Intelligent Automation And Soft Computing, 2020
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Vol. 26, no. 2, 253–260
https://doi.org/10.31209/2019.100000155

An Improved Crow Search Based Intuitionistic Fuzzy Clustering Algorithm for Healthcare Applications

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ABSTRACT

Intuitionistic fuzzy clustering allows the uncertainties in data to be represented more precisely. Medical data usually possess a high degree of uncertainty and serve as the right candidate to be represented as Intuitionistic fuzzy sets. However, the selection of initial centroids plays a crucial role in determining the resulting cluster structure. Crow search algorithm is hybridized with Intuitionistic fuzzy C-means to attain better results than the existing hybrid algorithms. Still, the performance of the algorithm needs improvement with respect to the objective function and cluster indices especially with internal indices. In order to address these issues, the crow search algorithm is modified by introducing the genetic operators like cloning and mutation operators. In addition to that, an archive of memory is created to store the best solutions of the iterations and these values are used for updating the position when the acquired solutions are not feasible. The results obtained are compared with other hybrid Intuitionistic fuzzy C-means algorithms and the performance of ICrSA-IFCM is high in terms of the objective function and cluster validity indices.

KEYWORDS: Intuitionistic Fuzzy Clustering, Improved Crow Search, Cloning, Mutation, Awareness Probability, Flight Length.

1 INTRODUCTION

NOWADAYS, a huge volume of data is available in all fields. It is mind-numbing to analyze all these data manually and to extract the useful patterns or knowledge. Lot of data is yet to be un-dwelled from this heap to pull out useful information. The increase in the dimensionality of data demands the exploratory analysis and summary of data. Clustering algorithms disseminate the objects in any dataset into several groups based on their characteristics. Partitional algorithms are capable of finding clusters based on similarity measures and update cluster centers using mean or medoid values. The decision on the allocation of objects determines whether a clustering algorithm is categorized into hard or soft. An object is allocated to only one cluster in case of a hard clustering algorithm like K-Means while an object exists in various clusters with different membership values in case of a soft clustering algorithm like Fuzzy C-Means (FCM).

Fuzzy sets (Zadeh, 1965) are the notations used to represent the uncertainties in the data. An Intuitionistic Fuzzy Set (IFS) is a higher order fuzzy set that goes a further level beyond fuzzy sets in addressing the confusion or ambiguity that arises while representing data. The IFS adds the hesitancy parameter to mention the lack of clarity in determining the belongingness of an object to a group. Atanassov (2003) represented an IFS as follows

$$IFS = \{< x, \mu_{IF}(x), \nu_{IF}(x) >| x \in X\}$$

where μIF denotes the membership and νIF represents the non-membership and the hesitancy or indeterminacy is given by $\pi_{IF}(x) = 1 - \mu_{IF}(x) - \nu_{IF}(x)$.

Optimization is an applied science (Corne et al., 1999) which explores the best values of the

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parameters of a problem that may take under specified conditions. Crow search is combined with Intuitionistic Fuzzy C Means (IFCM) algorithm (Parvathavarthini et al., 2017) and benchmark datasets from UCI repository are considered for testing its performance. However, the motivation for improved crow search is obtained due to the fact that the internal indices need to be improved and still the objective function values can be minimized. The presence of noise or ambiguity in medical datasets claims the usage of IFCM algorithms to show user's inability to represent data.

This work throws light on an Improved Crow Search Algorithm (ICrSA) and combines it with Intuitionistic fuzzy clustering algorithm. The IFCM algorithm is hybridized with Particle Swarm Optimization (IFCM-PSO) (Parvathavarthini et al., 2017), Cuckoo Search Algorithm (IFCM-CSA) and Crow Search Algorithm (IFCM-CrSA). The results of ICrSA-IFCM are compared with these algorithms and the proposed method shows its efficacy in terms of objective function and cluster validity indices.

Kuo et al., (2018) proposed evolutionary-based clustering algorithm by combining kernel IFCM with PSO, Genetic Algorithm (GA) and Artificial Bee Colony (ABC) algorithms.. The proposed method is executed over benchmark datasets and a customer segmentation case study is carried out to show better cluster construction when compared to existing algorithms. Hassaballah, & Ghareeb (2017) introduced a quality index measure for representing an image in the form of IFS and constructed a neighborhood based similarity to improve the image quality for visualization. A mathematical proof of the convergence of IFCM is given by Lohani et al toreveal the effectiveness of IFCM over benchmark and synthetic datasets through standard measurement indices.

Zhao et al., (2018) constructed IF images to compute the fitness function and fuzzy evaluation index is used for choosing the optimal solution. The number of clusters is automatically determined by the algorithm and this method proved to be robust against noise. Luo, & Zhao (2018) designed a new distance measure based on matrix norm for IFS and a strictly increasing (or decreasing) binary function. This measure is applied to both numerical and medical diagnosis problems and is proved to be successful in both the cases.

Binu (2015) explored the performance of PSO, GA and Cuckoo search by inspecting them against seven objective functions and assessed that PSO perfoms well with large data. The multiobjective immunized PSO algorithm (Nanda & Panda, 2013) automatically finds the possible groups in a dataset and optimizes two objective functions simultaneously to produce the best solution from the pareto optimal archive.

Chaira (2011) segmented CT scan brain images to identify tumor affected regions. Xu, & Wu (2010) proposed the IFCM algorithm for clustering numerical datasets related to the car market. Kaur, Soni, & Gosain (2011) presented an IFCM and kernel IFCM employing a novel distance metric that considers variation in the distance among data points within each cluster. Bhargava et al. (2013) hybridized rough set with IFS and applied it for medical diagnosis. Shanthi & Bhaskaran (2013) classified mammogram images as normal or abnormal after applying IFCM clustering over the images.

Ananthi, Balasubramaniam & Lim (2014) segmented gray scale images by finding entropy to calculate the threshold value for segmenting the image. Tripathy, Basu, & Govel (2014) introduced a spatial function to represent the likeliness of a pixel to its neighbors and segmented brain images. Lin (2014) proposed an evolutionary Kernel IFCM by taking the full advantage of the good points in the kernel space. The author made use of GA to optimize the algorithm. Balasubramaniam & Ananthi (2016) identified the deficiency of various nutrients in crop images by utilizing IFCM to impute the missing pixels in the incomplete image.

The novelty of the proposed method can be put forth in two aspects viz. the application of a trending optimization technique called crow search to clustering and implementation of clonal selection theory of Artificial Immune Systems by incorporating cloning and hypermutation operators into crow search.

This paper is organized as follows: Section 2 gives a glimpse on FCM and IFCM clustering algorithms, Section 3 throws a quick look on CSA, Section 4 presents the ICrSA-IFCM method, Section 5 analyzes the effect of proposed method on various benchmark medical datasets and Section 6 focuses on the conclusion and suggestions for future work.

2 FCM AND IFCM CLUSTERING ALGORITHMS

FCM (Bezdek, Ehrlich, & Full, 1984) allows an object to be present as a member of various clusters and shares the membership degrees of the data to those clusters. The data is fuzzified before running the FCM algorithm. The membership is computed as follows

$$U_{ij} = \frac{1}{\sum_{r=1}^{C}\left(\frac{dis(X_j,V_i)}{dis(X_j,V_r)}\right)^{\frac{2}{m-1}}}, \quad 1 \le i \le C, 1 \le j \le n, m = 2 \tag{1}$$

The cluster centers are updated by computing the mean values and the process is iterated till the same set of centroid values is obtained in the consecutive iterations.

IFCM is an extension of FCM with the starting step as Intuitionistic fuzzification, the distance measure is taken as IFS distance measure and the objective function is modified accordingly. Yager method of Intuitionistic fuzzification is used to convert the data into IF notation. The Yager generated fuzzy complement function is given by

$$\mu_i(d_j;\alpha)=1-(1-\overline{\mu_i}(d_j))^{\alpha} \tag{2}$$

$$\nu_i(d_j;\alpha)=(1-\overline{\mu_i}(d_j))^{\alpha(\alpha+1)} \tag{3}$$

where alpha takes the value in the range 0 to 1. The value for alpha is to be determined for each dataset so that the intuitionistic fuzzy entropy gets maximized. Entropy is computed as follows

$$IFE=\frac{1}{n\times D}\sum_{i=0}^{n-1}\sum_{j=0}^{D-1}\frac{2\mu_i(d_j)\nu_i(d_j)+\pi_i^2(d_j)}{\pi_i^2(d_j)+\mu_i^2(d_j)+\nu_i^2(d_j)} \tag{4}$$

The IF Euclidean distance is employed to assess the similarity between the seed values and other objects in the dataset. Based on this distance, the membership matrix is calculated as follows:

$$U_{ij}=\frac{1}{\sum_{r=1}^{C}\left(\frac{d(X_j,V_i)}{d(X_j,V_r)}\right)^{\frac{2}{m-1}}},\ 1\le i\le C,\ 1\le j\le n,\ m=2 \tag{5}$$

For each attribute or dimension in the dataset, a mass value or weight vector (Xu, & Wu, 2010) is assigned. The mass value is found using

$$ma_i(k+1)=\left\{\frac{U_{i1}(k)}{\sum_{j=1}^{n}U_{ij}(k)},\frac{U_{i2}(k)}{\sum_{j=1}^{n}U_{ij}(k)},\dots,\frac{U_{in}(k)}{\sum_{j=1}^{n}U_{ij}(k)}\right\},1\le i\le C \tag{6}$$

The new centroids are updated using the mass value as follows

$$V_i=\{[\sum_{j=1}^{D}ma_j\mu_{Xj},\sum_{j=1}^{D}ma_j\nu_{Xj}],1\le i\le C\} \tag{7}$$

The objective function of IFCM is computed as

$$J_m(x,y)\ =\ \sum_{i=1}^{c}\sum_{j=1}^{p}U_{ij}^{\ m}\left\|X'_j-C_i\right\|,\ \ 1\le m\le\infty \tag{8}$$

The process is repeated until the objective function is converged.

3 CROW SEARCH ALGORITHM

ASKARZADEH (2016) proposed the algorithm by simulating the behavior of crows. Crows are intelligent birds that can remember faces and places of food source. They live in flocks and they hide their food sources from other crows. Even then, a crow goes behind others to steal food. The algorithm aims at finding the better food source by utilizing a couple of parameters called Awareness Probability (AP) and Flight Length (fl).

The metaheuristic algorithm needs to initialize the population size n and the problem dimension d. The position of crow i at any point in time t is given as $X_i^t=\left[x_1^{\,t},\ x_2^{\,t},\dots,\ x_D^{\,t}\right]$ where i=1,2,…,N; t=1,2,…,itmax, and itmax refers to the number of iterations. The hiding position of crow A at time t is given by $m_{A,t}$.

The possibilities that the crow i trails crow j may have two consequences as determined by the awareness factor of crow j, viz,

- crow j is unaware of crow i following it and reaching its hiding place.
- crow j is aware of crow i and takes a random flight direction to fool crow i

The memory and position of crows are updated every iteration so that an optimal place for food source is found.

4 IMPROVED CROW SEARCH BASED IFCM (ICRSA-IFCM)

THE novelty of ICrSA-IFCM lies in two aspects

- Utilizing the unexplored crow search algorithm and hybridizing it with IFCM
- Making use of clonal selection and mutation operators

The steps in the proposed algorithm include

Step 1: Initialization

The initial population, number of clusters and algorithm specific parameters like fl and AP are initialized. The position matrix of crows is initialized randomly and the memory is also assigned the same values as that of the position because initially crows do not have any memory.

Step 2: Evaluation of fitness

Based on the distance matrix, the membership of each object is calculated and the fitness of each crow is found.

Step 3: Nondominated sorting

The entire swarm is applied with nondominated sorting as given in (Coello, Pulido, & Lechuga, 2004) to determine all the possible nondominated solutions.

Step 4: Updation of position and memory

If crow j reaches the hiding place of crow i due to the lack of its awareness probability, then the position is updated as follows else a random position is chosen

$$x_{A,t+1}=x_{A,t+1}+r_A.\,fl_{A,t}.(m_{B,t}-x_{B,t}) \tag{9}$$

If the fitness of the new position is higher than the previous one, the Archive is updated. For the consecutive iterations, the best solutions are selected at random from the archived solutions.

Step 5: Cloning

Now the updated positions are evaluated for their fitness and steps 2 and 3 are repeated. The nondominated solutions obtained are cloned.

$$Cl_{N\times D} = [nd_1, nd_2, \ldots, nd_n]^T \tag{10}$$

Step 6: Hypermutation

All set of cloned population undergoes the process of hypermutation. The number of times the mutation takes place is controlled by the mutation rate r_m. Therefore, the total number of mutations is calculated as

$$T_m = r_m \times N \times D \tag{11}$$

The initial values for mutation are taken as the cloned population and it is given by

$$HM = Cl_{N\times D} \tag{12}$$

Random numbers are selected to replace the worst solutions.

Step 7: Reselection of immune cells

Step 2 and 3 are repeated on the cloned and mutated population and best solution for the next generation is identified as

$$x_{A,t+1} = HM_{N\times D} \; if \;\; ND_2 < N \tag{13}$$

Otherwise,

$$Arc(i) = ND1(i) \; if \; \forall \; objectives \; ND1(i) < ND2(i)$$

else Arc(i)=ND2(i) (14)

Arc is a collection of nondominated solutions to store the best positions of the present generation. Hereafter, the new position and Arc are considered for the updation of position and memory of crows.

Step 8: Select best solution from memory that produces the minimal value for fitness function and has the highest accuracy

Step 9: Compute cluster validity indices

Pseudocode for ICrSA-IFCM

```
Convert data into intuitionistic fuzzy representation using Eq. (2), (3) and (4)
Initialize the swarm of N crows, C clusters and maximum iterations itmax
Initialize the parameters fl and AP
Initialize a random position matrix of crows of size NxD
Assign the memory of the crows same as that of the position of crows.
    While run < maxruns
      while t < itmax
        for A = 1 : N
            Compute membership matrix using Eq. (5) and find the fitness using Eq. (8)
            Apply nondominated sorting
            Choose crow B to follow crow A
            If $r_B$ >=$AP_{B,t}$ calculate new position using Eq. (9)
            Else assign a random position
          end if
            Apply Cloning on nondominated solutions using Eq.(10)
            Perform Hypermutation using Eq.(11) and (12)
        end for
        Ensure feasibility of new positions
        If it is feasible, Evaluate its finess and Update the memory
        else $m_{A,t+1}$=$m_{A,t}$
        end if
        Reselection of best solution from archive or memory using Eq.(13) and (14)
      end while
Locate the best position with least cost
    while iter < maxiterations
Calculate membership matrix using the best position
Evaluate mass values using Eq. (6) and Update cluster centers using Eq. (7)
    end while
end while
```

5 RESULTS AND DISCUSSION

THE algorithm is implemented in Matlab. By extracting suitable features of two parent evolutionary processes, hybrid methods provide better solutions than the individual process. The parameters supplied to the algorithm are listed in Table 1. Experiments are conducted with these values and the results of ICrSA-IFCM method are compared with other hybrid methods. The experiments are executed upto 100 runs and the mean values are taken for analysis. The benchmark data sets are taken from the UCI data repository (Asuncion & Newman, 2007) for experimentation purpose and their details are shown in Table 2.

Table 1 Parameters used for experimentation

Parameters	Values
Population (N)	20
Maximum iterations (itmax)	50
Flight length (fl)	2
Awareness Probability (Ap)	0.1
Mutation rate (rm)	0.1

The results are analyzed in two aspects: the first way using the fitness function values and the second one based on clustering indices. The best, worst and average values of the objective function are extracted from the run that has the highest average accuracy. Table 3 shows the fitness values compared with hybrid FCM, IFCM and hybrid IFCM algorithms.

The crow search optimization algorithm is relatively simple and it yields convincing results also. But it exhibits less accuracy with the internal indices like DB index. Also, when the number of clusters increases, there is a decline in the performance. To overcome these issues, the improved crow search algorithm is designed with two additional operations like cloning of the best solutions and hypermutation of the clones.

The mutation operation executed over the position vector helps in randomly choosing diversified positions and thus causes variations in the cloned position. Each crow is taken towards global best position and the next iteration is started from that position. The utilization of these features help in a detailed exploration of search space, locating multiple optima and also retaining certain local optimal solutions.

Table 2 Dataset description

Dataset	No. of instances	No. of attributes	No. of clusters
Breast tissue (BT)	106	10	6 or 4 (minute variation among 2 classes are ignored)
Contraceptive Method Choice (CMC)	1473	9	3
Haberman Survival (HS)	306	3	2
Wisconsin Breast cancer (WBC)	683	9	2

In addition to this, the best solutions in every iteration are memorized using the archive. Whenever there is a updation of position, the feasibility is checked and if it is not feasible, the values archived are utilized. This leads to the improvement in the results both in terms of fitness values and the cluster indices.

It can be observed from the table 3 that ICrSA-IFCM produces more consistent results than the other methods. In most of the cases, an optimal solution is achieved by the proposed methodology. CrSA-IFCM produces the least worst case value for the breast tissue dataset and for Wisconsin Breast Cancer dataset, the least best case value is obtained. The remaining values stand as a proof for the exemplary performance of ICrSA-IFCM.

The reason that CrSA-IFCM produces the least worst case for the breast tissue might be the fact that the complexity of the ICrSA-IFCM increases as the number of clusters increase. Therefore the convergence gets affected slightly when the worst case arises and also there is a hike in the cluster count (6 clusters in case of breast tissue). However, the least best case value obtained by WBC is very much closer to that of ICrSA-IFCM.

5.1 Cluster Validity indices

The cluster structure obtained as a result of clustering algorithm must be evaluated for its correctness and compactness. Therefore, various internal and external validity measures are needed to ensure the level upto which the clustering is performed in a right manner. In this work, three external indices like Rand Index, Adjusted Rand Index, F-Measure and an internal index named DB index are considered for the cluster quality evaluation.

The formula for DBIndex can be given as

$$\frac{1}{C}\sum_{i=1}^{C} max_j \frac{s(C_i)+s(C_j)}{d_c(C_i,C_j)} \tag{15}$$

where C denotes the number of clusters and s(C) is the average distance among the objects in cluster C.

The Rand index (Rand, 1971) measures the percentage of correct decisions made by an algorithm.

$$RI = \frac{YY + YN}{YY + NY + NN + YN} \tag{16}$$

where YY denotes True Positive, YN denotes the True Negative, NY denotes the False Positive and NN denotes False Negative.

The F-Measure (Van Rijsbergen, 1979) is defined as the harmonic mean of the precision and recall factors. A high F-measure value is obtained if both the precision and recall value is high. All the other cases result in a low F-measure. It can be computed using the formula

$$F = \frac{2YY}{2YY + NY + YN} \tag{17}$$

Adjusted Rand Index compares a couple of groups with varying cluster numbers. The value ranges from -1 to +1.

$$ARI = \sum_{i=1}^{C}\sum_{j=1}^{D}\binom{n_{ij}}{2}\binom{n}{2}^{-1}\sum_{i=1}^{C}\binom{n_i}{2}\sum_{j=1}^{D}\binom{n_j}{2}\bigg/\frac{1}{2}\left[\sum_{i=1}^{C}\binom{n_i}{2}+\sum_{j=1}^{D}\binom{n_j}{2}\right]-\binom{n}{2}^{-1}\sum_{i=1}^{C}\binom{n_i}{2}\sum_{j=1}^{D}\binom{n_j}{2} \tag{18}$$

The results of ICrSA-IFCM are compared with other hybrid FCM and IFCM methods.

Table 4 shows the results of Rand Index. It is evident that the proposed method works well with all the four datasets. The values reflect the highest average performance of all the 100 runs. Table 5 summarizes the results of F-measure and it can be observed that hybrid IFCM algorithms like cuckoo search and improved crow search produce the same results for breast tissue dataset. In case of Wisconsin breast cancer dataset, crow search produces slightly high results than improved crow search.

Table 6 demonstrates that the proposed method provides excellent results for Adjusted Rand index in case of all datasets. Table 7 illustrates the DB index values obtained. It is apparent that there is a significant decrease in performance of crow search algorithm. The improved crow search algorithm overcomes these drawbacks and exhibits an outstanding performance for all the datasets.

Table 3 Comparison of fitness values

Dataset	Objective function	FCM-PSO	FCM-CUCKOO	IFCM	PSO-IFCM	CSA-IFCM	CrSA-IFCM	ICrSA-IFCM
BT	Best	1.87	1.09	3.15	0.55	0.50	0.5513	0.5491
	Worst	1.94	1.67	4.25	0.60	0.59	0.5888	0.5994
	Average	1.91	1.54	3.21	0.59	0.60	0.5964	0.5916
CMC	Best	112.5	102.35	175.18	71.19	71.65	71.2306	70.97
	Worst	124.2	112.76	224.17	86.99	81.93	84.3621	83.40
	Average	113.1	109.54	183.21	72.44	75.28	72.1946	72.11
HS	Best	8.95	3.49	39.07	6.88	6.77	2.0849	2.0531
	Worst	9.45	4.51	51.01	7.42	6.87	2.1228	2.0996
	Average	8.98	3.94	40.26	6.90	6.88	2.8314	2.0911
WBC	Best	21.29	18.75	58.62	13.56	13.57	7.3072	7.3075
	Worst	24.60	21.31	76.10	14.82	14.82	7.9596	7.6728
	Average	22.58	20.05	60.76	15.19	15.19	8.7218	7.6003

Table 4 Comparison of Rand index values

Dataset	FCM-PSO	FCM-CUCKOO	IFCM	PSO-IFCM	CSA-IFCM	CrSA-IFCM	ICrSA-IFCM
BT	0.7729	0.8376	0.7283	0.8671	0.8588	0.8719	0.8925
CMC	0.5812	0.5591	0.5637	0.6457	0.5714	0.7947	0.7996
HS	0.6003	0.6034	0.5128	0.6127	0.6128	0.6812	0.7009
WBC	0.7579	0.8027	0.8027	0.8123	0.8452	0.8641	0.8937

Table 5 Comparison of F-Measure index values

Dataset	FCM-PSO	FCM-CUCKOO	IFCM	PSO-IFCM	CSA-IFCM	CrSA-IFCM	ICrSA-IFCM
BT	0.5071	0.5877	0.7013	0.8007	0.8018	0.7981	0.8018
CMC	0.5196	0.4904	0.6121	0.7589	0.6993	0.7543	0.7734
HS	0.6775	0.7272	0.6754	0.6842	0.7482	0.7604	0.7802
WBC	0.8606	0.8848	0.8848	0.8672	0.9138	0.9216	0.9211

Table 6 Comparison of Adjusted Rand index values

Dataset	FCM-PSO	FCM-CUCKOO	IFCM	PSO-IFCM	CSA-IFCM	CrSA-IFCM	ICrSA-IFCM
BT	0.3129	0.3145	0.2237	0.5926	0.4958	0.5684	0.6007
CMC	0.3487	0.3591	0.0510	0.5312	0.4097	0.7890	0.8016
HS	0.0166	0.1274	0.0297	0.2307	0.2307	0.2370	0.3955
WBC	0.7532	0.7521	0.7016	0.7867	0.7917	0.8076	0.8169

Table 7 Comparison of DB index values

Dataset	FCM-PSO	FCM-CUCKOO	IFCM	PSO_IFCM	CSA_IFCM	CrSA_IFCM	ICrSA_IFCM
BT	0.1059	0.0844	0.4851	0.1518	0.1287	0.2170	0.0838
CMC	0.4113	0.2206	0.3216	0.2580	0.2137	0.1261	0.1253
HS	0.3942	0.1450	0.5586	0.2767	0.2150	0.2072	0.1329
WBC	0.0049	0.0082	0.2938	0.0099	0.0045	0.1753	0.0040

6 CONCLUSION

The modified and improved crow search algorithm incorporates some genetic operators like cloning and mutation that makes it achieve favorable and exceptional results in case of all the above medical datasets. The approach is performing well with all the datasets and produces a quality cluster structure. In future, the mutation rate may be fixed by means of some soft computing method like neural networks.

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8 DISCLOSURE STATEMENT

NO potential conflict of interest was reported by the authors.

9 NOTES ON CONTRIBUTORS

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