Data Analytics

Unit - 4 [One - Shot]

Most important topics :

1. Mining frequent itemsets
2. Apriori algorithm
3. Flajolet - Martin (FM) algorithm.
4. K- means clustering techniques, Hierarchical ~~Heighrarchical~~ clustering.
5. CLIQUE and ProCLUS.

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Mining frequent itemsets :

- It involves finding reoccurring patterns, items or set of items in large datasets.
- This is crucial in fields like market Basket analysis, where it helps identify items that frequently re-occur in transactions.

* Key concept :

- Itemset : A collection of one or more items.

  e.g: { bread, butter, milk }

- Support : Frequency of occurrance of an itemset in data.

  e.g: if { milk, butter } appears in 3 out of 10 transactions, its support is 30%.

- Frequent itemset : An itemset whose support is greater than or equal to a user- defined minimum threshold.

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Apriori Algorithm :

- It is a classic algorithm used in data mining for mining frequent itemsets and relevent association rules.
- It uses bottom- up approach

where frequent subsets are extended one item at a time, and non - frequent subsets are pruned.

Steps of Apriori Algorithm :

Step 1: Generate candidate itemsets :

- Start with itemset of length 1.

- e.g: {bread}, {milk}, {butter}.

Step 2: Calculate support :

- Count the support for each candidate itemset.

- e.g: {bread} has 50%, {milk} has 20%.

Step 3: Prune non - frequent itemsets :

- Remove itemsets that do not meet the minimum support threshold.

- e.g: if minimum support is 30%, remove {milk} with 20% support.

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Step 4: Generate new candidates :

- Create new candidate itemsets by combining frequent itemsets.

- e.g: Combine {bread} and {butter} to form {bread, butter}.

Step 5: Repeat :

- Repeat the process for itemsets of increasing length until no more frequent itemsets can be generated.

Example: [Assume min. support threshold = 50%]

T1	{bread, milk}
T2	{bread, butter}
T3	{milk, butter}
T4	{bread, milk, butter}
T5	{bread, milk}

1. Generate candidate itemset :

{ bread } , { milk } , { butter }

2. Calculate support for each:

{ bread } :	4/5	= 80%
{ milk } :	4/5	: 80 %
{ butter } :	3/5	= 60 %

3. Frequent itemset :

all have support ≥ 50% .

{ bread }, { butter }, { milk }

4. Again generate candidate itemsets :

{ bread , milk } , { bread , butter }, { milk , butter }

5. Calculate support for each :

{ bread , milk } :	3/5	= 60%
{ bread , butter } :	2/5	= 40%
{ milk , butter } :	2/5	= 40%

6. Frequent itemset :

{ bread , milk } (pruned other sets).

No further candidate will be generated since there are no 2 - frequent itemsets to extend.

Hence ,

frequent itemsets :

1. { bread }, { milk } , { butter }

2. { bread , milk }

Flajolet - Martin (FM) Algorithm :

- It is a probablistic algorithm used to estimate the no. of distinct elements in a data stream.

- It utilizes the use of hash functions and the properties of bit patterns in the hash values to estimate the no. of distinct elements.

Algorithm :

Step 1 : Hashing elements : For each element in the data stream, apply a hash func^n that maps the element to a binary number.

Step 2: Trailing zeros: For each hashed value, determine the no. of trailing zeros.

Step 3: Maximum trailing zeros: Track the max no. of trailing zeros observed. If the max no. of trailing zeros is R, then we estimate that there are approx 2^R distinct elements.

Step 4: Averaging (Multiple Hash functions): To improve accuracy, use multiple independent hash functions and take the average of their estimates.

(#) K- means clustering algorithm:

- It is a popular unsupervised machine learning algorithm used to partition a dataset into k-clusters, where each data point belongs to the cluster with the nearest mean.

Algorithm:

1. Initialization:

- Choose the no. of clusters, k.
- Initialize k centroids randomly. These centeroids can be randomly selected from the dataset.

2. Assignment step:

- Assign each data point to the nearest centroid. This forms k clusters.
- Distance is usually measured using the Euclidian distance formula.

3. Updation:

- Recalculate the centroid of each cluster.
- The new centroid is mean of all the points assigned to that cluster.

4. Repeatition :

- Repeat assignments and update steps until the centroid do not change significantly, or max no of iterations is reached.

Heirarchical clustering :

- It is a method of cluster analysis that seeks to build a heirarchy of clusters.
- It can be divided into two main types :
  1. Agglomerative (Bottom-up)
  2. Divisive (Top-down)

i) Agglomerative clustering :

- Starts with each data point as a single cluster.
- Iteratively merges the closest clusters until all points are in a single clusters or a desired no. of clusters is reached.

★ Algorithm :

Step 1. Initialization :

- Start with n clusters (each data point is its own cluster)

Step 2. Compute proximity matrix :

- Calculate the distance (similarity) between every pair of clusters.

Step 3. Merge clusters :

- Find the pair of clusters with smallest distance
- Merge these two clusters into a single cluster.

Step 4. Update proximity matrix :

- Recalculate the distances between the new cluster and all the other clusters.

Step 5 Repeat :

- Repeat the merge and update steps until all points are merged into a single cluster or the desired no. of cluster is reached.

ii) Divisive clustering :

- Starts with all data points in one cluster.
- Iteratively splits the cluster into smaller clusters until each point is in its own cluster or a desired number of clusters is reached.

★ Algorithm :

Step 1 Initialization :

- Starts with all points in one cluster.

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Step 2 Split clusters :

- Identify the best way to split the cluster into two sub-clusters. (mostly uses k-means clustering)

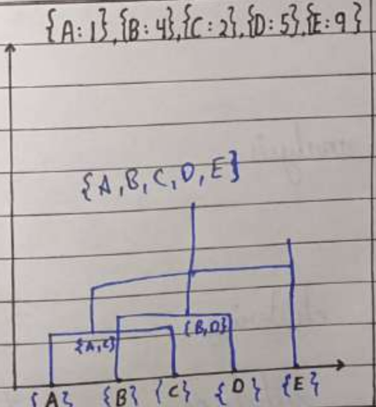
Step 3 Update clusters :

- Recalculate the distances b/w the new clusters and all other clusters (if applicable).

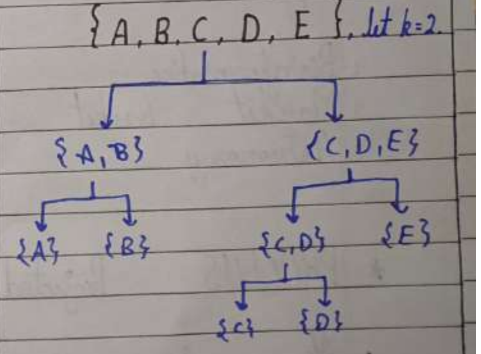
Step 4 Repeat :

- Repeat the split and update steps until each point is in its own cluster or the desired no. of clusters is reached.

e.g:



Agglomerative Clustering



Divisive Clustering

⊛ CLIQUE and PROCLUS :

* CLIQUE : Clustering in Quest

- It is a powerful and efficient clustering algorithm designed for high-dimensional data.
- It combines grid-based and density based clustering approaches to discover clusters in subspaces of high-dimensional spaces.
- CLIQUE is notable for its ability to automatically determine subspaces that are relevant for clustering.

Applications:

1. Bioinformatics
2. Market basket analysis
3. Astronomy

* PROCLUS : Projected clustering

- It is a subspace clustering algorithm specifically designed to handle high - dimensional data.
- It identifies clusters in lower dimensional subspaces where clusters are not visible in full - dimensional space but appear in some lower dimensional projections.

Applications :

1. Bioinformatics
2. Customer segmentation
3. Text mining

Thanks for watching !!

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