

Automatic Brain Tumor Detection and Segmentation from MRI Images

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Received: 22 October 2025 ; Accepted: 28 September 2026; Published: 1 October 2026

Abstract: A brain tumor is an abnormal growth of tissue in the central spine or brain that can cause the brain to become more pressured and interfere with normal brain function. Early detection of a brain tumor is extremely challenging for medical professionals. MRI images can be greatly impacted by noise and other environmental disruptions. As a result, diagnosing the tumor and its causes becomes challenging for medical professionals. Therefore, a methodology is presented to detect brain tumors and segment them from medical image. According to the studies, the region growing algorithm initializes the seed point either manually or semi-manually, which has an impact on the segmentation outcome. Therefore, an improved region growing algorithm is suggested for automatic seed point initialization. This paper presents an automated and integrated framework for the highly accurate detection and segmentation of brain tumors. The suggested methodology starts with image pre-processing to enhance image quality and reduce noise. The next step involves using the skull stripping developed algorithm, which is specifically made for precise brain mask extraction. The generated mask is crucial in automatically determining the tumor region's seed point, which removes the need for human intervention and reduces the variability of the results. Lastly, the entire tumor region is segmented using a region-growing algorithm that starts with the identified seed. Experimental results demonstrate that our proposed technique achieves robust performance and accurate results in detecting and segmenting brain tumor boundaries in MRI images, making it a promising tool for supporting clinical decision-making.

Keywords: Brain MRI Image; Brain Tumor; Detection; Morphological Filtering; Region Growing; Segmentation; Skull Stripping

1. Introduction

A brain tumor is a mass of tissue where the cells are growing out of control. It originates from a variety of cells, both inside and outside the brain. While secondary tumors spread to other parts of the body, primary tumors start in the brain itself. Depending on the cells or the origin derived from various tumor types, tumors can have a variety of origins. Gangliogliomas, for instance, are tumors that contain neoplastic neurons and are typically classified as grade I or low-grade tumors, indicating that the tumor is well-differentiated and grows slowly [1].

Meningioma, which can be grade I, II, or III and is slow-growing, is another example. It starts from the meninges, which are the three membranes that cover the brain and spinal cord [1]. Cognitive disorders, dizziness, muscular disorders, headache that can be persistent and acute, etc., are all signs of a brain tumor. Surgery (craniotomy), tomotherapy, radiotherapy, and chemotherapy are all used to treat them. Brain tumor deaths have increased over the past few decades in developed countries, although brain tumors are relatively uncommon, accounting for 1.4% of new cases annually [2]. In India, there are 5 to 10 cases of CNS tumors for every 100,000 people, and the number is on the rise. It makes up 2% of all cancers [3-4].

Abnormal blobs in the brain are indicative of brain tumors on MRI scans (or any other scan). These regions or blobs are typically brighter than the surrounding area and have a different illumination than the rest of the brain. Nevertheless, it is a very challenging task to segment the tumors in MRI images.

Zainab Ghayyib Abdul Hasan, "Automatic Brain Tumor Detection and Segmentation from MRI Images", *Annals of Emerging Technologies in Computing (AETiC)*, Print ISSN: 2516-0281, Online ISSN: 2516-029X, 1 October 2026, Vol. 10, No. 4, pp. 123-142, Published by [International Association for Educators and Researchers \(IAER\)](http://www.theiaer.org), DOI: 10.33166/AETiC.2026.04.005, Available: <https://aetic.theiaer.org/archive/v10/v10n4/p5.html>.

Tumors vary in position, size, and even textures. Segmenting the tumor based on characteristics such as illumination may run into problems like overlapping pixel intensities with normal tissues. In MRI images, identification and segmentation of brain tumors is crucial because it shows the presence of abnormal tissues for patient follow-up or treatment. The majority of brain tumors also result in edema [5], which can alter the pixel intensities surrounding the tumor and distort the surrounding structures.

This paper presents a new technique for the detection and segmentation of brain tumors in MRI images. The steps in the proposed methodology were image preprocessing, skull stripping involving the Bidirectional Horizontal Scan Algorithm and morphological refinement of the brain image, tumor candidate regions extraction, automatic seed point selection of the tumor region, and the brain tumor segmentation algorithm utilizes a region-growing technique that starts based on a selected seed point. This paper places a strong emphasis on the use of image processing because digital images have a number of issues, including the illumination issue mentioned above. As a result, the system may generate incorrect outputs if appropriate image preprocessing techniques are not used. Selecting appropriate methods is also essential because one of the main issues with image processing for datasets is that the method may work well for a specific kind of image but not for the full dataset.

2. Related Work

Numerous studies have been conducted using various segmentation techniques in the field of medical image segmentation, including brain tumors, breast cancer, and biometric processes [6-10]. However, brain tumor segmentation was a difficult task due to the indistinguishable boundaries between regions of the human brain tissues, the large variations in tissue structure, and its complexity [11]. Several brain image segmentation techniques have been developed for MRI images in recent years, and they have been evaluated using various evaluation parameters. One of the best methods for segmenting brain tumors is the region growing algorithm. Regions with similar pixels are primarily extracted using this method [12]. The initial seed point selection and the kind of similarity metric applied between nearby pixels have a significant impact on the region-growing algorithm's performance. However, choosing the best seed point is typically done by hand, and the algorithm as a whole is inconsistent. The reason for the inconsistency is that seed points are chosen at random from a set of possible seed points generated by computing the possibility of a seeds falling within a tumor region.

Thiruvankadam [13] explained that the most crucial stage in region-growing-based brain tumor segmentation is manual seed point selection.

Sarathi *et al.* [14] suggested a region-growing segmentation algorithm based on wavelet features for a 256x256 T1-weighted enhanced MRI image. They first convolved the 64x64 kernel with the 64x64 preprocessed brain images, and then they extracted wavelet features that were utilized as potential initial seed points until the optimal ROI was extracted. Significant wavelet feature points were utilized alternately as a possible initial seed. In this paper, the adjacent pixels to the seed point were included or excluded based on similarity properties such as entropy, standard deviation, variance, and mean. The results of the experiment demonstrated that the suggested method produced better performance outcomes with less computation time.

Ho *et al.* [15] proposed that the selection of the seed points was based on the intensity values of the brain tissue from its various regions. However, prior knowledge of the intensity and structure of the brain map is required. Therefore, multi-modal images were preferred in order to obtain detailed information on the brain images, and hence, in this work, a fusion of multi-modal images was used to automatically select the initial seed.

Cui *et al.* [11] developed an automatic image segmentation algorithm for brain tumors. The model primarily enhances the growth rules and seed point selection. The segmentation algorithm is made more robust by automatically choosing the seed point using the fusion information method with multimodal MRI images. Additionally, it makes use of the region growing while maintaining the co-constraint of spatial texture and intensity to largely preserve the local feature and boundary information of the brain tumor. surpasses other segmentation algorithms in terms of accuracy and computational cost.

Hachemi *et al.* [16] The author has created a novel automatic technique in this paper that is based on the multisegmentation of the brain tumor region. To define the desired classes, used a refined region-

growing algorithm based on quasi-Monte Carlo and expectation maximization techniques. A number of metrics were computed to assess the technique's performance. The fully automatic multisegmentation method created in this study performed well and may provide a fresh alternative to traditional methods for MRI tumor detection.

Biratu *et al.* [17] suggested an improved region-growing algorithm for initializing seed points automatically. For every input brain image, the skull was removed using a thresholding technique. The brain image is separated into eight blocks once the skull has been stripped. Then calculated the mean intensities for each block, and out of the eight blocks, the five with the highest mean intensities were chosen. Five distinct regions of interest (ROIs) were then produced by using the five maximum mean intensities as a seed point for the region-growing algorithm independently. The best region of interest was chosen as the final ROI after the five ROIs produced using the suggested method were assessed using the accuracy (Acc) against the ground truth (GT), intersection over union (IoU), and dice similarity score (DSS). Lastly, the common dataset, BRATS2015, was used to compare the final ROI with various cutting-edge deep learning algorithms.

Shiny & Sugitha [18], A region-growing method for automatic segmentation and tumor detection based on MRI texture is suggested. In order to detect the area and determine whether it is involved or not, this technique was used to separate the irregular tissues from regular tissues. This greatly aided the surgeon in accurately identifying the affected areas.

Bhunja [19] The author discusses traditional techniques for brain tumor segmentation with an emphasis on a detailed examination of region-growing segmentation from MRI images. Brain tumor images from Kaggle and the Image Processing Toolbox under Matlab software were utilized for the project's implementation.

In recent years, attention models and transformers have dominated the field of medical image segmentation. A representative example is the Swin-Unet architecture, which can capture complex anatomical structures and long-range contextual associations that traditional CNNs often overlook. This study focuses on constructing a robust baseline for the present comparative analysis; however, the revolutionary potential of these new architectures is acknowledged.

Thresholding and clustering methods [13] are considered simple and global methods of segmentation that always fail to perform well in heterogeneous tumors due to their inadequate consideration of spatial context. The "automated region growing" scheme proposed in the above studies [11, 14, 17] and improved in our study is undoubtedly an achievement of the field since it successfully combines human clinical intuition when a radiologist recognizes a focal point and technical effectiveness. The subjective assessment is transformed into a clear objective and mathematical procedure through mathematical modeling of focal initialization.

The issue of preprocessing and noise suppression is quite debatable in recent scientific works. Although the classical method of median filtering used in the above-mentioned articles [14, 18], due to its resistance to salt-and-pepper noise and computational efficiency, is criticized for causing over-smoothing, which can result in failing to preserve the delicate edges of high-grade gliomas (HGG). This contradiction is overcome since in our paper, while using median filtering at the preprocessing stage, our new algorithm of region growing includes dynamic intensity gradients that help avoid the problem of the edges' smoothing, thereby preventing the excessive blurring of complex lesion boundaries.

Table 1. Comparative analysis of existing Related Research on MRI tumor methodologies.

Reference	Methodology	Contextual Success & Clinical Transparency	Limitations & Contextual Failure	Computational Complexity	Robustness to Noise	Seed Selection
Kebede <i>et al.</i> (2020) [10]	Classifier-based Segmentation	Demonstrates generalizability of ML classifiers across different tissue types (e.g., breast cancer).	Requires complex feature engineering; partially suffers from "black-box" issues compared to region growing.	Moderate: Multi-stage pipeline (Noise removal -> K-Means & Feature Extraction -> SVM/KNN)	High: Includes explicit noise, tag, and pectoral muscle removal steps	Automatic
Cui <i>et al.</i> (2018) [11]	Region Growing with Co-constraint	Reduces manual reliance while maintaining	May fail if spatial co-constraints cannot	Low: Optimized for lower computational	Moderate: Automatic seed selection via	Automatic

		algorithmic transparency for clinicians.	distinguish overlapping intensities in necrotic cores.	cost than deep learning; uses multimodal fusion	fusion improves stability against local artifacts	
Angulakshmi & Priya (2017) [12]	Review of Automated Techniques (Comprehensive Review)	Highlights that CNNs achieve high accuracy in complex feature extraction.	CNNs act as a "black box" with high computational costs, hindering rapid clinical adoption.	Variable: Discusses a wide range of algorithmic complexities in the literature	Context-dependent: Reviews robustness across different method families	Literature Analysis
Kalaiselvi & Nagaraja (2015) [13]	FCM Clustering + Seeded Region Growing	FCM serves as an evolutionary bridge between basic thresholding and directed growing.	Struggles with High-Grade Gliomas (HGG) where FCM misclusters highly variable intensities.	Moderate: Two-stage (Clustering then Region Growing); modified objective functions	Moderate: Enhanced FCM membership values improve handling of tissue intensity overlaps	Semi-automatic (Seeded)
Sarathi <i>et al.</i> (2013) [14]	Feature Point Detector + Seeded Region Growing	Offers high computational efficiency, suitable for rapid pre-operative clinical workflows.	Heavy reliance on specific localized points may cause failure in multifocal lesions.	Moderate: Requires feature point detection stage before region growing	Moderate: Novel detector aims to isolate tumor points from background noise	Semi-automatic (Seeded)
Ho <i>et al.</i> (2016) [15]	Region Growing (Brain Extraction)	Specialized in T1-weighted MRI; successfully automates the removal of non-brain tissue (skull stripping).	Primarily designed for brain extraction rather than internal tumor segmentation; may lose peripheral brain pixels.	Low: Simple intensity distribution analysis and seed point selection	Insufficient evidence to report measured robustness to MRI noise Not Detailed: Primarily focused on skull stripping rather than denoising	Fully automatic
Hachemi <i>et al.</i> (2020) [16]	Improved Region-growing + Quasi-Monte Carlo	Highly interpretable; statistical integration improves handling of intra-tumor variance.	Computational cost rises with complex statistical models, negating the speed advantage.	Low: Extremely efficient (<30s on 2.4 GHz CPU); no training required	High: QMC sampling and constrained k-means provide robust statistical estimation	Fully automatic
Biratu <i>et al.</i> (2021) [17]	Enhanced Region Growing	Provides a balance between transparency and accuracy in brain MR images.	Can be sensitive to initial parameters if the tumor is highly diffuse or small.	Moderate: Includes skull stripping, block-wise mean analysis, and multi-ROI evaluation	Moderate: Preprocessing (skull stripping) and mean-intensity filtering reduce artifact impact	Fully automatic
Shiny & Sugitha (2022) [18]	Texture Analysis + Region Growing	Tailored for pre-operative planning; provides clear, interpretable visual results for surgeons.	May struggle with post-operative images where anatomy is distorted or contains artifacts.	Low-to-Moderate: Utilizes 2D MRI texture features to identify complex necrotic regions	Moderate: Aims to resolve ambiguities in complex necrotic tumor structures	Automatic
Bhunia (2023) [19]	Standard Region Growing Analysis	Proves the fundamental effectiveness of the algorithm for general MRI tumor detection.	Lacks advanced optimization for multi-modal sequences (T1c, FLAIR).	Low: Basic seed-based intensity thresholding and region expansion	Low: Highly sensitive to intensity variations and MRI noise	Semi-automatic / Automatic

Although the previous works [16, 17, 19] rightly pointed out the problem of manual seed selection, they do not take into consideration that the above-mentioned problem is more than just being time-consuming, as this does not meet the demands of current clinical practice. The actual, complex research gap includes three main points: (1) Inter-observer variability, where manual seed selection introduces significant differences among clinicians; (2) Seed selection in necrotic tumor cores, when traditional automated seeds frequently fail in the heterogeneous parts of an advanced tumor; and (3) A trade-off

between the "black-box" problem and computational speed, as CNNs are known for their accuracy but suffer from being so computationally expensive and hard-to-interpret that making hinders doctors' trust and adopting them in real-time. Thus, the developed algorithm solves the problem by introducing a fast, mathematically interpretable, and automatic seed selection procedure that is immune to inter-observer variability and specifically designed to address necrotic irregularities without using the additional complexity of deep learning.

In general, the literature analysis indicates that existing approaches towards the segmentation of brain tumors are focused on enhancing one facet of the problem at the expense of others. Thresholding and clustering provide easy implementation, but they demonstrate low robustness when applied to heterogeneous tumor environments. Traditional region growing algorithms increase spatial consistency but often require manual input or rigid growth parameters, thus limiting flexibility to different tumor types. On the other hand, recent deep learning algorithms allow obtaining accurate segmentation results but require a large amount of training data, significant computational resources, and operate as black boxes with limited interpretability. However, the suggested architecture is aimed at being a solution that concurrently addresses these limitations. It allows overcoming the problems associated with tumor heterogeneity and necrosis structures by implementing fully automatic seed selection, adaptive region-growing conditions, and computationally efficient image pre-processing. Therefore, the suggested study not only aims to enhance the accurate segmentation method but also to create a balanced approach combining automation, interpretability, computational efficiency, and trustworthy tumor delineation.

Figure 1 displays a comparative analysis of the literature performance and emphasizes the trade-off between the processing efficiency and the accuracy of segmentation. The simpler the algorithm used (e.g., Ho & Bhunia), the faster the processing speed; because they are of lower accuracy (88–91%), their clinical use for complex disorders is restricted. At the same time, more complex statistical algorithms (Hachemi) or algorithms based on metaheuristics (Shiny) have higher processing costs due to high accuracy levels (96–97%) achieved in real-time surgery situations. Algorithms of intermediate complexity, like Cui & Biratu, provide a better balance of around 95–96% accuracy in 10 seconds. It is important to note that there is a significant research gap related to developing a proposed method that breaks the linear trade-off and would provide both high accuracy and clinical-grade efficiency.

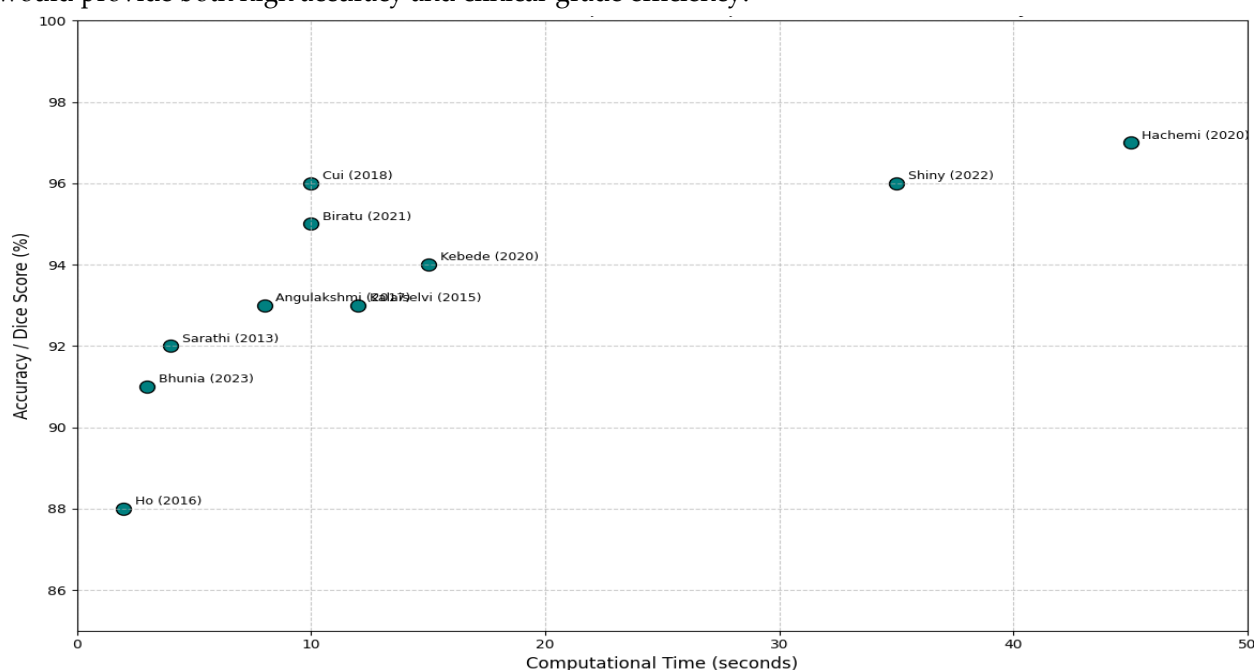


Figure 1. Literature performance comparison: computational time vs. accuracy

3. Proposed Methodology

The developed methodology is designed to detect brain tumors through automated analysis of 2D Magnetic Resonance Imaging (MRI). The process involves several essential stages, which can be seen in Figure 2 below.

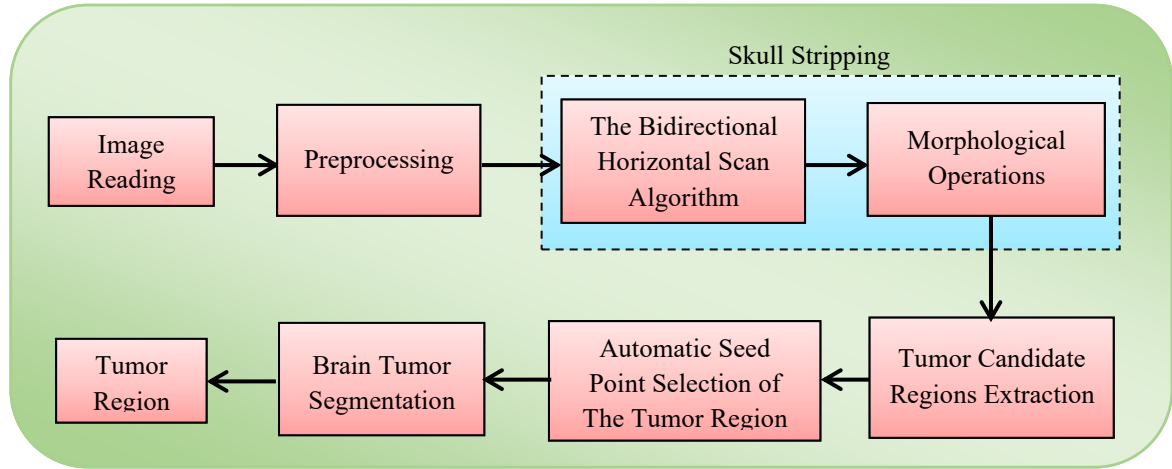


Figure 2. Flowchart of Proposed Methodology

3.1. Preprocessing

Converting image to grayscale: The input images, which come from an RGB color space, are converted into grayscale, as MRI imaging is primarily based on intensity. This makes the computation simple and standardizes the image format.

Applying Median Filter: Noise can be found in images captured in the medical field. In order to remove the noise from the image while maintaining the sharp edges, The median filter was applied to the grayscale image; that is a very good method for identifying anatomical boundaries.

3.2. Skull Stripping

3.2.1. The Proposed Algorithm for Bidirectional Horizontal Scan

Skull stripping is an essential step in order to eliminate non-cerebral tissues that might obstruct the ensuing tumor analysis. Within this methodology, an algorithm for removing the skull from a brain image was created. First, the original image is converted into a high-contrast binary image $I_{bw}(r, c)$, to clearly define the skull boundary. A bidirectional, horizontal scan of the image for each row r forms the basis of the algorithm:

Left-to-Right Scan: The algorithm scans from the left column ($c=1$) to the right for each row. It searches for the first bright pixel in $I_{bw}(r, c)$, which represents the left outer boundary of the skull. Once found, all bright pixels to its right in the grayscale image are set to zero. $C_{left}(r)$ is defined as the smallest column index c in row r where the skull region begins from the left, where W be the width of the image.

$$C_{left}(r) = \min\{c \mid I_{bw}(r, c) = 1 \wedge 1 \leq c \leq W\} \quad (1)$$

Right-to-Left Scan: Similarly, the algorithm scans each row from the right column ($c=n$) to the left, searching for the right outer boundary of the skull. Upon finding the first bright pixel from the right in $I_{bw}(r, c)$, all bright pixels to its left in the grayscale image are set to zero. $C_{right}(r)$ is defined as the largest column index c in row r where the skull region begins from the right.

$$C_{right}(r) = \max\{c \mid I_{bw}(r, c) = 1 \wedge 1 \leq c \leq W\} \quad (2)$$

The output image I_{out} can be defined as a function of the image I_{gray} without the skull region. For each pixel (r, c) , its value in the output image is its image I_{gray} value if it lies between the left and right of the skull boundaries, and zero otherwise.

$$I_{out}(r, c) = \begin{cases} I_{gray}(r, c), & \text{if } C_{left}(r) \leq c \leq C_{right}(r) \\ 0, & \text{otherwise} \end{cases} \quad (3)$$

In situations where the skull boundary is not contiguous, a safety heuristic that uses a 35-pixel ahead/behind is included to stop the algorithm from mistakenly removing brain tissue. This stage isolates the brain tissue for focused analysis.

3.2.2. Morphological Operations

Applying Erosion: The morphological operation known as erosion is done using a small disk-shaped structuring element. This results in a reduction of the brain area boundary, hence removing any thin connection to the skull that the stripping algorithm might have missed.

Applying Closing: A slightly larger structuring element is then used in a morphological closing operation. This step is essential for creating a solid and contiguous brain mask by filling in any small internal holes or gaps and smoothing the contour of the brain region.

The skull and other non-brain tissues are removed from each MRI $I(x,y)$ before analysis. This step's main goal is to isolate the intracranial volume to prevent high-intensity signals from extra-cranial sources (such as fat or skull marrow) from interfering with the subsequent tumor seed-finding algorithm.

Used a computationally efficient method based on global thresholding and morphological analysis for this purpose. First, a threshold is used to make an initial binary mask. MRI intensity distributions can be multi-modal, so the threshold method may not be optimal, but it works well as a first-pass binarization. Then, the binary image is processed to find all connected components and the largest component, which always corresponds to the brain parenchyma, while all the other components are removed.

This method is a pragmatic choice because it balances the need for speed and accuracy for our specific application. Even though established tools like FSL-BET offer superior anatomical precision, our approach works well for robustly and automatically isolating the brain region and is well-suited for rapid. The final result of this step is a skull-stripped image called $I_{\text{brain}}(x,y)$. This image is used as the input for the automated seed point initialization algorithm.

3.3. Tumor candidate regions extraction

High Thresholding: Based on the finding that many tumors show up as hyper-intense (abnormally bright) regions in specific MRI sequences, the tumor is segmented. An adaptive threshold is used to binarize the processed brain image. To maximize the inter-class variance by determining the optimal threshold, so the threshold T is scaled by a factor of two. This high thresholding technique is used to effectively isolate only the brightest pixels, which are strong candidates to be part of a tumor. The binarization is performed as:

$$\text{TumorMask}(x,y) = \begin{cases} 1 & \text{if BrainImage}(x,y) > (2 * T) \\ 0 & \text{otherwise} \end{cases} \quad (4)$$

Hole Filling: A hole-filling procedure is applied to the mask as the next step. This ensures that any possible tumor region is depicted as a solid object, which is consistent with the typical morphology of solid tumors.

3.4. Automatic seed point selection of the tumor region

A significant issue in region growing segmentation is the determination of the initial seed point. Manual selection lacks objectivity and results in low reproducibility. To address this problem, a deterministic algorithm for automated seed point initialization is introduced, designed to identify the most probable tumor candidate region.

Connected Components: The binary mask is used in a connected component analysis algorithm. This process puts all the connected non-zero pixels (pixels with a value of 1) into separate objects, or components. The output is a set of n components, $C = \{C_1, C_2, \dots, C_n\}$, where each part c_i is a set of pixel coordinates that belong to one continuous object.

Feature Extraction: For each identified component $ci \in C$, a set of features computed, with the area being the most important one. The area $A(ci)$ is defined as the total number of pixels in the component, which is equivalent to its cardinality.

$$A(ci) = |ci|$$

The algorithm operates on the assumption that the tumor corresponds to the largest hyperintense region in the image slice. Therefore, the component with the maximum area is selected as the primary tumor candidate region, denoted as C_{tumor} .

$$C_{\text{tumor}} = \arg \max ci \in C \{A(ci)\} \quad (5)$$

Seed Point Identification: The geometric centroid of the largest object chosen has been determined. This centroid's coordinates correspond exactly to the suggested tumor region seed point. The centroid coordinates (x_c, y_c) are calculated by averaging the coordinates of all pixels (x, y) belonging to C_{tumor} . Let $N = |C_{\text{tumor}}|$ represent the area of the chosen component. The centroid coordinates are given as follows:

$$x_c = \frac{1}{N} \sum_{(x,y) \in C_{\text{tumor}}} x \quad (8)$$

$$y_c = \frac{1}{N} \sum_{(x,y) \in C_{\text{tumor}}} y \quad (9)$$

The resulting seed point is $p_{\text{seed}} = (x_c, y_c)$. The process makes sure that the seed is centered at the largest connected component, which serves as the main object of study. This helps set up an accurate and repeatable starting point for the next phase of region-growing.

3.5. Brain Tumor Segmentation

After identification of the seed point, a seed region-growing algorithm is used for segmentation of the tumor. This process involves growth to the neighboring pixels satisfying the criteria of homogeneity from a seed point, which is often the center of the region with the maximum probability of a tumor. The basic idea behind the algorithm is the comparison of the intensity of the neighboring pixel with the intensity of the seed point to maintain homogeneity between the original region and the entire segmented region. The measure of similarity is obtained as follows:

$$\text{Similarity Score} = 1 - (|\text{Seed Intensity} - \text{Neighbor Intensity}| / 255) \quad (10)$$

When the similarity score of an adjacent pixel exceeds a specified value (threshold = 0.85), the pixel is added to the growing region. This process stops when there are no more neighboring pixels that meet this criterion, resulting in a contiguous binary mask that specifies the segmented tumor. A flowchart depicting the brain tumor segmentation technique is provided in Figure 2.

The block diagram illustrates the program implementation procedure. The procedure starts with initialization, where the required data structures are built: a binary output mask (segmented image), a visited matrix preventing repeated processing of the same pixels, and a First-In-First-Out (FIFO) queue containing seed point coordinates at first. The key element of this algorithm is an iterative loop running until the queue is empty. The queue used the BFS method to ensure the symmetric expansion of the region from the seed point. During each step of the loop, a pixel is dequeued, and its neighbors are methodically checked based on a set of criteria: the neighbor should be inside the image bounds, shouldn't be already visited, and should meet the homogeneity condition. If these conditions are satisfied and the similarity score of the neighbor is greater than the specified threshold, the position in the segmented image is set to 1, the neighbor becomes a part of the region, and is enqueued for further processing. The loop ends when the queue becomes empty, which means all homogeneous pixels belong to the region are processed. The resulting segmented image is a binary mask that accurately depicts the tumor's borders according to the algorithm's requirements.

4. Experimental Results and Discussion

4.1. Dataset Description

This work used "the Brain MRI Images for Brain Tumor Detection" dataset, which is an open-source dataset available on the Kaggle platform¹. This dataset consists of 253 brain Magnetic Resonance Imaging (MRI) scans, out of which 98 are non-tumor images, while 155 are brain tumor images. Experts collected the dataset from willing patients. JPEG images come in a variety of sizes and resolutions. These images were used to evaluate the effectiveness of the suggested framework for brain tumor identification. The suggested technique begins with preprocessing MRI scans to increase image quality and minimize noise. Subsequently, the tumor area was segmented using the suggested technique. The segmented tumor sections were then used to conduct further analysis and performance evaluations. The use of this publicly available dataset assures the repeatability of the experimental results and allows for comparison with other studies in the field of medical image processing. Figure 4 presents samples of these images.

¹ <https://www.kaggle.com/datasets/navoneel/brain-mri-images-for-brain-tumor-detection?resource=download>.

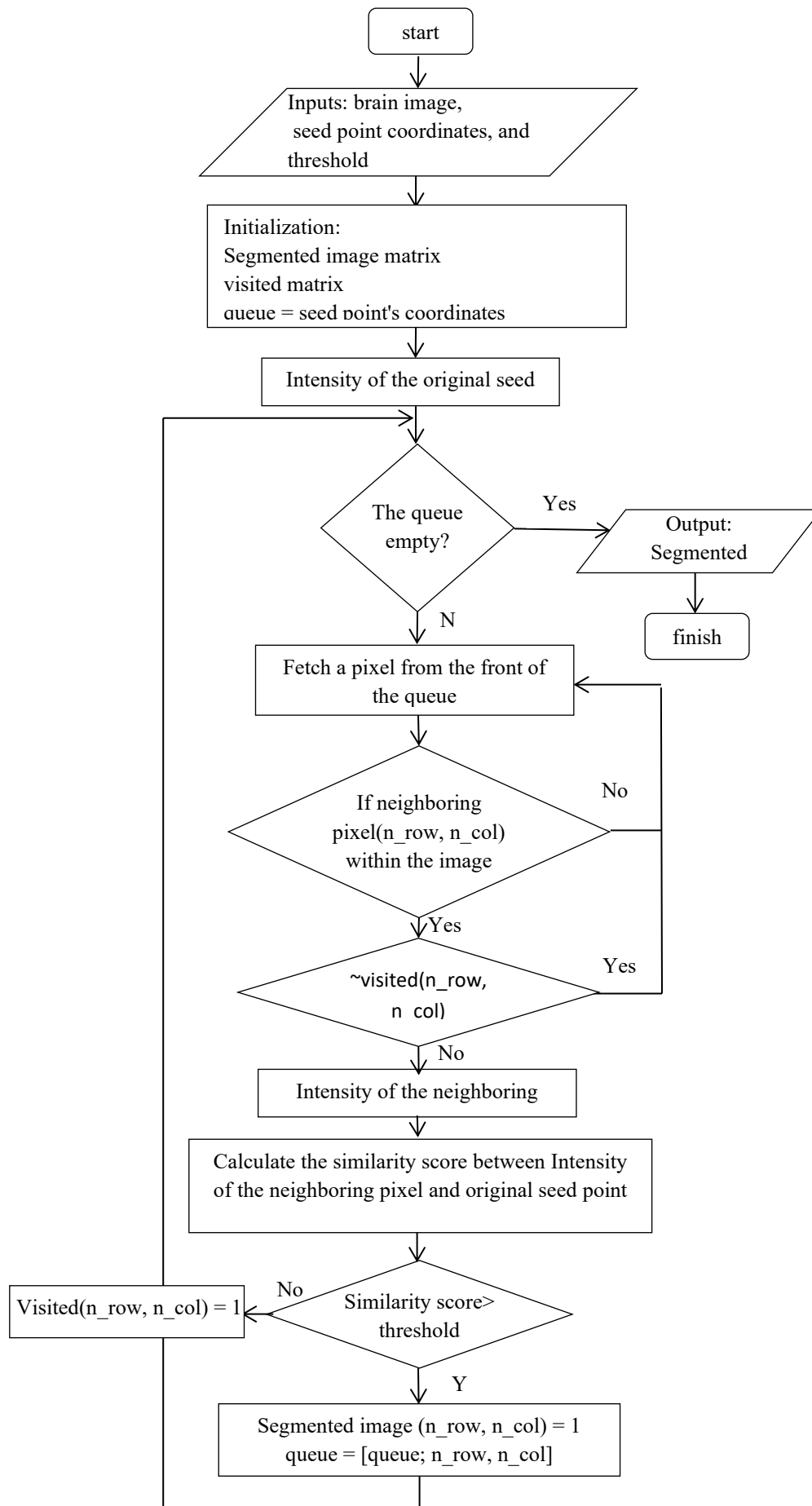


Figure 3. Flowchart for Brain tumor segmentation algorithm

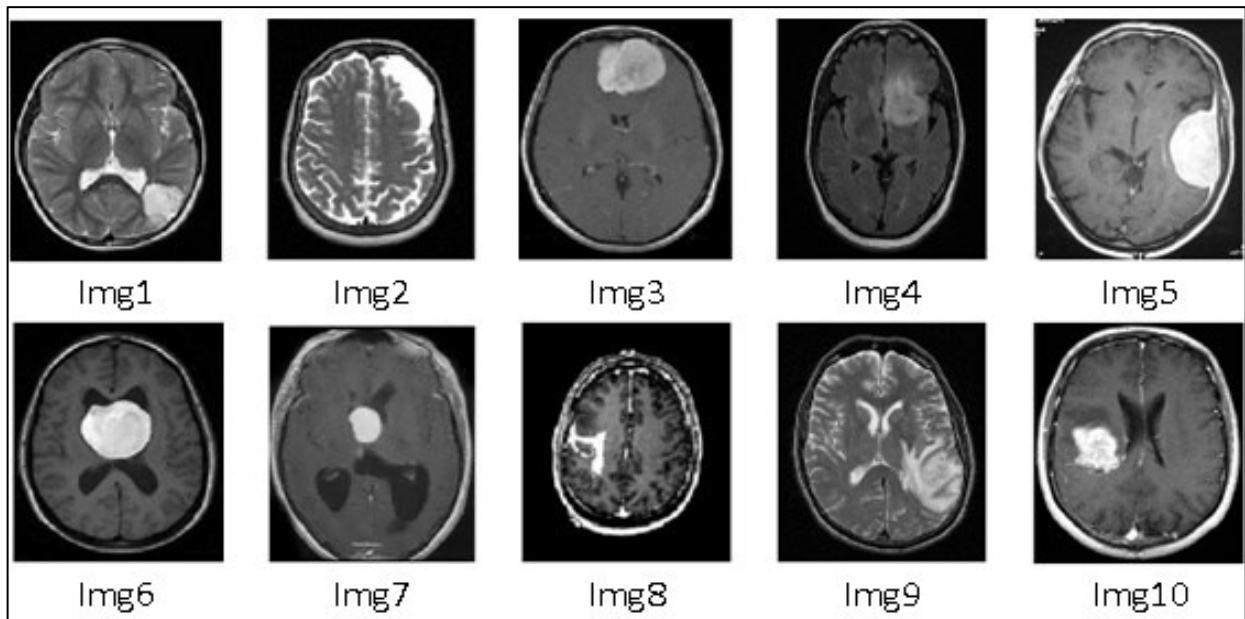


Figure 4. Samples of Brain MRI images from the database

4.2. Performance Evaluation of the Proposed Segmentation Method

The performance of the proposed technique was evaluated based on brain tumor segmentation accuracy using a dataset of 155 MRI images from different patients. In this part of the work, the results obtained from the application of the automatic seed point selection and detection and segmentation of the tumor region. The first step is the application preprocessing which involves converting the original image to grayscale and applying a Median Filter to reduce noise, which resulted in an enhanced and smooth image. The skull-stripping technique is a very important step to isolate the brain tissue, where the proposed Bidirectional Horizontal Scan Algorithm is used for skull removal from a brain image, and sequential morphology operations are applied to use to separate any weak connections to non-brain tissues and fill small gaps and smooth the brain contour, yielding a clear brain mask. The result is effective in extracting the brain region almost entirely, as illustrated in Figure 5, for ten images as samples.

The correct localization of the automatic seed point within the tumor is the primary factor that eliminates the need for manual intervention and ensures the success of the subsequent region growing algorithm in accurately delineating the tumor boundaries. A high-intensity threshold was applied to the isolated brain region to isolate the brightest areas, which often correspond to the tumor, as shown in Figure 6(b). Connected components were analyzed, and the object with the largest area was selected as the potential tumor region. Its centroid was then calculated to serve as the initial seed for the region growing process, as visualized in Figure 6(c), where the point is centered on the tumor. Finally, Figures 6 (d), (e) show the results of the experiments that used the method suggested in this paper. It showed detected and segmented images containing tumor areas of different shapes and sizes in MRI images. It shows that the suggested method has correctly removed the brain tumor.

To confirm the accuracy of the suggested segmentation algorithm, an expert radiologist manually drew the tumor boundaries to create the ground-truth reference. When these expert-defined masks were compared quantitatively, the result was an average Dice Score of 0.95 and an average Jaccard Score of 0.91. This high level of spatial overlap shows that our automated method accurately captures the complex pathological margins found in clinical practice. This shows that it is both accurate for diagnosis and a useful tool for computer-aided diagnosis.

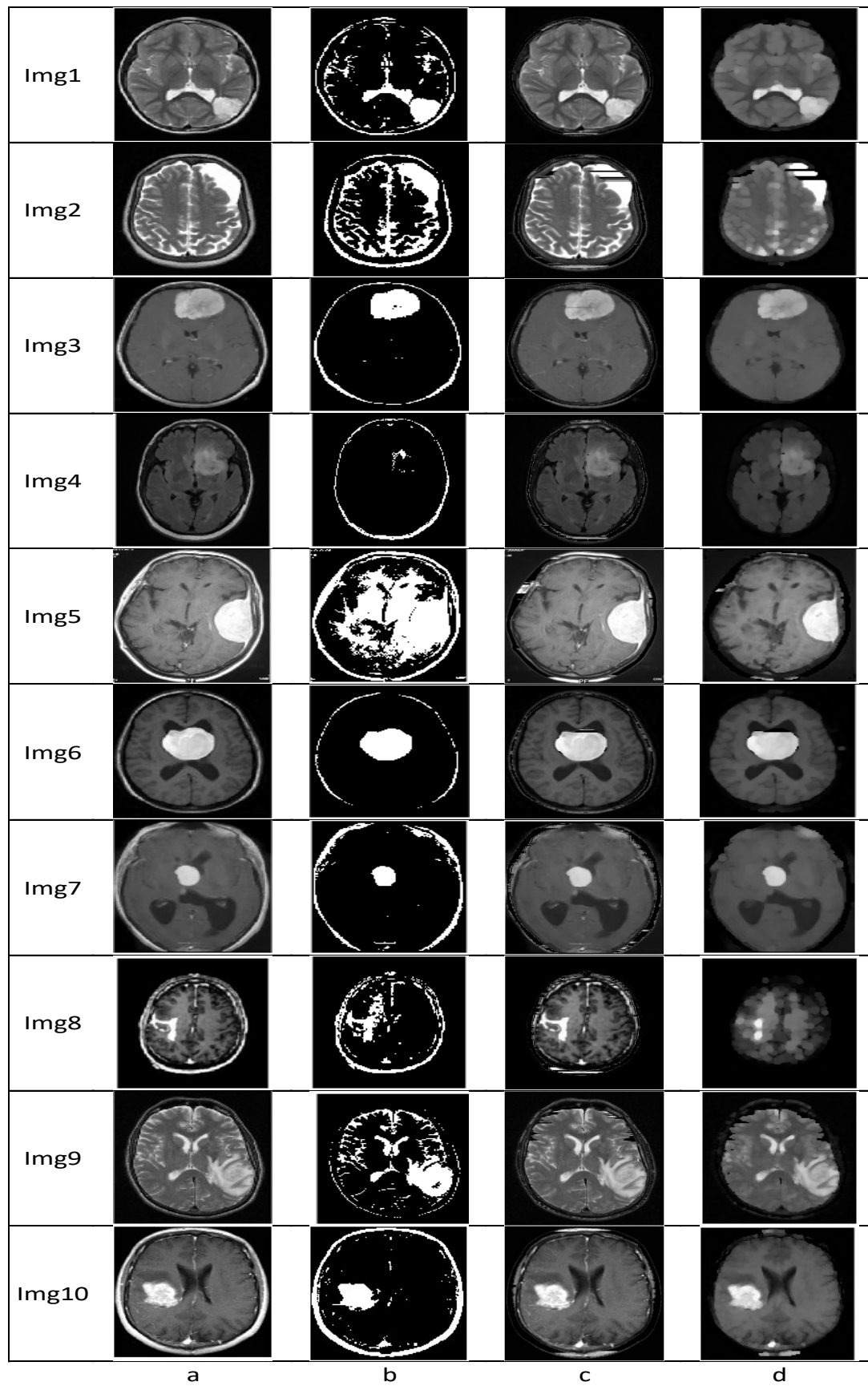


Figure 5. A skull removed from original brain images: a) Original MRI images, b) binary images, c) Bidirectional horizontal scan of the images and d) A skull removed after morphological optimization

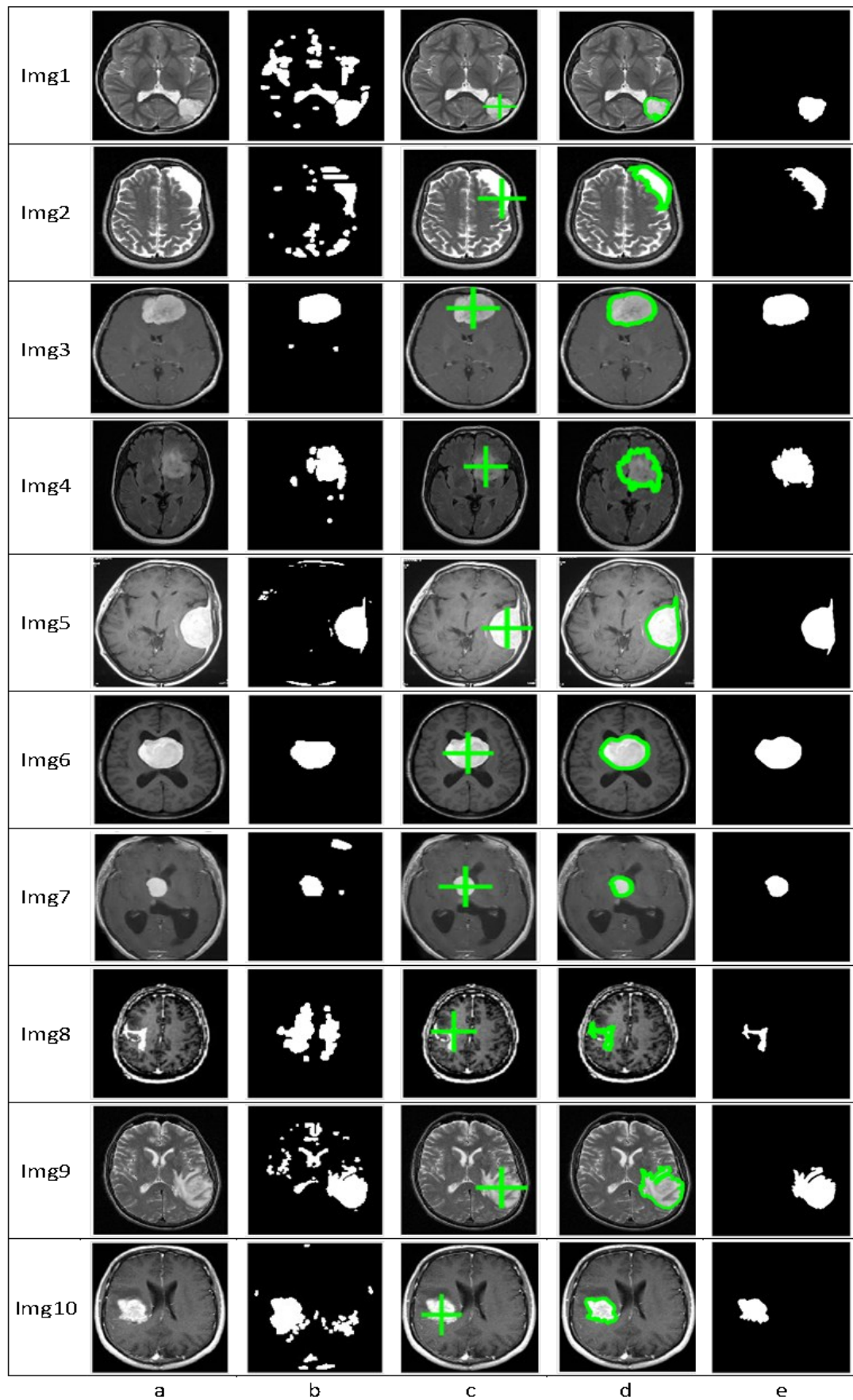


Figure 6. Experimental Results: a) images after Applying Median Filter b) Tumor candidate regions extraction, c) potential seed point for brain images, d) Detected tumor and e) Tumor alone image (Segmented image)

4.3. Impact of Preprocessing Techniques

To evaluate the effect of preprocessing filters on the final segmentation outcome, comparative visual analysis was performed using Anisotropic Diffusion (Anisodiff) and the Median filter together with the dynamic region-growing criteria, as shown in Figure 7. Although the Anisodiff algorithm performs better in terms of Rician noise and edge preservation, practical application on the particular dataset showed that the use of the median filter with the dynamic region-growing criteria outperformed more advanced techniques in certain clinical situations. Specifically, in cases where the tumor intensity is homogeneous but surrounded by low-contrast background noise, it effectively suppresses outliers without over-smoothing the intensity gradients used for the region-growing seeds.

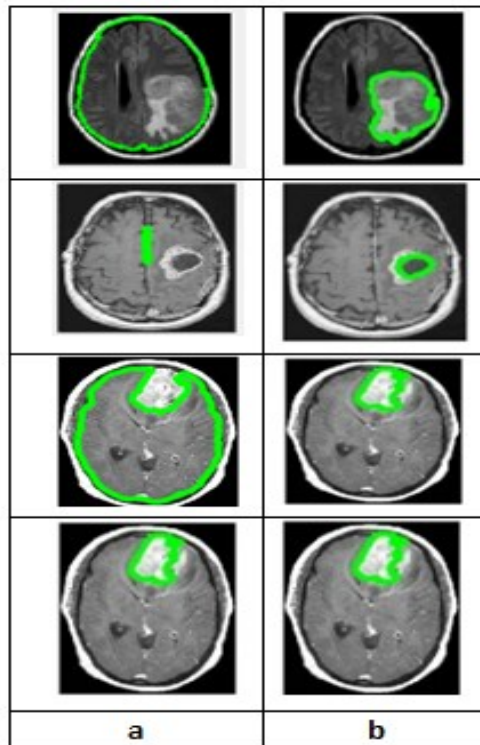


Figure 7. Comparative segmentation performance based on preprocessing techniques: (A) anisotropic diffusion vs. (B) median filter combined with our dynamic region-growing criteria.

Further, a quantitative analysis has been conducted to evaluate the efficacy of using median filtering as compared with anisotropic diffusion when combined with the suggested method of region-growing segmentation. As shown in Table 2, the median filter achieved a Similarity Coefficient (Dice) of 0.9524 and an Intersection over Union (IoU) of 0.9092, respectively. Significantly outperforming anisotropic diffusion, which achieved a 0.1687 Dice score and 0.0921 IoU. The results demonstrate that anisotropic diffusion is effective in noise elimination and edge preservation; it affects the local intensity correlation necessary for the proposed dynamic criteria used by the region growing. At the same time, the median filter preserves all the homogeneity characteristics that are crucial for accurate seed selection and consistent region growth, resulting in much better tumor segmentation performance. The small standard deviation of the median filter shows the robustness and consistency of the proposed preprocessing procedure for the analyzed MRI images. These data quantitatively corroborate median filtering's suitability as a preprocessing stage in the proposed scheme.

Table 2. Quantitative Comparison of Median Filtering and Anisotropic Diffusion Combined with Region Growing Segmentation Using Dice and IoU Metrics

Method	Dice	IoU	Std. Dice	Std. IoU
Median Filter + Region Growing	0.9524	0.9092	0.0092	0.0165
Anisotropic Diffusion + Region Growing	0.1687	0.0921	0.0050	0.0029

4.4. Comparison of Manual and Automated Seed Selection

To evaluate the effectiveness of the proposed automatic seed selection strategy, a qualitative comparison was conducted with conventional manual seed initialization. Figure 8 presents the results of brain tumor segmentation obtained using the region-growing algorithm with both manual and the proposed automated seed selection methods. The images in column (a) show the original Magnetic Resonance Imaging (MRI), where the user manually selected the initial seed point (shown by a crosshair or a bright spot). Column (b) shows the final segmentation outcome (outlined in green) that came from that manually placed seed. Column (c), on the other hand, shows the segmentation results that came from our developed automatic seed selection algorithm. The results show that the automatic method is effective and reliable. When using the manual method, the success of the segmentation process depends entirely on the user's skill and precision in selecting a suitable seed point. This process takes a lot of time and is also inherently subjective, which can lead to results that are inconsistent. For example, if a seed is accidentally placed in a necrotic or cystic region of the tumor with different signal intensity characteristics, the region-growing algorithm may fail to expand properly or terminate prematurely, implying that the tumor is not completely segmented. The automatic seed selection method, on the other hand, fixes these problems objectively and efficiently. The first advantage is time efficiency. As seen in Figure 9, the algorithm eliminates the need for manual intervention, which speeds up the processing of every case. The second and most important benefit is the ability to choose the best seeds. The suggested technique is designed to analyze the image's characteristics and automatically locate the seed point in the tumor mass's core—that is, in the region that is most uniform and has the maximum intensity—while avoiding edges and non-uniform areas. This deliberate decision ensures that the area-expanding process begins at a place that is accurately indicative of the tumor tissue, leading to a constant and thorough expansion that more fully encompasses the whole tumor region. It is evident by comparing columns (b) and (c) across the many cases that, for the most part, the automatic approach performs as well as the manual approach, and in certain instances, it even performs better by more precisely defining the tumor's boundaries.

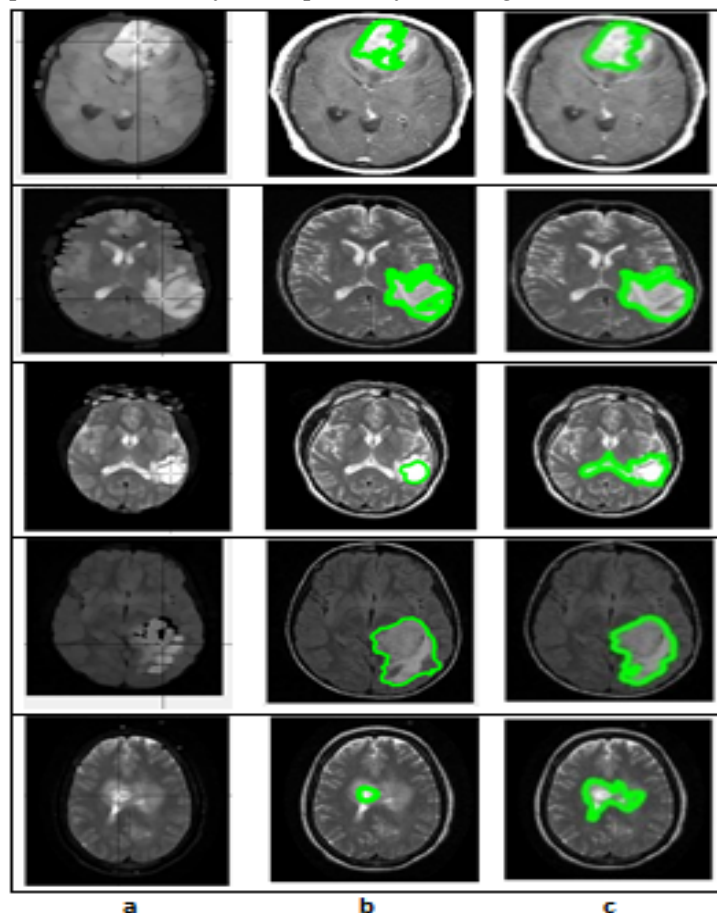


Figure 8. Comparative analysis of brain tumor segmentation: a) manual Seed point localization, b) Results of manual seed selection, and c) Results of the proposed automated seed selection method.

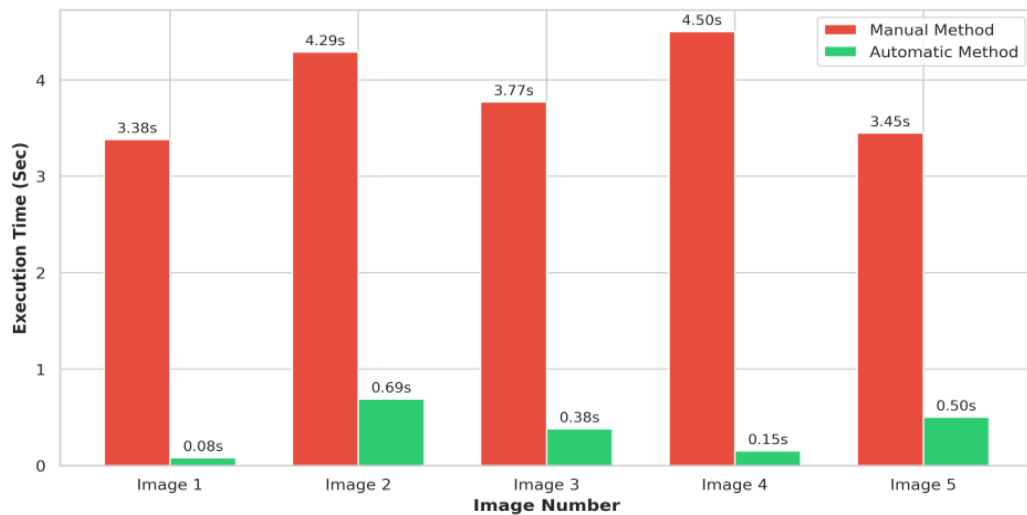


Figure 9. Comparative analysis of processing time between manual and automated seed selection across five representative MRI cases.

A comparison has been performed against the manual seed initialization in order to analyze the effectiveness of the suggested automated process. This is done by using two popular metrics used to measure the efficiency of segmentation, which are the Dice Similarity Coefficient (DSC) and the Jaccard Score. As seen from Table 3, the automated seeding method performs better than the conventional method. This shows that not only does automation of the seed selection process reduce time and effort, but it also improves the reliability and robustness of tumor segmentation. This is a significant step towards a completely automated diagnostic system.

Table 3. Quantitative Comparison Between Manual and Automated Seed Selection

Method	Dice Score	Jaccard Score
Manual	0.9299	0.8690
Automated	0.9524	0.9092

4.5. Sensitivity Analysis of the Similarity Threshold

A sensitivity analysis was performed using various threshold values to evaluate the similarity threshold effect on the proposed region-growing algorithm. where the value of the similarity threshold directly affects the accuracy of the segmentation by deciding whether nearby pixels are included in the expanding region. Figure 10 presents the qualitative segmentation results, while Table 4 summarizes the quantitative evaluation using Dice and IoU. As illustrated in Figure 10, a threshold value of 1.0 severely restricts region expansion, resulting in under-segmentation and failure to fully capture the tumor region. On the other hand, a low threshold value of 0.7 results in over-segmentation and excessive region expansion, which includes nearby healthy tissues, while threshold values of 0.9 and 0.8 provide better delineation. The best segmentation is obtained at a threshold of 0.85, which roughly resembles the ground-truth tumor borders. This observation is further confirmed by the quantitative results in Table 4, where the threshold value of 0.85 produced the highest Dice score and IoU. These results support the adopted similarity threshold in the suggested framework, which offers the best compromise between maintaining diffuse tumor borders and reducing both false-positive and false-negative segmentation errors.

Table 4. Quantitative Evaluation of Different Similarity Threshold Values

Threshold	Dice Score	IoU
1	0.0044	0.0022
0.9	0.9521	0.9085
0.85	0.9524	0.9092
0.8	0.9478	0.9009
0.7	0.2101	0.1174

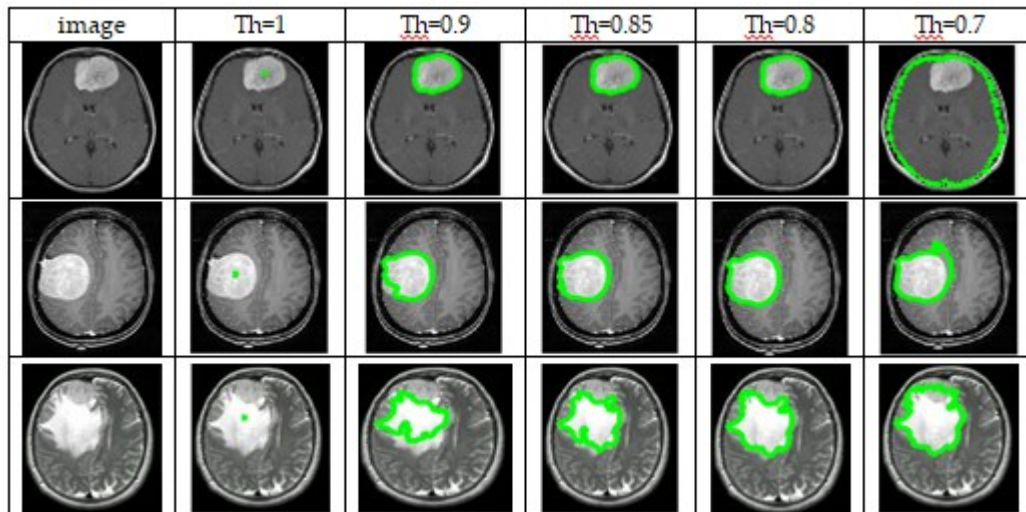


Figure 10. Effect of Different Similarity Threshold Values on Region-Growing Segmentation

4.6. Comparative Evaluation with State-of-the-Art Methods

A qualitative comparison of our suggested segmentation algorithm's performance against other well-known methods in Figure 11 for two MRI images. Figure 11(a) shows the original MRI images, while (b) presents the segmented image results using our proposal. Figures 11(c–f) show the corresponding segmentation results obtained using the methods of Sravanthi *et al.* [20], Bhunia [19], Joseph *et al.* [21], and Akram and Usman [22], respectively. The results demonstrate that the proposed approach effectively and precisely defined the tumor boundaries, maintaining the region's shape and preventing leakage into nearby healthy tissues.

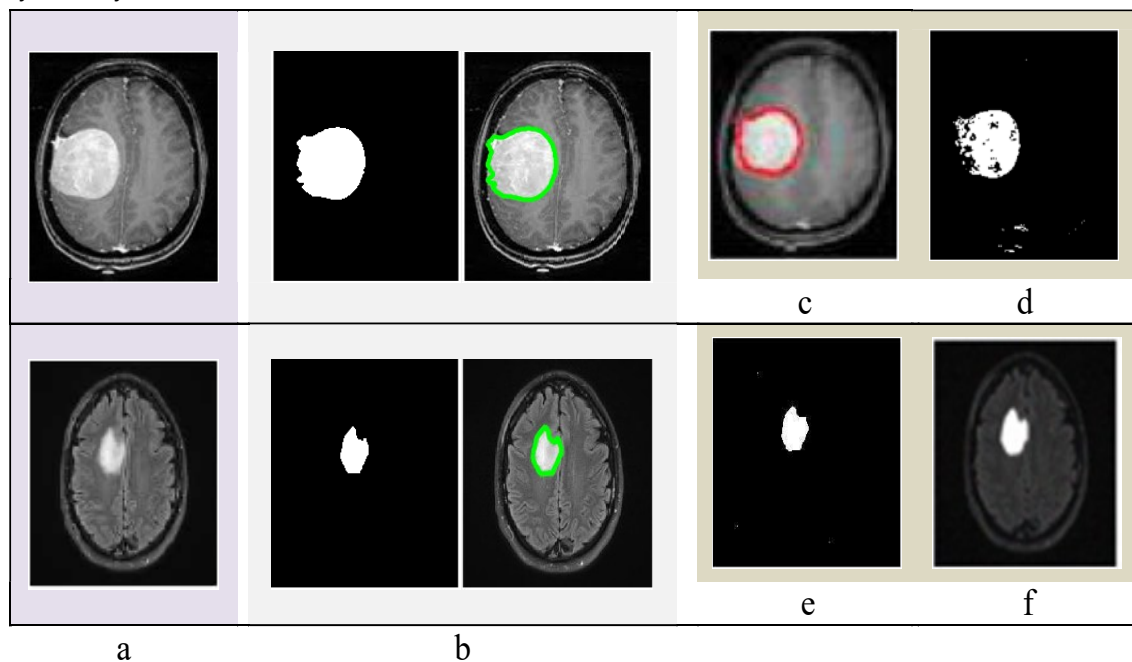


Figure 11. Comparison of tumor segmentation results using the proposed technique with the different techniques.

The Dice Similarity Coefficient (DSC) was utilized to compare the suggested technique with a number of existing brain tumor detection and segmentation techniques in order to offer a consistent quantitative assessment. The suggested strategy outperformed a number of recently published techniques, as seen in Table 5, with a Dice score of 0.95. The results show how well the suggested automatic region-growing framework works to precisely identify tumor locations in brain MRI images. The superior Dice score indicates a higher degree of overlap between the reference annotation and the segmented tumor region; the suggested method can achieve accurate tumor boundary extraction while

maintaining computational simplicity in comparison to more complicated machine learning and deep learning architectures.

Table 5. Comparison of Dice Score Between the Proposed Method and Recent Brain Tumor Segmentation Methods

Reference	Dice Score
Chand <i>et al.</i> [23]	0.78
Lin <i>et al.</i> [24]	0.85
Aleid <i>et al.</i> [25]	0.87
Mittal <i>et al.</i> [26]	0.89
Gunasekara <i>et al.</i> [27]	0.92
Ottom <i>et al.</i> [28]	0.92
Liu <i>et al.</i> [29]	0.93
Proposed method	0.95

4.7. Failure Analysis and Limitations

Even though the automated seed-growing algorithm works well and has robust performance in most clinical situations, a critical evaluation shows that there are some difficult cases where segmentation was suboptimal, as shown in Figure 12. process occasionally exceeds the actual pathological boundaries (leakage), particularly where the intensity levels are highly similar. When the lesion is diffuse or blurred, and the transition zones are not clearly defined, the algorithm may terminate prematurely without segmenting the full extent of the tumor. This is mainly due to the reliance of the algorithm on the local intensity gradients, which can be inconsistent in MRI images. Recognizing these cases is critical; it highlights the inherent difficulty in segmentation of high-grade gliomas with fuzzy boundaries and provides a concrete scientific basis for further research in this field. This would include the use of shape priors or intensity constraints from multiple spectra to improve robustness in complex clinical cases.

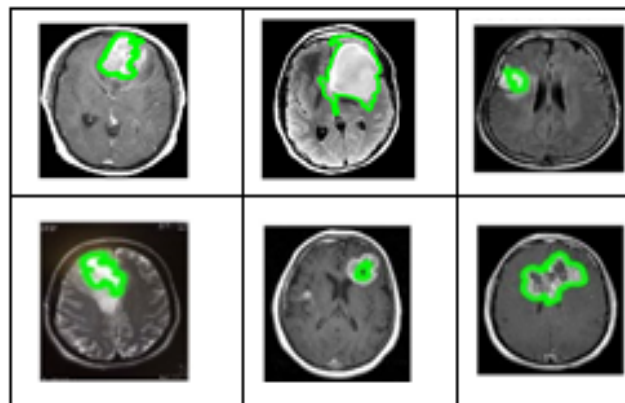


Figure 12. Analysis of challenging cases and suboptimal segmentation, illustrating boundary leakage and under-segmentation in complex tumor structures.

A limitation of the suggested segmentation methodology is its emphasis on single-lesion tumor detection. This method may not fully capture all diseased areas in situations involving multifocal or multiple tumors, even while it offers reliable and computationally efficient segmentation for pictures containing a single tumor. As a result, subsequent lesions with a smaller spatial extent may be unnoticed. In order to enhance the identification and segmentation of multifocal tumors, future work will use recursive connected-component analysis and multi-seed initialization to overcome this constraint.

5. Conclusion

This paper proposes a method for brain tumor detection and segmentation. This technique successfully developed and implemented a fully automated framework for segmenting brain tumors from MRI images. After the preprocessing step, which involves noise reduction and enhanced image quality, the main contribution of this work lies in the introduction of an integrated methodology that starts with an efficient skull stripping algorithm. This algorithm's usefulness extends beyond skull removal; it forms the basis for accurate and automated seed point recognition. A significant limitation of the popularly used

region-growing segmentation algorithm to identify the abnormality region on brain images has been effectively addressed by this method. A major challenge in using the region-growing algorithm to obtain an optimal ROI is the initialization of the seed point. In the proposed method, the seed point is automatically determined for each input brain image. The effectiveness of the suggested method in accurately and consistently segmenting brain MRI images to find and identify tumor regions has been shown by the experimental results. Future research could broaden the scope to test the algorithm on bigger and more varied datasets and incorporate further classification methods to identify the tumor's grade and type after segmentation.

CRedit Author Contribution Statement

Zainab Ghayyib Abdul Hasan: Conceptualization, Methodology, Software, Analysis, Investigation, Writing – Review & Editing.

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