

# Chapter 7. Cluster Analysis

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1. What is Cluster Analysis?
2. Types of Data in Cluster Analysis
3. A Categorization of Major Clustering Methods
4. Partitioning Methods
5. Hierarchical Methods
6. Density-Based Methods
7. Clustering High-Dimensional Data
8. Constraint-Based Clustering
9. Outlier Analysis
10. Summary



# What is Cluster Analysis?

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- Cluster: a collection of data objects
  - Similar to one another within the same cluster
  - Dissimilar to the objects in other clusters
- Cluster analysis
  - Finding similarities between data according to the characteristics found in the data
  - Grouping similar data objects into clusters



# Major Clustering Approaches

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- Partitioning approach:
  - Construct various partitions and then evaluate them by some criterion, e.g., minimizing the sum of square errors
  - Typical methods: k-means, k-medoids, CLARANS
- Hierarchical approach:
  - Create a hierarchical decomposition of the set of data (or objects) using some criterion
  - Typical methods: Diana, Agnes, BIRCH, ROCK, CHAMELEON
- Density-based approach:
  - Based on some density functions
  - Typical methods: DBSACN, OPTICS



# Centroid, Radius, and Diameter of a Cluster (for numerical data sets)

- **Centroid**: the “middle” of a cluster

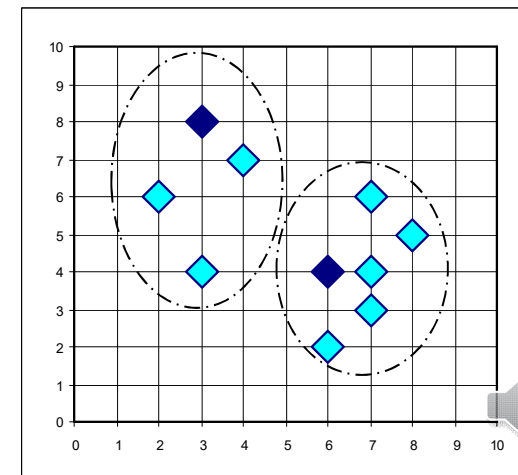
$$C_m = \frac{\sum_{i=1}^N (t_{ip})}{N}$$

- **Radius**: square root of an average squared distance from any point of the cluster to its centroid

$$R_m = \sqrt{\frac{\sum_{i=1}^N (t_{ip} - c_m)^2}{N}}$$

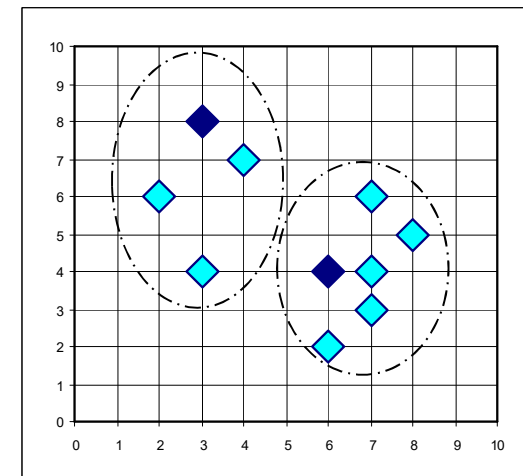
- **Diameter**: square root of an average squared distance between all possible pairs of points in the cluster

$$D_m = \sqrt{\frac{\sum_{i=1}^N \sum_{j=1}^N (t_{ip} - t_{jq})^2}{N(N-1)}}$$



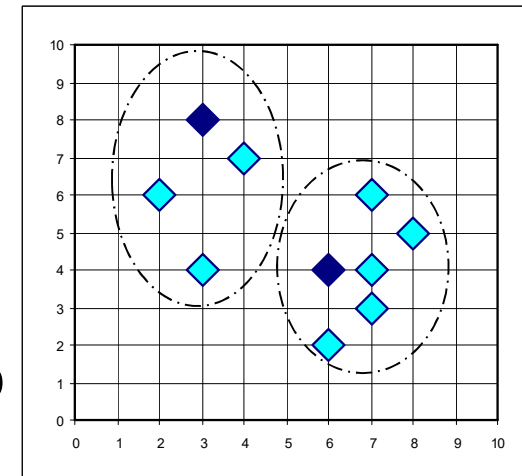
# Typical Alternatives to Calculate the **Distance** between Clusters

- Single link: smallest distance between an element in one cluster and an element in the other
  - $\text{dis}(K_i, K_j) = \min(t_{ip}, t_{jq})$
- Complete link: largest distance between an element in one cluster and an element in the other
  - $\text{dis}(K_i, K_j) = \max(t_{ip}, t_{jq})$



# Typical Alternatives to Calculate the **Distance between Clusters**

- Average: average distance between an element in one cluster and an element in the other
  - $\text{dis}(K_i, K_j) = \text{avg}(t_{ip}, t_{jq})$
- Centroid: distance between the centroids of two clusters
  - $\text{dis}(K_i, K_j) = \text{dis}(C_i, C_j)$
- Medoid: distance between the medoids of two clusters
  - $\text{dis}(K_i, K_j) = \text{dis}(M_i, M_j)$
  - **Medoid**: one chosen, centrally located (**real**) object in the cluster



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# Partitioning Algorithms: Basic Concept

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- Partitioning method: Construct a partition of a database ***D*** of ***n*** objects into a set of ***k*** clusters, having the **minimum sum** of squared distances of objects to their **representative** of a cluster

$$\sum_{m=1}^k \sum_{t_{mi} \in K_m} (C_m - t_{mi})^2$$

- Given a *k*, find a partition of *k clusters* that optimizes the chosen partitioning criterion
  - Global optimal: exhaustively enumerate all partitions
  - Heuristic methods: *k-means* and *k-medoids* algorithms
    - *k-means*: Each cluster is represented by the **centroid** of the cluster
    - *k-medoids* or PAM (Partition around medoids): Each cluster is represented by **one of the objects** in the cluster





# The *K-Means* Clustering Method

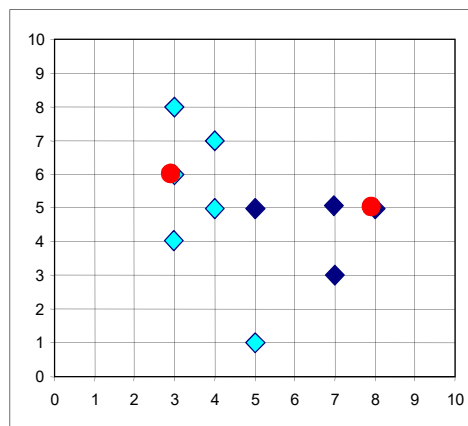
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- Given  $k$ , the *k-means* algorithm is implemented in four steps:
  - Partition objects into  $k$  nonempty subsets
  - Compute seed points as the **centroids** of the clusters of the current partition
    - The centroid is the center, i.e., *mean point*, of the cluster
  - Assign each object to the cluster with the nearest seed point
  - Go back to Step 2, stop when no more new assignment



# The *K-Means* Clustering Method

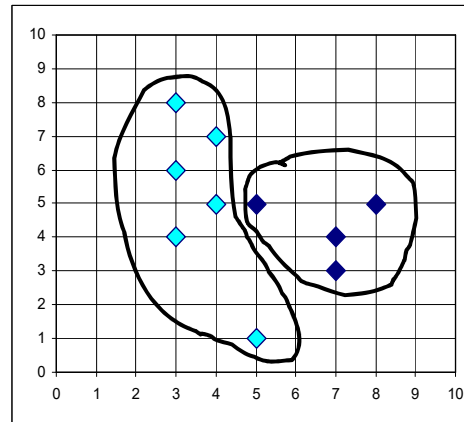
## ■ Example



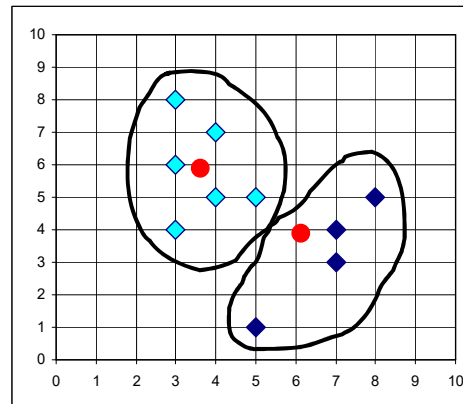
$K=2$

Arbitrarily choose  $K$  object as initial cluster center

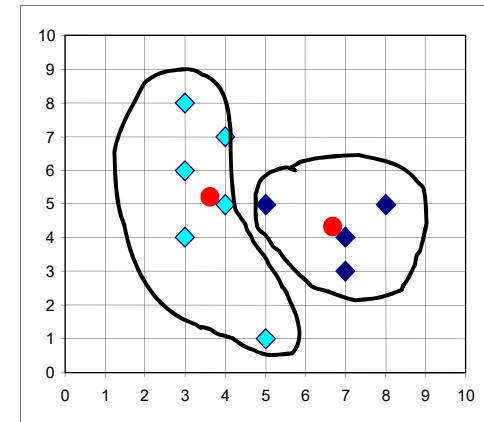
Assign each object to most similar center



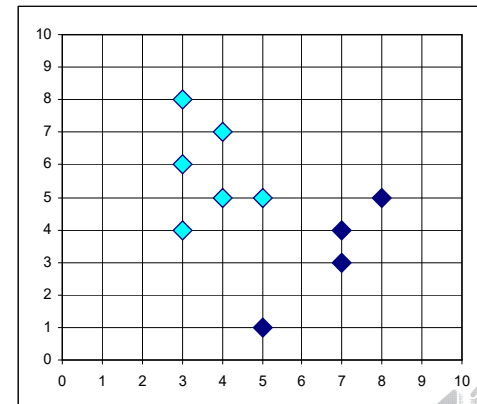
reassign



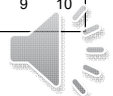
Update the cluster means



reassign



Update the cluster means



# Comments on the *K-Means* Method

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- Strength: *Relatively efficient*:  $O(n*k*t)$ , where  $n$  is # objects,  $k$  is # clusters, and  $t$  is # iterations. Normally,  $k, t \ll n$ 
  - Comparing: PAM:  $O(k(n-k)^2)$ , CLARA:  $O(ks^2 + k(n-k))$
- Comment: Often terminates at a *local optimum*
- Weakness
  - Applicable only when *mean* is defined (what about categorical data?)
  - Need to specify  $k$ , *the number of clusters*, in advance
  - Unable to handle *noises and outliers*
  - Not suitable to discover clusters with *non-convex shapes*



# Variations of the *K-Means* Method

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- Handling categorical data: *k-modes* (Huang'98)

- Idea: replacing means of clusters with **modes**

- X, Y: objects having m categorical attributes

- Dissimilarity  $d(X,Y)$ : the number of **total mismatches**

$$d(X, Y) = \sum_{j=1}^m \delta(x_j, y_j) \quad \text{where} \quad \delta(x_j, y_j) = \begin{cases} 0 & (x_j = y_j) \\ 1 & (x_j \neq y_j) \end{cases}$$

- **Mode** of  $X = \{X_1, X_2, \dots, X_n\}$  is a vector  $Q = \langle q_1, q_2, \dots, q_m \rangle$  that minimizes

$$D(X, Q) = \sum_{i=1}^n d(X_i, Q)$$

- Finding a mode for X

- Taking the value **most frequently occurring** for each attribute
      - Using a **frequency-based method** to update modes of clusters

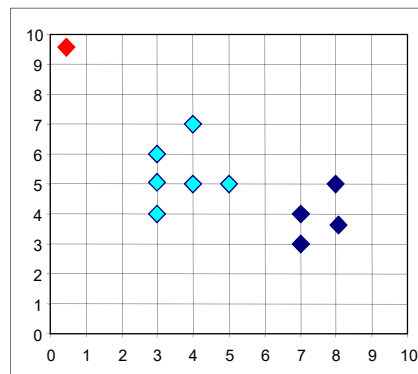
- A mixture of categorical and numerical data: *k-prototype* method



# What Is the Problem of the K-Means Method?

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- The k-means algorithm is sensitive to *outliers* !
  - An object with an extremely large value may substantially distort the distribution of the data
- K-Medoids: Instead of taking the **mean** value (i.e., *centroids*) of the object in a cluster as a reference point, *a medoids* can be used, which is the *most centrally-located object* in a cluster



# The *K-Medoids* Clustering Method

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- Find *representative* objects, called medoids, in clusters
  - *PAM* (Partitioning Around Medoids, 1987)
  - *CLARA* (Kaufmann & Rousseeuw, 1990)
  - *CLARANS* (Ng & Han, 1994): Randomized sampling



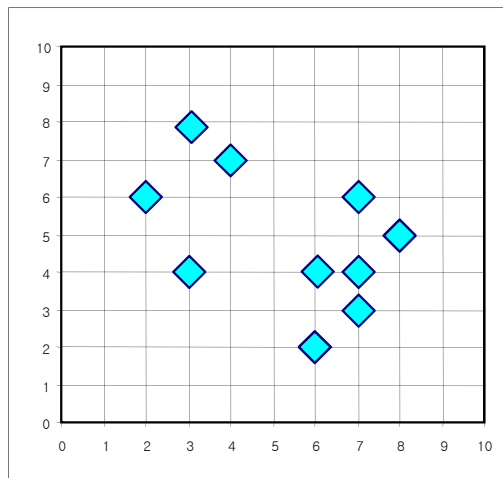
# PAM (Partitioning Around Medoids) (1987)

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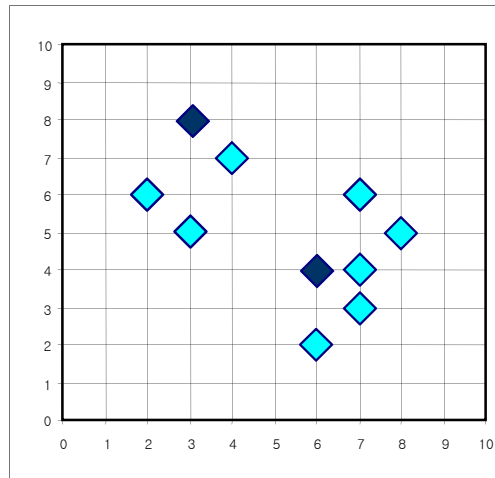
- PAM (Kaufman and Rousseeuw, 1987), built in Splus
- Use a **real object** to represent the cluster
  - Select  **$k$**  representative objects arbitrarily
  - For each pair of non-selected object  **$h$**  and **selected object (i.e., seed)  $i$** , calculate the total swapping cost  **$TC_{ih}$**
  - For each pair of  **$i$**  and  **$h$** ,
    - If  $TC_{ih} < 0$ ,  **$i$**  is replaced by  **$h$**
    - Then, each non-selected object is assigned to the most similar representative object
  - Repeat steps 2-3 until there is no change



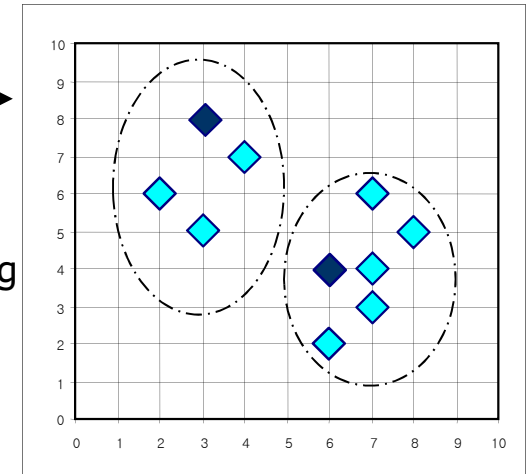
# A Typical K-Medoids Algorithm (PAM)



Arbitrary  
choose  $k$   
objects  
as initial  
medoids



Assign  
each  
remaining  
object to  
nearest  
medoids



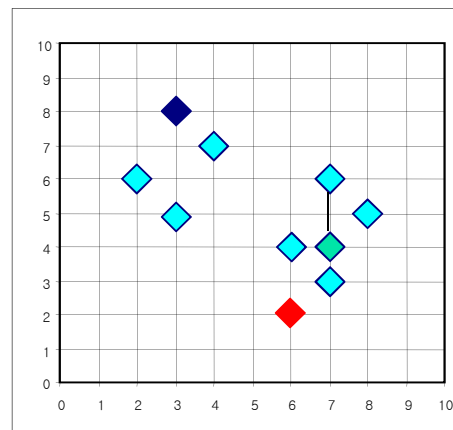
Total Cost = 20

$K=2$

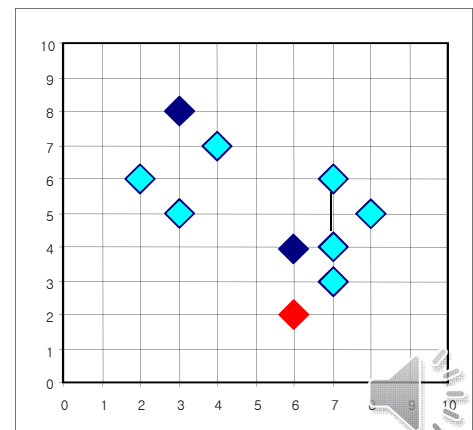
**Do loop  
Until no  
change**

Swapping  $O$   
and  $O_{\text{random}}$   
If quality  
is improved.

Total Cost = 26



Compute  
total cost of  
swapping



Randomly select a  
nonmedoid object,  $O_{\text{random}}$

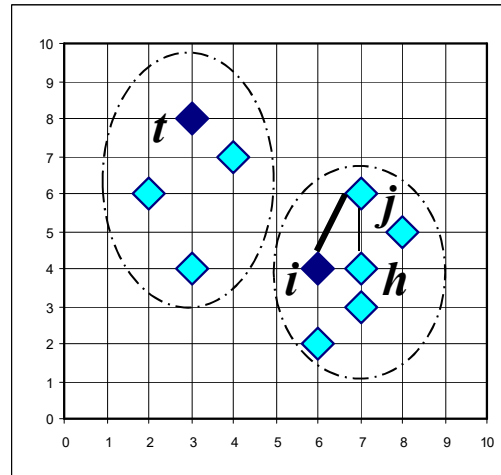


# PAM Clustering: Total swapping cost $TC_{ih} = \sum_j C_{jih}$

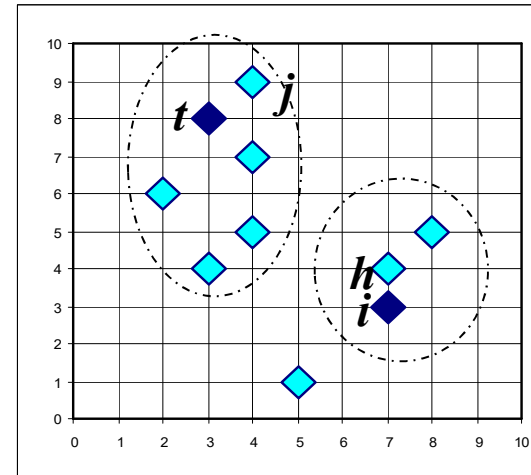
NewC - OldC

i: original seed  
h: new seed  
t: other seed  
j: non-seed

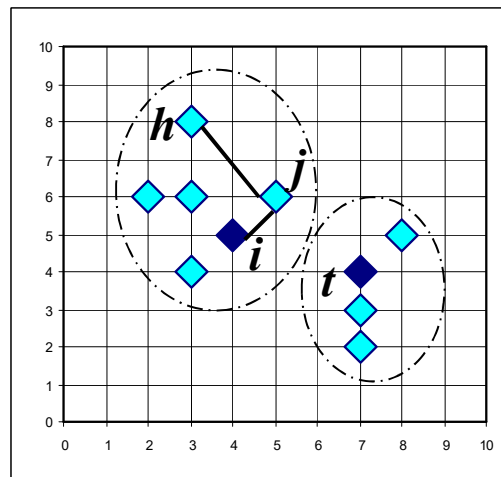
A: j belonged to i and now belongs to h  
B: j belonged to t and again belongs to t  
C: j belonged to i and now belongs to t  
D: j belonged to t and now belongs to h



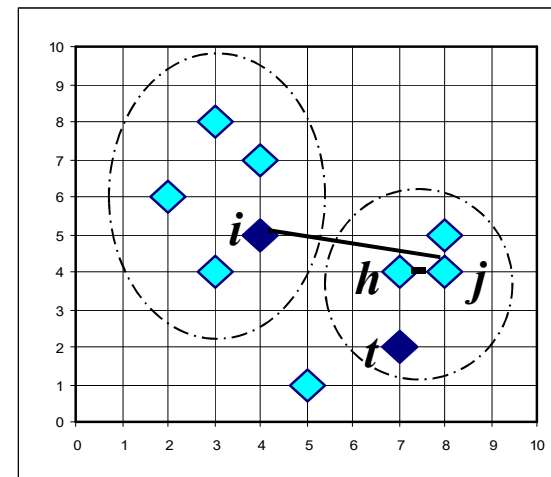
$$C_{jih} = d(j, h) - d(j, i)$$



$$C_{jih} = 0$$



$$C_{jih} = d(j, t) - d(j, i)$$



$$C_{jih} = d(j, h) - d(j, t)$$

# What Is the Problem with PAM?

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- PAM is more robust than k-means in the presence of noise and outliers
  - because a medoid is less influenced by outliers or other extreme values than a mean (i.e., centroid)
- PAM works efficiently for small data sets but **does not scale well** for large data sets.
  - $O(i * k * (n - k)^2)$  where  $n$  is # of data,  $k$  is # of clusters,  $i$  is # of iterations

➔ Sampling based method,

CLARA (Clustering LARge Applications)

# CLARA (Clustering Large Applications) (1990)

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- *CLARA* (Kaufmann and Rousseeuw in 1990)
  - Built in statistical analysis packages, such as S+
- It draws *multiple samples* of the data set, applies *PAM* on each sample, and gives the best clustering as the output
- Strength: deals with larger data sets than *PAM*
- Weakness:
  - Efficiency *depends on the sample size*
  - A good clustering based on samples will not necessarily represent a good clustering of the whole data set *if the sample is biased*

