EINCKM: An Enhanced Prototype-based Method for Clustering Evolving Data Streams in Big Data

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Abstract: Data stream clustering is becoming an active research area in big data. It refers to group constantly arriving new data records in large chunks to enable dynamic analysis/updating of information patterns conveyed by the existing clusters, the outliers, and the newly arriving data chunk. Prototype-based algorithms for solving the problem have their promises for simplicity and efficiency. However, existing implementations have limitations in relation to quality of clusters, ability to discover outliers, and little consideration of possible new patterns in different chunks. In this paper, a new incremental algorithm called Enhanced Incremental K-Means (EINCKM) is developed. The algorithm is designed to detect new clusters in an incoming data chunk, merge new clusters and existing outliers to the currently existing clusters, and generate modified clusters and outliers ready for the next round. The algorithm applies a heuristic-based method to estimate the number of clusters (K), a radius-based technique to determine and merge overlapped clusters and a variance-based mechanism to discover the outliers. The algorithm was evaluated on synthetic and real-life datasets. The experimental results indicate improved clustering correctness with a comparable time complexity to existing methods dealing with the same kind of problems.

1 INTRODUCTION

Recent advances in information and networking technologies have led to a rapidly growing flux of massive data interaction that has led to the emergence of Big Data witnessed in almost every sector of life ranging from the stock market, online shopping, banking, social media, and healthcare systems (Liu et al., 2013). Despite numerous attempts at defining the term, big data fundamentally refers to a huge volume of data that are generated by various applications and stored in different sources and locations. Big data requires frequent updating and analysis with the aim of the enhanced competitiveness and improved performance of organizations (Olshannikova et al., 2014).

Velocity is one of the known characteristics of big data. It means that data arrive and require processing at different speeds. While for some applications, the arrival and processing of data can be performed in batch analysis style, other analytics applications require continuous and real-time analyses of incoming data chunks (Islam, 2013). Data stream clustering is defined as the grouping of new data that frequently arrive in chunks with the objective of gaining understanding about underlying grouping patterns that may change over time in the data streams (Yogita and Toshniwal, 2012).

Most existing data stream clustering solutions follow the path of adapting existing static data clustering approaches and methods to the dynamic data stream scenarios, attempting to accommodate the capability of two-phase processing, i.e. offline-online or online-offline (Aggarwal et al., 2003) (Bhatia and Louis, 2004). There are mainly three schools of thoughts in data stream clustering, i.e. prototype-based, density-based, and model-based (Yogita and Toshniwal, 2012; Nguyen et al., 2015; Silva et al., 2013). Prototype-based algorithms initially divide data objects into imprecise prototype clusters and then iteratively refine the prototypes into final clusters (e.g. K-Means (MacQueen, 1967)). Density-based algorithms look for dense regions in each of which there is a high concentration of data points, and then the dense regions form clusters of similar data objects (e.g. DBSCAN (Ester et al., 1996)). Model-based algorithms consider the data points as the results of a statistical modeling process. Finding clusters of similar data points is equivalent to finding the

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distributions of the statistical model (e.g. Expectation Maximization (Dempster et al., 1977)). Prototype-based methods are favored due to their promises of simplicity, ease of implementation, and efficiency. However, most, if not all, prototype-based methods have their limitations, such as requiring the advanced setting of a number of clusters (K), lack of capability in discovering outliers, etc. The aim of our research is to develop an efficient dynamic clustering solution that improves existing prototype-based algorithms.

In this paper, a new algorithm called Enhanced Incremental K-Means (EINCKM) is presented. At any incremental round, the inputs of the algorithm consist of a newly arrived data chunk, summary of the current set of clusters, and a list of outliers from the previous iteration. The outputs of the algorithm include the summary of a set of modified clusters and a new list of outliers. The EINCKM algorithm applies a simple heuristic-based method to estimate the number (K) of new clusters to be constructed from the new chunk. In addition, a radius-based technique is used to decide how to merge overlapping new and existing clusters. Moreover, the algorithm utilizes a variance-based mechanism to discover the output outliers. The algorithm was evaluated on both synthetic and real-life datasets. The experimental results show that the proposed algorithm improves clustering correctness with a comparable time complexity to the existing methods of the same type. The structure of the algorithm is designed to be modular for easy accommodation of any further improvements.

The rest of this paper is organized as follows: Section 2 presents the state of the art of the related work on data stream clustering algorithms in the current literature. Section 3 explains the proposed algorithm. Section 4 presents a systematic evaluation of the performance of the algorithm and compares it with a selected number of existing algorithms through theoretical analysis and practical experiments using the synthesized and real-life datasets. A number of further issues regarding the proposed algorithm will be discussed in Section 5. Section 6 concludes the work and outlines the possible future directions of this research.

2 RELATED WORK

2.1 Existing Approaches for Clustering Data Streams

From a computation point of view, there are two approaches for data stream mining: incremental-learning and two-phase-learning (Nguyen et al., 2015). Both approaches of mining can be adopted for clustering purposes. Figure 1 illustrates the principles of the two approaches. In the incremental-learning approach, a model of clusters continuously evolves to fit changes made by incoming data chunks (Guha et al., 2000). On the other hand, the basic principle of the two-phase-learning approach is to split the clustering process into two phases. The first phase summarizes the data points into "pseudo" clusters, i.e. not finalized clusters. In the second phase, i.e. whenever a query about the clustering results is raised, the pseudo-clusters are modified to produce the finalized clusters (Aggarwal et al., 2003; Silva et al., 2013).

2.2 Existing Algorithms

Several prototype-based algorithms using the traditional K-Means clustering principles have been developed. The Adapt.KM algorithm (Bhatia and Louis, 2004) first finds K clusters in an initial dataset using the K-Means method. It then takes the minimum distance among the centroids of the clusters as a threshold. When a new data point arrives, if the distance between the data point and the centroid of its closest cluster is below the threshold, the data point is then added to the cluster.

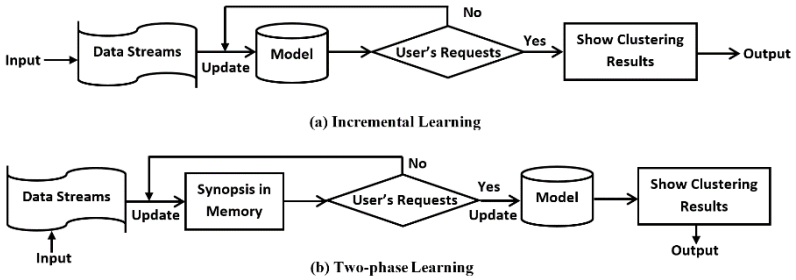


Figure 1: Computational approaches of data stream clustering (Nguyen et al., 2015).

The cluster centroid, as well as the threshold, are subsequently updated. If the distance is greater than the threshold, a new cluster is created for this new data point and the two closest existing clusters are merged followed by updating the centroid of the merged cluster and the threshold. The main limitation of this algorithm is its merging strategy. If there are a lot of outliers then clustering results will become meaningless.

Chakraborty and Nagwani later suggested an improvement, known as Inc.KM (Chakraborty and Nagwani, 2011), that uses the average distance between centroids as the threshold and ignores the data point with a distance greater than the threshold as an outlier. The drawback of this algorithm is that it ignores the outliers which may create a new cluster(s).

Guha, et al. (Guha et al., 2000) presented the STREAM algorithm. In the first phase, the algorithm evenly divides the stream into D chunks of equal size, finds S clusters in each chunk using the K-Median algorithm, and the centroids of the S clusters are weighted by the number of data points in each. After that, only the weighted centroids of all clusters are kept and treated as "data points" when a buffer of size m prototypes is accumulated. In the second phase, these m prototypes are further clustered into K cluster representations. The main shortcoming of STREAM is that it is unable to adapt to the evolution concept of data, i.e. merge, split, add, and delete clusters.

2.3 Merging Strategies for Overlapped Clusters

Merging overlapped clusters that may emerge during the updating phase is one of the most important steps in data stream clustering algorithms. It has an effect on the correctness of the resulting clusters. There exist three main strategies of merging clusters: matching, the conditional probability of intersection area, and cluster radius.

Spiliopoulou et al. (Ntoutsi et al., 2009) presented MONIC+ (Modeling and Monitoring Cluster Transitions) framework that computes the matching between clusters to capture their evolution. Clusters are only merged if they share at least a half of their memberships. Oliveira and Gama (Oliveira and Gama, 2012) produced MEC (Monitoring Clusters' Transitions) framework which relies on the conditional probability and a predefined merging threshold of 0.5. Conditional probabilities are computed for every pair clusters obtained at the consecutive time. The weakness of (Ntoutsi et al., 2009) and (Oliveira and Gama, 2012) is that information about the data points must be kept for each cluster, which is very expensive to maintain.

Zhang et al. (Zhang et al., 1996) presented BIRCH (Balanced Iterative Reducing and Clustering using Hierarchies) algorithm. To decide whether to add a new data point into the previous clusters or not, BIRCH depends on the radius (i.e. the average distance from memberships to the centroid of the cluster). Cao et al. (Cao et al., 2006) produced Denstream algorithm which relies on the radius r_{avg}, which is the average distance from the points in a micro-cluster to the centroid. The radius is then used to determine the merge of two closest micro-clusters. Although calculating radius in these two algorithms gives a very high probability for data points to belong to a cluster, they may consider some data points as outliers instead of members.

3 THE PROPOSED ALGORITHM

3.1 The Algorithm Framework

The general framework of the proposed EINCKM algorithm is depicted in Figure 2. The algorithm consists of the following main steps. Firstly, the outliers from the previous iteration are added into the incoming data chunk (step 1) in order to generate the K new clusters. The number K of new clusters is determined by an estimation function (step 2), which currently uses some heuristic rules to determine the value of K, but can be improved into a learning function to learn the best possible number of clusters for the new chunk. An Enhanced K-Means (EKM) algorithm is applied to the new data chunk (step 3) to discover the K new clusters. After that, a merging strategy is applied to the overlapped new and existing clusters of the last round using a radius-based technique to derive a set of modified clusters (steps 4, 5). Finally, data points that are currently members of the modified clusters are filtered using a variance-based mechanism to determine the outliers among them (step 6).

Figure 3 shows the pseudo-code of the EINCKM algorithm. The inputs are a data chunk of size M, a pool of outliers, the minimum number of data points per cluster, and a set of existing clusters summary. Each cluster summary is a tuple (N, LS, LSS, μ, R), where N is a number of data points, LS is the linear sum of the data points, LSS is the sum of squared data points, μ is the centroid, R is the radius. The outputs are K clusters and outliers.

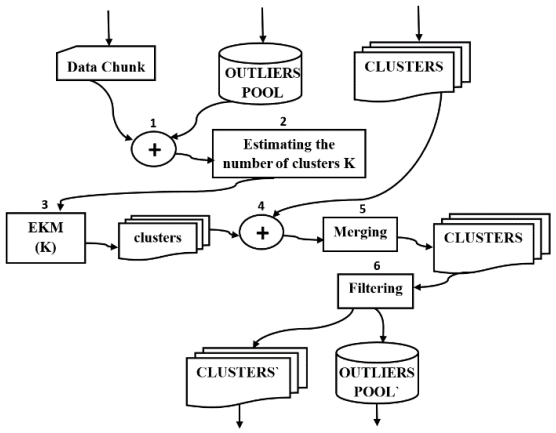


Figure 2: Main steps of the EINCKM algorithm.

EINCKM Algorithm:

Inputs:

CH : Data chunk of size M. Initially *CH = {}*

CF: Set of clusters summary $(N, LS, LSS, \boldsymbol{\mu}, R)$; //Previous clustering summary of T clusters. Initially, *CF = {}*

Po: Pool of outliers; //Previous Pool of W outliers. Initially, *Po = {}*.

$MinPts$: Minimum number of data points per cluster.

Outputs:

CF`: Modified CF;

Po`: Modified Po;

Algorithm Steps:

1. $CH = CH \cup Po$;
2. $\langle K, Ini\rangle = Estimate(CH, CF)$; //Estimate K and the initial centroids
3. $cf = EKM(CH, K, Ini)$;//cf is a structure contains cf.member as cluster members & cf.summary as cluster summary.
4. $For\ i = 1\ to\ K$ //Find the cluster summary of new clusters.
   Calculate $\mu_i\ and\ \sigma_i\ of\ S_i$; //$S_i$ is a cluster in cf.
   Set R_i as $(2 * \sigma_i)$ from μ_i;
   Calculate cluster summary for S_i//i.e. N, LS, L SS.
5. $CF = Merge(CF, cf)$; //Merge overlapping clusters.
6. $\langle CF, Po\rangle = Filter(CF, cf, MinPts)$; //Filter outliers

Figure 3: Pseudo-code of the proposed algorithm.

3.2 Main Functions of the Algorithm

We intend to keep the *Estimate* function simple and hence it determines the number of clusters K and initial centroids Ini using heuristics (see Figure 4). For the first iteration, the number of clusters is set to $K = \sqrt{N/2}$ where N is the number of data points in the new chunk plus the number of outliers in the previous pool. For the later iterations, K is set to the K value of the previous iteration (in Section 4.1 we will explain why we select K in this way). Parameter Ini refers to the collection of the initial centroids. For the first iteration, the initial centroids are assigned as randomly selected data points in the data collection, but for later iterations, the centroids of the clusters of the previous iteration are taken as the initial centroids for the current round. The *EKM* function is an enhanced K-Means method that uses K and Ini determined by the *Estimate* function. The intension is to minimize the nondeterministic results of clustering caused by different random seeds.

Estimate Function:

$\langle K, Ini\rangle = Estimate(CH, CF)$

$If\ (K_{old} = \emptyset)$ then//K_{old} is the number of clusters in CF

{

$K = SQRT(\text{size}(CH)/2)$;

$Ini = rand(K, CH)$;

}

$Else$

{

$K = K_{old}$;

$Ini = \{\mu_i\}$;//μ_i in CF

}

Figure 4: Pseudo-code for the Estimate Function.

The *Merge* function (see Figure 5) first creates a pairwise centroid distance matrix D for all clusters. It then locates a pair of closest clusters with the minimum distance. If the distance is less than or equal to the radius of the smaller cluster, then the two clusters are merged into a single cluster with updated cluster summary and memberships for the data points involved. One row and one column of the matrix D need to be updated to modify the distances of the newly merged cluster with the other clusters. The process is repeated until this criterion cannot be satisfied by any pair of clusters in the matrix D.

Merge Function:

$CF = Merge(CF, cf)$

1. $CF = CF \cup cf.summary$;
2. Calculate the pairwise distance matrix D for distances between $\mu_i\ and\ \mu_j$ in CF;// $(i \neq j)$
3. Repeat
   (A) Locate S_i, S_j in CF where$Dist_c_{min}(\mu_i, \mu_j) = argmin(D)$
   (B) Find $R_{min} = argmin(R_i, R_j)$
   (C) $If\ Dist\_c_{min} <= R_{min}$ then
   {
   (a) $S_i = S_i + S_j$;// Merging two clusters and reassigned the memberships
   (b) Calculate μ_i, σ_i for cluster S_i in CF;
   (c) Set R_i as $(2 * \sigma_i)$ from Cn_i
   (d) Modify D
   (e) Update cluster summary for S_i
   }

Until no more merge clusters

Figure 5: Pseudo-code for the Merge Function.

Extracting the outliers from the final clusters is done by calling the *Filter* function (see Figure 6) which uses the variance of each cluster and MinPts threshold to distinguish outliers. It scans the data points in each final cluster and compares their distance to the centroid with the radius of that cluster. If the distance is greater than the radius, the data point is considered as an outlier.

Filter Function:

$\langle CF, Po\rangle = Filter\ (CF, cf, MinPts)$
  $For\ i = 1\ to\ size(cf)$
  {
    $For\ j = 1\ to\ size(S_i)$// cf.member
    {
      $D = dist(p(j), \mu_i)$;// p is a data point in S_i
      $If\ D > R_i$ then $Po = Po \cup p(j)$;
    }
    $If\ size\ (S_i) < MinPts$ then $Po = Po \cup S_i$;
    Update cluster summary for S_i
  }

Figure 6: Pseudo-code for the Filter Function.

4 EVALUATION OF EINCKM

4.1 Logical Evaluation

Our evaluation of correctness focuses on the three main functions of the algorithm. The *Estimate* function only approximates the value of K and initial centroids. Since the number of clusters is normally smaller than the number of data points, using the square root of half of the data points as suggested in (Kodinariya and Makwana, 2013) is sensible as the initial estimate.

The *Merge* function depends on the general characteristics of the normal distribution to calculate the cluster radius. The cautious merge strategy ensures that the centroid of the smaller cluster not only belongs to the big cluster, but also close to the centroid of the big cluster. The *Filter* function extracts the outliers from the final clusters using their variance. Using the understanding of the normal distribution, the function excludes some data points outside the radius as an outlier, ensuring the high quality of the clusters.

The number of clusters in each iteration is affected by the *Estimate* and *Merge* functions. It could be increased or decreased at one round of clustering. In other words, the number of clusters is determined after each round of clustering.

Regarding completeness, unlike Inc.KM, the proposed algorithm does not lose any data point during the clustering process. If a data point does not belong to any clusters, it will be kept in the pool as outliers. If the outliers kept in the pool are considered belonging to a default cluster, the proposed algorithm is complete.

The time complexity of EINCKM is determined by the time complexity of its main functions. First, the time complexity of *EKM* algorithm is estimated as $O(NKI)$ where N is the total number of data points in a chunk plus the outliers in the input pool, K is the number of clusters, and I is the number of iterations until the clusters converge. The estimated time complexity of the *Merge* function is $O((T+k)^2)$ where T is the number of clusters of previous iteration and k is the number of clusters from a new chunk. The estimated time complexity of *Filter* function is $O(N)$ because each data point within the chunk and the previous pool is determined as a cluster member or an outlier. Therefore, the time complexity of EINCKM is estimated as $O(M(NKI)+(T+k)^2+N)$, where M is the chunk size.

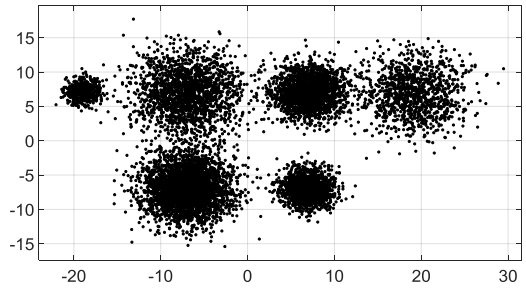
The time complexity of the Adapt.KM algorithm is estimated as $O(M(NKI+k(k-1)+N(K+1)))$. The time complexity of the Inc.KM algorithm is estimated as $O(M(NKI+k(k-1)+NK))$. The time complexity of STREAM is estimated as $O(M(NKI)+2k+N)$. Comparing the Big O notations across the different algorithms shows that STREAM is the fastest among the algorithms. The proposed EINCKM algorithm time complexity depends on $(T+k)^2$ whereas the Inc.KM and the Adapt.KM algorithms depend on MK^2 and $M(K^2+1)$. Since in most cases, the number of clusters is much fewer than the number of data points within a chunk, the proposed algorithm should be marginally faster than Inc.KM and Adapt.KM but slower than STREAM.

4.2 Empirical Evaluation

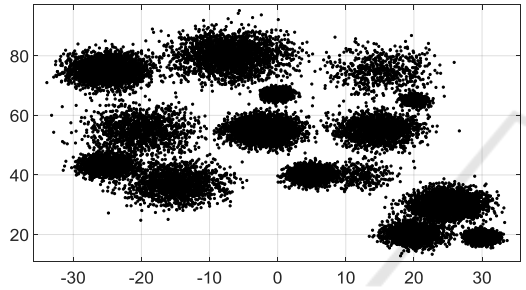
Different approaches to evaluate clustering algorithm performance exist in the literature (Kremer et al., 2011). In order to evaluate the correctness of the proposed algorithm, we have decided to use the evaluation by the reference method, i.e. to find if the algorithm can return the known clusters in a given ground truth. To do so, we generated three synthetic datasets (DS1, DS2, and DS3) of 10000, 30000, and 50000 data points respectively of two dimensions. The DS1 contains six clusters; DS2 contains fifteen clusters, and DS3 contains thirty clusters. Clusters in each of the three datasets have different sizes. Each cluster is generated randomly by following a normal distribution of a different mean and variance. Figure 7 (a, b, c) shows the scatterplots of the three datasets. The details of the normal distributions used for generating the datasets are given in Appendix1.

For real-life dataset, we selected the Network Intrusion Detection (NID) dataset from the KDD Cup'99 repository. This dataset contains TCP connection logs for 14 days of local network traffic (494,021 data points). Each data point corresponds to a normal connection or attack. The attacks split into four main types and 22 more specific classes: denial-of-service (DOS), unauthorized access from a

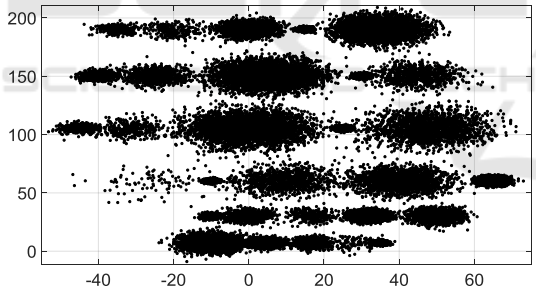
remote machine (R2L), unauthorized access to local user privileges (U2R), and surveillance (PROBING). We used all 34 continuous attributes as in (Aggarwal et al., 2003) and (Cao et al., 2006).



(a) Scatterplot of dataset DS1.



(b) Scatterplot for dataset DS2.



(c) Scatterplot for dataset DS3.

Figure 7: Overview of synthesized datasets.

To evaluate correctness, we used three commonly used evaluators: purity, entropy, and the sum of squared errors (SSE). Purity was used in (Cao et al., 2006), entropy in (Karypis and George, 2001), and SSE in (Aggarwal et al., 2003). Purity refers to the proportion of the data points belonging to a known cluster that are assigned as members of a cluster by the algorithm. The higher the proportion of purity (between [0, 1]) is, the more certain that the algorithm has found the original clusters and the better the algorithm is (Silva et al., 2013). Entropy reflects the number of the data points from different known clusters in the original dataset that are assigned to a cluster by the algorithm. The value of this measure is between $[0, Log_2 N]$ where N is the number of known clusters involved. The smaller value of the entropy is, the fewer members of the known clusters are mixed in the clusters discovered by the algorithm, and the better the clustering algorithm is (Nguyen et al., 2015). SSE is a commonly used cluster quality measure. It evaluates the compactness of the resulting clusters. Low scores of SSE indicates better clustering results as the clusters contain less internal variations (Silva et al., 2013). The efficiency of an algorithm was measured by the amount of time in seconds taken for the algorithm in completing the clustering task.

MATLAB was used to build an implementation of the EINCKM algorithm and the experiment framework. For the Adapt.KM and Inc.KM algorithms, we split a given dataset into two parts: the dynamic arriving data chunks of a certain size and the initial dataset before the arrival of the first dynamic data chunk. We randomly selected (e.g. DS1) an initial collection of 1000 data points as the initial dataset and the remaining 9000 were randomly selected as data points in the dynamic chunks. Our proposed algorithm does not treat the initial dataset and later arrived chunks differently, and hence an empty set of existing clusters and an empty set of outliers were assumed as the inputs when the first chunk is processed. For STREAM and EINCKM algorithms, we randomly selected all the chunks with size 100 data points. The idea behind the random selection of the data points is to investigate the behavior of the algorithms when there is no control on the sequence of data points, i.e. we did not select specific data points from specific groups in the original datasets. No assumption was made that the initial data chunk represents the entire data domain. In order to minimize the effect of random choice of data points, the experiments were repeated 100 times, and the average is calculated.

Figure 8 shows the details of comparison results between the known clusters and the output clusters from the Inc.KM, Adapt.KM, STREAM, and EINCKM algorithms respectively. EINCKM has the highest purity. This is the result of the stringent merge strategy deployed and the exclusion of some data points as outliers. Inc.KM also has good purity by ignoring the outliers, but this strategy denies the opportunity for some ignored outliers to become members of some clusters at a later stage. Adapt.KM has the poorer purity because of its merging strategy, i.e. combining two closest clusters could belong to different clusters in the original dataset. STREAM

has the lowest purity because it selects randomly initial centroids as one property of K-Median and this leads to clusters contain data points belong to different clusters in the original dataset.

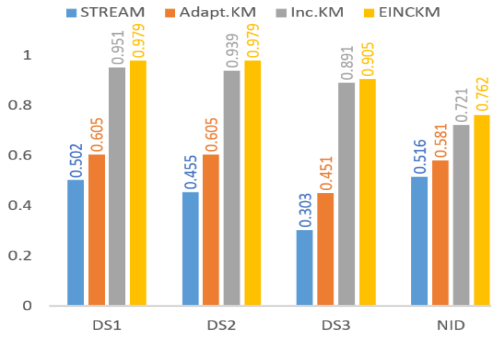


Figure 8: The purity measurement.

As shown by Figure 9, Inc.KM has the lowest entropy because it deletes all the outliers. EINCKM has the second lowest level because adding the outliers to the new data chunk may group them into different clusters comparing with original dataset. STREAM has the third level because the random initial centroids could lead to getting output clusters including some data points from other clusters. Adapt.KM has the highest level of entropy because its merging approach is getting output clusters contain many data points belong to different clusters in the original dataset.

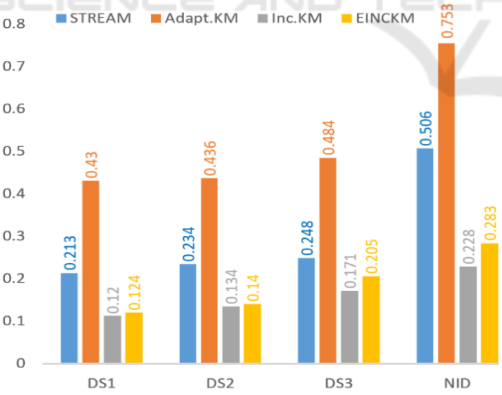


Figure 9: The entropy measurement.

The EINCKM has the lowest SSE because it produces compact and more stable clusters as a result of merging criterion and keeps the outliers separately (see Figure 10). In.KM has the second level because it gives us almost balanced clusters. STREAM has the third level because it presents different cluster sizes every time. Adapt.KM has the highest level because it produces bigger clusters during the merging process.

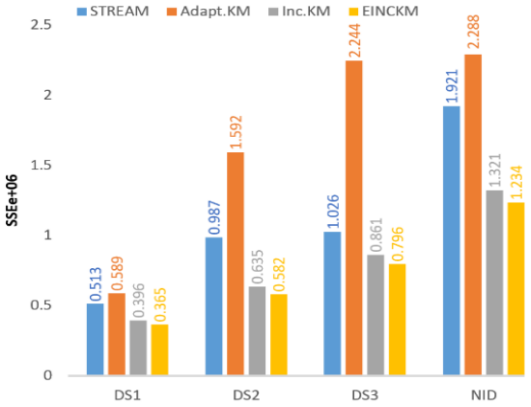
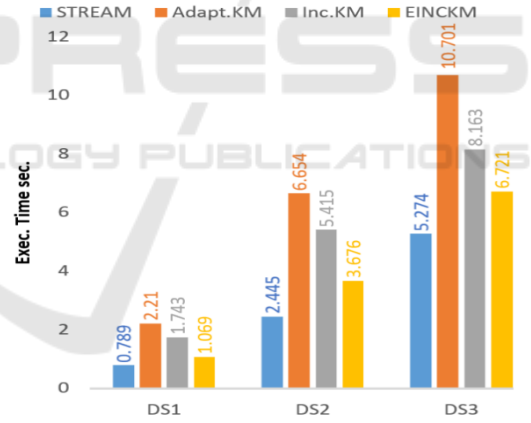
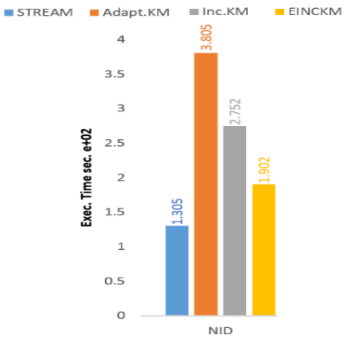


Figure 10: The SSE measurement.

Test results are shown in Figure 11 (a, b) confirm the logical analysis on efficiency: the STREAM algorithm has the minimum execution time followed by the EINCKM algorithm which in turn is better than both Inc.KM and Adapt.KM. The pattern is consistent across the synthesized and the real-life datasets.



(a) The efficiency measurement for synthesized dataset.



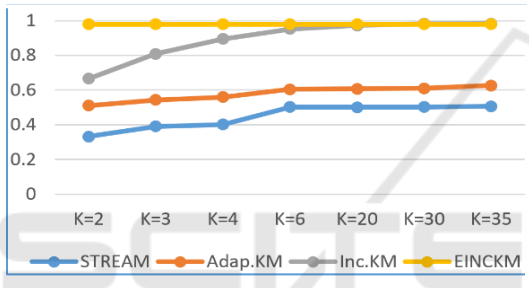
(b) The efficiency measurement for real-life dataset.

Figure 11: The efficiency measurement.

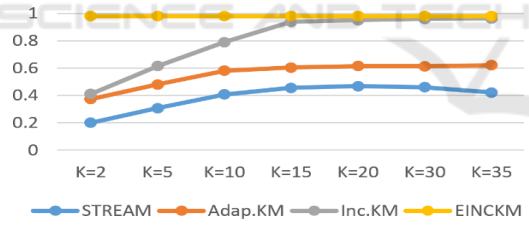
5 DISCUSSIONS

5.1 Adaptive Number of Clusters K by EINCKM

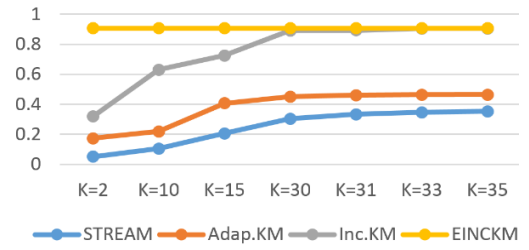
Our algorithm determines the number of clusters K automatically whereas the others require a predefined K. The empirical study results presented in the previous section compared those algorithms against the proposed algorithm when they were using the appropriate K values. However, those algorithms would have performed much worse if inappropriate K values were used. Figure 12 (a, b, c) shows the purity differences of the existing algorithms from the proposed algorithm when different K values were chosen. The results clearly demonstrate that the proposed algorithm outperform the others.



(a) Different values of K for DS1 dataset.



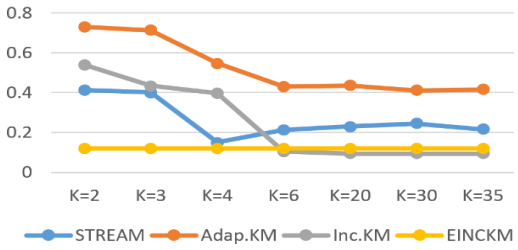
(b) Different values of K for DS2 dataset.



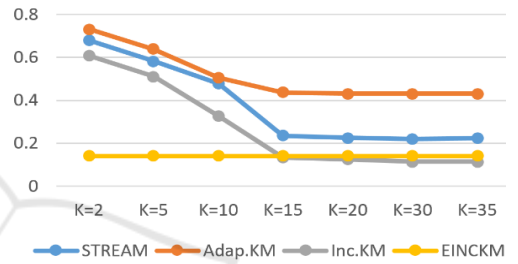
(c) Different values of K for DS3 dataset.

Figure 12: The purity measurements of the algorithms for synthesized datasets when different values of K were used.

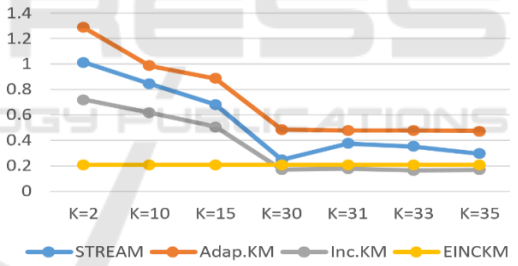
Figure 13 (a, b, c) shows the differences between the algorithms for the entropy correctness metric over the synthesized datasets. We have also tested the performances on SSE and performances on the real-life dataset NID, but will not present the results here due to space constraint. All test results indicate the same performance gaps between the proposed algorithm and the existing ones.



(a) Different values of K for DS1 dataset.



(b) Different values of K for DS2 dataset.



(c) Different values of K for DS3 dataset.

Figure 13: The entropy measurements of the algorithms for synthesized datasets when different values of K were used.

5.2 Refinements of EINCKM

One advantage of the EINCKM algorithm is its highly modular structure where the essential operations of the algorithm, i.e. estimating the value of K, the K-Means performed on the new data chunk, the merge operation, and the filter operation, are designated to functions. This means that we can continuously improve each function without changing the structure of the algorithm.

As for the further improvement of each function within the algorithm, first we do realize that using a heuristic estimation at the start of the algorithm may

be too trivial, and may not guarantee optimal results. We have noted the work presented in (Pio et al., 2014) that used the principal component analysis (PCA) to estimate the value of K before the K-Means clustering is conducted on the newly arrived data chunk, and consider adopting the method in the future improved version of the algorithm. Besides, machine learning solutions may be investigated to predict a more suitable value for K based on past clustering history on the previous chunks.

Besides, both the merge strategy and filtering scheme are currently quite simply in order to limit the amount of processing time. In fact, both the merging strategy and the filtering scheme may be further improved through learning. This is one area for future research that we intend to investigate.

5.3 Adaptation of EINCKM to Concept Drift

Concept Drift has been recognized as one major issue in data stream clustering and classification (Nguyen et al., 2015). In clustering, concept drift refers to the evolutionary changes to cluster models over time. Static data clustering only has one concept: the global model of clusters whereas data stream clustering may have multiple concepts that evolve over time. We identified concept drift at two levels: the adaptation level and change monitoring level.

At the adaptation level, our algorithm, by following the incremental approach of data stream clustering, always refines the existing model of clusters in light of the newly arrived data chunk, and hence always adapts to the changes reflected by new clusters added into the model or modification to the existing clusters via merging.

At the change monitoring level, the proposed algorithm itself does not keep a history trail of the changed cluster models. In fact, implementation of the algorithm may use variable parameters to keep a single copy of the new model of clusters, over-writing the previous model. However, this problem can be solved by adding an outer loop in the data streaming clustering process where the proposed algorithm can be called when a new chunk arrives, the refined new model of clusters can be recorded into a permanent file. Then from time to time, a monitoring task over the stored versions of the cluster model can be undertaken to identify the changes from one version to the next. It can be an interesting problem to investigate further about how to mine evolving patterns among the past cluster models. This task requires developing a new kind of algorithm for the "second order" discovery.

6 CONCLUSION AND FUTURE WORK

In this paper, we presented a new algorithm EINCKM for data stream clustering. The algorithm emphasizes on simplicity, modularity, and adaptivity. The key ideas of the algorithm are to estimate the number of clusters (K) using heuristics, merge the overlapped clusters using a radius-based technique based on statistical information, and to filter outlier using a variance-based mechanism. The algorithm addressed two significant problems of prototype-based methods: using a fixed predefined value of K and produce clusters as well as outliers. The evaluation on some synthesized datasets and real dataset has shown that the algorithm produces correct and good quality clusters with low time complexity.

Our future work will focus on enhancing the algorithm. Since the algorithm is modular, those enhancement efforts can focus on the main functions within the algorithm. The *Estimate* function can be improved with learning capability to more accurately estimate the value of K for later rounds of calling the algorithm. A more adaptive strategy based on learning of mixture models of Gaussians can be developed for the *Merge* function, and a fuzzy and shape based cluster radius could be embedded into the *Filter* function to identify real outliers.

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APPENDIX 1

The following tables show the details and specify the distribution of each of the three synthesized datasets.

Table 1: Parameters details of DS1.

K	Mean		STD		SZ
	X	Y	X	Y	
K1	5	7	2	2	20000
K2	16	7	3	3	11000
K3	5	-7	1.5	1.5	15000
K4	-5	7	3	3	18000
K5	-16	7	1	1	5000
K6	-5	-7	2.5	2.5	31000

Table 2: Parameters details of DS2.

K	Mean		STD		SZ
	X	Y	X	Y	
K1	20	20	2	2	2000
K2	5	40	1.5	1.5	2600
K3	30	19	1.1	1.1	3400
K4	12	40	2.5	2.5	300
K5	25	30	2.4	2.4	3100
K6	-15	37	3.5	3.5	1600
K7	-25	43	1.8	1.8	2100
K8	1	67	1.2	1.2	1500
K9	15	55	2.9	2.9	1700
K10	-2	54	2.3	2.3	4000
K11	-20	55	3.9	3.9	1300
K12	15	75	3.8	3.8	600
K13	20	65	0.9	0.9	500
K14	-7	80	4.1	4.1	2300
K15	-25	75	2.7	2.7	3100

Table 3: Parameters details of DS3.

K	Mean		STD		SZ
	X	Y	X	Y	
K1	7	7	2.5	2.5	800
K2	30	7	3.5	3.5	110
K3	-11	7	1.9	1.9	3500
K4	-35	7	3.9	3.9	2900
K5	45	7	1.1	1.1	1290
K6	7	30	3.4	3.4	300
K7	32	30	2.2	2.2	5000
K8	-15	30	3.1	3.1	700
K9	-30	30	1.2	1.2	600
K10	50	30	3.3	3.3	1700
K11	-15	60	1.2	1.2	900
K12	45	60	5.9	5.9	2000
K13	10	60	6.4	6.4	1000
K14	-50	60	7.9	7.9	100
K15	75	60	1.7	1.7	4300
K16	1	105	7.5	7.5	4000
K17	25	105	1.3	1.3	1650
K18	-35	105	4.4	4.4	350
K19	-60	105	2.4	2.4	400
K20	60	105	7.7	7.7	1900
K21	5	150	6.4	6.4	5000
K22	30	150	0.9	0.9	1200
K23	-30	150	4.4	4.4	800
K24	-60	150	2.4	2.4	500
K25	60	150	5.5	5.5	800
K26	7	190	3.6	3.6	2500
K27	25	190	0.8	0.8	750
K28	-20	190	4.2	4.2	250
K29	-50	190	2.8	2.8	350
K30	50	190	5.6	5.6	4350