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Research Article

Detecting Brain Tumors Using an Adapted DE Algorithm with the Otsu Technique

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ABSTRACT

Brain tumors require precise and prompt detection techniques because they pose a serious challenge to medical diagnosis and treatment. In order to improve brain tumor diagnosis from medical imaging data, this work presents a novel method that combines the Otsu methodology with a customized Differential Evolution (DE) algorithm. For segmentation, the Otsu approach is used for accurate thresholding, and the DE algorithm is specifically tailored to improve the process. This study assesses the efficacy of the suggested methodology through thorough testing and analysis using a variety of datasets, including MRI and CT scans. Comparing the results to traditional methods, it is clear that the accuracy of tumor detection and the quality of segmentation have significantly improved. The integrated approach exhibits favorable outcomes for advancing computer-aided diagnostic systems, offering medical practitioners a reliable means for early tumor identification and subsequent treatment planning.

Keywords: control parameters; optimisation; segmentation; Otsu technique, thresholding

1. INTRODUCTION:

Brain tumor is forceful and probably fatal diseases. Effective treatment and surgery of brain tumor require pre-detection. Magnetic resonance imaging (MRI) based investigations have developed as a preferred method for diagnosis among other available methods like computed tomography (CT) . Segmentation of tumor areas from MRI images is an essential part of the estimated diagnosis. MRI images are less clear, large intensities, similar intensities of skull and tumor make it's quite hard to diagnose the infected region. Thus, automatic detection of the infected tumorous part with precision is a complicate work for the medically authorized radiologists. So, there is an acute aim to the development of automated segmentation of the tumorous part suited for MRI based images . Significant processes have been started many conventional techniques such as thresholding, edge detection and region based algorithms (clustering or watershed techniques). These well-developed conventional algorithms have time scaling limits or some other limitations that make it confined for efficient MRI images segmentation. Therefore, local segmentation techniques like wavelet and decomposition based methods have attracted the researchers to get the piece wise smoothness structure of the complex nature medical images . However, the quality and complexity of medical imaging are increasing day by day, so proper approach and technique are needed to analyze and solve these difficulties. The automatic detection of these brain tumors is therefore an important task, including the selection of suitable attributes from the medical image, data normalization, and specific classification which is a challenge. This study is an approach to an innovative competitive system, which is an essential aspect for the proper production of reliable results.

The selection of a medical image is a method that divides the interest region (ROIs) from the extreme environments and encompasses trying to split all of the encouraging spots from the sad regions. However, this is limited to limited human involvement, therefore feature extraction of the true tumors from the mind MRI image is a tough task. To be successful in MRI brain tumor images, a nice feature isolation function is the important premise. A tough image selection plan is crucial because a functionally distinct, reliable tumor image from the well interlaced background parts is possible to be obtained just after that. In the medical image selection, the Otsu technique was already employed, the main plan of this method is to optimize the histogram gain. A dense MRI result will be attainable using it, especially for general brain group IRM and T2-W expansion filmmaking . For any medicinal institution, it's necessary to get an early and clear image diagnosis of brain tumors having an accurate resolution. However, it is not an easy task as the selection of an accurate brain tumor image needs extremely unite focus and cautiousness because it is very hard to separate the tumor spot from the bordering concerning tissues in the compressed and weak edge pictogram .

Differential Evolution (DE) algorithms have been successfully utilized in this field to improve segmentation accuracy and efficiency. Several studies have investigated the application of DE in MRI image segmentation, with a focus on optimizing thresholding techniques and enhancing segmentation algorithms. [1] introduced an adaptive DE algorithm designed for optimal multi-level thresholding in MRI brain image segmentation, aiming to enhance the accuracy of segmenting brain images by optimizing the thresholding process using DE. [2] proposed a transformed DE algorithm combined with Kapur's thresholding for tumor detection in MRI images. Their study concentrated on improving the segmentation of MRI images by integrating DE with thresholding methods to enhance tumor detection accuracy. [3] developed a beta DE algorithm for determining optimal threshold levels in image segmentation, specifically focusing on enhancing the segmentation process by utilizing a variant of DE to optimize threshold selection in image segmentation tasks. Moreover, DE has found applications in various other image segmentation tasks. For example, [4] utilized a modified DE algorithm for contrast and brightness enhancement in satellite images, demonstrating the versatility of DE in different imaging domains. In summary, DE algorithms, including adaptive and transformed variants, have demonstrated potential in enhancing MRI image segmentation by optimizing thresholding techniques and improving segmentation accuracy. These studies underscore the promise of DE in advancing medical image analysis and contributing to more precise diagnostic procedures. Owing to this factor, an adaption of Differential Evolution algorithm has been developed and tested with some variants. This technique was then combined with Otsu thresholding approach to segment the MRI imagery.

2. METHODS AND METHODOLOGY:

To develop an algorithm for detecting brain tumors using an adapted Differential Evolution (DE) algorithm with the Otsu technique, it is essential to consider various existing methodologies and techniques in the field of brain tumor detection. The adaptation of the DE algorithm with the Otsu technique can enhance the accuracy and efficiency of brain tumor detection. Scholars have investigated its use in thresholding MRI, CT, and X-ray images, showing increases in accuracy over conventional techniques [5] .[6] used MRI scans to detect brain tumours using a GA-based method for multi-level thresholding. They showed that GAs could dynamically modify threshold levels to better catch tumour borders. Nevertheless, GAs can be computationally demanding, frequently requiring a significant amount of computing power and time to converge, particularly when dealing with high-resolution pictures. GAs are nevertheless beneficial because of their versatility and flexibility in spite of this drawback. DE has been very helpful in enhancing multi-level thresholding, which is crucial for intricate medical imaging with several layers of intensity, such as PET or MRI scans. The adaptation of the DE algorithm can help in optimizing the parameters for tumor detection, while the Otsu technique can aid in image segmentation by automatically determining the threshold value for image binarization. This combination can lead to improved segmentation of brain tumor regions in medical images, particularly in Magnetic Resonance Imaging (MRI) scans.Variant of DE with Kapur's entropy was used for brain MRI segmentation and verified [7]. Their findings showed that DE-based thresholding was more accurate than traditional thresholding in defining tumour boundaries and lowering noise. Furthermore, adaptive DE algorithms—like those developed by [8]—have been investigated for automatic thresholding adjustments, demonstrating even greater segmentation accuracy by accounting for patient-specific image fluctuations. [9] developed a PSO-based multi-level thresholding method for MRI brain scans, achieving better accuracy than traditional methods and faster convergence compared to GA. The PSO-based approach was particularly effective for images with irregular boundaries, such as brain tumors, where traditional methods often struggle.

Hybrid techniques that combine two or more algorithms have been investigated to further improve performance due to the drawbacks of employing a single EA type. For instance, in order to detect tumours in MRI images, [10] combined DE with GA. This hybrid algorithm produced more reliable and accurate segmentation by combining the diversity of GA with the quick convergence of DE. By fusing the advantages of EAs, hybrid algorithms frequently perform better than single EAs, providing more accuracy and efficiency.The advantages and disadvantages of various EAs in medical picture thresholding are highlighted in numerous comparison studies [11]. GA is renowned for its resilience in managing intricate segmentation jobs, but DE and PSO are favoured for their speed and ease of use. Especially for high-resolution MRI and CT images, hybrid approaches seem to strike a balance between the trade-offs between accuracy and processing load.There are still difficulties in spite of these developments. EA-based thresholding continues to face challenges due to its high computing cost, sensitivity to beginning conditions, and requirement for parameter adjustment. Furthermore, algorithm performance may be impacted by variations in image quality between machines and patients, necessitating the use of adaptive algorithms that exhibit strong generalisation across a range of datasets.

Different algorithms and methods for detecting brain tumours have been proposed in a number of research. A model combining template-based K-means and improved fuzzy C-means (TKFCM) algorithm for detecting human brain tumours in MRI images was proposed by [13], while Mustaqeem et al. [12] presented an effective brain tumour detection algorithm using watershed and thresholding-based segmentation. The importance of segmentation algorithms in precisely identifying tumour locations is demonstrated by these investigations. Furthermore, [14] demonstrated the value of sophisticated algorithms in raising detection accuracy by presenting a technique for strengthening the accuracy of brain tumour identification in MRI images utilising super-pixel and the Fast Primal Dual Algorithm. Furthermore, [15] reviewed U-Net's efficacy in brain tumour segmentation in MRI scans, highlighting the significance of deep learning methods in diagnosis. Additionally, utilising data science, namely deep learning techniques, [16] suggested a novel approach for brain tumour identification that can shed light on the use of sophisticated algorithms in medical imaging. showed how Convolutional Neural Networks (CNNs) may be used to detect brain tumours, demonstrating the potential of artificial neural networks for precise MRI image analysis [17].

In conclusion, by leveraging the insights from these studies and incorporating the adapted DE algorithm with the Otsu technique, a robust algorithm for detecting brain tumors can be developed. This algorithm can potentially improve the accuracy, efficiency, and reliability of brain tumor detection in medical imaging, ultimately aiding in early diagnosis and treatment of brain tumors.

3. METHODOLOGY:

3.1 Classical Differential Evolution

Differential Evolution (DE) algorithm is a potent optimisation method that has been applied extensively in many different domains because of its ease of use and efficiency in resolving challenging optimisation issues. Price and Storn [18] first proposed Differential Evolution (DE) in 1997. Scalar addition and multiplication are carried out using DE rather than by Genetic Algorithms (GA), which use a recombination and mutation mechanism [19]. With its distinct advantages over other population-based algorithms like Simulated Annealing, Genetic Algorithms, Particle Swarm Optimisation, and others, the DE method has found widespread application in engineering, signal processing, and picture processing. Multi-model stochastic optimisation, or DE, is a population based technique that excels in multimodal optimisation problems with multiple cost functions [20].

An initial set of possible solutions with certain values is produced during initialisation. These solutions are referred to as the best or base vector. The following phase is mutation, in which a trial vector is created by utilising one randomly chosen individual and another randomly chosen individual for every potential individual in the population. The trial vector and the population member are then compared in recombination, and the superior of the two is chosen to create the new generation's population. Therefore, by comparing the individual to the newly suggested solution, the recombination process aims to improve the individual, and the better individual is chosen for the new generation population. It chooses the best candidate solution. For a variety of optimisation problems, the DE algorithm effectively explores the solution space, adjusts to changing conditions, and converges towards optimal solutions by iteratively performing these processes.

Algorithm typically involves several key steps that are crucial for its operation:

Population Initialization: The first step of the DE method is to randomly initialise a population of potential solutions in the search space. Every candidate solution shows how the optimisation problem might be solved. The population of NP candidate solutions denoted by $X_{i,G}$ is used by DE, where the population is represented by G, generation of population and the population is represented by index $i = 1,2...NP$. Given any variable $X_{i,G}$, choose three vectors $X_{r1,G}, X_{r2,G}$ and $X_{r3,G}$ that are arbitrary divergent from one another for any given variable.

Mutation: By upsetting the population's current solutions, new candidate solutions are produced in the mutation step. In order to obtain the donor vector, this perturbation is usually accomplished by combining a scaled transformation between two randomly chosen solutions to a third solution.

$$V_{i,G} = X_{r1,G} + F \times (X_{r2,G} - X_{r3,G}) \quad (1)$$

The mutation factor F is a constant between 0 and 2. DE/rand/1 is the designation for the aforementioned approach. One DE approach is distinguished from another by the mutation function.

Crossover: The crossover operation combines information from different candidate solutions to create new candidate solutions called trial vector $U_{i,G}$. This step enhances the diversity of the population and helps explore the search space more effectively. With crossover probability $C_r \in [0,1]$, the components of donor vector relocate to trial vector. C_r is selected collectively with population size NP.

$$U_{j,i,G+1} = \{V_{j,i,G+1} \quad if rand_{i,j}[0,1] \leq C_r \; or if j = I_{rand} \; X_{j,i,G+1} \quad if \; rand_{i,j}[0,1] > C_r \; or if j \neq I_{rand} \quad (2)$$

Here $rand_{i,j} \approx \cup[0,1]$ and I_{rand} is a random numeral from 1,2,3...N.

Selection: Based on their fitness values, the selection stage establishes which candidate solutions will make it to the following generation. According to the "survival of the fittest" theory, solutions with higher fitness values have a higher chance of being chosen for the following generation. The target vector $X_{i,G}$ and trial vectors $V_{i,G}$ are combined, and the function's lowest result is carried over to the following generation.

$$X_{i,G+1} = \{U_{i,G+1} \quad if f(U_{i,G+1}) \leq f(X_{i,G}) where i = 1,2,3\ldots N \; X_{i,G} \quad otherwise \quad (3)$$

Termination Criteria: Until a stopping requirement is satisfied, the algorithm repeatedly goes through the mutation, crossover, and selection phases. Maximum number of repetitions, achieving a particular degree of convergence, or other predetermined circumstances could constitute this criterion.

Adapted Differential Evolution technique

By altering the control parameters, DE variants are created. DE is further sensitive to changes in mutation factor F compared to CR value. In the standard DE method, a mutation factor F is employed, which has a constant value between 0 and 2. A control parameter F1 that accepts random values between 0 and 1 was also used in a few additional DE variations. Three control factors are used in this case by the adaptive DE mutation strategy: F2 is the product of F and F1. In each cycle, F and F1 take random values, which significantly improves the convergence behavior.

$$F2 = F \times F1$$

$$X' = F \times X_{r1,G} + F2 \times (F \times (X_{best,G} - X_{r2,G}) - F1 \times (X_{best,G} - X_{r3G})) \quad (4)$$

This strategy's employment of three different control parameters greatly increases the donor vector's value, which in turn greatly increases the Adaptive DE algorithm's efficacy. Two sets of difference vectors are employed here. Thus, the optimal perturbation is achieved sooner. The mutation probability increases when three control factors are used. The higher the mutation chance, the shorter the CPU time. By selecting the vectors at random, the algorithm is prevented from acting greedily. The technique converges earlier than the conventional strategies by introducing the optimal vector value. The population diversity taken into consideration is increased when many difference vectors are used. The adaptive DE approach uses the same crossover and selection process as the traditional DE approach.

3.2 Image thresholding

The simplest approach of image segmentation is thresholding. The primary objective of thresholding is to eliminate the pixels from the imagery that represent an item. For both colour and greyscale photos, there are numerous thresholding techniques. The two primary approaches for thresholding colour images are neighbourhood-based and histogram-based. Data ranges are divided into classes of the same size to create histograms. Three RGB values are provided for every pixel in colour images. A three-dimensional histogram is created for every colour value in the histogram-based approach, and threshold values are plotted. To acknowledge an object, arbitrary pixel values are assigned to threshold-separated regions. Determining the amount of image segments will determine whether thresholding is multilevel or bilevel. Two parts of the image are distinguished in bilevel thresholding. T is the symbol for the threshold value. The grey values of background pixels are smaller than T, whereas those of object pixels are larger than T. Using multilevel thresholding, an image is divided into multiple discrete areas. With this method, the image is divided into distinct brightness zones based on multiple thresholds. There are numerous object pixels and a single backdrop. The separation of the foreground and background items into non-overlapping sets facilitates the segmentation of the greyscale image into discrete parts. This technique is most effective when used with complex or vibrant visuals.

3.3 Otsu Multi-level thresholding

Threshold selections are the diversely beneficial for application such as image segmentation, image edge detection, co-occurring frequency matrices, image color tests and touchless gesture recognized systems. Otsu formulated a simple objective function under two class gaussian distribution and formed a simple algorithm for the maximum class separations of all classes, so it settled the highest peaks. Later on, the normalized (n-1) between class variance has become very popular in various fields[21]. Optimum threshold value is calculated form the histogram. After that, otsu segmentation technique is applied to segment image by more than two regional value between 0 to 1 and more than three independent variables in the range of 0 to 1, which give the best image segmentation results; because of statistical properties of image that follow chi-square distribution curve their peak value is attained, more peaks can be found at threshold value where pixel are class based on the gray level then it is noticed that it represented as a classification curve.The steps involved in Otsu thresholding for image segmentation can be outlined as follows:

Histogram Computation: Calculate the histogram of the recorded imagery to represent the distribution of pixel intensities.

Computing Histogram Statistics: Compute the probabilities of occurrence of each intensity level in the imagery histogram.

Computing Cumulative Distribution and mean intensity value: Calculate the cumulative distribution function (CDF) of pixel intensities from histogram and mean intensity value of the image.

Between-Class Variance Calculation: Calculate the between-class variance for each possible threshold value. This involves finding the threshold that raises the between-class variance, which signifies optimal separation between the object and background regions.

Threshold Selection: Choose the threshold value that efficiently separates the image into foreground (object) and background areas by maximising the between-class variance.

Image Segmentation: Apply the selected threshold to the input image to create a binary mask where pixels with intensities above the threshold belong to the object region, and pixels below the threshold belong to the background region.

Assuming m thresholds, we can divide the image into m-1 classes, with C_0 representing the grey level between 0 and t_1-and C_1 representing the grey level between t_1 and t_2-1. L is the grey scale level 256, while C_m is the grey level between t_m and L-1. The method maximises the objective function to obtain the ideal value. The weights are specified as follows and are represented by the notation $w_0, w_1, \ldots . w_m$.

$$w_0(t) = \sum_{i=0}^{t_1-1} p_i \quad , \quad w_1(t) = \sum_{i=t_1}^{t_2-1} p_i \quad , \ldots . \quad w_m(t) = \sum_{i=t_m}^{L-1} p_i \tag{5}$$

The following is the objective function for multi-level thresholding:

$$Maximize\ J(n) = \sigma_1 + \sigma_2 + \cdots \sigma_m \quad (6)$$

where, σ is the class variance. The definition of the variance is:

$$\sigma_0 = w_0(\mu_0 - \mu_T)^2 \quad , \quad \sigma_1 = w_1(\mu_1 - \mu_T)^2 \quad , \ldots \quad \sigma_m = w_m(\mu_m - \mu_T)^2 \quad (7)$$

The probability distribution defines the classes $C_0, C_1, \ldots C_m$ as follows:

$$C_0 = \frac{p_0}{w_0(t)} \cdot\cdot \frac{p_{t_1-1}}{w_0(t)} \quad , \quad C_1 = \frac{p_{t_1}}{w_1(t)} \cdot\cdot \frac{p_{t_2-1}}{w_1(t)} \ , \ldots \quad C_m = \frac{p_{tm}}{w_m(t)} \cdot\cdot \frac{p_{L-1}}{w_m(t)} \quad (8)$$

For the classes $C_0, C_1, \ldots C_m$,the mean levels $\mu_0, \mu_1, \ldots \mu_m$ are denoted as:

$$\mu_0 = \sum_{i=0}^{t_1-1} \frac{ip_i}{w_0} \quad , \quad \mu_1 = \sum_{i=t_1}^{t_2-1} \frac{ip_i}{w_1} \ \ldots \quad \mu_m = \sum_{i=t_m}^{L-1} \frac{ip_i}{w_m} \quad (9)$$

3.4 Applying Otsu multi-level thresholding on Adaptive DE

The simple thresholding method assigns the threshold value manually but it delivers poor output for accurate categorization of images. So, the adaptive DE algorithm with Otsu thresholding technique has been introduced. Otsu technique segregates the image into parts and then identifies the dimensions of components of the image based on appearance of pixel values. The histogram of the image is employed in each part, and then in every class the possibility of pixels lie is taken into account by pixel intensity. The significance of the unimodal histogram approach is that it minimizes a convolution classification within category variables variance and maximize overall class variance. Subsequent to the compact value of distribution workload, Otsu technique is used for thresholding of MRI images. The Otsu technique undertakes multi-thresholding on intensity values founded on the features with the least total value of intra-class variation, and the utmost in-between class variation. This method outlines the general steps involved in detecting brain tumors using the adapted DE algorithm integrated with the Otsu technique. Obtain medical imaging data containing brain images. During preprocessing, normalize the intensity values of the images to ensure consistency and remove any noise or artifacts present in the images through filtering techniques if necessary. Initialize parameters for the Adaptive DE algorithm, such as population size, crossover rate, mutation rate, and maximum number of iterations. Define parameters for the Otsu technique, such as the number of intensity levels. Generate an initial population of candidate solutions, where each solution represents a potential segmentation of the brain image. Evaluate the fitness of each solution using a fitness function that measures the quality of segmentation, considering factors like tumor coverage and smoothness of boundaries. Iterate until convergence or reaching the maximum number of iterations. Apply adaptive DE operators to generate new candidate solutions. Evaluate the fitness of the new solutions. Select the best-performing solutions to form the next generation. Apply the Otsu technique to determine an optimal threshold for segmenting the brain image into tumor and non-tumor regions based on pixel intensities. Combine the segmented regions obtained from the adaptive DE algorithm with the binary mask generated by the Otsu technique. Refine the segmentation boundaries using morphological operations to improve accuracy. Obtain the final segmented image, where brain tumors are delineated from the surrounding tissue. Quantitatively assess the performance of the algorithm using metrics such as similarity coefficient and accuracy.

4. STUDY OF EXPERIMENTS AND RESULTS:

1. 4.1 Experimental Result from ADE

Utilising MatLab R2017b on an i7 core processor running a 64-bit operating system, the simulated experiment was carried out. The 25 benchmark functions that were expected during CEC 2005 were taken into account in this experiment. It is possible to categorise these functions into four classes: unimodal, basic multimodal, expanded multimodal, and hybrid composite multimodal. Five different mutation techniques of DE algorithms were compared with ADE. In their study, Storn and Price claimed that the choice of value F, not C_r, influences DE. A smaller F accelerates the rate of convergence, while a higher F value generally places the mutant vector in a widely dispersed search space. Therefore, the midpoint of the range taken into consideration, 0.8, is used as the value of F in this study. Table 1 is a tabulation of the results obtained.

Table 1. Comparative outcomes between various DE and ADE techniques

Function	**DE/ best/1**	**DE/ best/2**	**DE/ rand/1**	**DE/ best-to-rand/1**	**DE/ rand/2**	**Adaptive DE**
F1	13.76	58.6	13.12	51.2	89.67	**11.21**
F2	7.25	11.05	11.62	6.4	**5.12**	11.65
F3	6.89	11.78	41.2	7.42	10.28	**6.1**
F4	7.67	7.32	11.6	11.4	8.5	**6.9**
F5	18.1	**4.75**	10.32	8.75	6.35	10.45
F6	14.23	15.4	16.3	17.8	9.75	**9.01**
F7	131.5	135.3	142.6	132.9	165.7	**130.1**
F8	10.8	7.67	8.12	**7.02**	15.13	12.3
F9	8.31	4.87	5.76	6.23	7.12	**4.01**
F10	162.9	153.2	154.5	157.6	**146.24**	151.8
F11	**12.15**	17.75	17.72	18.9	33.23	20.4
F12	**97.21**	98.7	99.13	98.65	110.12	101.5
F13	142.5	82.2	37.8	110.3	101.6	**30.13**
F14	103.1	97.1	97.12	100.8	87.2	**51.4**
F15	41.25	105.8	38.13	84.8	101.34	**30.23**

The aforementioned outcomes are attained for dimensionality 50 and vtr = 1.0e-015. The 25 benchmark functions were implemented for different vtr (1.0e-016, 1.0e-10, 1.0e-014) and dimensionalities (75, 100, 150, and 200). The variation ADE produced better results across all experimental circumstances. ADE's effectiveness was verified using statistical research. The results in Table 1 were subjected to the Kruskal Wallis and Freidman's tests, which are reported in Table 2. Based on how well they worked, the strategies were graded. When compared against the other five techniques, ADE was scored as the best for both tests, and the results are shown in table 3.

Table 2. Statistical Test Results

	F test	Kruskal Wallis test
Chi square	21.32	5.21
Dimension	50	50
Asymptotic Significance	0.006	0.38

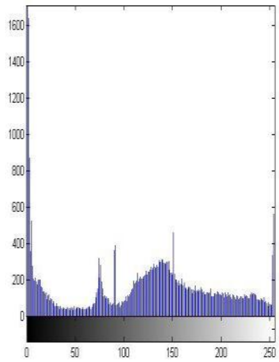
Table 3. Comparing the average of different methods using the F test and Kruskal Wallis

Strategy	F test	Kruskal Wallis test
DE / best-to-rand/ 1	3.56	82.1
DE / rand / 1	2.89	67.5
DE / rand / 2	3.02	69.76
DE / best /2	4.75	71.2
DE / best / 1	3.4	86.2
ADE	2.4	64.2

4.2 Multi-level thresholding based results

Digital imaging requires an efficient and reliable method for image segmentation. Since colour photos convey more information than greyscale images, they are in high demand. Even though a number of segmentation approaches have been developed, their accuracy and effectiveness remain lacking. As the need to address this inefficiency grows, more efficient methods for colour image segmentation are sought. Sample MRI images from www.sciencephoto.com were subjected to Otsu multilevel thresholding and the proposed ADE approach. A few MRI sample photos from www.sciencephoto.com were then subjected to multi-level Otsu thresholding. Figure 1 shows the original MRI scans, their histogram, and segmented pictures using the ADE and Kapur's approaches with Otsu. These photos' performance is compared to that of the conventional DE technique using multi-level thresholding based on the ADE algorithm. Table 4 shows the calculated ideal threshold values. According to the results, threshold values utilising ADE are superior than those using the traditional DE technique. The result of changing the ADE approach's mutation strategy in contrast to the DE technique is an improvement in the outcome.

(a)



(b)

(c)

(d)

Figure 1: a) Original Imagery b)Histogram c) Segmented imagery with Otsu d) Segmented imagery with Adaptive DE and Otsu

Table 4. Values attained for the threshold

Image	Number of thresholds(m)	Optimal threshold values	
		DE with Otsu method	Adaptive DE with Otsu
Image 1	2	40,51	41,52
	3	42,104,117	42,106,120
	4	103,172,178,184	105,170,180,186

The peak to signal ratio (PSNR) and CPU time are utilised to confirm the algorithms' performance. The quality difference relating the initial and segmented images on the basis of mean square error (MSE) is known as PSNR. It is distinguished by:

$$PSNR(\sigma, s) = 20log_{10}\left[\frac{255}{\sqrt{MSE(\sigma,s)}}\right] \quad (10)$$

where s is the segmented imagery and σ is the original imagery. The mean square error (MSE) is stated as follows if the image size is m ×n:

$$MSE = \frac{1}{m*n}\sum_{i=0}^{m-1}\sum_{j=0}^{n-1}[\sigma(m,n) - s(m,n)] \quad (11)$$

A higher PSNR number means that there is less noise in the imagery. The two imagery under consideration are compared using the structural similarity index, or SSIM. In contrast to PSNR, an evaluation criterion for the reconstructed image, it is based on the image's visual structure. The definition of the mean intensity of a picture x is:

$$\mu_x = \frac{1}{N}\sum_{i=1}^{N} x_i \quad (12)$$

The definition of an image x's standard deviation is:

$$\sigma_x = \left(\frac{1}{N}\sum_{i=1}^{N}(x_i - \mu_x)^2\right)^{\frac{1}{2}} \quad (13)$$

The definition of the SSIM between a picture x and a reference image y is:

$$SSIM(x,y) = \frac{(2\mu_x\mu_y + C_1)(2\sigma_{xy} + C_1)}{(\mu_x^2 + \mu_y^2 + C_2)(\sigma_x^2 + \sigma_y^2 + C_2)} \tag{14}$$

where the constants C_1 and C_2 are found. SSIM's value falls between 0 and 1.Table 5 displays the results acquired for SSIM, PSNR and CPU time for the sample images in question.

Table 5. SSIM,PSNR and CPU time comparison

Image	Threshold (m)	SSIM		PSNR		CPU Time	
		Otsu with DE	Otsu with Adaptive DE	Otsu with DE	Otsu with Adaptive DE	Otsu with DE	Otsu with Adaptive DE
Imagery 1	2	0.86	0.95	31.05	32.8	2.8	2.12
	3	0.86	0.90	31.2	32.4	2.6	2.0
	4	0.89	0.94	33.5	32.1	2.56	2.1

For precise diagnosis, treatment planning, and disease monitoring, including cancer, tumour segmentation in MRI imaging is crucial. There are several benefits to using the ADE with Otsu approach for this assignment since it can effectively and precisely identify and segment tumours, even in big datasets, potentially lowering manual error and enhancing consistency. This method can detect and define tumour boundaries with high accuracy. When opposed to radiologists' manual segmentation, this method can automate the process, greatly reducing the amount of time needed.

A sample of segmented tumour using this technique is shown in figure 2.

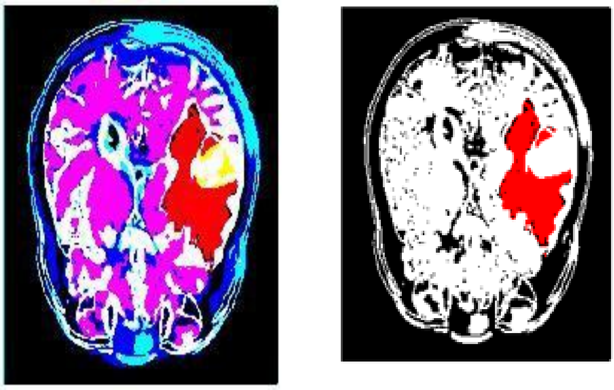


Figure 2. Segmented tumour regions from Images

5. CONCLUSION:

Brain tumor is the most harmful and aggressive kind of cancer causative of 2.6% of all cancer deaths globally. Diagnosing brain tumors is a difficult task and needs comprehensive knowledge and training. CT and MRI scans are considered the pre-eminent techniques for the detection and screening of brain tumors. At present, the tumor region in the MRI image is identified by the radiologist manually. The detection and treatment of brain tumor at an early stage can inhibit it from growing farther or stop it from advancing to severe complications. Various image segmentation techniques like watershed, edge-based, thresholding, and clustering techniques have been projected to detect and differentiate the areas of interest. The standard thresholding method and various adaptation of the simple method are inefficient in the segmented MRI images due to the inappropriate selection on the initial threshold value and the distribution of the histogram.

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