

## **Introduction to Data Mining**

### Lecture #15: Clustering-2

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## In This Lecture

- Learn the motivation and advantage of BFR, an extension of K-means to very large data
- Learn the motivation and advantage of CURE, an extension of K-means to clusters of arbitrary shapes





# BFR Algorithm CURE Algorithm

## BFR: Extension of k-means to large data



# **BFR Algorithm**



- BFR [Bradley-Fayyad-Reina] is a variant of k-means designed to handle very large (disk-resident) data sets
- Assumes that clusters are normally distributed around a centroid in a Euclidean space
  - Standard deviations in different dimensions may vary
    - Clusters are axis-aligned ellipses
- Efficient way to summarize clusters
   (want memory required O(clusters) and not O(data))



## **BFR Algorithm**

- Points are read from disk one main-memory-full at a time
- Most points from previous memory loads are summarized by simple statistics
- To begin, from the initial load we select the initial
   *k* centroids by some sensible approach:
  - Take k random points
  - Take a small random sample and cluster optimally
  - Take a sample; pick a random point, and then
     *k-1* more points, each as far from the previously selected points as possible



## **Three Classes of Points**

### 3 sets of points which we keep track of:

### Discard set (DS):

Points close enough to a centroid to be summarized

#### Compression set (CS):

- Groups of points that are close together but not close to any existing centroid
- These points are summarized, but not assigned to a cluster

#### Retained set (RS):

Isolated points waiting to be assigned to a compression set



## **BFR: "Galaxies" Picture**



**Discard set (DS):** Close enough to a centroid to be summarized **Compression set (CS):** Summarized, but not assigned to a cluster Retained set (RS): Isolated points



## **Summarizing Sets of Points**

# For each cluster, the discard set (DS) is <u>summarized</u> by:

- The number of points, N
- The vector SUM, whose i<sup>th</sup> component is the sum of the coordinates of the points in the i<sup>th</sup> dimension
- The vector SUMSQ: i<sup>th</sup> component = sum of squares of coordinates in i<sup>th</sup> dimension



# Summarizing Points: Comments

- 2d + 1 values represent any size cluster
  - **d** = number of dimensions
- Average in each dimension (the centroid) can be calculated as SUM<sub>i</sub> / N
  - SUM<sub>i</sub> = i<sup>th</sup> component of SUM
- Variance of a cluster's discard set in dimension i
   is: (SUMSQ<sub>i</sub> / N) (SUM<sub>i</sub> / N)<sup>2</sup>
  - And standard deviation is the square root of that

### Next step: Actual clustering

**Note:** Removing the "axis-aligned" clusters assumption would require storing full covariance matrix to summarize the cluster. So, instead of **SUMSQ** being a *d*-dim vector, it would be a *d x d* matrix, which is too big! U Kang





## The "Memory-Load" of Points

### **Processing the "Memory-Load" of points (1):**

- 1) Find those points that are "sufficiently close" to a cluster centroid and add those points to that cluster and the DS
  - These points are so close to the centroid that they can be summarized and then discarded
- 2) Use any main-memory clustering algorithm to cluster the remaining points and the old RS
  - Clusters go to the CS; outlying points to the RS Discard set (DS): Close enough to a centroid to be summarized. Compression set (CS): Summarized, but not assigned to a cluster Retained set (RS): Isolated points UKang



## The "Memory-Load" of Points

**Processing the "Memory-Load" of points (2):** 

- 3) DS set: Adjust statistics of the clusters to account for the new points
  - Update Ns, SUMs, SUMSQs
- 4) Consider merging compressed sets in the CS
- 5) If this is the last round, merge all compressed sets in the CS and all RS points into their nearest cluster

**Discard set (DS):** Close enough to a centroid to be summarized. Compression set (CS): Summarized, but not assigned to a cluster Retained set (RS): Isolated points **U** Kang



## A Few Details...

- Q1) How do we decide if a point is "close enough" to a cluster that we will add the point to that cluster?
- Q2) How do we decide whether two compressed sets (CS) deserve to be combined into one?



## How Close is Close Enough?

 Q1) We need a way to decide whether to put a new point into a cluster (and discard)

#### BFR suggests two ways:

 High likelihood of the point belonging to currently nearest centroid (and, the point far from all other centroids)

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The Mahalanobis distance is small (< t)</p>





## **Mahalanobis Distance**

#### Normalized Euclidean distance from centroid

For point  $(x_1, ..., x_d)$  and centroid  $(c_1, ..., c_d)$ 

- 1. Normalize in each dimension:  $y_i = (x_i c_i) / \sigma_i$
- 2. Take sum of the squares of the  $y_i$
- 3. Take the square root

$$d(x,c) = \sqrt{\sum_{i=1}^{d} \left(\frac{x_i - c_i}{\sigma_i}\right)^2}$$

 $\sigma_i$  ... standard deviation of points in the cluster in the *i*<sup>th</sup> dimension



## **Mahalanobis Distance**

If clusters are normally distributed in **d** dimensions, then after transformation, one standard deviation =  $\sqrt{d}$ 

 Accept a point for a cluster if its M.D. is < t (a parameter), e.g. 2 standard deviations





## **Picture: Equal M.D. Regions**

#### Euclidean vs. Mahalanobis distance



# Should 2 CS clusters be combined?

# Q2) Should 2 CS subclusters be combined?

- Compute the variance of the combined subcluster
  - N, SUM, and SUMSQ allow us to make that calculation quickly
- Combine if the combined variance is small (< s)</li>







# BFR Algorithm CURE Algorithm

## CURE: Extension of k-means to clusters of arbitrary shapes



## **The CURE Algorithm**

### Problem with BFR/k-means:

- Assumes clusters are normally distributed in each dimension
- And axes are fixed ellipses at an angle are *not OK*



#### CURE (Clustering Using REpresentatives):

- Assumes a Euclidean distance
- Allows clusters to assume any shape
- Uses a collection of representative points to represent clusters





# **Starting CURE**

#### **2** Pass algorithm. Pass 1:

- 1) Pick a random sample of points that fit in main memory
- 2) Initial clusters:
  - Cluster these points hierarchically group nearest points/clusters

### **3)** Pick representative points:

- For each cluster, pick a sample of points, as dispersed as possible
- From the sample, pick representatives by moving them (say) 20% toward the centroid of the cluster



# **Starting CURE**

#### **2** Pass algorithm. Pass 1:

#### 4) Merge clusters

- Merge two clusters that are sufficiently close (<t)</li>
  - Cluster distance: minimum distance of representative points
- Repeat, until there are no more sufficiently close clusters



## **Example: Initial Clusters**









# **Finishing CURE**

#### Pass 2:

Now, rescan the whole dataset and visit each point *p* in the data set

#### Place it in the "closest cluster"

Normal definition of "closest":
 Find the closest representative to *p* and assign it to representative's cluster



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## **Summary: Clustering**

 Clustering: Given a set of points, with a notion of distance between points, group the points into some number of clusters

### Algorithms:

- Agglomerative hierarchical clustering:
  - Centroid and clustroid
- □ *k*-means:
  - Initialization, picking k
- **BFR**
- **CURE**



# **Questions?**