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Classification of Brain Tumor using Dendritic Cell-Squirrel Search Algorithm in a Parallel Environment

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ABSTRACT Magnetic Resonance Imaging is a vital imaging tool for detecting brain malignancies in medical diagnosis. The semantic gap between low-level visual information collected by MRI equipment and high-level information stated by the doctor, on the other hand, is the biggest stumbling block in MR image classification. Large amount of medial image data is generated through various imaging modalities. For processing this large amount of medical data, considerable period of time is required. Due to this, time complexity becomes a measure challenge in medical image analysis. As a result, this paper offers analysis for brain tumour classification method named as Dendritic Cell-Squirrel Search Algorithm-based Classifier in the parallel environment. In this paper a parallel environment is proposed. In the experimentation the input dataset is divided into datasets of equal sizes and given as the input on the multiple cores to reduce the time complexity of the algorithm. Due to this, brain tumor classification becomes faster. Here initially, pre-processing is performed applying Gaussian Filter and ROI, it improves the data quality. Subsequently segmentation is done with sparse fuzzy-c-means (Sparse FCM) for extracting statistical and texture features. Additionally, for feature selection, the Particle Rider mutual information is used, which is created by combining Particle Swarm Optimization (PSO), Rider Optimization Algorithm (ROA), and mutual information. The Dendritic Cell-SSA algorithm, which combines the Dendritic Cell Algorithm and the Squirrel Search Algorithm, is used to classify brain tumors. With a maximum accuracy of 97.79 percent, sensitivity of 97.58 percent, and specificity of 98 percent, the Particle Rider MI-Dendritic Cell-Squirrel Search Algorithm-Artificial Immune Classifier outperforms the competition. The experimental result shows that the proposed parallel technique works efficiently and the time complexity is improved up to 99.94% for Particle Rider MI-Dendritic Cell- Squirrel Search Algorithm-based artificial immune Classifier and 99.92% for Rider Optimization-Dendritic Cell –Squirrel Search Algorithm based Classifier as compared to sequential approach.

KEYWORDS Particle Swarm Optimization; Mutual Information; Rider Optimization Algorithm; Dendritic Cell Algorithm; Squirrel Search Algorithm; Parallel Processing.

I. INTRODUCTION

MEDICAL Image analysis plays a vital role in diagnosis of various diseases. The analysis of multidimensional medical images is a critical task due to its size, structure and shape. Brain tumor is the most leading cause of cancer-related deaths. The detection of this disease at the early stage improves the patient's chance for successful treatment to a great extent and reduces the risk of death. In Computer-aided diagnosis using multidimensional images, effective techniques for feature extraction, feature selection and classification are required. Another highlighting point for processing the medical image requires considerable amount of time. Due to this, time complexity becomes a measure challenge in medical image analysis. As a result, this paper offers analysis for brain tumor classification method named as Dendritic Cell-Squirrel Search Algorithm-based Classifier [11] in the parallel environment. In this research paper a parallel processing environment is proposed to reduce the execution time. An experimental result shows that the proposed algorithm gives the promising results in parallel environment. Here, the preprocessing is carried out with the help of region of interest and Gaussian filter. The preprocessed image is given towards the sparse FCM for segmentation task. After that, segmented image goes for the

feature extraction task, where statistical and texture features are focused. Finally, the feature selection and classification is carried out using particle rider mutual information [11] and dendritic cell-squirrel search based artificial immune classifier [11], respectively.

Motivations

1 As mentioned in the introduction, analyzing multidimensional medical imaging is a crucial task. The most common cancer-related deaths are brain tumours. Early diagnosis of these diseases greatly increases the chances of a successful therapy for the patient.
2 In the realm of medicine, medical image analysis and processing are extremely important, particularly in non-invasive therapy and clinical research.
3 Appropriate interpretation and analysis of MR images takes time as the size of the images grows larger with technological advancements.
4 Because of their ease, parallelism, and convergence of the population towards the global optimal solution in a particular search space, swarm intelligence and artificial immune systems are more popular than traditional optimization methods.
5 The previous approaches and existing approaches are time-consuming, have a low convergence rate, are inefficient, and have low accuracy, specificity and sensitivity.

The goal of this research is to develop a novel parallel environment for faster brain tumour classification for the newest proposed methods named as dendritic-Squirrel Search Algorithm [11]. To remove noise and artifacts from the image, Region of Interest and Gaussian filters are used. Sparse Fuzzy C Means Clustering [12] has also been applied for segmentation to obtain segments. The statistical and texture features are taken from each segment to create a feature vector. For feature selection, the Particle Rider Mutual Information [11] is used, which is developed by combining Particle Swarm Optimization [13], Rider Optimization Algorithm [14], and Mutual Information [15]. The selected features are induced by Artificial Immune Classifier (AIC) [16] in order to determine the tumorous regions. The Dendritic Cell-SSA algorithm [11], which combines the dendritic cell algorithm [17] with the Squirrel search algorithm [18], is used to train the Artificial Immune Classifier. The Artificial Immune Classifier weights are optimized using the suggested Dendritic Cell-SSA technique [11].

The major contribution of the paper is designed and developed parallel processing environment for faster brain tumor classification in such way that accuracy, sensitivity and specificity are also preserved.

The remainder of the paper is divided into the following sections: Section 2 discusses the traditional brain tumour detection methodologies that were used in the literature, as well as the obstacles that were encountered, which served as the inspiration for designing the proposed parallel image processing technique. The proposed strategy for detecting brain tumours using AIC is then presented in Section 3. The results of the proposed method in comparison with other approaches are shown in Section 4, and the conclusion is given in Section 5.

II. LITERATURE REVIEW

Mohammad Taherdangkoon *et al.* [1] investigated that ACO provides high precision when it comes to clustering. It also makes implementation easier. ACO [25] is less vulnerable to initialization errors and requires less computation time, making it a promising option for improving performance. When compared to other optimization methods such as GA and PSO, they have better segmentation quality, accuracy, and stability. Lokesh P. Gagnani *et al.* [2] stated that resolving the problem of hyper parameter selection in a support vector machine is a critical task. The hybridization of simplified swarm optimization and Particle Swarm Optimization with Exchange Local Search is used to tackle this problem. The optimal parameters are provided by SSO-ELS. Due to its ease of implementation, PSO provides the best parameters. When compared to the CS-PSO approach, this will result in better classification accuracy. Mona Soliman *et al.* [3] proposed that for thermography breast cancer imaging, an effective automated computer diagnosis approach is proposed. PSO, GWO, MFO, and FA are four swarm strategies proposed in this paper. FA outperforms the others due to effective information sharing among the individuals. As a result, the pace of convergence accelerates. FA has a lesser likelihood of entrapment in local optima. B. Uma Shankar *et al.* [4] studied that the key feature of nature-inspired computation is the adaptable framework's collective synergy. In a context of uncertainty, imprecision, and ambiguity, this will lead to the integration of expert knowledge and the provision of low-cost solutions. This will solve the challenges that are complex and ill-defined. As a result, nature-inspired computers can be used to do excellent medical image analysis. M. Prema Kumar *et al.* [5] proposed that when compared to mathematical algorithms and other heuristic optimization techniques, the PSO algorithm has the following advantages: simple concept, straightforward implementation, robustness to control parameters, and computational efficiency. Thus, it provides an efficient image fusion of mammographic images. Mahua Bhattacharya *et al.* [6] suggested that in search strategy, PSO provides the maximization of the similarity metric. PSO is a global optimization technique with a high efficiency due to the low number of iterations. As a result, medical image registration is improved. IztokFister Jr *et al.* [7] carried out a brief review of nature inspired computing algorithms. A comprehensive list of all algorithms is also presented in this paper for the task of optimization. The categories in the list are divided into four, in particular Swarm intelligence based, bio-inspired based, Physics and chemistry based and other algorithms. Gabriele Magna et al. [8] proposed an artificial immune system for detecting mammographic anomalies in order to detect breast cancer. Because of its highly distributed, adaptive, and self-organizing nature, the proposed algorithm performs efficiently. Pattern recognition applications are also a result of this, when combined with learning and memory. B. V. Kavetha *et al.* [9] proposed the use of an artificial immune system (AIS) to diagnose breast cancer and it is addressed in this article. The principle of negative selection is used by AIS. This is used to do classification and discrimination of the input images. The notion of negative selection was inspired by the process of picking positive and negative patterns during image pixel mutation. The input image is classified as self-nonself discrimination by NSA. In this case, a benign tumor is considered self-patterns, while a malignant tumor is considered nonself. Because of this proposed strategy,

classification performance is improved. S. Valarmathy *et al.* [10] proposed the AIS-GA to accomplish an automatic MRI classification. Positive cases are dealt with efficiently by AIS, and the patterns it has learned can be examined explicitly. They have a self-organizing feature that reduces the amount of effort required to optimize the parameters. GA, on the other hand, is a simple population-based optimization technique that employs the appropriate objective function. It also works well in noisy conditions, with no failures for local minima or maxima. When compared to other approaches, the proposed algorithm outperforms them.

III. METHODOLOGY

Fig. 1 shows the block diagram of the Brain MRI Classification.

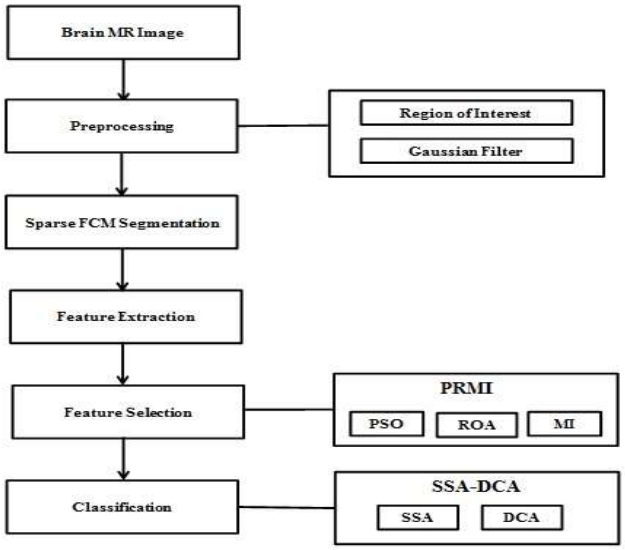


Figure 1. Block Diagram of Hybrid Classification Method [11]

In this, preprocessing is carried out with the help of region of interest (ROI) and Gaussian filter. The segmentation process is completed with the help of the sparse FCM [20]. From the segmented image, statistical features and local derivative patterns are extracted. After that, feature selection task is achieved by using the hybridization of three algorithms named as PSO [21], ROA [22] and MI and SSA DCA AIC [11]. Lastly, classification is done with the integration of the SSA [24] and DCA [23] [11].

A.PROPOSED METHODOLOGY FOR PARALLEL DATA PROCESSING

Parallel computing has traditionally been utilized for scientific computing and modeling of scientific issues, particularly in natural and technical sciences like meteorology. As a result, parallel software and hardware, and also high-performance computing, were developed. Main central processing unit (CPU) or processor manufacturers began to build power-efficient CPUs with several cores to address the concerns of power usage and overheating. The processor's core is its computational unit, and in multi-core computers, each core is autonomous and can use the same memory at the same time. Parallel computing has come to desktop PCs thanks to multi-core CPUs. As a result, parallelizing serial programs has become a common programming task.

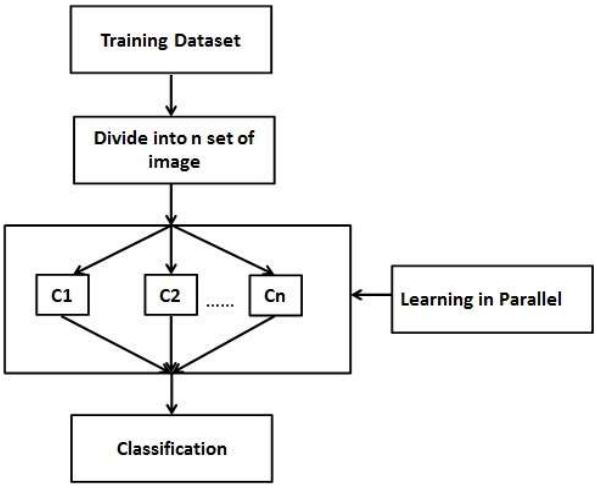


Figure 2. Proposed Block Diagram for Parallel Data Processing

Parallel processing is the use of two or more computers or processors working together to address a single problem. It is a type of computer architecture where a computation or programme is run simultaneously by several processors. By spreading the burden among several processors, each of which completes the operation simultaneously, parallel computing makes it possible to carry out large computations. Most supercomputers use parallel computing principles to operate. Another name for this method of computing is parallelization. The basic objective of parallel computing is to increase the amount of computing power available for time-saving, efficient processing.

Advantages of Parallel Data processing.

- Time can be saved by parallel data processing since it enables applications to execute faster.
- More complex problems can be quickly resolved.
- Compared to serial computing, parallel data processing is far more suitable for modeling, simulating, and understanding complex real-world phenomena. Many issues are so large and complex that addressing them on a single computer is impractical or impossible, especially with limited computer memory.

As shown in Fig. 2, multiple computer cores are used in parallel computing to deal with multiple tasks at the same time. Parallel computing, unlike serial computing, divide a major task into its component parts and multitask them. Simulating and analyzing and real-world situations are ideally suited to parallel computer systems. In this paper, the major task is to classify the brain tumor from MR images. The actual process is described in Fig. 1. To reduce the time complexity, the input brain MR image dataset is divided into equal size datasets. After that, each and every divided input dataset is processed on separate computer core. To check the efficiency of the proposed system, four performance metrics, in particular accuracy, sensitivity, specificity and time complexity are measured in the following sections.

B. THE PROPOSED ALGORITHM

Let T_F be a set of all available n training input images. The data set T_F is divided into training set T_t and testing T_{Test} as per cross validation method. In the proposed approach a

dataset is horizontally partitioned into n disjoint subsets with round robin method.

The dataset is partitioned into n subsets of data. Let $\{T_1, T_2, ...T n\}$ be the set of instances, where $T_t = T_1 \cup T_2 \cup T_{3.....} T_n$. Let $|T_t|$ is the cardinality of the training dataset where,

$$|T_t| = |T_1| + |T_2| + ...|T_n|$$

The partitioned training data is stored on separate computer core. Each computer core processes the input training data. The learning is done in parallel on n computer core. The accuracy, sensitivity and specificity are compared along with the time complexity.

The steps for proposed parallel data processing algorithm are summarized as follows:

i. Partitioning the training dataset randomly.
ii. Each dataset is processed on separate computer core in parallel.
iii. Each core applies both methods for brain tumor classification
iv. Accuracy, sensitivity and specificity are measured for the both methods.
v. Comparison and analysis of the both methods
vi. Both methods are used for the K fold analysis.
vii. Again accuracy, sensitivity and specificity are calculated.
viii. Runtime analysis is done.

IV. Experimental Results and Discussions

Assessment of the proposed strategy using brain tumor detection dataset is elaborated in this section on the basis of accuracy, sensitivity and specificity and runtime analysis. The analysis is done by varying training data and K-fold. In addition, the effectiveness of Particle Rider MI + Dendritic Cell-SSA-based AIC [11] is analyzed.

A. EXPERIMENTAL FRAMEWORK

The approach is performed in MATLAB using a PC with Windows 10 operating system, 8 GB RAM, and an Intel i3 Intel core processor.

B. DATASET DESCRIPTION

The experimentation of the Particle Rider MI+Dendritic Cell-SSA-based AIC [11] is performed using BRATS and Simulated BRATS datasets considering accuracy, sensitivity and specificity. The BRATS and Simulated BRATS datasets are taken from BRATS 2015 [19] which poses various severity levels of images. From BRATS database, 30 patients brain MRI is considered. Here, the image of every patient is collected as four modalities, like T1, T1C, T2, and FLAIR. Each modality generates from 130 to 176 brain slices that are used in the analysis. In this dataset, all the datasets are manually segmented, by one to four rates, which follow the similar annotation protocol, approved by experienced doctors.

C. EVALUATION METRICS

The performance of Particle Rider MI+Dendritic Cell-SSA-based AIC [21] is employed for analyzing the methods including accuracy, sensitivity and specificity.

$$Accuracy = \frac{T^p + T^n}{T^p + T^n + F^p + F^n}$$

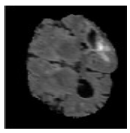
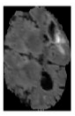
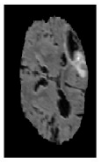
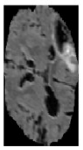
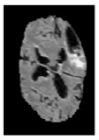
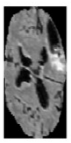
$$Sensitivity = \frac{T^p}{T^p + F^n}$$

$$Specificity = \frac{T^n}{T^n + F^p}$$

D. EXPERIMENTAL RESULTS

The experimental results are shown in **Table 1** below, with sample input brain MR images in the first column. The input brain MR images after preprocessing are shown in the second column. The third column displays segmented output brain MR images. Finally, LDP applied brain MR images are displayed in the last column. Here, the input dataset is divided into three equal size datasets named as DB1, DB2 and DB3. Later on, these partitioned input datasets are processed in parallel. Later on K-fold analysis is also performed by taking the 10 folds for the same partitioned data named as DB_K1, DB_K2 and DB_K3. Lastly, the speed up calculation due to the parallel data processing along with analysis in terms performance measure is discussed.

Table 1. Experimental analysis for sample input brain MR Image [11].

a) Input MR brain image	b) ROI extracted image	c) Segmented output image by Sparse FCM	d) LDP applied image
			
			
			

The methods employed for the analysis include: Rider Optimization Algorithm+Dendritic Cell-SSA-based AIC and Particle Rider MI+Dendritic Cell-SSA-based AIC [11].

E. COMPARATIVE ANALYSIS

The comparative analysis of the PSO+NSA, PSO+CSA, ACO+NSA, ACO+ CSA, ABC+NSA, ABC+CSA, Rider Optimization Algorithm + Dendritic SSA AIC [11] and

Particle Rider MI+Dendritic Cell-SSA-based AIC [11] with accuracy, sensitivity, and specificity parameters is evaluated. The analysis is performed for partitioned training data and K-fold analysis is also carried out for partitioned dataset.

Preliminary experimentation to verify feasibility for proposed approach.

Table 2. Analysis of various performance measures using various proposed methods for brain tumor image classification on complete, unpartitioned BRATS dataset. The performance is measured by using training data as test data.

Data set / Methods	BRATS Training Dataset		
	Accuracy (%)	Sensitivity (%)	Specificity (%)
PSO+NSA	81.78	86.70	48.12
PSO+CSA	81.94	94.77	91.87
ACO+NSA	85.36	95.16	91.96
ACO+CSA	86.24	96.43	92.06
ABC+NSA	87.45	96.60	95.35
ABC+CSA	88.75	97.02	95.45
PSO+DCA	95.22	97.19	95.75
Rider Optimization Algorithm+ Dendritic Cell-SSA_based AIC	97.69	97.50	98.00
Particle Rider MI+ Dendritic Cell- SSA-based AIC	97.79	97.58	98.00

Table 2 illustrates the analysis of the complete, un-partitioned dataset. The Particle Rider MI with dendritic cell-Squirrel Search outperforms all other methods and gives the maximum accuracy of 97.79%, sensitivity of 97.58% and specificity of 98%. This is considered as the preliminary experimentation which is used to compare with the analysis of the partitioned dataset [11].

Table 3. Analysis of various performance measures using various proposed methods for brain tumor image classification on complete, unpartitioned BRATS dataset. The performance is measured by using K fold analysis.

Data set using K Fold Analysis / Methods	BRATS Dataset for K fold Analysis		
K=10	Accuracy (%)	Sensitivity (%)	Specificity (%)
PSO+NSA	70.29	59.23	62.08
PSO+CSA	75.43	80.10	72.59
ACO+NSA	79.78	87.51	75.88
ACO+CSA	82.53	91.70	78.61
ABC+NSA	87.08	92.80	83.35
ABC+CSA	87.17	93.27	86.29
PSO+DCA	88.00	93.30	89.42
Rider Optimization Algorithm+ Dendritic Cell-SSA_based AIC	97.55	97.10	98.00
Particle Rider MI+ Dendritic Cell- SSA-based AIC	97.65	97.30	98.00

Table 3 illustrates the analysis of the unpartitioned dataset using K- fold analysis. Here, K=10 is considered. The Particle Rider MI with dendritic cell-Squirrel Search outperforms all other methods and gives the maximum accuracy of 97.65%, sensitivity of 97.30% and specificity of 98%.

The K-Folds analysis is popular and simple to comprehend, and it generally produces a less unbalanced model than other methods. Because every input image from the original dataset has a chance to appear in the training and test sets. The optimal value of k is chosen here which K=10. [11]

Analysis using the training data

The analysis of methods is performed using BRATS dataset considering reduced training data and K-fold with accuracy, sensitivity and specificity parameters. From BRATS database, 30 patients' brain MRI is considered.

Here, the image of every patient is collected as four modalities, like T1, T1C, T2, and FLAIR. Each modality poses from 130 to 176 slices of brain that are considered in the analysis. This dataset is partitioned into three equal parts consisting of 10 patients in each dataset. The three datasets are named as DB1, DB2 and DB3.

Table 4. Analysis using partitioned Training BRATS dataset DB1, DB2 and DB3

Partitioned Data set / Methods	DB1			DB2			DB3		
	ACC (%)	SEN (%)	SPE (%)	ACC (%)	SEN (%)	SPE (%)	ACC (%)	SEN (%)	SPE (%)
PSO+NSA	64.74	94.73	62.02	75.94	95.06	62.74	62.37	94.41	59.57
PSO+CSA	69.65	94.91	67.42	80.03	95.24	65.37	79.21	94.58	77.97
ACO+NSA	85.30	95.08	79.61	83.74	95.42	78.62	81.23	94.75	80.08
ACO+CSA	85.91	95.12	81.19	86.39	95.47	80.04	84.93	94.76	84.27
ABC+NSA	88.69	95.26	85.61	92.86	95.60	94.23	88.60	94.92	88.45
ABC+CSA	91.68	95.29	90.72	93.59	95.65	94.33	91.54	94.93	91.20
PSO+DCA	96.26	95.43	97.40	96.59	95.78	97.70	95.93	95.09	97.10
ROA+ Dendritic-SSA_based AIC	96.35	95.47	97.40	96.68	95.83	97.70	96.02	95.10	97.10
Particle Rider MI+ Dendritic Cell-SSA-based AIC	96.43	95.61	97.40	96.77	95.96	97.70	96.10	95.26	97.10

Table 4 illustrates the analysis of partitioned dataset. The dataset is divided into three equal sizes named as DB1, DB2 and DB3, among all the methods, the Particle Rider MI with dendritic cell-Squirrel Search gives the maximum accuracy of 96.43%, sensitivity of 95.61% and specificity of 97.40% for DB1, for DB2 the maximum accuracy of 96.77%, sensitivity of 95.96% and specificity of 97.70% and for DB3 maximum accuracy of 96.10%, sensitivity of 95.26% and specificity of 97.10%.

Analysis using K-Fold

K-Fold Analysis considering partitioned BRATS dataset. The dataset named as DB_K1, DB_K2 and DB_K3.

Table 5. Analysis using partitioned BRATS DB_K1,DB_K2 and DB_K3 using K fold analysis.

Partitioned Data set K -Fold Analysis / Methods	DB_K1			DB_K2			DB_K3		
K=10	ACC (%)	SEN (%)	SPE (%)	ACC (%)	SEN (%)	SPE (%)	ACC (%)	SEN (%)	SPE (%)
PSO+NSA	65.39	88.47	62.82	53.00	85.68	49.08	60.86	88.52	58.19
PSO+CSA	77.05	89.12	63.20	61.23	89.46	59.08	69.12	88.79	60.28
ACO+NSA	77.49	89.29	65.11	74.67	89.63	61.54	77.87	88.95	64.97
ACO+CSA	80.24	92.51	70.38	77.34	89.79	62.90	78.42	92.27	66.36
ABC+NSA	84.07	93.90	77.37	83.88	93.88	79.10	81.70	93.56	73.42
ABC+CSA	86.06	94.05	83.34	84.27	94.23	80.22	84.28	93.90	78.99
PSO+DCA	92.03	94.23	97.40	92.25	95.06	97.70	91.24	94.75	97.10
ROA+ Dendritic-SSA based AIC	92.11	94.92	97.40	92.33	95.42	97.70	91.89	95.09	97.10
PRMI+ Dendritic-SSA-based AIC	92.20	95.08	97.40	93.09	95.78	97.70	91.97	95.26	97.10

Table 5 illustrates the analysis of partitioned dataset for K-fold analysis. Here, K=10 folds are considered for every partitioned dataset. The divided datasets are named as DB_K1, DB-K2 and DB_K3, the Particle Rider MI with dendritic cell-Squirrel Search gives the maximum accuracy of 92.20%, sensitivity of 95.08% and specificity of 97.40% for DB_K1, for DB_K2 the maximum accuracy of 93.09%, sensitivity of 95.78% and specificity of 97.70% and for DB_K3 maximum accuracy of 91.97%, sensitivity of 95.26% and specificity of 97.10%.

Table 6 provides the analysis for the two optimal methods named as Rider Optimization Algorithm + Dendritic Cell-SSA based AIC and Particle Rider MI+ Dendritic Cell- SSA-based AIC which gives the better results among all the methods. This already shown in Table 5 and Table 6.

Table 6.Analysis for Partitioned BRATS dataset

Training Data / K-Fold	Metrics	Dataset is Partitioned					
		Rider Optimization Algorithm + Dendritic Cell-SSA based AIC (1) in %			Particle Rider MI+ Dendritic Cell- SSA-based AIC (2) in %		
Training Data	**Dataset**	DB1	DB2	DB3	DB1	DB2	DB3
	Accuracy (%)	96.35	**96.68**	96.02	96.43	**96.77**	96.1
	Sensitivity (%)	95.47	**95.83**	95.1	95.61	**95.96**	95.26
	Specificity (%)	97.4	**97.7**	97.1	97.4	**97.7**	97.1
K-fold K=10	**Dataset**	DB_K1	DB_K2	DB_K3	DB_K1	DB_K2	DB_K3
	Accuracy (%)	92.11	**92.33**	91.89	92.2	**93.09**	91.97
	Sensitivity (%)	94.92	**95.42**	95.09	95.08	**95.78**	95.26
	Specificity (%)	97.4	**97.7**	97.1	97.4	**97.7**	97.1

Table 7.Analysis for Partitioned BRATS and Unpartitioned dataset

		Dataset is not Partitioned		Dataset is Partitioned		Δ in %	
Training / k-fold	Metrics	Rider Optimization Algorithm+ Dendritic-SSA_ based AIC (1)	Particle RiderMI+ Dendritic Cell-SSA-based AIC (2)	(1)	(2)	Δ_1	Δ_2
Training data	Accuracy (%)	97.69	97.79	96.68	96.77	1.03	1.04
	Sensitivity (%)	97.50	97.58	95.83	95.96	1.71	1.66
	Specificity (%)	98.00	98.00	97.7	97.7	0.13	0.31
K-Fold	Accuracy (%)	97.55	97.65	92.33	93.09	5.35	4.67
	Sensitivity (%)	97.10	97.30	95.42	95.78	1.73	1.56
	Specificity (%)	98.00	98.00	97.7	97.7	0.13	0.31

Table 7 illustrates the analysis of the partitioned and unpartitioned dataset in terms of accuracy, specificity and sensitivity. The better results from partitioned data are taken into consideration for the analysis. It is observed that the slight change in the performance for the two optimal methods named as Rider Optimization Algorithm + Dendritic Cell-SSA based AIC and Particle Rider MI+ Dendritic Cell- SSA-based AIC is noticed. But the execution time is significantly improved which is shown in Table 8. Time complexity plays the measure role in brain tumor classification. The early and accelerated classification can help doctors and medical practitioners. The main purpose of this paper is to give the better classification results for brain MR image in minimum time. This is achieved with the help of the proposed parallel data processing algorithm which is shown in Fig. 2. The experimental results of the proposed parallel data processing are given in Table 8, where significant enhancement is shown in runtime analysis.

Let A_S be the accuracy, SPE_S - the specificity, and SEN_S - the sensitivity in the sequential processing. Similarly, A_P is the accuracy, SEN_P is the sensitivity, and SPE_P is the specificity in parallel processing. The following are the computations to analyze enhancement in the performance measure.

Accuracy in sequential (A_S) processing for Rider Optimization Algorithm+ Dendritic-SSA_ based AIC is

$$= \Delta_{1(A_{S1})} = \left(\frac{A_{S1} - A_{P1}}{A_{S1}} \right) * 100 = 1.03\%.$$

Sensitivity in sequential (SEN_S) processing for Rider Optimization Algorithm+ Dendritic-SSA_ based AIC is

$$\Delta_{1(SEN_{S1})} = \left(\frac{SEN_{S1} - SEN_{P1}}{SEN_{S1}} \right) * 100 = 1.71\%.$$

Specificity in sequential (SPE_S) processing for Rider Optimization Algorithm+ Dendritic-SSA_ based AIC is

$$\Delta_{1(SPE_{S1})} = \left(\frac{SPE_{S1} - SPE_{P1}}{SPE_{S1}} \right) * 100 = \text{-}0.13\%.$$

Accuracy in sequential (A_S) processing for Proposed Particle Rider MI+ Dendritic Cell- SSA-based AIC is

$$\Delta_{2(A_{S2})} = \left(\frac{A_{S2} - A_{P2}}{A_{S2}} \right) * 100 = 1.04\%.$$

Sensitivity in sequential (SEN_S) processing for Proposed Particle Rider MI+ Dendritic Cell- SSA-based AIC is

$$\Delta_{2(SEN_{S2})} = \left(\frac{SEN_{S2} - SEN_{P2}}{SEN_{S2}} \right) * 100 = 1.66\%.$$

Specificity in sequential (SPE_S) processing for Proposed Particle Rider MI+ Dendritic Cell- SSA-based AIC is

$$\Delta_{2(SPE_{S2})} = \left(\frac{SPE_{S2} - SPE_{P2}}{SPE_{S2}} \right) * 100 = 0.31\%.$$

Similarly the speed up is calculated for both methods when the K-fold analysis is used. The analysis is shown in Table 6.

Comparative discussion

Table 7 illustrates the analysis of PSO+NSA, PSO+CSA, ACO+NSA, ACO+ CSA, ABC+NSA, ABC+CSA, **Rider Optimization Algorithm + Dendritic Cell-SSA based AIC**[11] **and Particle Rider MI+ Dendritic Cell- SSA-based AIC**[11] for partitioned BRATS dataset as well as complete BRATS dataset considering training data percentage and K-Fold. The Dendritic Cell-SSA-AIC has the maximum performance in terms of accuracy, sensitivity, and specificity when used with MRI for brain tumour classification. This is because AIC classifiers are trained with Dendritic Cell-SSA, which has a high convergence momentum and accuracy. The computational complexity of segmentation based on Sparse FCM is reduced. The Particle Rider MI's feature selection method selects the most informative features, resulting in the highest classification accuracy. Furthermore, the AIC classifier is self-organizing and necessitates good characteristics. As a result, the new strategy improves overall speed while reducing errors. Tables 9 and 10 indicate that the ROA+ Dendritic Cell-SSA based AIC and Particle Rider MI+ Dendritic-SSA-based AIC methods use less time than alternative techniques. These methods eliminate the problems that existing techniques have, such as high time consumption, low convergence rate, low efficiency, and accuracy specificity and sensitivity.

Table 8 illustrates the analysis based on the time

Table 8. Analysis based on time

Sr. No	Name of the Method	Execution Time in Sec.		Speed Up in %
		In Sequence (T_S) (Dataset not Partitioned)	In Parallel (T_P) (Dataset is Partitioned)	Delta (Δ)
1	PSO+NSA	44.49	9.36	78.97
2	PSO+CSA	39.21	5.64	85.61
3	ACO+NSA	37.21	6.50	82.52
4	ACO+CSA	44.88	6.48	85.57
5	ABC+NSA	41.93	10.64	74.63
6	ABC+CSA	43.90	10.59	75.88
7	PSO+DCA	43.57	0.03	99.94
8	**Rider Optimization Algorithm +Dendritic Cell-SSA_based AIC**	**37.39**	**0.03**	**99.92**
9	**Particle RiderMI+DendriticCell-SSA-based AIC**	**39.31**	**0.02**	**99.94**

$$\Delta = \left(\frac{T_S - T_P}{T_S} \right) * 100,$$

where, Δ is the speed up parameter, T_S is the execution time when the dataset is not partitioned, and T_P is the execution time when the dataset is partitioned for parallel processing.

Table 8 illustrates the analysis based on the time when the dataset is partitioned into equal sizes. It is observed that the Rider Optimization Algorithm +Dendritic Cell-SSA based AIC and Particle Rider MI+Dendritic Cell-SSA-based AIC gives better results in addition to lower execution time when it is compared to other methods. By comparing Table 6 and Table 7, it is observed that when the dataset is partitioned into equal sizes and they are processed in parallel on three cores, the time complexity is improved significantly with preserving accuracy, sensitivity and specificity. Here, the number of partitioned datasets and the number of core for processing is same. This is also explained in Fig. 3, which depicts the stepwise task.

V. Conclusions

This paper presents the analysis of ROA+ Dendritic Cell-SSA based AIC and Particle Rider MI+ Dendritic Cell- SSA-based AIC in the parallel environment for the task of brain tumor classification. A novel parallel environment is proposed to reduce the time complexity. The experimental results show that the proposed technique works efficiently and the time complexity is improved up to 99.94% for Particle Rider MI+ Dendritic- SSA-based AIC and 99.92% for ROA+ Dendritic Cell-SSA based AIC. This is due to the feature of parallel computing to run the method more effectively by executing a large number of computations over different multiple cores. As a result, significant delays in model computation from learning to classification are avoided. For brain tumor classification, initially, Gaussian filters and Region of interest are used for removing noise and artifacts present in the image. Then, Sparse Fuzzy C Means clustering is applied for segmentation task. After that, statistical features and texture features are extracted in the feature extraction task. Lastly, The Particle Rider Mutual Information is employed for feature

selection which is developed by combining Particle Swarm Optimization, Rider Optimization Algorithm, and mutual information. Finally, the brain tumor classification is performed with the help of Artificial Immune Classifier, which is trained using dendritic cell-SSA algorithm which is the combination of the dendritic cell algorithm and squirrel search algorithm. The methods provide superior performance with maximal accuracy of 96.77%, sensitivity of 95.97%, and specificity of 97.70%. For K-fold analysis, the maximum accuracy of 93.08%, sensitivity of 95.79%, and specificity of 97.70%. Other MR Image datasets will be used in the future to calculate the efficiency of the suggested technique. Furthermore, enhanced optimization using deep learning approaches will be investigated in order to improve the efficiency of existing methods.

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