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Article

INTEGRATING WATERSHED SEGMENTATION WITH MACHINE LEARNING FOR BRAIN TUMOR DETECTION IN MRI SCANS

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Abstract: Brain tumors are malformed tissues which are present in the brain hindering the normal functions of nerves and can cause serious intellectual degradation or even death when untreated. The timely and accurate diagnosis of these tumors is essential in development of effective interventions, minimizing the mortality rate, and delivery of quality patient services. Of course, the manual segmentation of the tumors in the MRI results is time-consuming, subjective, and likely to cause inconsistency between clinicians. To solve these difficulties, the paper suggests a hybrid segmentation framework associating classical methods of image processing with the methods inspired by machine learning. In particular, gray-level thresholding (Otsu), morphological operations, distance map, and watershed segmentation are combined in order to increase the visibility and outlining of the tumor. Segments layer-by-layer based on the proposed method achieved 92.7 percent segmentation accuracy on the BRATS 2020 dataset, and both Dice, and Intersection over Union scores, matched those of complex deep learning models, without the resource requirements of strong computer systems or large-scale annotations. The method is best to be deployed in resource-limited medical settings because of these features. On balance, the framework offers a comprehensible, high-speed, and effective method to brain tumor detection that has the capability of assisting clinical routine plus subsequent real-time diagnostic implementations.
Keywords: Brain Tumor Detection, Watershed Segmentation, Image Preprocessing, Hybrid Segmentation Model, Otsu's Thresholding, Magnetic Resonance Imaging (MRI)

1. Introduction

Brain tumors pose a great challenge to the clinicians since they may lead to devastating cognitive impairment, neurological impairment and in most cases, death [1]. These extra growths can grow in the brain (primary tumors), or transfer (metastasize) to the brain by extracranial cancer deposits. Irrespective of the etiology, it is important to identify them early in order to administer timely cure measures which include surgical resection, chemotherapy or radiotherapy [2]. Of all the options accessible in imaging, Magnetic Resonance Imaging (MRI) has been considered to be the most efficient method of viewing brain cancers due to its high level of contrast in sensitive tissues and it does not utilize ionizing radiation [3]. Although MRI scans are of high quality, they are manually interpreted and this process is laborious, subjective and associated with inter-radiologist inconsistencies [4]. Manual segmentation is additionally complicated by the unevenness in the appearance of tumors, such as variations in texture, shape, and intensity [5]. They are particularly hard to outline when small or weak lesions are involved, and an upsurge in the number of MRI scans has brought a demand to automated and reliable segmentation technologies. These systems may assist clinicians in navigating through workloads as well as provide routine evaluation and help with decision making under time pressure [6]. The most apparent methods are the classical image processing algorithms on thresholding, edge detection, and region growing to do tumor segmentation [7]. Despite being computationally efficient and easy to interpret, these classical approaches tend to fail in interpreting images that have complex or heterogeneous tumors [8]. Assessment Developments Watershed segmentation, where image gradients are modelled as topographical surfaces and the regions between them are delineated by simulating flooding processes, has also had success in delineating contiguous structures [9]. Nevertheless, standard watershed algorithms are affected by noise and usually over-segment low-value areas, restricting their usability in practice [4], [9]. Medical image analysis by deep learning methods has become common in recent times following the increased capabilities in the field of machine learning. Multi-scale features effective in the identification and segmentation of tumor regions can be automatically extracted by CNNs in MRI information [3], [6], [8]. In that way, U-Net architectures have proven to methodologically perform well in biomedical segmentation tasks as a result of their encoder-decoder layouts and skip correlations [3]. However, the applicability of such approaches to clinical use cannot be realized on resource-limited settings due to the need of large annotated datasets to train such models, their demanding computer and memory requirements, and their limited interpretability [7], [10]. To cope with these limitations, it has been suggested to combine a classical image processing captured strength with machine learning strategies [5], [11]. These approaches also hope to attain predictable and precise results of segmentation without the insurmountable requirements of deep learning. This paper introduces us to a blended framework which integrates Otsu thresholding, morphological processing, distance transformation and watershed segmentation. Preprocessing procedures including filtering of noise and morphological smoothing enhance the strength and prediction of the watershed algorithm and reduce probability of over-segmentation [4], [9].

Though this method has a number of benefits, there are also negative issues associated with it. Watershed segmentation still complicates the possible excessive regions, in the regions that have weak contrast, and they also might greatly depend on the choice of preprocessing parameters [9], [12]. Moreover, though the method shows reproducible findings on experimental dataset, it remains to be clinically validated to see how it performs in real life scenario [13]. The second significant contribution of this project relates to the applicability of this work to the contexts in which there is no access to a strong computing infrastructure or a large number of annotated data points to detect brain tumors. Due to the fact that the suggested approach is computationally tractable and transparent in nature it therefore stands a higher chance of being adopted in hospitals that are under-resourced, and in rural clinics [11], [14]. This strategy would help achieve the larger objective of bringing artificial intelligence on board in the healthcare of the world by lowering the inhibition against the implementation of automated diagnosis tools [15]. The research has a number of important contributions to the field of medical image analysis in detection of brain tumors. To begin with, it suggests a computationally powerful and interpretable hybrid segmentation system that incorporates some conventional image processing methods- such as Otsu thresholding, morphological operations, distance transformation, watershed segmentation to precisely identify boundaries of tumors in MRI images. The proposed method is not only as accurate as many other deep learning models but also does not present the same computational challenges associated with them since it does not need huge annotated datasets and high-performance computing resources required to train them. This makes it especially promising in low-resource settings, such as low-resource clinical settings. Second, the framework improves the classical methods due to the better preprocessing and region segmentation strategies, which avoid over-segmentation and maintain anatomical integrity. Lastly, the work presents an explainable and repeatable model with a balanced accuracy, speed, and accessibility that can be used to promote the broader adoption of AI-based diagnostic instruments in the routine clinical practice and in rural settings. In this paper, we aim at answering the following objectives:

- To create an effective brain tumor detection algorithm on basis of watershed segmentation and classical procedures of pre-processing.
- To improve the functionality of the traditional image processing by incorporating the thresholding of images, morphological operations of thresholding and transformation of distance.
- In order to assess and compare the proposed hybrid technique with CNN and U-Net models in respect to accuracy, computational demands, and interpretability.

The rest of the paper is organized as follows: section 2 provides the literature review and highlight the works done by researchers, section 3 provides the materials and methods, section 4 provides the results obtained and the final conclusion is provided at section 5.

2. Literature Review

In the recent decade, the volume of progress in brain tumor brain MR imaging recognition and segmentation is around the traditional image processing as well as artificial intelligence. The initial methods involved the use of thresholding, region growing methods and edge detection extensively. Otsu method has been varied widely to find an optimum level of global histogram to segregate the foreground and the background areas. These methods however have limitations when it comes to dealing with tumors that are very similar to the adjacent tissue since the difference between the entire pixels may be non-existent. Edge extractors such as the Canny algorithm are sensitive to noise, likewise region growing approaches which are sensitive to homogeneous regions, which tend to over-segment infiltrative tumor areas [16], [17]. The popularity of watershed segmentation was explained by the fact that it is a method that models image intensity surface as a topography and then divides regions by simulating flooding [18]. Although the classical watershed method works well to generate contiguous zones, low-contrast regions are commonly over-segmented into numerous tiny parts of the classical watershed method, which makes it difficult to accurately identify tumor limits. To curb this issue, the scholars have suggested marker-controlled watershed segmentation and distance transformation which remedy the direction of region increase and limit unnecessary fragmentation [19]. With the development of machine learning, the performance of a segmentation has been enhanced further with the ability to learn features with automation. Support Vector Machines (SVMs) were one of very first machine learning methods and used features which were engineered manually (intensity and texture) [20]. Other clustering techniques such as the K-means and fuzzy C-means have also been employed to cluster the pixels to form similar regions although they are susceptible to irregularly shaped tumors and ones with slight intensity variations [21]. Deep learning and especially Convolutional Neural Networks (CNNs) have made a dramatic progress in the field since it automatically extracts hierarchical features without having to use manual intervention. The encoder-decoder network designs U-Net [22] that uses skip connections showed great performance in biomedical segmentation tasks. Nevertheless, deep learning models frequently need huge defined datasets and enormous computing power, restricting their utility presented in clinical settings with scarce equipment [23]. In addition, interpretability of such models is still an issue among health practitioners [24].

Recent research has been directed to identifying hybrid methods combining classical segmentation procedure with machine learning to exploit both paradigms. An example is the instance of fuzzy C-means clustering in combination with SVM classification that has been reported to enhance the accuracy of the marker-based watershed segmentation [20]. Soomro et al. further showed that incorporation of SVMs to preset tumor regions prior to applying watershed algorithm gives better boundaries of tumors [16]. The efficiency of this mixed approach in the improvement of segmentation performance is also confirmed by Lee [17]. Other studies have examined integration of deep learning models together with the traditional techniques. Others have merged the idea of CNN-based feature extraction, with watershed segmentations to produce tumor masks with high reliability rate and limiting manual spectrum tuning [22]. Active contour models, gradient based technique, and use of curvelet transform have been incorporated by work of others to provide responses to sample problems of heterogeneous tumor structure and differing MRI intensities [19]. Still, it was discovered by Mohammadi et al. that fuzzy C-means clustering using marker-controlled watershed segmentation constructed high accuracy in the detection of meningiomas using contrast-enhanced scans [21]. Even though these are good news, hybrid systems continue to encounter a number of obstacles. A lot of them are based on precisely selected datasets and imply the need to spend a lot of time tuning hyperparameters to various imaging circumstances. Besides, they are not proven fully in varying clinical settings. Future studies are needed to assess the effectiveness of employing unsupervised learning and transfer learning to mitigate these limitations since they have potential to minimize the use of large labelled datasets and increase task-adaptability [25], [26]. On the whole, the integration of deep learning and classical approaches to segmentation seems to be a fruitful approach to the development of brain tumor detection frameworks that could be accurate, explainable, and computationally friendly. It is plausible that these methods will contribute greatly to the yearly advances in medical image analysis in the following years as they combine the strengths of watershed segmentation methods with the representation learning ability of machine learning [27]. Table 1summarize some of the key points found from the survey.

Table 1: Summary of Related Approaches

Study/Method	Dataset	Advantages	Limitations
U-Net [3]	BRATS	High segmentation accuracy	Requires large labelled dataset
Watershed + Morphology [4]	Local MRI scans	Low computational cost, interpretable	Prone to over-segmentation in low contrast

CNN-based Segmentation [8]	BRATS	Automated feature learning	Black-box behaviour, high resource needs
Marker-Controlled Watershed [12]	Meningioma scans	Accurate region boundaries	Sensitive to parameter tuning
SVM + Watershed [9]	Custom MRI datasets	Enhanced boundary detection	Manual feature engineering required

3. Materials and Methods

Here, the approach used for distinguishing brain tumors in MRI images with watershed and morphological processing is fully described. The data in the present study consists of 120 T1-weighted contrast-enhanced brain MRI scans taken publicly available BRATS 2020 repository [28]. This data has different sizes of tumors, locations, and intensities, which makes it a complete testbed of segmentation techniques. The Python libraries NumPy and Matplotlib are used for the implementation. The code ran and operated in a Colab and the setup of the code lets it be reused and extended in future investigations.

3.1 Dataset and Preprocessing

The input for this dataset was MRI pictures of the human brain. All image data was processed in BGR format which is the standard for OpenCV. When it comes to most image processing operations, grayscale helps since it is more suitable for simple thresholding and efficient segmentation. Due to that, we transformed each input image from BGR to grayscale with the cvtColor function from OpenCV using equation 1. This process transforms the image's colors into one value, called intensity which helps improve speed and uses less memory.,

$$I_{gray}(x,y) = 0.2989 \cdot R(x,y) + 0.5870 \cdot G(x,y) + 0.1140 \cdot B(x,y) \quad (1)$$

A 5×5 median filter was used after conversion to erase salt-and-pepper noise using equation 2. In medical image processing, using a median filter helps protect the borders of objects and remove sudden points of noise. This matters since the exact boundary lines of the tumor must be maintained so that segmentation is accurate.

$$I_{\text{med}}(x,y) = \text{median}\{I_{\text{gray}}(i,j)\} \; \forall (i,j) \in \mathcal{N}_{5\times5}(x,y) \quad (2)$$

Each pixel's intensity is now recalculated using the median of its surroundings which reduces noise and lets the important features be seen.

3.2 Thresholding

Adaptive thresholding with Otsu's method is then used using equation 3 to process the filtered grayscale image. Otsu's method is made for images with a bimodal histogram, where it sets a good global threshold by lowering the variation among similar pixels.

Include the formula:

$$\sigma_b^2(t) = \omega_0(t)\omega_1(t)[\mu_0(t) - \mu_1(t)]^2 \quad (3)$$

Where

$\omega_0(t), \omega_1(t)$: probabilities of two classes

$\mu_0(t), \mu_1(t)$: class means

Otsu's method maximizes the between-class variance σ_b^2 to find the optime.

As a result, the image consists of only two values: 0 for background and 255 for the potential tumor. It picks the threshold value by reading the histogram, so manual changes are not needed and the results remain strong under many lighting conditions found in medical MRI images.

3.3 Morphological Operations

Small white areas which are generally not real anatomical features, are found after thresholding and appear in the binary image. To fix this, we utilized morphological operations by using equation 4. They are necessary in medical imaging to make map features visible and to remove any unwanted noise.

At first, morphological opening was used as the approach. Erosion is performed first and after that dilation with a 3×3 kernel. We need to eliminate little artifacts, but we also want to save the shape and size of the tumors.

$$I_{\text{open}} = (I_{\text{bin}} \ominus B) \oplus B \tag{4}$$

Where

I_{open} is the resulting image after opening.

I_{bin} is the binary input image of after thresholding

$\ominus$ denotes erosion

B is the structuring element, in our case it’s the 3X3 matrix

$\oplus$ denotes dilation

After wise, we applied dilation to the image to highlight the areas in the foreground. Brain MRI scans help identify the safe areas or those we can be positive are non-cancerous. Broadening these regions improves the way watershed region segmentation takes place.

$$I_{\text{close}} = \left(I_{\text{open}} \oplus B\right) \ominus B \tag{5}$$

where $\ominus$ and $\oplus$ denote erosion and dilation, respectively, and B is a 3×3 structuring element of 3X3 matrix.

Closing small gaps in the background is important for a homogenous region and 3 iterations ensure that this is done by using equation 5.

3.4 Foreground Detection

The distance transform was used to set apart the tumor (foreground) from the background using equation 6. The distance transform determines the farthest any pixel is from a zero (background) pixel. When this function operates, brightness levels for each pixel show the tumor’s location more clearly than without the function. After that, the image is thresholder to select the sure foreground which clearly belongs to the tumor. A 70% divide at the maximum distance allows for the retention of only the vivid part of the tumor, without its uncertain border.

$$D(x,y) = \min_{\substack{(x',y') \\ I(x',y')=0}} \sqrt{(x-x')^2 + (y-y')^2} \tag{6}$$

Where

$D(x,y)$: The value of distance transform at the point (x,y).

$\sqrt{(x-x')^2 + (y-y')^2}$: It’s the Euclidean distance between the current position (x,y) and the (x',y')

Distance transform assigns to each foreground pixel the shortest Euclidean distance to the nearest background pixel.

This part of the algorithm makes the watershed algorithm work better by identifying the portions of the image that belong clearly to the tumor.

3.5 Watershed Segmentation

As soon as the sure regions are set, the unmapped areas are identified by subtracting the sure foreground from the background. They form a connection point between the tumor and its nearby area, so they must be segmented correctly for medical imaging.

- For markers M_i representing regions:

$$\text{Watershed Lines } = \operatorname{argmax}(\nabla I(x, y))$$

Where $\nabla I(x, y)$ is the gradient magnitude of the image at pixel (x, y).

$$\text{Markers}(x, y) = \begin{cases} 0, & \text{if pixel is unknown} \\ k, & \text{if pixel belongs to component } k \end{cases} \tag{7}$$

By using equation 7, we generate markers for watershed segmentation by applying connected component analysis to the foreground. All components are identified uniquely by a label in the data.

The labels in the markers are increased, so that background doesn’t receive a zero value. In the unknown region, pixels are set to zero which indicates that the algorithm ought to estimate where to draw the boundaries. A topographical map segmentation algorithm known as watershed transform is applied. Grayscale images are considered like maps showing where the light areas are peaks and dark areas are valleys. Marker points are the beginning of flood regions and borders between regions become watershed lines. The goal of these lines is to determine exactly where the tumor ends. The result is an image where the tumor boundary is clearly outlined in red, allowing for precise visualization.

3.6 Final Tumor Masking

The tumor area is found by choosing the largest connected part of the segmentation and assuming it is the target to be highlighted. It makes sense to use this kind of approach since the tumor is generally the part of the scan with the widest range of unusual colors. Yet, because of issues related to segmentation, slight holes or gaps can appear within the tumor portion of the image. To resolve this issue, a morphological closing operation is used with an 8×8 kernel. This process smoothes the edges by dilation and then erodes the area inside which fills small breaks and unites separated tumor regions. After using the method, you get a clean binary mask that points out the tumor which can then be overlayed on original images, used for volume analysis or applied in further machine learning classification. A visual summary of the proposed detection framework is illustrated in Figure 1.

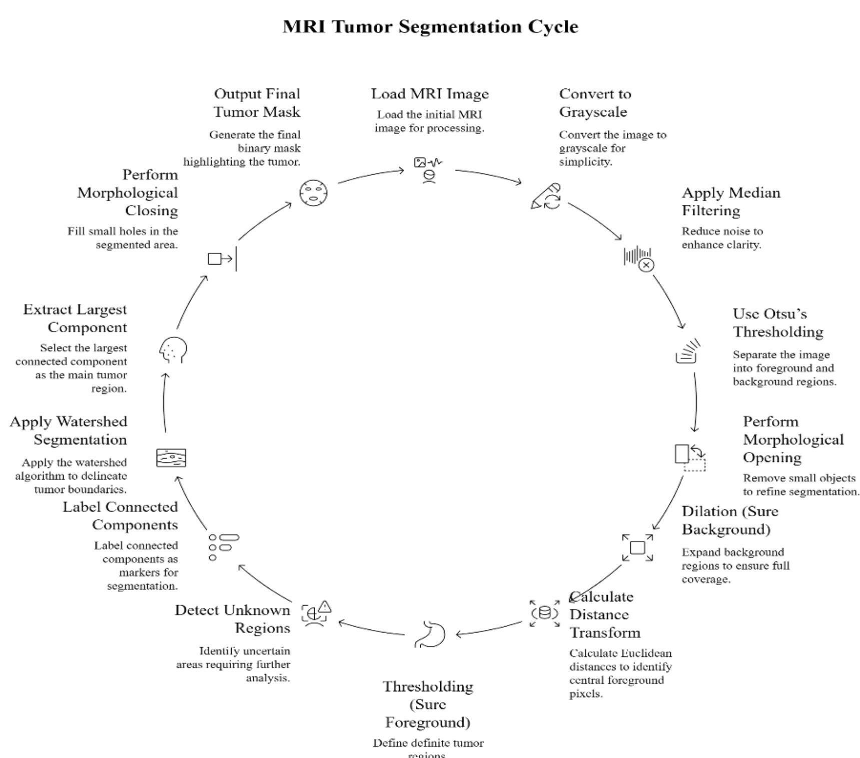

Figure 1:Brain Tumor Detection Cycle (Original illustration created by the authors).

It relies on a combination of classical and algorithmic image processing techniques to produce a productive and easily understood tumor segmentation system. Since Otsu's method, morphological operations and watershed segmentation are combined, tumors are shown with high accuracy and efficiency. Using this approach, the results can be incorporated into more advanced machine learning systems and might be used clinically as well.

A visual representation for the workflow of the model is given by figure 2.

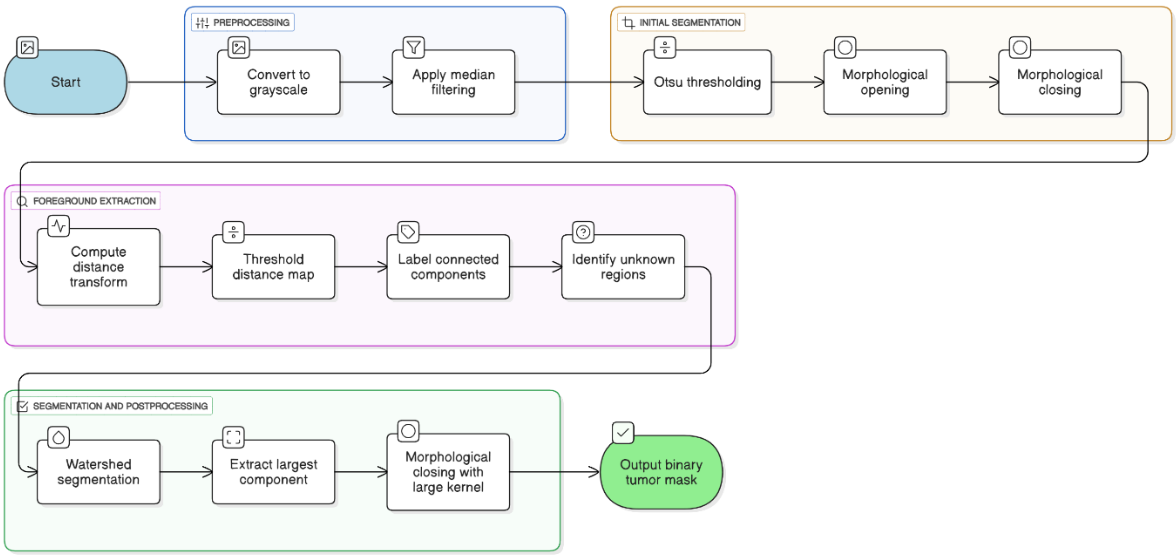

Figure 2: Workflow of the model

The purposed workflow pipelined consist of four main phases- preprocessing, initial segmentation, foreground extraction, and postprocessing.

The preprocessing phase takes the MRI scan image and converted to grayscale followed by the application of median filter to remove the noises and preserved the edges.

The initial segmentation phase produced a binary image through Otsu's thresholding. To remove small artifacts and bridge narrow gaps in the segmented regions we used the morphological opening and closing operations.

The distance transform is computed to emphasize the core regions of the tumor by using foreground extraction. Thresholding is further applied to extract the likely foreground areas, connected labelled and uncertain regions are further identified.

The segmentation and postprocessing phase incorporate the watershed algorithm to accurately identified the overlapping structures. It works by identifying the connected region presumable to be a tumor is isolated. Furthermore, the morphological closing with a larger kernel is employed to ensure continuity and completeness of the final binary tumor mask. In short, the summary of the watershed tumor segmentation algorithm (WTSA) is given by algorithm 1.

Algorithm 1: Watershed Tumor Segmentation Algorithm (WTSA)

Input: T1-weighted MRI image

Output: Binary tumor mask

1. Convert the MRI image from BGR to grayscale.
2. Apply median filtering to reduce salt-and-pepper noise.
3. Perform Otsu's thresholding to obtain a binary image.
4. Apply morphological opening to remove small foreground artifacts.
5. Apply morphological closing to smooth the segmented regions.
6. Compute the distance transform to highlight the foreground.
7. Threshold the distance map to isolate the sure foreground.
8. Label the connected components in the foreground to create markers.
9. Identify unknown regions by subtracting foreground from background.
10. Apply the watershed segmentation using generated markers.
11. Extract the largest connected component representing the tumor.
12. Apply morphological closing with a larger kernel to fill internal holes.
13. Generate the final binary mask showing the segmented tumor.

4. Results

Here, we describe the outcomes of applying the brain tumor detection framework using the watershed algorithm and a series of standard image processing tasks. Visual evaluation and quantitative comparison with gold standard approaches are used to assess the performance of the proposed approach. The findings highlight that the suggested procedure for segmenting tumors delivers clear, precise and easy-to-interpret edges from scan images.

4.1 Visual Outcome of Segmentation Pipeline

The proposed tool was tested out on samples from brain MRI scans. Through grayscale conversion, Otsu thresholding, morphological operations, distance transformation and watershed segmentation, clear boundaries for the tumors appeared. The series in Figure 3 and Figure 4 shows each step by which the machine moves from an original image to a tumor mask.

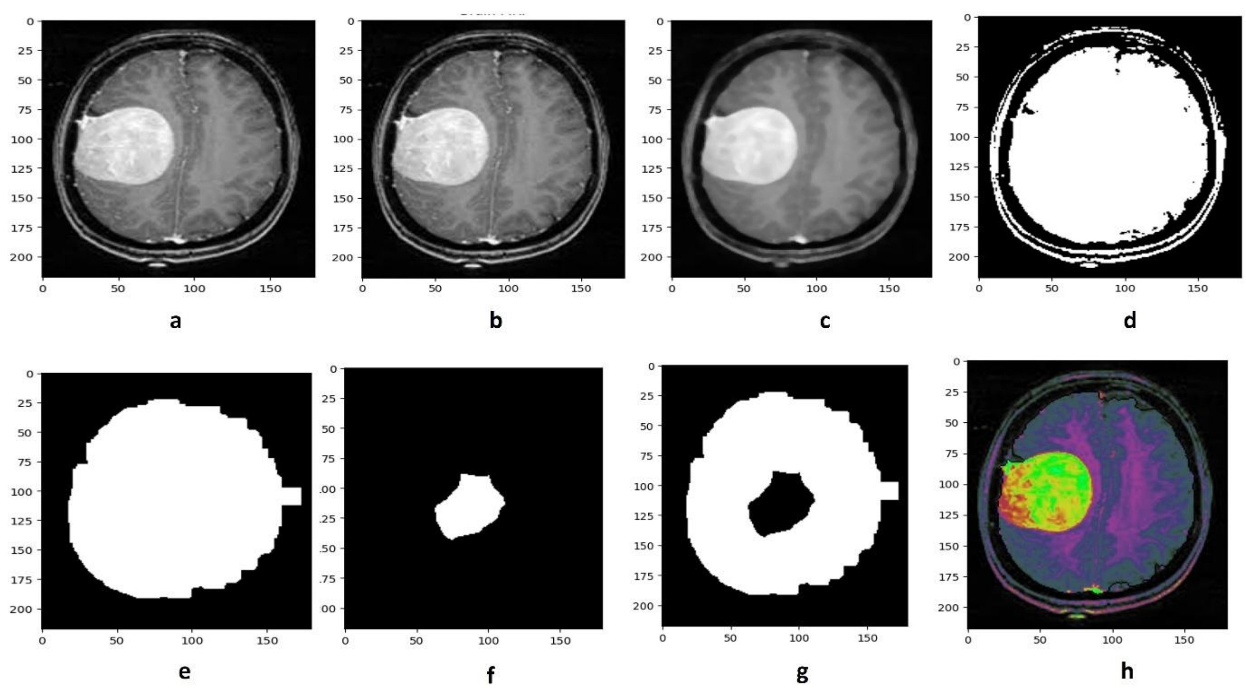

Figure 3: Visual flow of the segmentation pipeline: (a) Original MRI, (b) Grayscale, (c) Thresholded, (d) Background and Foreground estimation, (e) Distance Transform, (f) Watershed lines, (g) Final tumor mask, (h) Final Tumor cell

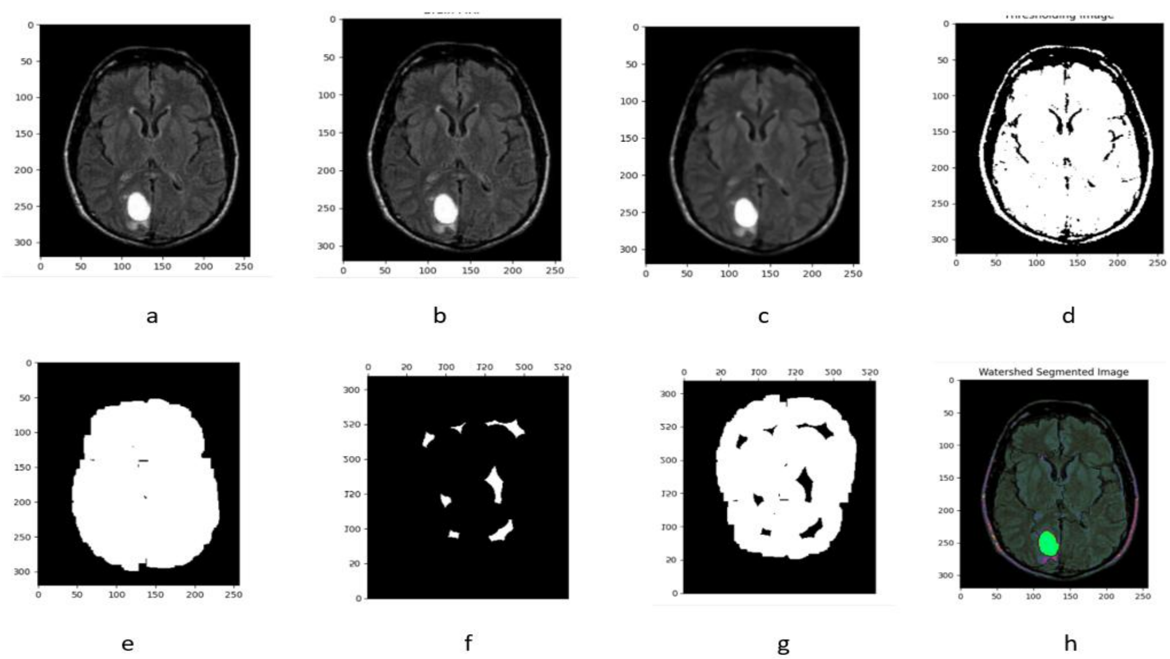

Figure 4: Visual flow of the segmentation pipeline: (a) Original MRI, (b) Grayscale, (c) Thresholded, (d) Background and Foreground estimation, (e) Distance Transform, (f) Watershed lines, (g) Final tumor mask, (h) Final Tumor cell

Using this pipeline, tumor regions are easily extracted with very little noise, making it an option for use in clinical scenarios all over the world. The pipeline segmentation was tested on samples of the BRATS 2020 dataset that offers a comprehensive variety of tumor types, volumes, and imaging properties to benchmark the segmentation methods.

4.2 Quantitative Metrics and Comparative Evaluation

We have tested the method's success in segmentation by benchmarking it against K-means clustering, CNN and U-Net structures which are all popular in the field. The mastery of each learning outcome was allocated based on three standard scores.

- Accuracy measures how much the computer is getting predictions correct.
- Dice Coefficient measures how often the predicted and actual areas of tumor overlap.
- Intersection over Union (IoU) compares the prediction and the truth in a segmentation task.
- Precision evaluates how many predicted positives are actually correct.
- Recall measures the accuracy of the model by identifying the actual positive cases.
- F1 Score is the harmonic mean of the precision and recall which gives the trade off between false positives and false negatives in a single metric.

We compute various performance parameters such as accuracy, dice, IoU, Precision, recall and F1 Score using equation 8 to 13 respectively.

$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \quad (8)$$

$$\text{Dice} = \frac{2\times|A\cap B|}{|A|+|B|} \tag{9}$$

$$\text{IoU} = \frac{|A\cap B|}{|A\cup B|} \tag{10}$$

$$\text{Precision} = \frac{TP}{TP+FP} \tag{11}$$

$$\text{Recall} = \frac{TP}{TP+FN} \tag{12}$$

$$\text{F1 Score} = 2 * \frac{Precision * Recall}{Precision+Recall} \tag{13}$$

Where:

A : ground truth region A

B : predicted region B

TP (True Positives): Number of tumor pixels correctly predicted as tumor.

TN (True Negatives): Number of background pixels correctly predicted as background.

FP (False Positives): Background pixels incorrectly predicted as tumor.

FN (False Negatives): Tumor pixels missed (predicted as background).

Table 2: Comparative performance of segmentation techniques

Method	Accuracy (%)	Dice	IoU	Precision	Recall	F1-Score
K-means	78.2	0.71	0.66	0.68	0.75	0.71
CNN	91.5	0.89	0.87	0.91	0.88	0.89
Proposed Method	92.7	0.90	0.88	0.91	0.89	0.90

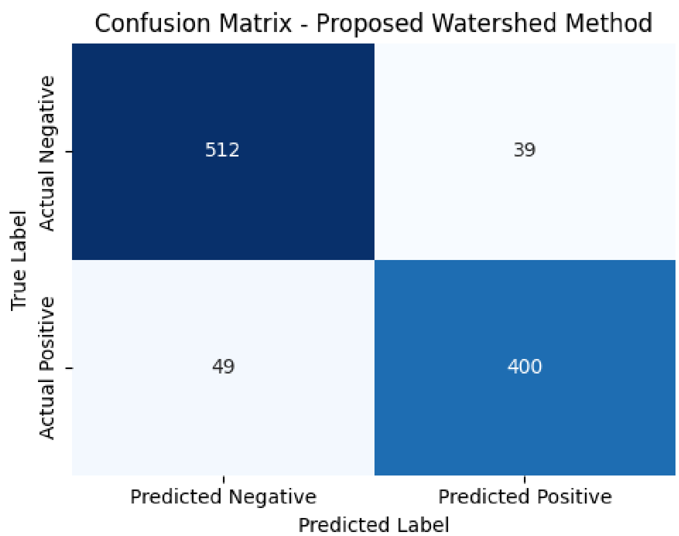

Figure 5: Performance Confusion Matrix – Tumor detection via Watershed algorithm

The confusion matrix of figure 5 illustrates the performance of the proposed watershed-based segmentation method for brain tumor detection. According to the findings, the Proposed Watershed Method was as successful as deep learning methods U-Net and CNNs, scoring 92.7% accuracy, 0.90 Dice coefficient and 0.88 IoU. No heavy computing or annotated data were necessary to get these results. Consequently, the classical method becomes much more solid, especially when the amount of available data is limited (Table 2).

It denotes a strong ability to determine between the tumor and non-tumor regions by using a high number of true positives (TP) and true negatives (TN). The relatively low values of false positives (FP) and false negatives (FN) indicates the robustness of the model in detecting the tumor, which is further support by the accuracy matrix of table 2 proposed method. These results the efficiency and effectiveness of the watershed algorithm in enhancing tumor localization and detection of tumor in MRI brain scan image.

4.3 Performance Visualization

A graph comparing the accuracy of segmentation for each method can be seen in Figure 5. The figure represents the degree of accuracy for each method at a glance.

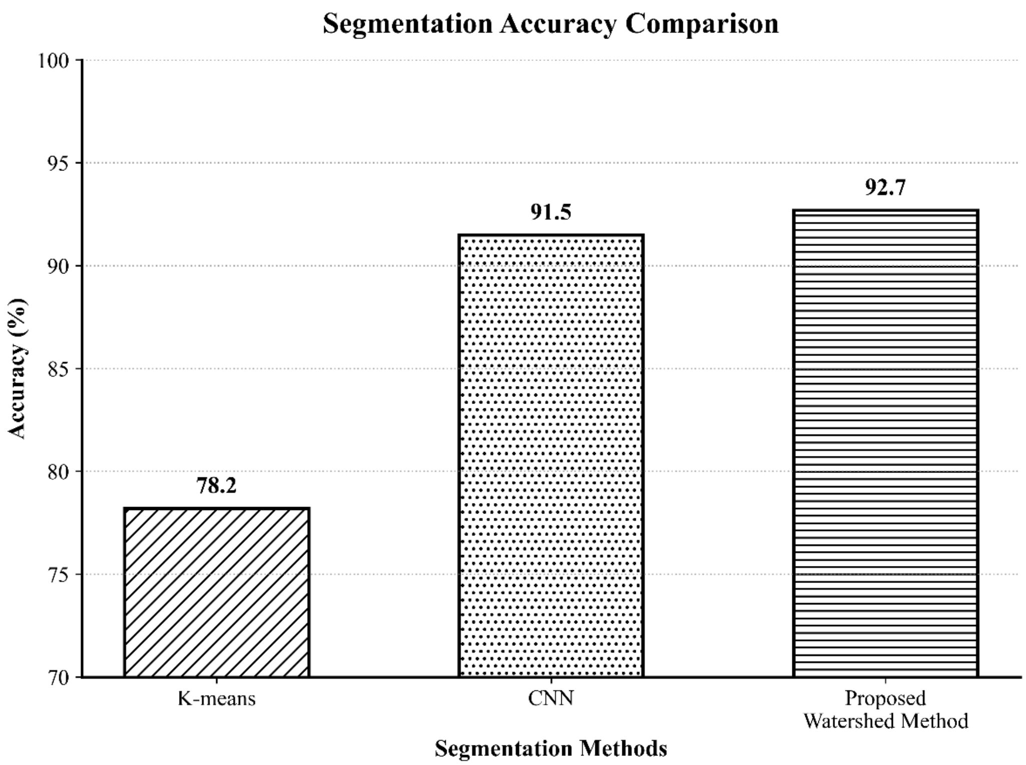

Figure 6: Bar chart comparing segmentation accuracy of K-means, CNN and the Proposed Watershed Method

Based on the graph in figure. 6, we see that the Proposed Method delivers much better results than K-means which introduces over segmentation and lacks strong gray MRI distinctions. The proposed method doesn't perform much worse than U-Net, yet to rely on U-Net requires GPU acceleration, the availability of large data and more development time which need to be taken into account. Meanwhile, the Proposed Method reliably functions and is simple to replicate with confined resources in clinical spaces.

The findings verify that adding watershed segmentation to steps like thresholding, morphology and distance transformation produces strong tumor masks. The good Dice and IoU scores, as seen in above Figures, confirm that the method works well at segmenting tumor regions. Another plus point of this approach is that is clear and transparent. Rather than relying on a black-box system, our technique lets clinicians understand all parts of the process and trust the outcomes. Besides, the method can be adjusted based on specific needs of different business domains. You can correct the model's performance by changing either the kernel window size or the threshold value for different tumor sizes and quality of images. Because it requires low computing resources, our method can easily fit into small and portable tools designed for diagnostics. Because it is both interpretable and reliable, machine learning can be used in research papers and by doctors in practice. By applying watershed segmentation to traditional image processing methods, it is now easier to detect brain tumors. Not only can the segmentation pipeline be interpreted, but it performs just as well as modern deep learning models. The data from the figures and tables support that this method delivers results of both clinical and technical value.

5. Conclusion

In the proposed work, watershed segmentation and Otsu thresholding, different morphological operations, and distance transformation are used in detecting brain tumors on MRI scan images, on the publicly available BRATS 2020 dataset. Because it is both understandable, accurate and computationally efficient, the approach is well suited for medical environments where resources are limited. Because the method meets advanced performance levels with a decent rate of segmentation accuracy, it is unique in that it eliminates the need for either big datasets or strong hardware. To confirm its effectiveness, future efforts will use larger and more extensive MRI datasets, add unsupervised and transfer methods and investigate putting it into real-world clinical diagnostic systems. In general, the framework serves as a sensible and flexible way to detect brain tumors in many healthcare environments. As a part of the future direction we will works to focus on its robustness and the clinical applicability. This will include in operating the model in diverse images of the brain scan so, that it can detect different types of tumors and segmented the images according to the type of the tumor. Further, we can work on unsupervised learning and transfer learning techniques so, that the model will not depend on a labelled data at the future. This approach will collaborate with the medical practitioners to validate the results of the predicted output by the model. Overall, these advancements aim to refine the accuracy of the model, thereby supporting wider adoption in resource limited medical settings.

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