Partitions Methods



Major Clustering Approaches

- Partitioning algorithms: Construct various partitions and then evaluate them by some criterion
- Hierarchy algorithms: Create a hierarchical decomposition of the set of data (or objects) using some criterion.
 - Can be agglomerative and divisive approach
- Density-based: based on connectivity and density functions
 - Grow the cluster as long as the density in the neighborhood exceeds some threshold
- Grid-based: based on a multiple-level granularity structure
- Model-based: A model is hypothesized for each of the clusters and the idea is to find the best fit of that model to each other

Major Clustering Approaches

Method	General Characteristics
Partitioning methods	- Find mutually exclusive clusters of spherical shape - Distance-based - May use mean or medoid (etc.) to represent cluster center - Effective for small- to medium-size data sets
Hierarchical methods	 Clustering is a hierarchical decomposition (i.e., multiple levels) Cannot correct erroneous merges or splits May incorporate other techniques like microclustering or consider object "linkages"
Density-based methods	 Can find arbitrarily shaped clusters Clusters are dense regions of objects in space that are separated by low-density regions Cluster density: Each point must have a minimum number of points within its "neighborhood" May filter out outliers
Grid-based methods	- Use a multiresolution grid data structure - Fast processing time (typically independent of the number of data objects, yet dependent on grid size)



Partitioning Algorithms: Basic Concepts

- Partitioning method: Discovering the groupings in the data by optimizing a specific objective function and iteratively improving the quality of partitions
- K-partitioning method: Partitioning a dataset D of n objects into a set of K clusters so that an objective function is optimized (e.g., the sum of squared distances is minimized, where c_k is the centroid or medoid of cluster C_k)
 - A typical objective function: Sum of Squared Errors (SSE) $SSE(C) = \sum_{i=1}^{K} \sum_{j=1}^{K} ||x_i c_k||^2$

Partitioning Algorithms: Basic Concepts

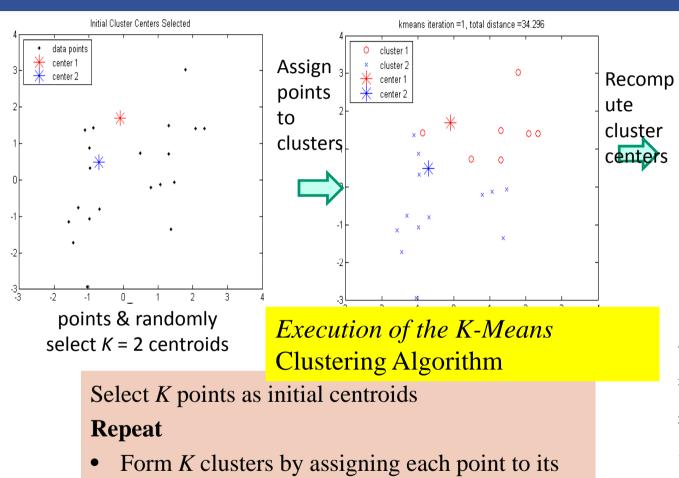
- Problem definition: Given K, find a partition of K clusters that optimizes the chosen partitioning criterion
 - Global optimal: Needs to exhaustively enumerate all partitions
 - Heuristic methods (i.e., greedy algorithms): K Means, K-Medians, K-Medoids, etc.



The K-Means Clustering Method

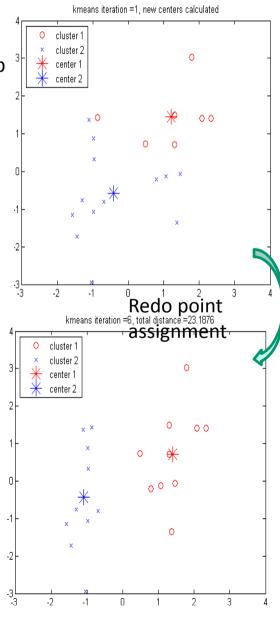
- <u>K-Means</u>: Each cluster is represented by the center of the cluster
- Given K, the number of clusters, the K-Means clustering algorithm is outlined as follows
 - Select K points as initial centroids
 - Repeat
 - Form K clusters by assigning each point to its closest centroid based on the distance measures
 - Re-compute the centroids (i.e., mean point) of each cluster
 - Until convergence criterion is satisfied
- · Different kinds of measures can be used
 - Manhattan distance (L_1 norm), Euclidean distance (L_2 norm). Cosine similaritu

Example: K-Means Clustering



- closest centroid
- Re-compute the centroids (i.e., *mean point*) of each cluster

Until convergence criterion is satisfied



A Simple example showing the implementation of k-means algorithm

Individual	Variable 1	Variable 2
1	1.0	1.0
2	1.5	2.0
3	3.0	4.0
4	5.0	7.0
5	3.5	5.0
6	4.5	5.0
7	3.5	4.5



Example: *K-Means* Clustering

Step 1:

<u>Initialization</u>: Randomly we choose following two centroids (k=2) for two clusters.

In this ca

Individual	Variable 1	Variable 2
1	1.0	1.0
2	1.5	2.0
3	3.0	4.0
4	5.0	7.0
5	3.5	5.0
6	4.5	5.0
7	3.5	4.5

0,7.0).

	Individual	Mean Vector
Group 1	1	(1.0, 1.0)
Group 2	4	(5.0, 7.0)



Step 2:

 Thus, we obtain two clusters containing:

$$m_1 = (\frac{1}{3}(1.0 + 1.5 + 3.0), \frac{1}{3}(1.0 + 2.0 + 4.0)) = (1.83, 2.33)$$

 $m_2 = (\frac{1}{4}(5.0 + 3.5 + 4.5 + 3.5), \frac{1}{4}(7.0 + 5.0 + 5.0 + 4.5))$

• Their new centroids are: = (4.12,5.38)

Individual	Centrold 1	Centrold 2
1	0	7.21
2 (1.5, 2.0)	1.12	6.10
3	3.61	3.61
4	7.21	0
5	4.72	2.5
6	5.31	2.06
7	4.30	2.92

$$d(m_1,2) = \sqrt{|1.0 - 1.5|^2 + |1.0 - 2.0|^2} = 1.12$$

$$d(m_2,2) = \sqrt{|5.0 - 1.5|^2 + |7.0 - 2.0|^2} = 6.10$$



Example: *K-Means* Clustering

Step 3:

- Now using these centroids we compute the Euclidean distance of each object, as shown in table.
- Therefore, the new clusters are:
 {1,2} and {3,4,5,6,7}
- Next centroids are: m1=(1.25,1.5) and m2=(3.9,5.1)

Individual	Centroid 1	Centroid 2
1	1.57	5.38
2	0.47	4.28
3	2.04	1.78
4	5.64	1.84
5	3.15	0.73
6	3.78	0.54
7	2.74	1.08



Example: *K-Means* Clustering

Step 4 :

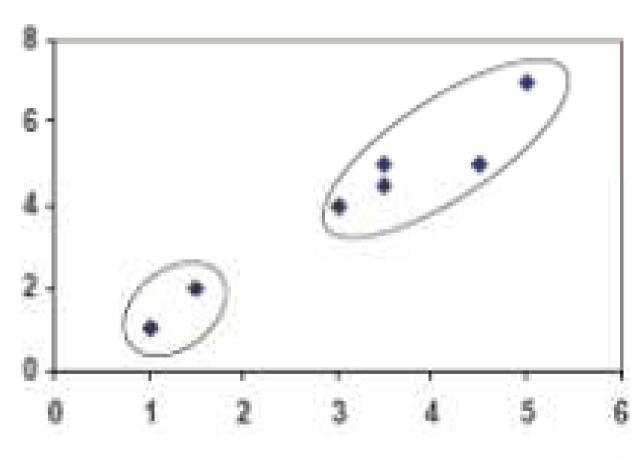
The clusters obtained are: $\{1,2\}$ and $\{3,4,5,6,7\}$

- Therefore, there is no change in the cluster.
- Thus, the algorithm comes to a halt here and final result consist of 2 clusters {1,2} and {3,4,5,6,7}.

Individual	Centroid 1	Centroid 2
1	0.56	5.02
2	0.56	3.92
3	3.05	1.42
4	6.66	2.20
5	4.16	0.41
6	4.78	0.61
7	3.75	0.72



PLOT





(with K=3)

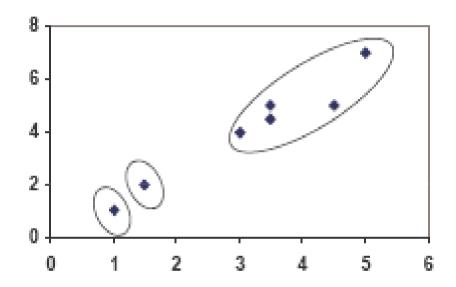
Individual	m ₁ = 1	m ₂ = 2	m ₃ = 3	cluster
1	0	1.11	3.61	1
2	1.12	0	2.5	2
3	3.61	2.5	0	3
4	7.21	6.10	3.61	3
5	4.72	3.61	1.12	3
в	5.31	4.24	1.80	3
7	4.30	3.20	0.71	3

Individual	m ₁ (1.0, 1.0)	m ₂ (1.5, 2.0)	m ₃ (3.9,5.1)	cluster
1	0	1.11	5.02	1
2	1.12	0	3.92	2
3	3.61	2.5	1.42	3
4	7.21	6.10	2.20	3
5	4.72	3.61	0.41	3
6	5.31	4.24	0.61	3
7	4.30	3.20	0.72	3

clustering with initial centroids (1, 2, 3)



PLOT



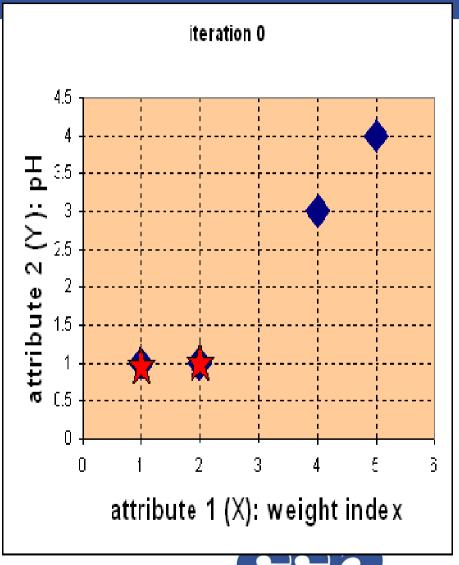


Object	Attribute1 (X): weight index	Attribute 2 (Y): pH
Medicine A	1	1
Medicine B	2	1
Medicine C	4	3
Medicine D	5	4



Step 1:

- Initial value of
 centroids: Suppose
 we use medicine A
 and medicine B as
 the first centroids.
- Let c_1 and c_2 denote the coordinate of the centroids, then $c_1=(1,1)$ and $c_2=(2,1)$



 Objects-Centroids distance : we calculate the distance between cluster centroid to each object. Let us use Euclidean distance, then we have distance matrix at iteration O is

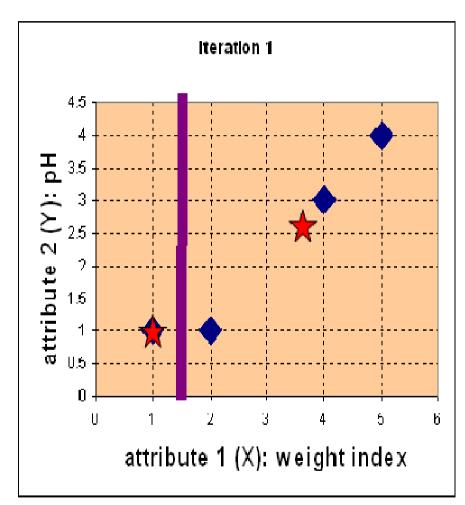
$$\mathbf{D}^{0} = \begin{bmatrix} 0 & 1 & 3.51 & 5 \\ 1 & 0 & 2.33 & 4.24 \end{bmatrix} \quad \begin{array}{c} \mathbf{c}_{1} = (1,1) & group - 1 \\ \mathbf{c}_{2} = (2,1) & group - 2 \\ & A & B & C & D \\ \hline \begin{bmatrix} 1 & 2 & 4 & 5 \\ 1 & 1 & 3 & 4 \end{bmatrix} \quad \begin{array}{c} X \\ Y \end{array}$$

- · Each column in the distance matrix symbolizes the object.
- The first row of the distance matrix corresponds to the distance of each object to the first centroid and the second row is the distance of each object to the second centroid.
- For example, distance from medicine C = (4, 3) to the first centroid $\mathbf{c}_1 = (1,1)$ is $\sqrt{(4-1)^2 + (3-1)^2} = 3.61$ and its distance to the second centroid is $\mathbf{c}_2 = (2,1)$ is $\sqrt{(4-2)^2 + (3-1)^2} = 2.83$

<u>Step 2:</u>

- Objects clustering: We assign each object based on the minimum distance.
- Medicine A is assigned to group 1, medicine B to group 2, medicine C to group 2 and medicine D to group 2.
- The elements of Group matrix below is 1 if and only if the object is assigned to that group.

$$\mathbf{G}^0 = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 1 & 1 \end{bmatrix} \quad \begin{array}{c} group - 1 \\ group - 2 \end{array}$$





- <u>Iteration-1, Objects-Centroids distances</u>: The next step is to compute the distance of all objects to the new centroids.
- · Similar to step 2, we have distance matrix at iteration 1 is

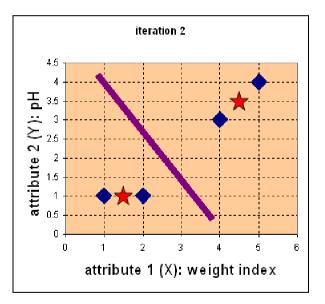
$$\mathbf{D}^{1} = \begin{bmatrix} 0 & 1 & 3.61 & 5 \\ 3.14 & 2.36 & 0.47 & 1.89 \end{bmatrix} \begin{array}{c} \mathbf{c}_{1} = (1,1) & group - 1 \\ \mathbf{c}_{2} - (\frac{11}{3}, \frac{8}{3}) & group - 2 \\ A & B & C & D \\ \hline \begin{bmatrix} 1 & 2 & 4 & 5 \\ 1 & 1 & 3 & 4 \end{bmatrix} \begin{array}{c} X \\ Y \end{array}$$



- Iteration-1, Objects
 clustering: Based on the new
 distance matrix, we move the
 medicine B to Group 1 while
 all the other objects remain.
 The Group matrix is shown
- Iteration 2, determine centroids: Now we repeat step 4 to calculate the new centroids coordinate based on the clustering of previous iteration. Group 1 and group 2 both has two members, thus the new centroids are $c_1 = (\frac{1+2}{2}, \frac{1+1}{2}) = (1\frac{1}{2}, 1)$ and $c_2 = (\frac{4+5}{2}, \frac{3+4}{2}) = (4\frac{1}{2}, 3\frac{1}{2})$

$$\mathbf{G}^{1} = \begin{bmatrix} 1 & 1 & 0 & 0 \\ 0 & 0 & 1 & 1 \end{bmatrix} \quad \begin{array}{c} group - 1 \\ group - 2 \end{array}$$

$$A \quad B \quad C \quad D$$





• <u>Iteration-2, Objects-Centroids distances</u>: Repeat step 2 again, we have new distance matrix at iteration 2 as

$$\mathbf{D}^{2} = \begin{bmatrix} 0.5 & 0.5 & 3.20 & 4.61 \\ 4.30 & 3.54 & 0.71 & 0.71 \end{bmatrix} \quad \mathbf{c}_{1} = (1\frac{1}{2}, 1) \quad group - 1 \\ \mathbf{c}_{2} = (4\frac{1}{2}, 3\frac{1}{2}) \quad group - 2 \\ A \quad B \quad C \quad D \\ \begin{bmatrix} 1 & 2 & 4 & 5 \\ 1 & 1 & 3 & 4 \end{bmatrix} \quad X \\ Y$$



Real-Life Numerical Example of K-

Means Clustering iteration-2, Objects clustering: Again, we assign each object based on the minimum distance.

$$\mathbf{G}^{2} = \begin{bmatrix} 1 & 1 & 0 & 0 \\ 0 & 0 & 1 & 1 \end{bmatrix} \quad \begin{array}{c} group - 1 \\ group - 2 \end{array}$$

$$A \quad B \quad C \quad D$$

- We obtain result that ${\bf G}^2-{\bf G}^1$. Comparing the grouping of last iteration and this iteration reveals that the objects does not move group anymore.
- Thus, the computation of the k-mean clustering has reached its stability and no more iteration is needed..



We get the final grouping as the results as:

Object	Feature1(X): weight index	<u>Feature2</u> (Y): pH	Group (result)
Medicine A	1	1	1
Medicine B	2	1	1
Medicine C	4	3	2
Medicine D	5	4	2



Discussion on the K-Means Method

- Efficiency: O(tKn) where n: # of objects, K: # of clusters,
 and t: # of iterations
 - Normally, K, t << n; thus, an efficient method
- K-means clustering often terminates at a local optimal
 - Initialization can be important to find high-quality clusters
- Need to specify K, the number of clusters, in advance
 - There are ways to automatically determine the "best"
 K
 - In practice, one often runs a range of values and selected the "best" K value

Discussion on the K-Means Method

- Sensitive to noisy data and outliers
 - Variations: Using K-medians, K-medoids, etc.
- K-means is applicable only to objects in a continuous n-dimensional space
 - Using the K-modes for categorical data
- Not suitable to discover clusters with non-convex shapes
 - Using density-based clustering, kernel K-means, etc.

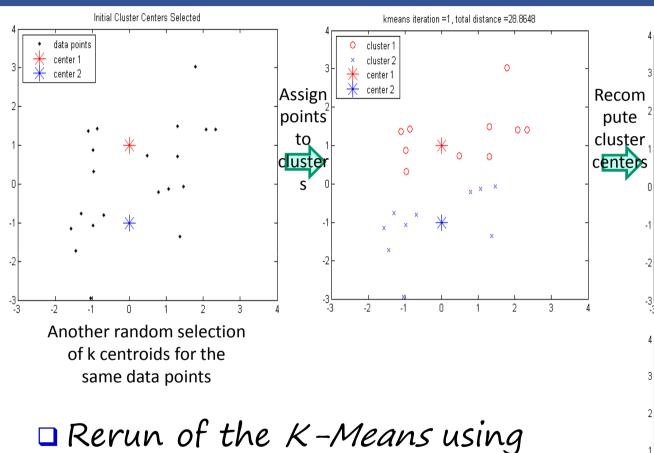


Initialization of K-Means

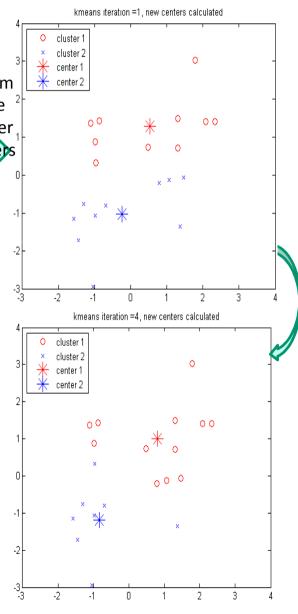
- Different initializations may generate rather different clustering results (some could be far from optimal)
- · Original proposal: Select K seeds randomly
 - Need to run the algorithm multiple times using different seeds
- There are many methods proposed for better initialization of k seeds
 - The first centroid is selected at random
 - K-Means++,k-median,k-mediods



Example: Poor Initialization May Lead to Poor Clustering



- Rerun of the *K-Means* using another random *K* seeds
- □ This run of K-Means generates a poor quality clustering

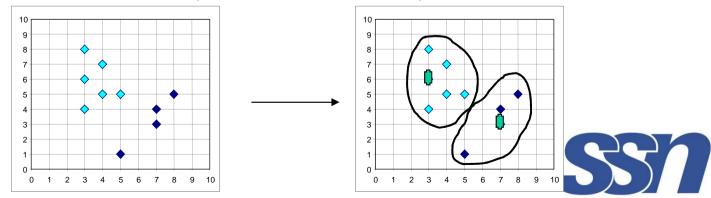


K-Mediods

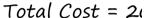
- Consider six points in 1-D space having the values
- 1, 2, 3, 8, 9, 10, and 25, respectively.
- By visual inspection we may partition the points into the clusters {1,2,3} and {8, 9,10} where point 25 is excluded which is an outlier.
- How would k-means partition the values?
- If we apply k-means using mean 2 and 9 and $c1\{1,2,3\}$ {8,9,10,25} with cluster variation as 196
- With mean as 3.5 and 14.67 for c1{1,2,3,8} and c2{9,10,25} the cluster variation as 189.67
- Assigns 8 to different cluster due to the prsence of outliers

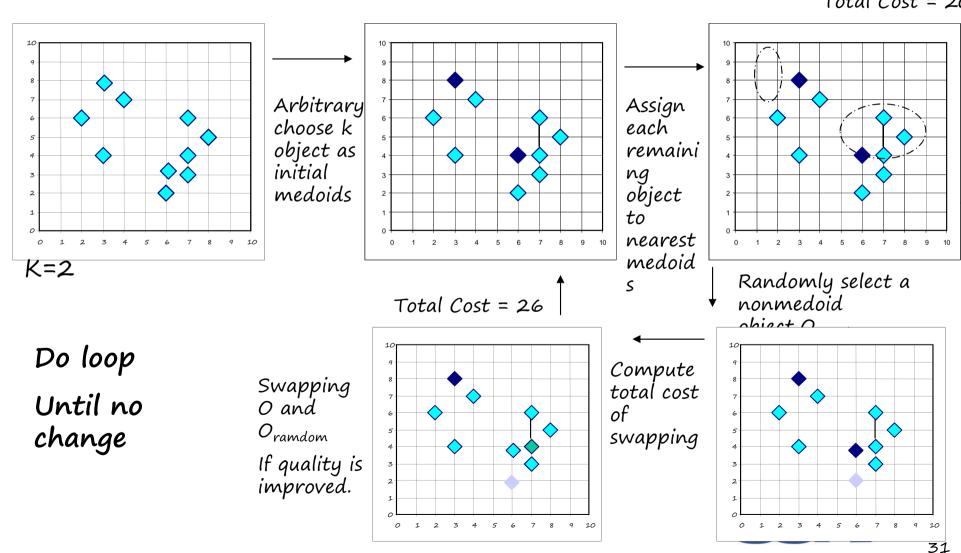
K-Mediods

- Avoid taking the mean value of the object as reference point.
- Actual objects to represent the clusters medoids can be used, which is the most centrally located object in a cluster
- Assign other similar objects as representative object to the cluster.
- The absolute-error criterion is defined as $E = \sum_{i=1}^{E} \sum_{p \in C_i} dist(p, i)$
- O_i representative object and P all objects in the data set



PAM: A Typical K-Medoids Algorithm





Algorithm for PAM

- The K-Medoids clustering algorithm:
 - Select K points as the initial representative objects (i.e., as initial K medoids)
 - Repeat
 - Assigning each point to the cluster with the closest medoid
 - Randomly select a non-representative object o_i
 - Compute the total cost S of swapping the medoid m with o_i
 - If S < O, then swap m with o_i to form the new set of medoids
 - Until convergence criterion is satisfied

Discussion on K-Medoids Clustering

- K-Medoids Clustering: Find representative objects (medoids)
 in clusters
- PAM (Partitioning Around Medoids:
 - Starts from an initial set of medoids
 - Iteratively replaces one of the medoids by one of the non-medoids if it improves the total sum of the squared errors (SSE) of the resulting clustering
 - PAM works effectively for small data sets but does not scale well for large data sets (due to the computational complexity)
 - Computational complexity: PAM: O(K(n K)²) (quite expensive!)

Discussion on K-Medoids Clustering

- Efficiency improvements on PAM
 - CLARA (Kaufmann & Rousseeuw, 1990):
 - PAM on samples; $O(Ks^2 + K(n K))$, s is the sample size
 - CLARANS (Ng & Han, 1994): Randomized re-sampling,
 ensuring efficiency + quality



K-Medians: Handling Outliers by Computing Medians

- Medians are less sensitive to outliers than means
 - Think of the median salary vs. mean salary of a large firm when adding a few top executives!
- *K-Medians*: Instead of taking the **mean** value of the object in a cluster as a reference point, **medians** are used $(L_1$ norm as the distance measure)
- The criterion function for the K-Medians algorithm:

$$S = \sum_{k=1}^{K} \sum_{x_{i \in C_k}} |x_{ij} - med_{kj}|$$

