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Enhancing MRI-based Early Brain Tumor Detection with Entropy-driven Fuzzy C-Means and Elephant Herding Optimization.

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Abstract

Accurate and rapid brain tumor segmentation in Magnetic Resonance Imaging (MRI) remains a critical challenge for early diagnosis and effective treatment. Conventional methods often struggle with inherent tumor heterogeneity (variations in solid tumor, edema, necrosis) and noise, leading to segmentation inaccuracies. This work presents a novel hybrid approach specifically designed to address these limitations. It combines Entropy-driven Fuzzy C-Means (EnFCM) and Elephant Herding Optimization (EHO) algorithms. EnFCM, a novel contribution, utilizes information entropy to optimize the clustering of brain tissues and tumor sub-regions. This effectively handles the issue of overlapping intensities in MRI scans, where tissues might have similar intensity values. EHO, inspired by elephant herding behavior, further refines the cluster centers (centroids) identified by EnFCM. This iterative process enhances segmentation accuracy by ensuring optimal positioning within complex tumor regions.

This combined EnFCM-EHO approach tackles limitations associated with noise and complex tumor characteristics, potentially leading to faster and more precise segmentation results. The proposed method's effectiveness is evaluated on the BraTS benchmark dataset. Keywords: Elephant Herding Optimisation (EHO), Entropy-based Fuzzy C- means clustering (EnFCM), Brain Tumour Segmentation (BraTS) dataset, Magnetic resonance imaging (MRI).

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1. Introduction

A tumour is a malformed mass or bulge of cells that forms as a result of unrestricted cell growth and division. Non-cancerous benign tumours often grow slowly(Li, Set al.,2023).One of the remarkable aspects of these infections is that they tend to remain localized and do not spread to nearby tissues or migrate throughout the body; they appear to stay in one area. Although they are not malignant, if they push on neighbouring tissues or organs, they can nevertheless lead to complications. Malignant tumours are malignant growths that have the ability to spread into adjacent tissues and metastasize to other areas of the body. Malignant tumours are more hazardous and, if left untreated, can be fatal.

The brain's cortex, breast, lungs, as well as numerous other organs and tissues, are just a few of the bodily areas where tumours can develop. The place of origin, dimension, and kind of a tumour all affect its manifestations and signs(Abdusalomovet al.,2023).It is crucial to seek medical advice from a qualified practitioner for an accurate assessment and diagnosis if someone has concerns about having a tumour or is exhibiting worrying symptoms. Clinicians may perform essential examinations and imaging procedures to identify the type of tumour and create a successful approach to therapy. Individuals never be afraid to ask for medical help if they have concerns regarding a tumour or another illness because early discovery and prompt medical intervention can result in improved treatment results.

Although brain tumours can develop at any stage of life, some forms are more frequent in certain ages. The likelihood of developing a brain tumour tends to rise with ageing with rates peaking in the 65+ age group. About 2% of all instances of cancer are caused by brain tumours. In India, an estimated 30,000 new instances of brain tumours are identified every year(Ramaraj, K et al.,2022). Even though they are less frequent than certain other cancers, brain tumours can nonetheless have a profound effect on patients and their families. The type of tumour, where it is located, the patient's age, and their general health are all important considerations when determining the future outlook for brain tumours. Though certain brain tumours can be more successfully treated than others, some have a better prognosis. The average 5-year survival rate for all varieties of brain tumours is roughly 36%. Surgery, radiation exposure, chemotherapy, personalised therapy, and immunotherapy are all possible forms of therapies for brain tumours(Miao, Y et al.,2023). The course of medication is determined by the grade, spot, and dimension of the tumour in addition to the patient's general condition.

Migraines, epilepsy, difficulties with remembering, psychological and behavioural modifications, trouble communicating, speech slurring, complications in understanding language, trouble paying attention, disorientation, alterations in judgement, problems in coordination as well as balancing, fluctuating emotions, anger, mood disorders, vision impairment, double sight, decrease in peripheral sight, tinnitus are some of the typical manifestations of brain tumours(Zhang, R et al.,2023). A medical expert should be consulted for a precise assessment and diagnosis, as similar signs may also be brought on by a number of other diseases.

The majority of brain tumours have an unknown specific source. When brain cells proliferate abnormally, brain tumours can form, although the cause of this unusual development is frequently unknown (Walbert, T. and Stec, N.E., 2023). The possibility of getting brain tumours has, however, been linked to a number of risk factors and genetic disorders. Ages between 40 and 70, biological variables, heritage, being subjected to enormous amounts of ionising radiation, impaired systems of immunity, variables related to the environment, and perpetual usage of cell phones are a few examples of potential reasons and associated risks.

The greatest opportunity for a successful treatment frequently comes from a cancer diagnosis made when it is most treatable. Investigations reveal that early identification of cancer using screening methods may preserve human lives in the case of certain cancers. Only those at higher risk are advised to get screening testing for other malignancies (Mitusova, K et al., 2022). The following techniques are used to identify tumours: (i) During a physical examination, the physician may search for anomalies that could be signs of cancer, like alterations in skin tone or an expansion of an organ; (ii) Laboratory examinations - Blood and urine tests, complete blood counts can identify an unusually high or low WBC; (iii) Imaging tests - Scans such as CT scans, bone scans, MRIs, PET scans, ultrasounds, and X-rays may be used to diagnose cancer; (iv) Biopsy: A physician takes a small number of cells to be examined in a lab. There are numerous approaches to sample collection. Most of the time, a biopsy is required to make a certain cancer diagnosis. Physicians examine specimens of cells using a microscope in a laboratory setting. Normal cells have a consistent appearance, comparable dimensions, and a well-organized layout. Cancer cells appear less organized, with a range of sizes and no discernible organization.

Viewing internal bodily tissue, organs, skeletons, and many other structures using an MRI, a non-invasive method (Ramaraj, K et al., 2022). It creates interior images of the body using radio waves and powerful magnetic fields. MRI scanners create cross-sectional, 3D images of the human body without the use of radiation, in contrast to X-ray and CT scans. MRI is frequently used by medical professionals to observe body parts that are difficult to see using other imaging methods. Cardiovascular disease, ischemic stroke, muscular and bone abnormalities, tumours, and numerous other medical conditions can all be diagnosed with MR imaging. A strong magnet and radio waves are used in an MRI to take segments of our body as pictures. The resulting slices are put together to produce intricate representations of the interior of our body that can highlight potential tumour sites. MRI produces images of the body's soft tissue regions, which can occasionally be difficult to observe with other imaging techniques. Some malignancies can be found and located with great accuracy using MRI. A contrast agent, which is a particular dye that may occasionally be infused into the veins prior to or during our MRI examination, may cause tumors to appear brighter in the images. It may assist in choosing the most appropriate course of medication and show whether a malignancy has progressed.

Medical image processing includes the use and investigation of human body 3D image collections, typically from a CT or MRI scanner, to identify diseases, direct healthcare procedures like surgical preparation, or for study. Images are made better for human

interpretation as a result(Asif, S et al.,2023). Images can be analyzed, and data can be extracted for automated assessment. Any specified density as well as contrast can be achieved by manipulating the image's pixels. Images may be conveniently stored and accessed. Research on medical image processing focuses on creating software and methods that allow for the automatic or semi-automatic extraction of essential details from clinical images. The process of identifying and extracting areas of interest (ROIs) from 2D/3D images of various image modalities is known as medical image segmentation. By separating just relevant areas, medical picture segmentation enables a more accurate examination of anatomical information, which is one of its main advantages. With the use of segmentation for medical imaging, entities may be easily identified, their pixels can be divided into groups, and computer vision models can be trained using this method of labelling.

A prevalent method called clustering entails dividing pixels into groups that reflect their similarity, with each cluster accounting for a segment. A clustering method's fundamental goal is to arrange unlabeled pixels into homogenous groups with the greatest degree of similarity, i.e., to accomplish the greatest degree of similarity within the clusters and the greatest degree of dissimilarity between the clusters(Cao, L et al., 2023). The two primary types of clustering methods, hard and soft, can be generally divided based on the cluster development. The data items are grouped using a technique called hard clustering, where each item is exclusively ascribed to one cluster. A technique for grouping data items so that a single item can reside in several clusters is called soft clustering.

The most prevalent clustering technique, fuzzy c-means clustering (FCM), improves the efficiency of clustering by periodically revising the membership degree and the cluster centres. The main metrics used to assess the FCM algorithm's effectiveness are within cluster compactness and between cluster divergence. The main advantages of FCM are (i) that it performs most effectively with overlapped data sets and is superior to the k-means algorithm in this regard; and (ii) that unlike k-means, where each data point ought to merely correspond to one cluster centre, where each data point has been allocated membership to each cluster centre, allowing data points to belong to multiple cluster centres(Ramaraj, K et al.,2020). The shortcomings of FCM are (i) Apriori definition of the number of clusters (ii) FCM can be computationally more costly than conventional methods of clustering, as they require optimization over many membership degrees (iii) Selecting the appropriate amount of clusters and membership functions may be difficult, and might necessitate specialist expertise or an extensive amount of experimentation (iv) Euclidean distance calculations can inequitably weigh the underlying variables and (v) For minimum value of β , the better outcome may achieve as well as number of iterations are increased.

The EnFCM algorithm, which uses entropy-based fuzzy clustering, operates using a similarity threshold. In contrast to FCM, EnFCM uses actual cluster centres that are selected from the data points(Moradi, M et al.,2023). The quantity and calibre of clusters can be altered by altering this variable. Here, the data points' entropy values are initially estimated, and the data point with the lowest entropy value is chosen as the cluster centre. The data points are grouped according to a threshold level of similarity in this iterative technique.

Outliers are data points that are not chosen for inclusion in any of the clusters. The EnFCM helps generate better clusters with a maximum of related pixels.

An optimization problem, such as maximizing or minimizing an objective function, can be used to describe nearly all tasks in image processing. More intricate and expansive mathematical representations are needed to solve image processing challenges, resulting in the need for more effective optimization methods. In the area of image processing, machine learning and optimization are becoming more significant. The Metaheuristics Algorithm (MA) excels at resolving certain NP-hard problems and quickly locating the ideal or nearly ideal solution. Such algorithms have gained a lot of popularity because of their benefits, which include being simple to build, eliminating local optima, and being adaptable and versatile. The Elephant Herding Optimization (EHO) algorithm is one of the Swarm intelligence optimization algorithms (Abidi, M.H et al., 2023). Two operators in this algorithm—the clan updating operator and the separating operator—define the elephants' herding behaviour. EHO can offer less time-intensive solutions to challenging real-world issues.

To recognize and extract the cancer and non-tumor sections from MR brain pictures, a hybrid automated system has been created. This technique combines EnFCM for clustering operations and EHO for improved optimization. On the dataset from the Brats challenge, the effectiveness of the generated algorithm was examined. The segmented results are contrasted with their respective in-repository ground truth images. To determine the effectiveness of the proposed strategy, performance metrics are compared to the results of cutting-edge methodologies.

The most important contributions of this research are outlined below:

- The combination of the EHO-EnFCM technique is proposed in this article as an innovative approach for segmenting tumour and non-tumor sections.
- We use a method to dramatically improve dissection accuracy, enabling it to concentrate only on the complete tumour part while removing extraneous data.
- The proposed technique has been extensively evaluated for brain tumour segmentation applications on several BraTS datasets. Our system has shown substantial enhancements for the delineation of increased and central brain tumour parts in regard to a variety of performance criteria, proving the viability of the presented approach.

The manuscript is structured as follows: Section 1 introduces the motivation behind the work and the contribution delivered. Section 2 represents the review on segmentation approaches employed by previous researchers. Section 3 defines the dataset utilized. Section 4 exemplifies the background works and the proposed hybrid technique. Section 5 demonstrates and discusses the proposed method outcomes. The conclusion of the work is signified in Section 6.

The following segment reviews and provides illustrations of the results, benefits, and drawbacks of the several studies that have examined the segmentation of brain tumours using various clustering and optimization strategies in the last few years.

A Convolutional neural network approach was introduced by Malathi et al. (2019) for automatic segmentation of tumors. Additionally, it utilizes a high-quality gliomas brain picture from the BRATS 2015 database. With the use of tensor flow, which implements high-level mathematical operations utilizing anaconda frameworks, the proposed study segments brain tumors. The outcome demonstrates that the employed strategy aids in boosting tumor detection as well as tumor specification to the solely tumor site.

A brain tumor segmentation and classification method based on automatic discriminative learning was proposed by Balaha and Hassan (2023) utilizing the Sparrow Search Algorithm (SpaSA), a metaheuristic optimizer. UNet models are used in the segmentation process. Using pre-trained CNN models, learning as well as SpaSA optimization are carried out. Two different dataset kinds are produced. One has two classes, whereas the other has four. 99.19% accuracy is the average. Eleven related papers are compared with the proposed strategy.

The current systems could be more effective in pinpointing the tumor's precise location and concealed edge features with the least amount of computational effort. In their research, Kurdi et al., (2023) applied the Harris Hawks optimized convolution network (HHOCNN) to address these problems. The candidate region approach uses the notion of line segments to study border regions, which minimizes the loss of concealed edge features. With fault tolerance, CNN computes the precise location of the tumor. Utilizing MATLAB to develop the suggested HHOCNN system, its performance was assessed using metrics for pixel accuracy, accuracy, error rate, specificity, and sensitivity. The Harris Hawks optimization approach, which draws inspiration from nature, reduces the misclassification error rate and raises the overall tumor identification rate to 98% on the Kaggle dataset.

Zheng et al., (2023) use zernike moments to determine the primary image characteristics, and for the final diagnosis, a support vector machine-based optimal classification methodology is applied. A modified arithmetic optimization is employed to optimize image segmentation, resulting in a very effective system. The suggested method is tested on the Figshare dataset, and the segmented outcomes are compared with six distance methods to demonstrate the effectiveness of the developed system.

Ren et al., (2023) developed a completely novel pipeline technique for the MRI-based automated cancer diagnosis. The features that are pertinent are first extracted from the pre-processed source images that have been provided. The best ANN is then used to incorporate the features into a diagnosis method. The courtship learning-based water strider algorithm is an enhanced metaheuristic that determines both feature selection and classification. The suggested system's effectiveness has been evaluated using the Brain-Tumor-Progression dataset.

Deep CNN and significant data augmentation methods were used by (Sajjad et al., 2019). to develop a method for grading brain tumours. They used the expanded dataset to train a deep CNN and then used a test set of MRI images to assess its performance. The findings demonstrated that CNN was very accurate in its ability to categorize brain tumours into distinct categories and that the model's performance had been enhanced by the utilization of data augmentation approaches.

An investigation on recognizing and categorization of tumours using classifiers based on DL approaches that extract features from MR brain images was presented by Habiba et al. (2022). Utilizing the InceptionV3 and DenseNet201 models, the authors used a publically accessible repository and a transfer learning methodology. In order to enhance the classification outcomes and prevent overfitting, data augmentation was used. Six densely linked convolutional layers formed the Brain-Deep Net model, a deep CNN that extracts features from dense layers. Compared to the other models, the dense layers are more effective in extracting features from brain MRI. With a classification accuracy of 96.3%, the model was able to identify the three distinct brain tumors types.

A DL approach was put forth by Ranjbarzadehet al., (2021) to identify the tumour from brain MRI . The pre-processing phase solves the overfitting and computational complexity problems. On the BraTS 2018 tumour dataset, segmentation was carried out using a cascade CNN, which produced better dice score values. The many SOTA methods for segmenting liver tumours were covered by Gul et al. (2022). The traditional research results and dataset information are compared and reviewed in this work. Future scholars can acknowledge those strategies by looking at the performance measures of traditional methodologies.

BrainMRNet, a tumour dissection technique that uses CNN and hypercolumn algorithms for feature extraction, was introduced by Togacar et al. (2020). Despite whether augmentation methods were utilised or not, this procedure produced superior results and was substantially more effective than alternative ways. To assess the effectiveness of the algorithm, the measured metric values are contrasted with traditional approaches. In order to create an automatic segmentation method for neck and head cancers in CT and PET images, Oreiller et al. (2022) employed U-net . The new approach produced a dice value of 75.91% when dissecting the overall tumour volume.

A relative entropy-based fuzzy clustering approach was proposed by Zarinbal et al. (2014). As a metric of cluster variation, relative entropy is a function of the variance between two distributions. The cluster distinction is optimized by the developed technique by minimizing distances inside the clusters. The effectiveness of the recommended approach for separating the noise was evaluated using seven assessments, three statistical representations, datasets of the iris plant, and three images. Relevant membership degrees were subsequently allocated for the findings recorded. The proposed method delivers the most precise outcomes in all cases for membership degree assignment and noise recognition.

By altering the training set, Cocoscoet al. (2003) introduced a novel technique for identifying oddities from brain tissues . For lowering samples from earlier tissue probability maps made by an erroneous mark, the minimum spanning tree is utilised. These samples are then used by the K-NN classifier to recognise the infected tissues in the brain image.

Employing a Hidden Markov Random Field (HMRF) System with Expect-Maximization, Zhang et al. (2001) automatically segmented brain MR images. This HMRF methodology is computationally expensive, more susceptible to noise, and rarely produces findings that are reliable. For the purpose of enhancing brain MRI, Rajinikanth et al. (2017) established a technique employing meta-heuristic to extract the central tumour and edoema . This

technique integrates entropy, Teaching Learning based optimisation, and active contour-based segmentation. On FLAIR, T1-CE, and T2 images, the suggested technique was tested.

By introducing an energy reduction strategy to create the geodesic active region, Firouzian et al.(2011) developed a technique for autonomously dissecting intracranial aneurysm in CTA images . On 11 datasets, the method was tested, and the dissected outcomes are significantly more accurate than those displayed by manual segmentation.

Using computational intelligence and artificial intelligence, Chaudhury and Sau (2023) proposed an automatic segmentation approach for identifying breast cancer from raw medical images. When compared to traditional recurrent neural networks (RNNs), the Gated Recurrent Units (GRU) perform better. Testing the developed algorithm on the Wisconsin Diagnostic Breast Cancer (WDBC) dataset confirmed its effectiveness.

Heidari et al. (2023) used the DL algorithm to classify lung cancer based on aggressiveness and identify the malignant lung nodules in lung CT images . Federated Learning (FL), which uses blockchain for data authentication, is used to train the model. Patients with lung cancer are categorised in local mode using the CapsNets approach. The CIA dataset, Kaggle Data Science Bowl (KDSB), LUNA 16, and the local dataset were used to train and test the recommended technique. Finally, in-depth tests of the proposed approach are carried out using Python and some of its well-known libraries, including Scikit-Learn and TensorFlow.

Although earlier research has improved the detection and delineation of abnormalities in multimodal images, the performance metric values still have the opportunity to improve. In this study, a novel EHO-EnFCM algorithm is suggested to improve the rate of accuracy and DC while also speeding up the calculation. No researchers tested or disseminated the combination of the generated techniques among the wider community of scientists.

2. Methods

2.1 Dataset Description

A brain tumour segmentation dataset called BraTS is composed of both real and synthetic images, with each of them being segmented into high- and low-grade gliomas (HG and LG). The collection includes gliomas images with a variety of grades acquired in multiple sequences(Ramaraj, K et al. ,2021). BraTS images are gathered from many organizations at standard medical examinations, employing dedicated scanner and imaging methods. The quality of images produced by these data collection methods varies greatly and can represent a variety of clinical interventions.

2.2 EHO - Elephant Herding Optimization

Elephants are sociable animals that reside in families made up of females and their young. One of the biggest mammals in Africa and Asia is the elephant. There are various subspecies of elephants in both Asia and Africa. Elephants use a subsonic vibration that transmits quicker than sound over ground along with air for interpersonal interaction over large distances(Wu, Z.Qet al. ,2023). Elephant males communicate with their clan by sending low-

frequency vibrations. The optimization method has been modeled after the traits of elephants, which include living in clans under the direction of a matriarch and separating the male elephants from their clan once they attain puberty. The males typically reside elsewhere, whereas females choose to reside with relatives. Until they entirely separate from their families, they will progressively become detached from them. After researching actual elephant herding behaviour, Wang et al. created the EHO method that they proposed in 2015. In EHO, the following presumptions are taken into account.

I. The elephant population is made up of a few clans with predetermined amounts of elephants.

II. In every generation, a preassigned number of male elephants will detached from their clan to resideseparately inn remote area from the chief elephant community.

III. Elephants in every clan will be led by a matriarch.

Clan updating operators

Elephants belong to different clans coexist peacefully under the leadership of a matriarch. Each clan comprises aprecise number of elephants. For the intent of modelling, we consider that every clan comprises an identical number of elephants at all times. The matriarchal bond affected the elephant's position in the clan. This behavior is accomplished using the Clan Updating operator in the EHO technique.

All elephants of a clan reside united beneath the matriarch's control, based on the specifications given. The matriarch C_i in a clan C_i has an impact on each elephant's newly amended position within that clan. The elephant j 's amended position in the C_i clan can be determined by

$$x_{new,ci,j} = x_{ci,j} + \alpha * (x_{best,ci} - x_{ci,j}) * r \quad (1)$$

Where,

$x_{new,ci,j}$ = elephant new position j in clan C_i

$x_{ci,j}$ = elephant old position j in clan C_i

$x_{best,ci}$ = best elephant in the clan C_i ie. Matriarch

α = scale factor range [0,1]

The best elephant in all clan is evaluatedby

$$x_{new,ci,j} = \beta * x_{center,ci} \quad (2)$$

Where,

β = scale factor [0,1], whichregulates the impact of $x_{center,ci}$ on assessing the best one.

$x_{new,ci,j}$ = new individual elephant

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$x_{center,ci}$ = Center individual of clan ci

The center individual is

$$x_{center,ci,d} = \frac{1}{n_{ci}} * \sum_{j=1}^{n_{ci}} x_{ci,j,d} \quad (3)$$

Where,

n_{ci} = elephants count in clan ci

$x_{ci,j,d}$ = d^{th} dimension of $x_{ci,j}$, where $(1 \leq d \leq D)$

The clan ci centre is modified by (3)

Separating operator

Once a male elephant attains adulthood, he is allowed to reside independently and is expelled from the family herd. Consider that each new generation of adult male elephants is kept apart from the clan group. As a result, in the EHO method, the iterative process functions as a separation operator.

An individual elephant with the least fitness in each group incorporates the separation operator and is represented as

$$x_{worst,ci} = x_{min} + (x_{max} - x_{min} + 1) * rand \quad (4)$$

Where,

$x_{worst,ci}$ = worst individual in clan ci

x_{min} = lower bound

x_{max} = upper bound

$rand$ = stochastic distribution [0,1]

Figure 1 shows the EHO technique's pseudo code.

```

(1) Begin
(2) Initialization. Set the initialize iterations  $G = 1$ ; initialize the population  $P$  randomly; set maximum generation  $MaxGen$ .
(3) While stopping criterion is not met do
(4)   Sort the population according to fitness of individuals.
(5)   For all clans  $ci$  do
(6)     For elephant  $j$  in the clan  $ci$  do
(7)       Generate  $x_{new, ci, j}$  and update  $x_{ci, j}$  by Equation (1).
(8)       If  $x_{ci, j} = x_{best, ci}$  then
(9)         Generate  $x_{new, ci, j}$  and update  $x_{ci, j}$  by Equation (2).
(10)      End if
(11)     End for
(12)   End for
(13)   For all clans  $ci$  do
(14)     Replace the worst individual  $ci$  by Equation (4).
(15)   End for
(16)   Evaluate each elephant individual according to its position.
(17)    $T = T + 1$ .
(18) End while
(19) End.

```

Figure 1. Pseudo code of EHO

2.3 Fuzzy C-means algorithm (FCM)

Fuzzy C-means (FCM) algorithm, which was established by Bezdek after Dunn originally suggested it. A data point's membership values can be determined by FCM, which can then iteratively modify the values according to the predetermined number of clusters (Amiya, G et al., 2022). A data point can therefore belong to any cluster that has associated membership values.

Here are the most significant advantages of clustering:

1. the ease with which noisy data and outliers can be handled;
2. the capacity to handle data containing multiple sorts of variables.

Consider $X = \{x_1, x_2, \dots, x_n\}$ is the finite set of elements and $v = \{v_1, v_2, \dots, v_c\}$ as the cluster center.

The objective function of FCM is;

$$J_{FCM} = \sum_{i=1}^N \sum_{j=1}^c u_{ij}^m \|x_i - v_j\|^2 \quad (5)$$

Where,

N – samples count

c – clusters count

m – fuzzy exponent, ($m > 1$)

x_i – grayscale at i^{th} pixel (k- dimensional data measured)

v_j – cluster center (d- dimensional)

u_{ij} – membership degree of x_i in the cluster j , ($0 \leq u_{ij} \leq 1$)

$\|x_i - v_j\|^2$ – Euclidean distance between i^{th} pixel and cluster center v_j

The membership function u_{ij} is,

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$$u_{ij} = \frac{1}{\sum_{k=1}^c (\|x_i - v_j\|^2 / \|x_i - v_k\|^2)^{1/(m-1)}} \quad (6)$$

The cluster center v_j is,

$$v_j = \frac{\sum_{i=1}^N u_{ij}^m x_i}{\sum_{i=1}^N u_{ij}^m} \quad (7)$$

Till it satisfies the termination condition, continuing the iteration process, $\max_{ij} \left\{ \left| u_{ij}^{(k+1)} - u_{ij}^{(k)} \right| \right\} < \varepsilon$

Where, ε – stopping criterion between 0 and 1

k – iteration counts

This approach is affined to a J_{FCM} local minimum. In the noiseless image, FCM produces improved accuracy and is especially responsive to noisy images. By including greyscale and local information between pixels in the FCM clustering, effectiveness is increased.

2.4 Entropy-based Fuzzy Clustering (EnFCM)

In accordance with the degree of similarity at every point in the data, entropy is determined. The data point in the centre of the cluster exhibits a relatively small entropy value, making it more probable that it will be selected as the cluster core. The initial cluster node is proposed to be the data point with the lowest entropy. Data points are removed from the cluster centre selection list if they fall below a threshold equivalent to this cluster centre in the subsequent rounds (Cardone, B et al., 2023). The data points that closely resemble the chosen cluster centre should fit there with the greatest likelihood, and it is uncertain whether they belong to any other cluster centres. Till there are no more data points, the iteration will be repeated. This approach has benefits over more traditional ones in that (i) there are fewer computation challenges because the entropy is assessed once, and (ii) fewer parameters are required for the calculation.

Entropy parameter tends to offer the below mentioned things while processing images:

1. The entropy values of each pixel are considered.
2. A pixel with a low entropy value is picked to represent the centre of the cluster and is margined over a specific area in the image.
3. FCM will then explore clustering the pixels that share the cluster core most closely or have a high degree of similarity.
4. Additional pixels with differences are grouped under other clusters for better organization.
5. This operation causes border cohesion/overlap while marginating the pixels, and it also takes longer overall to build the boundaries.

Consider a set of N data points in M -dimension, where a vector of M values (i.e., $x_{i1}, x_{i2}, \dots, x_{iM}$) represents each data point x_i , $i = 1, \dots, N$. In the range $[0.0, 1.0]$, the values of each dimension are standardized.

The Euclidean distance between any two data points (e.g., i and j) is assessed as

$$D_{ij} = \sqrt{\sum_{k=1}^M (X_{ik} - X_{jk})^2} \quad (8)$$

where, D_{ij} = distance between the x_i and x_j data points.

The similarity between any two points can be determined as

$$S_{ij} = e^{-\alpha D_{ij}} \quad (9)$$

where S_{ij} is the similarity between x_i and x_j normalized in the range [0.0, 1.0].

Entropy concerning another data point at one data point is:

$$E = -S \log_2 S - (1 - S) \log_2 (1 - S) \quad (10)$$

where S is the similarity measure and E assumes a maximum of 1.0 if S is 0.5, and the least of 0.0 if S is 0.0 or 1.0. At data point x_i , the average entropy for all other data points is calculated as:

$$E_i = -\sum_{j \in X}^{j \neq i} (S_{ij} \log_2 S_{ij} + (1 - S_{ij}) \log_2 (1 - S_{ij})) \quad (11)$$

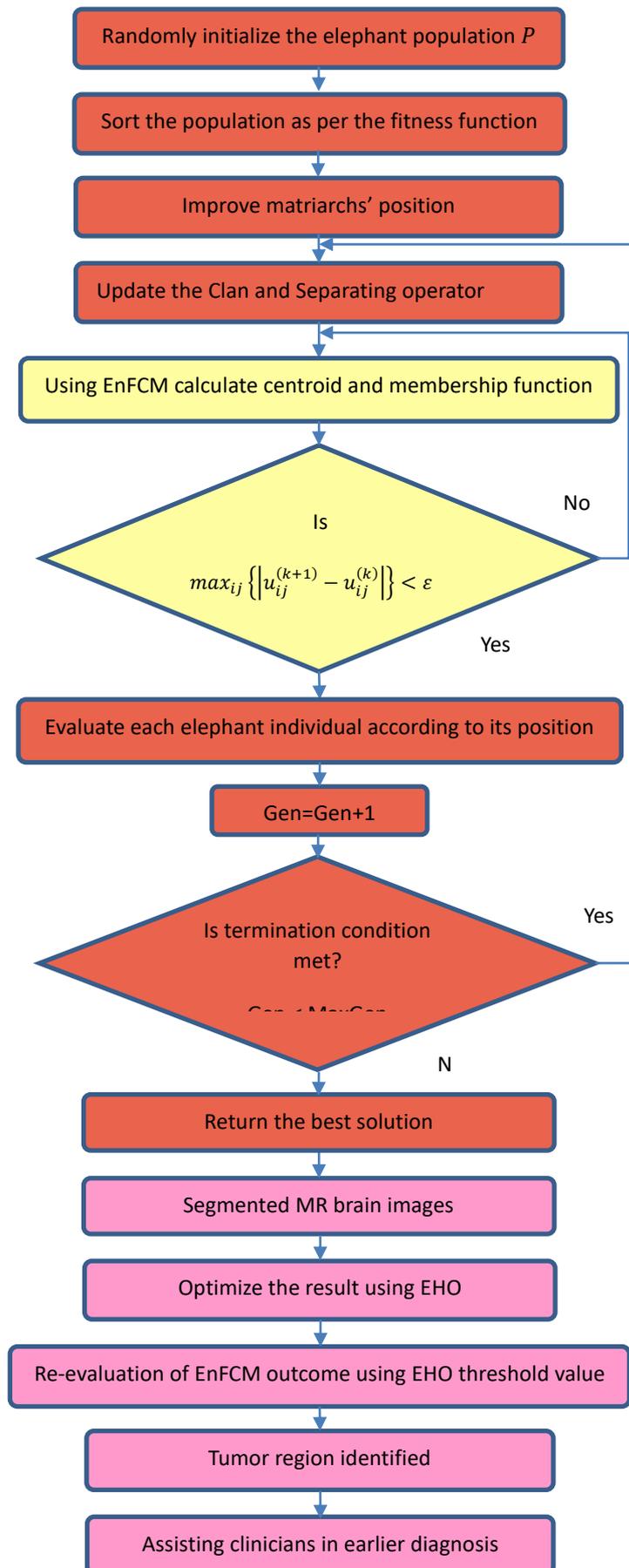


Figure 2. Workflow for EHO-EnFCM Technique

If similarity against distance is shown, a larger curvature for a large α value will be exist in the curve. The similarity value is allotted as 0.5 to automatically calculate α , only when the two data point's distance have a mean distance of all data point pairs, and it is represented as, $\alpha = -\ln 0.5/\bar{D}$

Where, \bar{D} - mean distance among the data points pairs.

The threshold is among the data points in the same cluster, according to the interpretation of the β parameter, which can be thought of as a resemblance or correlation. The range of β is in between [0.0, 1.0]. The input data with N data points are represented by the threshold value ' T ' in the algorithm.

The Entropy-based Fuzzy Clustering (EnFCM) algorithm is given below:

1. Calculate entropy for every x_i in T for $i = 1, \dots, N$.
2. Choose $x_{i_{min}}$ with the least entropy.
3. Reject $x_{i_{min}}$ and the data points having similarity with $x_{i_{min}}$ larger than β from T .
4. If T is not becomes empty then go to Step 2.
5. $x_{i_{corr}}$ (To account for the objective function for accurate and vulnerable clustering, a new parameter has been offered as the initial of its kind, ensuring that the boundaries between the clusters are depicted with no cohesiveness, disorientation, or blurred vision) signifies the correlated datapoint that are lower than β and in acquiesce/belonging to the threshold T .

$$x_{i_{corr}} \leq \beta \in T \quad (12)$$

5. Therefore, the minimum FCM objective function can be modified or reformulated as follows:

$$J(U, C) = \sum_{i=1}^N \sum_{j=1}^C (u_{ij})^m \|x_{i_{corr}} - c_j\|, 1 \leq m \leq \infty \quad (13)$$

2.5 Proposed EHO based EnFCM Clustering:

The suggested approach uses EnFCM clustering and the EHO algorithm to precisely identify and delineate any anomalies existing in the brain MRI. Figure 2 depicts the proposed method's execution.

3 Results

The newly developed EHO-EnFCM approach discovered and fragmented the tumour region visible in the MR images, aiding in an earlier identification. The efficacy of the dissection outcomes of the developed technique is validated by comparing it with their respective ground truth images. Figure 3 displays the results of segmenting BraTS MR images using the EHO-EnFCM method.

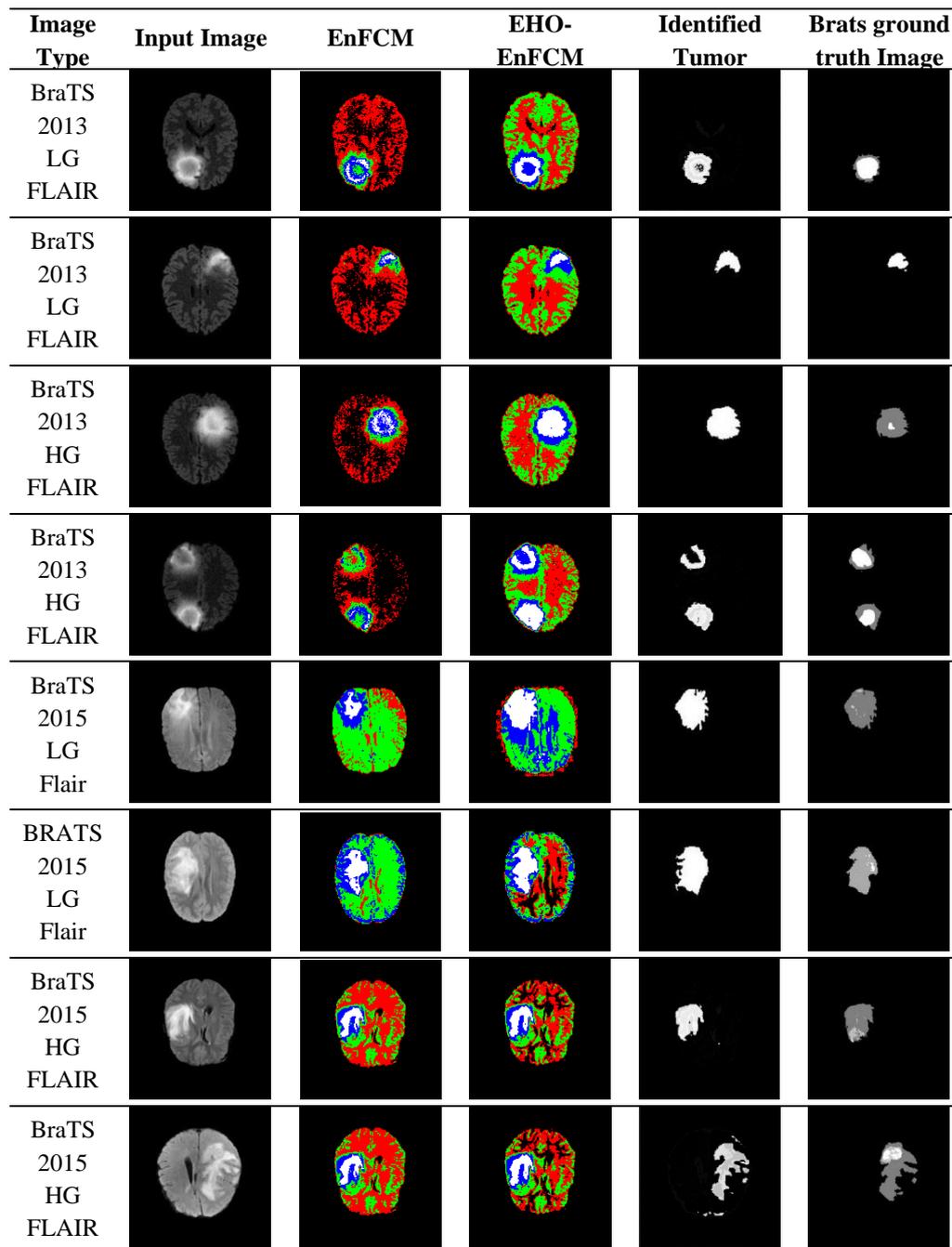


Figure 3. Segmented outcomes of developed EHO-EnFCM algorithm

The developed algorithm's performance measures, including Tanimoto coefficient index (TC), mean squared error (MSE), dice score (DS), peak signal to noise ratio (PSNR), and computing time (T), are assessed and shown in Table 1 and 2.

Table 1. Performance metrics

Performance Metrics	Formula	Description
Mean Squared Error (MSE)	$MSE = \frac{1}{CD} \sum_{i=0}^{C-1} \sum_{j=0}^{D-1} [A(i,j) - B(i,j)]^2$	When looking for inequalities, the MSE is the sum of the squared errors

	Where, C - rows D - columns i - rows'incremental operator j - columns'incremental operator	between the input (A) and dissected (B) images.
Peak Signal to Noise Ratio (PSNR)	$PSNR = 10 \log_{10} \left(\frac{Peak\ Value^2}{MSE} \right)$	PSNR in dB is a measure of the quality between the input and the segmented image. The better quality is indicated by an elevated PSNR level.
Tanimoto Co-efficient index (TC)	$T(A, G) = \frac{ A \cap G }{ A \cup G }$	The term TC refers to the ratio between the intersection and union over the pixels that comprise the input and golden images. The pixel similarity between the input's pixels and the golden image is quantified as DS. The bigger amount of comparable pixels present in both pictures is indicated by an elevated DS.
Dice Score (DS)	$D(A, G) = 2 \times \frac{T(A, G)}{1 + T(A, G)}$	The algorithm's computing time, expressed in seconds, indicates how long it took to finish the tumor delineation operation.
Computational Time (T)	NA	

Table 2 Performance metric values of proposed algorithm

Data resource	TIME	MSE	PSNR	TC	DS
BraTS Challenge Dataset	27.34	0.3067	53.2981	58.0497	80.1212
	27.58	0.3193	53.1231	57.5378	79.0521
	26.16	0.2556	54.0886	59.1461	79.2907
	27.14	0.2724	53.8130	59.6745	80.4956
	26.70	0.2731	53.8020	58.1525	80.0431
	26.66	0.2583	54.0441	57.5488	79.0834
	27.43	0.2944	53.4750	56.0985	80.2070
	25.86	0.3199	53.1145	59.9806	79.9319
	25.81	0.2832	53.6440	56.8906	80.7672
	25.01	0.2517	54.1561	55.8948	79.5889
	27.86	0.2643	53.9431	56.2128	80.9894

	26.53	0.3064	53.3021	55.3850	80.9651
	27.10	0.2848	53.6199	58.7678	80.3245
	27.47	0.3165	53.1607	56.1506	80.1553
	25.77	0.2788	53.7118	59.5731	79.3731
	26.05	0.2981	53.4208	55.7011	79.4034
	25.83	0.3137	53.2003	58.8856	80.6473
	25.99	0.3091	53.2644	59.6507	80.6379
	25.53	0.2800	53.6926	57.4057	79.9314
	27.50	0.2958	53.4543	58.4739	80.4670
AVG	26.57	0.29	53.57	57.76	80.07

4 Discussion

The following is a description of the mean performance values obtained for segmenting the tumour from multiple BraTS datasets: The attained average computational time, MSE, PSNR, TC and DS are 26.57 Sec, 0.29, 53.57 dB, 57.76 % and 80.07 %, respectively.

The DC values acquired by conventional researchers while analysing similar datasets are contrasted to the Dice Score values gained through the new EHO-EnFCM methodology on testing various BraTS datasets. Figure 4 shows a comparison of the aforementioned DC values.

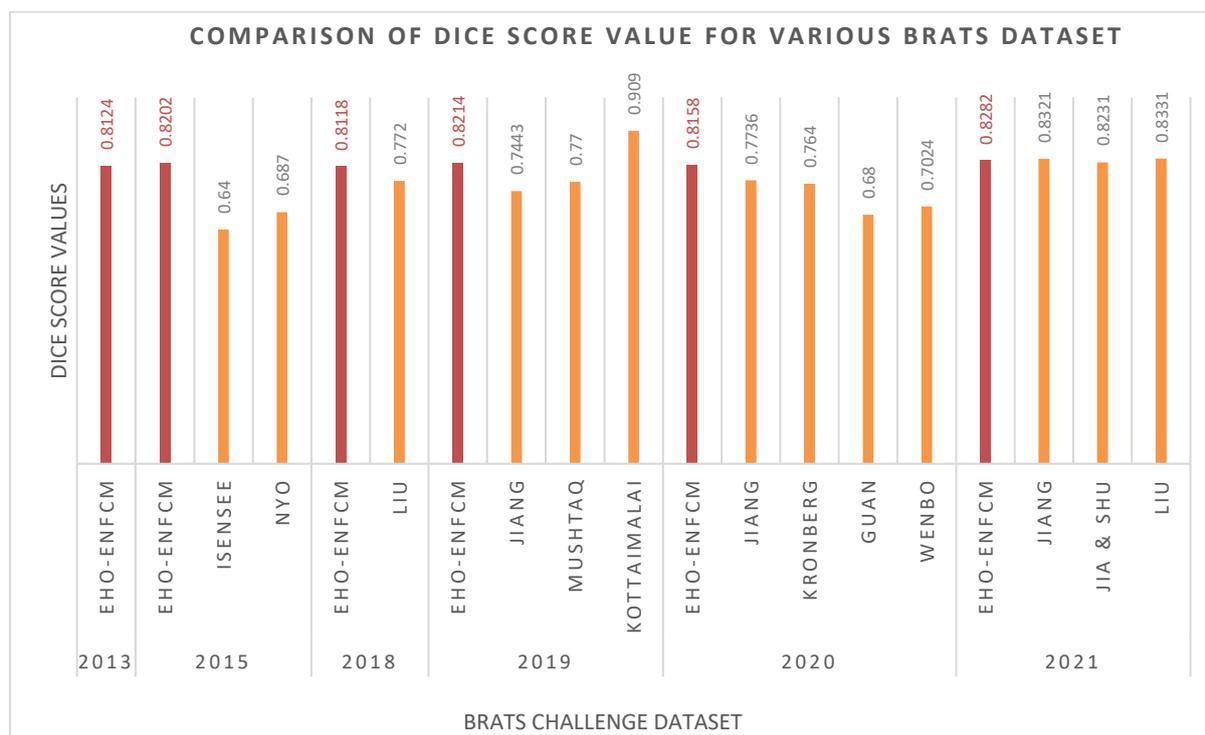


Figure 4. Comparison of DC values

The novel contribution of the proposed work is listed below: Utilization of fuzzy c means clustering itself has few shortcomings include boundary overlapping, intensity inhomogeneity and increased computational time. This can be overcome by the integration of entropy values

of the pixels (change in pixels) with conventional FCM. The EHO algorithm assists in forming the optimized clusters with less computational complexity. The hybrid algorithm delivers better tumor segmented outcomes with superior performance metric values.

5 Conclusion

The clusters' local approximations of the pixels are recognised, and similarities between them are determined. Elephant herding habit imitates and helps generate clusters of like pixels that resemble the development of a clan. The recommended approach assists in processing brain MR images that are complicated by issues including noise invasion, intensity inhomogeneity, and atypical tumours in a variety of dimensions, forms, and positions. The tumor dissected images are verified with the corresponding ground truth images to determine the resemblance. As a result, the innovative EHO and EnFCM approach produces a value of 80.07% as a dice score.

On images with single or numerous tumours and varied forms and spots, the proposed EHO-EnFCM approach performed exceptionally well. These logical conclusions might open the door to precise disease identification in patients. The suggested approach could be incorporated into therapeutic procedures to allow accurate estimation of strangeness throughout therapy, leading to faster diagnosis. The segmented results unambiguously demonstrate that cancers are broken down in a respectable amount of time and that by maximizing the variable, this process might speed up even more. The future direction of the research aims to improve PSNR, TC, and DS while reducing MSE and time for computation.

Declarations

Ethical Approval

Not Applicable

Competing interests

The authors have no competing interests.

Author's contributions

Baiju Karun: Conceptualization, Methodology, Software, Writing - Original Draft
Arunprasath Thiyagarajan: Supervision, Data Curation, Writing - Review & Editing
Pallikonda Rajasekaran Murugan: Writing - Review & Editing, Investigation
Rakhee Makreri: Writing - Review & Editing, Formal analysis, Methodology
Kottaimalai Ramaraj: Visualization, Formal analysis, Methodology

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Availability of data and materials

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