

A powerful and efficient evolutionary optimization algorithm based on stem cells algorithm for data clustering

Research Article

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Abstract: There are many ways to divide datasets into some clusters. One of most popular data clustering algorithms is K-means algorithm which uses the distance criteria for measuring the data correlation. To do that, we should know in advance the number of classes (K) and choose K data points as an initial set to run the algorithm. However, the choice of initial points is a main problem in this algorithm which may cause the algorithm to converge to a local minimum. Some other data clustering algorithms have been proposed to overcome this problem. The methods are Genetic algorithm (GA), Ant Colony Optimization (ACO), PSO algorithm, and ABC algorithms. In this paper, we employ the Stem Cells Optimization algorithm for data clustering. The algorithm was inspired by behavior of natural stem cells in the human body. We developed a new data clustering based on this new optimization scheme which has the advantages such as high convergence rate and easy implementation process. It also avoids local minimums in an intelligent manner. The experimental results obtained by using the new algorithm on different well-known test datasets compared with those obtained using other mentioned methods demonstrate the better accuracy and high speed of the new algorithm.

Keywords: data clustering • K-means algorithm • stem cells optimization algorithm

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1. Introduction

Data Clustering is an important issue and a key part of many fields such as data mining [1, 9], math programming [13], scientific analysis [3] and image segmentation [11, 16]. Data clustering aims at dividing a dataset into some classes

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without knowing any pre-information about the kind of relations exists between classes. There are many ways to do data clustering. One of the popular algorithms is the K-means algorithm [5]. The algorithm tries to put the entire dataset S into K clusters (i.e. C_1, C_2, \dots, C_k) by randomly selecting K data points as a set of cluster centers. To do that, the clusters are formed such that the existing data in each cluster should have the minimum Euclidean distance to the center of that cluster. Hereby, following conditions should be satisfied:

$$\bigcup_{i=1}^K C_i = S, \quad (1)$$

where S is the entire data set. Moreover, there should be at least one point in each cluster, such that:

$$C_k |_{k=1, \dots, K} \neq \Phi, \quad (2)$$

where Φ is an empty set. Final condition is that there should not be any data point jointly existing in two different clusters which can be expressed as follow:

$$C_k \cap C_j = \Phi |_{k \neq j}. \quad (3)$$

By settling these conditions, total Euclidean distance between the data points and the cluster centers is iteratively minimized such that the center of each cluster becomes the best represent of that cluster. Total Euclidean distance is defined as:

$$E = \sum_{j=1}^K \sum_{x_i \in C_j}^{N_j} \|x_i - Z_j\|, \quad (4)$$

where x_i is i^{th} data point and belongs to the cluster C_j , Z_j is the center of C_j , K is the number of clusters and N_j is the number of data points in C_j . Selection of K data points as the initial centers of the clusters affects significantly the performance of the algorithm. Another fundamental problem in K-means algorithm is that as the dataset gets large, it increasingly converges to local minima, and even after repeated application the global optimum cannot be obtained. To overcome these drawbacks, many clustering algorithms have been introduced recently. For instance, the K-Medoid algorithm [7] uses a different distance criterion to determine the best representative of each cluster. Other proposed methods used certain optimization algorithms in order to achieve optimal response (correctly classified data points). For instance, the Genetic algorithms have been widely employed for data clustering [6, 8]. In [8], the responses are expressed as a string of bits and the algorithm starts using a population consisting of a series of initial responses and obtains ideal responses using a proposed Genetic algorithm and continues its process until achieving a convergence to a global minimum. It should be noted that the optimization of the K-means algorithm using Genetic algorithm increases only the speed of reaching final response and improves little the performance of K-means algorithm, although it improves somewhat the problem of local minimum convergence.

Data clustering approach has been also extended by the algorithms based on the social behavior of ants known as ant colony optimization (ACO) algorithms [14, 18]. For instance, in [14] an algorithm was implemented using the increase of pheromone evaporation rate on data closer to the cluster centers and achieved responses far better than previous algorithms. Some researchers have used recently particle swarm optimization (PSO) algorithm for data clustering [4, 10]. Van Der Merwe and Engelbrecht [10] optimized the K-means algorithm using PSO and demonstrated much better performance than previous algorithms. In this method, K-means algorithm was used only in forming initial population of particles and then PSO classifies data points using this initial solution.

More recently, [19] has introduced a clustering algorithm using artificial bee colony (ABC) algorithm that showed better performance than K-means algorithm. It proposed to avoid from local minimums using bee algorithm as an optimization procedure, however it took many iterations to achieve the optimal response and the entire process was very long.

In this paper, we propose to classify various types of data using one of the newest optimization algorithms, we called it stem cells algorithm (SCA). By applying this optimization algorithm with our proposed scheme for data clustering, we have clustered well known test datasets faster and more precisely than previous methods.

2. Stem cells optimization algorithm

Most naturally-based optimization algorithms are introduced because of their simplicity and because they have been shown to effectively solve complex optimization problems in nature.

Stem cells are found in all multi-cells of body organs where they are able to become a full organ. Research in this field was conducted by Ernest A. Mc Culloch and James E. Till [2, 15] and their activities were focused on investigating embryonic stem cells which are part of the inner blastocysts cells group. In their research they have reached an important conclusion which is that stem cells may result in changes in some organs of body. The problems of some adult human organs can also be resolved using the ability of embryonic stem cells in cell division and becoming a full organ. We present an optimization scheme using two important features of stem cells in the real world including their ability to self reproduce.

The stem cells optimization algorithm was first proposed in our previous work [17]. This algorithm is like other optimization algorithms in that it is based on population and the idea of evolutionary process, but it is different in that it uses minimal constraints and has a simpler implementation than the others. This algorithm converges faster than other optimization algorithms because of its simplicity and its ability to escape from local minima. Population is placed in a range of members (stem cells forming initial population) in this algorithm and it starts with the minimum. Considering that each population member of each stem cell (e.g. in genetic algorithm, chromosomes and in particle swarm algorithm, birds or fish, etc.) indicates an optimal answer for all considered problems, increasing the population at each iteration is related to the problem space, but defining a large population in this type of algorithms results in abundant iterations to achieve optimal response which consequently raises many problems. Meanwhile defining the population in an interval and increasing the population according to the space of the considered problem are especially advantageous in implementation by resulting in few iterations in simple problems and increasing the speed of convergence. To perform the proposed algorithm, first, the space of problem is divided into sections which can be done completely in a random process. Then, the initial population is distributed in the whole space of the problem in a random and uniform manner. Considering the goal of all optimization algorithms, including stem cells algorithms, which is to obtain a response with respect to variables of the problem, a matrix of variables should be formed at the beginning of the process. In the proposed algorithm, the initial matrix is composed of the stem cell characteristics. It consists of liver cells, intestinal cells, blood cells, neurons, heart muscle cells, pancreatic islets cells and so on.

Thus, the initial matrix is defined as follows:

$$\text{Population} = \begin{bmatrix} X_1 \\ X_2 \\ \dots \\ X_N \end{bmatrix}$$

$$X_i = \text{Stem Cells} = [SC_1, SC_2, \dots, SC_N] \quad (5)$$

$$i = 1, 2, \dots, N,$$

where initialized parameters of proposed algorithm are defined as:

$$\begin{aligned} \{M = & \text{Maximum number of stem cells,} \\ P = & \text{population size, } \{10 < P \leq M\} \\ C_{\text{Optimum}} = & \text{best of stem cell in each iteration,} \\ \chi = & \text{penalty parameter for prevent grow stem cell,} \\ sc^i = & i^{\text{th}} \text{ stem cell in the population.} \end{aligned}$$

After determination of the criterion function based on the nature of the problem, the cost of each stem cell is calculated using this criterion function. Two memories are defined for each cell, local memory and global memory. The cost of each stem cell is stored in local memory. A group of cells, representing each area, is defined first. Each cell area, which has the best cost related to other cells stores the cost in its global memory. This process is also done in other regions.

Then, only the best cells of each area are extracted and employed in a self-renewal process. Next, information of the best cells of each area is shared and the cell that has the best cost is selected. This cell has a greater contribution in the self-renewal process of the next iteration than the other cells selected from each area. It should be noted that, however, the entire renewal operation of cells contains just a part of participated population in the next iteration (e.g. 60%) and the rest of the population will be selected randomly using uniform contribution of new cells having no information about considered space. Moreover, cell renewal process depends on the space of the problem, i.e. how big the feature space is, and is performed such that more non-uniformity of renewal process is applied for high dimensional problems. The self-renewal operation of stem cells is computed by:

$$SC_{Optimum}(t+1) = \zeta SC_{Optimum}(t), \quad (6)$$

where t denotes the iteration number, $SC_{Optimum}$ is the best stem cell in each iteration and $\zeta \in [0, 1]$ is a random number, however, it can be considered as fixed. For instance, we considered $\zeta=0.96$ if the selected cell was an exact renewal of the same cell as itself and ζ if it had its opposite point.

Figure 1 shows an example of self-renewal characteristics of stem cells until reaching to the best cell.

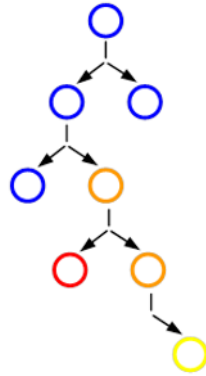


Figure 1. Self-renewal stem cells feature, where the color circle shows the stem cell and the yellow circles are the best stem cell in final iteration when the algorithm converges to optima.

This process will continue until it reaches to the goal which is finding the best cell (getting an optimal response) while having the lowest cost function value. The best cell should also have the most power relative related to other cells. This is obtained from the following equation:

$$x_{ij}(t+1) = \mu_{ij} + \varphi(\mu_{ij}(t) - \mu_{kj}(t)), \quad (7)$$

where x_{ij} denotes the i^{th} stem cell position for the solution dimension j , t is the iteration number, μ_{ij} and μ_{kj} are two randomly selected stem cells for the solution dimension j , and if $\mu_{ij}(t) - \mu_{kj}(t) = \tau$ then $\varphi(\tau)$ produces a random variable in the interval of $[-1, 1]$.

Finally, the best stem cell is selected when it has the most power relative related to the other cells. This comparative power is obtained using following relation.

$$\varsigma = \frac{SC_{Optimum}}{\sum_{i=1}^N SC_i}, \quad (8)$$

where ς denotes the comparative power of stem cells, $SC_{Optimum}$ is stem cells selected in terms of cost, and N is the final population size when the best answer is obtained and the algorithm stops.

In fact, this relative power is one of the most important features mentioned before and is the main characteristic of stem cells in being converted to multiple organs. Now we propose a new clustering method in which we overcome the problem of convergence to local optima using flexibility of stem cells algorithm. Finding the exact centers of categories with the minimum Euclidean distance (Eq. 4), can be a significant help to achieve an optimal response in real data clustering.

3. Proposed method for data clustering

After defining required constraints and inserting initial parameters for stem cells algorithm (SCA), the criterion to stop the algorithm should be defined. The algorithm starts with an initial population where each cell in the population indicates a clustering response as K category centers. The initial K centers are selected in a completely random manner without any prior information about the data. Then the distance of each data point to each center is calculated using Eq. 4. A data point is considered to be a member of the category with the center to which it has the minimum distance. Then, the difference between each data point (cell) and its center is computed and stored in the local memory of that cell. Note that this difference is a vector. The average of difference vectors in each category is also computed and defined as \vec{E}_i . This vector shows how well a center represents its category. The length and direction of this vector quantifies the deviation of the current center from a more representative center. So, we can use this vector to replace the old center by the new and better representative center using the following equation:

$$\vec{Z}_{i-new} = \vec{Z}_{i-old} + \alpha \vec{E}_i, \quad (9)$$

where $i \in 1, \dots, K$, K is the number of clusters, and α is a learning rate which adjusts the steps in each iteration towards the better representing center. The learning rate is a positive number with following impact; if it is too small then the convergence might be unnecessarily slow, but if it is too large then the convergence might overshoot and miss the best center. A value between zero and one is recommended.

This process will continue until the stopping criterion is met or the number of iterations reaches to the predefined maximum. The pseudo-code for the proposed data clustering algorithm is as follows:

Begin

Generate an initialize population randomly

{Uniform distribution of a part of stem cells in the search space}

Evaluate the objective function for the initialize population

Sort the initial population based on objective function values

Calculate the comparative power based on below equation :

$$\left\{ \varsigma = \frac{SC_{Optimum}}{\sum_{i=1}^N SC_i} : \text{Comparative Power} \right\}$$

Choose the best of stem cells based on fitness values & comparative power value (in initial population)

do {

Place the best of stem cells as initial K centroids object that are clustered

do {

Assign each object to stem cells as initial cluster using equation below :

$$E = \sum_{j=1}^K \sum_{x_i \in C_j} \|x_i - Z_j\|^2$$

}

While (the centroids still move)

add average of difference between each stem cells with center of cluster in each group

to center by equation below :

$$\vec{Z}_{i-new} = \vec{Z}_{i-old} + \alpha \vec{E}_i$$

}

```

do {
renewal of the best of stem cells based on below equation :
  { $SC_{Optimum}(t + 1) = \chi * \zeta * SC_{Optimum}(t)$ ,  $t$  represent of iteration}
  { $\chi$  = penalty parameter for prevent grow renewal stem cell}
do {
Generate the part of population as initial stem cells for next iteration
Use the whole of population for neighborhood search
In each iteration : Find the best stem cell, replace with respective stem cell and
  compare with stem cells in previous iteration.
}
}
{If the best fitness value of stem cell is better than the stem cells in previous iteration,
the best stem cell do Self – renewal by  $SC_{Optimum}(t + 1) = \zeta * SC_{Optimum}(t)$ 
and, So compute Comparative Power for stem cells and choose the best stem cell according to
Comparative Power and fitness value,
Best Solution
Until ( $i = M$ )
Cycle = Cycle + 1
Until (Cycle = Max _Iteration)
END

```

4. Experimental results

In order to evaluate the performance of the new data clustering algorithm, a set of well-known datasets have been used. They are known as Vowel, Iris, Crude Oil, Control Chart, Wood Defects, and Wine. Table 1 shows the characteristics of each dataset including the number of objects, features and classes. We have also compared the results obtained using the proposed algorithm with those using standard K-mean algorithm, genetic algorithm (GA), artificial bee colony (ABC) algorithm, Particle Swarm Optimization (PSO), Ant colony Optimization (ACO). Table 2 shows the parameters used in each algorithm in our experiments. Table 3 shows the results obtained by applying the different clustering algorithms to different test datasets with the cost function calculated as follows:

$$Cost\ function = \sum_{j=1}^N [min (\|Y_j - Z_i\|) \quad for \quad i = 1, 2, \dots, K], \quad (10)$$

Y = input data,

Z = cluster center,

N = number of input data,

K = number of cluster center.

Here, we compute the Euclidean distances between each input data and all cluster centers and then determine the minimum of these distances and finally sum all minimums for all input data. The mean, minimum and maximum cost function values were computed for each algorithm over 100 different runs on each dataset. As can be seen, the proposed algorithm demonstrates better results in obtaining lower mean value with minimum difference between min and max values for all datasets. We also computed the running time of each algorithm in clustering different datasets. The

characteristics of the computer on which the algorithms were run are: Macintosh OS, Two 2.93GHz 6-Core Intel, 64GB Ram, and the graphic card is ATI Radeon HD 5870 1GB.

The results obtained are shown in Table 4. As can be seen, the proposed algorithm has better performance than the other algorithms. The running time for each algorithm is the time when the algorithm achieves its best result. The SCA typically took less time than the other algorithms to achieve its best result. It is mostly due to the fact that SCA has fewer constraints, fewer parameters to be computed and fewer loops, which causes it achieves the result in far fewer iterations than other algorithms. In order to assess the speed of convergence of different clustering algorithms, we computed the curve of objective function value versus the number of iterations for all mentioned clustering algorithms and for all test datasets. Figures 2 through 7 show these curves. As can be seen, the proposed algorithm achieved a better objective function value in fewer iterations for all datasets.

Table 1. Datasets used in experiments and their characteristics.

Dataset Name	Number of Objects	Number of features	Number of Classes
Vowel	871	3	6
Iris	150	4	3
Crude Oil	56	5	3
Control Chart	1500	60	6
Wood Defects	232	17	13
Wine	178	13	3

Table 2. Parameters used in the clustering algorithms.

Algorithm	Parameter	Value
K-mean	Maximum number of iterations	1000
GA	Crossover probability	0.8
	Mutation probability	0.001
	Population size	100
ABC	Number of bees (employer and onlooker)	20
	Number of sites selected for neighborhood search	10
	Number of bee recruited for best sites	5
	Number of iterations	500
PSO	Number of Swarm	100
	C_1	1.9
	C_2	2.1
	ω_{max}	1
	ω_{min}	0.5
	Number of iterations	500
ACO	Number of ants	50
	Probability threshold for maximum trail	0.95
	Local search probability	0.01
	Evaporation rate	0.01
SCA	Number of stem cells	20
	ζ_{max}	0.98
	ζ_{min}	0.01
	Number of iterations	200

Table 3. Clustering results obtained by applying the algorithms for 100 different runs on each dataset.

Dataset	Algorithm	F_{mean}	$F_{min} = best$	$F_{max} = worst$	Standard deviation
Vowel	K-means	161775.693	159663.874	162783.433	987.27
	GA	162075.665	161874.655	162916.664	3210.3
	PSO	159445.333	158779.667	160389.254	3672.7
	ACO	159668.442	157996.333	160113.226	28100.3
	ABC	158889.455	156556.722	159778.446	2460
	SCA	150003.662	149988.333	150024.277	6.871
Iris	K-means	106.91276	102.45724	109.09872	13.89
	GA	99.38548	97.01237	100.85462	13.42
	PSO	98.98634	96.06847	100.31864	0.362
	ACO	98.65729	97.12787	99.98212	0.381
	ABC	98.32564	97.54622	99.73824	0.067
	SCA	98.01275	97.89834	98.04839	0.0002
Crude Oil	K-means	288.82759	285.87367	289.98628	42.632
	GA	286.22478	283.67278	287.76576	51.118
	PSO	280.69238	278.14945	281.97271	43.993
	ACO	280.12158	279.02278	281.41328	39.594
	ABC	279.65824	277.29441	279.97223	11.782
	SCA	277.00425	276.97324	277.01968	0.0032
Control Chart	K-means	2724.652	2562.453	2728.356	823.76
	GA	2548.281	2478.462	2692.662	34.782
	PSO	2124.789	2074.225	2127.436	26.378
	ACO	2094.622	2071.113	2114.218	29.463
	ABC	2049.792	2041.334	2050.001	16.832
	SCA	1968.257	1968.102	1968.271	0.0382
Wood Defects	K-means	185262.76	184672.23	186919.44	893.37
	GA	176728.22	175862.28	177169.33	2764.2
	PSO	155987.86	154241.32	156095.21	2977.3
	ACO	155026.17	154622.56	156001.65	2170.78
	ABC	153718.67	153267.34	153992.73	2660.48
	SCA	148393.25	148299.36	148412.78	3.671
Wine	K-means	17895.434	17682.589	17901.381	733.74
	GA	16928.633	16184.662	17128.885	0.0089
	PSO	16468.256	16074.730	16822.387	0.00058
	ACO	16411.116	16167.413	16912.223	0.00098
	ABC	16298.023	16133.336	16454.452	0.0172
	SCA	16104.618	16095.332	16112.376	0.000016

Table 4. Cost time obtained by applying the different algorithms.

Dataset	Algorithm	Real Time in Second
Vowel	K-means	0.0214
	GA	0.0017
	PSO	0.0009
	ACO	0.0026
	ABC	0.0005
	SCA	0.000102
Iris	K-means	0.0183
	GA	0.00889
	PSO	0.00232
	ACO	0.00764
	ABC	0.00187
	SCA	0.00627
Crude Oil	K-means	0.7642
	GA	0.0983
	PSO	0.0378
	ACO	0.0674
	ABC	0.0139
	SCA	0.0123
Control Chart	K-means	0.572
	GA	0.0832
	PSO	0.0196
	ACO	0.0362
	ABC	0.0128
	SCA	0.0016
Wood Defects	K-means	0.1295
	GA	0.0793
	PSO	0.0096
	ACO	0.0361
	ABC	0.0082
	SCA	0.00014
Wine	K-means	0.1978
	GA	0.0561
	PSO	0.0067
	ACO	0.0092
	ABC	0.0052
	SCA	0.00082

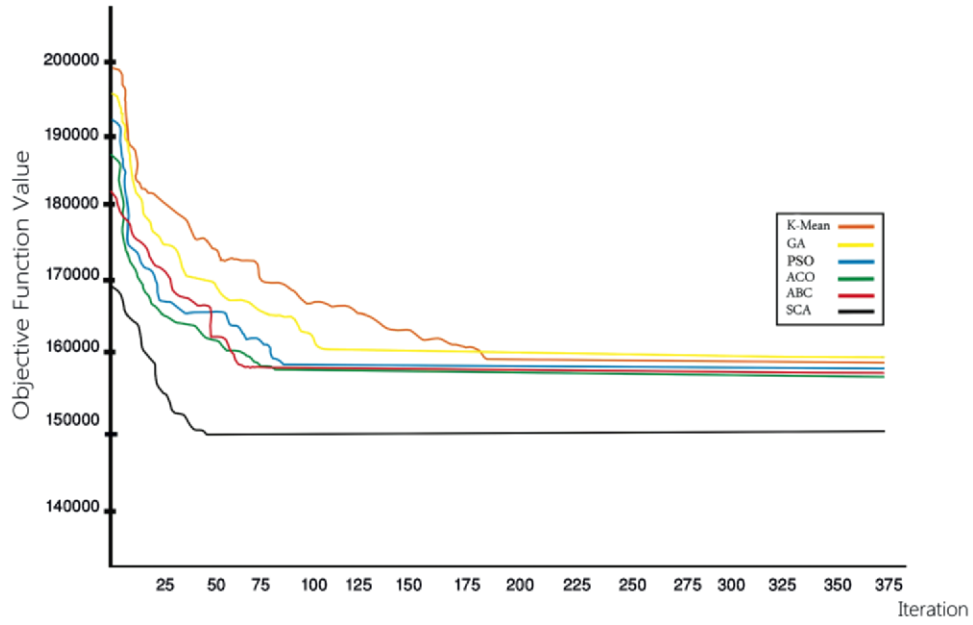


Figure 2. Convergence characteristic of clustering algorithms in reaching best solutions on Vowel test data.

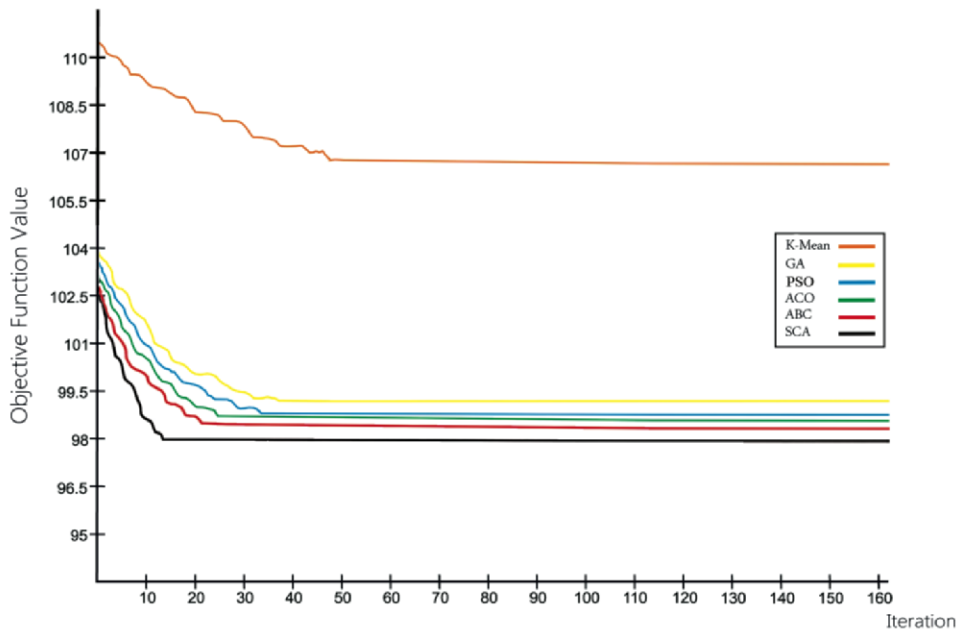


Figure 3. Convergence characteristic of clustering algorithms in reaching best solutions on Iris test data.

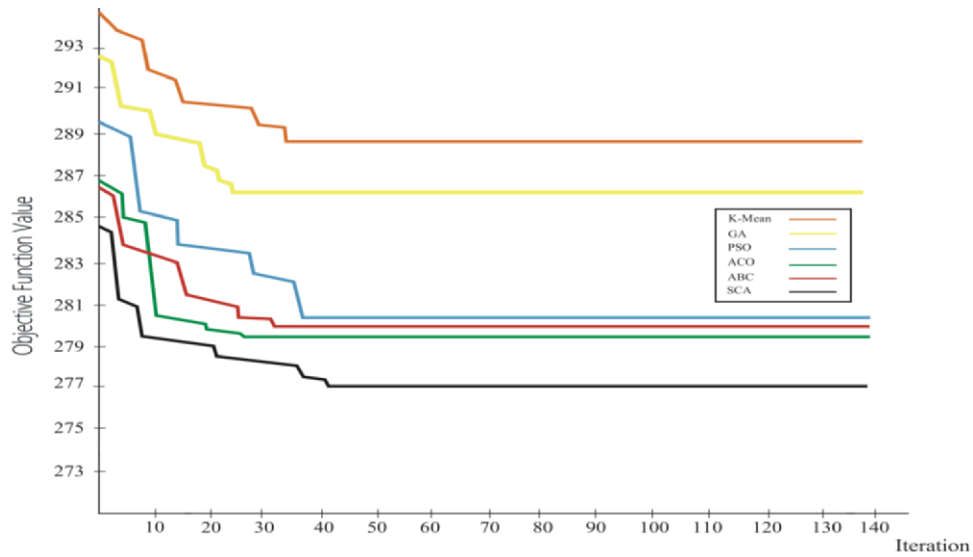


Figure 4. Convergence characteristic of clustering algorithms in reaching best solutions on Crude Oil test data.

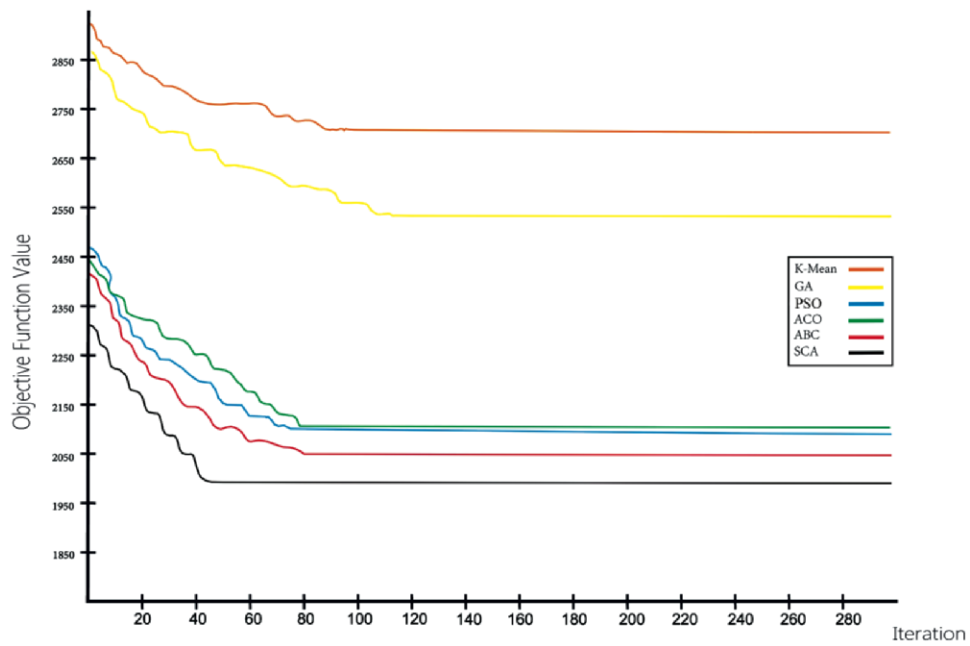


Figure 5. Convergence characteristic of clustering algorithms in reaching best solutions on Control Chart test data.

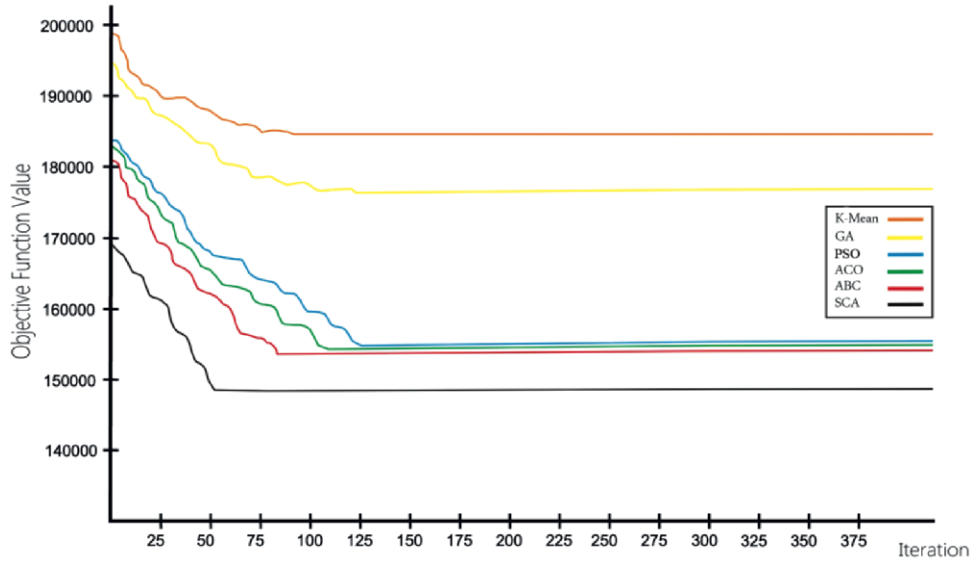


Figure 6. Convergence characteristic of clustering algorithms in reaching best solutions on Wood Defects test data.

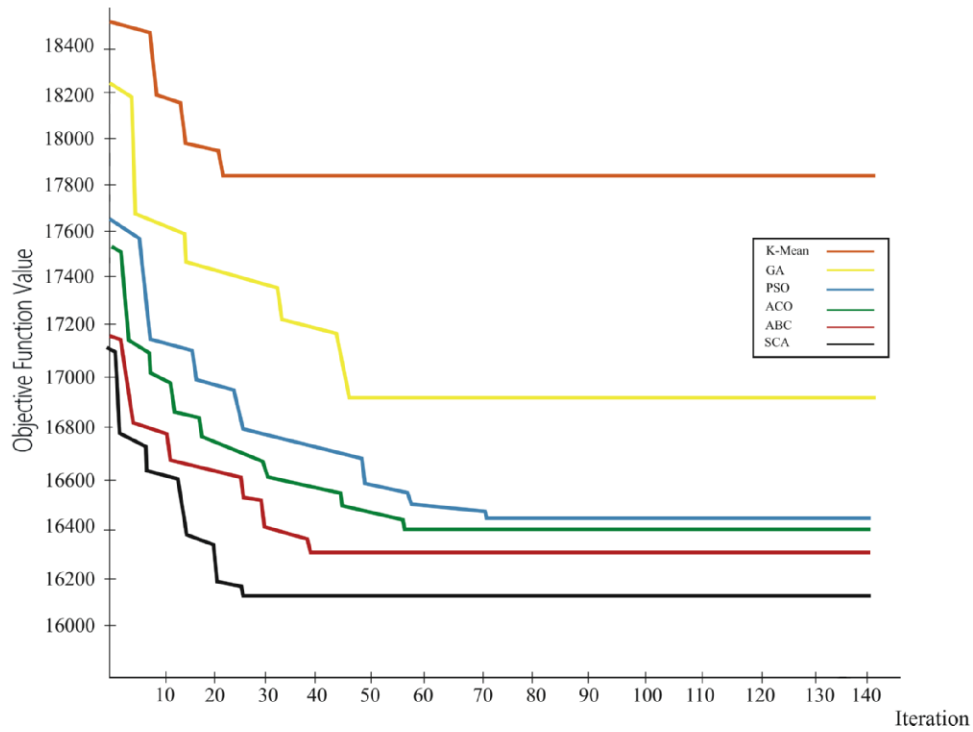


Figure 7. Convergence characteristic of clustering algorithms in reaching best solutions on Wine test data.

5. Conclusion

This paper has presented a new method for data clustering using the setm cells algorithm (SCA), and demonstrated superior clustering performance in fewer iterations than other algorithm. The SCA not only converges faster to a solution than other algorithms, its also more effectively avoids being trapped in local minima. Experimental results have demonstrated the superiority of the proposed method.

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