

Brain Tumor Segmentation via Efficient Thresholding and Binary K-Means Integration

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Abstract—In medical image segmentation, the identification, characterization, and visualization of a tumor's dimension and region are considered to be very crucial, tedious, and time-consuming tasks. In spite of intensive research, segmentation is still one of the most challenging problems in the medical field due to the variety of image content. In this paper, we propose a new hybrid method for detecting and segmenting tumors in T2-weighted magnetic resonance imaging (MRI) brain scans. The approach begins with an efficient thresholding technique, followed by conventional morphological filtering, and then applies the binary K-means clustering algorithm. Experimental results and performance metrics demonstrate that the proposed method effectively identifies and segments tumors in MRI brain scans with significant accuracy.

Keywords— Brain tumor segmentation, T2-weighted MRI, Efficient thresholding, Binary K-means clustering, Silhouette Coefficient.

I. INTRODUCTION

In digital image processing and computer vision, image segmentation is the process of segregating the digital image into multiple regions or parts, often based on the characteristics of the pixels [1]. The key objective of image segmentation is to improve the meaning of a digital image by changing its representation. It is widely used to localize the objects and boundaries in the image. The results of image segmentation appear as a set of regions that cover the entire digital image information [2]. Thus, image segmentation plays a very significant role during the medical image analysis.

The human body is composed of large number of cells. Cell is defined as basic structural and functional unit of life. New cells are formed in the human body, and old cells die by the process called cell division. But, any sort of disturbance in cell division cycle causes severe complications. Tumor is one of them. The National Cancer Institute define a tumor as an abnormal mass of tissue that forms when cells divide more than they should or do not die when they should [3]. Tumors are mainly of two types, some tumors are benign (non-cancerous cells), while others are malignant (cancerous cells). The presence of a tumor in the brain, specifically, prevents the brain from functioning normally and causes an adverse effect

on the human body because the brain is considered to be one of the most complex organs of the body.

To study the anatomy of the brain tumor in detail, many useful imaging techniques are used nowadays, such as MRI, computed tomography (CT), positron emission tomography (PET), single-photon emission computed tomography (SPECT), magnetic resonance spectroscopy (MRS), ultrasound (US), and X-rays [4]. These imaging tests provide the information about the size, shape, location, and type of the tumor lesion. Many clinical experts believe that of the aforementioned techniques, MRI is the most reliable and standard approach for studying brain tumors, as it involves no ionizing radiation and is based on magnetic fields and radio waves [2]. MRI provides high-resolution scans of brain tumors in different anatomical planes (axial, coronal, and sagittal) with excellent soft tissue contrast and wide clinical availability. MRI can be performed in different modalities, such as T1-weighted, T2-weighted, and FLAIR, each emphasizing distinct tissue characteristics [5]. Among these, T2-weighted imaging holds particular importance, as it highlights differences in water content, making it especially effective in detecting edema and delineating tumor boundaries, which are crucial for diagnosis and treatment planning.

Early detection and segmentation of the brain tumor in patients increases the survival rate and life expectancy [2], otherwise it can be fatal. For this, a lot of study has been done, and a variety of methods are proposed in order to segment the brain tumor from the medical images, like thresholding technique, Otsu's binarization method, the region growing technique, the watershed algorithm, the level-set method, K-means clustering, and fuzzy-C means clustering. All methods and techniques provide meaningful information to clinical experts for medical image analysis. But the development of a single segmentation method that can be used for all kinds of medical images is still a problem [6]. Even, selecting the proper segmentation method can be a critical choice. Thus, there is no unified accepted approach for segmentation in digital image processing and computer vision. To overcome

this, researchers introduced hybrid techniques, which incorporate two or more methods in order to get effective and consistent results by maximizing their strengths and minimizing their weaknesses.

In this paper, we introduce a new hybrid method that integrates efficient thresholding with binary K-means clustering to accurately detect and segment tumors in T2-weighted MRI brain scans. This approach is designed to overcome the limitations of each individual method by leveraging their respective strengths. First, the given MRI brain scan is resized and converted to grayscale if necessary. Next, efficient thresholding is applied to transform the scan into a binary form, which facilitates the application of binary K-means clustering. As suggested in [23], binary K-means performs better on dichotomous data than on real-valued data. To further enhance tumor detection with high precision, our method incorporates morphological filtering between the thresholding and clustering stages. Finally, the tumor boundary is calculated in the processed image, demonstrating the effectiveness of the proposed approach. Experimental results show that the method achieves more accurate segmentation compared to using each technique individually. By integrating efficient thresholding with binary K-means, the proposed approach reduces the number of iterations, improves execution time, and produces a more precisely segmented tumor.

This paper is structured as follows: Section II provides an overview of the scientific advancements in the field of brain tumor segmentation over the past several years. Section III presents the proposed methodology, including a brief introduction to the core methods along with their mathematical formulations. Section IV describes the dataset and materials used in this study. Section V reports and discusses the experimental results obtained from the evaluation of the proposed method. Finally, Section VI concludes the study and outlines possible directions for future work.

II. LITERATURE REVIEW

Over the past decade and beyond, brain tumor segmentation has emerged as a key focus in medical imaging. Researchers are particularly interested in hybrid approaches that combine traditional techniques, since no single method can fully capture the complex structure and behavior of brain tumors on its own. These hybrid methods represent a promising step toward more precise and efficient tumor detection, ultimately contributing to earlier and more accessible diagnoses.

Early efforts, such as the work by Wu et al. [7] demonstrated the potential of combining K-means clustering with histogram-based clustering for segmenting brain tumors in MRI scans. Their findings marked an important starting point for hybrid approaches in medical image analysis.

In 2012, Dessai et al. [8] proposed a multithreaded framework that employed K-means clustering in combination with morphological operations to segment multiple MRI brain scans in parallel. They found that this hybrid approach

significantly improved execution time and provided accurate segmentation by effectively identifying tumors across different MRI slices. Based on their findings, they suggested that integrating clustering with morphological processing in a multithreaded environment enhances both the efficiency and accuracy of brain tumor detection.

Vijay and Subhashini [9] introduced a brain tumor detection method using K-means clustering for automatic MRI segmentation in 2013. Their technique focused on separating key brain tissues—White Matter (WM), Gray Matter (GM), Cerebrospinal Fluid (CSF), and tumor regions. They highlighted that unsupervised methods like K-means reduce preprocessing and don't require large training datasets. K-means was also found to be fast, reliable, and simpler compared to more complex algorithms like fuzzy clustering, making it a strong standalone candidate for automatic brain tumor segmentation.

K. Sinha and G. R. Sinha [10] conducted a comparative study to evaluate the effectiveness of different segmentation techniques for brain tumor detection in MRI scans. Their work focused on three methods: K-means clustering combined with the watershed algorithm, optimized K-means using a genetic algorithm, and optimized Fuzzy C-means with a genetic algorithm. To address the limitations of traditional K-means—particularly its sensitivity to initial cluster centres—they introduced optimization strategies that made the algorithm more accurate and faster to converge. Their findings showed that the genetic Fuzzy C-means approach outperformed the others by effectively reducing over-segmentation and enhancing computational efficiency. This study highlights the value of integrating evolutionary algorithms with classical clustering techniques for more precise tumor localization and extraction.

In 2015, Abdel-Maksoud et al. [2] suggested a hybrid approach for brain tumor segmentation in MRI scans by combining K-means and Fuzzy C-means clustering algorithms. The method involved four stages: pre-processing, hybrid clustering, tumor extraction using thresholding and level set techniques, and validation. To overcome the limitations of Fuzzy C-means in noisy environments, the authors combined it with K-means to enhance both robustness and efficiency. They also proposed an automatic cluster initialization strategy to reduce execution time. Experimental results showed that the proposed hybrid method achieved higher segmentation accuracy and faster processing than several state-of-the-art algorithms.

Further contributions came from Sharif et al. [11] who presented a method that emphasizes accurate brain tumor segmentation and effective classification from MRI scans. The approach begins with pre-processing, where manual skull stripping and Gaussian filtering are applied to remove noise and isolate the region of interest (ROI). Tumor segmentation is then carried out using an improved thresholding technique based on binomial mean, variance, and standard deviation, enabling precise separation of tumor tissues from healthy brain regions. For classification, the method involves extracting geometric and texture features, selecting the most discriminative ones using a Genetic Algorithm, and finally utilizing a Support Vector Machine (SVM) with a linear kernel to classify tumor malignancy with high accuracy.

In 2020, Trivedi et al. [12] introduced an Otsu K-means (OKM) approach for brain tumor segmentation. This method combines Otsu thresholding with K-means clustering, allowing accurate localization of tumor regions in MRI scans without the need for large training datasets. Using the BRATS dataset and MRI modalities such as T2-weighted and FLAIR, the method successfully segmented the whole tumor and its subcomponents—necrosis, edema, and both enhancing and non-enhancing regions. The approach achieved strong Dice scores and offers a straightforward alternative to deep learning techniques, which typically require significantly more data and computational resources.

In 2021, Khan et al. [13] proposed a method aimed at improving brain tumor detection from MRI scans, placing particular emphasis on the segmentation process. The approach begins with image pre-processing, after which K-means clustering is applied to clearly separate tumor regions from normal brain tissues. While classification is also performed to distinguish between benign and malignant tumors, the key strength of this work lies in its segmentation-driven framework. By effectively isolating the tumor regions, the method achieved higher accuracy compared to existing techniques when evaluated on the BraTS 2015 dataset.

In a recent study, Deepa et al. (2025) proposed a robust methodological framework for brain tumor detection and severity estimation using K-means clustering on MRI scans [14]. Their approach begins with preprocessing to enhance image quality, followed by segmentation through K-means clustering to differentiate between healthy and tumor-affected tissues based on intensity differences. Post-processing techniques are then applied to refine the segmentation and extract features such as tumor size, shape, and spatial distribution. The percentage of tumor involvement is quantitatively assessed and validated against expert-annotated ground truth, demonstrating the method's promising accuracy and effectiveness in supporting diagnosis and treatment planning.

Based on the reviewed studies, it is evident that existing approaches exhibit several limitations, such as sensitivity to noise, dependence on global or average intensity thresholding, and the limitation of standard K-means in handling binary data, since its centroid calculations often yield fractional values between 0 and 1 rather than the discrete values {0,1} of the thresholded image. These shortcomings highlight the need for a more reliable hybrid method that can refine the data prior to clustering and enhance the accuracy of tumor boundary detection. The proposed methodology, designed to address these gaps, is presented in the following section.

III. PROPOSED METHOD

In this paper, a new hybrid method is proposed for brain tumor segmentation using T2-weighted MRI brain scans. The approach involves a sequence of carefully designed steps: efficient thresholding to enhance image contrast, morphological operations to eliminate noise, artifacts, and refine anatomical structures, and binary K-means clustering for accurate segmentation. To assess the quality of segmentation, the silhouette coefficient is employed as a

performance metric. Each stage of the methodology is aimed at improving the precision and reliability of tumor identification. A detailed explanation of each step is presented in the following subsections.

A. Efficient Thresholding

Thresholding is one of the most fundamental steps in medical image segmentation, where grayscale images are converted into binary form to separate potential tumor regions (foreground) from surrounding healthy tissues (background) [15]. However, conventional approaches—such as global mean or Otsu-based thresholding—often perform sub-optimally on MRI brain scans due to challenges such as intensity inhomogeneity, low contrast, and overlapping intensity distributions between tumor and normal tissues. These limitations highlight the need for a composite thresholding strategy that integrates multiple statistical cues to achieve more reliable separation under diverse imaging conditions [11, 16].

To address this challenge, we propose a new composite threshold, through which efficient thresholding is performed prior to segmentation with binary K-means. This composite threshold is specifically designed for T2-weighted MRI brain scans, where tumors often appear with high contrast against surrounding tissues. It combines three complementary intensity descriptors which are given as follow:

- **Global Mean (statistical descriptor):**

For an image $I(x, y) \in \mathbb{R}^{M \times N}$, the global mean of all pixel intensities is defined as [17]:

$$T_{mean} = \frac{1}{M \cdot N} \sum_{x=1}^M \sum_{y=1}^N I(x, y) \quad (1)$$

This provides a baseline separation point between foreground and background.

- **Otsu's Threshold (probabilistic descriptor):**

A threshold T_{Otsu} is computed using Otsu's method, which separates foreground and background intensities by minimizing intra-class variance [18].

- **Midpoint of Intensity Range (range-based descriptor):**

The midpoint of the intensity range between maximum and minimum intensity values introduces adaptability to varying image contrast levels as [19]:

$$T_{mid_range} = \frac{\max(I) + \min(I)}{2} \quad (2)$$

- **Composite Threshold:**

Finally, the composite threshold is defined as:

$$T = T_{mean} + T_{Otsu} + T_{mid_range} \quad (3)$$

The binarization is then performed under composite threshold T as:

$$I_{bin}(x, y) = \begin{cases} 1, & \text{if } I(x, y) > T, \\ 0, & \text{otherwise.} \end{cases} \quad (4)$$

This composite thresholding method combines statistical mean intensity, probabilistic Otsu thresholding, and range-based intensity extremes. This fusion helps overcome the limitations of single-threshold methods in low-contrast or intensity-inhomogeneous regions, while also performing efficiently on high-contrast T2-weighted MRI scans. In such images, where tumors typically appear brighter against the background, the method ensures sharper delineation of tumor boundaries and minimizes false segmentation of surrounding tissues. This innovation enhances the consistency and robustness of binarization, making it a reliable step for subsequent segmentation with binary K-means. Although its strength lies in exploiting the contrast characteristics of T2-weighted images, the modality-specific design may limit its direct applicability to other MRI sequences such as T1 or FLAIR.

B. Morphological Operations

Morphological operations are image processing techniques that work by passing a small predefined shape, called a structuring element, over an image to refine its geometric structure [20]. They are widely used in medical imaging for tasks such as removing noise, closing small gaps, smoothing boundaries, and isolating relevant structures [21]. Their importance lies in improving the quality of segmented regions so that subsequent analysis is more accurate and reliable.

In this work, morphological operations [20] are applied to enhance the thresholded image and remove unwanted artifacts. First, a function is used to fill enclosed background areas within the detected region, ensuring that the tumor mask is continuous and free from internal gaps. This strengthens the structural integrity of the segmentation, which is essential for accurate analysis. After that, an opening operation—erosion followed by dilation—is performed using a predefined structuring element. Mathematically, this is represented as:

$$I_{bin} \circ B = (I_{bin} \ominus B) \oplus B. \quad (5)$$

Here, I_{bin} denotes the binarized image, and B represents the structuring element. The erosion (\ominus) eliminates small noise and thin protrusions, and dilation (\oplus) restores the main shape. Together, these operations smooth the tumor boundaries, preserve its essential geometry, and produce a refined region suitable for reliable feature extraction and classification.

C. Binary Kmeans

After applying efficient thresholding and morphological filtering, the MRI brain tumor scan reduces to dichotomous

data containing only two intensity levels. At this stage, employing standard K-means [22] is not a best choice, since it assumes continuous variables and relies on Euclidean distance. Dichotomous data violate these assumptions, as centroids computed by averaging binary values (0/1) produce non-binary results that lack physical meaning in a binary mask. Studies have shown that for binary variables, specialized distance measures such as Hamming, Jaccard, or Dice significantly improve clustering accuracy. Holmes Finch in [23] reported that tailored distance metrics achieve 60–90% correct cluster recovery for binary data—substantially higher than Euclidean-based approaches.

Binary K-means constrains centroids to remain binary and replaces Euclidean distance with Hamming distance [24, 25]. The data consist of binary vectors (0 or 1), and the algorithm iteratively assigns each pixel to one of two clusters. Centroids are then updated bit by bit using majority voting across cluster members [25].

Formally, for binary feature vectors $\rho_i \in \{0,1\}^n$ for $i = 1, 2, \dots, N$, binary K-means minimizes [25]:

$$\min_{c_1, c_2} \sum_{j=1}^2 \sum_{\rho_i \in C_j} d_H(\rho_i, \mu_j),$$

where the Hamming distance is defined as:

$$d_H(\rho_i, \mu_j) = \sum_{k=1}^n |\rho_{ik} - \mu_{jk}|, \quad (6)$$

and the centroid μ_j is updated as:

$$\mu_{jk} = \begin{cases} 1, & \sum_{\rho_i \in C_j} \rho_{ik} \geq \frac{|C_j|}{2}, \\ 0, & \text{otherwise.} \end{cases} \quad (7)$$

This ensures that centroids $\mu_j \in \{0,1\}^n$, $j \in \{1,2\}$ always remain binary, lying at the corners of the hypercube [25].

Binary K-means is also particularly relevant for MRI brain tumor segmentation because the image is reduced to a two-tone map (foreground vs. background). It naturally produces two clusters that correspond to tumor and non-tumor regions by grouping similar binary patterns. Unlike standard K-means, which may arbitrarily split binary tones, binary K-means preserves the discrete structure and suppresses residual noise more effectively [23, 25].

Several alternatives exist for handling categorical or binary data, including K-modes and K-prototypes (which use modes instead of means) [24], bisecting K-means (hierarchical splitting with Euclidean distance) [26], and kernel K-means with Hamming kernels [27]. While these methods have merit, binary K-means is both simpler and faster, making it attractive for segmentation tasks.

We incorporate binary K-means with Hamming distance in our proposed method. This alignment with the dichotomous structure of thresholded MRI brain scans ensures clusters with tighter internal similarity and lower within-cluster variance. As a result, segmentation accuracy improves

compared to the standard K-means approach, as demonstrated in the experimental results section that follows. The following figure presents the flowchart of our proposed method.

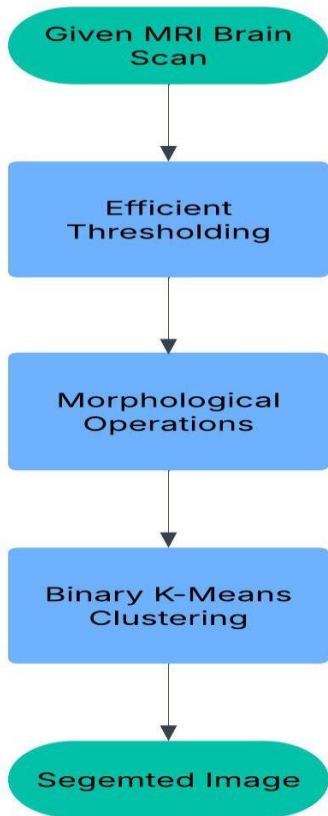


Figure 1. Flowchart of the Proposed Method

D. Silhouette Coefficient

The Silhouette Coefficient is a well-established performance metric used to evaluate the quality of clustering results, particularly in scenarios where ground truth labels are not available. First introduced by Peter J. Rousseeuw in 1987, it combines two essential aspects of clustering—cohesion and separation—into a single quantitative measure [28]. Cohesion refers to how close a data point is to other points in the same cluster, while separation measures how far the point is from points in the nearest neighbouring cluster. This makes the silhouette coefficient especially useful in unsupervised learning tasks, such as medical image segmentation, where accurate evaluation of cluster boundaries is critical.

Mathematically, for each data point i , the intra-cluster distance $a(i)$ is calculated as the average distance between i and all other points in the same cluster. The nearest-cluster distance $b(i)$ is then computed as the smallest average distance between i and all points in any other cluster. The silhouette coefficient for point i is defined as:

$$s(i) = \frac{b(i) - a(i)}{\max\{a(i), b(i)\}} \quad (8)$$

The value of $s(i)$ ranges from -1 to 1 , where a score close to 1 indicates that the point is well-clustered, and a score near 0 suggests that the point lies between two clusters, and a score close to -1 signals possible misclassification [28]. The overall silhouette score for a dataset is obtained by averaging $s(i)$ over all points.

The importance of the silhouette coefficient lies in its ability to provide a reliable, unsupervised evaluation of clustering quality. Since it does not require labelled data, it is highly applicable to domains such as medical imaging, where annotated datasets may be limited or costly to produce. Moreover, it simultaneously accounts for intra-cluster compactness and inter-cluster distinctiveness, allowing researchers to assess both aspects in one metric. Apart from the Elbow method, it is also widely used for selecting the optimal number of clusters by comparing average silhouette scores for different K values, and for comparing the effectiveness of various clustering algorithms. In medical image segmentation tasks such as brain tumor detection—high silhouette scores can indicate that the segmented tumor region is clearly distinguishable from surrounding tissues, thereby increasing confidence in the segmentation results and supporting clinical decision-making.

For these reasons, we incorporated the silhouette coefficient as a key performance metric in our proposed method, since its importance and efficacy make it highly suitable for evaluating clustering-based medical image segmentation.

IV. MATERIAL AND DATASET:

To evaluate the performance of our proposed segmentation method, we used Dataset_66, which consists of 66 T2-weighted MRI brain scans, each with dimensions of 256×256 pixels. These scans are sourced from the Harvard Whole Brain Atlas Database [29]. The T2 modality is selected due to its high contrast, superior visualization of soft tissue and quiet challenging to segment as compared to T1 or PET scans.

The dataset focuses on two pathological classes: benign (non-cancerous) and malignant (cancerous) tumors, comprising 12 and 54 scans respectively. This setup provides a practical basis for testing the accuracy and robustness of our proposed segmentation method under real-world problems.

V. EXPERIMENTAL RESULTS AND DISCUSSION

This section presents the qualitative and quantitative results of the proposed method, evaluated on T2-weighted MRI brain scans from the dataset described in previous section. The implementation was carried out using MATLAB (R2019a) and MATLAB Online. All experiments were conducted on a system equipped with an Intel Core i5 processor (2.4 GHz), 8 GB of RAM, and an NVIDIA GPU with 1 GB of VRAM.

A. Qualitative Evaluation

Qualitative results for the five test images are presented in the following figure, illustrating the different stages and demonstrating the effectiveness of the proposed method.

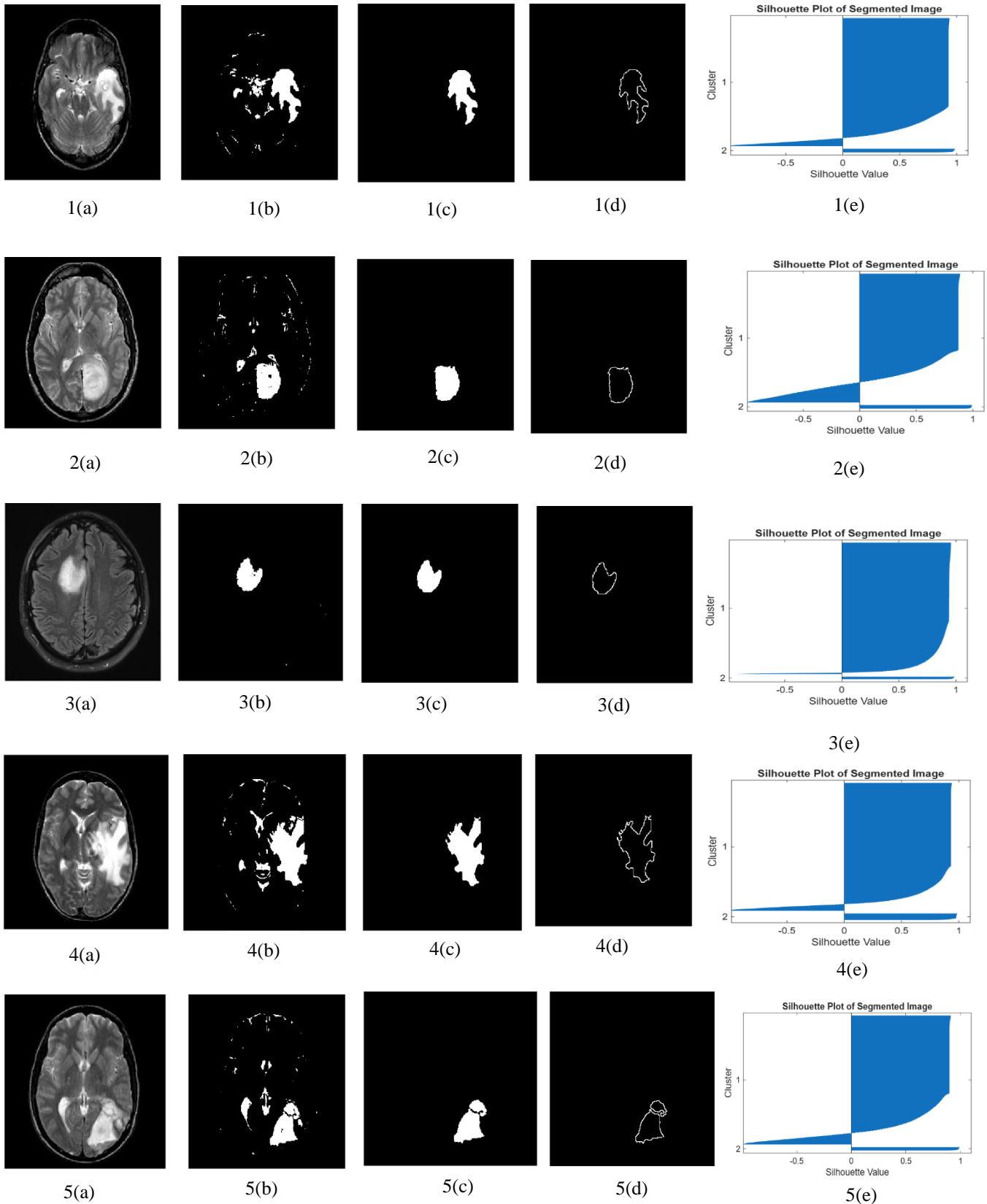


Figure 2. Qualitative results of the proposed method on five test images, each shown in five stages: (a) original MRI brain scan, (b) thresholded image, (c) segmented tumor, (d) tumor boundary, and (e) Silhouette Coefficient representation

B. Quantitative Evaluation

In the absence of ground truth, the Silhouette Coefficient is commonly used as an unsupervised metric to quantitatively assess the quality and consistency of segmented images. It captures the compactness of intra-cluster pixels and the separation between clusters. The following table presents the Silhouette Coefficient values for the five test images, which effectively reflect the segmentation performance of the proposed method.

Table 1. Silhouette coefficient values for five test images

Image No.	Silhouette Coefficient
1	0.77
2	0.58
3	0.87
4	0.79
5	0.69
Average	0.74

C. Computational Efficiency

To evaluate computational efficiency, the execution time is measured for each test image. The results indicate that the proposed method is computationally efficient, achieving segmentation in an average time of less than 0.30 seconds per image.

Table 2. Execution time of segmentation for five test images

Image No.	Execution Time of Segmentation Phase (in seconds)
1	0.29
2	0.31
3	0.30
4	0.29
5	0.27
Average	0.29

VI. CONCLUSION AND FUTURE WORK

In this work, we present a new hybrid method for segmentation of MRI brain scans by combining efficient thresholding with binary K-means clustering. The process begins by converting the image into a binary format through thresholding, followed by morphological operations to refine the tumor region. Next, binary K-means clustering is applied for precise tumor delineation and boundary extraction. The proposed method is evaluated on T2-weighted MRI brain scans, and its performance is assessed using the silhouette coefficient to highlight segmentation quality and effectiveness. In addition to quantitative evaluation,

qualitative results visually confirm that the segmented tumor regions are more precise and well-defined. Furthermore, computational efficiency is demonstrated through reduced execution time, indicating that the proposed approach is not only accurate but also faster and more resource-efficient. Experimental results collectively show that the method significantly improves segmentation accuracy, making it a more efficient and effective technique for brain tumor segmentation.

The proposed Efficient Thresholding (ET) technique in this work, has been applied to T2-weighted MRI brain scans, where tumors typically appear bright and exhibit high intensity. However, its performance may be limited in other modalities, such as T1 or FLAIR, where tumor intensity characteristics differ. Future work will therefore focus on adapting the hybrid formulation through modality-specific weighting or adaptive rules to improve its generalizability across different MRI sequences. In addition, we aim to extend the proposed method to a wider range of medical imaging modalities, including CT scans, PET scans, ultrasound, X-rays, and mammograms, in order to enhance its applicability across diverse diagnostic scenarios. Furthermore, we plan to adapt this approach for tumor detection and segmentation in various anatomical regions beyond the brain, such as the lungs, liver, breast, and other critical organs, thereby ensuring a more versatile and comprehensive framework for medical image analysis. These efforts will help validate the effectiveness and generalizability of our method across diverse imaging datasets and medical conditions.

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