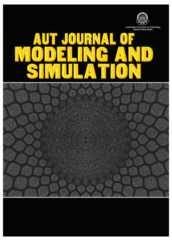

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NGTSOM: A Novel Data Clustering Algorithm Based on Game Theoretic and Self-Organizing Map

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ABSTRACT: Identifying clusters is an important aspect of data analysis. This paper proposes a novel data clustering algorithm to increase the clustering accuracy. A novel game theoretic self-organizing map (NGTSOM) and neural gas (NG) are used in combination with Competitive Hebbian Learning (CHL) to improve the quality of the map and provide a better vector quantization (VQ) for clustering data. Different strategies of Game Theory are proposed to provide a competitive game for non-winning neurons to participate in the learning phase and obtain more input patterns. The performance of the proposed clustering analysis is evaluated and compared with that of the K-means, SOM and NG methods using different types of data. The clustering results of the proposed method and existing state-of-the-art clustering methods are also compared which demonstrates a better accuracy of the proposed clustering method.

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1- Introduction

Identifying clusters is an important factor in data analysis. Generally, for extracting data, eliminating duplicate data, and making these data usable, several techniques have been proposed as data mining methods [1]. As a result, data mining has emerged as an important area of research [2]. Clustering can be considered as the most important thing in unsupervised learning. Clustering involves finding a structure within a collection of unlabeled data. The cluster is referred to as sets of data that are similar to each other. In clustering, data can be split into clusters where the similarity between the data in each cluster is minimum and the similarity between the data within different clusters is maximum [3]. So far, numerous data clustering approaches have been proposed.

Below, we provide a short overview of the most important clustering algorithms proposed in the literature.

In [4], the K-means clustering algorithm is proposed. The K-Means method is one of the partition-based data clustering methods in data mining. This method, despite its simplicity, is a basic method for many other methods of questing (such as Fuzzy-based decompositions). In the K-means algorithm, at first, the K number of input patterns are randomly selected for algorithm initialization. Then, the n-K remaining members are assigned to the nearest cluster. After assigning all members, the cluster centers are recalculated and assigned to the clusters according to the new centroids, and this continues until the centroids of the clusters stay constant. In [5], the K-Medoids algorithm was proposed to solve the problem of the K-means algorithm. Each cluster was defined by the most central medoid in which it is located. First, K data are considered as initial centroids (medoid) and then each data is assigned to the closest Medoid, and the initial clusters are formed. In an iteration-based process, the most central data in each cluster is considered as the new centroid and each data is assigned to the nearest centroid. The remaining steps of this algorithm match the K-means algorithm. The Fuzzy C-means (FCM) algorithm [6], [7] puts forward a concept called partial membership. In fact, in the FCM algorithm, each data belongs to all clusters. The degree of belonging is represented by a partial membership determined by a fuzzy clustering matrix. A genetic algorithm-based K-means (GA-K-means) algorithm was proposed in [8] to provide a global optimum for the clustering. In this method, the K-means clustering algorithm was used as a search operator instead of a crossover. A biased mutation operator was also proposed for clustering that helps the K-means algorithm to avoid local minima. In [9], the global K-means method was developed which is a gradual method for clustering; in this algorithm, at each step, a cluster centroid is dynamically calculated using a global search method based on iterative running the K-means algorithm and adds the appropriate initial points. However, it is not appropriate for clustering medium-sized and large-scale datasets due to its heavy computational burden. K-means++ algorithm was proposed in [10] for obtaining initial centroids for K-means algorithm that yields the near-optimal solution. The main drawback of the K-means++ is its inherent sequential nature, which limits the effectiveness of the method for the high-volume data. An artificial bee colony K-means (ABC-K-means) clustering approach was proposed in [11] for optimal partitioning of data objects into a fixed number of clusters. The reference [12] introduced a hybrid algorithm, named DE-K-means, that is a combination of differential evolution and K-means algorithms. The differential evolution optimization algorithm was used as a global optimization method and the resultant clustering solutions were fine-tuned and corrected using the K-means algorithm.

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Data clustering with SOP [13] has found wide applications in artificial neural networks. However, SOM clustering method often fails to deliver satisfactory results, especially when clusters have arbitrary shapes. Therefore, the weakness of this method at accurately and efficiently detecting the non-spherical clusters makes it more effective on synthetic datasets rather than the real dataset.

The reference [13] developed a hybrid clustering technique of the K-means++ and SOM algorithm to improve the clustering accuracy. However, the aforementioned limitation of the K-means++ was not addressed [22].

In this paper, we propose a novel data clustering method called NGTSOM that presents more accurate clustering results for the various types of synthetic and real datasets, compared to SOM algorithm and its improved version. The proposed method is a combination of game theory-based optimization techniques and SOM to develop a novel clustering method. In the game theory, each player has a pay-off function and a strategy set. Where each player's strategy is optimal given the strategies of all other players. In [14] different strategies were proposed to provide a more selective mechanism for the weight adaptation of neurons. This enables the winning neuron to select one among its neighbors to update its weight and therefore avoids the complexity of the original SOM algorithm where the weight vectors of all neighboring neurons are updated.

Unlike the previous studies where the weight vectors of dead neurons are far from the input patterns without having any chance to contribute in the learning phase, several different strategies are assigned to the non-winning neurons to provide a competitive game and improve the vector quantization. The neighborhood is defined based on the neurons' distances in the input space to accelerate the learning process and enhance the quality of the map when compared to the original SOM where the neighborhood is defined based on the neurons' distances in the two-dimensional lattice. A NGTSOM is proposed in this paper based on a new technique to make a proper selection of initial values of neuron's weights. Besides, five new strategies are proposed to increase the non-winning neuron's participation in the learning phase and enhance the clustering performance.

The rest of the paper is organized as follows. Section 2 provides a brief description of the original SOM algorithm and game theory concepts. It also explains the proposed clustering method. Section 3 demonstrates a case study where the mean squared errors (MSEs) are calculated for the proposed method and the existing K-means, the original SOM, SOM++ and NG clustering. Finally, section 4 concludes the paper.

2- Methodology

A. SOM Algorithm

SOM is an unsupervised artificial neural network (ANN) that performs the VQ or clustering tasks [15]. The distribution of the n-dimensional input patterns is estimated using the neurons arranged in a two-dimensional lattice in the network.

Let $X = [x_1, x_2 \dots x_n]$ represent an arbitrary input pattern and $M_i = [m_{i1}, m_{i2}, \dots, m_{in}]$ denote the weight vector of neuron i. An iterative process is used for the training of SOM. For each iteration, the Euclidean distances between the neurons and a pattern randomly selected from the set of input patterns are calculated. The neuron whose distance is the minimum is chosen as the winning neuron with the weight vector m_c. The best matching unit (BMU) is the winning neuron calculated by:

$$\|X - M_c\| = min_i \{\|X - M_i\|\} \tag{1}$$

The weight vectors of the neurons are then updated according to

$$M_i(t+1) = M_i(t) + h_{ci}(t)\left[X(t) - M_i(t)\right] \tag{2}$$

where h_{ci} is the neighborhood function given by

$$h_{ci}(t) = \alpha(t).\exp\left(-\frac{\|r_c - r_i\|^2}{2\sigma^2(t)}\right) \tag{3}$$

In the above relation, $0<\alpha(t)<1$ is the learning rate. r_c and $r_i \in R_2$ are the positions of the winning neuron and neuron i in the two-dimensional lattice of units. The parameter σ is used to control the neighborhood size.

B. Game Theory

Game theory is the study of situations where players with conflicting interests are involved [16]. A strategy set and a payoff function are defined for each player. The strategies determine players' actions in each stage of the game. The pay-off for each player is governed by both his and the other players' actions. The players' objective is to maximize their payoffs. Two major classes of the game are non-cooperative and cooperative games. Each player's action is independent of others' in a non-cooperative game, whereas in the cooperative games the players can choose to form coalitions and establish cooperation.

C. The Proposed Data Clustering Method

A NGTSOM is proposed in this paper to achieve better clustering results. The proposed clustering method uses a hybrid approach based on a new technique to make a proper selection of initial values of neurons' weights for SOM method along with the game theories approach to provide a better clustering performance. The steps of NGTSOM algorithm are as follows:

2- 1- Proposed method for a proper selection of initial values of neurons' weights

Let $X=[x_1,\dots,x_n]$ be a set of n data. The selection of K initial points as the initial weights of neurons is as follows:

1. Remove duplicate data vectors (temporarily) and store them in the new dataset $X`=[x`_1,\dots,x`_m]$, (X→X`).

2. Sort the data vectors in the dataset X in ascending order based on their infinity (Chebychev) norms. The Chebychev norm of any vector $V=[V_1,V_2,\dots,V_n]$ in a d-dimensional space, R^d, is calculated by:

$$\|V\|_\infty = \max\{|V_1|,|V_2|,\dots,|V_d|\} \tag{5}$$

3. Divide the dataset X`, consisting of m elements, into K sub-datasets, with P=|m / k| , according to Eq. (6), such that the elements of are distributed among the sub-datasets $X`_1$ to $X`_k$.

$$\begin{aligned} X'_1 &= [x'_1,\dots,x'_P], \\ X'_2 &= [x'_{P+1},\dots,x'_{2P}], \\ &\vdots \\ X'_K &= [x'_{(K-1)\times(P)+1},\dots,x'_{KP}]. \\ X' &= \bigcup_{k=1}^{K} X'_k \end{aligned} \tag{6}$$

4. Now, we have K sub-datasets where each one is used to determine only one of the K initial weights of neurons. Eq. (7) is used to determine each of the K initial weights from the sub-datasets {X`₁, X`₂,..., X`ₖ}.

$$\text{init}WTF_l = \frac{\sum_{i=1}^{P}(x'_i)}{P}, \ (1 \le l \le K) \qquad (7)$$

where x_i is the related data for the l-th sub-dataset.
Fig. 1 shows the flowchart of the proposed method to determine the initial weights of neurons.

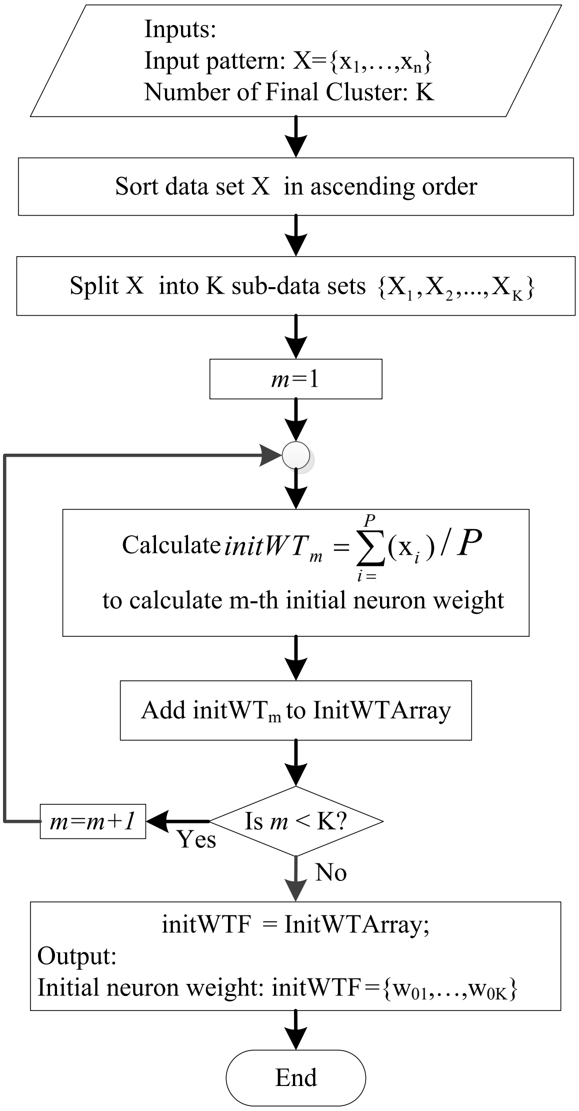

Inputs:
Input pattern: X={x₁,…,xₙ}
Number of Final Cluster: K
Sort data set X in ascending order
Split X into K sub-data sets $\{X_1, X_2, ..., X_K\}$
$m=1$
Calculate $initWT_m = \sum_{i=}^{P}(x_i)/P$
to calculate m-th initial neuron weight
Add initWT$_m$ to InitWTArray
Is m < K?
Yes
$m=m+1$
No
initWTF = InitWTArray;
Output:
Initial neuron weight: initWTF={w₀₁,…,w₀K}
End

Fig. 1. Flowchart for the proposed method to determine the initial weights of neurons

2- 2- Proposed strategies to improve the quality of the map

To resolve the shortcomings of the original SOM and enhance the quality of the map, five strategies are proposed as follows:

Strategy A: Winning neuron and its neighbors adjust their weights to approach the input pattern and minimize the Euclidean distance.

The following strategies are assigned to the non-winning neurons based on their situations and the current iteration number.

Strategy O: An equal probability is considered for the patterns distributed within the input space. Therefore, the non-winning neurons may increase their chance of reaching a pattern by moving in the opposite direction of the winning neuron. This strategy is more appropriate at early iterations.

Strategy S: Another strategy for the non-winning neurons is to stay in their current positions. This is more applicable to the recent winning neurons or the neurons which have won many times as they most likely approached regions with sufficient input patterns.

Strategy R: The neurons, which have not won for a long time are probably wandering in regions without sufficient or any input patterns. Strategy R requires random moves for these neurons to increase their chance of approaching regions with sufficient input patterns. This strategy is more applicable at early iterations.

Strategy B: The last strategy for the non-winning neurons involves approaching the neuron defined as the best player. The best player is identified using an error variable E_c calculated by:

$$E_c(t) = E_c(t-1) + \|X - M_c\| \qquad (8)$$

The error variable is the sum of the cumulative error of the neuron and the Euclidean distance between the input pattern and BMU. A counter is calculated for the number of wins the neuron achieved to become BMU.

The average cumulative error is then calculated by dividing the error variable of (5) by the counter variable. Then, The neurons with small average cumulative errors are selected as the best players.

Table 1 summarizes the proposed strategies considered for each neuron.

Table 1. proposed strategies for neurons

Neuron	Strategy
Winning neuron and its neighbors	A (Approach): Winning neuron and its close neighbors move towards the input pattern
Non-winning neurons	O (Opposite): Neurons move in the opposite direction of the winning neuron
	S (Stay): Neurons stay in their current positions
	R (Random): Neurons move to random positions in the input space
	B (Best player to approach): Neurons approach a neuron surrounded by ample input patterns

The topology of the input data is preserved by the topographic mapping of SOM. It means that the close input patterns remain close to the trained map [15].

The topology preserving the property of the map needs defining the neighborhood function based on the distance between neurons in the 2-D lattice, which this lattice domain is not appropriate for the proposed strategies. NG as a SOM-based method is used in this paper to define the neighborhood based on the neurons' distances in the input space rather than their distances in the lattice [21].

The neurons are ranked based on their distances from the input pattern where an integer k_i is assigned to represent their proximities. For example, 0 is assigned for neuron i_0 as the closest neuron, 1 for neuron i_1 as the second-closest and so on. NG adjusts the weight vectors of the neurons as:

$$M_i(t+1) = M_i(t) + \alpha(t) * \exp\left(\frac{-k_i}{\sigma(t)}\right)\left[X(t) - M_i(t)\right] \qquad (9)$$

The neighboring relationship between neurons is determined using CHL in combination with NG [21].

Fig. 2 shows the flowchart for the developed NGTSOM.

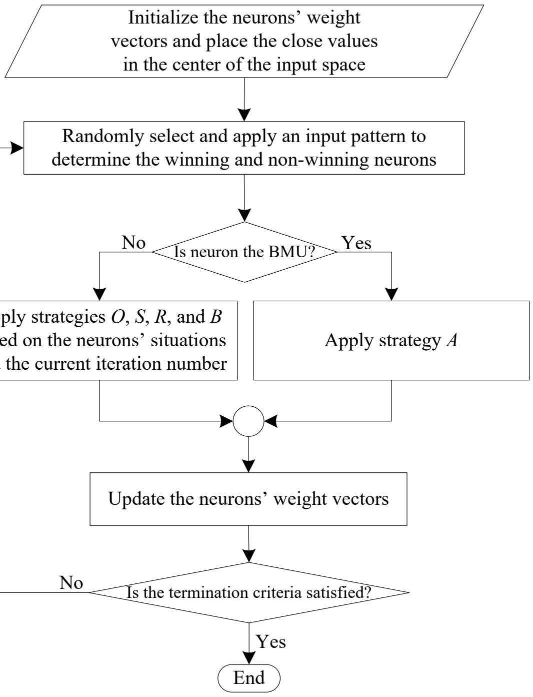

Initialize the neurons' weight vectors and place the close values in the center of the input space
Randomly select and apply an input pattern to determine the winning and non-winning neurons
Is neuron the BMU?
No
Yes
Apply strategies *O*, *S*, *R*, and *B* based on the neurons' situations and the current iteration number
Apply strategy *A*
Update the neurons' weight vectors
Is the termination criteria satisfied?
No
Yes
End

Fig. 2. Flowchart for the proposed clustering method (NGTSOM)

D. Time complexity

The Proposed NGTSOM algorithm has a time complexity of the order $n^2.K$, i.e. $O(n^2.K)$, where n is the total number of data, K is the number of clusters.

Table 2 provides the time complexity orders for the proposed method and well-known clustering algorithms, namely K-means++, original K-means, K-medoids, FCM, SOM, SOM++ algorithm.

Table 2. Comparison of time complexities in the proposed NGTSOM algorithm and several well-known clustering algorithms.

Algorithm	Time complexity
K-means++	O(n.K)
K-means	O(n.K)
K-medoids	$O(n^2.K)$
FCM	$O(n.K^2)$
SOM	$O(n^2.K)$
NG	$O(n^2.K)$
SOM++	$O(n^2.K)$
NGTSOM	$O(n^2.K)$

Time complexities comparison in Table 2 shows that the proposed NGTSOM algorithm is faster than K-medoids and competes equally with FCM, SOM, NG, and SOM++. The time complexity of K-means++ and K-means is better than that of our proposed algorithm. However, as the data volume increases, the K-means++ algorithm may not be as efficient as our proposed method due to its sequential initialization [18].

3- Case Studies

This section evaluates the clustering accuracy of the proposed NGTSOM and its comparison with the K-means, SOM, and NG, based on the type of the test data. Dynamic validity index (DVI) [19] and Mean Squared Error (MSE) are used as the performance indicators given by:

$$DVI = \min_{k=1,2,\ldots,K} \{IntraRatio(k) + InterRatio(k)\} \qquad (10)$$

where the IntraRatio and InterRatio are defined as follows.

$$IntraRatio(k) = \frac{Intra(k)}{MaxIntra} \qquad (11)$$

$$InterRatio(k) = \frac{Intra(k)}{MaxInter} \qquad (12)$$

$$Intra(k) = \frac{1}{N}\sum_{i=1}^{k}\sum_{x-C_i}\|x-c\| \qquad (13)$$

$$Intra(k) = \max_{i=1,2,\ldots,K}(Intra(i)) \qquad (14)$$

$$Inter(k) = \frac{Max_{i,j}\left(\|c_i - c_j\|^2\right)}{Min_{i\neq j}\left(\|c_i - c_j\|^2\right)}\sum_{i=1}^{k}\left(\frac{1}{\sum_{j=1}^{k}\|c_i - c_j\|^2}\right) \qquad (15)$$

Here, IntraRatio stands for the overall compactness of clusters whereas the InterRatio represents the overall separation of clusters. The lesser is the value of DVI, the more is the quality of the clusters [20].

$$MSE = \frac{1}{K.N}\sum_{k=1}^{K}\sum_{i=1}^{N}\left\|X_i^{(k)} - C_k\right\|^2 \qquad (16)$$

where N is the number of data points in the cluster k, and $X_i^{(k)}$ is a data point in the cluster k.

DVI and MSE values are calculated for different clustering algorithms, including the proposed NGTSOM, K-means, original SOM and NG method.

Tables 3 to 9 and Table 11 show the comparison results of different clustering methods for image data, Birch-sets, S-sets, A-sets, Dim-sets, Unbalance, Categorical, Shape sets, UCI datasets and large datasets respectively, that are presented in Figures 3 to 9, and Table 10 respectively. These data are available online at joensuu [23], uci websites [24]. Fig. 10 shows the processing time of different clustering algorithms on the twenty-sample dataset.

A. Image data

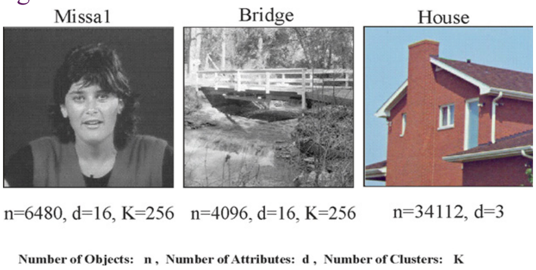
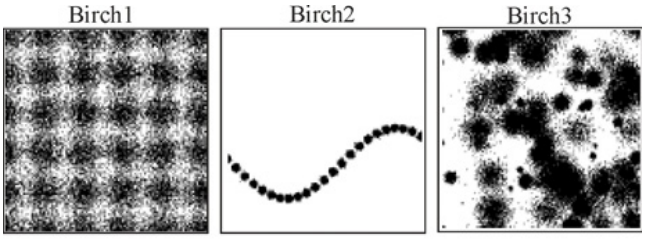

Missa1
Bridge
House
n=6480, d=16, K=256
n=4096, d=16, K=256
n=34112, d=3
Number of Objects: n , Number of Attributes: d , Number of Clusters: K

Fig. 3. The image datasets used for the case study

Table 3. dvi and mse values for different clustering techniques

DATASET	VALIDITY INDEX	Algorithm				
		K-MEANS	NG	SOM	SOM++	NGTSOM
Missa1	DVI	0.5430	0.5790	0.5429	0.5761	0.5226
	MSE	8.5057	8.7217	8.5051	8.7043	8.3833
Bridge	DVI	3.0756	3.2438	3.0558	3.3010	3.03225
	MSE	23.7018	24.7107	23.5826	25.0539	23.4412
House	DVI	2.9509	2.7775	2.6919	2.5666	2.5326
	MSE	22.9531	21.9127	21.3991	20.6473	20.4433

B. Birch-sets



n=100000, d=2, K=100

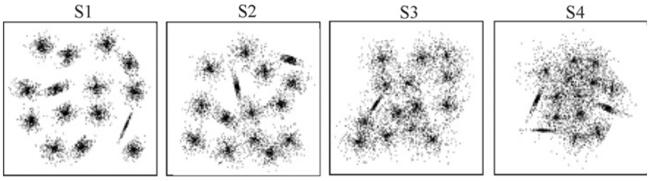
Number of Objects: n, Number of Attributes: d, Number of Clusters: k

Fig. 4. The Birch-sets data

Table 4. mse errors for different clustering techniques (*10^4)

DATASET	VALIDITY INDEX	Algorithm				
		K-MEANS	NG	SOM	SOM++	NGTSOM
Birch1	DVI	5.6669	6.1914	5.9981	6.3002	5.2162
	MSE	1.5933	1.6245	1.6056	1.4758	1.4304
Birch1	DVI	4.6916	5.0187	4.8518	4.9087	4.5475
	MSE	0.1626	0.1269	0.1174	0.1206	0.1206
Birch1	DVI	1.5424	1.3588	5.7178	5.6998	4.8064
	MSE	0.9075	0.8711	0.9303	0.8468	0.805

C. S-sets



n=5000, d=2, K=15

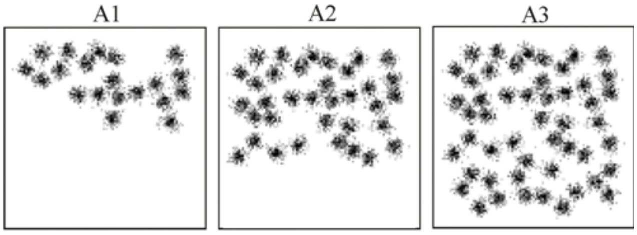
Number of Objects: n, Number of Attributes: d, Number of Clusters: k

Fig. 5. The S-sets data

Table 5. mse errors for different clustering techniques (*10^4)

Algorithm Dataset	VALIDITY INDEX	K-MEANS	NG	SOM	SOM++	NGTSOM
S1	MSE	2.6005	2.0783	1.6908	1.6916	1.6869
	DVI	5.1876	4.9176	4.8369	4.5842	4.4209
S2	MSE	2.3075	2.0659	2.0528	2.0604	2.0478
	DVI	5.7909	5.4935	6.6971	5.2468	4.6535
S3	MSE	2.5657	2.3913	2.6033	2.3829	2.388
	DVI	4.1596	4.1037	4.255	3.2771	3.546
S4	MSE	2.4049	2.2835	2.2958	2.3187	2.2679
	DVI	5.1257	4.8086	4.7388	4.8341	4.7124

D. A-sets



n=3000, d=2, K=20 n=5250, d=2, K=35 n=7500, d=2, K=50

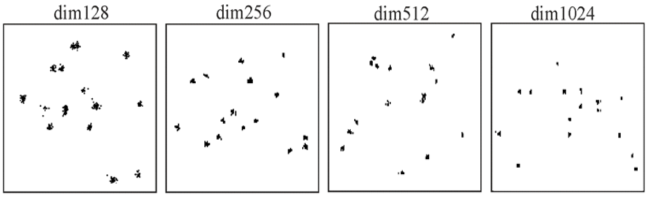
Number of Objects: n, Number of Attributes: d, Number of Clusters: k

Fig. 6. The A-sets data

Table 6. mse errors for different clustering techniques (*10^3)

Algorithm Dataset	VALIDITY INDEX	K-MEANS	NG	SOM	SOM++	NGTSOM
A1	MSE	1.0289	0.9889	0.8985	0.9541	0.9045
	DVI	7.4801	7.1703	6.2614	7.3365	6.2857
A2	MSE	1.2635	0.918	0.9077	0.9778	0.9157
	DVI	6.8725	5.0229	5.8155	5.8148	5.6643
A3	MSE	1.0208	0.9846	0.9914	0.9662	0.9588
	DVI	4.4269	4.1524	4.6915	4.6384	4.3779

E. Dim-sets



n=1024, d=128, K=16 n=1024, d=256, K=16 n=1024, d=512, K=16 n=1024, d=1024, K=16

Number of Objects: n, Number of Attributes: d, Number of Clusters: k

Fig. 7. The Dim-sets data

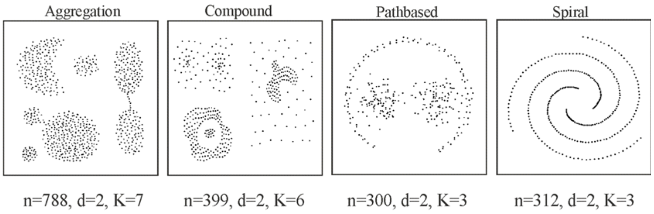
Table 7. mse errors for different clustering techniques (*10^5)

Algorithm / Dataset	VALIDITY INDEX	K-MEANS	NG	SOM	SOM++	NGTSOM
dim0128	MSE	1.2187	0.8003	0.8411	0.1184	0.1014
	DVI	6.1818	7.5285	6.4593	4.3152	4.1253
dim0256	MSE	1.1413	0.8158	0.9016	0.3293	0.1516
	DVI	4.3574	3.858	3.3955	3.4779	3.2682
Dim0512	MSE	1.143	0.6788	0.2209	0.4409	0.0353
	DVI	9.6591	8.6686	6.013	7.2092	4.7449
Dim1024	MSE	0.3041	0.4117	0.1646	0.456	0.1451
	DVI	5.8128	6.3031	4.8413	6.5526	4.5804

Table 8. mse errors for different clustering techniques

Algorithm / Dataset	VALIDITY INDEX	K-MEANS	NG	SOM	SOM++	NGTSOM
Aggregation	MSE	1.2102	1.1972	1.1931	1.1811	1.1546
	DVI	5.1546	5.1251	5.1802	5.1595	5.0771
Compound	MSE	1.0207	0.9045	0.9027	0.9105	0.9017
	DVI	4.0955	4.1309	3.995	3.6298	3.6667
Pathbased	MSE	1.6132	1.617	1.6133	1.6118	1.6115
	DVI	5.9863	5.2928	5.3845	5.3392	5.2758
Spiral	MSE	1.9629	1.9668	1.9664	1.9623	1.9601
	DVI	7.1675	7.4465	6.9785	6.6029	6.2503

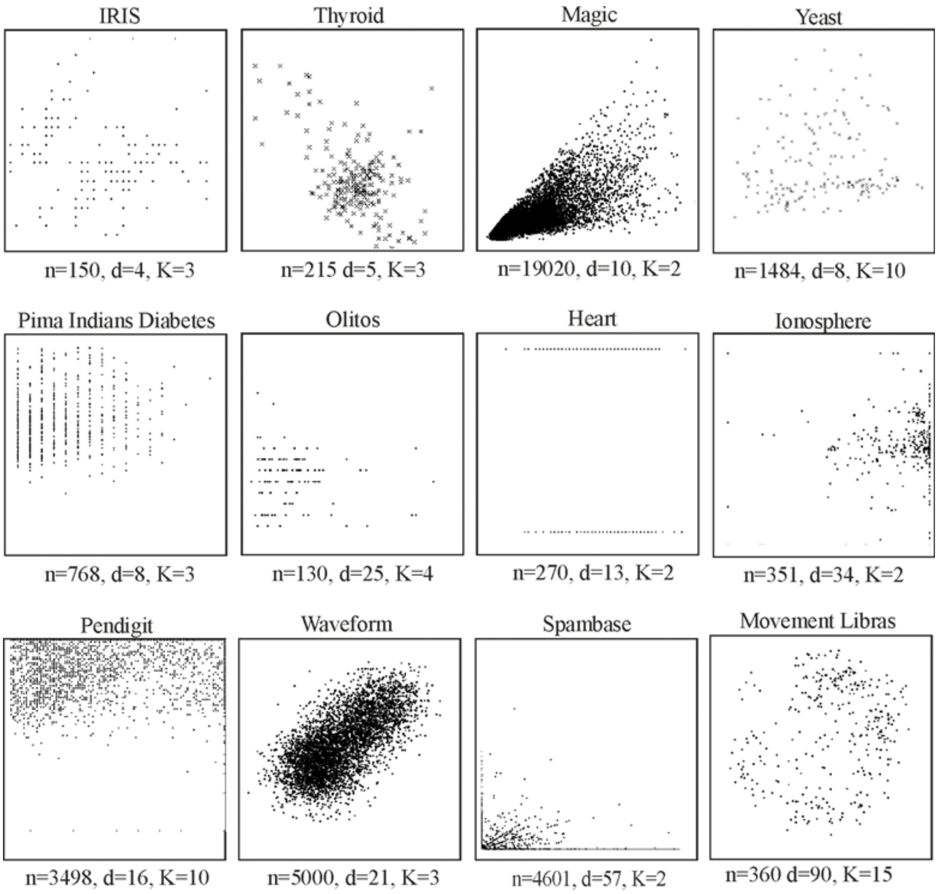
F. Shape sets



Number of Objects: n, Number of Attributes: d, Number of Clusters: k

Fig. 8. The Shape datasets

G. UCI datasets



Number of Objects: n, Number of Attributes: d, Number of Clusters: K

Fig. 9. UCI datasets

Table 9. mse errors for different clustering techniques

Algorithm Dataset	VALIDITY INDEX	K-MEANS	NG	SOM	SOM++	NGTSOM
IRIS	MSE	215866	215212	215520	215529	214495
	DVI	1295198	1291272	1293120	1293174	1286971
Thyroid	MSE	236827	236871	238243	238141	236738
	DVI	1421963	1421226	1429459	1428847	1420429
Magic	MSE	9.3126	9.7127	8.8655	9.6523	8.8655
	DVI	25.4663	25.6051	22.6442	23.4909	22.6442
Yeast	MSE	0.3301	0.2808	0.2127	0.1948	0.1951
	DVI	4.0689	2.5875	1.0434	3.3596	5.7953
P. I. D	MSE	8.4753	8.374	8.545	8.3702	8.1982
	DVI	20.0709	17.9303	23.0292	17.0702	21.4675
Olitos	MSE	0.7497	0.728	0.7269	0.7297	0.7265
	DVI	2.3994	4.0355	6.7595	4.8228	4.9689
Heart	MSE	3.0472	3.0372	3.0552	3.0372	3.0372
	DVI	11.6673	11.4215	11.0389	10.0729	10.0729
Ionosphere	MSE	0.0669	0.0669	0.067	0.0668	0.0667
	DVI	4.6634	4.5145	4.5756	5.026	3.8892
M. Libras	MSE	0.0102	0.0098	0.01	0.0098	0.0098
	DVI	4.6749	4.5501	4.9735	5.9531	4.5981
Spambase	MSE	5.238	3.6863	3.6092	4.1615	3.5919
	DVI	15.6314	13.2686	13.2296	13.5156	13.0776
Waveform	MSE	0.2424	0.2428	0.2427	0.2426	0.2424
	DVI	5.3735	5.4301	5.4291	5.4249	5.3735
Pendigit	MSE	3.8447	3.8298	3.7758	3.784	3.7795
	DVI	11.9137	11.6872	11.3694	12.4451	11.0395

H. Large datasets

Table 10. large datasets used for the case study

Algorithm Dataset	Number of objects	Number of attributes	Number of clusters
ConfLongDemo	164,860	3	11
MiniBooNE	130,065	50	---
MNIST	10000	748	10
KDDCUP04Bio	145751	74	2000

Table 11. mse errors for different clustering techniques

Algorithm Dataset	VALIDITY INDEX	K-MEANS	NG	SOM	SOM++	NGTSOM
ConfLongDemo	MSE	47.51651	44.70387	40.199705	43.300355	37.2299
	DVI	96.24162	91.50179	86.54654	88.52581	76.35052
MiniBooNE	MSE	342.651	336.173	331.4545	359.9345	331.4545
	DVI	693.9291	677.8689	663.3355	721.0998	663.3355
MNIST	MSE	120.651	121.60603	107.76003	103.76453	100.24753
	DVI	246.145	249.5109	216.0154	209.584	206.847
KDDCUP04Bio	MSE	8105.0631	8105.0631	8653.4586	8905.1184	8105.0631
	DVI	16212.94	16212.94	17311.81	17811.7	16212.94

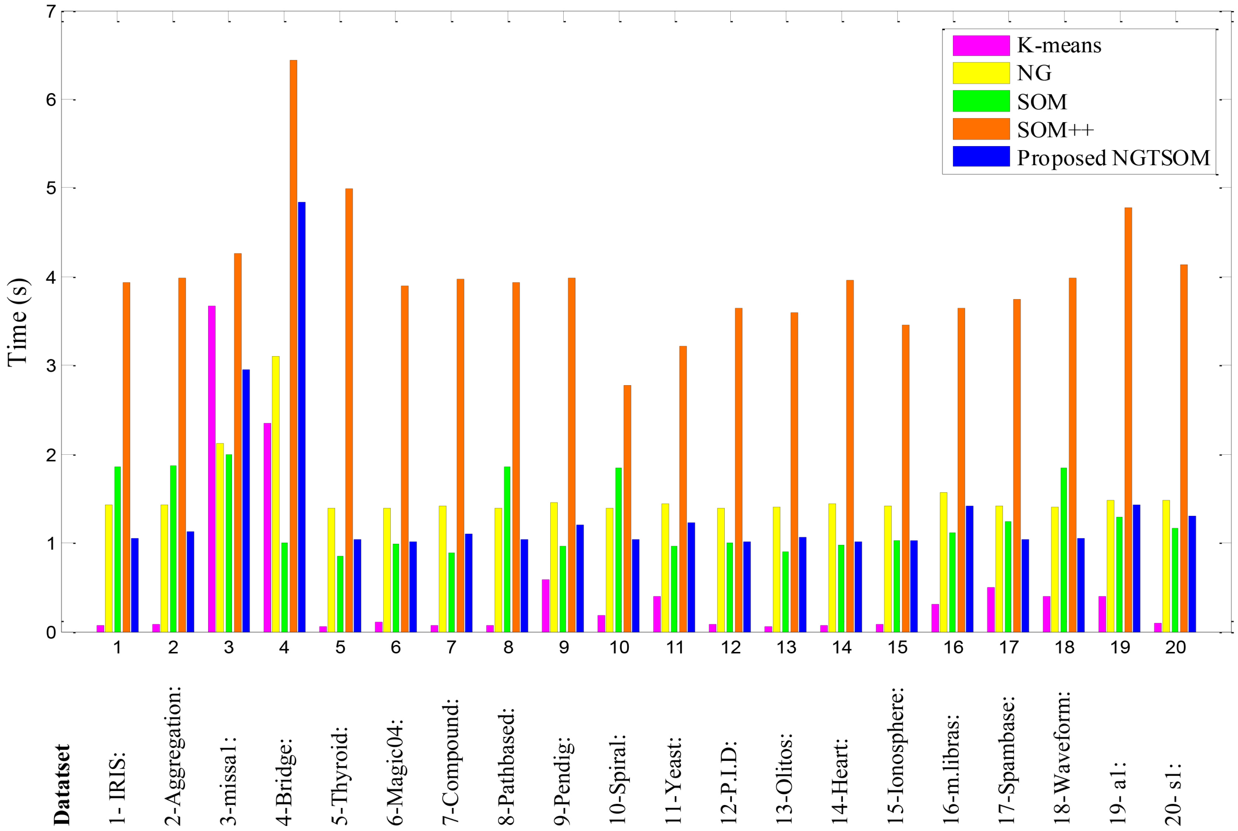


Fig. 10. The Running times for different clustering methods

The calculated MSE values show that the proposed NGTSOM improves the quality of the clustering when compared to the other clustering methods.

Based on the results presented in Fig.10, the proposed NGTSOM algorithm has a faster processing time than the SOM++ and NG method and is comparable with SOM clustering approach.

4- CONCLUSION

In this paper, a novel Game theory-based data clustering algorithm is proposed by combining a new initialization method, Game theory, and SOM algorithm. The performance of the proposed NGTSOM is evaluated using several different synthetics and real datasets and the results show a significant accuracy improvement for the proposed data clustering model. This is due to the more competitive game provided by the proposed strategies. It resolves the major problem of the existing clustering techniques where the weight vectors of non-winning neurons are far from the input patterns without having any chance to contribute in the learning phase. The proposed NGTSOM were compared with K-means, NG, SOM and SOM clustering algorithm. The comparison results demonstrate the improved clustering quality of the proposed NGTSOM.

REFERENCES

[1] R. Duwairi, M. Abu-Rahmeh, A novel approach for initializing the spherical K-means clustering algorithm, Simulation Modelling Practice and Theory, 54 (2015) 49-63.

[2] H. Mashayekhi, J. Habibi, S. Voulgaris, M. van Steen, GoSCAN: Decentralized scalable data clustering, Computing, 95(9) (2013) 759-784.

[3] S.M.R. Zadegan, M. Mirzaie, F. Sadoughi, Ranked k-medoids: A fast and accurate rank-based partitioning algorithm for clustering large datasets, Knowledge-Based Systems, 39 (2013) 133-143.

[4] J. MacQueen, Some methods for classification and analysis of multivariate observations, in: Proceedings of the fifth Berkeley symposium on mathematical statistics and probability, Oakland, CA, USA., 1967, pp. 281-297.

[5] H.-S. Park, C.-H. Jun, A simple and fast algorithm for K-medoids clustering, Expert systems with applications, 36(2) (2009) 3336-3341.

[6] J.C. Dunn, A fuzzy relative of the ISODATA process and its use in detecting compact well-separated clusters, (1973).

[7] S. Miyamoto, K. Umayahara, Methods in hard and fuzzy clustering, in: Soft computing and human-centered machines, Springer, 2000, pp. 85-129.

[8] T. Johnson, S.K. Singh, Genetic algorithms based enhanced K Strange points clustering algorithm, in: Computing and Network Communications (CoCoNet), 2015 International Conference on, IEEE, 2015, pp. 737-741.

[9] A. Likas, N. Vlassis, J.J. Verbeek, The global k-means clustering algorithm, Pattern recognition, 36(2) (2003) 451-461.

[10] D. Arthur, S. Vassilvitskii, k-means++: The advantages

of careful seeding, in: Proceedings of the eighteenth annual ACM-SIAM symposium on Discrete algorithms, Society for Industrial and Applied Mathematics, 2007, pp. 1027-1035.

[11] C. Zhang, D. Ouyang, J. Ning, An artificial bee colony approach for clustering, Expert Systems with Applications, 37(7) (2010) 4761-4767.

[12] W. Kwedlo, A clustering method combining differential evolution with the K-means algorithm, Pattern Recognition Letters, 32(12) (2011) 1613-1621.

[13] T. Kohonen, The self-organizing map, Proceedings of the IEEE, 78(9) (1990) 1464-1480.

[14] S. Wu, T.W. Chow, Clustering of the self-organizing map using a clustering validity index based on inter-cluster and intra-cluster density, Pattern Recognition, 37(2) (2004) 175-188.

[15] Y. Dogan, D. Birant, A. Kut, SOM++: integration of self-organizing map and k-means++ algorithms, in: International Workshop on Machine Learning and Data Mining in Pattern Recognition, Springer, 2013, pp. 246-259.

[16] A. Neme, S. Hernández, O. Neme, L. Hernández, Self-Organizing Maps with Non-cooperative Strategies (SOM-NC), in: WSOM, Springer, 2009, pp. 200-208.

[17] A.P. Engelbrecht, Computational intelligence: an introduction, John Wiley & Sons, 2007.

[18] L. Pavel, Game theory for control of optical networks, Springer Science & Business Media, 2012.

[19] J. Shen, S.I. Chang, E.S. Lee, Y. Deng, S.J. Brown, Determination of cluster number in clustering microarray data, Applied Mathematics and Computation, 169(2) (2005) 1172-1185.

[20] S. Subramani, S. Balasubramaniam, Post mining of diversified multiple decision trees for actionable knowledge discovery, in: International Conference on Advanced Computing, Networking and Security, Springer, 2011, pp. 179-187.

[21] T. Martinetz, K. Schulten, A" neural-gas" network learns topologies, (1991).

[22] B. Bahmani, B. Moseley, A. Vattani, R. Kumar, S. Vassilvitskii, Scalable k-means++, Proceedings of the VLDB Endowment, 5(7) (2012) 622-633.

[23] http://cs.uef.fi/sipu/datasets.

[24] https://archive.ics.uci.edu/ml/datasets.

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