Autonomous Data Density based Clustering Method

Plamen P. Angelov
and Xiaowei Gu
School of Computing and Communications
InfoLab21, Lancaster University,
Lancaster, LA1 4WA, UK.
E-mail: p.angelov@lancaster.ac.uk

German Gutierrez
and Jose Antonio Iglesias
and Araceli Sanchis
Computer Science Department
Carlos III University of Madrid, Madrid, Spain,
E-mails: {ggutierr, jiglesia, masm}@inf.uc3m.es

***Abstract*—It is well known that clustering is an unsupervised machine learning technique. However, most of the clustering methods need setting several parameters such as number of clusters, shape of clusters, or other user- or problem-specific parameters and thresholds. In this paper, we propose a new clustering approach which is fully autonomous, in the sense that it does not require parameters to be pre-defined. This approach is based on data density automatically derived from their mutual distribution in the data space. It is called ADD_clustering (Autonomous Data Density based clustering). It is entirely based on the experimentally observable data and is free from restrictive prior assumptions.**

This new method exhibits highly accurate clustering performance. Its performance is compared on benchmarked data sets with other competitive alternative approaches. Experimental results demonstrate that ADD_clustering significantly outperforms other clustering methods yet does not require restrictive user- or problem-specific parameters or assumptions. The new clustering method is a solid basis for further applications in the field of data analytics.

Index terms- *fully autonomous clustering; data density; mutual distribution; data analytics.*

I. Introduction

Clustering has long been widely used for finding underlying groups and patterns within the data. We have already entered the Era of Big Data. Clustering as an unsupervised machine learning method is currently a very hot topic in the field of data processing and considered as one of the most effective tools for extracting information from data and, thus, one of the ways to address the Big Data problems.

Traditional clustering methods require user inputs based on some *prior* knowledge or different assumptions (including number of clusters, the shape of clusters, etc.) to work efficiently. In most practical cases, however, the *prior* knowledge is very limited and the assumptions made are always too ideal to be true. The requirement of *prior* knowledge or assumptions does, no doubt, limit the traditional clustering methods abilities in data analytics and information discovery [1].

In this paper, we propose a new autonomous clustering algorithm named ADD_clustering (Autonomous Data Density-based clustering). The novelty of this new algorithm is that it is entirely based on the data and their mutual distribution in the data space. There is no need for predefined specific thresholds or any kind of user inputs in the proposed method. Additionally, ADD_clustering method works equally effectively with various types of distance/similarity metrics and arbitrary number of dimensions of data. It starts from scratch, self-defines the data pattern in terms of density, and exhibits a highly accurate clustering performance. To the best of our knowledge, this is the first clustering method with such characteristics of real autonomy.

The remainder of this paper is organized as follows: section II introduces some related published techniques for further comparison. Section III provides the theoretical basis of the proposed method. The detailed demonstration of ADD_clustering method is given in section IV. Experimental results and analysis are shown in section V and section VI is providing the conclusions.

II. Related Work

The clustering problems has been addressed in different context in many disciplines such as data mining, information retrieval or pattern recognition. However, as far as we know, there is still no clustering method which does not require any kind of user- or problem- specific parameter. Nonetheless, our proposed method will be compared with several well-known methods, such as *mean shift* clustering, *K-means* clustering, as well as with some recent advanced (*DDCAR* [2] and *eClustering* [3]) methods. These four methods need some kind of *prior* knowledge. In this section, we will detail their most important aspects:

- *Mean shift clustering* [4] method considers an empirical probability distribution function around the data samples and the cluster centres or modes of the underlying distribution are represented by dense regions in the data space. After each iteration, the candidate solution shifts closer to the nearest mean and, finally, converges to the nearest mode or cluster centre. The direction of change is estimated by the gradient of the kernel density. The Mean shift clustering method requires the user to pre-define the kernel size. Clustering results are susceptible to different kernel sizes. Without any *prior* knowledge of the data, it is very hard to decide the kernel sizes.
- The well-known *k-means* clustering [5] method starts with k seed data points to be used as cluster centres and all the remaining data samples are assigned to the nearest cluster centres. Then, the means of the k clusters are calculated and set as the new centres. Other data

samples are reassigned again. This process continues until the clusters do not change any more. The K-means clustering method supports different types of distances as well as high dimensional data. Despite of its excellent performance, *k-means* clustering algorithm requires a user input, namely the number of clusters, which is an impossible task for users without *prior* knowledge.

- *DDCAR* [2] method is also based on the data density. By using the data density calculations to estimate the initial radius, *DDCAR* can be defined as a data-driven automated clustering method. Compared with other current clustering methods, *DDCAR* only needs users to set the minimum size of clusters, which is a great advance. However, *DDCAR* is still not totally free of user input. The minimum size of clusters can still influence the accuracy of the method. In addition, *DDCAR* currently only supports 2-dimensional data with Euclidean type of distance.
- *Evolving clustering (eClustering)* uses proximity based potential value to determine the cluster centres. The favourite characteristics of *eClustering* [3] are that it automatically identifies the number of clusters and also handles the outliers. Nonetheless, *eClustering* requires users to decide the initial radius of the clusters. The initial radius of clusters will be different with various types of datasets. As a result, deciding the initial radius will need users to have *prior* knowledge on the data, or *eClustering* might not achieve the best performance.

III. Theoretical Basis of The Proposed Method

In this section, three cornerstone non-parametric estimators of data ensemble properties (cumulative proximity, density, eccentricity, typicality) defined within the TEDA framework [1], [6], [7] and used within the proposed ADD_clustering method will be described.

First of all, let us define several basic notions. In this paper, R^p is defined as the real data space consisted of p dimensional data points. $\{x_1, x_2, \ldots, x_k\}$ is a series of data points belonging to R^p, k denotes the time instant when the last data sample arrives. Within the data space R^p, the distance $d(x, y)$ is defined as a measurement of dissimilarity between the two data points x and y. The proposed ADD_clustering algorithm can work with various types of distance metrics including Euclidean, Mahalanobis, and a recently introduced, direction-aware distance [6] metric.

A. Cumulative Proximity

Cumulative proximity, π_k is a representation of the closeness of a certain data point to all other data points, which is obtained in a direct way by summing the distance or dissimilarity measures between all points, see Fig.1 as an example of the cumulative proximity for a dataset which has *100* data samples per cluster. The cumulative proximity of data point x_i is expressed as (1):

$$\pi_k(x_i) = \pi_{ik} = \sum_{j=1}^{k} d^2(x_i, x_j) \tag{1}$$

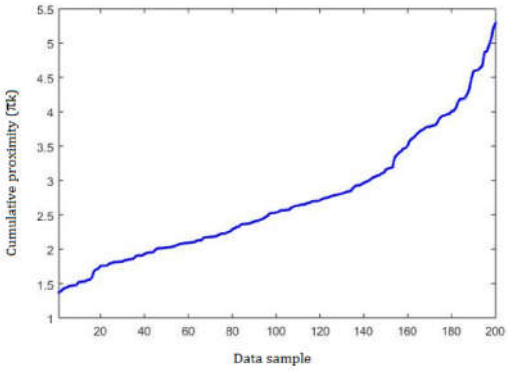


Fig. 1: Example of cumulative proximity

For the case of Euclidean type of distance, we have [1], [6], [7]:

$$\pi_k(x_i) = k((x - \mu_k)^T (x - \mu_k) + X_k - \mu_k^T \mu_k) \tag{2}$$

where $\mu_k = \frac{1}{k} \sum_{i=1}^{k} x_i$.

For Mahalanobis type of distance, we have [1], [6], [7]:

$$\pi_k(x_i) = k((x - \mu_k)^T \Sigma_k^{-1} (x - \mu_k) + X_k - \mu_k^T \Sigma_k^{-1} \mu_k) \tag{3}$$

where $X_k = \frac{1}{k} \sum_{i=1}^{k} x_i^T \sum_k^{-1} x_i$.

Normally, the data points which are close to the centre of the group will have much lower cumulative proximity than the data points close to the edge of the group. Thus, naturally, outliers will have high π_k value and a point with minimum π_k is a natural candidate to be a cluster centre.

B. Eccentricity

Eccentricity [1], [7] is another very important indicator of the ensemble properties of the data. It plays a critical role in the proposed method.

Eccentricity can be considered as normalized cumulative proximity π_k and is defined as follows [6]:

$$\xi_k(x) = \frac{2\pi_k(x)}{\sum_{i=1}^{k} \pi_k(x_i)} \quad , \sum_{i=1}^{k} \pi_k(x_i) > 0 \quad k > 1 \tag{4}$$

where the normalization coefficient 2 is due to the fact that, in the sum, each distance is counted twice [1], [7]. Obviously, the range of eccentricity values is from 0 to 1 and it sums to 2 [1], [7].

With the increase of the number of data samples, the value of eccentricity $\xi_k(x)$ will fall down quickly to zero, which is inconvenient for computation. In order to overcome this problem, the standardized eccentricity is introduced [6] as:

$$\epsilon_k(x) = k\xi_k(x) = \frac{2\pi_k(x)}{E(\pi_k(x))} \quad , \; E(\pi_k(x)) > 0 \quad k > 1 \tag{5}$$

where $E(\pi_k(x)) = \frac{1}{k} \sum_{i=1}^{k} \pi_k(x)$ is the mean cumulative proximity. Correspondingly, the range of possible values for $\epsilon_k(x)$ is $\epsilon_k(x) < k$

and the sum of all $\epsilon_k(x)$ values is

$$\sum_{i=1}^{k} \epsilon_k(x_i) = 2k \tag{6}$$

C. Data Density

Density plays a very important role in the proposed algorithm. Data density is inversely proportional to the eccentricity and is defined in [6] as:

$$D_k(x_i) = \frac{1}{\epsilon_k(x_i)} = \frac{E(\pi_k(x))}{2\pi_k(x_i)} \tag{7}$$

Obviously, the closer a particular data point is to other points, the smaller its cumulative proximity is, and the higher its density is. Although, cumulative proximity and density can both provide effective information about the data pattern, density is comparatively superior because it is: 1) Monotonic; 2) Maximum valu[is]; 3) Asymptotically tends to zeros when π_k tends to infinity. Therefore, it has properties similar to a likelihood and probability [6].

IV. ADD Clustering Algorithm

ADD_clustering is a novel method based entirely on the empirical observations (discrete data samples) and the density of this data. The proposed method does not require any user- or problem- specific threshold to be predefined and can extract the cumulative proximity, eccentricity and density of the data samples. Compared with other previously published methods, the proposed ADD_clustering algorithm has the following advantages:

- No *prior* knowledge of the dataset is needed;
- No initial user input is required;
- Entirely based on the data and its mutual distribution in the data space;
- No need to choose a model of the data distribution (e.g. Gaussian, etc.).

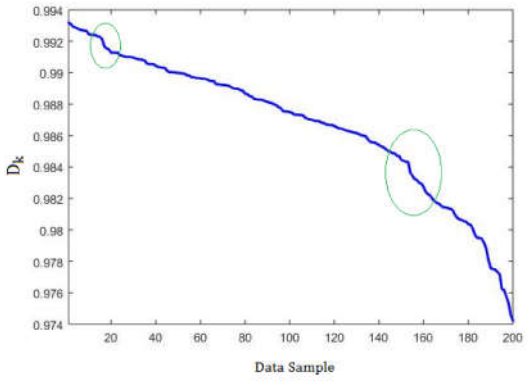
In the remaining part of this section we will explain in detail the three stages of our method: 1) initial centre and radius formation; 2) centre and radius updating; 3) clusters final adjustment.

A. Stage 1. Initial Centre and Radius

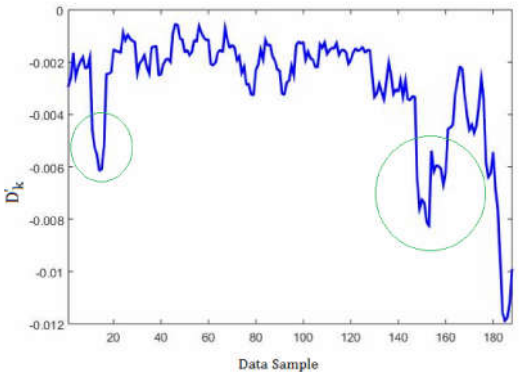
The first stage of our method consists in finding out the initial centre and radius of the new cluster in the particular datasets $\{x_1, x_2, \ldots, x_k\}$. The global cumulative proximity $\pi_k(x)$, eccentricity ξ (or standardised eccentricity $\epsilon_k(x)$), density $D_k(x)$ of every data point are obtained by formulas (1),(4),(5), and (7). By ranking the global density values of all data points in descending order, the data point with the highest density is selected as the initial centre of the newly formed cluster:

$$x^{*1} \leftarrow x^{j*},\ j* = argmax_{i=1}^{k} D_k(x_i) \tag{8}$$

Because, the density is higher closer to the cluster centres and lower towards the edges, there would always be a change in the gradient of the density when data samples belonging to different clusters are grouped together. It is well known that the change of gradient is an indication of an inflexion point and change of the sign of the second derivative [8]. As we can see in the example in Fig.2a (based on the dataset as previously described), there are several inflexion points in the rate of density reduction, which indicate the end/edge of a cluster.



(a) D_k



(b) D'_k

Fig. 2: Examples of ranked global density(D_k) and smoothed differential density(D'_k)

However, the density drop is susceptible to small variations. Therefore, the globally ranked densities of the data points should be further processed by applying a moving window average difference operation to zoom in as follows:

$$D'_k(x) = \frac{1}{N} \sum_{i=0}^{N-1} [D_k(x+i+N) - D_k(x+i)] \tag{9}$$

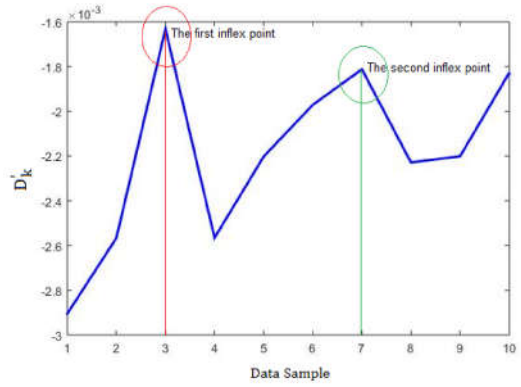
where $2N$ is the width of the moving window, a value of $N = 6$ can be used for all problems and data sets. It has to be stressed that the value 6 is not a problem- or user- specific parameter and is the same for all problems. Moreover, its slight variations do not influence the result. It is merely a way to zoom in and focus on the changes of D_k.

Compared with regular difference operation [2] , the average difference operation is less susceptible to the influence of noise and different data patterns, namely it is more robust.

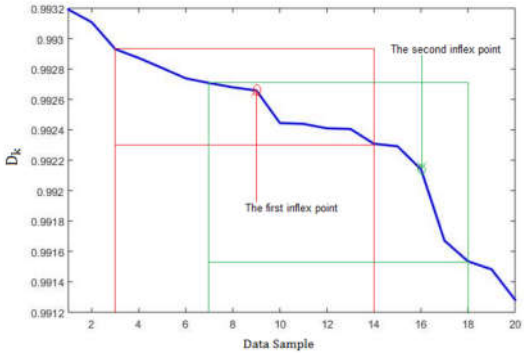
After the moving window average difference operation is applied, the smoothed differential density $D'_k(x)$ will have larger drops/jumps as shown in Fig. 2b (based on the same data as previously).

To ensure the purity [9] of the initial members of the new cluster, we select the first turning point of $D'_k(x)$, which indicates that there is a change in the speed of the descent of the densities in the data points shown in Fig. 3.

Then, the initial radius of the new cluster can be defined by calculating the distance between the initial centre and the first inflexion point point, $D_k(x+2N-1)$. By finding all data points within the distance of the initial radius from the initial centre, the prototype of a new cluster is obtained, and the first step is finished.



(a) The first turning point in D'_k



(b) The corresponding changing area in D_k

Fig. 3: Examples of the first turning point in the smoothed differential density(D'_k) and the ranked global density(D_k)

B. Stage 2. Centre and Radius Updating

At the end of the previous stage, a prototype of the newly formed cluster is built, but the cluster is not fully formed yet; we should update the centre and radius to let in more samples belong to the new cluster.

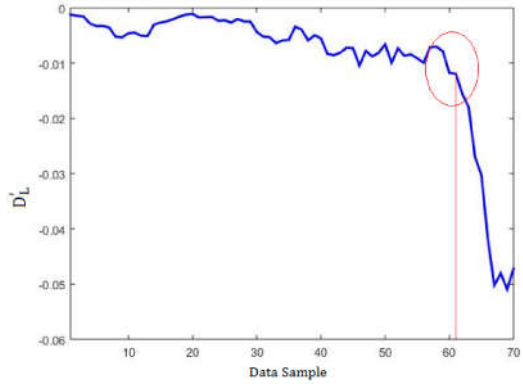
Again, formulas (2), (4), (5) and (7) are used to calculate the ***local*** density and the equation (9) is used for smoothing and differencing the *local* density after it is ranked in descending order. We denote the smoothed differential *local* density as $D'_L(x)$.

There are two conditions that can occur in regards to the smoothed differential *local* density.

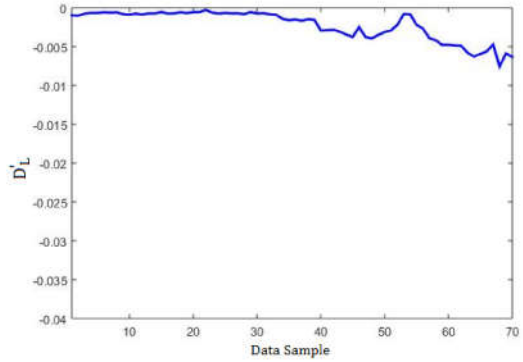
Condition 1. There is a big drop in $D'_L(x)$;

Condition 2. There is only a steady drop with normal fluctuations in $D'_L(x)$.

Examples of Conditions 1 and 2 are shown in Fig. 4a and 4b respectively using the same data as the previous.



(a) Condition 1



(b) Condition 2

Fig. 4: Illustrative examples of the smoothed differential *local* density

The well-known Chebyshev inequality [10] describes the probability of the distance between a certain data sample x and the mean value to be larger than $n\sigma$. For Euclidean type of distance it has the following form:

$$P(d^2(\mu, x) \leq n^2\sigma^2) \geq 1 - \frac{1}{n^2} \tag{10}$$

where $d(\mu, x) = \|\mu - x\|$.

Here, we use the Chebyshev inequality to help us distinguish the two conditions:

$$\textit{Condition 1: } (D'_L(x_m) - \mu_L)^2 \geq n^2\sigma_L^2 \tag{11}$$

$$\textit{Condition 2: } (D'_L(x_m) - \mu_L)^2 < n^2\sigma_L^2 \tag{12}$$

where x_m is the data point having the maximum value in $D'_L(x_m)$ in the new cluster, the μ_L and σ_L are the mean and standard deviation of $D'_L(x_1), D'_L(x_2) \ldots D'_L(x_{m-1})$. $n = 3$ is used for all problems and is well known from the literature [10].

If condition 1 is met, it means that the new cluster actually contains samples from two or more clusters. The transition between the two clusters is exactly the point when $D'_L(x)$ drops. The centre of the new cluster is updated based on the points that belong to this cluster, and the radius of the newly formed cluster is updated by:

$$r = d(x_1, x_m) \tag{13}$$

If condition 2 is met, it means the cluster is not fully spread, the centre should not be updated, while the radius should be enlarged letting all samples of this initial cluster to be included in the new cluster.

After the centre and radius become stable during updating and the members of the newly formed cluster do not change any more, we can declare that the centre and radius updating operation is finished and a new cluster is formally formed. Then, we can remove all the data points belonging to the new cluster from the dataset and go back to stage 1 to form another cluster.

C. Stage 3. Clusters Final Adjustment

When all the possible clusters have already been formed and the data points left in the dataset are not available to form a new cluster, stages 1 and 2 are finished, but the clusters formed are not always ideal. Because of the fact that the clusters are formed one by one sequentially, and in each time only one new cluster is formed, sometimes there will be overlaps between the spreads of influences of some clusters. Therefore, the clusters should be adjusted before the whole clustering process is finished.

First of all, we define several conditions:

Condition 3. If the distance between the centres of two clusters satisfies the following inequality:

$$d(x_i^*, x_j^*) \leq min(r_i, r_j) \tag{14}$$

Then the two clusters are defined as *double-centres-overlapped*.

Here x_i^* and x_i^* denote the centres of the *i-th* and *j-th* clusters, r_i and r_j are the radii correspondingly.

Condition 4. If the distance between the centres of two clusters satisfies the following inequality:

$$min(r_i, r_j) < d(x_i^*, x_j^*) \leq max(r_i, r_j) \tag{15}$$

Then the two clusters are defined as *single-centre-overlapped*.

Condition 5. If the distance between the centres of two clusters satisfies the following inequality:

$$max(r_i, r_j) < d(x_i^*, x_j^*) \leq r_i + r_j \tag{16}$$

Then the two clusters are defined as *slightly-overlapped*.

Condition 6. If more than half of the members of a cluster are closer to the centres of its neighbouring clusters than to their own centre, namely for them

$$d(x_i^*, x_j^*) < d(x_i^*, x_i^*) \tag{17}$$

Then the cluster is defined as a *loose cluster*. Here x_i^k is the *k-th* member of the *i-th* cluster.

Condition 7. If more than half of the members of a cluster are in the area of influences of two or more clusters, namely:

$$d(x_i^k, x_j^*) < r_j \tag{18}$$

Then we regard this cluster as being *group-covered* by others.

Condition 8. If the average distance of the members of a cluster to the centre of a nearby cluster is smaller than its radius, namely:

$$\frac{1}{M^i} \sum_{k=1}^{M^i} d(x_i^*, x_j^*) < r_j \tag{19}$$

Then we regard this cluster as being *single-covered* by some other cluster(s). Here M is the member number of the *i-th* cluster.

If there are *loose clusters*, clusters being *double-centres-overlapped*, clusters being *single-centre-overlapped* by more than two clusters or clusters being *group-covered*, we call these *significantly overlapping cases*.

If there are clusters being *single-centre-overlapped* by two clusters or clusters being *single-centre-overlapped* and *single-covered* by one cluster, we call these *moderately overlapping cases*.

If there are clusters being *slightly-overlapped* or clusters being *single-centre-overlapped* by one cluster, we call these *slightly overlapping cases*.

The final adjustment is divided into three steps.

Step 1: in this step, we will eliminate all the *significantly overlapping cases*.

Firstly, we check Rule 1.

Rule 1: If cluster C_i meets condition 6, and is *double-centres-overlapped* or *single-centre-overlapped* with most other clusters, then C_i should be split and all its members are re-assigned to the nearest clusters according to the following formula:

$$\text{Cluster\_label} = argmin_{i=1,2,\ldots,K} d(x, x_i^*) \tag{20}$$

where *K* is the number of clusters.

Then, Rule 2 and Rule 3 are executed:

Rule 2: If clusters $C_i, C_j, \ldots$ meet Condition 3 in regard to them, then clusters $C_i, C_j, \ldots$ should merge together.

Rule 3: If cluster C_i meets condition 3 with $C_j, C_k, \ldots$ while $C_j, C_k, \ldots$ only meets condition 4, then the largest one in $C_i, C_j, C_k, \ldots$ should be split and all its members are re-assigned to the nearest clusters using equation (20).

Because of the execution of the three rules above, the original structure of existing clusters is being changed largely, most of the *significantly overlapping* clusters have been split or merged, Rule 4 is used further to clear the remaining cases.

Rule 4: If cluster C_i meets Condition 6 or Condition 7, or is *single-centre-overlapped* by more than three clusters, then cluster C_i should be split and all its members are re-assigned to the nearest clusters using equation (20).

Once Rules 1-4 are not used any more, Step 1 is finished and the final adjustment comes to Step 2.

Step 2: Since the *significantly overlapping cases* have been resolved, the *moderately overlapping cases* are eliminated in this step, here, Rule 5 and Rule 6 are used.

Rule 5: If cluster C_i is *single-centre-overlapped* by two clusters then cluster C_i should be split and all its members are re-assigned to the nearest clusters using equation (20).

Rule 6: If cluster C_i is *single-centre-overlapped* and *single-covered* by cluster C_j, then C_i and C_j should be merged together.

Once there is one cluster that meets Rules 5 and 6 any more, all the *moderately overlapping cases* have been removed and the final adjustment comes to the last step.

Step 3: In this step, we simply find all the *slightly overlapping cases* and reassign the members of the overlapping clusters, which meet equation (18), to the nearest clusters using equation (20).

Finally, for the remaining data points, we assign them to the nearest clusters using equation (20), which concludes the final adjustment.

D. Overall Clustering Process

The overall clustering process is summarised as follows

Algorithm ADD_clustering:

- *A. While* remaining data points in the dataset are available (or able to form a new cluster):
  1) Calculate the global density, D_k of each data point by equation (7);
  2) Rank the global density, D_k in descending order and smooth the ranked densities by equation (8);
  3) Detect the first inflexion point, see Fig.3a;
  4) Declare the initial centre x_i^* and radius r_i and find the initial cluster members;
  5) **While** the members of the new cluster are still changing their allocation
     - Calculate the local density, D_L, of the new cluster;
     - Rank the local density in descending order and smooth the ranked densities;
     - **If** (Condition 1 or Condition 2 is met) Then:
       * Update the radius and all data points that belong to the new cluster;
     - **End If**
  6) **End While**
  7) A new cluster is formed;
  8) Remove from the dataset the data points that belong to the new cluster;
- *End While*
- *B. While* the existing clusters exhibit overlaps
  1) **While** there are *significantly overlapping cases*
     - **If** (Rule 1 is met) **Then**
       * Split the cluster and reassign the members to the nearest cluster by equation (20);
     - **End If**
     - **If** (Rule 2 is met) **Then**
       * Merge the clusters;
     - **End If**
     - **If** (Rule 3 is met) **Then**
       * Split the cluster and reassign the members to the nearest cluster by equation (20);
     - **End If**
     - **If** (Rule 4 is met) **Then**
       * Split the cluster and reassign the members to the nearest cluster by equation (20);
     - **End If**
  2) **End While**
  3) **While** there is no *significantly overlapping case* any more
     - **If** (Rule 5 is met) **Then**
       * Split the cluster and reassign the members to the nearest cluster by equation (20);
     - **End If**
     - **If** (Rule 6 is met) **Then**
       * Merge the clusters;
     - **End If**
  4) **End While**
  5) **While** there is no *significantly overlapping case* or *moderately overlapping case* any more
     - **If** (*slightly overlapping case* is found) **Then**
       * Reassign the overlapping members to the nearest clusters by equation (20);
     - **End If**
  6) **End While**
- *C.* Assign remaining unclustered data points to the nearest clusters by equation (20);
- *End ADD_clustering*

V. Experimental results and analysis

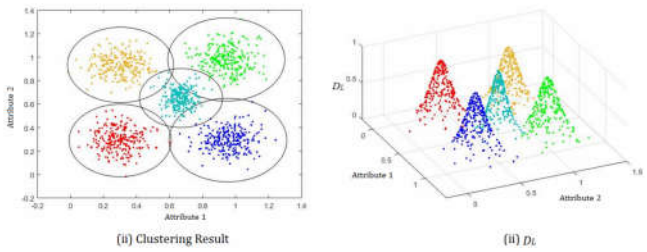
In order to test the performance of the newly proposed ADD_clustering method, several artificial and benchmark datasets were used in numerical experiments. The artificial datasets were used to test the accuracy of the method, and the benchmark datasets were used to ensure that the method is applicable to real cases.

A. Datasets

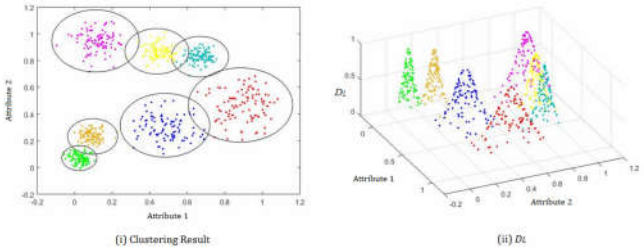
Two artificial and two benchmark datasets were used in experiments with Euclidean type of distance:

1) The first dataset contained 5 clusters with 250 samples per cluster.
2) The second dataset had 7 clusters with 100 samples in each one.
3) Climate Dataset [11].
4) Iris Dataset [12].

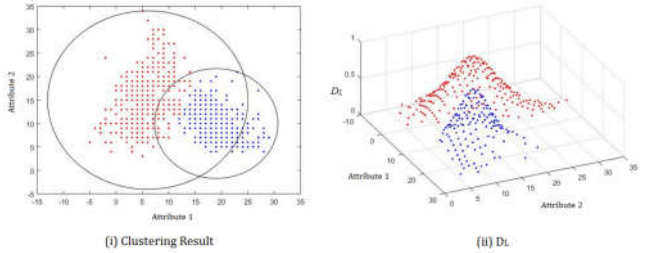
The datasets include clusters with very close proximity and chains of noise. The clustering results and the data density values are shown in Fig. 5.



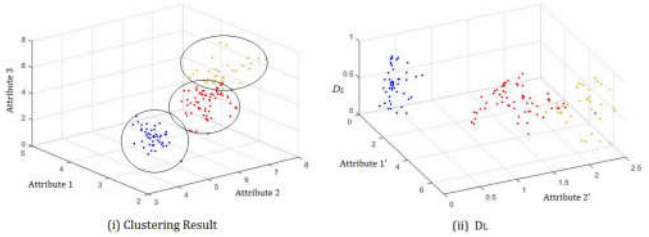
(a) 5 x 250 Gaussian Dataset



(b) 7 x 100 Gaussian Dataset



(c) Benchmark Data - Climate Dataset



(d) Benchmark Data - Iris Dataset

Fig. 5: The four datasets (two artificial, Climate and Iris) used in the experimentation.

B. Results

For further comparing, the quality of the proposed ADD_clustering method with different existing methods including *Mean-shift* clustering, *K-means* clustering, *DDCAR* and *eClustering*, a number of measures of the performance were considered:

1) *Input*: the parameters that have to be predefined.
2) *NoC*: is the number of clusters in the result.
3) *Accuracy*: is a measure of the number of samples that are correctly assigned to their original clusters.
4) *AverPurity*: is a measure of the average purity of the clusters but can disguise poor results [9].
5) *MaxPurity*: is the maximum cluster purity [9].
6) *MinPurity*: is the minimum cluster purity [9].

In this paper, the quality of clustering and the number of clusters in the results together directly decide the correctness and effectiveness of the proposed ADD_clustering method. In order to get the most accurate result, the number of clusters should be exactly the same with the original dataset, and the clustering accuracy should be as high as possible. Therefore, *clustering accuracy* and *NoC* both are the most important measures. In this paper, the focus is on a new method for data analytics, which is based entirely on the empirical observations of data samples and the cumulative proximity of these data.

The comparative results for the artificial and benchmark datasets with Euclidean type of distance are shown in Table I, where *ks* denotes the kernel size in the *mean shift* clustering method; *mcs* denotes the minimum cluster size in *DDCAR* method; *r* denotes the initial radius in *eClustering* method; *N* denotes the number of clusters in the *K-means* algorithm.

Analysing the results, we can compare ADD_clustering method with the other techniques listed above as follows:

- *Mean shift* clustering method: Although, there are no requirement regarding the *prior* information of the number of clusters and the embedded assumptions on the shape of the clusters, Mean shift clustering method actually needs users to predefine the kernel size. As we can see from the table, different kernel sizes can largely influence the clustering result. To exhibit good clustering performance using the mean shift clustering method, users have to decide the kernel size first either based on *prior* knowledge or trying many times before finding the ultimate one.
- *K-means* clustering method has quite high accuracy compared with other algorithms, and can additionally work with different types of distance metrics. However, the high accuracy is based on the *prior* knowledge of the number of clusters in the datasets, which normally is unknown for users. With enough *prior*-knowledge, K-means clustering is quite accurate.
- *DDCAR algorithm* is comparable with ADD_Clustering in terms of user input, but needs users to predefine the minimum size of clusters, which requires some *prior* knowledge about the datasets compared with other techniques. However, ADD_Clustering is totally free of any user input. The results of DDCAR algorithm normally contain many clusters with few members. The distribution of the datasets can be misrepresented largely. In contrast, ADD_Clustering can give clustering results with fewer and much more accurate clusters, which effectively reflect the distribution of datasets. In addition, DDCAR is not applicable for clustering the datasets with more than 2 dimensions, which is also a serious disadvantage compared with ADD_Clustering.
- *eClustering* algorithm requires users to select the original

TABLE I: Clustering Results Comparison with Euclidean Type of Distance

Methods	Data	Inputs	NoC	Accuracy	AverPurity	MaxPurity	MinPurity
ADD_Clustering	5*250	**None**	5	**0.9928**	**0.9928**	**1.0000**	**0.9690**
Mean Shift		ks=0.1	9	0.9640	0.9864	1.0000	0.9394
		ks=0.2	5	0.9928	0.9928	1.0000	0.9690
DDCAR		mcs=10	24	0.9125	0.9152	1.0000	0.5000
eClustering		r=0.05	2	0.2712	0.2712	0.6692	0.2238
		r=0.01	2	0.2712	0.2712	0.6692	0.2238
Kmeans		N=5	5	0.9928	0.9928	1.0000	0.9840
ADD_Clustering	7*100	**None**	7	**0.9986**	**0.9986**	**1.0000**	**0.9615**
Mean Shift		ks=0.1	11	0.9029	0.9914	1.0000	0.9709
		ks=0.2	5	0.7114	0.7114	1.0000	0.4975
DDCAR		mcs=10	17	0.9571	0.9786	1.0000	0.9259
eClustering		r=0.05	5	0.4771	0.5129	1.0000	0.3636
		r=0.01	1	0.4771	0.5300	1.0000	0.3636
Kmeans		N=7	7	0.7929	0.8529	1.0000	0.5025
ADD_Clustering	Climate	**None**	2	**0.9824**	**0.9824**	**0.9883**	**0.9764**
Mean Shift		ks=4	7	0.7141	0.9741	1.0000	0.9474
		ks=6	2	0.9474	0.9474	0.9976	0.9773
DDCAR		mcs=10	7	0.5141	0.5224	1.0000	0.5149
eClustering		r=0.5	1	0.5071	0.5071	0.5071	0.5071
		r=0.01	1	0.5071	0.5071	0.5071	0.5071
Kmeans		N=2	2	**0.9824**	**0.9824**	**0.9883**	**0.9764**
ADD_Clustering	Iris	**None**	3	**0.8933**	**0.8933**	**1.0000**	**0.7742**
Mean Shift		ks=0.8	5	0.6867	0.8133	1.0000	0.5455
		ks=1.2	2	0.6667	0.6667	1.0000	0.5000
DDCAR		mcs=10	Not applicable				
eClustering		r=0.5	4	0.6067	0.6733	1.0000	0.5797
		r=0.01	4	0.5533	0.6733	1.0000	0.5246
Kmeans		N=3	3	**0.8933**	**0.8933**	**1.0000**	**0.7742**

radius of clusters. As we can see in the Table 1, the selection of the initial radius can influence the clustering results largely. Choosing the most suitable initial radius can be a very hard task for users without any *prior* knowledge of the datasets. In addition, accuracy and purity is not as high as all other methods.

From the comparisons we can see, that ADD_Clustering method can achieve extremely high accuracy without any *prior* knowledge. This feature makes the ADD_clustering method a very effective algorithm when it is applied in the field of data analysis.

VI. Conclusion

A novel, fully autonomous clustering method, ADD_clustering, is introduced in this paper. The proposed method is totally data-driven and free of any kind of user inputs. This method starts "from scratch", and automatically defines all the clusters on the basis of the data density alone. Numerical experiments show that, without any user input, this method can exhibit excellent clustering performance compared with other methods that use various kinds of *prior* knowledge or assumptions. Because of the advantages of no requirement for user inputs and self-generating the estimators of ensemble data properties of the clustered datasets, this new method is a very attractive and effective tool in the field of data analytics.

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