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Brain MRI Segmentation Using an Improved Bat Optimization Algorithm

W. Renhua[1,*]

[1] Department of Electronic Engineering, Tsinghua University, Beijing, China

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ABSTRACT

Magnetic Resonance Imaging (MRI) is a non-invasive and widely adopted diagnostic modality that provides high-resolution information for the assessment of neurological disorders and the characterization of brain structures. Accurate segmentation of brain MRI images is a fundamental step in computer-aided medical image analysis because it enables the identification and spatial delineation of anatomical regions and provides essential information for subsequent diagnostic and clinical decision-making processes. However, conventional manual segmentation performed by radiologists is time-consuming, labor-intensive, and subject to inter- and intra-observer variability. Moreover, the complex morphology and intensity variations of soft tissues, together with image noise and system-induced artifacts, can substantially reduce segmentation accuracy and make the reliable identification of tissue boundaries challenging. To address these limitations, this study proposes an automated brain MRI segmentation framework based on an Improved Bat Optimization Algorithm (IBOA). The proposed approach integrates the global search capability of the bat-inspired optimization mechanism with the K-means clustering algorithm, in which the optimization procedure is employed to determine more appropriate initial cluster centroids. This hybrid strategy aims to reduce the sensitivity of conventional K-means clustering to the random initialization of centroids and consequently improve the reliability and accuracy of the segmentation process. The performance of the proposed framework is evaluated through quantitative simulations implemented in the MATLAB environment and is benchmarked against alternative state-of-the-art segmentation approaches. The experimental results demonstrate that the proposed method achieves a segmentation accuracy of 99.5%, consistently outperforming the considered baseline methods. These findings indicate that the integration of metaheuristic optimization with clustering-based segmentation can provide an effective computational framework for accurate and automated analysis of brain MRI images. The proposed method therefore offers considerable potential for supporting computer-aided brain image analysis and reducing the limitations associated with conventional manual segmentation.

1. INTRODUCTION

Clustering is a foundational analytical methodology within machine learning and data mining, aimed at partitioning data vectors into distinct groups such that highly homogeneous samples are localized within the same

[*] Corresponding Author: weirenhua@gmail.com
Department of Electronic Engineering, Tsinghua University, Beijing, China

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cluster while heterogeneous samples are segregated. Operating in an unsupervised manner without requiring historical class labels, this technique uncovers latent structural topographies within high-dimensional datasets. Consequently, it aids in data pattern analysis, structural dimensionality reduction, and feature pre-processing for down-stream machine learning tasks. The technical significance of clustering becomes particularly prominent when processing massive volumes of big data where manual annotations are unavailable or costly to curate [1-3].

The application areas of clustering span broadly across diverse industrial sectors and scientific domains. In targeted marketing, customer clustering facilitates data-driven market segmentation and personalized service delivery. In computational biology and clinical medicine, clustering specific gene expression profiles or histopathological tissue samples can significantly enhance diagnostic precision and biomolecular data interpretation. Furthermore, in computer vision and digital image processing, clustering serves as a primary tool for image segmentation, object isolation, and automated descriptor extraction. Previous research has also demonstrated the effectiveness of vocabulary-based image representation and fuzzy weighting strategies for improving image classification performance, highlighting the importance of appropriate feature representation and weighting in image analysis [20].

Within wireless sensor networks (WSNs) and Internet of Things (IoT) frameworks, cluster-based node topologies optimize energy dissipation and prolong net network longevity [4-7].

Despite its high architectural significance, clustering introduces several prominent theoretical and computational challenges. One of the most critical bottlenecks is determining the mathematically optimal number of clusters (k), which is often evaluated heuristically or via unsupervised validity indices. Additionally, sensitivity to high-frequency noise and spatial outliers, severe computational complexity when scaling to massive datasets, and the presence of non-linear, non-convex data topologies complicate data partitioning. Conventional partitional algorithms such as standard K-means or hierarchical clustering frequently exhibit poor performance under non-ideal conditions, demonstrating extreme sensitivity to initial seed initialization and an inherent tendency to get trapped in sub-optimal local minima.

To overcome these architectural limitations, evolutionary computation and swarm intelligence frameworks are widely deployed. Metaheuristics such as the Genetic Algorithm (GA), Particle Swarm Optimization (PSO), and the Bat Optimization Algorithm possess the mathematical capability to globally explore the complex search landscape of cluster configurations. By instantiating a stochastic population of candidate solution vectors, enforcing evolutionary selection mechanics, and dynamically updating multi-agent position coordinates, these algorithms successfully escape local traps. This endows the hybrid system with enhanced flexibility and robustness when partitioning hyper-dimensional, non-linear data structures [8-12].

In summary, hybridizing data clustering with evolutionary optimization paradigms facilitates the attainment of highly accurate, stable, and reproducible solutions. This combined approach finds extensive utilization in big data analytics, biological data processing, high-resolution image and video segmentation, and advanced industrial monitoring. Leveraging this hybrid execution yields superior segmentation alignment, lower objective minimization error, enhanced model generalization, and efficient feature learning from complex datasets.

2. EXISTING METHODS

Several digital image segmentation methodologies have been proposed across various literature sources. In study [1], the process of brain tumor extraction is investigated, where second-order texture descriptors specifically contrast, correlation, energy, and homogeneity are computed. During the pre-processing phase, high-frequency background noise is suppressed utilizing a median filter. Subsequently, the spatial region exhibiting the maximum signal intensity is isolated as the prospective tumor mass. Finally, the processed images are categorized using a Support Vector Machine (SVM). The mean classification accuracy of this framework reached 93.05%, demonstrating an enhanced operational profile over conventional baseline models.

Paper [2] provides a comprehensive review of diverse segmentation techniques tailored for tumor-bearing brain MRI scans, including artificial neural networks, edge-detection operators, intensity thresholding, and partitional clustering. Brain MRI slices are frequently characterized by inherent noise artifacts and intensity inhomogeneity (bias field), rendering precise tissue segmentation a highly complex task. Furthermore, the high morphological variability in the shape, spatial position, and volumetric size of tumors significantly complicates the segmentation pipeline. This comparative study was conducted to identify and isolate the mathematically optimal approach for brain MRI tissue partitioning.

Brain tumor segmentation aims to delineate the pathological tumor volume from surrounding cranial tissues, such as adipose tissue, edema, healthy gray/white matter, and cerebrospinal fluid (CSF). One foundational strategy exploited in this domain is intensity thresholding. In this approach, decision-making is executed directly based on the gray-level intensity values of individual pixels; specifically, if the gray-scale intensity of a pixel exceeds a predefined threshold, its value is substituted with a maximum value (maxval), otherwise, it is forced to zero (black background). In study [4], this thresholding strategy was evaluated using 14 tumor-bearing brain MRI scans. The empirical profiles verified that this method can differentiate the tumor mass from adjacent cerebral tissues, and the resulting segmentation masks were validated against ground-truth tumor volumes.

In paper [5], a novel unsupervised brain tissue segmentation algorithm is introduced that seamlessly integrates anatomical prior knowledge with the 3D structural characteristics of volumetric images. Incorporating spatial priors restricts the optimization search space for each specific tissue class, thereby increasing the computational throughput of the algorithm. To benchmark its execution, a synthetic digital brain phantom dataset was generated, upon which extensive validation experiments were conducted.

In the digitizing and computer-aided analysis of clinical MRI scans, brain tumor segmentation constitutes a critical and decisive challenge for accurate clinical diagnosis; hence, the segmentation framework must be precise, stable, and computationally efficient.

Clustering algorithms have been widely adopted to satisfy these requirements. In study [6], standard K-means (KM) and Fuzzy C-means (FCM) clustering algorithms are deployed to isolate and extract brain tumor boundaries. A comparative analysis between these two partitional paradigms indicates that the FCM algorithm delivers superior performance; the segmentation precision achieved via the FCM approach was reported at 93%. More recent research has further demonstrated that advanced deep-learning architectures combining residual U-Net structures with Transformer layers can substantially improve medical image segmentation, particularly for tumor localization, by capturing both local and long-range spatial dependencies [21].

In paper [7], a multi-faceted approach for brain MRI classification and structural tumor segmentation is evaluated. High-fidelity tumor extraction is uniquely critical in neuro-oncology due to the structural complexity of human brain anatomy. In this research, high-level features are extracted by factoring in structural parameters such as spatial configuration, morphology, dimensions, and positional coordinates within the image matrix. Following descriptor extraction, a tumor classification pipeline is executed to distinguish the pathological tumor volumes from healthy cerebral tissues.

3. PROPOSED METHODOLOGY

The proposed methodology is driven by a hybrid architecture combining the K-means clustering algorithm and an Improved Bat Optimization Algorithm. The mathematical and operational steps of the proposed framework are detailed below.

3.1. The K-means Algorithm

The K-means method is a classical unsupervised learning algorithm extensively applied to resolve partitioning and clustering problems in machine learning [13-15]. Machine learning paradigms are generally divided into supervised and unsupervised learning categories. Supervised learning models a function that maps an incoming input vector to an output space based on historical, labeled training pairs (input-target couples), thus requiring explicit data annotations. Conversely, unsupervised clustering uncovers structural patterns without pre-existing labels.

In K-means clustering, the core mathematical objective is to minimize intra-cluster variance (the distance between observations belonging to the same cluster) while maximizing inter-cluster separation (the distance between distinct cluster partitions). Consequently, data points assigned to an identical cluster are forced close together in the feature space, while separate clusters are pushed apart, ensuring high internal cohesion and distinct cluster separation.

The standard operational pipeline of the K-means algorithm is structured as follows:

Initialize Cluster Count: Define the target number of desired cluster partitions (k).

Seed Initial Centroids: Randomly assign an initial spatial coordinate to serve as the centroid for each of the k clusters.

Compute Proximity Metrics: Calculate the Euclidean distance from every discrete data observation to all k cluster centroids.

Assign Data Points: Map each data observation to its nearest spatial centroid.

Update Cluster Centroids: Recompute the coordinates of each centroid by calculating the mathematical mean of all data observations assigned to that specific cluster partition.

Iterate for Convergence: Recursively loop through steps 3 to 5 until the centroid coordinates stabilize (i.e., spatial displacement falls below a defined tolerance threshold), signifying global algorithmic convergence.

3.2. Improved Bat Optimization Algorithm

The Bat Optimization Algorithm is an evolutionary, swarm intelligence-based metaheuristic. It was developed by mimicking the foraging behavior of microbats and their unique capacity to navigate and detect prey using echolocation. The core concept of the metaheuristic is that each individual bat represents a candidate solution vector within the problem search space. By dynamically adjusting its position and velocity vector while traversing this space, the swarm iteratively converges toward the global optimum [16-17].

Within the operational loop of the Bat Algorithm, each bat is characterized by a dynamic frequency, velocity, and position vector, which are updated iteratively. The frequency parameter governs the step size and spatial exploration reach of the bat, velocity dictates the rate of position modification, and the position coordinates define the current candidate solution in the objective landscape.

Furthermore, two critical parameters namely loudness (A) and pulse emission rate (r) regulate the behavioral dynamics of the swarm. The loudness typically decays mathematically as the individual approaches an optimal solution, whereas the pulse emission rate increases progressively. This dynamic interplay preserves a strict balance between global exploration and local exploitation.

Due to its mathematical simplicity, rapid convergence characteristics, and exceptional flexibility in solving continuous and combinatorial optimization problems, the Bat Algorithm has been extensively adopted across engineering, machine learning, network optimization, and image processing. Moreover, it can be hybridized with alternative heuristics such as the Genetic Algorithm (GA) or Particle Swarm Optimization (PSO) to boost its accuracy in hyper-complex optimization landscapes.

A major advantage of the Bat Algorithm is its intrinsic capacity to maintain a fine-tuned trade-off between broad search-space exploration and localized solution exploitation. This characteristic prevents the population from stagnating in sub-optimal local minima, significantly increasing the probability of discovering the global maximum or minimum. Consequently, this algorithm has attracted substantial interest for resolving challenging, real-world engineering optimization, industrial scheduling, and intelligent system design problems.

The Improved Bat Algorithm (IBA) is an advanced, augmented variant of the classical Bat Algorithm engineered to enhance numerical precision and optimization throughput when handling highly complex search landscapes, such as multi-UAV path planning in highly dynamic environments. In this variant, several mathematical modifications are applied to overcome the structural limitations of the baseline algorithm including insufficient search coverage, premature convergence, stagnation in local optima, and low population diversity. Specifically, incorporating a bounded sine function, a dynamic expansion factor, and a non-linear modulation mapping broadens the spatial search boundaries, limits premature stagnation, and drastically reduces the probability of getting trapped in local minima.

Furthermore, genetic operators are embedded within the optimization loop to maintain an effective population pool, ensuring high structural diversity and preventing performance degradation over successive iterations. To optimize initial target allocation, the A^* pathfinding algorithm is deployed as a pre-initializer; subsequently, by hybridizing the Hungarian assignment method with genetic crossover operations, the target search envelope is expanded, substantially upgrading solution quality. These architectural enhancements accelerate the global convergence rate and boost optimization accuracy. Experimental results demonstrate that the Improved Bat Algorithm significantly outperforms both the classical BA and competitive metaheuristics like the Chaotic Cuckoo Search Whale Optimization Algorithm (CCWOA) and the Opposition-Based Uniform Mutation Particle Swarm Optimization Algorithm (OUMPOA) in tracking and trajectory mapping, yielding a 34.64\% improvement in the fitness function value and a 30.29\% reduction in convergence time relative to the baseline Bat Algorithm [18].

3.3. Core Steps of the Proposed Methodology

The comprehensive execution blueprint of the proposed framework which seamlessly hybridizes the Improved Bat Algorithm (IBA) and K-means clustering (Figure 1) is structured sequentially through the following operational phases:

Data Acquisition and Pre-processing: First, the raw input data corpus, comprising medical images or specific target data arrays, is compiled and subjected to standardized pre-processing pipelines. This critical preliminary phase encompasses high-frequency noise suppression, data intensity normalization, and tensor transformation to format the dataset appropriately for downstream optimization and clustering routines.

Initial Cluster Assignment (K-means Initialization): In this stage, the standard K-means algorithm is executed to establish a preliminary partitioning of the data space into discrete clusters. The target cluster count (k) is defined, and initial centroids are initialized. The data points are iteratively mapped to their nearest spatial centroids, and the cluster centers are updated recursively until mathematical convergence is achieved. This step effectively bounds and structures the search space, providing localized initialization constraints for the subsequent heuristic optimization phase.

Centroid Optimization via the Improved Bat Algorithm: Following the initial cluster allocation, the Improved Bat Algorithm is applied to globally optimize the spatial localization of the cluster centers and discover superior partitioning topographies. During this evolutionary phase, structural modifications specifically the incorporation of a bounded sine modulation function, a dynamic expansion factor, and non-linear mapping functions are enforced. These operators expand the search envelope, limit premature population stagnation, and mitigate the probability of the swarm getting trapped in sub-optimal local minima.

Population Diversity Maintenance via Genetic Operators: To counter the natural decay of population diversity inherent to the baseline Bat Algorithm and bolster the probability of discovering global optima, genetic algorithm (GA) operations are concurrently integrated into the optimization loop. This hybrid configuration ensures that the candidate cluster centroids and their corresponding search trajectories maintain high structural diversity, empowering the multi-agent system to explore the global objective landscape thoroughly.

Terminal Partitioning and Data Classification: Upon termination of the metaheuristic optimization phase, the definitive optimized cluster centroids are extracted, and every data vector is systematically mapped to its optimal partition. This terminal phase executes a final proximity evaluation, calculating the distance of each data point to the optimized centroids to establish conclusive cluster membership boundaries.

Performance Evaluation and Validation: Finally, the operational throughput of the proposed hybrid methodology is rigorously quantified using robust statistical metrics, including classification accuracy, precision, sensitivity, and convergence velocity. The resulting performance profiles are benchmarked against conventional baseline models to validate the empirical efficacy of combining K-means partitioning with the Improved Bat Algorithm.

Here is the professional, publication-ready English translation of the Figure 1 caption and Section 4 (Simulation Results), incorporating precise medical image segmentation and metaheuristic optimization terminology.

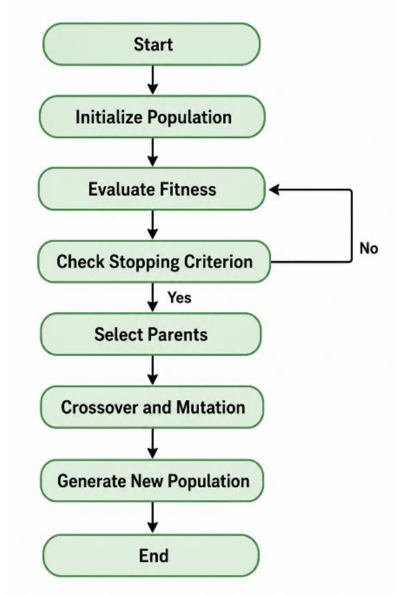

Fig. 1. Flowchart of the proposed methodology.

4. SIMULATION RESULTS

The proposed methodology and the existing comparative techniques were implemented within the MATLAB software environment developed by MathWorks. The hardware configuration utilized for the simulations consisted of an Intel(R) Core™ i5-4460 CPU @ 3.2 GHz processor equipped with 16 GB of Random Access Memory (RAM). The initialized operational parameters for the Bat Optimization Algorithm are compiled in Table 1.

Table 1. Parameters of the Bat Optimization Algorithm.

Parameter Name	Description	Value
$r0$	Initial Pulse Emission Rate	0.5
$\propto$	Positive Constant 1	0.99
γ	Positive Constant 2	0.01
Population	Population Size	20
Iteration	Maximum Iterations	100

These parameters were tuned to establish an optimal balance between the convergence speed and the classification precision of the algorithm. The hybrid K-means and Improved Bat Algorithm framework was applied to brain MRI scans, such as the sample illustrated in Figure 2, and the corresponding segmentation output partitioned into four distinct clusters is displayed in Figure 3. Furthermore, the optimization convergence profile tracking the objective function minimization for each processed image is illustrated in Figure 4.

To comprehensively validate the diagnostic efficacy of the proposed framework, evaluation trials were conducted on a cohort of 300 sample images extracted from the benchmark Brain Tumor Dataset hosted on figshare.com [19]. The comparative benchmarking results regarding the classification accuracy of the evaluated algorithms are plotted in Figure 5.

The principal architectural advantage of the proposed framework over existing state-of-the-art approaches lies in the optimal determination of initial cluster centroids driven by the Improved Bat Algorithm. Effectively, by seamlessly hybridizing the localized partitioning capabilities of the K-means routine with the global exploration mechanics of the Improved Bat Algorithm, the net clustering performance and tissue segmentation throughput are substantially enhanced.

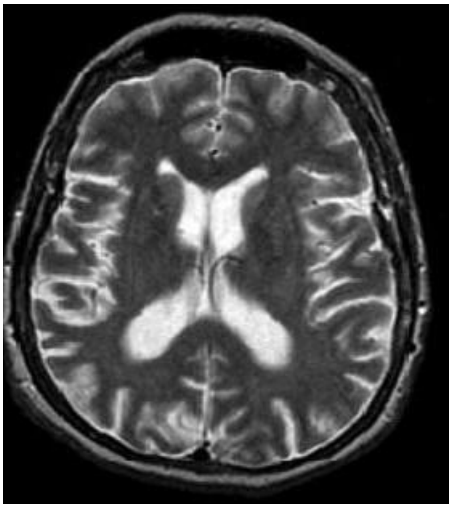

Fig. 2. Representative sample of brain MRI scans.

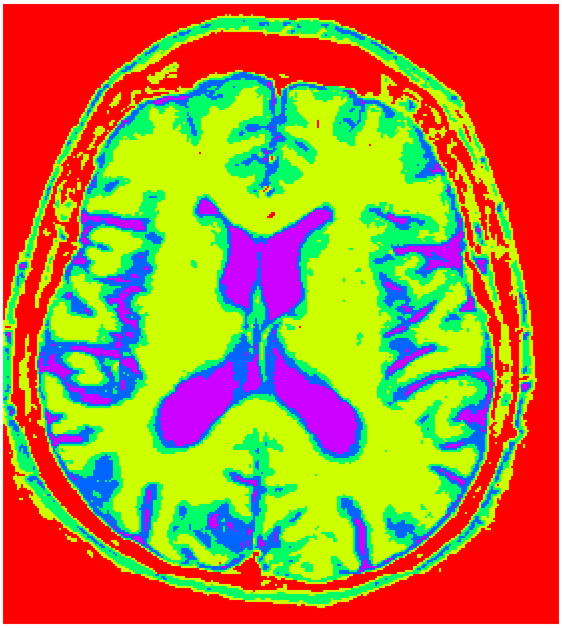

Fig. 3. Implementation output of the proposed methodology on the above image.

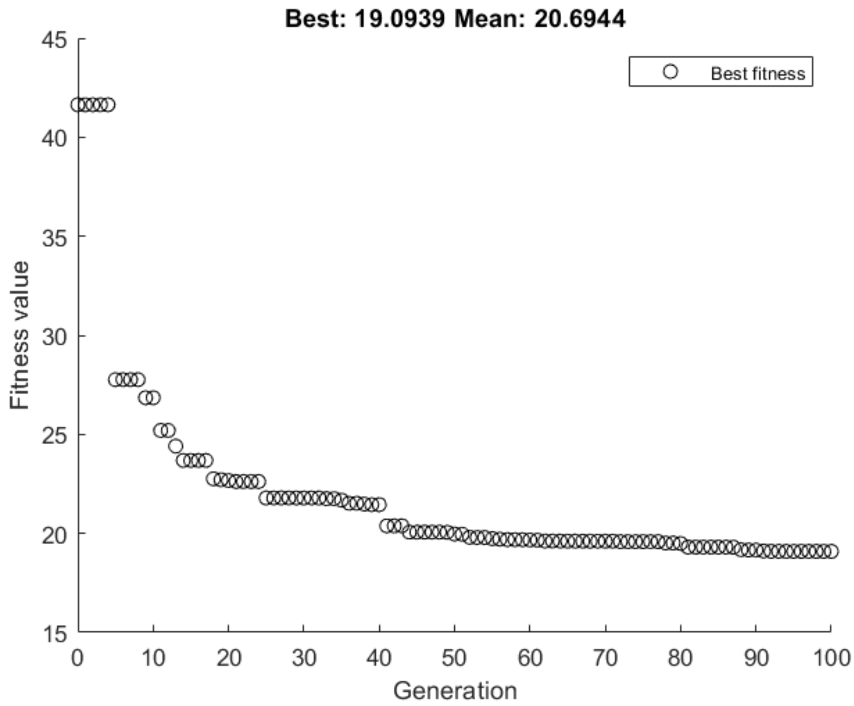

Fig. 4. Optimization convergence profile.

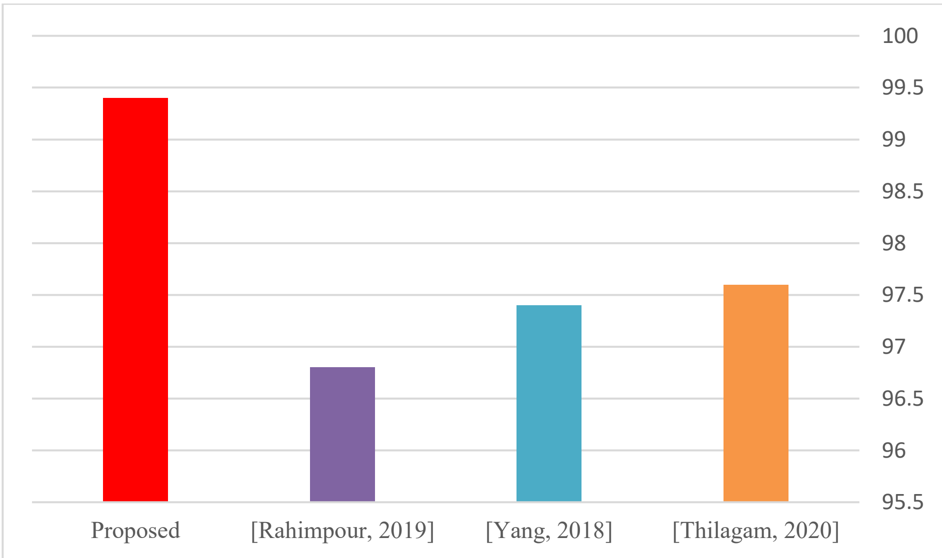

Fig. 5. Comparative accuracy analysis between the proposed method and existing state-of-the-art approaches.

5. CONCLUSION

The empirical findings of this study demonstrate that hybridizing the K-means clustering algorithm with the Improved Bat Algorithm (IBA) provides a highly effective and robust paradigm for data clustering and image segmentation. Utilizing the K-means routine as a preliminary initialization phase substantially accelerates the overall optimization process and establishes mathematically sound baseline clusters. Building upon this initialization, the

Improved Bat Algorithm augmented with specialized architectural modifications including a bounded sine modulation function, a dynamic expansion factor, and non-linear mapping operators successfully broadens the search envelope, mitigates premature population stagnation, and dramatically refines the fidelity of the final cluster configurations.

Comprehensive simulation profiles and comparative evaluations verify that the proposed hybrid methodology yields superior classification accuracy, enhanced precision, and optimized convergence latency compared to conventional baseline frameworks. In conclusion, this study validates that the intelligent integration of partitional clustering routines with evolutionary metaheuristics can significantly elevate the structural performance of complex data-driven systems, offering a highly reliable and stable solution for diverse medical image processing applications.

Declaration

We acknowledge that we used ChatGPT to enhance the academic writing of our manuscript while ensuring the originality and integrity of our work.

Transparency Statement

The data supporting this study are available upon reasonable request to the corresponding author, subject to ethical and confidentiality considerations.

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Declaration of Interest

The authors declare that they have no competing interests.

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