Lecture 6 Descriptive Analytics

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Agenda

- Introduction
- **Clustering:**
- K-means
- K-means++
- k-medoids (PAM)
- Applying Clustering on Big Data
- **Association Rules**
- Applying Association Rules on Big Data



Introduction

Introduction

Descriptive Analytics use Descriptive Data Mining techniques which use Unsupervised Machine Learning techniques.

Descriptive Analytics



Descriptive Data Mining



Unsupervised
Machine Learning



Clustering

Clustering

- > Clustering is used to identify groups of similar objects in a multivariate data sets.
- As a data mining function, cluster analysis serves as a tool to gain insight into the distribution of data to observe characteristics of each cluster.
- Clustering analysis is broadly used in many applications in data mining:
 - Clustering can be used in **image processing**, for example, in a video k-means analysis can be used to **identify objects** in the video.
 - Clustering can help markets **characterize their customer groups** based on the purchasing patterns.
 - Clustering helps in **classifying documents** on the web for **information discovery**.
 - Clustering is used in outlier detection applications as detection of credit card fraud.

- There are different types of clustering methods, including:
 - Partitioning clustering
 - Hierarchical clustering
 - Fuzzy clustering
 - Density-based clustering
 - Grid-based clustering
 - Model-based clustering
 - Constraint-based clustering

> Partitioning clustering:

- Suppose we are given a database of 'n' objects, the partitioning method constructs 'k' partition of data. Each partition will represent a cluster where each cluster contains at least one object, and each object must belong to exactly one cluster.
- For a given number of partitions (say k), the partitioning method will create an initial partitioning.
- Then it uses the iterative relocation technique to improve the partitioning by moving objects from one cluster to other.

>Hierarchical clustering:

- This method creates a hierarchical decomposition of the given set of data objects. There are two approaches here:
 - **Agglomerative Approach:** Known also as the <u>bottom-up</u> approach. In this, we start with each object forming a separate group. It keeps on merging the objects or groups that are close to one another until the termination condition holds.
 - **Divisive Approach:** Known also as the <u>top-down</u> approach. In this, we start with all of the objects in the same cluster. In the continuous iteration, a cluster is split up into smaller clusters until the termination condition holds

>Fuzzy clustering:

- Fuzzy clustering is also known as **soft** method. Standard clustering approaches produce partitions, in which each observation belongs to only one cluster. This is known as **hard** clustering.
- In Fuzzy clustering, items can be a member of more than one cluster. Each item has a set of membership coefficients corresponding to the degree of being in a given cluster.

> Density-based clustering:

• In density-based clustering, clusters are defined as areas of **higher density** than the remainder of the data set. Objects in sparse areas - that are required to separate clusters - are usually considered to be **noise** points.

➤ Grid-based clustering:

- In this method, the objects together form a **grid**. The object space is divided into **finite number of cells** that form a grid structure.
- Cells are chosen randomly until all cells are traversed.
- The density of a cell 'c' is calculated and if this density is greater than threshold density, then mark cell 'c' as a new cluster.
- The densities of the neighboring cells are calculated and based on the threshold value it is decided to merge it with cell 'c'.

➤ Model-based clustering:

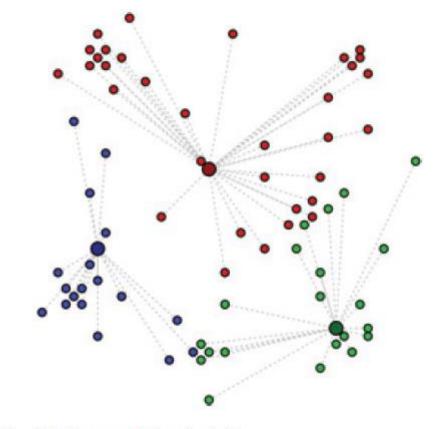
- **Model-based clustering** assumes that the data were generated by a **model** and tries to recover the original **model** from the data. The **model** that we recover from the data then defines **clusters** and an assignment of objects to **clusters**. A commonly used criterion for estimating the **model** parameters is maximum likelihood.
- This method provides a way to automatically determine the number of clusters based on standard statistics, taking outlier or noise into account.

➤ Constraint-based clustering:

• In this method, the clustering is performed by the incorporation of **user or application-oriented constraints.** A constraint refers to the user expectation or the properties of desired clustering results. Constraints provide us with an interactive way of communication with the clustering process.



- Given a collection of objects each with n measurable attributes, *k-means* is an analytical technique that, for a chosen value of k, identifies k clusters of objects based on the objects' proximity to the center of the k groups.
- The center is determined as the arithmetic average (mean) of each cluster's n-dimensional vector of attributes.
- ➤ It is a Partitioning clustering method.



Possible k-means clusters for k=3

- The k-means algorithm to find k clusters can be described in the following four steps:
 - 1. Choose the value of k and the k initial guesses for the centroids.
 - 2. Compute the distance from each data point to each centroid. Assign each point to the closest centroid. This defines the first k clusters.
 - For a given point, **pi** (pi1, pi2, ..pin) and a centroid, **q**, (q1, q2,..qn) where n is the number of features, the distance, **d**, between pi and q, is expressed as shown in the following equation:

$$d(p_{I},q) = \sqrt{\sum_{j=1}^{n} (p_{IJ} - q_{J})^{2}}$$

- The k-means algorithm to find k clusters can be described in the following four steps (cont.):
 - 3. Compute the centroid, the center of mass, of each newly defined cluster from Step 2. The centroid, **q**, of a cluster of **m** points, where each point pi has n features(pi1, pi2, ..pin), is calculated as in the following equation:

$$(q_1, q_2, ..., q_n) = \left(\frac{\sum_{i=1}^m p_{i1}}{m}, \frac{\sum_{i=1}^m p_{i2}}{m}, ..., \frac{\sum_{i=1}^m p_{in}}{m}\right)$$

- 4. Repeat Steps 2 and 3 until the algorithm converges to an answer.
 - Convergence can be reached when the computed centroids do not change or the centroids and the assigned points oscillate back and forth from one iteration to the next.

Determining the Number of Clusters (i.e. K):

- The value of k can be chosen based on a reasonable guess or some predefined requirement.
- However, even then, it would be good to know how much better or worse having k clusters versus k-1 or k+1 clusters would be in explaining the structure of the data.
- Next, a heuristic using the **Within Sum of Squares** (WSS) metric is examined to determine a reasonably **optimal value of k**.

- Determining the Number of Clusters (i.e. K):
 - **WSS** is defined as shown in the following equation:

WSS =
$$\sum_{l=1}^{M} d(p_l, q^{(l)})^2 = \sum_{l=1}^{M} \sum_{l=1}^{n} (p_{ij} - q_j^{(l)})^2$$

• WSS is the sum of the squares of the distances between each data point and the closest centroid. M is the number of objects in the dataset. The term $q^{(i)}$ indicates the closest centroid that is associated with the ith point. If the points are relatively close to their respective centroids, the WSS is relatively small. Thus, if k + 1 clusters do not greatly reduce the value of WSS from the case with only k clusters, there may be little benefit to adding another cluster.

>Advantages:

- Fast convergence for clustering small datasets
- Easy to implement

>Drawbacks:

- Computationally expensive for large datasets
- Doesn't guarantee to converge to a global minimum. It is sensitive to the centroids' initialization. Different setups may lead to different results.
- Strong sensitivity to outliers



- >K-means algorithm is sensitive to the initialization of the centroids.
- To overcome the above-mentioned drawback we use **K-means++**.
- **K-means++** algorithm ensures a smarter initialization of the centroids and improves the quality of the clustering.
- ➤ **K-means++** is an algorithm for choosing the initial values for the K-means clustering algorithm.
- Apart from initialization, the rest of the algorithm is the same as the standard K-means algorithm.

- The steps of choosing the centroids are as follows:
 - 1. Randomly select the first centroid from the data points which means that all points have an equal probability of getting selected.
 - 2. For each data point compute its distance from the nearest, previously chosen centroid.
 - 3. Select the next centroid from the data points such that the probability of choosing a point as centroid is directly proportional to its distance from the nearest, previously chosen centroid. (i.e. the point having maximum distance from the nearest centroid is most likely to be selected next as a centroid)
 - 4. Repeat steps 2 and 3 until k centroids have been sampled.

- >K-means++ intuition:
 - By following the mentioned procedure for initialization, we pick up centroids that are far away from one another.
 - This increases the chances of initially picking up centroids that lie in different clusters.
 - K-means++ is more likely to converge and run faster than K-means.



Clustering: k-medoids (PAM)

Clustering: k-medoids

- **K-Medoids** (also called as Partitioning Around Medoid **PAM**).
- The PAM algorithm searches for k representative objects in a data set (**k medoids**) and then assigns each object to the closest medoid in order to create clusters.
- These medoids are actual observations from the dataset and not computed points (mean value) like in the case of k-means.
- Its aim is to minimize the sum of dissimilarities between the objects in a cluster and the center of the same cluster (medoid).
- It is known to be less sensitive to outliers than k-means.

Clustering: k-medoids

>PAM algorithm steps:

- 1. Randomly pick k observations as initial medoids.
- 2. Compute the distances between the observations and medoids.
- 3. Assign each point to the nearest medoid.
- 4. Pick a new observation (non-medoid) in each cluster and consider its swap with the correspondent medoid.
- 5. Compute the cost after such swap.
- 6. Select the best swap (if any) that decreases the cost function (sum of all distances from a non-medoid object to the medoid for the cluster it is in).



- We now consider how to reformulate **K-means** algorithms for solving the clustering problem on **Big Data**.
- > We will formulate this algorithm using MapReduce technique.
- Fach iteration of standard k-means can be divided into two phases, the first of which computes the sets of points closest to mean μi, and the second of which computes new means of these sets.
- These two phases correspond to the **Map** and **Reduce** phases of the MapReduce algorithm.

- The Map phase operates on each point x in its split.
- For a given x, find the mean µi (the cluster) which minimizes the squared distance between x and the mean.
- Then a <key-value > pair is emitted with this mean's index i as key and the value x i.e <i, x>
- Note that in order for the Map function to compute the distance between a point x and each of the means, each machine in our distributed cluster **must have the current set of means**. We must therefore **broadcast** the new means at each iteration.

The output of the map phase is huge, so a **combiner** is used to minimize the size of the data.

The combiner calculates the average of the data instances for each cluster id, along with the number of the instances.

>It outputs < i, (cluster mean, number of instances)>

The **reduce phase** calculates the means by iterating over the values of the same cluster index.

The shared means values have to be updated to the new computed values.

>All the mentioned procedure is repeated until the convergence criterion is met.



Association Rules

Association Rules

- Association rules method is an unsupervised learning method.
- This is a descriptive method often used to discover interesting relationships hidden in a large dataset.
- The disclosed relationships can be represented as rules or frequent itemsets.
- > Here are some possible questions that association rules can answer:
 - Which products tend to be purchased together?
 - Of those customers who are similar to this person, what products do they tend to buy?
 - Of those customers who have purchased this product, what other similar products do they tend to view or purchase?

Association Rules: Overview

- For example, given a large collection of transactions in which each transaction consists of one or more items:
- ⇒association rules go through the items being purchased to see what items are frequently bought together and to discover a list of rules that describe the purchasing behavior.
- The goal with association rules is to discover interesting relationships among the items.
- The relationship occurs too frequently to be random and is meaningful from a business perspective.

Association Rules: Overview



Rules

Cereal → Milk (90%)

Bread → Milk (40%)

Milk → Cereal (23%)

Milk → Apples (10%)
...

...

The general logic behind association rules

when cereal is purchased, 90% of the time milk is also purchased.

Association Rules: Overview

- Each of the uncovered rules is in the form $X \to Y$, meaning that when item X is observed, item Y is also observed.
- In fact, because of their popularity in mining customer transactions, association rules are sometimes referred to as *market basket analysis*.
- Each transaction can be viewed as the shopping basket of a customer that contains one or more items.
- This is also known as an *itemset*.
- An itemset containing *k* items is called a *k-itemset*.

Association Rules: Overview

- The term *itemset* generally refers to a collection of items or individual entities that contain some kind of relationship.
- This could be:
 - a set of retail items purchased together in one transaction,
 - a set of hyperlinks clicked on by one user in a single session,
 - a set of tasks done in one day,
 - others

Association Rules: Apriori Algorithm

- ➤ Apriori is one of the earliest and the most fundamental algorithms for generating association rules.
- It pioneered the use of support for pruning the itemsets and controlling the exponential growth of candidate itemsets.
- This approach eliminates the need for all possible itemsets to be enumerated within the algorithm, since the number of all possible itemsets can become exponentially large.

Association Rules: Apriori Algorithm

- ➤One major component of Apriori is **support**.
- \triangleright Given an itemset L, the **support** of L is the percentage of transactions that contain L.
- For example, if 80% of all transactions contain itemset {bread}, then the support of {bread} is 0.8.
- A *frequent itemset* has items that appear together often enough. The term "often enough" is formally defined with a *minimum support* criterion.
- If the minimum support is set at 0.5, any itemset can be considered a frequent itemset if at least 50% of the transactions contain this itemset.

Association Rules: Apriori Algorithm

- If an itemset is considered frequent, then any subset of the frequent itemset must also be frequent.
- This is referred to as the *Apriori property* (or *downward closure property*).
- For example, if 60% of the transactions contain {bread,jam}, then at least 60% of all the transactions will contain {bread} or {jam}.
- In other words, when the support of {bread,jam} is 0.6, the support of {bread} or {jam} is at least 0.6.
- The Apriori property provides the basis for the Apriori algorithm.

- The Apriori algorithm takes a bottom-up iterative approach to uncovering the frequent itemsets by:
 - <u>first</u> determining all the possible items (or 1-itemsets, for example {bread}, {eggs}, {milk}, ...)
 - and then identifying which among them are frequent.
- Assuming the minimum support threshold (or the minimum support criterion) is set at 0.5:
 - the algorithm identifies and retains those itemsets that appear in at least 50% of all transactions
 - and discards (or "prunes away") the itemsets that have a support less than 0.5.

- In the **next iteration** of the Apriori algorithm:
 - the identified frequent 1-itemsets are paired into 2-itemsets (for example, {bread,eggs}, {bread,milk}, {eggs,milk}, ...)
 - and again evaluated to identify the frequent 2-itemsets among them.
- ➤ At each iteration, the algorithm checks whether the support criterion can be met;
 - if it can, the algorithm grows the itemset, repeating the process until it runs out of support or until the itemsets reach a predefined length.

- To generate the association rules, find all the rules of the frequent itemset such that these rules have higher confidence value than the threshold or minimum confidence.
- Confidence is the percent of transactions that contain both X and Y out of all the transactions that contain X and computed as follows:

$$Confidence(X \rightarrow Y) = \frac{Support(X \land Y)}{Support(X)}$$

Example: Suppose we have the following dataset that has various transactions, and from this dataset, we need to find the frequent itemsets and generate the association rules using the Apriori algorithm:

TID	ITEMSETS	
T1	А, В	
T2	B, D	
T3	В, С	
T4	A, B, D	
T5	A, C	
T6	В, С	
T7	A, C	
T8	A, B, C, E	
T9	A, B, C	

>Step-1: Assume minimum support count is 2, Calculate the support count for each itemset and prune those items with support count less than the minimum support count.

Itemset	Support_Count
Α	6
В	7
С	5
D	2
E	1

Itemset	Support_Count
Α	6
В	7
С	5
D	2

Item E is pruned since it doesn't satisfy the minimum support count criteria

➤ Step-2: Create pairs of the frequent itemsets that are identified in Step-1 and again calculate the support count for each itemset and prune those itemsets with support count less than the minimum support count.

Itemset	Support_Count
{A, B}	4
{A,C}	4
{A, D}	1
{B, C}	4
{B, D}	2
{C, D}	0



Itemset	Support_Count
{A, B}	4
{A, C}	4
{B, C}	4
{B, D}	2

➤ Step-3: Expand the frequent itemsets that are identified in Step-2 to include 3 items and again calculate the support count for each itemset and prune those itemsets with support count less than the minimum support count.

Itemset	Support_Count
{A, B, C}	2
{B, C, D}	1
{A, C, D}	0
{A, B, D}	0



Itemset	Support_Count
{A, B, C}	2

>Step-4: Generating the association rules; we will now apply on the last frequent itemset reached (generally frequent itemsets from the other iterations are considered).

Rules	Support	Confidence
A ^B → C	2	Sup{(A ^B) ^C}/sup(A ^B)= 2/4=0.5=50%
B^C → A	2	Sup{(B^C) ^A}/sup(B ^C)= 2/4=0.5=50%
A^C → B	2	Sup{(A ^C) ^B}/sup(A ^C)= 2/4=0.5=50%
C→ A ^B	2	Sup{(C^(A ^B)}/sup(C)= 2/5=0.4=40%
A→ B^C	2	Sup{(A^(B ^C)}/sup(A)= 2/6=0.33=33.33%
B→ B^C	2	Sup{(B^(B ^C)}/sup(B)= 2/7=0.28=28%

- >Step-4: We will exclude the rules that have less confidence than the minimum threshold (50%).
- Therefore, the rules selected will be:
 - $\{A, B\} \rightarrow C$
 - $\{B, C\} \rightarrow A$
 - $\{A, C\} \rightarrow B$

Association Rules: Evaluation of Candidate Rules

- > We have seen two measures which are: Support and Confidence.
- There are other measures such as: Lift and Leverage
- Lift measures how many times more often X and Y occur together than expected if they are statistically independent of each other. Lift is a measure of how X and Y are really related rather than coincidentally happening together:

$$Lift(X \to Y) = \frac{Support(X \land Y)}{Support(X) * Support(Y)}$$

A larger value of lift (greater than 1) suggests a greater strength of the association between X and Y.

Association Rules: Evaluation of Candidate Rules

Leverage is a similar notion, but instead of using a ratio, leverage uses the difference. Leverage measures the difference in the probability of X and Y appearing together in the dataset compared to what would be expected if X and Y were statistically independent of each other.

Leverage
$$(X \rightarrow Y)$$
 = Support $(X \land Y)$ - Support (X) * Support (Y)

A larger leverage value indicates a stronger relationship between X and Y.

Association Rules: Evaluation of Candidate Rules

Confidence is able to identify **trustworthy rules**, but it cannot tell whether a **rule is coincidental**. Why?

A high-confidence rule can sometimes be misleading because confidence does not consider support of the itemset in the rule consequent.

Measures such as lift and leverage not only ensure interesting rules are identified but also **filter out the coincidental rules**.



- A MapReduce job splits the input transaction database into various blocks, and a mapper is invoked once for each transaction passed as arguments.
- The map task parses one transaction at a time and extracts each itemset included in the transaction it received as input.
- After processing, the mapper sends the itemset to the partitioner by emitting the itemset and frequency as <key, value> pair, where 'key 'is a candidate itemset and 'value' is 1.

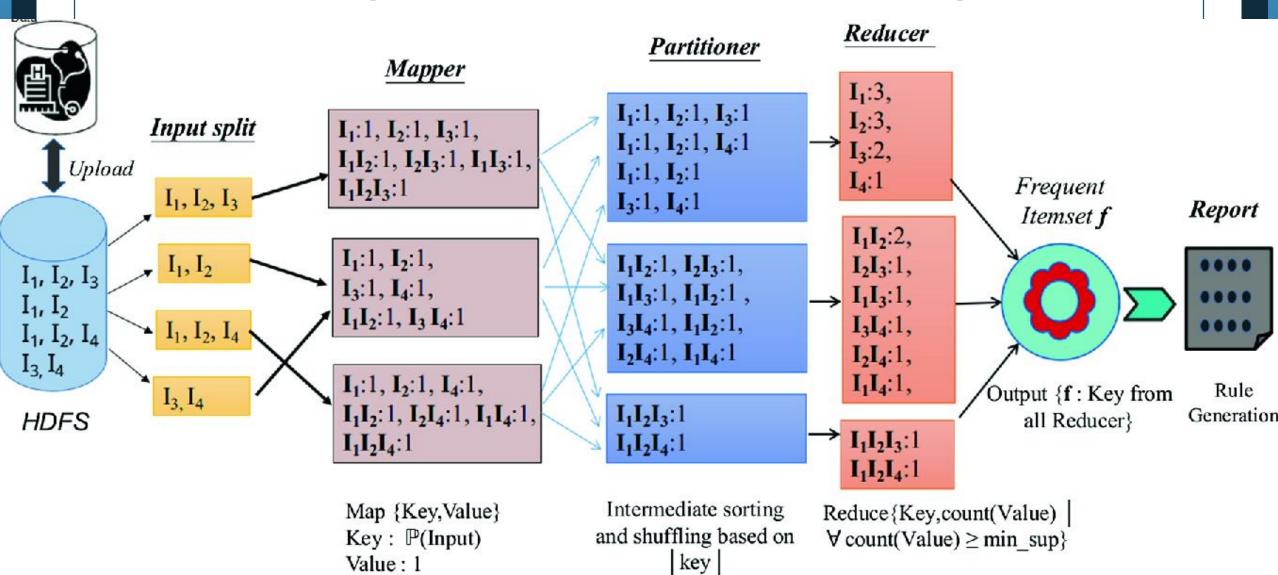
- The partition task collects all the intermediate <key, value > pair emitted from the map task as its input.
- Based on the **key size**, i.e., the size of each itemset, the partitioner specifies that all the values for each itemset are grouped together and maps all the values of a single key to go to the same reducer.

The output of all partitioner are shuffled and exchanged to make the list of values associated with the same key as <key,list(value) > pairs.

The **reduce task** collects each key passing all the values emitted against the same key as arguments, i.e., <key,list(value)> pairs emitted by partitioner task.

Then, it **sums up** the values of respective keys. Candidate itemset whose sum of values is **supportcount<minimum_support_count** is discarded.

The result from all reducers is written to the output file.



References

- ➤ Bodoia, M. (2016). MapReduce Algorithms for k-means Clustering. Stanford University
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Thank You