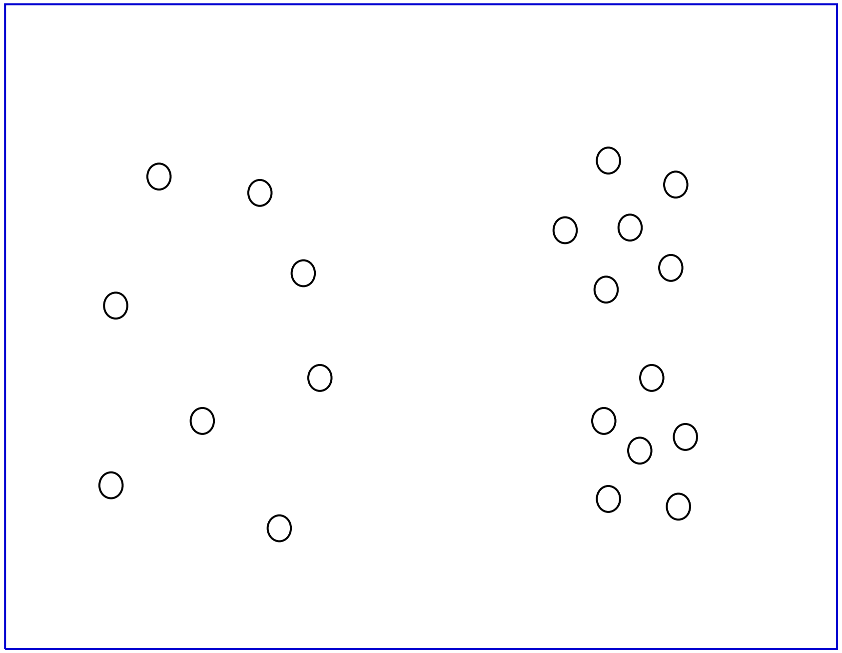
Topics:

- Clustering
- Informative linear projections
- Embedding and manifold learning
- Metric learning
- Autoencoders
- Deep nets

Clustering in $\mathbf{R}^p$



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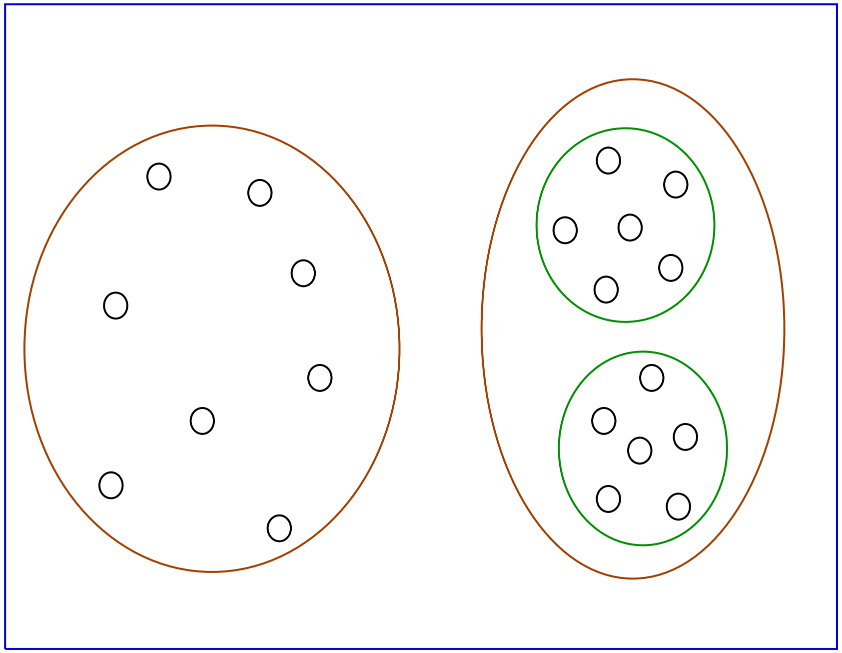

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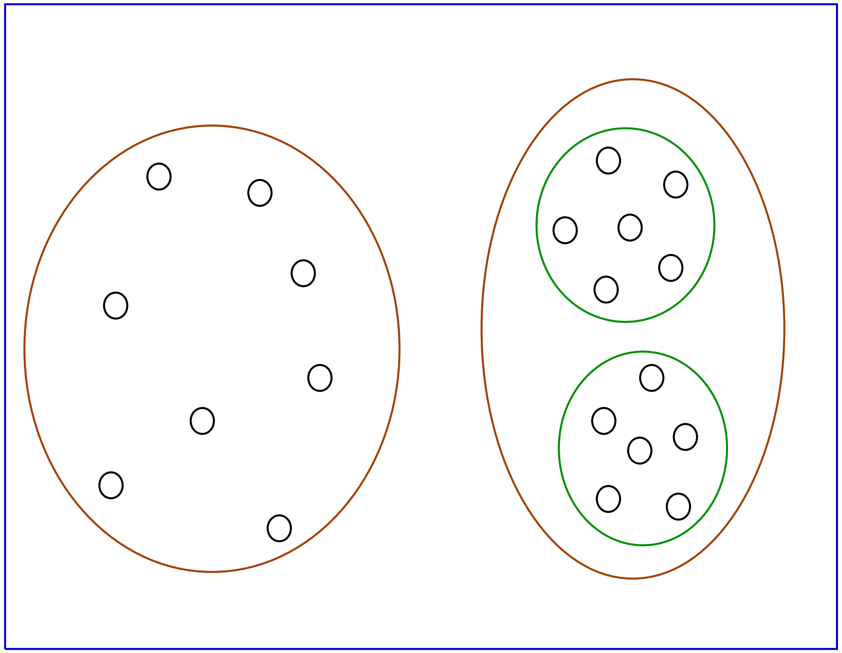

Two common uses of clustering:

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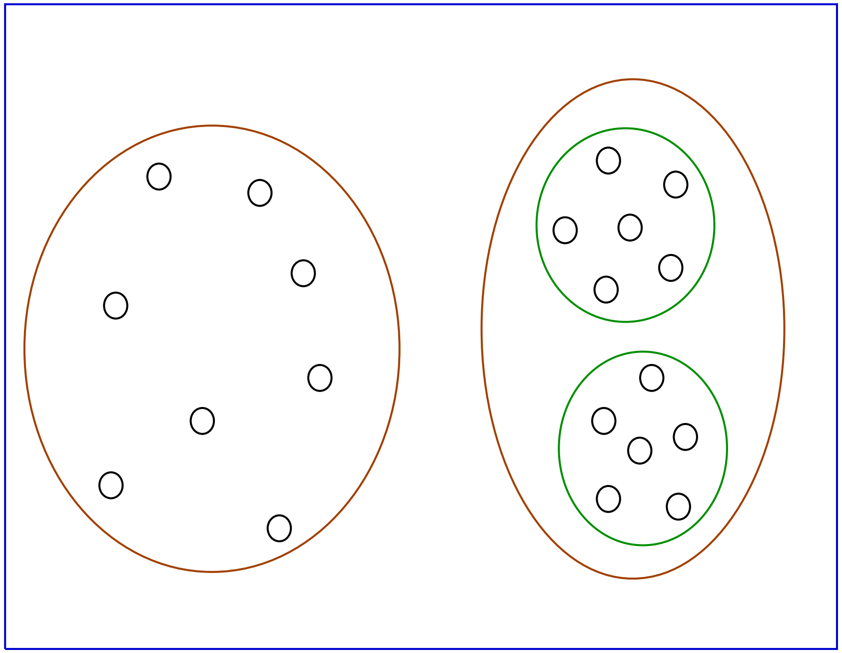

Two common uses of clustering:

- Vector quantization

  Find a finite set of representatives, that provides good coverage of a
  complex, possibly infinite, high-dimensional space
- Finding meaningful structure in data

  Finding salient grouping in data.

Widely-used clustering methods

1. *K* -means and its many variants
2. EM for mixtures of Gaussians
3. Agglomerative hierarchical clustering

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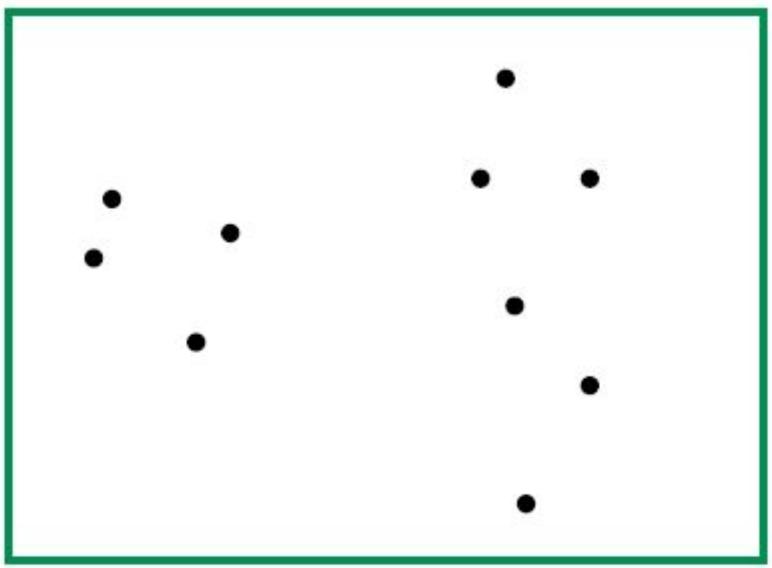
The *k*-means optimization problem

- Input: Points $x_1, \ldots, x_n \in \mathbb{R}^p$; integer k
- Output: "Centers", or representatives, $\mu_1, \ldots, \mu_k \in \mathbb{R}^p$
- Goal: Minimize average squared distance between points and their nearest representatives:

$$\text{cost}(\mu_1, \ldots, \mu_k) = \sum_{i=1}^{n} \min_j \|x_i - \mu_j\|^2$$



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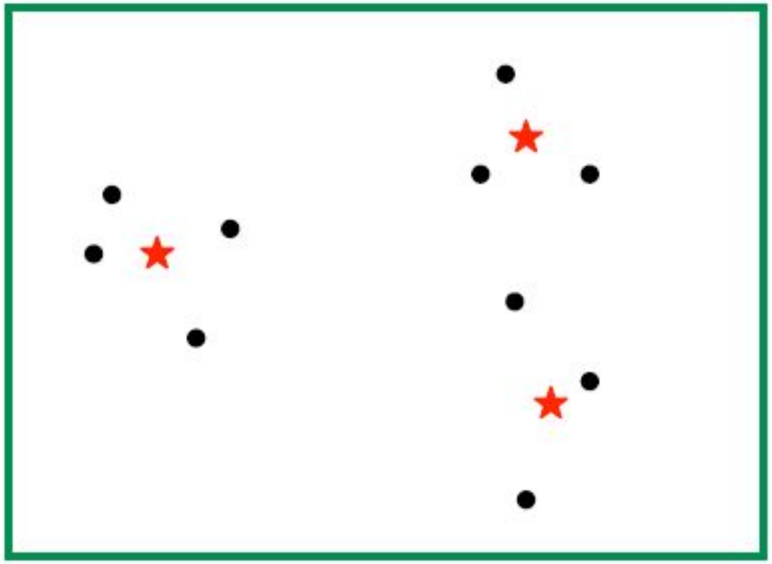

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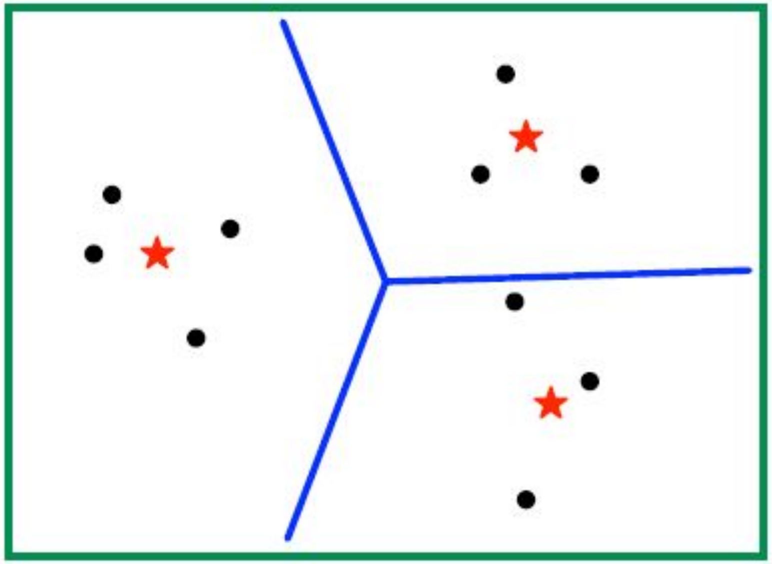

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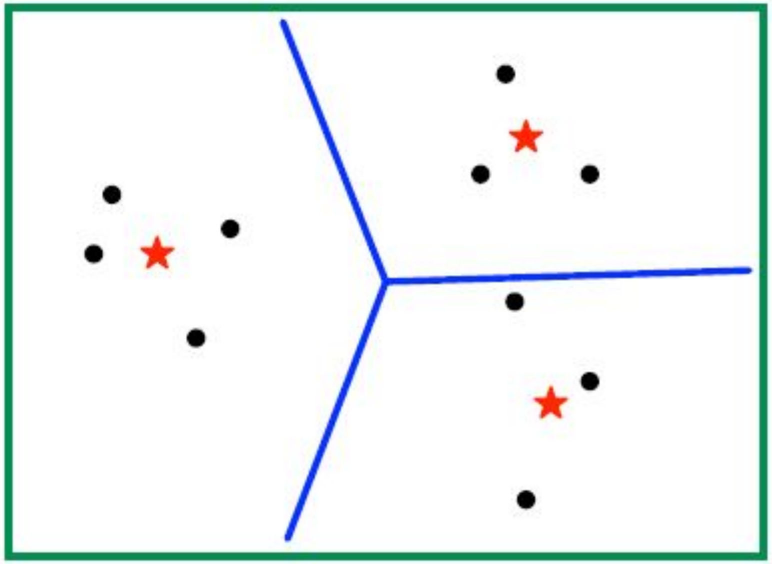

The centers carve $\mathbb{R}^p$ up into k convex regions: μ_j's region consists of points for which it is the closest center.

Lloyd's *k*-means algorithm

The *k*-means problem is NP-hard to solve. The most popular heuristic is called the "*k*-means algorithm".

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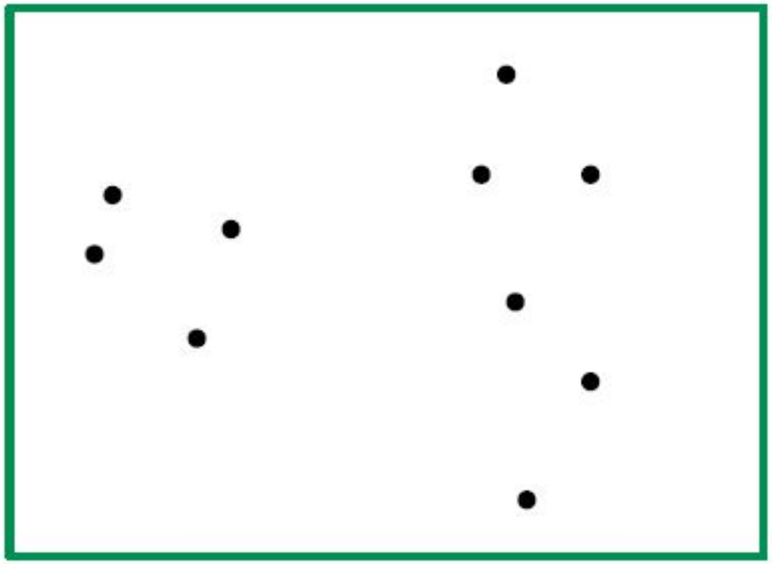

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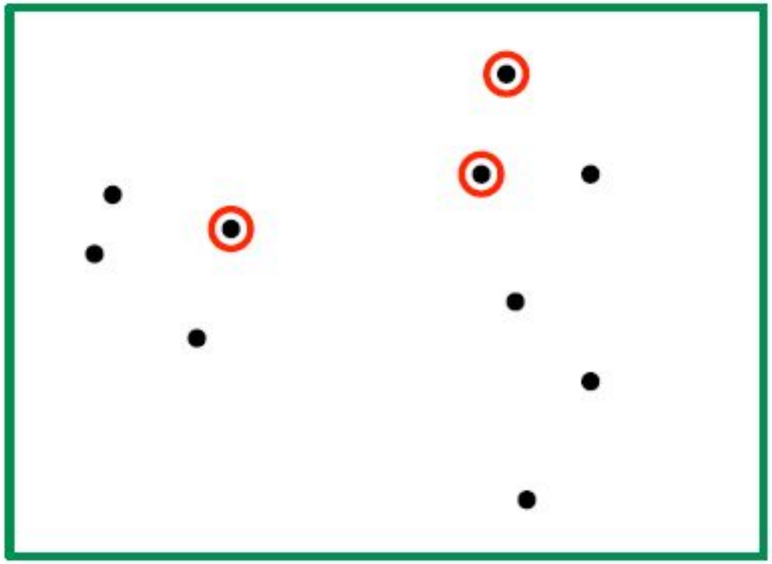

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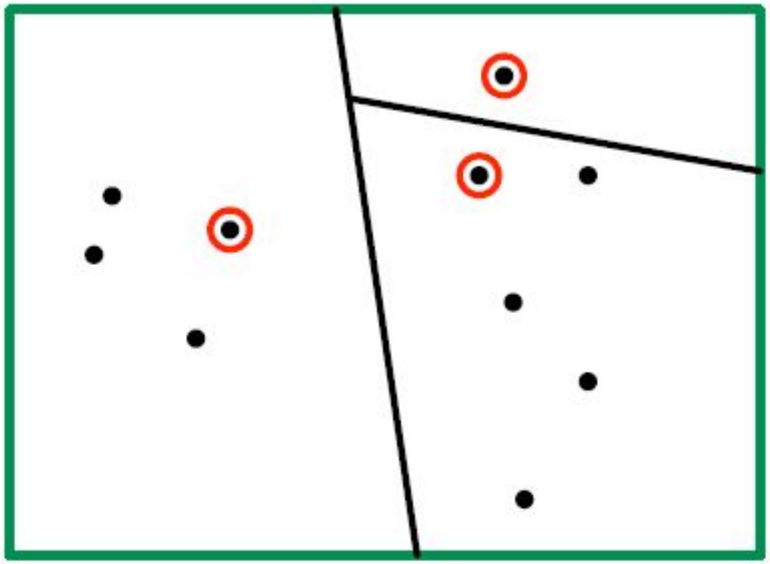

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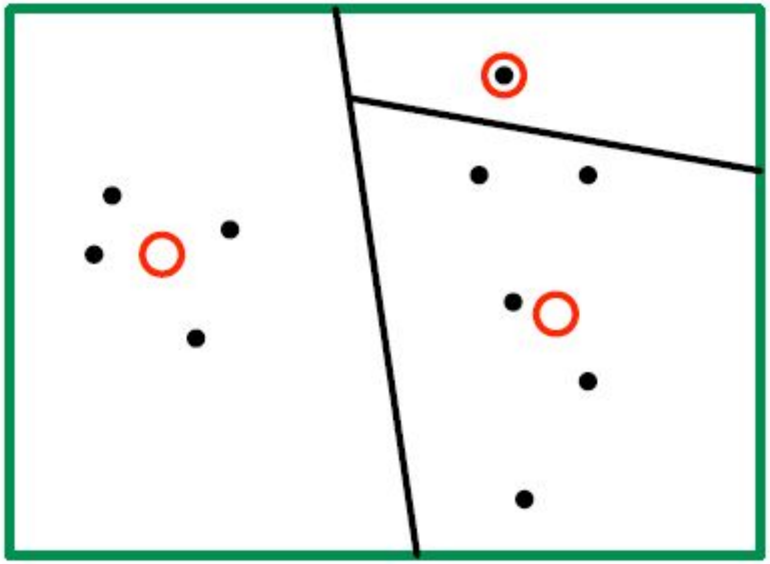

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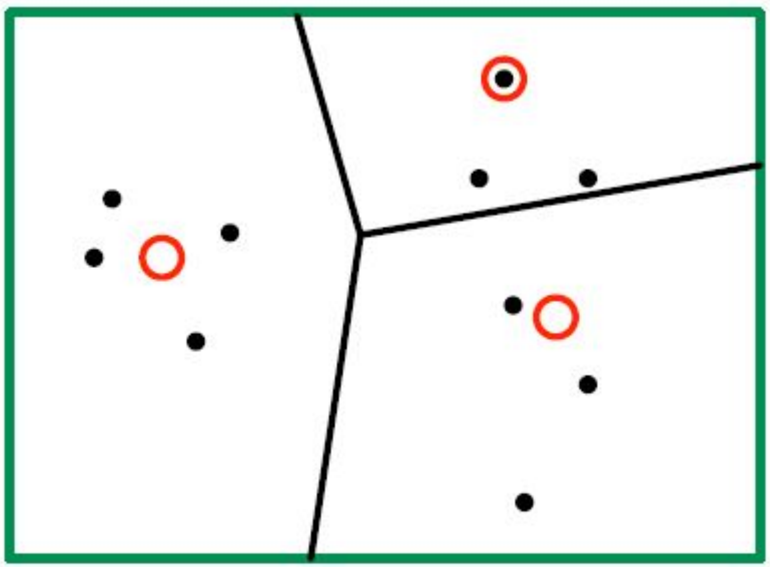

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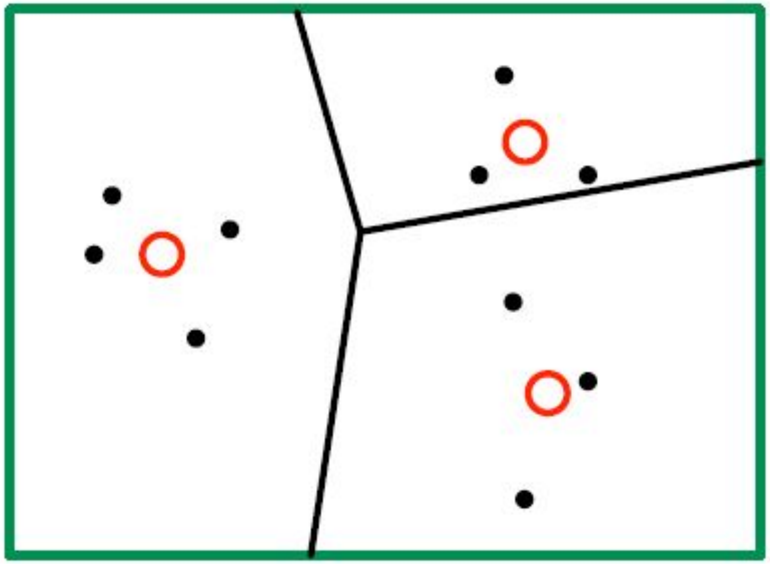

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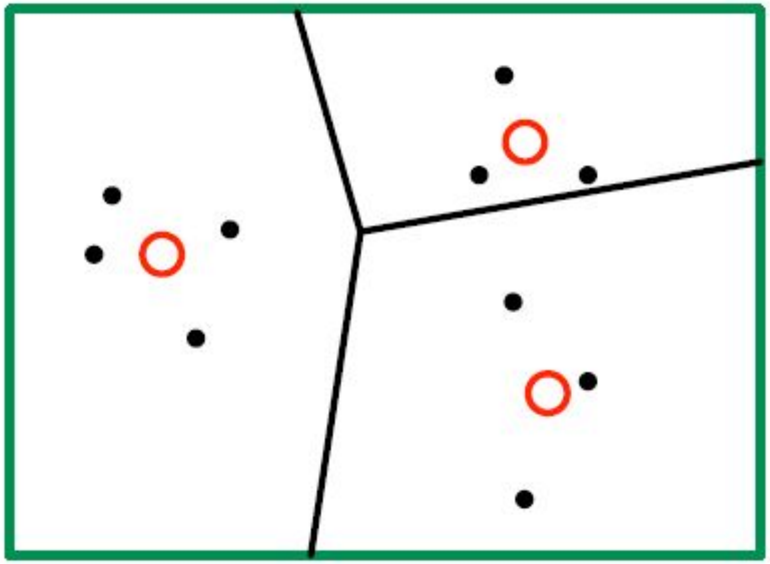

Each iteration reduces the cost $\Rightarrow$ convergence to a local optimum.

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Typical practice: choose *k* data points at random as the initial centers.

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A particularly good initializer: *k*-**means++**

- Pick a data point x at random as the first center
- Let $C = \{x\}$ (centers chosen so far)
- Repeat until desired number of centers is attained:
  - Pick a data point x at random from the following distribution:

$$\Pr(x) \propto \text{dist}(x, C)^2,$$

    where $\text{dist}(x, C) = \min_{z \in C} \|x - z\|$
  - Add x to C

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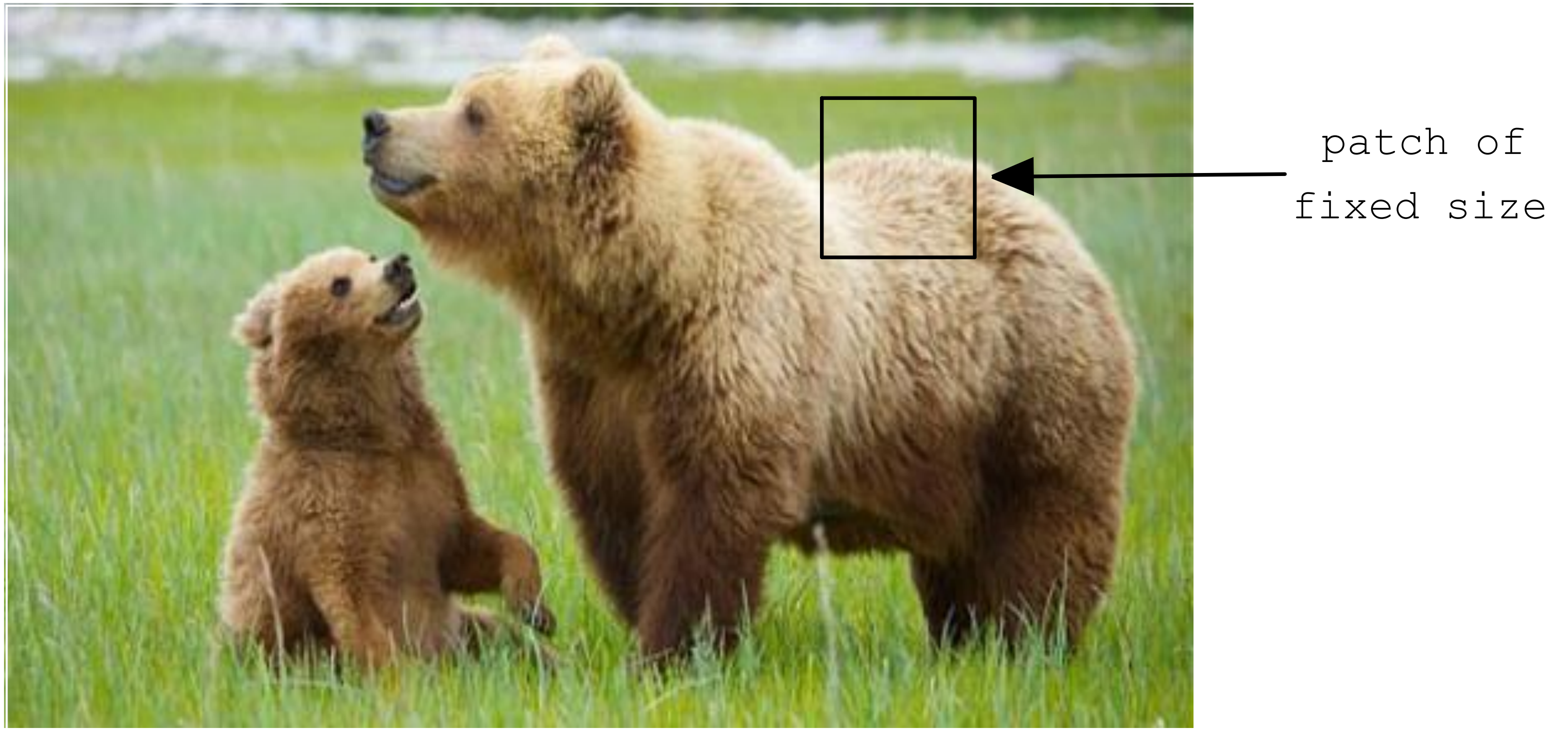

- Look at all $\ell \times \ell$ patches in all images. Extract features for each.
- Run k-means on this entire collection to get k centers.
- Now associate any image patch with its nearest center.
- Represent an image by a histogram over $\{1, 2, \ldots, k\}$.

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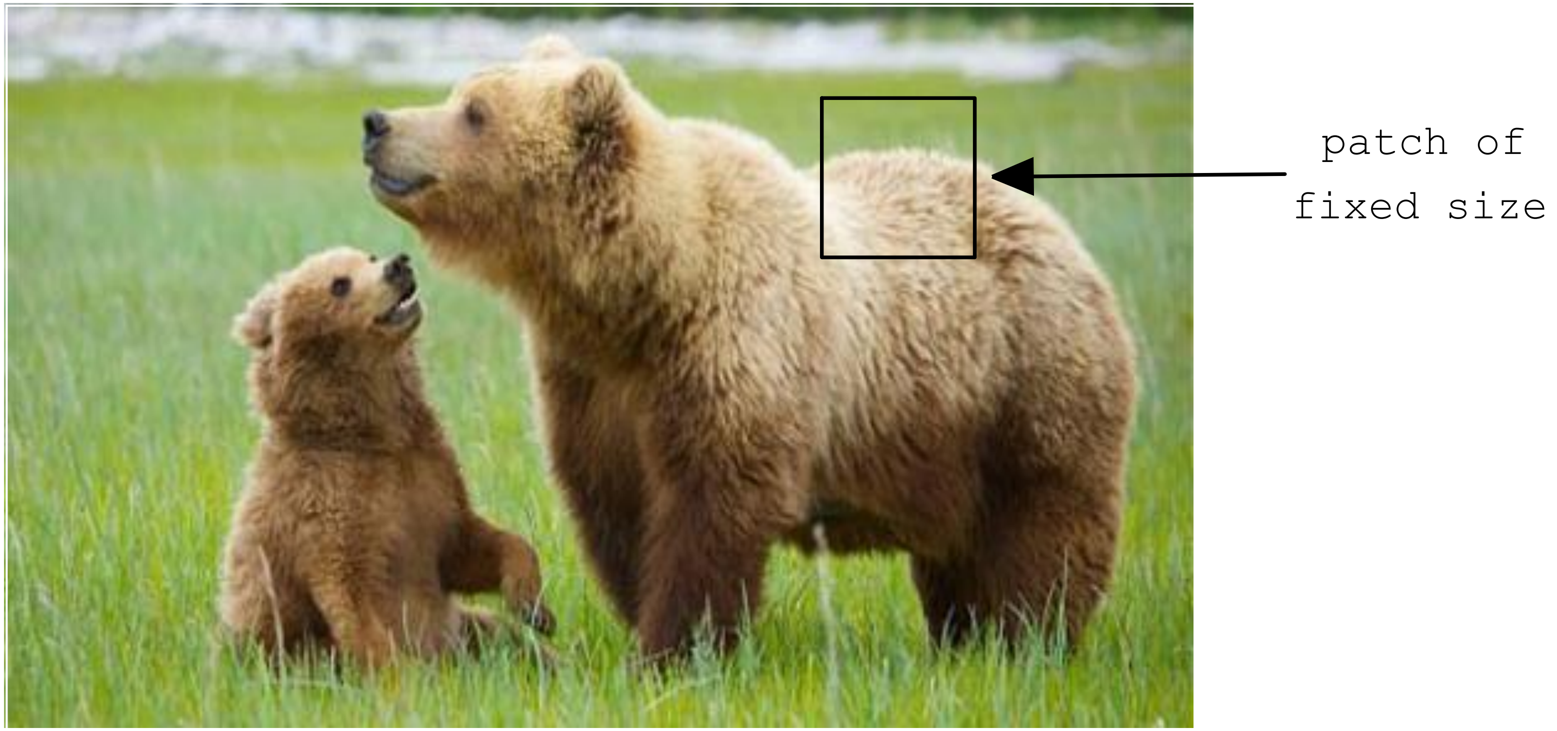

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Such data sets are truly enormous.

Streaming and online computation

Streaming computation: for data sets that are too large to fit in memory.

- Make one pass (or maybe a few passes) through the data.
- On each pass:
  - See data points one at a time, in order.
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Online computation: an even more lightweight setup, for data that is continuously being collected.

- Initialize a model.
- Repeat forever:
  - See a new data point.
  - Update model if need be.

Example: sequential *k*-means

1. Set the centers $\mu_1, \ldots, \mu_k$ to the first k data points
2. Set their counts to $n_1 = n_2 = \cdots = n_k = 1$
3. Repeat, possibly forever:
   - Get next data point x
   - Let μ_j be the center closest to x
   - Update μ_j and n_j:

$$\mu_j = \frac{n_j \mu_j + x}{n_j + 1} \quad \text{and} \quad n_j = n_j + 1$$

K -means: the good and the bad

The good:

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- Effective in quantization.

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Is there is a similarly-simple algorithm in which clusters of more general shape are accommodated?

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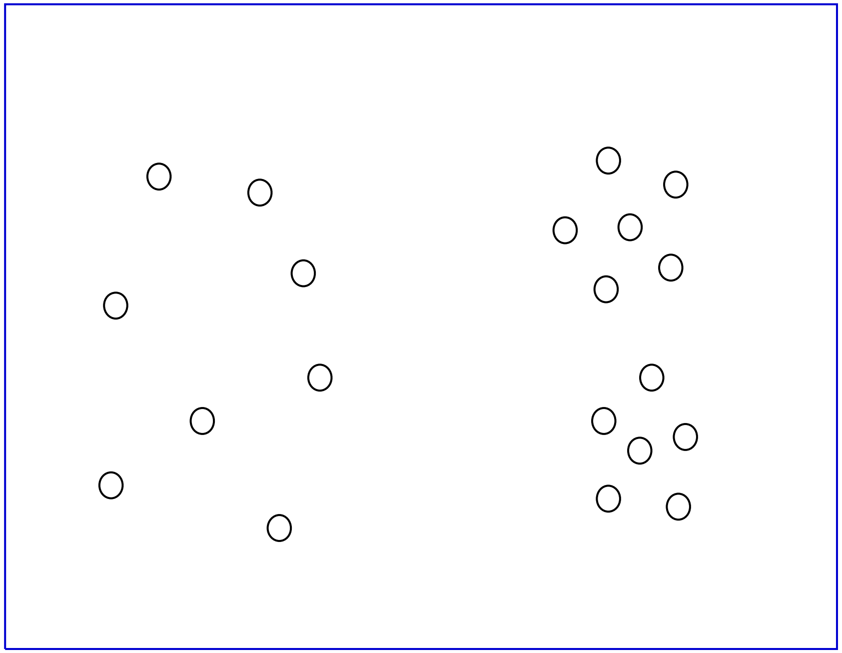
Hierarchical clustering

Choosing the number of clusters (*k*) is difficult.



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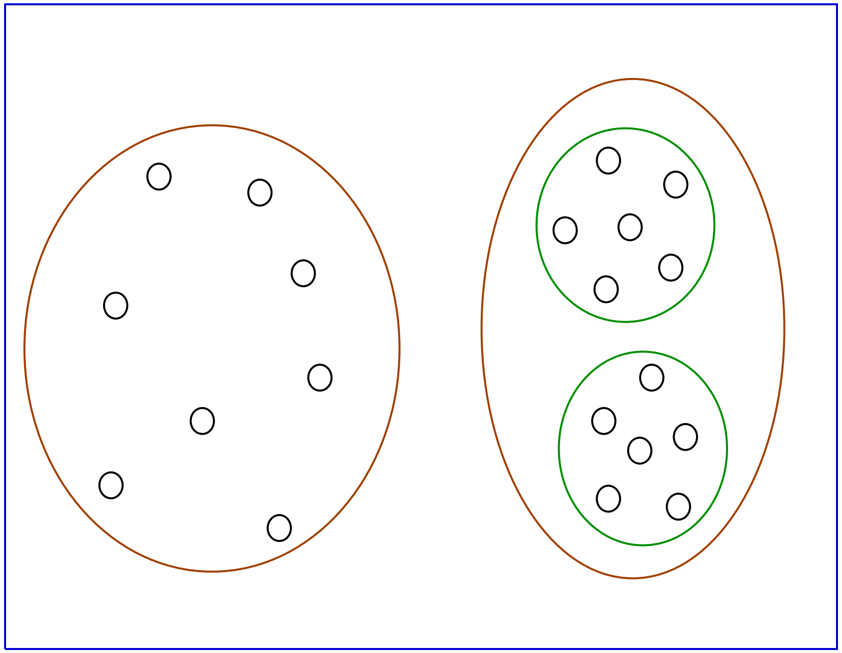

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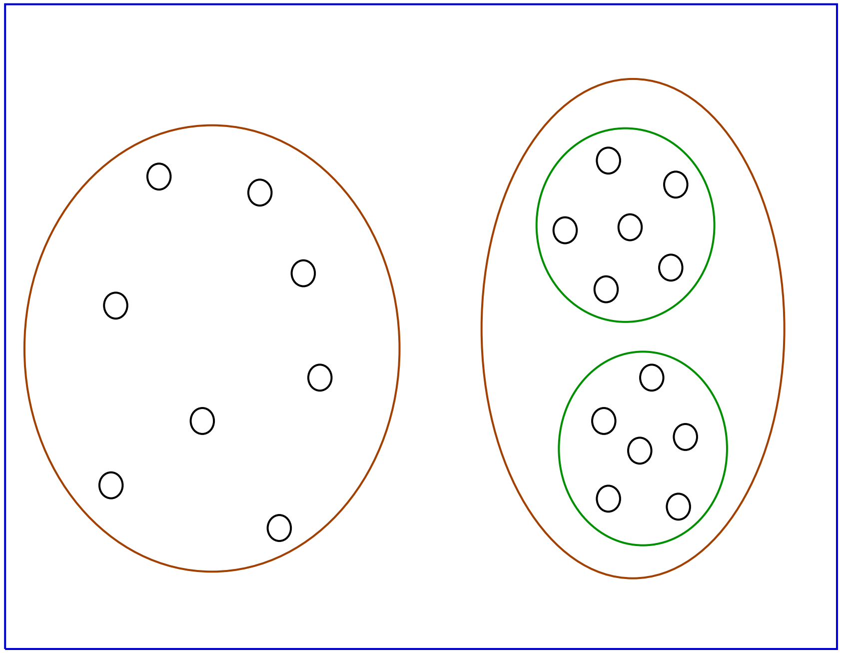

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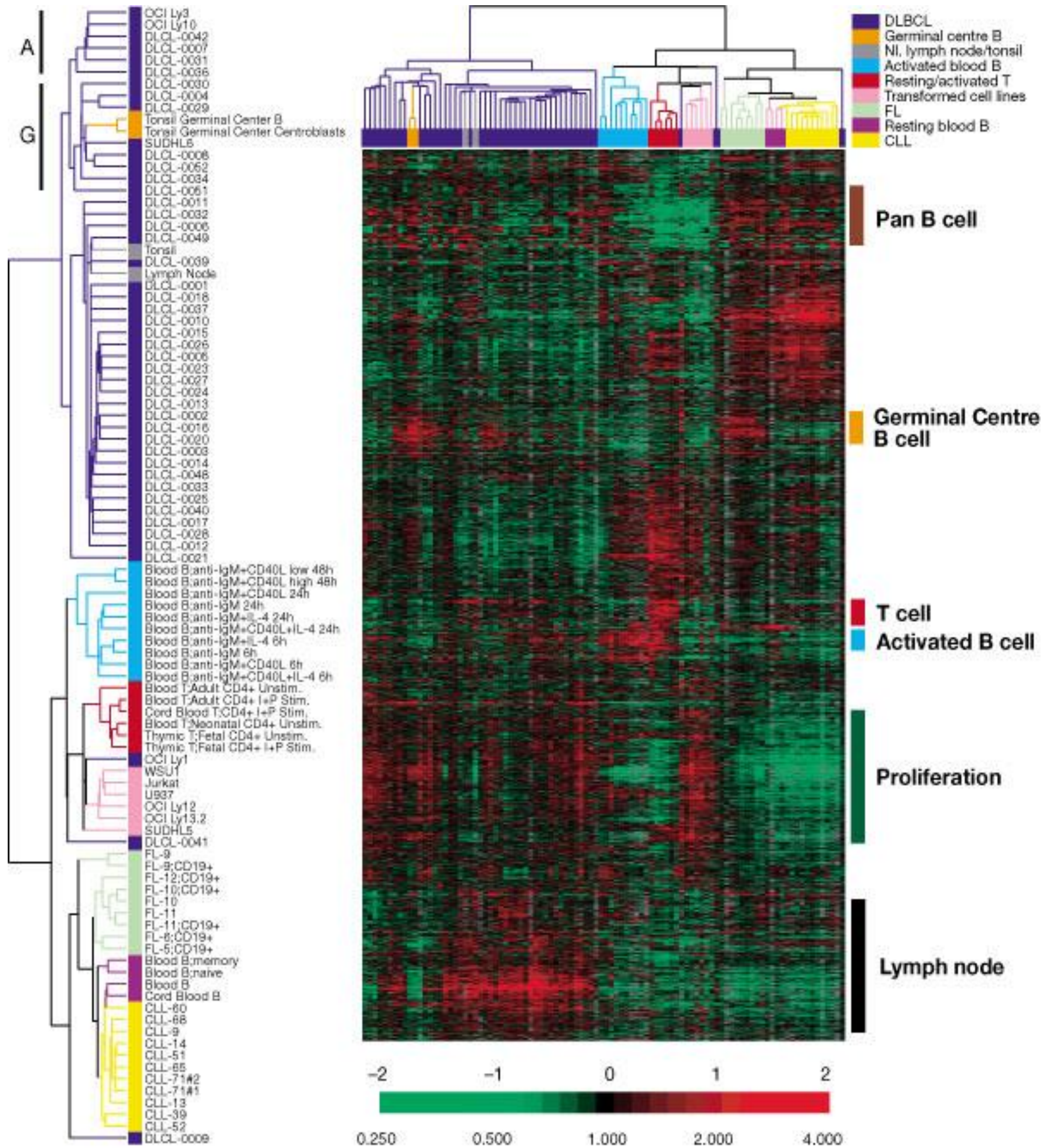
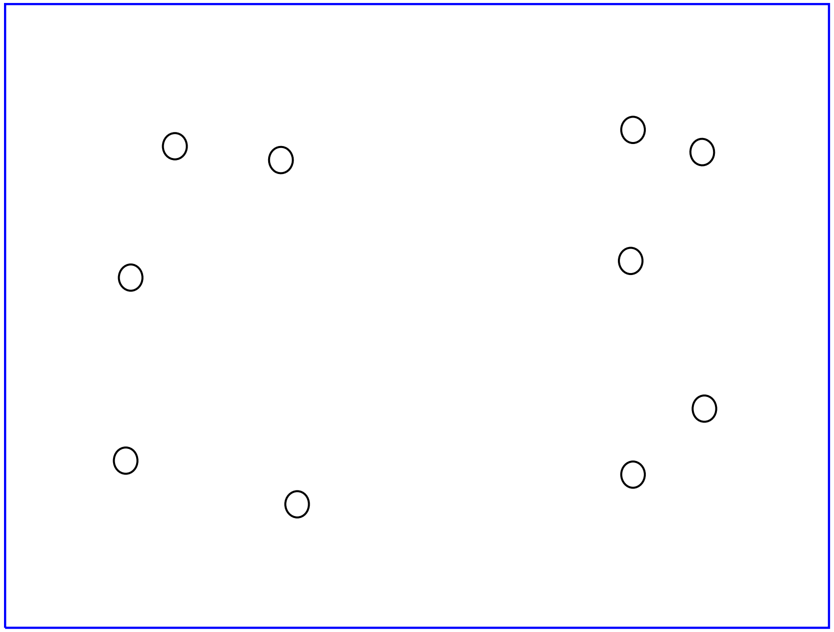
Hierarchical clustering avoids these problems.

Example: gene expression data



The single linkage algorithm



- Start with each point in its own, singleton, cluster
- Repeat until there is just one cluster:
  - Merge the two clusters with the closest pair of points
- Disregard singleton clusters

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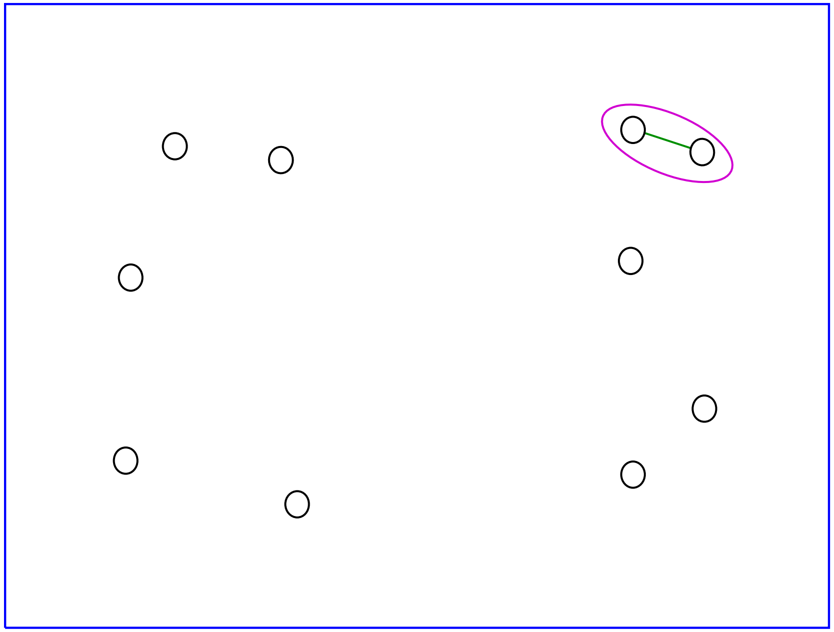

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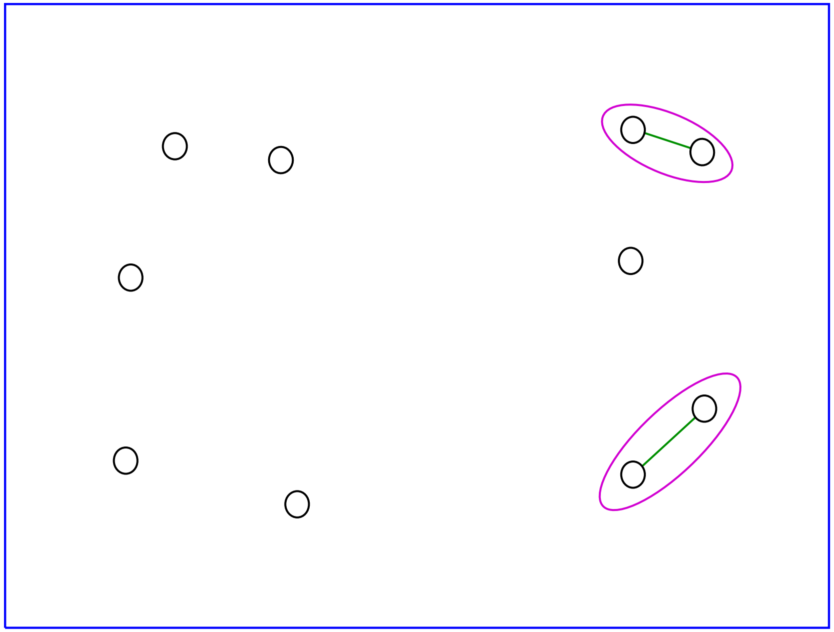

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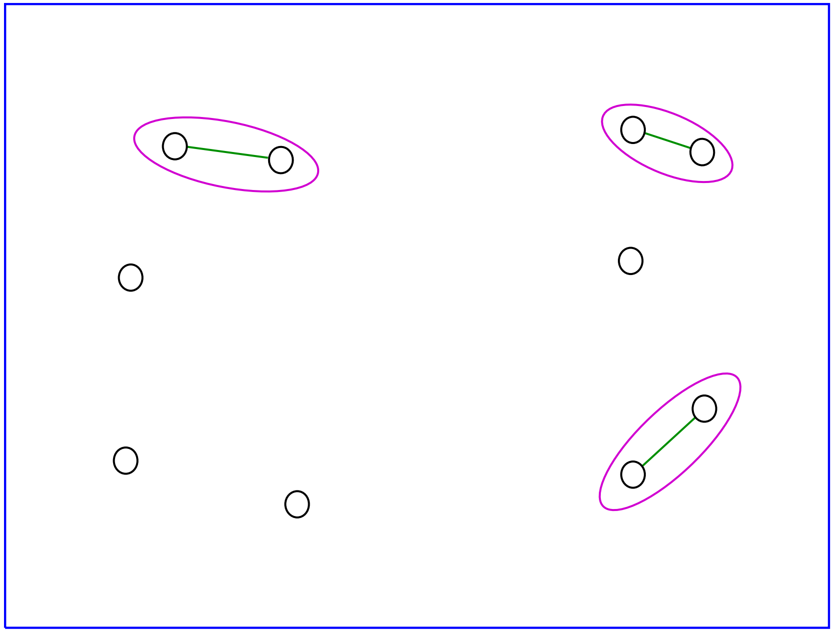

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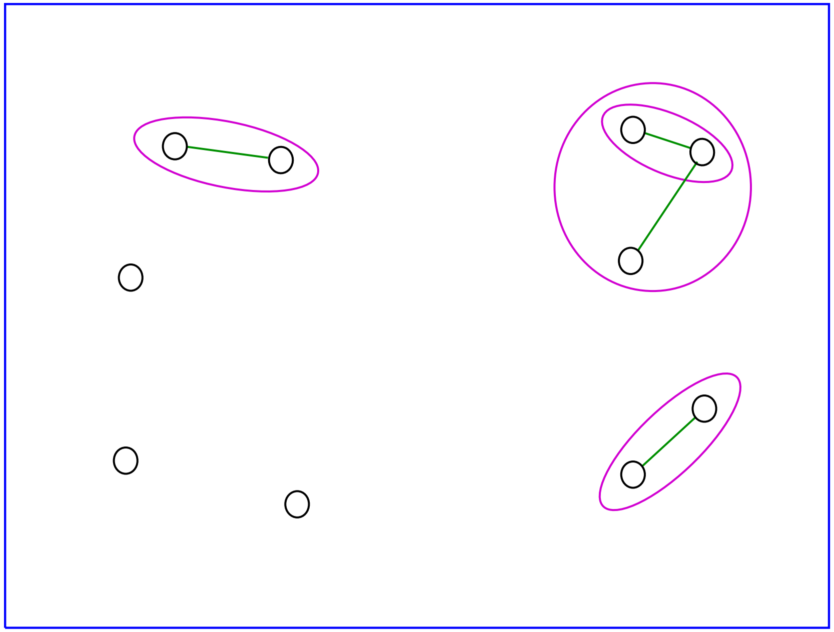

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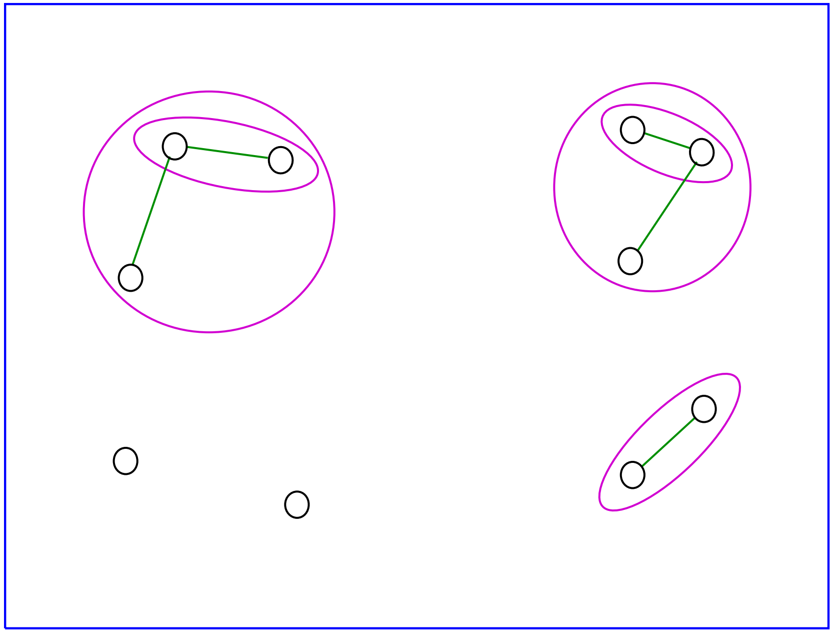

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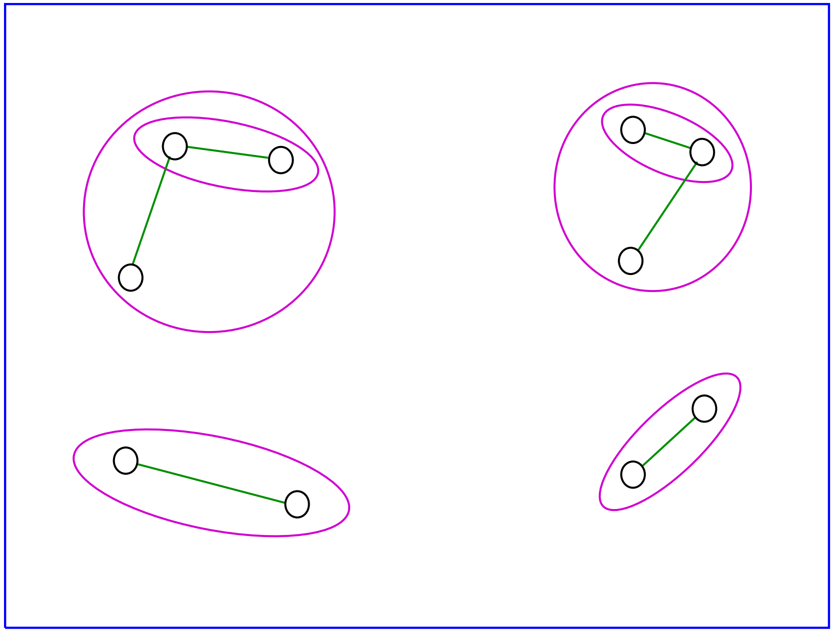

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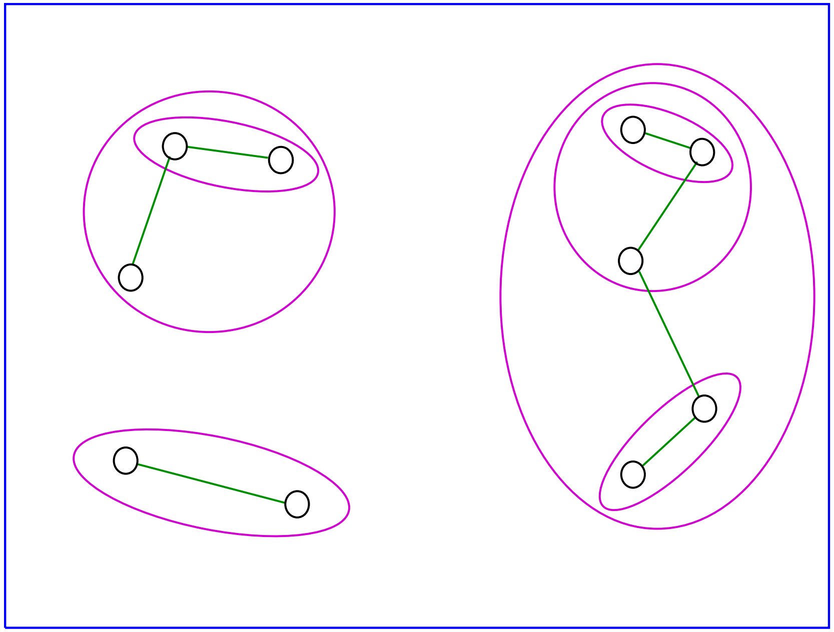

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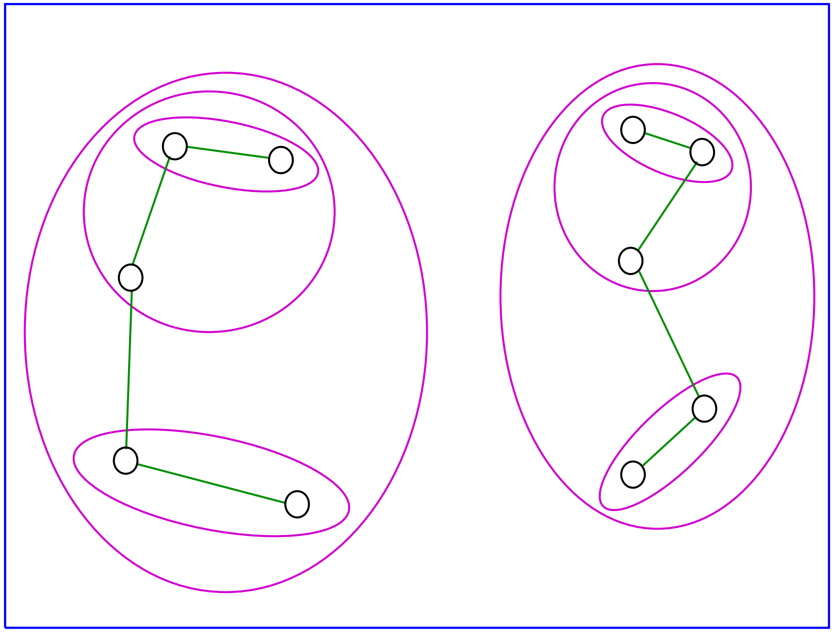

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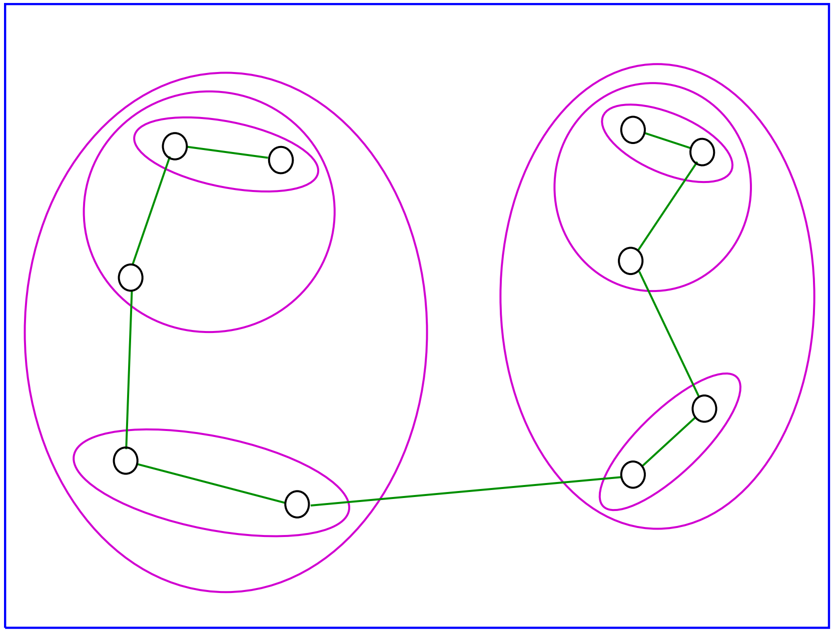

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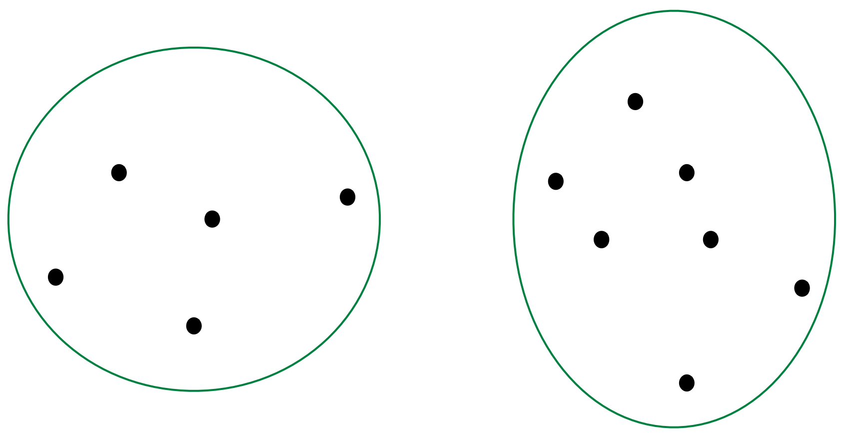

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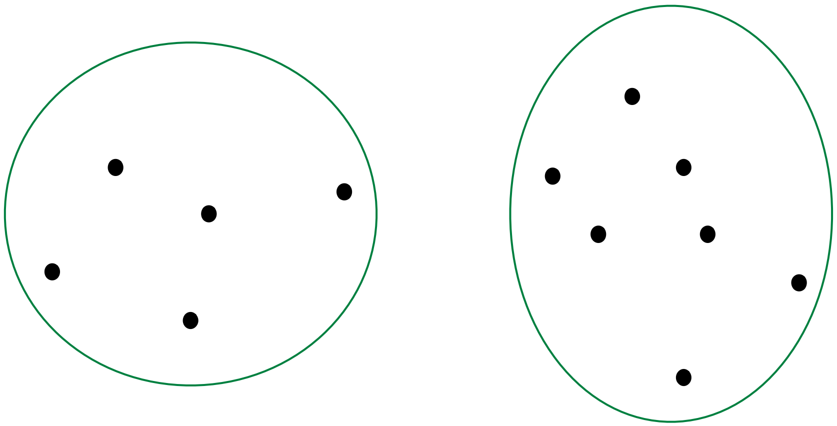

- Single linkage

$$\mathrm{dist}(C, C') = \min_{x \in C, x' \in C'} \|x - x'\|$$

- Complete linkage

$$\mathrm{dist}(C, C') = \max_{x \in C, x' \in C'} \|x - x'\|$$

Average linkage

Three commonly-used variants:

1. Average pairwise distance between points in the two clusters

$$\text{dist}(C, C') = \frac{1}{|C| \cdot |C'|} \sum_{x \in C} \sum_{x' \in C'} \|x - x'\|$$

2. Distance between cluster centers

$$\text{dist}(C, C') = \|\text{mean}(C) - \text{mean}(C')\|$$

3. Ward's method: the increase in k-means cost occasioned by merging the two clusters

$$\text{dist}(C, C') = \frac{|C| \cdot |C'|}{|C| + |C'|} \|\text{mean}(C) - \text{mean}(C')\|^2$$

(penalize merging of large clusters)