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Brain Tumor Prediction and Segmentation with Morphological Region-based Active Contour Model and Refinement using Boltzmann Monte Carlo Method in MRI Images

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Abstract

Objectives: The primary goal of the research work is to accurately detect the precise location of the brain tumor in the radiological Magnetic Resonance Imaging (MRI) images of human brain using segmentation method. **Methods:** In this research work, we introduce mainly the Morphological Region-based Active Contour model and Boltzmann Monte Carlo method (MACB model), involving a comprehensive three-step methodology for the segmentation of the brain, MRI images in order to detect brain tumor. The initial step involves pre-processing which includes Gaussian filtering for noise reduction and Contrast Limited Adaptive Histogram Equalization (CLAHE) technique to enhance image features. In the second step, we identify tumor-related clusters using morphological operations and delineate the tumor regions using Active Contour (Snake) model to get a segmented image. In the final step, the Boltzmann Monte Carlo method is used to refine the edges of the segmented image. To evaluate the effectiveness of this approach, the 2D brain tumor datasets, available in the public domain, are used. The first dataset is taken from Kaggle website and has 3064 MRI human brain images and its respective ground truth images which is used for segmentation. The second dataset is used for visualization of segmented tumor, available in the same Kaggle website. **Findings:** The Performance metrics for finding similarity between the segmented images generated using the proposed MACB model and the ground truth images, available in the first dataset, exhibit higher values. That is, the proposed method has achieved higher values of Dice Similarity Coefficient (DSC): 93.26%, Jaccard Co-efficient: 86.44%, Sensitivity: 97.27%, Specificity: 99.43% and Pixel accuracy: 98.95%. **Novelty:** In this research work, MACB model is proposed for the detection, segmentation, and refinement process of brain tumor by incorporating Boltzmann Monte Carlo method with Morphological Region-Based Active Contour model. This novel approach has resulted in enhanced precision and efficiency in the brain tumor segmentation

process.

Keywords: Brain Tumor Segmentation; Morphological Operation; Active Contour; Boltzmann Monte Carlo Method; Magnetic Resonance Imaging

1 Introduction

The Human brain is the control centre for all organs of the body[1]. Brain tumors are the growth of abnormal cells in the brain. In a normal brain, new cells typically begin growing when old cells cease their growth and become damaged. However, in the case of a person with a tumor, the growth of cells becomes aberrant, with new cells growing even when the old cells are undamaged[2]. The brain tumors are of two types: non-cancerous tumors, which are called benign and cancerous tumors, which are called malignant. Benign tumors are non-progressive and have uniformity in structure that originate in the brain. This kind of tumor is less aggressive and cannot expand in the body. On the other hand, malignant tumors are active cancerous tumors and have non-uniformity in structure that spread rapidly throughout the body. Furthermore, there are two categories of malignant tumors: primary malignant tumors that originate in the brain and transfer to other body parts and secondary malignant tumors that initiate in other body regions and spread to the brain. Meningioma, pituitary, and glioma tumors are common types of brain tumors. Meningioma arises in the thin membranes, i.e., tissues surrounding the spinal cord and brain. Gliomas arise within the glial cells of the brain. Pituitary tumors grow when cells in the pituitary gland near the brain grow in an abnormal pattern. One of the most life-threatening disorders is a brain tumor[3] the structure of brain tumor is as shown in Figure 1(a), (b) & (c)[4].

Brain tumor diagnosis consists of tumor detection, segmentation, and classification processes. Early detection of brain tumors is crucial for effective treatment planning in the healthcare sector. Successful treatment is challenging, and the chances of survival significantly diminish if the tumor spreads to nearby tissues.
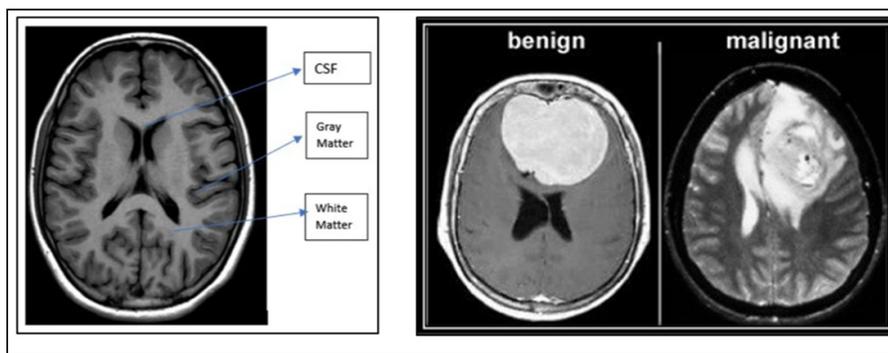
Fig 1. (a) Normal Brain (b) Benign brain tumor (c) Malignant brain tumor

The techniques, such as Computed Tomography (CT), Magnetic Resonance Imaging (MRI)- a method most commonly used to detect tumor, Single Photon Emission Computed Tomography (SPECT), Positron Emission Tomography (PET), Functional MRI (fMRI) and Ultrasound (US), precisely identify brain tumors and provide valuable insights about their size, location, shape and other features. MRI provides information about the anatomy of human tissues and it is considered to be a standard technique. It uses radio frequency signals with a powerful magnetic field to produce images of human tissues. However, the brain tumor segmentations are used for localizing and isolating different tumor tissues inside the brain MRI images[5].

Image segmentation plays a vital role in image processing, especially in medical imaging for identifying and defining regions of interest (ROI). This is particularly essential for locating, detecting and outlining tumor structure with abnormalities in various medical imaging modalities. In recent years, extensive research efforts have been dedicated to the segmentation of brain tumors. As of 2022[6], there are approximately 7,00,000 individuals in the United States, diagnosed with primary brain tumors annually and about 85,000 people are projected to be added every year. To address this issue, several research works have been conducted to segment brain tumors accurately at early stages.

Kulshreshtha, A. and Arpita Nagpal[7] have proposed an improved fully automatic segmentation (IFAS) Convolutional Neural Network model and trained on morphologically enhanced images to detect brain tumors. The average dice similarity observed is 88%.

Kabirat Sulaiman Ayomideet et al.[8] have proposed a research work that combines Deep CNN characteristics and an SVM classifier, powered by GoogleNet's convolution neural network (CNN) to segment brain tumors. The modified GoogleNet's pooling layer that has been implemented after the previous inception module is used to extract features. It has achieved Classification accuracy of 98.64%, precision of 93.17%, recall of 98.60%, F-measure of 97% by using the dataset with 3064 brain MRI images.

Shekari, M. and Rostamian, M.[9] have used Fuzzy clustering, morphological reconstruction, and active contour segmentation model. It has achieved an average segmentation accuracy of 99.06%, Sensitivity of 92.10%, Dice of 92%, and Precision of 92.05% and Jaccard of 86%.

Zahra Shahvaranet et al.[10] have used K- means clustering and morphological region-based active contour model for tumor extraction. The Gaussian distribution has been used to model local image intensities. The spatial correlation between neighbouring voxels has also been modelled using Markov random field. It is evaluated on BraTS2013 dataset that yields better performance on tumor segmentation with mean Dice similarity coefficients of 91.79% and 89.10%, which are respectively obtained on High-grade tumors and Low-Grade tumors.

Sheela, C.J.J. and Suganthi, G.[11] have proposed a segmentation algorithm that uses Active Contour model and Fuzzy–C Means method to optimize the edge pixels, providing a Dice-score of 82.5%, 64% and 53% for meningioma, glioma, and pituitary type tumors respectively. Also, an overall accuracy of 91% is achieved for 3064 MRI images comprising 1426 Glioma, 708 Meningioma and 930 Pituitary type tumors.

Santhosh Kumar et al.[12] have proposed a unique approach for segmenting brain MRI images by combining nonlinear filtering, k-means clustering, active contour modelling, thresholding, and morphological post-processing. It has achieved an Accuracy of 97.38%, Sensitivity of 82.01%, Precision of 97.20%, Dice Co-efficient of 85.82%.

EliseeIlunga et al.[13] have introduced the Localized Region-based Active Contour Model (LRACM), Local Gaussian Distribution Fitting (LGDF), Localized Chan-Vese (C-V) and Localized Active Contour Model with Background Intensity Compensation (LACM-BIC). It has achieved a Dice Index of 93.20% on BraTS2012 dataset.

Kaiqiong Sun et al.[14] have proposed an automated adjustment method for the smoothing parameter in region-based active contour model for obtaining the segmentation quality. This is comparable to those, obtained by traditional region-based active contour model, without the cumbersome trial of smoothing parameter.

Shumoos Al-Fahdawiet al.[15] have introduced the Fundus-Deep Net system, which includes image pre-processing incorporated with the SoftMax layer and Discriminative Restricted Boltzmann Machine (DRBM) that specifically identifies eight different ocular diseases.

X. Ye et al.[16] have introduced Restricted Boltzmann Machine as one of the hidden layers in Deep Learning networks for face detection on a video with high detection speed.

T. Pramananda Perumal, K.R. Srivaishnavi, D.L. Asha Rani, and K.P.N. Murthy[17] have outlined the Boltzmann sampling and non-Boltzmann sampling algorithm to remove the noise from an image.

Pai[18] has proposed Boltzmann Metropolis Algorithm for positive parameter selection of SVM model, which is important to forecast the accuracy of the SVM Model.

Nicholas Metropolis[19] has proposed that the Monte Carlo integration over configuration space seem to be a feasible approach for statistical mechanical problems.

The above literature survey shows that the use of traditional techniques[9–13] (viz. thresholding, edge-based segmentation methods, clustering methods, morphological operations methods, and active contour models) and CNN deep learning segmentation algorithms[7,8], along with image optimization techniques has achieved improved segmentation in terms of Dice Similarity Coefficient (DSC) and Jaccard Coefficient. Image optimization techniques/refinement process play a key role in the brain tumor segmentation process. Along with image segmentation, the image refinement process will delineate the tumor region in the brain MRI images precisely.

In the existing methods, various standard optimization techniques like Fuzzy C-Means[9], K-Means Clustering[10] and Particle Swarm Optimization (PSO)[11] have been used to refine segmented tumor region in the brain MRI images with good accuracy. In general, image optimization techniques have many important advantages such as

- Enhanced Image Quality and Segmentation Accuracy,
- Improved Feature Extraction, and
- Artifact Reduction and Edge Preservation.

The objectives of our research work are to use traditional segmentation methods viz. Morphological Operations (for identifying the tumor clusters), Active Contour Snake Model (to delineate the tumor regions) and Boltzmann Monte Carlo (Markov Chain Monte Carlo) method to refine the edges of the segmented contour (region). In contrast to the previous approaches, in the proposed research work, the Boltzmann Monte Carlo method is used instead of standard image optimization techniques. This method combines the random sampling techniques of Monte Carlo simulations with the Boltzmann probability distribution and tries to produce a refined tumor region with improved values of DSC, Jaccard Coefficient, Sensitivity, Specificity and Pixel accuracy.

The main objective of the proposed research work is to design an accurate and efficient image segmentation model to detect the various types /classes of brain tumors in MRI images. This paper is organized as follows. In Section 2, we briefly describe the dataset for brain tumor segmentation, the flow diagram of the proposed MACB model for brain tumor segmentation, brain MRI image pre-processing methods, MRI image segmentation methods viz. Morphological operations, Active contour (Snake) model and Boltzmann Monte Carlo method (MACB model) and its implementation. In Section 3, we present our results and discussions on a) Performance metrics between the ground truth and segmented images (using first dataset), b) Visualization of tumor outline marked and segmented using MACB model (using second dataset) c) Analyzing Performance metrics for segmentation of tumor in the brain MRI images using the proposed MACB model (by using first dataset) d) Performance metrics analysis of various existing methods e) Comparative analysis of Performance metrics for tumor segmentation in the brain MRI images using the proposed MACB model and existing methods. In Section 4, we highlight the principal outcome of the research work.

2 Methodology

2. 1 Dataset for Brain Tumor Segmentation

Magnetic Resonance Imaging (MRI) is an advanced medical imaging technique, which is used to produce high-quality images[20] of the parts in the human body. The MRI images are often used while treating brain tumors. In this paper, we use two brain MRI images datasets.

The first dataset for comparing automatically segmented image with their corresponding ground truth image to assess performance metrics and another dataset is used for visualizing and verifying the MACB model capability to segment various types of brain tumor images at different locations in the brain. The public dataset, created by Nikhil Tomar and retrieved from Kaggle[21] is used for 2D brain tumor segmentation in this research work. This dataset contains 6128 images comprising 3064 brain tumor images and 3064 corresponding ground truth images of the brain tumor images.

The second dataset is sourced from Kaggle, by combining datasets from Figshare and Br35H. This contains 7023 images (5712 in the training dataset and 1311 in the testing dataset)[22] of human brain MRI images from 233 patients. In this research work, only the training datasets are used which are classified into four classes. That is, the classified images are 1321 glioma images, 1339 meningioma images, 1595 images with no tumors, and 1457 pituitary images. Those brain MRI images are used for visualizing whether the tumor in the brain image is segmented accurately or not.

2.2 Implementation

This research work is implemented in MATLAB R2023b by using two Public Datasets as given in Section 2.1. The machine, used for this computation, is Lenovo LAPTOP-8T6ALGF9. It is equipped with Intel (R) Core (TM) i3-8145U CPU @ 2.10GHz and 36.0 GB RAM. The device runs a 64-bit version of Windows 11 Home Edition. The various standard Performance metrics[11] such as Dice Similarity Coefficient Jaccard Coefficient, Sensitivity, Specificity and Pixel accuracy are calculated.

2.3 Flow diagram

The proposed MACB model aims to perform brain tumor segmentation in MRI images. Figure 2 illustrates the sequential steps, which are involved in constructing the proposed model for brain tumor segmentation. It starts with pre-processing, followed

by Contrast Limited Adaptive Histogram Equalization (CLAHE) technique and morphological operations, in order to identify whether brain tumor is present or not in the MRI images. Subsequently, if brain tumor is present, an Active Contour (Snake) model is used to draw a contour to segment the tumor and Boltzmann Monte Carlo method is used to refine the contour position by accepting or rejecting perturbations, based on energy changes. The combination of the above three methods is termed as "MACB" model which is a novel approach. The detected brain tumor region is evaluated using appropriate metrics such as Dice Similarity Coefficient, Jaccard Coefficient, Sensitivity, Specificity and Pixel accuracy.
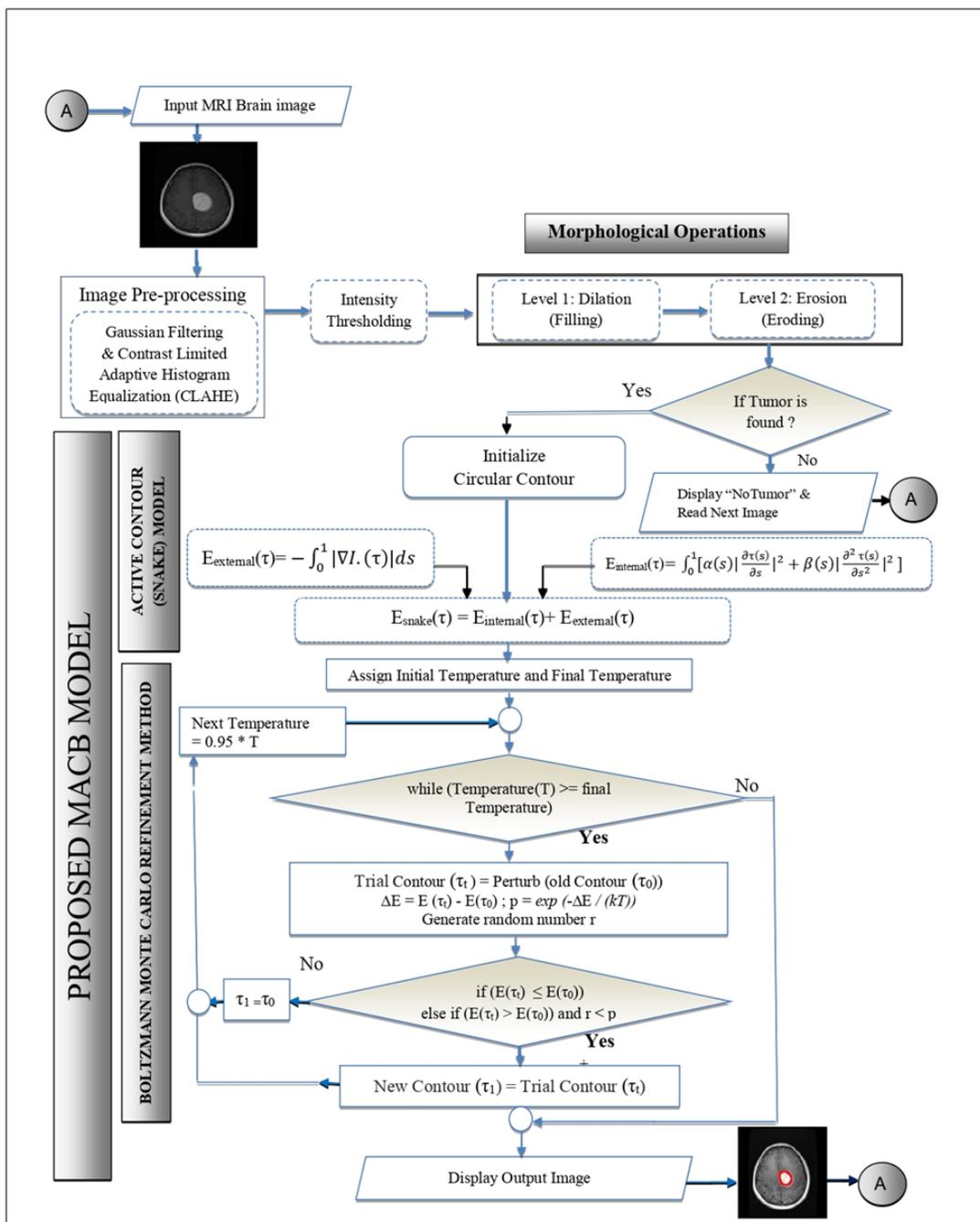

Fig 2. Flow diagram of the p roposed MACB model

2.4 MRI Images Pre-processing

The input image is subjected to 3 x 3 Gaussian filtering kernels [23] for effective smoothing of images and reduces noise in the image. The Contrast Limited Adaptive Histogram Equalization (CLAHE) technique is applied to improve the contrast between the region of interest and the background. It enhances the quality of the low-quality brain MRI images. The Block Size (BS) and Clip Limit (CL) are two primary parameters in CLAHE that are significantly responsible for improving brain MRI image quality [24]. The histogram illustrating the frequency distribution of the original image is shown in Figure 3(a). The histogram of the original image is relatively flat which indicates that the image is mostly medium gray, with a relatively small range of pixel values. The histogram, shown in Figure 3 **(b)**, is much wider, with peak values between 0 and 255, which are the black and white values, respectively. This indicates that the image has a much wider range of pixel values, enhancing both bright and dark areas of the image.
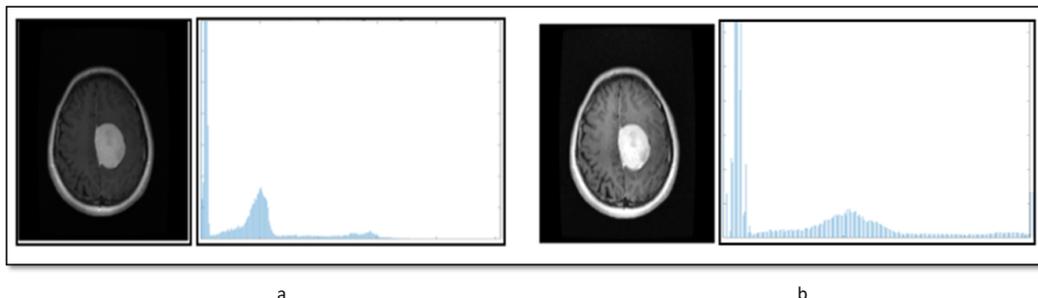

Fig 3. (a) Histogram of the Original Image, (b) Histogram of the CLAHE Image

2.5 Brain MRI Images Segmentation using MACB model

In MACB model, initially we identify tumor-related clusters using morphological operations. In the second step, we delineate the tumor regions using Active Contour (Snake) model to get a segmented image. In the final step, the Boltzmann Monte Carlo method is used to refine the edges of the segmented image, which is obtained through active contour method.

2.5.1 Morphological Segmentation Operations

The morphological operations are used to detect he tumor-related clusters. The morphological operations are dilation, erosion, opening and closing. Among them, the most basic morphological operations are dilation and erosion. Dilation adds pixels; it causes the objects to grow in size whereas erosion removes the pixels at boundaries of the objects and causes the objects to shrink or become thin in size [25]. In this research work, closing operations are only performed. A closing operation is nothing but combination of dilation, followed by erosion. The equation for closing operation is as follows.

$$Clo\sin g\ operation: I \bullet B = (I \oplus S) \Theta S \qquad (1)$$

Where, I is a 2D input image, B and S are the structuring elements, which are neighbourhood around each pixel and used for morphological operations; $(I \oplus S)$ (=A) represents dilation operation which involves shifting S over I; $A \Theta S$ represent results of the erosion operation, obtained by eroding the previously dilated image (A).

2.5.2 Active Contour (Snake) model and Boltzmann Monte Carlo Method
a) Initialization of Contour:
The initialization step guides the subsequent evolution of the active contour during the segmentation of brain MRI images. The initial contour utilizes the region properties of the segmented tumor, specifically the centroid coordinates, obtained through the region props function. If a cluster of tumor region is identified, that is, if the centroid of cluster is not empty, the function creates a circular initial contour around the tumor by specifying a number of points in the contour and a radius proportional to the image dimensions.
b) Active Contour evolution (Snake model to delineate the tumor:
The one of the most popular traditional region-based active contour models, viz. Chan and Vese (CV) model is used in this research work [14]. An active contour method normally uses an energy minimization technique for accurate tumor delineation
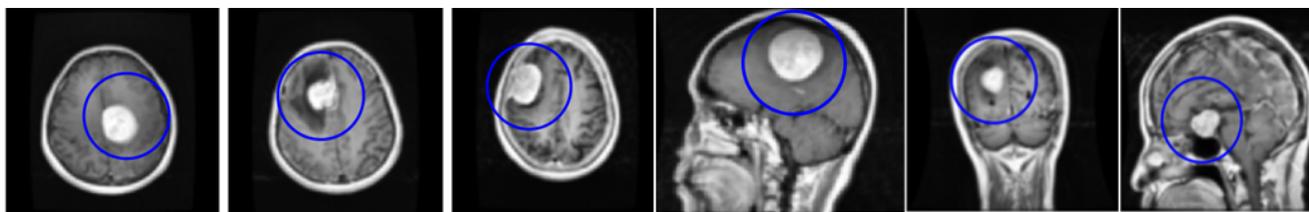
Fig 4. Locating the tumor at different regions of the brain in various brain MRI images during the initialization of contour

and segmentation in brain MRI image. A contour, τ has two energy functions associated with it. They are namely internal and external energies. The internal energy measures desired properties of a contour's shape, such as smoothness and continuity. The external energy is derived from a selected functional image, to measure desired features such as edges, lines, regions, and texture. The internal energy, apriori information, regularises the external energy, aposteriori information. The Snake model deforms an estimated initial contour by an energy minimization technique [26]. That is, it is the minimization of the total energy over the entire shape of the contour, τ. The total energy is defined as follows [27,28].

$$E_{snake}\ (\tau)\ =\ E_{internal}\ (\tau)\ +\ E_{external}\ (\tau) \tag{2}$$

Where, $E_{snake}\ (\tau)$ is the total energy of the contour τ, composed of the internal energy $E_{internal}\ (\tau)$ and external energy $E_{external}\ (\tau)$.

The internal energy term can be expressed as follows [27]

$$E_{internal}(\tau)\ =\ \int_{s=0}^{1} [\alpha\,(s)|\frac{\partial\tau\,(s)}{\partial s}|^2 + \beta\,(s)|\frac{\partial^2\,\tau\,(s)}{\partial s^2}|^2\ ].ds \tag{3}$$

Where, the first term simulates the surface tension of the contour and the second term is the acceleration term which simulates the rigidity of the contour, τ. $\alpha(s)$ and $\beta(s)$ are the controlling strengths(weighting parameters) associated with the surface tension and rigidity terms and is the arc length parameter along the contour, τ.

The external energy term can be expressed as follows [27].

$$E_{external} = \int_{0}^{1} E_{external}\ (\tau\,(s))\,.ds \tag{4}$$

where the external energy function, $E_{external}(\tau(s))$ can be defined as - $\gamma|\nabla I(\tau\,(s))\ |.ds$ and ∇I represents the gradient of the image I at the location [x(s),y(s)] of the contour, τ [12].

c) Contour Refinement process using Boltzmann Monte Carlo method:

The Boltzmann Monte Carlo/Markov Chain Monte Carlo (MCMC) method is used to hone/refine the resultant contour (τ_0) which is obtained through Active Contour model, over a period of time. The refinement process is described as follows.

Step 1 (Initialization): This process begins by introducing a temperature parameter (T) which is initially set to 100. The temperature decay rate (ρ) is fixed as 0.95. The end value of the temperature parameter for convergence is set to 0.01. Within the contour refinement process loop, the resultant contour (τ_0), previously obtained from the Active contour model, is given as input for MCMC method.

Step 2 (Proposed contour): A contour is proposed by perturbing the pixels of the existing resultant contour (τ_0) randomly and hence the change in energy (ΔE) between the trial contour (τ_t) (Energy=E (τ_t)) and old contour (τ_0) (Energy=E(τ_0)) is assessed. The perturbation of a pixel point (x_i, y_i) in the contour can be represented as

$$(xi',\ yi')\ =\ (xi\ + \Delta x,\ yi\ + \Delta y) \tag{5}$$

where (xi', y_i') are proposed/updated pixel points, (x_i, y_i) are current pixel points and (Δx, Δy) are random perturbations in (x_i, y_i).

After perturbing the old contour, a trial contour is either accepted or rejected according to probability values (p) and energy differences (ΔE). In Boltzmann Monte Carlo method, the probability (p) for accepting /rejecting the proposed /perturbed contour can be calculated using the following equation.

$$p=\ exp\ (-\triangle E/(kT)) \tag{6}$$

$$\triangle E \ = \ E\left(\tau_t\right) - E\left(\tau_0\right) \tag{7}$$

Where, ΔE is the Change in energy between old contour ($E(\tau_0)$) and trial contour ($E(\tau_t)$),

T is the temperature of the system and

k is the Boltzmann constant.

Step 3 (Acceptance tests): The following equations are employed to determine the acceptance or rejection of the proposed contour.

$$\left.\begin{array}{l} Accept\ the\ trial\ contour: \ a)\ if\ E\left(\tau_t\right) \ \leq \ E\left(\tau_0\right) \\ \qquad\qquad\qquad b)\ if\ E\left(\tau_t\right) \ > \ E\left(\tau_t\right) \\ \qquad\qquad\qquad then\ generate\ a\ random\ number,\ r\ where\ 0 \ \leq \ r \ \leq \ 1\ and \\ \qquad\qquad\qquad if\ r \ < \ p;\ (here\ p\ is\ calculated\ using\ Eqn.(\mathbf{6})). \end{array}\right\} \tag{8}$$

Reject the trial contour otherwise [18,19].

Step 4 (Incumbent solutions):

a) If the trial contour is accepted, then set the trial contour as the new contour (i.e., $\tau_1 = \tau_t$).

Now we have the Markov chain, $\tau_0 \rightarrow \tau_1$. (OR)

b) If the trial contour is rejected, then keep the old contour (i.e., $\tau_1 = \tau_0$).

c) To obtain the next new contour (τ_2), reduce the temperature using the Equation (9) as follows.

$$New\ temperature \ = \ Current\ temperature * \rho,\ where\ 0 \ < \ \rho \ < \ 1 \tag{9}$$

In this research work, ρ is set to 0.95.

d) Now, carry out the above operations from Step 2 on τ_1 and generate τ_2 and repeat this process. Generate the long Markov Chain $\tau_0 \rightarrow \tau_1 \rightarrow \tau_2 \rightarrow \tau_3 \rightarrow \ldots$until the convergence (final) temperature = 0.01 is reached, indicating that the system has attained a thermal equilibrium and no further significant changes occur in the contour. Ultimately, the resulting last contour denotes the final refined configuration.

Fig 5. Temperature decay versus iterations

Figure 5 shows how the temperature decreases over iterations according to the decay rate until it reaches the thermal equilibrium. That is, Figure 5 visually represents the process of temperature decay towards thermal equilibrium through iterative steps where rate of change of temperature becomes negligible and the system reaches a stable state.

3 Results and Discussion

This section presents experimental results, obtained through computational analysis of brain tumor segmentation. The performance metrics of brain tumor segmentation of both previously published works (existing methods) and current research work are compared.

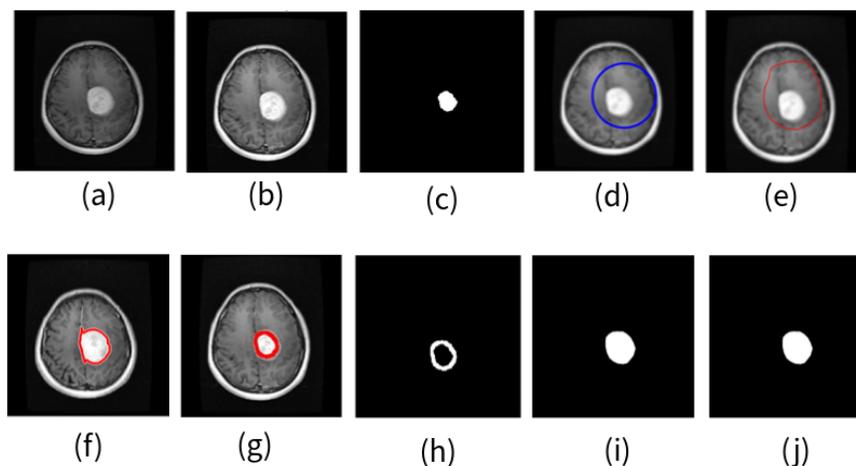## 3.1 Experimental results of Brain tumor segmentation of brain MRI images using MACB model

Fig 6. Experimental Results of BrainTumor Segmentation: Various stages - (a) Input brain MRI image **(b)** Enhanced image using CLACHE method **(c)** Eroded image using Morphological operations **(d)** Initialization of Contour using Centroid method **(e)** Contour evolution during Active Contour Process **(f)** Detection of contour using Active Contour method **(g)** Outlined image after MCMC Refinement **(h)** Outline of contour (tumor outline) **(i)** Final Segmented image using MACB model **(j)** Manual Ground truth image, available in the first dataset, for finding similarity

3.2 Performance evaluation

3.2.1 Performance metrics between the ground truth and segmented images (using first dataset)

In this research work, we have employed the MACB model to segment brain tumor from brain MRI images.

In **Supplementary table A**, the manually generated ground truth images (B), available in the first dataset, obtained from the Kaggle website, are compared with the segmented images (A), generated by the proposed MACB model. The performance metrics for finding similarity between images A and B are given in the **Supplementary table A**.

The values of Performance metrics in **Supplementary table A** indicate that the MACB model is performing well in segmenting the tumor in brain MRI images. The Performance metrics are DSC, Jaccard coefficient, Sensitivity, Specificity and Pixel accuracy. The Performance metrics for finding similarity between the segmented images generated using the proposed MACB model and the ground truth images, available in the first dataset, exhibit higher values.

3.2.2 Visualization of tumor outline marked and segmented using MACB model (using second dataset)

In **Supplementary table B**, the second dataset is used for visualization of tumor outline marked and tumor segmented using proposed MACB model. The second dataset has four-tumor classes viz. glioma, meningioma, pituitary, and no tumor. The ground truth images are not available in this dataset in order to compare with segmented images as in the case of first dataset. The tumor outline marked and segmented using MACB model in the brain MRI images in the second dataset are given in the **Supplementary table B** for visualization.

The images in **Supplementary table B** show better tumor outlined areas and segmentation in brain MRI images of the tumor classes- glioma, meningioma, pituitary and no tumor. The visual clarity of the segmented regions highlights the algorithm's capability to segment the tumors more accurately.

3.2.3 Analyzing Performance metrics for segmentation of tumor in the brain MRI images using the proposed MACB model (by using first dataset)

Table 1 shows the Performance metrics (average) values of segmentation of tumor in brain MRI images using the proposed MACB model (by using first dataset) without and with Boltzmann Monte Carlo Refinement method.

That is, esp. Dice Similarity Coefficient (DSC), Jaccard Coefficient, Sensitivity, Specificity and Pixel accuracy are given in Table 1 without and with Boltzmann Monte Carlo Refinement method.

Table 1. Performance metrics analysis of segmentation of tumor in the brain MRI images using MACB model (by using first dataset)

Method	Dataset	DSC	Jaccard Coefficient	Sensitivity	Specificity	Pixel accuracy
Without Boltzmann Monte Carlo Refinement method	3064 brain MRI images	92.27%	85.07%	93.23%	99.13%	97.47%
With Boltzmann Monte Carlo Refinement method (Proposed MACB model)	3064 brain MRI images	**93.26%**	**86.44%**	**97.27%**	**99.43%**	**98.95%**

The Dice Similarity Coefficient (DSC) quantifies the overlap between the predicted segmented region (of the image) and the ground truth image. It increases from 92.27% to 93.26% with the Boltzmann Monte Carlo Refinement method, indicating improved segmentation performance and better alignment with the ground truth image.

The Jaccard coefficient measures the similarity between the segmented and ground truth regions. It increases from 85.07% to 86.44% with Boltzmann Monte Carlo Refinement method and signifies improvement in delineating tumor boundaries.

The Sensitivity significantly rises from 93.23% to 97.27%, indicating a notable improvement in tumor detection with the ability to identify tumor pixels correctly, minimizing missed lesions.

The Specificity measures the model's ability to identify non-tumor pixels correctly. The slight increase from 99.13% to 99.43% suggests a minor enhancement in distinguishing non-tumor pixels.

The Pixel accuracy represents the correctness of pixel classification over the total number of pixels, specifying the overall correctness of the tumor segmentation. Its improvement, from 97.47% to 98.95% with Boltzmann Monte Carlo Refinement method, indicates better overall segmentation Pixel accuracy. Overall, as shown in Table 1, after applying the Boltzmann Monte Carlo method for refinement process, the Performance metrics values for brain tumor segmentation in the MRI images have improved. Hence, this novel approach (the proposed MACB model) has resulted in enhanced precision and efficiency in the brain tumor segmentation process.

3.2.4 Performance metrics analysis of various existing methods

Table 2 presents a comprehensive comparison of various existing methods in the field of image segmentation of tumor in brain MRI images and their corresponding performance metrics. Each method is associated with a reference, year of publication, dataset used and Performance metrics evaluation. These Performance metrics values provide insights into the effectiveness of each method in segmenting tumor in brain MRI images.

Table 2. Performance metrics analysis of segmentation of tumor in the brain MRI images by the existing methods

Reference	Year of research work	Existing method/model	Dataset	Performance metrics evaluation	
				Metrics	Values
[1]	2010	Fuzzy approach	256 Slices of normal brain and 256 slices of meningioma.	Jaccard coefficient	84.00%
[1]	2011	Enhanced Possibilistic Fuzzy C-Means	Not specified	Jaccard coefficient	82.10%
[29]	2011	Gradient vector flow	120 images	Sensitivity Pixel accuracy	95.40% 92.80%
[30]	2015	Morphological Region-Based Initial Contour	STARE dataset 20 images DRIVE dataset 20 images	DSC Sensitivity Specificity Precision Pixel accuracy	75.70% 74.21% 98.13% 82.46% 97.44%
[31]	2016	Convolutional Neural Network (CNN)	241 brain MRI images	DSC Sensitivity Precision	88.00% 89.00% 88.00%
[32]	2017	Local Binary Pattern and Histogram Orientation	Glioma Dataset	DSC	93.00%
[1]	2018	FCM based Segmentation	250 brain MRI images	Pixel accuracy	98.67%
[33]	2019	Active Contour model (ACM) and Neural Networks (NN)	250 brain MRI images	DSC	88.30%

Continued on next page

Table 2 continued					
(11)	2020	Active contour model (ACM) & FCM Optimization	233 Patients, 3064 slices (Glioma -1426 Meningioma-708, pituitary-930)	DSC Sensitivity Specificity	82.50% 71.00% 97.50%
(10)	2021	K-Means, Morphological Active Contour model (ACM)	250 images	DSC	91.79%
(9)	2023	Fuzzy clustering, Morphological reconstruction and Active contour model (ACM)	250 images	DSC Jaccard coefficient Sensitivity Precision	92.00% 84.00% 92.10% 92.05%
(12)	2023	Non- Linear Filters and Active Contour model (ACM)	Brain MRI Dataset 400 images	DSC Sensitivity Precision Pixel accuracy	85.82% 82.01% 97.20% 97.38%

3.2.5 Comparative analysis of Performance metrics for tumor segmentation in the brain MRI images using the proposed MACB model and existing methods
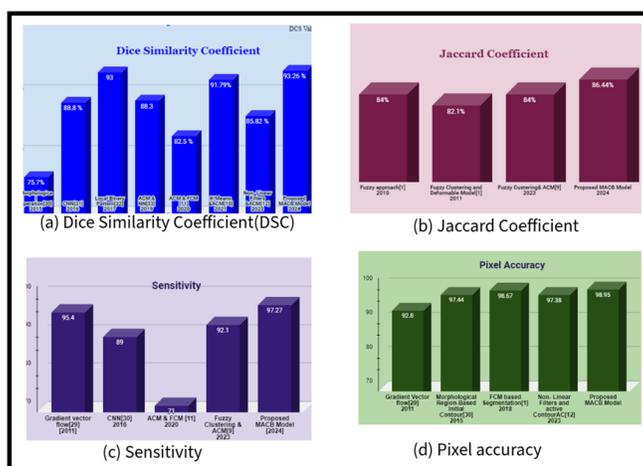
Fig 7. Comparative analysis of Performance metrics for tumor segmentation in the brain MRI images using the proposed MACB model and existing methods

Tables 1 and 2 provide a comprehensive overview of values of Performance metrics. Table 1 highlights the higher values of Performance metrics for tumor segmentation in the brain MRI images using the proposed MACB model than that for all other models. The proposed MACB model outperforms the existing methods (Table 2). Hence, the segmentation of brain tumor in the brain MRI images is accurate and essential for diagnosis, early detection, and treatment planning for the disease. The various existing methods have been developed for this purpose, each with its own advantages and limitations.

S. Singh and V. Saxena [34] have proposed an automated solution utilizing a CNN for brain tumor classification and a hybrid approach by integrating graph-based and threshold segmentation techniques to locate the tumor region accurately in magnetic resonance (MR) brain images and has shown the highest Jaccard coefficient value among the five test images as 93.86%. But, in our research work, we have used 3064 MRI images for segmentation using MACB model and achieved the highest Jaccard coefficient value of 94.86% for one of the MRI images.

Here, we compare the Performance metrics of the existing methods with the proposed MACB model in Figure 7. The comparative analysis for tumor segmentation in the brain MRI images using the proposed MACB model and existing methods are visually represented through the bar charts, illustrating the metrics such as Dice Similarity Coefficient (DSC) in Figure 7**(a)**, Jaccard Coefficient in Figure 7**(b)**, Sensitivity in Figure 7**(c)** and Pixel accuracy in Figure 7 **(d)**.

The bar charts in Figure 7 illustrate that the proposed MACB model performs better than existing methods in delineating brain tumor boundaries accurately as we compare their performance metrics.

3.3 Research findings:

This research paper proposes a new tumor identification and segmentation method that incorporates Gaussian filtering kernels, Contrast Limited Adaptive Histogram Equalization (CLAHE), Morphological segmentation operation, Active Contour model and Boltzmann Monte Carlo /MCMC method. While comparing with other existing methods, the MACB model uses the Boltzmann Monte Carlo method for the first time to refine the contour, which is earlier generated by Active contour model for Brain tumor segmentation in brain MRI images. The efficacy of the proposed MACB method in attaining precise tumor segmentation is demonstrated while comparing with other existing methods/studies in MRI images. Further, this approach shows significance in the field of medical image processing and tumor analysis. The proposed MACB model outperforms the existing methods (given in Table 2) in detecting the brain tumor in the MRI images. The proposed MACB model takes lesser running time while comparing with CNN segmentation methods, which need large amount of time to train the network.

4 Conclusions

In this research work, a new image segmentation process, the MACB model, is proposed for the detection, segmentation and refinement process of brain tumor by incorporating Boltzmann Monte Carlo method with Morphological Region-Based Active Contour model. This process shows good performance and exhibits improved Dice Similarity Coefficient (DSC) and Jaccard Coefficient using larger dataset of images while comparing with the other previous works /existing methods which have mostly used small datasets and standard optimization techniques such as Fuzzy C-Means, K-Means Clustering and Particle Swarm Optimization (PSO) etc. The proposed MACB model outperforms the existing methods (given in Table 2) in detecting the brain tumor in the MRI images and takes lesser running time while comparing with CNN segmentation methods which need large amount of time to train the network. Since, this novel approach (the proposed MACB model) has resulted in enhanced precision and efficiency in the brain tumor segmentation process, it could be a useful tool for radiologists for diagnosing and segmenting the brain tumor in the MRI images.

In the future work, it is better to focus on classification of the segmented tumor images (using the proposed MACB model) with classes viz. glioma, meningioma, no tumor and pituitary (using second dataset) and to get improved classification performance metrics. This research work contributes to medical image analysis for health care in the medical field.

Hence, it is recommended to carry out the classification analysis of segmented and unsegmented images using Machine Learning (ML) algorithms and CNN models [35] in the future. We expect that the segmented brain MRI images may yield better classification accuracy.

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References

1) Kaifi R. A Review of Recent Advances in Brain Tumor Diagnosis Based on AI-Based Classification. *Diagnostics*. 2023;13(18):1–32. Available from: https://dx.doi.org/10.3390/diagnostics13183007.

2) Wadhwa A, Bhardwaj A, Verma VS. A review on brain tumor segmentation of MRI images. *Magnetic Resonance Imaging*. 2019;61:247–259. Available from: https://dx.doi.org/10.1016/j.mri.2019.05.043.

3) Ullah N, Khan JA, Khan MS, Khan W, Hassan I, Obayya M, et al. An Effective Approach to Detect and Identify Brain Tumors Using Transfer Learning. *Applied Sciences*. 2022;12(11):1–17. Available from: https://dx.doi.org/10.3390/app12115645.

4) Mane V, Chivate A, Ambekar P, Chavan A, Pangavhane A. Brain Tumor Detection using Convolutional Neural Network. In: Proceedings of International Joint Conference on Advances in Computational Intelligence;vol. 2019 of Algorithms for Intelligent Systems ((AIS)). Singapore. Springer. 2024;p. 449–461. Available from: https://doi.org/10.1007/978-981-97-0180-3_35.

5) Abd-Ellah MK, Awad AI, Khalaf AAM, Hamed HFA. A review on brain tumor diagnosis from MRI images: Practical implications, key achievements, and lessons learned. *Magnetic Resonance Imaging*. 2019;61:300–318. Available from: https://dx.doi.org/10.1016/j.mri.2019.05.028.

6) Rezazadeh R. The Concept of Centralization and Decentralization : An Analysis and Evaluation. *International Review of Administrative Sciences*. 1961;27(4):425–430. Available from: https://dx.doi.org/10.1177/002085236102700407.

7) Kulshreshtha A, Nagpal A. IFAS: improved fully automatic segmentation convolutional neural network model along with morphological segmentation for brain tumor detection. *International Journal of Information Technology*. 2024;16(3):1517–1525. Available from: https://dx.doi.org/10.1007/s41870-023-01572-5.

8) Ayomide KS, Aris TNM, Zolkepli M. Improving Brain Tumor Segmentation in MRI Images through Enhanced Convolutional Neural Networks. *International Journal of Advanced Computer Science and Applications*. 2023;14(4):670–678. Available from: https://dx.doi.org/10.14569/ijacsa.2023.0140473.

9) Shekari M, Rostamian M. Brain tumor segmentation from MRI using FCM clustering, morphological reconstruction, and active contour. *Multimedia Tools and Applications*. 2024;83(14):42973–42998. Available from: https://dx.doi.org/10.1007/s11042-023-17233-5.

10) Shahvaran Z, Kazemi K, Fouladivanda M, Helfroush MS, Godefroy O, Aarabi A. Morphological active contour model for automatic brain tumor extraction from multimodal magnetic resonance images. *Journal of Neuroscience Methods*. 2021;362. Available from: https://dx.doi.org/10.1016/j.jneumeth.2021.109296.

11) Sheela CJJ, Suganthi G. Brain tumor segmentation with radius contraction and expansion based initial contour detection for active contour model. *Multimedia Tools and Applications*. 2020;79(33-34):23793–23819. Available from: https://dx.doi.org/10.1007/s11042-020-09006-1.

12) Veeramalla SK, Hindumathi V, Reddy TV, Pattan AB, Nandan TPK. Segmentation of MRI Images Using A Combination of Active Contour Modelling and Morphological Processing. *Journal of Mechanics in Medicine and Biology*. 2023;23(04):1–24. Available from: https://dx.doi.org/10.1142/s021951942340002x.

13) Ilunga–Mbuyamba E, Avina–Cervantes JG, Cepeda–Negrete J, Ibarra–Manzano MA, Chalopin C. Automatic selection of localized region-based active contour models using image content analysis applied to brain tumor segmentation. *Computers in Biology and Medicine*. 2017;91:69–79. Available from: https://dx.doi.org/10.1016/j.compbiomed.2017.10.003.

14) Sun K, Qin L, Zeng S, Li Y. Automatic Smoothing Parameter Adjustment of Region-Based Active Contour Using Edge Information. In: 2016 8th International Conference on Intelligent Human-Machine Systems and Cybernetics (IHMSC). IEEE. 2016. Available from: https://doi.org/10.1109/IHMSC.2016.163.

15) Al-Fahdawi S, Al-Waisy AS, Zeebaree DQ, Qahwaji R, Natiq H, Mohammed MA, et al. Fundus-DeepNet: Multi-label deep learning classification system for enhanced detection of multiple ocular diseases through data fusion of fundus images. *Information Fusion*. 2024;102:1–11. Available from: https://dx.doi.org/10.1016/j.inffus.2023.102059.

16) Ye X, Ji B, Chen X, Qian D, Zhao Z. Probability Boltzmann Machine Network for Face Detection on Video. In: 2020 13th International Congress on Image and Signal Processing, BioMedical Engineering and Informatics (CISP-BMEI). IEEE. 2020;p. 138–147. Available from: https://doi.org/10.1109/CISP-BMEI51763.2020.9263555.

17) Pramanandaperumal T, Srivaishnavi KR, Rani DL, Murthy KPN. Boltzmann and Non-Boltzmann sampling for image processing. *Indian Journal of Economics and Development*. 2017;5(9):1–8. Available from: https://www.i-scholar.in/index.php/ijed/article/view/176178.

18) Pai PF, Hong WC. Support vector machines with simulated annealing algorithms in electricity load forecasting. *Energy Conversion and Management*. 2005;46(17):2669–2688. Available from: https://dx.doi.org/10.1016/j.enconman.2005.02.004.

19) Metropolis N, Rosenbluth AW, Rosenbluth MN, Teller AH, Teller E. Equation of State Calculations by Fast Computing Machines. *The Journal of Chemical Physics*. 1953;21(6):1087–1092. Available from: https://dx.doi.org/10.1063/1.1699114.

20) Patil RC, Bhalchandra AS. Brain tumor extraction from MRI images using MATLAB. *International Journal of Electronics, Communication and Soft Computing Science & Engineering (IJECSCSE)*. 2012;1(4):1–4. Available from: http://www.hep.upatras.gr/class/download/psi_epe_iko/5-Brain-Tumour-Extraction-from-MRI-Images-Using-MATLAB.pdf.

21) Tomar N. Brain Tumor Segmentation. 2021. Available from: https://www.kaggle.com/datasets/nikhilroxtomar/brain-tumor-segmentation/data.

22) Nickparvar M. Brain Tumor MRI Dataset. 2021. Available from: https://www.kaggle.com/datasets/masoudnickparvar/brain-tumor-mri-dataset.

23) Kumar A, Sodhi SS. Comparative Analysis of Gaussian Filter, Median Filter and Denoise Autoenocoder. In: 2020 7th International Conference on Computing for Sustainable Global Development (INDIACom);vol. 2020. IEEE. 2020;p. 45–51. Available from: https://doi.org/10.23919/INDIACom49435.2020.9083712.

24) Tenghongsakul K, Kanjanasurat I, Archevapanich T, Purahong B, Lasakul A. Deep transfer learning for brain tumor detection based on MRI images. In: 2022 The 4th International Conference on Electronics Communication Technologies (ICECT 2022) ;vol. 2497 of Journal of Physics: Conference Series. IOP Publishing. 2023;p. 1–9. Available from: https://dx.doi.org/10.1088/1742-6596/2497/1/012015.

25) Pandey SK, Bhandari AK. Morphological active contour based SVM model for lung cancer image segmentation. *Multimedia Tools and Applications*. 2024. Available from: https://dx.doi.org/10.1007/s11042-023-18092-w.

26) Gunn SR, Nixon MS. A robust snake implementation; a dual active contour. *IEEE Transactions on Pattern Analysis and Machine Intelligence*. 1997;19(1):63–68. Available from: https://dx.doi.org/10.1109/34.566812.

27) Das B, Banerjee S. Parametric Contour Model In Medical Image Segmentation. In: Deformable Models. Topics in Biomedical Engineering. International Book Series ((ITBE));New York, NY, USA. Springer. 2007;p. 31–74. Available from: https://doi.org/10.1007/978-0-387-68343-0_2.

28) Shenbagarajan A, Ramalingam V, Balasubramanian C, Palanivel S. Tumor Diagnosis in MRI Brain Image using ACM Segmentation and ANN-LM Classification Techniques. *Indian Journal of Science and Technology*. 2016;9(1):1–12. Available from: https://dx.doi.org/10.17485/ijst/2016/v9i1/78766.

29) Kazerooni AF, Ahmadian A, Serej ND, Rad HS, Saberi H, Yousefi H, et al. Segmentation of brain tumors in MRI images using multi-scale gradient vector flow. In: 2011 Annual International Conference of the IEEE Engineering in Medicine and Biology Society. IEEE. 2011;p. 7973–7976. Available from: https://doi.org/10.1109/IEMBS.2011.6091966.

30) Rad AE, Rahim MSM, Kolivand H, Amin IBM. Morphological region-based initial contour algorithm for level set methods in image segmentation. *Multimedia Tools and Applications*. 2017;76(2):2185–2201. Available from: https://dx.doi.org/10.1007/s11042-015-3196-y.

31) Pereira S, Pinto A, Alves V, Silva CA. Brain Tumor Segmentation Using Convolutional Neural Networks in MRI Images. *IEEE Transactions on Medical Imaging*. 2016;35(5):1240–1251. Available from: https://dx.doi.org/10.1109/tmi.2016.2538465.

32) Abbasi S, Tajeripour F. Detection of brain tumor in 3D MRI images using local binary patterns and histogram orientation gradient. *Neurocomputing*. 2017;219:526–535. Available from: https://doi.org/10.1016/j.neucom.2016.09.051.

33) Soleymanifard M, Hamghalam M. Segmentation of Whole Tumor Using Localized Active Contour and Trained Neural Network in Boundaries. In: 2019 5th Conference on Knowledge Based Engineering and Innovation (KBEI). IEEE. 2019. Available from: https://doi.org/10.1109/KBEI.2019.8735050.

34) Singh S, Saxena V. Classification and Segmentation of MRI Images of Brain Tumors Using Deep Learning and Hybrid Approach. *International journal of electrical and computer engineering systems*. 2024;15(2):163–172. Available from: https://dx.doi.org/10.32985/ijeces.15.2.5.

35) Saxena V, Singh S, Singh KV. MRI Brain Tumor Prediction using Azure Streamlit Framework and Analysis of CNN Activation Functions. *Indian Journal Of Science And Technology*. 2023;16(37):3129–3138. Available from: https://dx.doi.org/10.17485/ijst/v16i37.427.