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Clustering Data Streams Based on Shared Density between Micro-Clusters

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ABSTRACT: Micro-clusters represent local density estimates by aggregating the information of many data points in a defined area. On demand, a (modified) conventional clustering algorithm is used in a second offline step to recluster the micro-clusters into larger final clusters. For reclustering, the centers of the micro-clusters are used as pseudo points with the density estimates used as their weights. However, information about density in the area between micro-clusters is not preserved in the online process and reclustering is based on possibly inaccurate assumptions about the distribution of da ta within and between micro-clusters (e.g., uniform or Gaussian). This paper describes DBSTREAM, the first micro-cluster-based online clustering component that explicitly captures the density between micro-clusters via a shared density graph. The density information in this graph is then exploited for reclustering based on actual density between adjacent micro-clusters. We discuss the space and time complexity of maintaining the shared density graph.

KEYWORDS: Data Streams, Density Based Clustering, Micro Cluster

I. INTRODUCTION

In recent years demands of data stream clustering increases rapidly .Data stream are observed in network monitoring, critical scientific application, weather monitoring and astronomical applications, elect ronic business, stock trading ,social networks ,sensor network etc. In these applications ,data stream arrives continuously and evolve significantly over time.

1.1 Background

There are many technologies available which facilitates us to record day to life transactions at rapid rate. Such process lead to large volume of continuous data. This data term as 'Data Stream'. Data streams are highly dynamic, massive and unbounded in nature. Due to these characteristics real-time data stream clustering is challenging problem. Data stream clustering puts additional constraints on clustering algorithms. Clustering in data stream environment needs some special requirements due to data stream's characteristics such as clustering in bounded memory and within limited processing time as well as with single pass over evolving data streams.

1.2 Motivation

Data stream clustering is generally divided in two phases online and offline. Online phase summarized data into many micro clusters and then in offline phase micro clusters are merged and form macro cluster.[1]Reclustering is offline process hence its does not have limited time bound. In literature various data stream clustering methods are discussed like hierarchical and partitioning which are use to create spherical-shape clusters. Density based clus tering is one of the most important method to discover non-spherical shape and outliers. DENCLUE, DBSCAN, OPTICS, are density based clustering algorithm. These algorithm focuses on dense area of data points in data space and identify as cluster as they are separated by low density area .Another important method of clustering is grid based. Grid based clustering method has fast processing time and it is not depended on number of data points.

II. LITERATURE SURVEY

In this paper we address the issue of overwhelmingly large output size. We also specify a bound on the number of extra sets that are allowed to be covered. We examine different problem variants for which we demonstrate the hardness of

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the corresponding problems and we provide simple polynomial-time approximation algorithms. We give empirical evidence showing that the approximation methods work well in practice [1].

The algorithms for finding frequent patterns are complete: they find all patterns that occur sufficiently often. Completeness is a desirable property,of course. How-ever,in many cases the collection of frequent patterns is large,and obtaining a global understanding of which pat-terns are frequent and which are not is not easy. Even re-stricting the output to the border of the frequent item-set collection does not help much in alleviating the problem. The case when the input is the original database is per-haps the most interesting open algorithmic question. This case presents significant difficulties. First,computing the border in time polynomial to its size is a main open prob-lem. Furthermore,the size of the border can be exponential in the size of the database,and therefore one cannot afford looking at the whole search space—some kind of sampling method needs to be applied [2].

This goal,however,is different from our set-tingwhereweaskforthe k sets that best approximate the frequent item-set collection in the sense of set coverage. The work on frequent closed item sets attempts to compress the collection of frequent sets in a lossless manner,while for the condensed frequent item sets the idea is to be able to reduce the output size by allowing a small error on the support of the frequent item sets. The second set, Course,is from anonymized student/course registra-tion data in the Department of Computer Science at the University of Helsinki. Frequent course sets were obtained using a support threshold of 2.2%,yielding a collection of size 1637 [3].

Diabetes is part of the growing epidemic of non communicable diseases, with a high burden for the society on developing countries in future.For suppressing the development of diabetes mellitus and the onset of complications to manage their healthcare or personal data. We aim to apply association rule mining to electronic medical records to discover sets of risk factors. The four methods summaries the high risk of diabetes. Our extension to the bottom up summarization algorithm produced the most suitable summary [4].

Association rules are implications that associate a set of potentially interacting conditions (e.g. high BMI and the presence of hypertension diagnosis) with elevated risk. The use of association rules is particularly beneficial because in addition to quantifying the diabetes risk, they also readily provide the physician with a “justification”, namely the associated set of conditions. This set of conditions can be used to guide treatment towards a more personalized and targeted preventive care or diabetes management [5].

A clinical application of association rule mining to identify sets of co-morbid conditions that imply significantly increased risk of diabetes. Association rule mining on this extensive set of variables resulted in an exponentially large set of association rules. The main contribution is a comparative evaluation of these extended summarization techniques that provides guidance to practitioners in selecting an appropriate algorithm for a similar problem [6].

Association rule mining to identify sets of risk factors and the corresponding patient subpopulations who are at significantly increased risk of progressing to diabetes.An excessive number of association rules were discovered impeding the clinical interpretation of the results. For this method to be useful, the number of rules is used for clinical interpretation is make feasible [7].

Many of these rules are slight variants of each other leading to the obfuscation of the clinical patterns underlying the ruleset. One remedy to this problem, which constitutes the main focus of this work, is to summarize the ruleset into a smaller set that is easier to overview. We first review the existing rule set and database summarization methods, then propose a generic framework that these methods fit into and finally, we extend these methods so that they can take a continuous outcome variable (the martingale residual in our case) into account [8]

The significance is usually defined by the context of applica-tions. Previous studies have been concentrating on how to compute top-ksignificant patterns or how to remove redundancy among patterns separately. There is limited work on finding those top-kpatterns which demonstrate high-significance and low-redundancy simultaneously. In this paper, we study the problem of extracting redundancy-aware top-kpatterns from a large collection of frequent patterns. We first examine the evaluation functions for measuring the combined significance of a pattern set and propose theMMS(Maximal Marginal Significance) as the problem formulation [9].

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The second example isdocument theme extraction, where each document (or each sentence) is treated as a transaction. The goal is to extract the frequent patterns of term occurrence, calledthemes, buried in a large set of documents. Given a document set, the top- kfrequent patterns returned by a mining algorithm are not necessarily the bestkthemes one can find. Many frequent term sets could overlap significantly with each other. Such overlapping may render top-k important themes very redundant [10].

In this paper, we formulate the redundancy-aware top-kpattern extraction problem through a general rank-ing model which integrates two measures, significance and redundancy, into one objective function. We first examine the evaluation functions for measuring the com-bined significance of a pattern set and propose theMMS (Maximal Marginal Significance) as the problem formu-lation. TheMMSproblem is equivalent to searching a constrained rooted minimum spanning tree on the directed redundancy graph such that the overall weights on the root node and on the edges in the tree are maximized. The constraint specifies that the root must be the most significant pattern in the tree [11].

To extract redundancy-aware top-kpatterns, we ex-amined two problem formulations:MASandMMS. We studied a unified greedy approach to compare these two functions and show that MMSis a reasonable formulation to our problem. We further present an improved algorithm forMMSand show that the performance is bounded byO(logk). We present two case studies to examine the performance of our proposed approaches. BothMMSalgorithms are able to find high-significant and low-redundant top-kpatterns. Particularly, in block correlation experiments, we observe that our improved algorithm performs better. This study opens a new direction on finding both diverse and significant top-kanswers to querying, search- ing, and mining, which may lead to promising further studies [12].

In this paper, we study the problem of compressing frequent-pattern sets. Typically, frequent patterns can be clustered with a tight-ness measure±(called ±-cluster), and arepre-sentative patterncan be selected for each clus-ter. Unfortunately, finding a minimum set of representative patterns is NP-Hard. We develop two greedy methods,RPglobalandRPlo- cal. The former has the guaranteed compres-sion bound but higher computational com-plexity. The latter sacrifices the theoretical bounds but is far more efficient. Our per-formance study shows that the compression quality usingRPlocalis very close to RPglobal, and both can reduce the number of closed frequent patterns by almost two orders of magnitude. Furthermore, RPlocalmines even fasterthan FPClose, a very fast closed frequent-pattern mining method. We also show that RPglobaland RPlocal can be combined to- gether to balance the quality and efficiency [13].

There have been many scalable methods developed for frequent-pattern mining. However, the real bottleneck of the problem is not at the efficiency but at the usability. Typically, ifminsupis high, min-ing may generate only commonsense patterns, how-ever, with a lowminsup, it may generate an explosive number of results. This has severely restricted the us-age of frequent-pattern mining. To solve this problem, it is natural to explore how to “compress” the patterns, i.e., find a concise and succinct representation that describes the whole col-lection of patterns. Two major approaches have been developed in this direction: lossless compression and lossy approximation [14].

TheRP-globalmethod has theoretical bound, and works well on small collections of frequent patterns. TheRPlo-calmethod is quite efficient, and preserves reasonable compression quality. We also discuss a combined ap-proach, RPcombine, to balance the quality and effi-ciency. TheRPlocal method can be used as sampling procedure as we did in RPcombine, since it is efficient and achieves con-siderable compression. Second, the compressed pat-tern sets generated by our method can be used for queries of finding approximate supports [15].

The objective of the clustering is to minimize the number of clusters (hence the number of repre-sentative patterns). Finally, we show the problem is equivalent to set-covering problem, and it is NP-hard w.r.t. the number of the frequent patterns to be com-pressed. We propose two greedy algorithms: the first one, RPglobal, has bounded compression quality but higher computational complexity; whereas the second one, RPlocal, sacrifices the theoretical bound but is far more efficient [16].

III. EXISTING SYSTEM AND ITS LIMITATION

Density-based clustering is a well-researched area and we can only give a very brief overview here. DBSCAN and several of its improvements can be seen as the prototypical density-based clustering approach. DBSCAN estimates the density around each data point by counting the number of points in a user-specified eps neighborhood and applies user-specified thresholds to identify core, border and noise points. In a second step, core points are joined into a cluster if

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they are density-reachable (i.e., there is a chain of core points where one falls inside the eps-neighborhood of the next). Finally, border points are assigned to clusters. Other approaches are based on kernel density estimation (e.g., DENCLUE) or use shared nearest neighbors (e.g., SNN, CHAMELEON).

However, these algorithms were not developed with data streams in mind. A data stream is an ordered and potentially unbounded sequence of data point's X ¼hx 1; x2; x3; ...i. It is not possible to permanently store all the data in the stream which implies that repeated random access to the data is infeasible. Also, data streams exhibit concept drift over time where the position and/or shape of clusters changes, and new clusters may appear or existing clusters disappear. This makes the application of existing clustering algorithms difficult. Data stream clustering algorithms limit data access to a single pass over the data and adapt to concept drift. Over the last 10 years many algorithms for clustering data streams have been proposed. Most data stream clustering algorithms use a two-stage online/offline approach

Reclustering methods based solely on micro-clusters only take closeness of the micro-clusters into account. This makes it likely that two micro-clusters which are close to each other, but separated by an area of low density still will be merged into a cluster. Information about the density between micro-clusters is not available since the information does not get recorded in the online step and the original data points are no longer available. Fig. 1a illustrates the problem where the micro-clustersMC1 and MC2 will be merged as long as their distance d is low. This is even true when density-based clustering methods (e.g., DBSCAN) are used in the offline reclustering step, since the reclustering is still exclusively based on the micro-cluster centers and weights.

Disadvantages:

1. These algorithms were not developed with data streams in mind. It is not possible to permanently store all the data in the stream which implies that repeated random access to the data is infeasible.
2. This leads to a problem when the data points within each cell are not uniformly distributed and two dense cells are separated by a small area of low density.

IV. PROPOSED SYSTEM ARCHITECTURE

Reclustering represents the algorithm's offline component which uses the data captured by the online component. For simplicity we discuss two-dimensional data first and later discuss implications for higher-dimensional data. For reclustering, we want to join MCs which are connected by areas of high density. This will allow us to form macro-clusters of arbitrary shape, similar to hierarchical clustering with single-linkage or DBSCAN's reachability, while avoiding joining MCs which are close to each other but are separated by an area of low density.

For two-dimensional data the intersection factor a has a theoretical maximum of 0.391 for an area of uniform density when the two MCs are optimally packed (the centers are exactly r apart). However, in dynamic clustering situations MCs may not be perfectly packed all the time and minor variations in the observed density in the data are expected. Therefore, a smaller value than the theoretically obtained maximum of 0.391 will be used in practice. It is important to notice that a threshold on a is a single decision criterion which combines the fact that two MCs are very close to each other and that the density between them is sufficiently high.

Two MCs have to be close together or the intersecting area and thus the expected weight in the intersection will be small and the density between the MCs has to be high relative to the density of the two MCs. This makes using the concept of a -connectedness very convenient.To remove noisy MCs from the final clustering, we have to detect these MCs. Noisy clusters are typically characterized as having low density represented by a small weight. Since the weight is related to the number of points covered by the MC, we use a user-set minimum weight threshold to identify noisy MCs. This is related to min Points in DBSCAN or Cm used by D-Stream

In dimensions higher than two the intersection area becomes an intersection volume. To obtain the upper limit for the intersection factor a we use a simulation to estimate the maximal fraction of the shared volume of MCs (hyper-spheres) that intersect in d ¼ 1; 2 ;; 10; 20 and 50-dimen-sional space. The results are shown in Table 1. With increasing dimensionality the volume of each hyper sphere increases much more than the volume of the intersection. This leads at higher dimensions to a situation where it becomes very unlikely that we observe many data points in the intersection. This is consistent with the problem known as the curse of dimensionality which effects distance-based clustering as well as Euclidean density estimation. This also effects other density based algorithms (e.g., D-Stream's attraction) in the same way. For high-dimensional data we plan to extend a subspace clustering approach like HPStream to maintain a shared density graph in lower-dimensional subspaces.

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Advantages:

1. This improves performance and, in many cases, the saved memory more than offset the memory requirement for the shared density graph.
2. Shared-density reclustering already performs extremely well when the online data stream clustering component is set to produce a small number of large MCs.

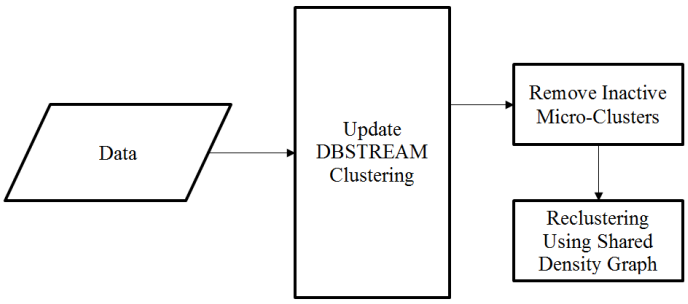

Figure 01. Proposed System Architecture

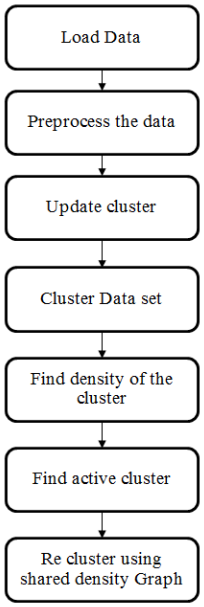

Figure 02. Flow of the system

4.1 MODULES:

1. Load Dataset
2. Update Cluster
3. Find Density of Micro cluster
4. Recluster using shared density

1. Load Dataset

- Load dataset which related to our system.
- Load data set into data base and show the loaded database.
- The input of Big Data comes from social networks (Facebook, Twitter, LinkedIn, etc.), Web servers, satellite imagery, sensory data, banking transactions, etc.
- Load remote sensing data into database.
- Pre-process data for remove irrelevant data.

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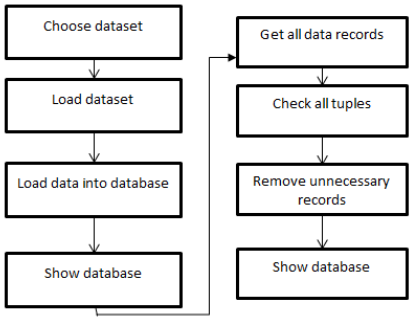

Figure 03. Load Dataset

2. Update Cluster:

- First, we find all MCs for which x falls within their radius. This is the same as asking which MCs are within r from x, which is the fixed-radius nearest neighbor problem which can be efficiently solved for data of low to moderate dimensionality.
- If one or more neighbors are found then we update the MCs by applying the appropriate fading, increasing their weight and then we try to move them closer to x using the Gaussian neighborhood function
- Next, we update the shared density graph

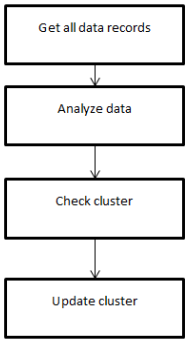

Figure 04.Update Cluster

3. Find Density of Micro-cluster:

- In this module find shared density of the each micro cluster.
- Produce the density of the micro cluster result in graph structure.

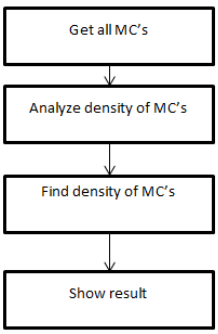

Figure 05. Find Density of Micro-cluster

4. Recluster using shared density:

Reclustering represents the algorithm's offline component which uses the data captured by the online component. For simplicity we discuss two-dimensional data first and later discuss implications for higher-dimensional data. For

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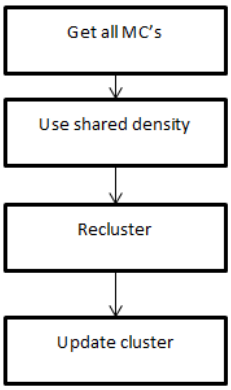

Figure 06.Recluster using shared density:

V. CONCLUSION

In this paper, we have developed the first data stream clustering algorithm which explicitly records the density in the area shared by micro-clusters and uses this information for reclustering. We have introduced the shared density graph together with the algorithms needed to maintain the graph in the online component of a data stream mining algorithm. Although, we showed that the worst-case memory requirements of the shared density graph grow extremely fast with data dimensionality, complexity analysis and experiments reveal that the procedure can be effectively applied to data sets of moderate dimensionality. Experiments also show that shared-density reclustering already performs extremely well when the online data stream clustering component is set to produce a small number of largeMCs. Other popular reclustering strategies can only slightly improve over the results of shared density reclustering and need significantly more MCs to achieve comparable results. This is an important advantage since it implies that we can tune the online component to produce less micro-clusters for shared-density reclustering. This improves performance and, in many cases, the saved memory more than offset the memory requirement for the shared density graph.

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