Clustering Analysis – Hierarchical Clustering

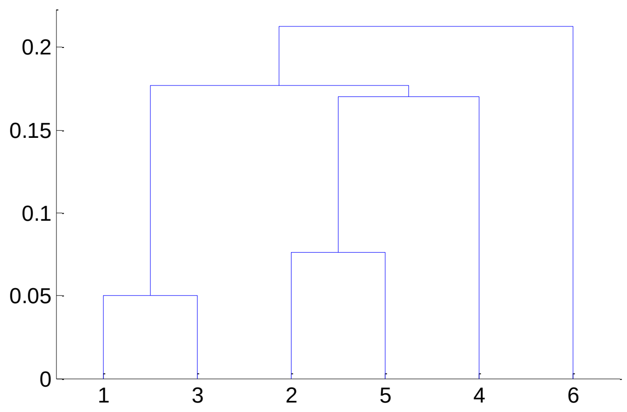
Rina BUOY

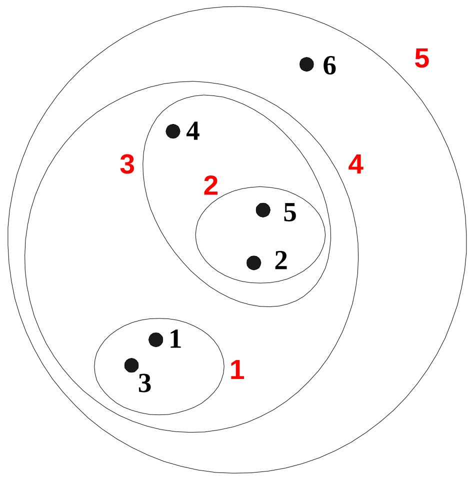
AMERICAN UNIVERSITY OF PHNOM PENH

STUDY LOCALLY. LIVE GLOBALLY.

Hierarchical Clustering

- Produces a set of nested clusters organized as a hierarchical tree
- Can be visualized as a dendrogram
  - A tree like diagram that records the sequences of merges or splits





Strengths of Hierarchical Clustering

- Do not have to assume any particular number of clusters
  - Any desired number of clusters can be obtained by ‘cutting’ the dendrogram at the proper level

- They may correspond to meaningful taxonomies
  - Example in biological sciences (e.g., animal kingdom, phylogeny reconstruction, …)

Hierarchical Clustering

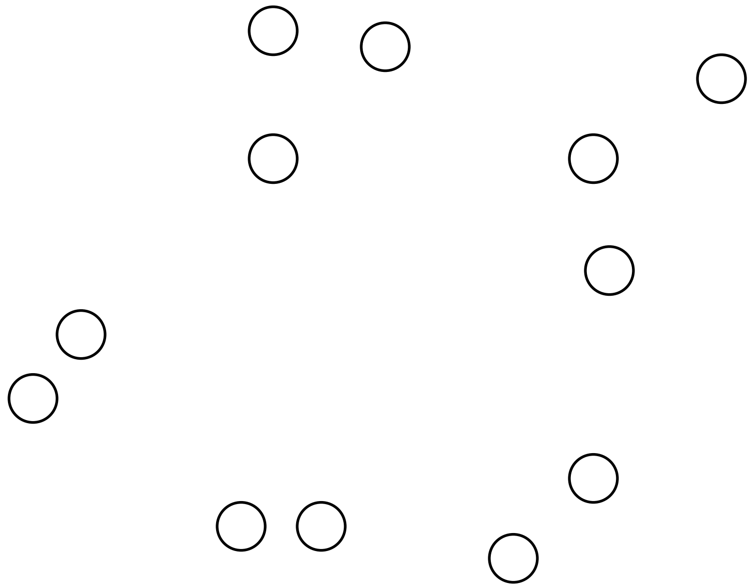
- Two main types of hierarchical clustering
  - Agglomerative:
    - Start with the points as individual clusters
    - At each step, merge the closest pair of clusters until only one cluster (or k clusters) left
  - Divisive:
    - Start with one, all-inclusive cluster
    - At each step, split a cluster until each cluster contains an individual point (or there are k clusters)
- Traditional hierarchical algorithms use a similarity or distance matrix
  - Merge or split one cluster at a time

Agglomerative Clustering Algorithm

- **Key Idea: Successively merge closest clusters**
- Basic algorithm
  1. Compute the proximity matrix
  2. Let each data point be a cluster
  3. **Repeat**
  4. Merge the two closest clusters
  5. Update the proximity matrix
  6. **Until** only a single cluster remains
- Key operation is the computation of the proximity of two clusters
  - Different approaches to defining the distance between clusters distinguish the different algorithms

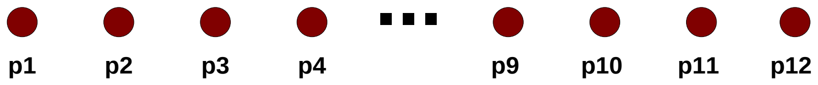
Steps 1 and 2

- Start with clusters of individual points and a proximity matrix



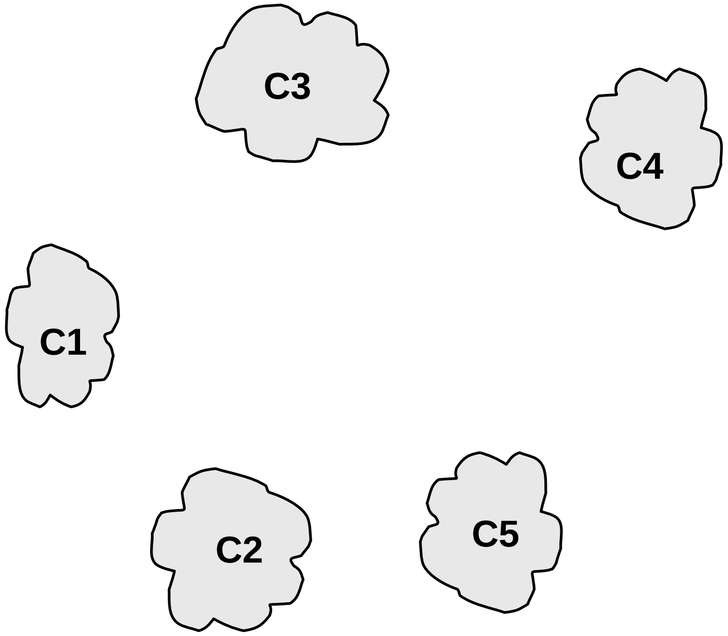
	p1	p2	p3	p4	p5	. . .
p1						
p2						
p3						
p4						
p5						
.						
.						
.						

Proximity Matrix



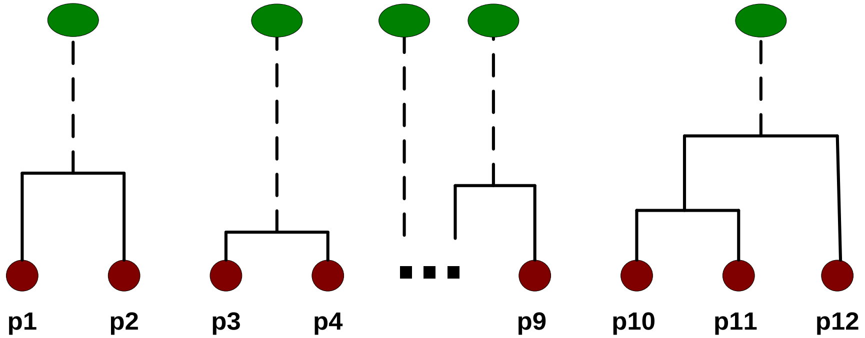
Intermediate Situation

- After some merging steps, we have some clusters



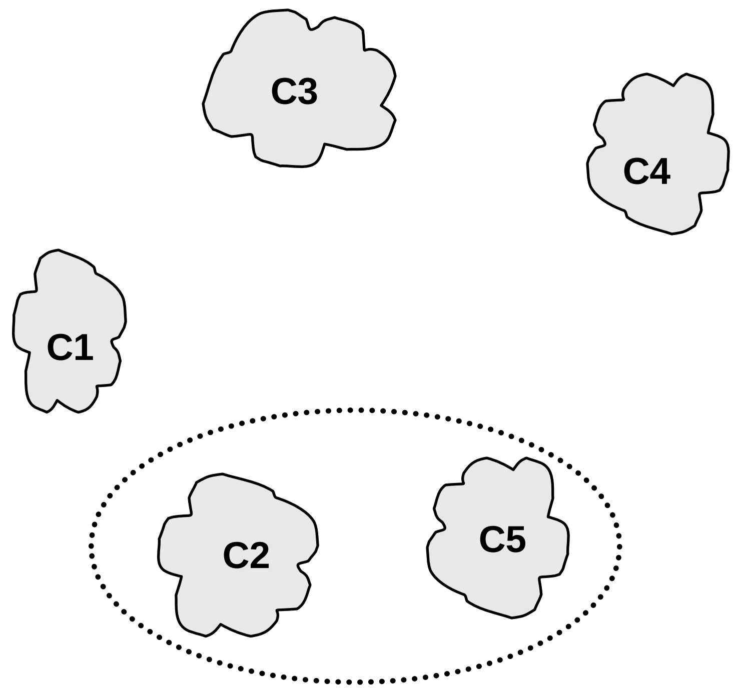
	C1	C2	C3	C4	C5
C1					
C2					
C3					
C4					
C5					

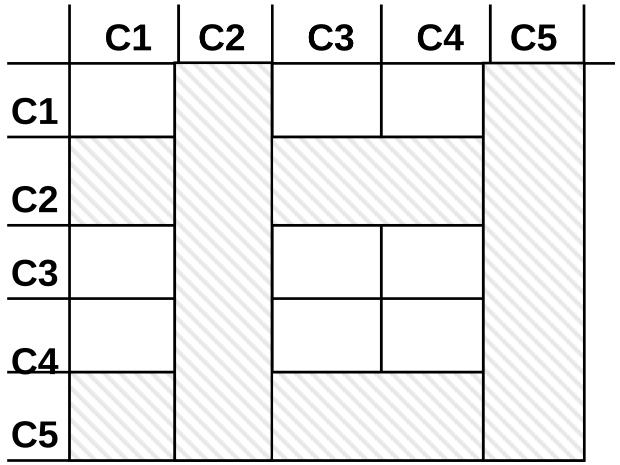
Proximity Matrix



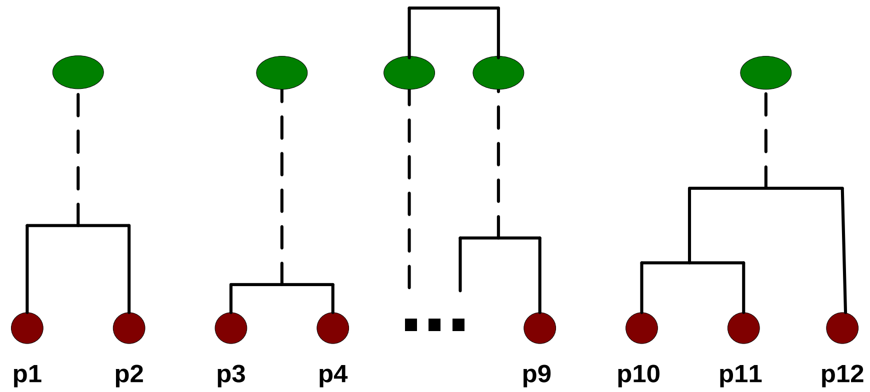
Step 4

- We want to merge the two closest clusters (C2 and C5) and update the proximity matrix.



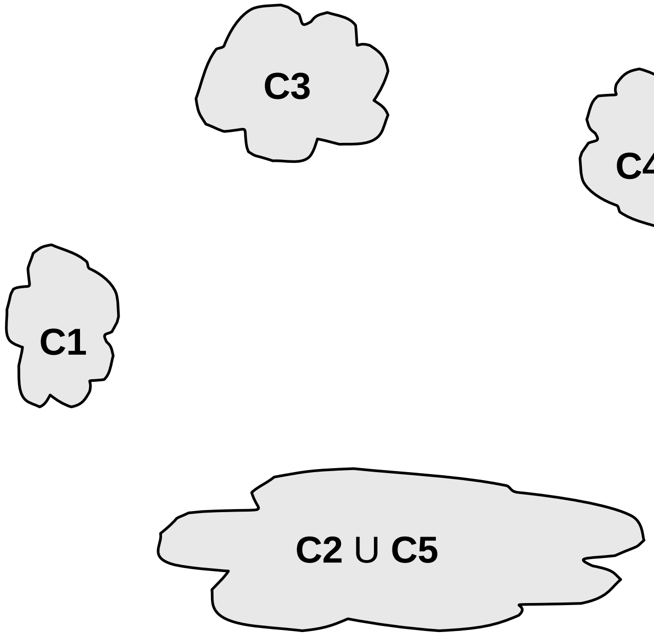


Proximity Matrix



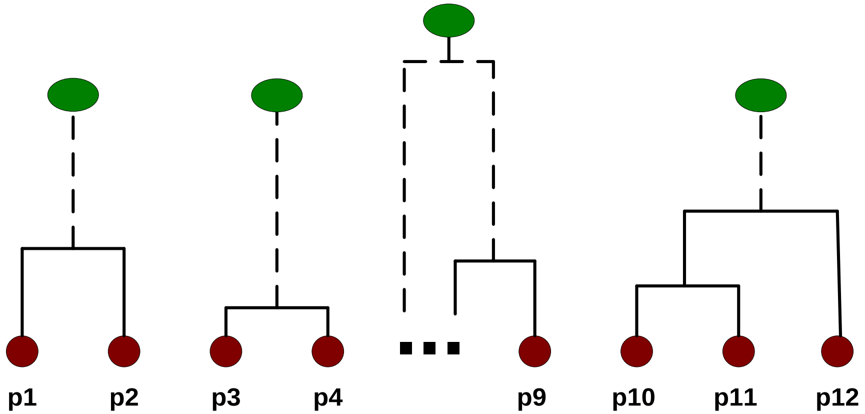
Step 5

- The question is “How do we update the proximity matrix?”

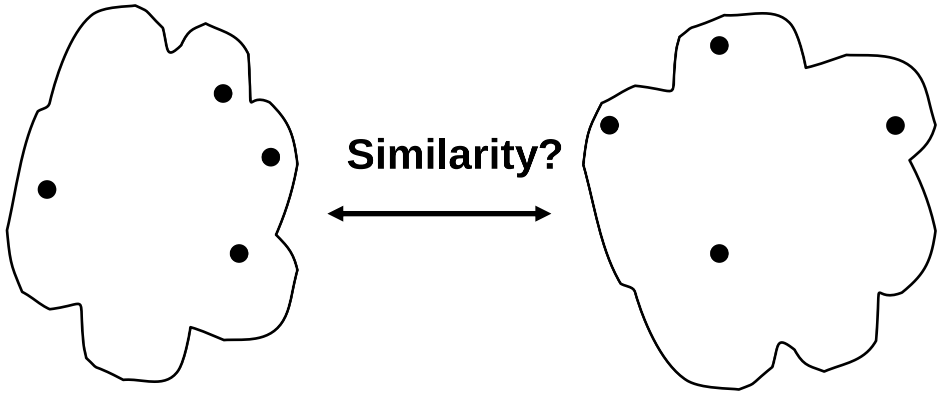


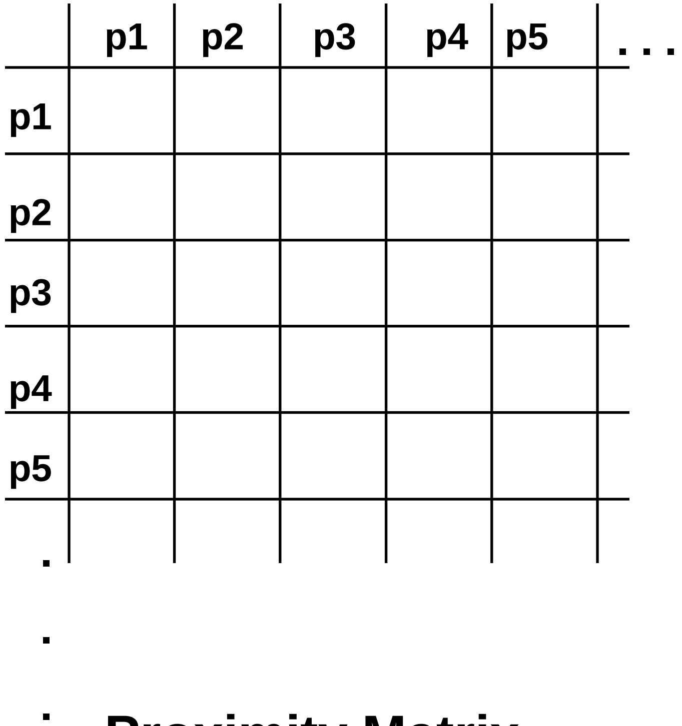
	C1	C2 U C5	C3	C4
C1		?		
C2 U C5	?	?	?	?
C3		?		
C4		?		

Proximity Matrix



How to Define Inter-Cluster Distance

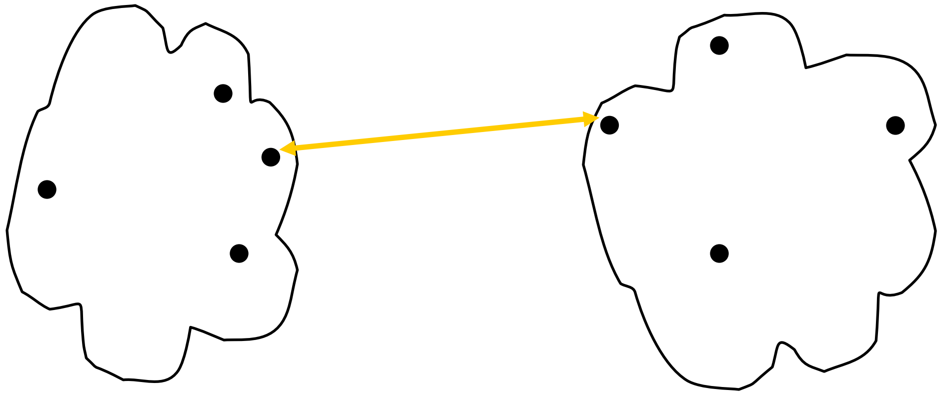




Proximity Matrix

- MIN
- MAX
- Group Average
- Distance Between Centroids
- Other methods driven by an objective function
  - Ward's Method uses squared error

How to Define Inter-Cluster Similarity



	p1	p2	p3	p4	p5	. . .
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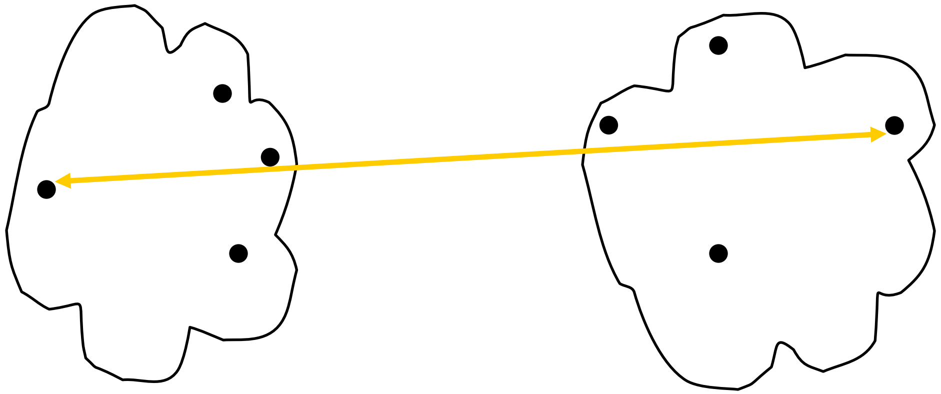

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Proximity Matrix

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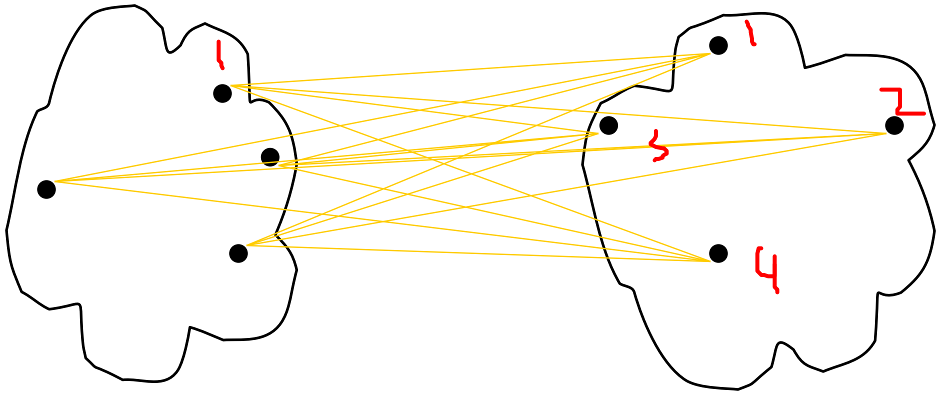

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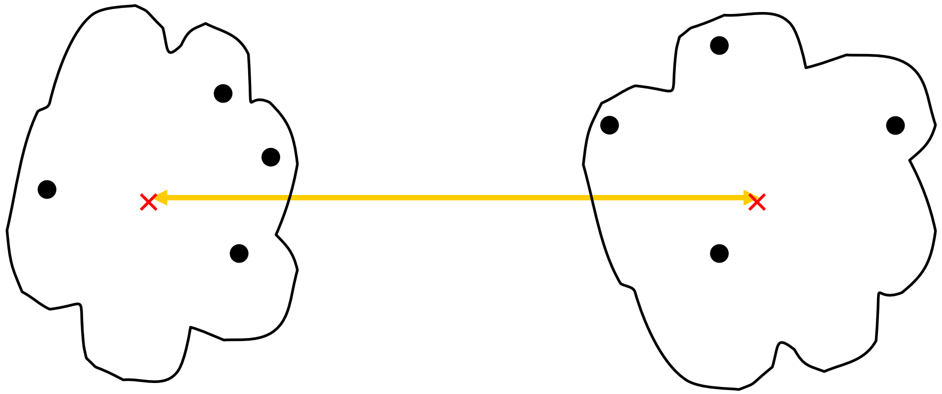
How to Define Inter-Cluster Similarity



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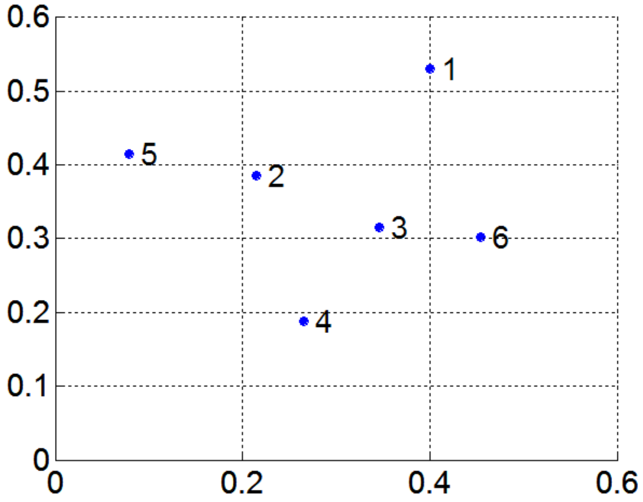
p2						
p3						
p4						
p5						
.						
.						
.						

Proximity Matrix

- MIN
- MAX
- Group Average
- Distance Between Centroids
- Other methods driven by an objective function
  - Ward's Method uses squared error

MIN or Single Link

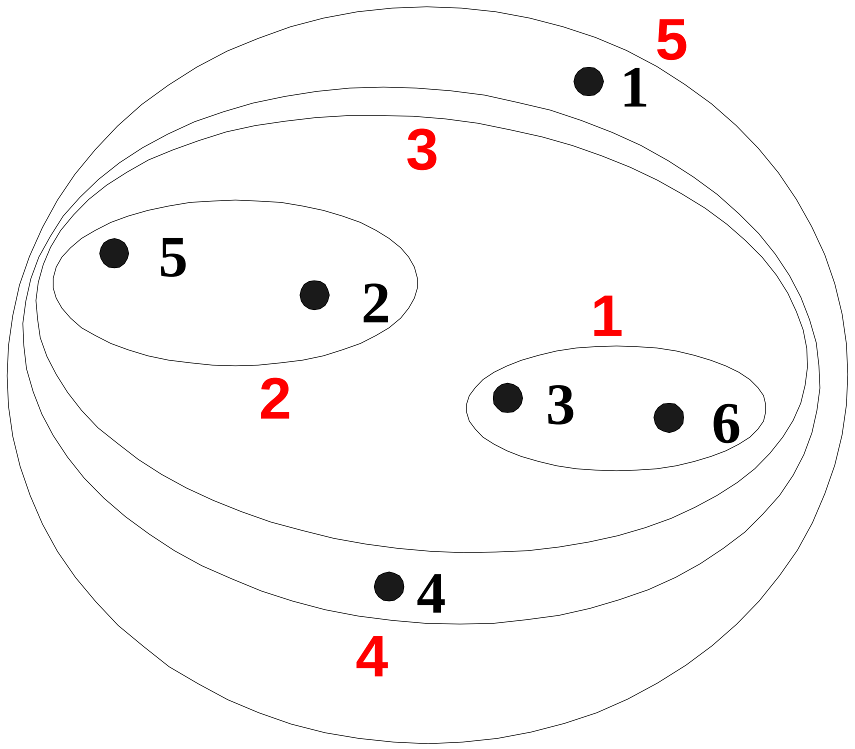
- Proximity of two clusters is based on the two closest points in the different clusters
  - Determined by one pair of points, i.e., by one link in the proximity graph
- Example:

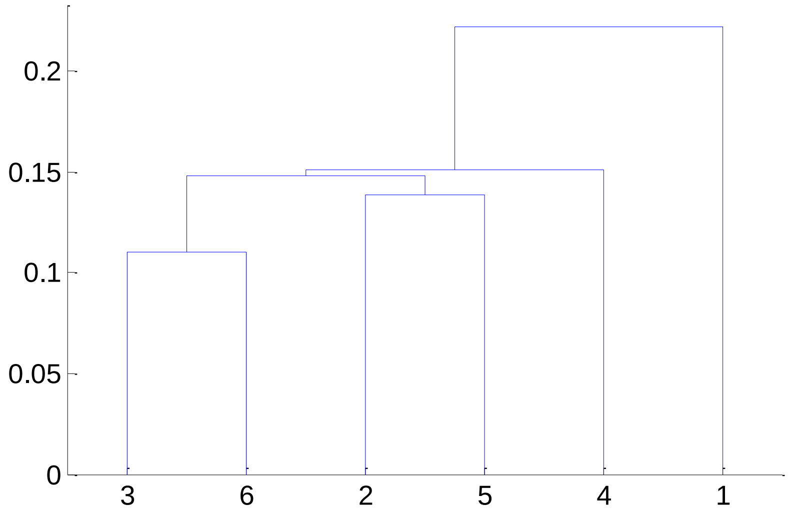


Distance Matrix:

	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.15	0.28	0.11
p4	0.37	0.20	0.15	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00

Hierarchical Clustering: MIN

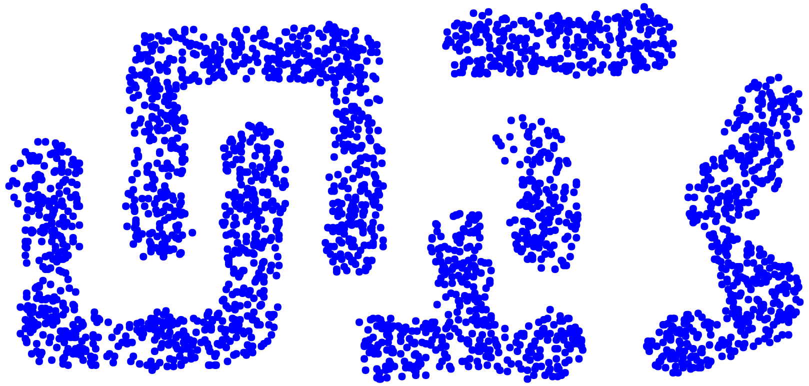




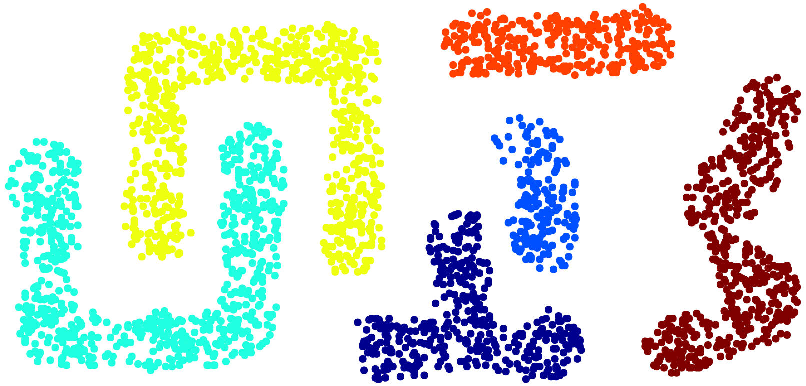
Nested Clusters

Dendrogram

Strength of MIN



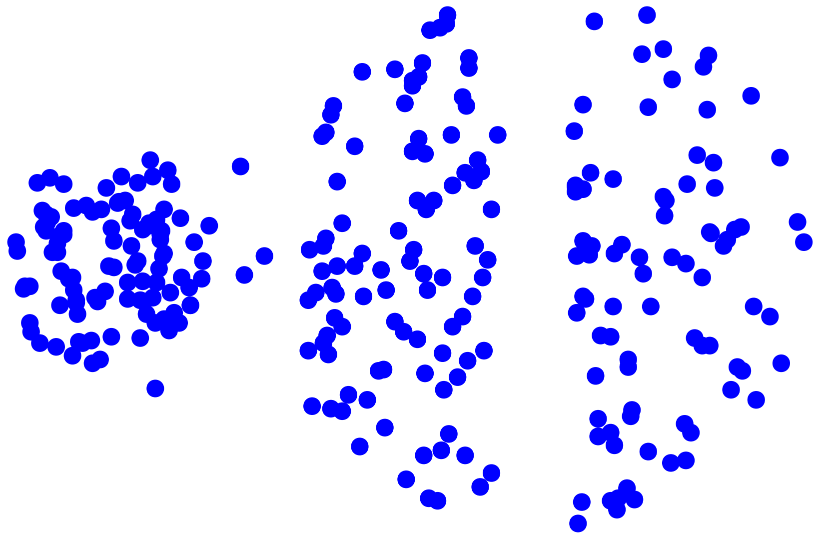
Original Points



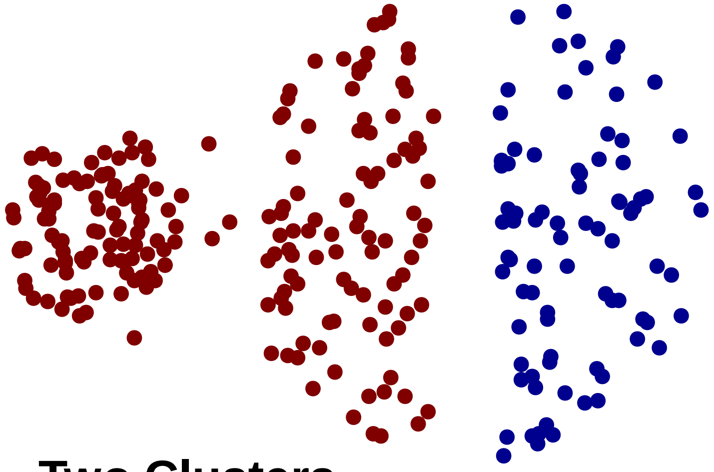
Six Clusters

- **Can handle non-elliptical shapes**

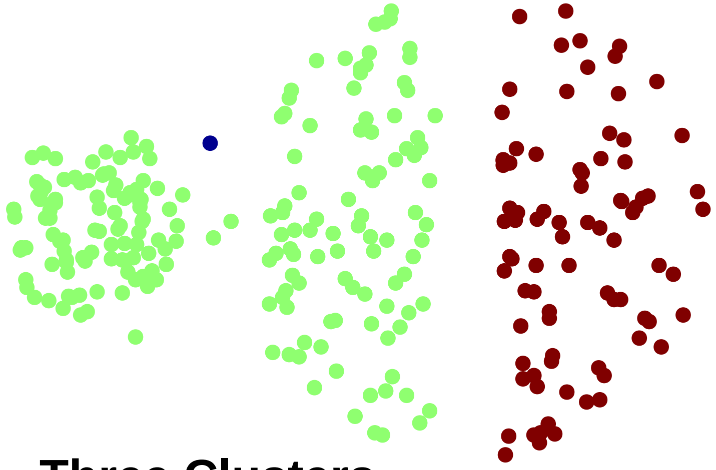
Limitations of MIN



Original Points



Two Clusters

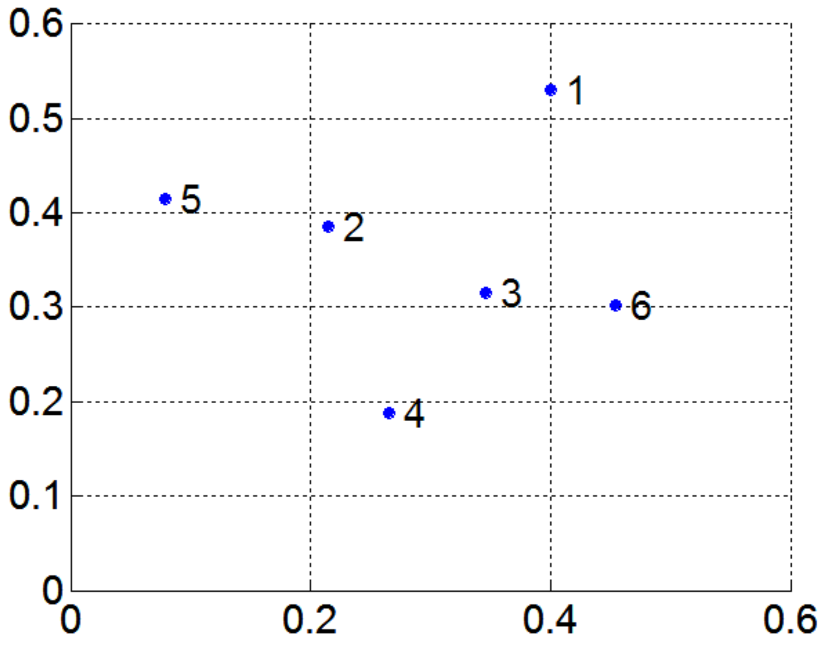


Three Clusters

- **Sensitive to noise**

MAX or Complete Linkage

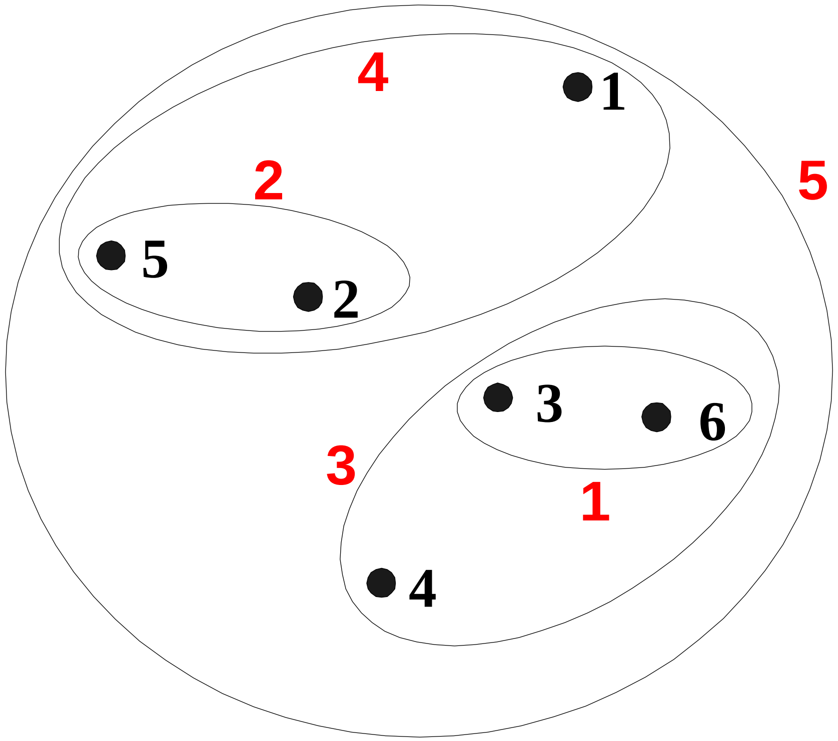
- Proximity of two clusters is based on the two most distant points in the different clusters
  - Determined by all pairs of points in the two clusters



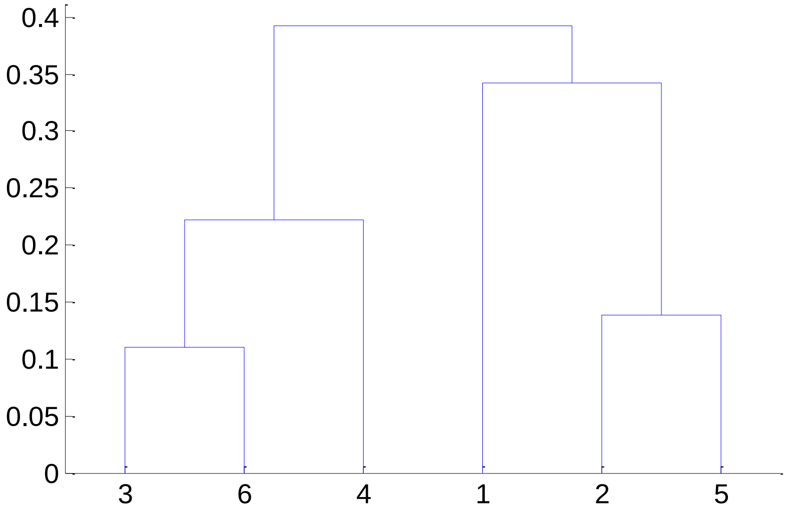
Distance Matrix:

	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.15	0.28	0.11
p4	0.37	0.20	0.15	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00

Hierarchical Clustering: MAX

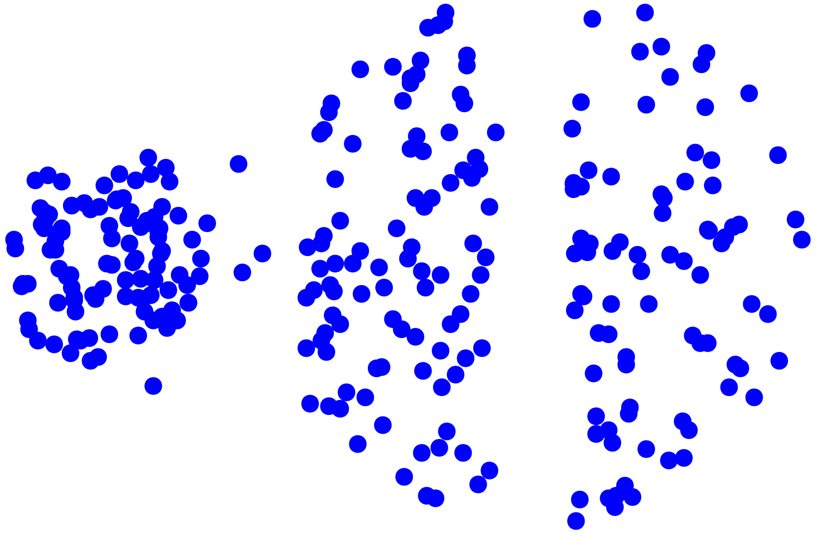


Nested Clusters

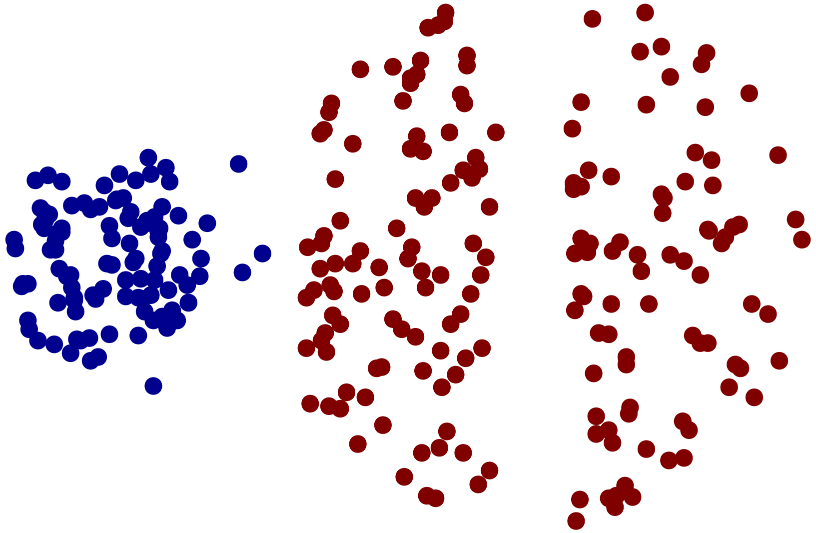


Dendrogram

Strength of MAX



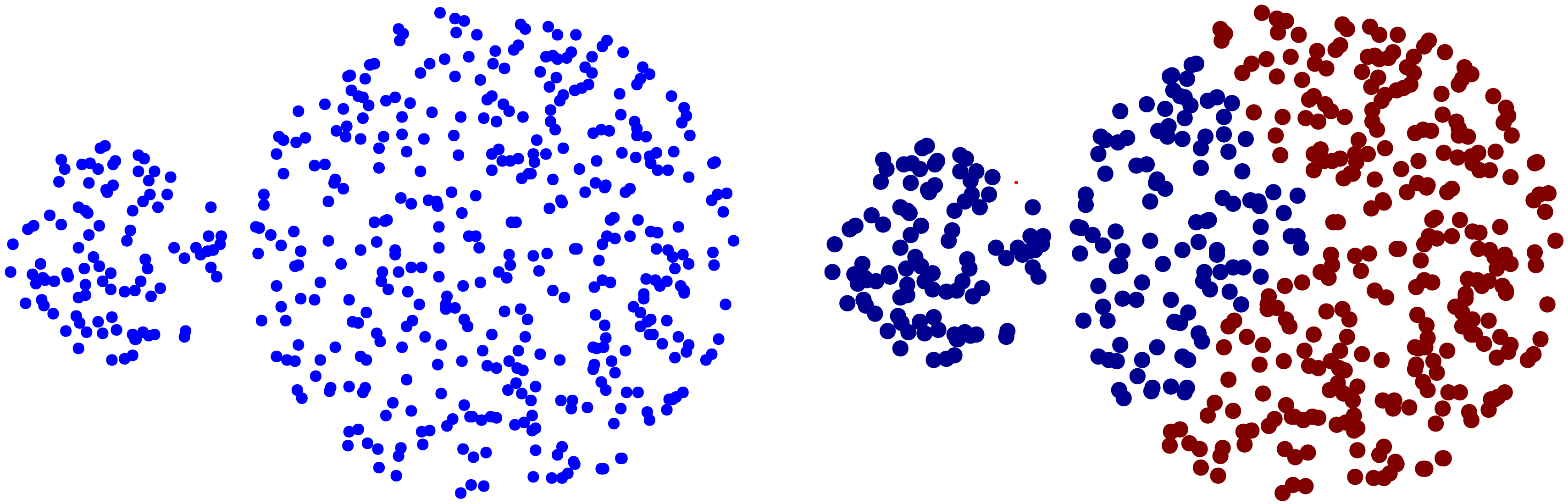
Original Points



Two Clusters

- **Less susceptible to noise**

Limitations of MAX



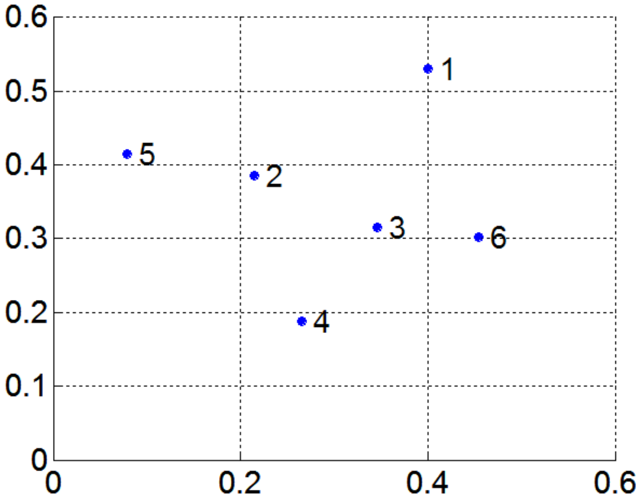
Original Points Two Clusters

- Tends to break large clusters
- Biased towards globular clusters

Group Average

- Proximity of two clusters is the average of pairwise proximity between points in the two clusters.

$$\text{proximity}(\text{Cluster}_i, \text{Cluster}_j) = \frac{\displaystyle\sum_{\substack{p_i \in \text{Cluster}_i \\ p_j \in \text{Cluster}_j}} \text{proximity}(p_i, p_j)}{|\text{Cluster}_i| \times |\text{Cluster}_j|}$$



Distance Matrix:

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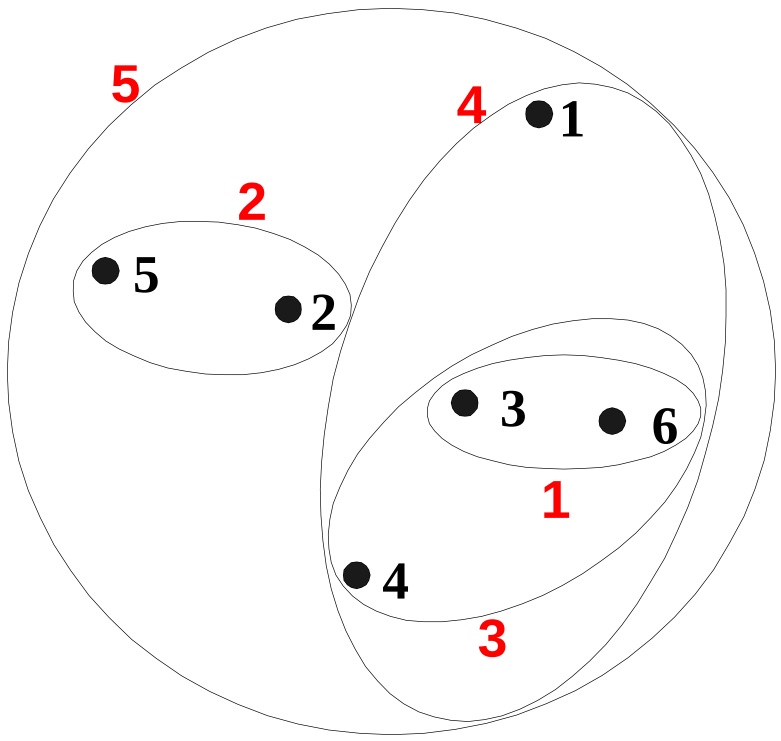
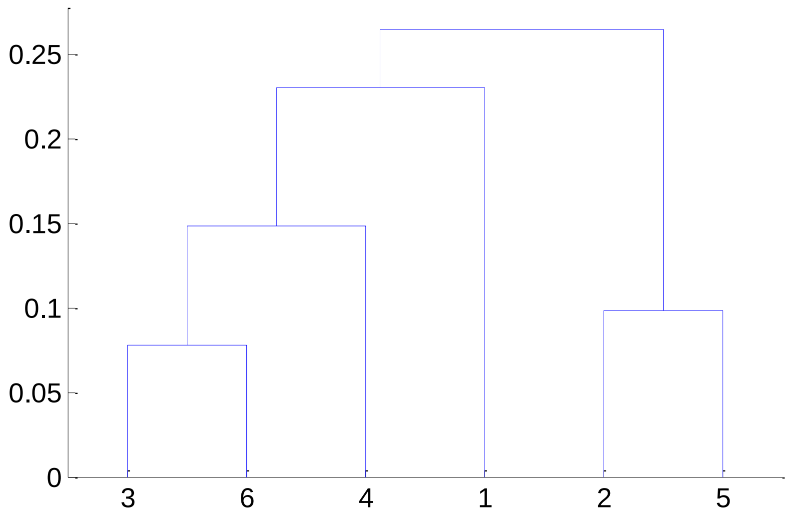
p3	0.22	0.15	0.00	0.15	0.28	0.11
p4	0.37	0.20	0.15	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00

Hierarchical Clustering: Group Average





Nested Clusters **Dendrogram**

Hierarchical Clustering: Group Average

- Compromise between Single and Complete Link

- Strengths
  - Less susceptible to noise

- Limitations
  - Biased towards globular clusters

Cluster Similarity: Ward's Method

- Similarity of two clusters is based on the increase in squared error when two clusters are merged
  - Similar to group average if distance between points is distance squared
- Less susceptible to noise
- Biased towards globular clusters
- Hierarchical analogue of K-means
  - Can be used to initialize K-means

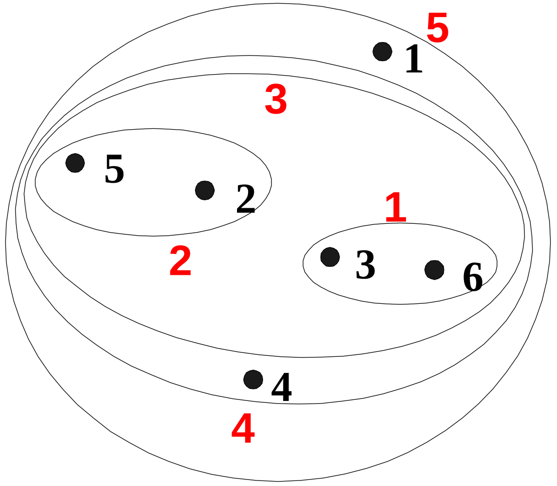
The Ward distance between two clusters A and B is calculated as follows:

$$D_{\text{Ward}}(A, B) = \frac{n_A n_B}{n_A + n_B} \times \text{dist}^2(A, B)$$

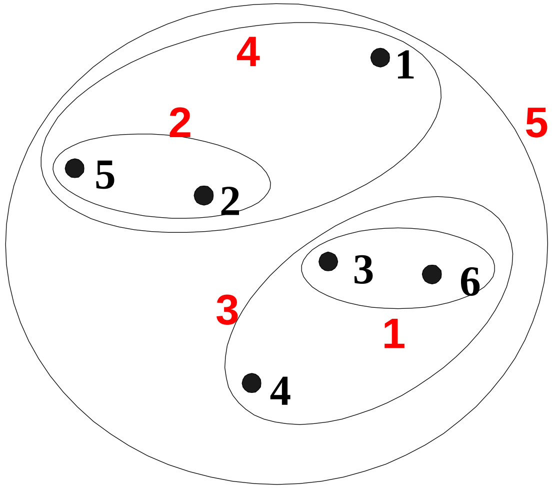
Where:

- n_A and n_B are the number of observations in clusters A and B, respectively.
- $\text{dist}(A, B)$ is the distance between the centroids of clusters A and B.

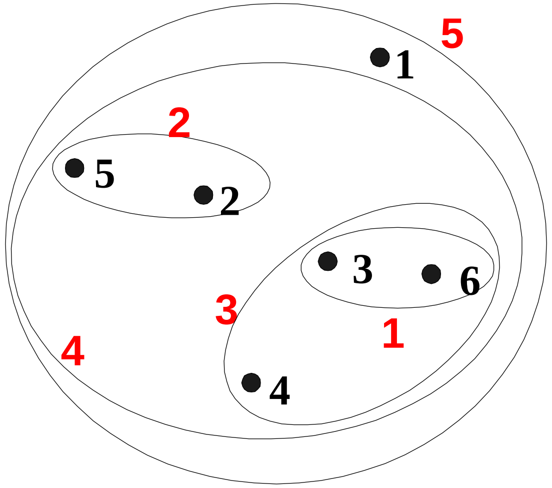
Hierarchical Clustering: Comparison



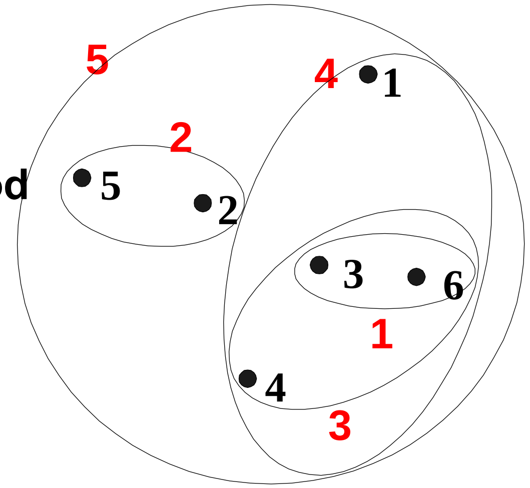
MIN



MAX



Group Average



Ward's Method

Hierarchical Clustering: Time and Space requirements

- $O(N^2)$ space since it uses the proximity matrix.
  - N is the number of points.

- $O(N^3)$ time in many cases
  - There are N steps and at each step the size, N^2, proximity matrix must be updated and searched
  - Complexity can be reduced to $O(N^2 \log(N))$ time with some cleverness

Hierarchical Clustering: Problems and Limitations

- Once a decision is made to combine two clusters, it cannot be undone

- No global objective function is directly minimized

- Different schemes have problems with one or more of the following:
  - Sensitivity to noise
  - Difficulty handling clusters of different sizes and non-globular shapes
  - Breaking large clusters

Density Based Clustering

- Clusters are regions of high density that are separated from one another by regions on low density.

DBSCAN

- DBSCAN is a density-based algorithm.
  - Density = number of points within a specified radius (Eps)

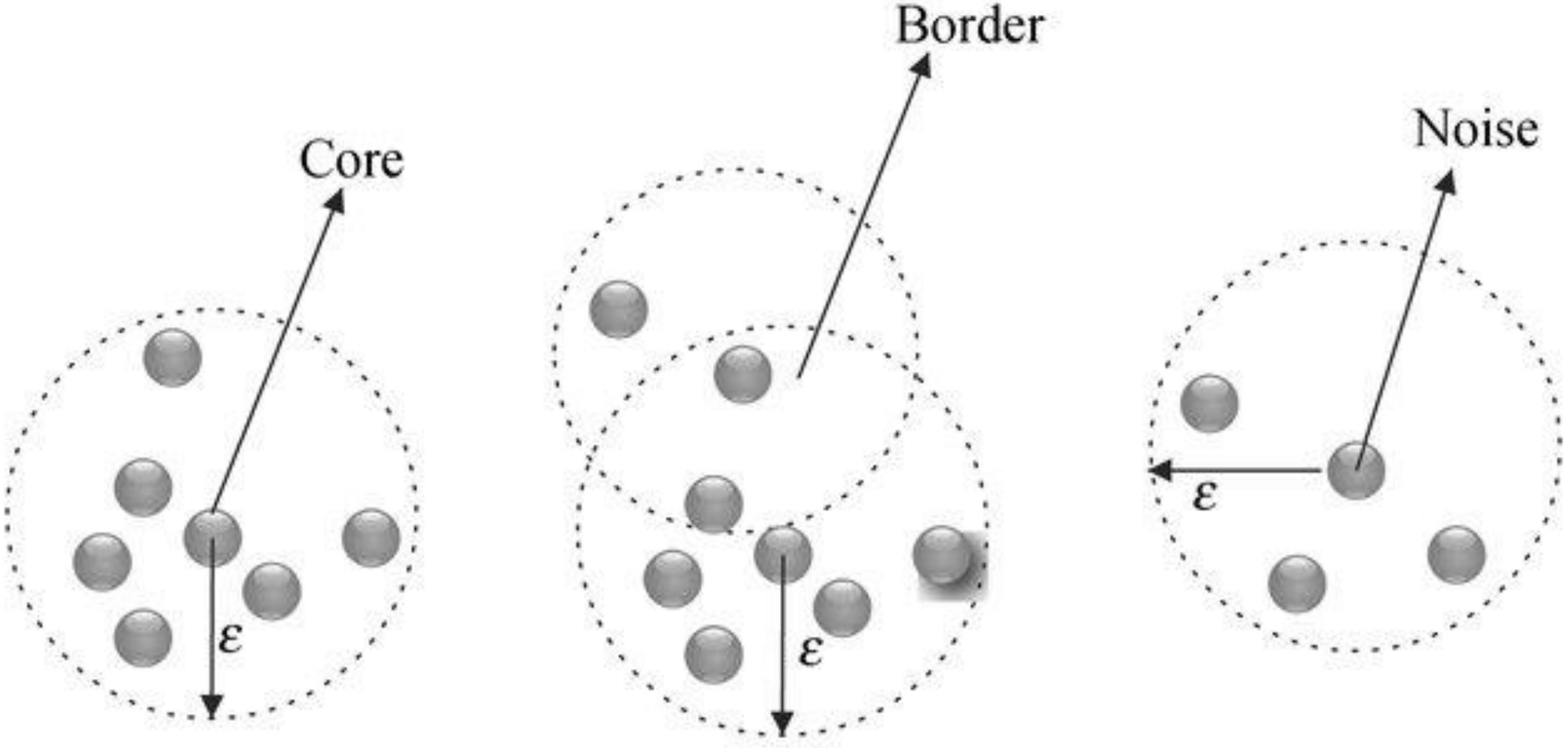
  - A point is a core point if it has at least a specified number of points (MinPts) within Eps
    - These are points that are at the interior of a cluster
    - Counts the point itself

  - A border point is not a core point, but is in the neighborhood of a core point

  - A noise point is any point that is not a core point or a border point

DBSCAN: Core, Border, and Noise Points

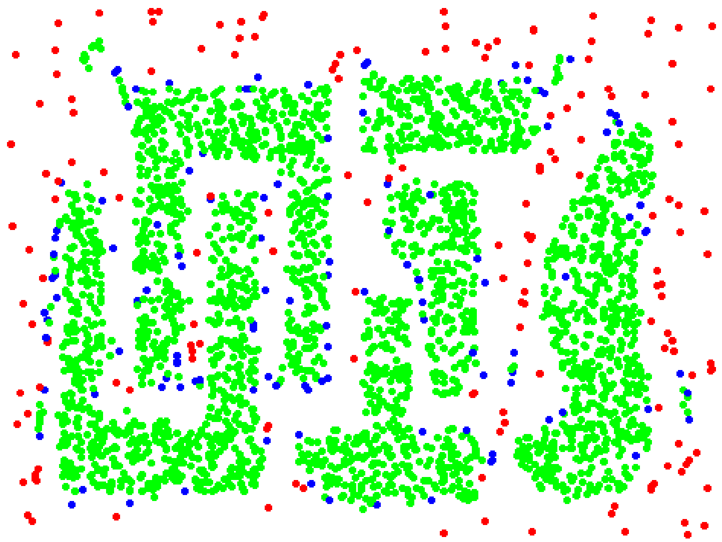
MinPts = 7



https://www.researchgate.net/publication/258442676_On_Density-Based_Data_Streams_Clustering_Algorithms_A_Survey/figures?lo=1

DBSCAN: Core, Border and Noise Points

Original Points



Point types: core, border and noise

Eps = 10, MinPts = 4

DBSCAN Algorithm

- Form clusters using core points, and assign border points to one of its neighboring clusters

1: Label all points as core, border, or noise points.

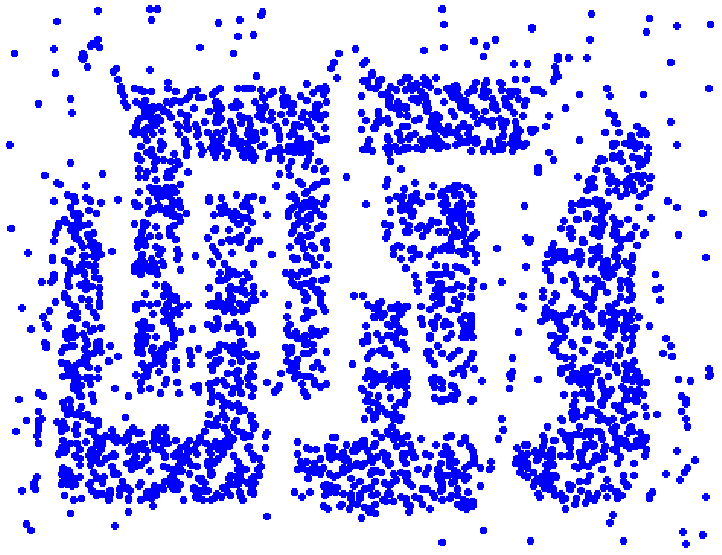
2: Eliminate noise points.

3: Put an edge between all core points within a distance *Eps* of each other.

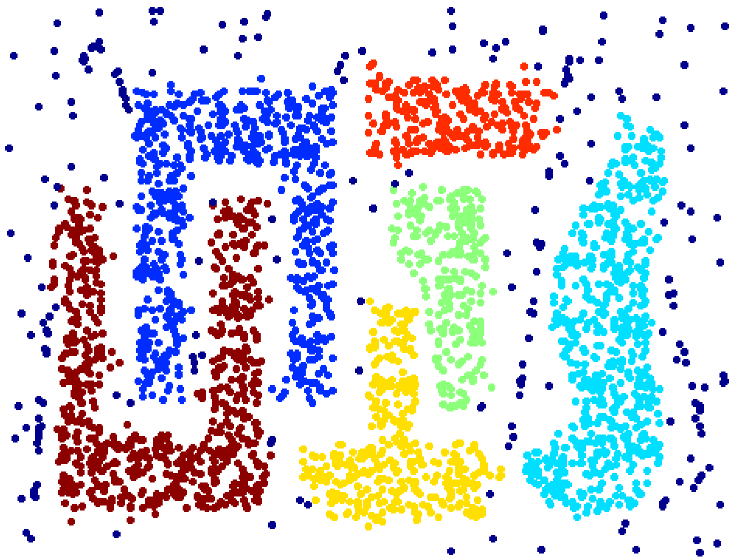
4: Make each group of connected core points into a separate cluster.

5: Assign each border point to one of the clusters of its associated core points

When DBSCAN Works Well



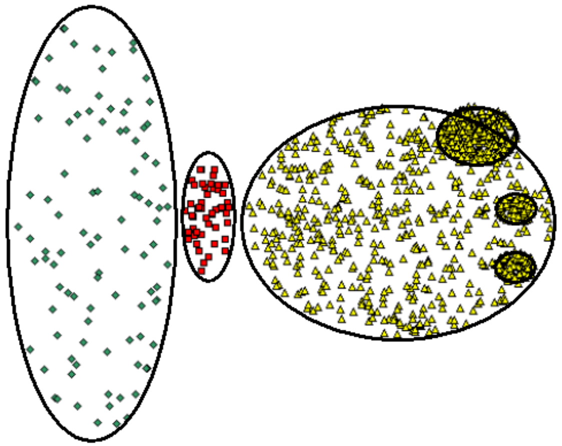
Original Points



Clusters (dark blue points indicate noise)

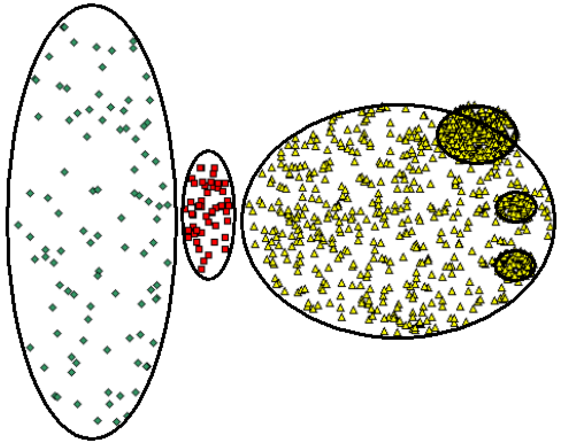
- **Can handle clusters of different shapes and sizes**
- **Resistant to noise**

When DBSCAN Does NOT Work Well

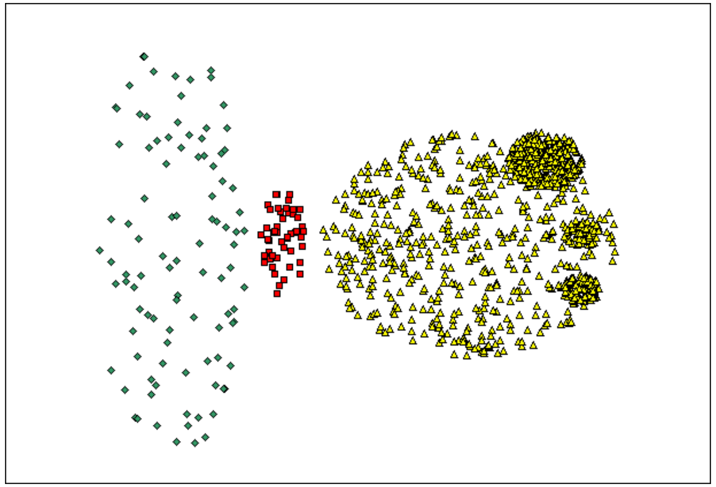


Original Points

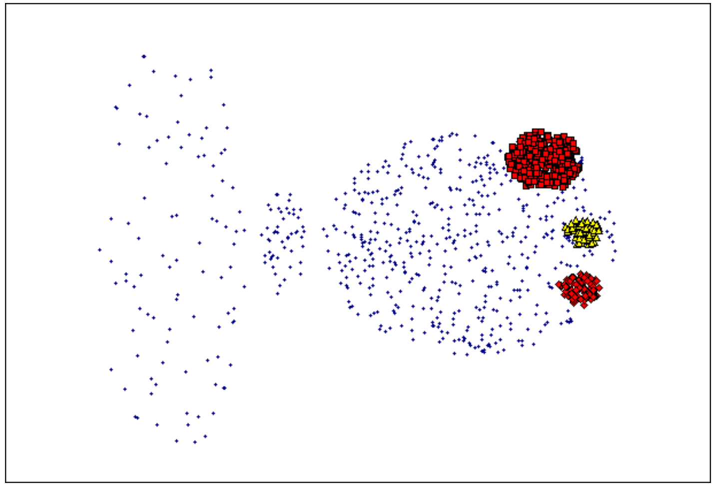
When DBSCAN Does NOT Work Well



Original Points



(MinPts=4, Eps=9.92).



(MinPts=4, Eps=9.75)

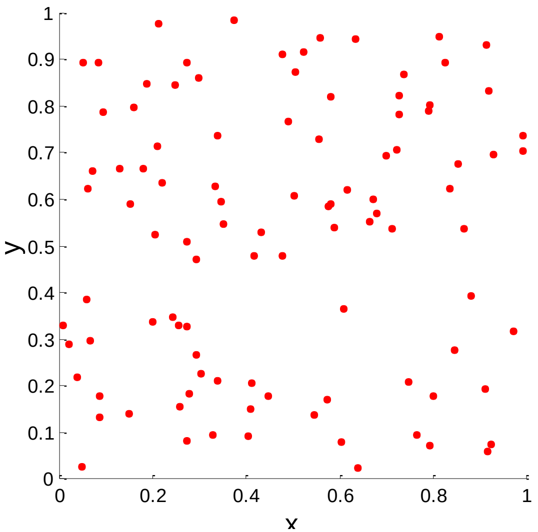
- **Varying densities**
- **High-dimensional data**

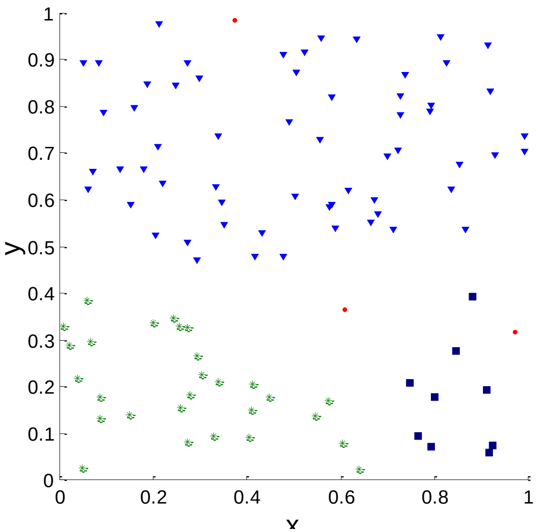
Cluster Validity

- For supervised classification we have a variety of measures to evaluate how good our model is
  - Accuracy, precision, recall
- For cluster analysis, the analogous question is how to evaluate the “goodness” of the resulting clusters?
- But “clusters are in the eye of the beholder”!
  - In practice the clusters we find are defined by the clustering algorithm
- Then why do we want to evaluate them?
  - To avoid finding patterns in noise
  - To compare clustering algorithms
  - To compare two sets of clusters
  - To compare two clusters

Clusters found in Random Data

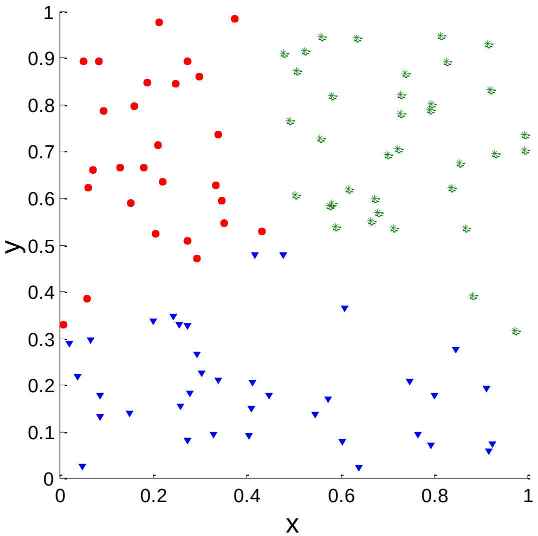
Random Points

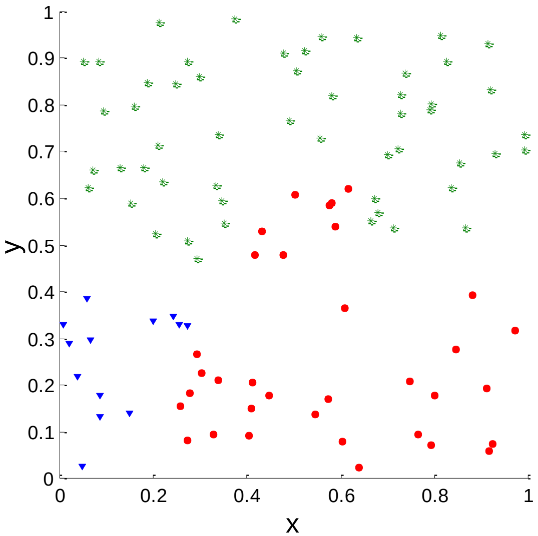




DBSCAN

K-means





Complete Link

Measures of Cluster Validity

- Numerical measures that are applied to judge various aspects of cluster validity, are classified into the following two types.
  - Supervised: Used to measure the extent to which cluster labels match externally supplied class labels.
    - Entropy
    - Often called *external indices* because they use information external to the data
  - Unsupervised: Used to measure the goodness of a clustering structure *without* respect to external information.
    - Sum of Squared Error (SSE)
    - Often called *internal indices* because they only use information in the data

- You can use supervised or unsupervised measures to compare clusters or clusterings

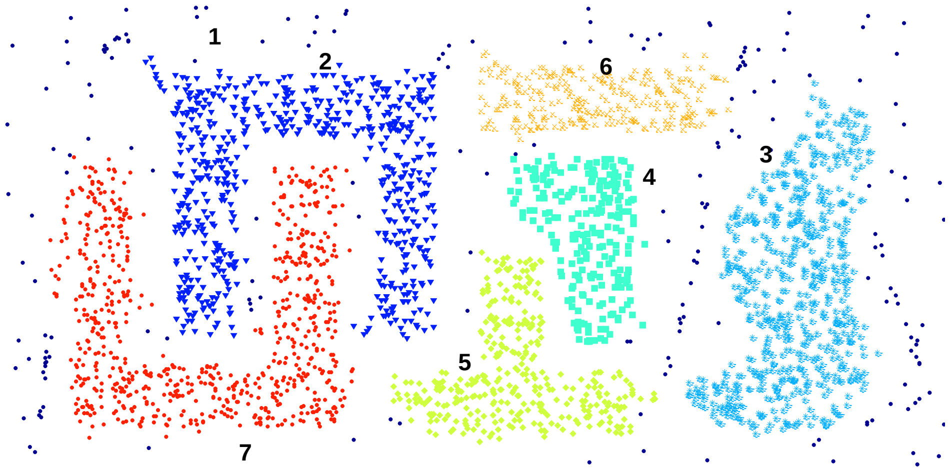
Unsupervised Measures: Cohesion and Separation

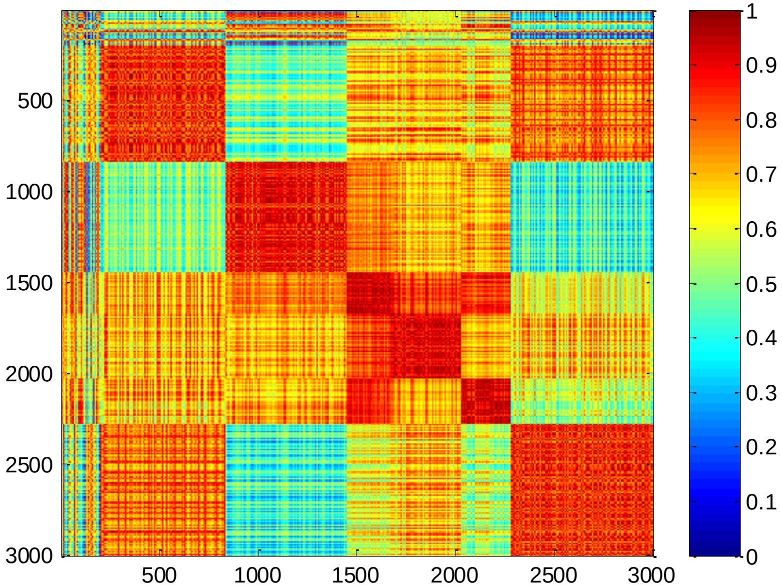
- Cluster Cohesion: Measures how closely related are objects in a cluster
- Cluster Separation: Measure how distinct or well-separated a cluster is from other clusters

- Example: Squared Error
  - Cohesion is measured by the within cluster sum of squares (SSE)
    $$SSE = \sum_i \sum_{x \in C_i} (x - m_i)^2$$
  - Separation is measured by the between cluster sum of squares
    $$SSB = \sum_i |C_i| (m - m_i)^2$$

Where $|C_i|$ is the size of cluster *i*

Judging a Clustering Visually by its Similarity Matrix

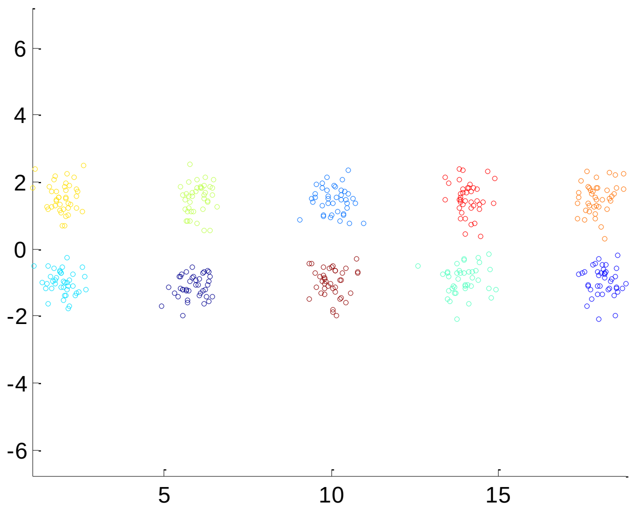


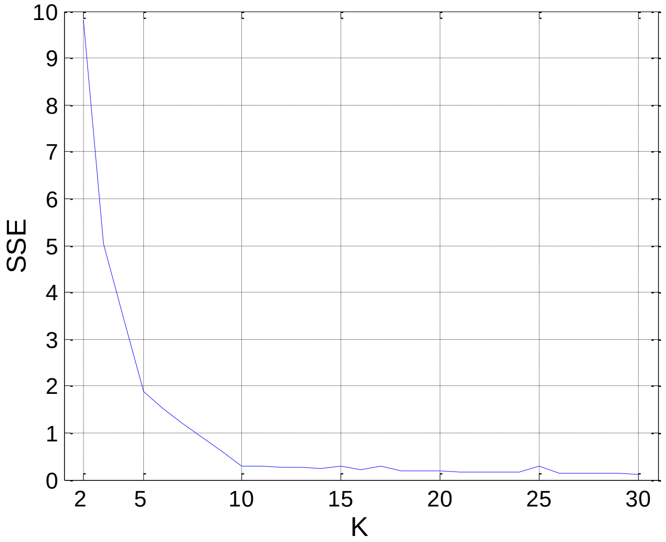


DBSCAN

Determining the Correct Number of Clusters

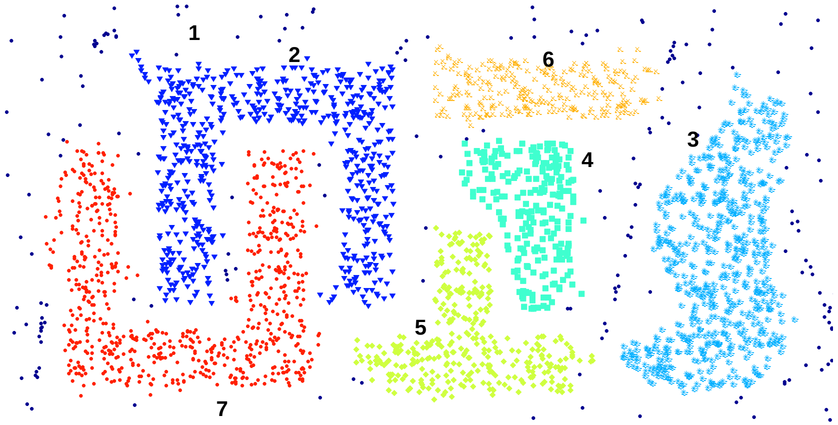
- SSE is good for comparing two clusterings or two clusters
- SSE can also be used to estimate the number of clusters

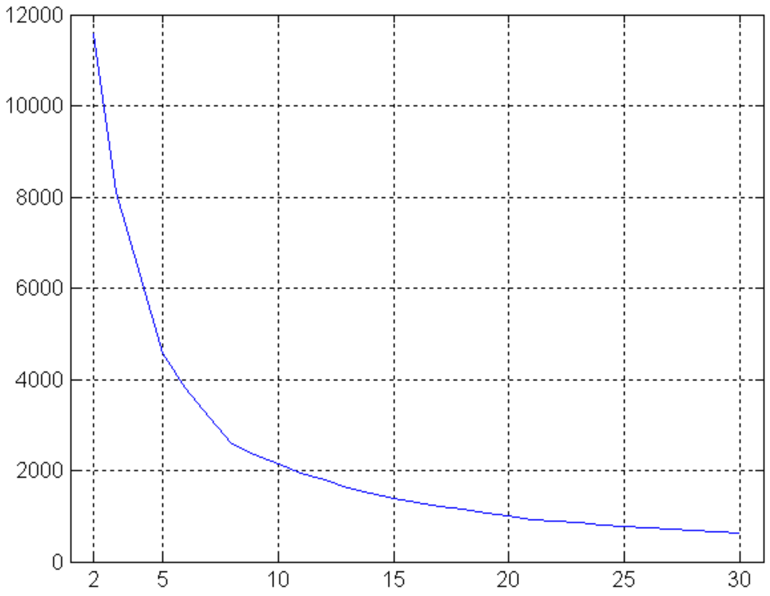




Determining the Correct Number of Clusters

- SSE curve for a more complicated data set





SSE of clusters found using K-means

Final Comment on Cluster Validity

"The validation of clustering structures is the most difficult and frustrating part of cluster analysis.

Without a strong effort in this direction, cluster analysis will remain a black art accessible only to those true believers who have experience and great courage."

***Algorithms for Clustering Data*, Jain and Dubes**

- H. Xiong and Z. Li. *Clustering Validation Measures*. In C. C. Aggarwal and C. K. Reddy, editors, Data Clustering: Algorithms and Applications, pages 571–605. Chapman & Hall/CRC, 2013.