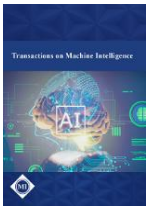
Transactions on Machine Intelligence 3(4) (2020) 211-217

ISSN Online: 2821-1693

Transactions on Machine Intelligence

Journal Homepage: https://tmachineintelligence.ir/index.php/TMI



Fully Automated Brain Tumor Segmentation in MRI Images Using a Modified Level Set Method

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ARTICLE INFO

Article History:
Received 2 July 2020
Received in revised form 9 October 2020
Accepted 5 December 2020
Available online 5 December 2020

Keywords:
Image Segmentation, Level Set, Brats 2017, Glioma, Brain Tumor

ABSTRACT

Gliomas are among the most common types of brain tumors found in adults, originating from glial cells and infiltrating surrounding brain tissues. Accurate identification and segmentation of these tumors are crucial for diagnosis, treatment planning, and patient monitoring. Despite significant advancements in medical imaging and computational analysis, glioma detection remains challenging due to the high variability in tumor shape, size, and location across different patients. Conventional segmentation methods, particularly level set approaches, often require manual intervention, limiting their efficiency and reproducibility in clinical settings. In this study, we propose a fully automated glioma segmentation method based on a modified level set framework. Unlike traditional semi-automatic level set techniques, our approach eliminates the need for manual initialization, thereby improving consistency and reducing operator dependency. The proposed method enhances boundary detection and region refinement, leading to more accurate segmentation results. To evaluate the effectiveness of our approach, we conducted extensive experiments using the standard BraTS 2017 dataset. Performance was assessed through both quantitative and qualitative evaluation metrics, including the Dice similarity coefficient. Our method achieved an average Dice coefficient of **79%** for the entire tumor, demonstrating its reliability and effectiveness compared to conventional techniques. The fully automated nature of this approach offers promising potential for integration into clinical workflows, aiding radiologists and medical professionals in the early detection and precise delineation of gliomas.

1. INTRODUCTION

Brain tumors, a form of cancer [1-5], are the second leading cause of mortality in children, adults, and the elderly, according to the World Health Organization [6][7]. The abnormal growth of cells results in a mass in the brain, known as a brain tumor. The growth rate of the tumor may be rapid or slow, depending on the type of tumor and the patient's health condition. Tumors originating in the brain are termed primary tumors (such as glioblastoma,

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http://dx.doi.org/10.47176/TMI.2020.211

multiforme, meningioma, astrocytoma, etc.), whereas tumors that originate elsewhere in the body and spread to the brain are known as secondary tumors [8].

Imaging techniques allow doctors and researchers to evaluate the activities and disorders present in the human brain before performing surgery. Among various medical imaging techniques, magnetic resonance imaging (MRI) provides more contrast information about brain tissues [9]. Conventional MRI imaging techniques that can offer morphological information of the scanned area include T1, T2, and FLAIR images. These images are complementary and together provide the most accurate information for tumor description [10]. In this paper, FLAIR MRI images are used to identify and segment the entire tumor. It is essential for a physician to accurately identify and localize the brain tumor initially to evaluate the proposed method.

In image processing, brain tumor segmentation means separating the unhealthy brain tissue, i.e., the tumor, from the healthy brain tissue [11]. Brain tumor segmentation is a broad research area. Since it plays a crucial role in MRI image processing and machine vision, it is considered a significant step in most medical applications. Various methods have been developed for brain tumor segmentation, one of which is the level set method. Our objective is to utilize the level set method in brain tumor segmentation. Sections 2 and 3 introduce the tools used in the proposed method. In section 4, we explain our proposed method. Section 5 presents the results obtained from simulating our proposed method, and section 6 provides a general conclusion of this paper.

2. BRATS2017 DATASET

The dataset used in this paper is the BraTS 2017 dataset. This dataset includes 285 training samples (210 samples belonging to malignant tumors (HGG) and 75 samples belonging to benign tumors (LGG)) and 46 testing samples across four MRI imaging modalities (T1, T2, T1c, and FLAIR). The test data includes ground truth maps. Ground truth maps are data where multiple expert physicians have meticulously labeled the tumor regions. Figure 1 shows some HGG FLAIR images from the Brats2017 dataset along with their corresponding ground truth maps. The test data in this set do not have ground truth maps. Therefore, to evaluate proposed methods in tumor segmentation, online tools are used. The results from these tools are primarily presented as Dice coefficient metrics for the three main tumor regions: the whole tumor (all tumor components), the core tumor (all tumor components except edema), and the active tumor (only active cells). However, due to the lack of access to these tools and our focus on FLAIR images, we evaluate our method using a portion of the training data that contains ground truth maps and Equation (1).

$$Dice = \frac{2(TP)}{2(TP)+FN+FP} \tag{1}$$

where TP is the number of pixels correctly identified as tumor, FP is the number of pixels incorrectly identified as tumor, and FN is the number of pixels that are part of the background but mistakenly identified as tumor.

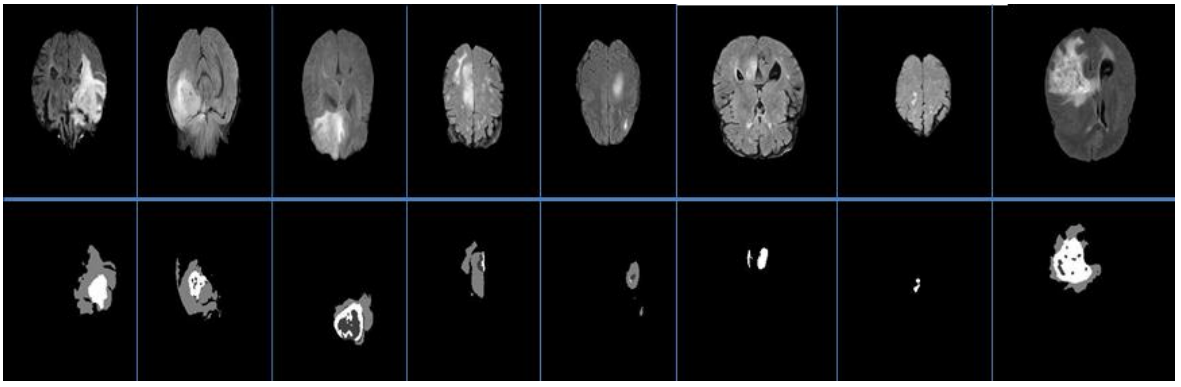

Fig.1. Examples of HGG FLAIR Images from the Brats2017 Dataset with Corresponding Ground Truth

3. LEVEL SET METHOD

Today, image segmentation has been used in many studies [12-14]. The level set method is a type of deformable model used for image segmentation. The main idea behind deformable models is to initially define a preliminary curve and then associate a series of energies with this initial curve. Finally, using a series of methods, this energy is minimized so that the initial curve aligns with the boundaries of the desired object in the image.

Deformable models can be divided into two categories based on whether the initial curve is parametric or non-parametric: level sets and active contours. Active contours have issues such as high sensitivity to the location and size of the initial curve, which are largely addressed by the level set method.

The level set function is defined as $\Phi(i,j,t)$, where (i,j) are the coordinates in the image plane and t is time. If Ω is the image domain and C is the initial curve, the level set function divides the image domain into three parts at any moment:

$$\begin{aligned} C &= \{(i,j) \in \Omega : \varphi(i,j) = 0\} \\ inside(C) &= \{(i,j) \in \Omega : \varphi(i,j) > 0\} \\ outside(C) &= \{(i,j) \in \Omega : \varphi(i,j) < 0\} \end{aligned} \tag{2}$$

This function is divided into two types: region-based and edge-based. In this paper, to address the intensity inhomogeneity in MRI images, which is an intrinsic characteristic of these images, we use Li's method [15], a region-based method. In this method, the following energy function is defined for the level set function:

$$\varepsilon(\Phi,c,b) = \int \sum_{i=1}^{N} e_i(x) M_i(\Phi(x)) dx \tag{3}$$

where $M_i(\Phi(x))$ is the membership function for each region with similar intensity, defined as follows:

$$e_i(x) = \int K(y-x) |I(X) - m_i|^2 dy \tag{4}$$

Here, (x, y) represents the intensity at point (x, y), m_i denotes the cluster centers, and k is a kernel function.

By minimizing Equation (3), this method can simultaneously segment the image and estimate the bias field, which can then be used to correct the intensity inhomogeneity. The process of minimizing Equation (3) is iterative, updating Φ, b, and c in each iteration until Equation (3) converges.

4. PROPOSED METHOD

Figure 2 shows the flowchart of our proposed method. In this method, the input image first passes through a power filter. As observed in Figure 1, in brain MRI images, the tumor has a higher grayscale intensity, close to 255. The power filter brightens the pixels closer to 255 and darkens the pixels closer to zero. Next, the image passes through a mean filter to blur and darken areas that are not part of the tumor but have high grayscale values. Then, the image is binarized to obtain a rough outline of the tumor. Subsequently, the coordinates of the bounding box of this tumor are determined and used as the initial curve for the level set algorithm. This process transforms the level set method, previously semi-automatic with manually input initial curves, into a fully automatic method, leading to precise segmentation results.

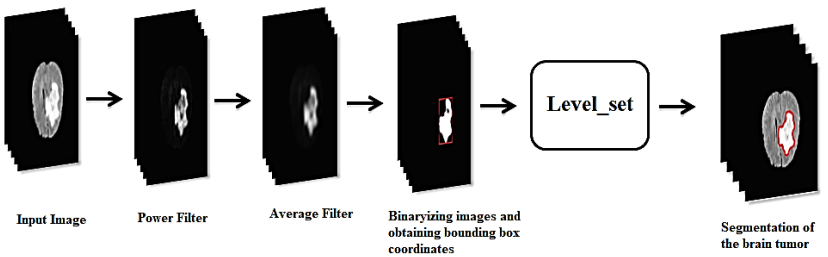

Fig.2. Flowchart of the Proposed Method

5. RESULTS

In the proposed method, image segmentation is performed using the level set algorithm. In [12], Li and colleagues demonstrated through multiple experiments that the only parameter in the level set algorithm that can be varied to achieve different results is the number of iterations used to update the level set method. Here, we apply our proposed method with 10, 20, 30, 40, 50, and 60 iterations. The results obtained from these experiments are shown in Figure 3.

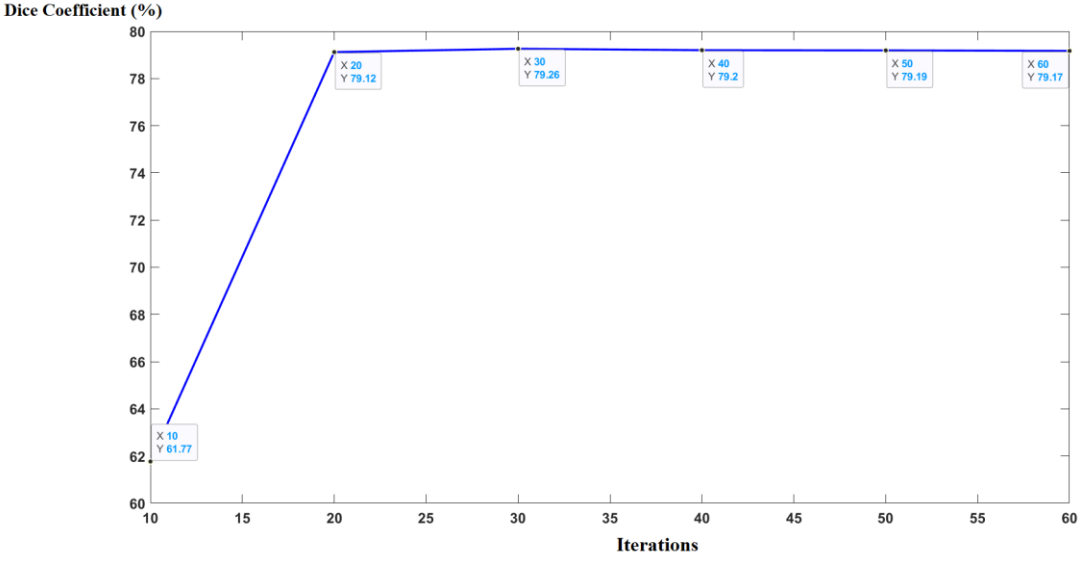

Fig.3. Comparison of Dice Coefficient for Six Experiments with Different Iteration Numbers

Based on Figure 3, it is observed that our proposed method achieves high accuracy for more than 20 iterations. Since each iteration is time-consuming and there is no significant difference in accuracy beyond 20 iterations, we conduct our experiment with 20 iterations. Ultimately, our proposed method achieves a Dice coefficient of 79.12%. Some of the output results of our proposed method, along with the corresponding ground truth maps, are shown in Figure 4.

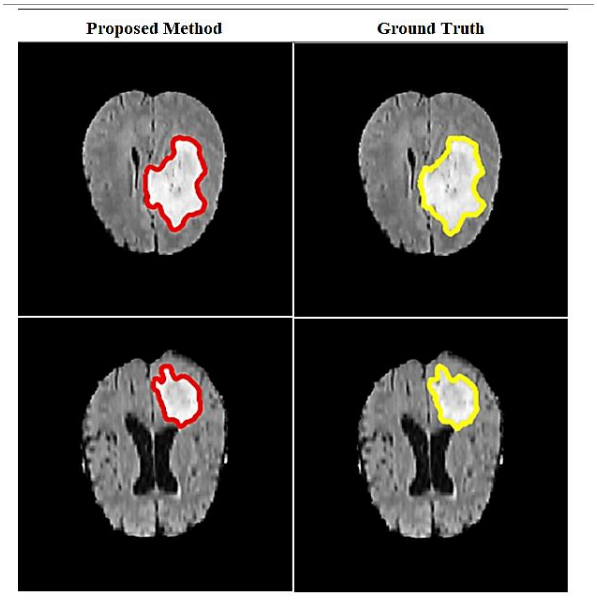

Fig.4. Comparison Between Some Results Obtained from the Proposed Method and the Ground Truth

Next, we compare our proposed method with the conventional level set method. This comparison is shown in Table 1.

Table 1. Comparison of the Proposed Method and the Level Set Algorithm

Method	Dice Coefficient (%)
Present Study	79.12
Algorithm of equal levels	69.86

As expected, the proposed method demonstrates higher accuracy than the conventional method, due to the appropriate selection of the initial curve around the brain tumor. Figure 5 illustrates the segmentation output results of both methods for one image. In this figure, the impact of appropriately selecting the initial curve is clearly visible; in the conventional level set algorithm, the initial curve might be selected from an inappropriate location, resulting in segmenting the entire brain instead of the tumor.

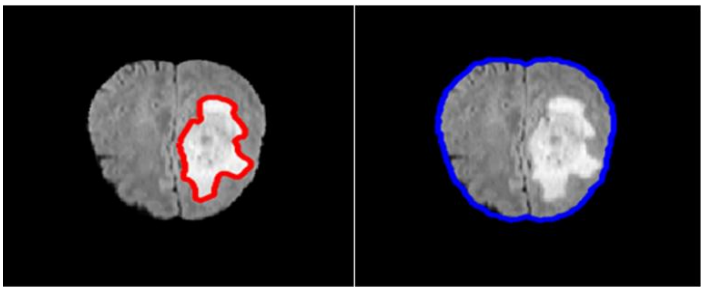

Fig.5. Comparison of the Output Result of the Proposed Method (Left) with the Conventional Level Set Method (Right)

6. CONCLUSION

In this paper, we presented a fully automatic method using the level set approach. In the conventional level set method, the initial curve is selected manually, making this method semi-automatic. Additionally, sometimes the manually selected initial curve is not appropriately placed, leading to segmentation errors. Here, we proposed a method that automates the level set method and improves segmentation accuracy.

In the future, we aim to expand our proposed method and enhance its accuracy. Our goal is to develop a fully automatic method with high accuracy and speed to quickly detect and accurately segment tumors. This advancement can significantly assist specialized physicians in better treating the disease.

Transparency Statement

The data supporting this study are available upon reasonable request to the corresponding author, subject to ethical and confidentiality considerations.

Acknowledgments

We would like to express our gratitude to all individuals who contributed to this project.

Declaration of Interest

The authors declare that they have no competing interests.

Funding

This research received no specific grant from any funding agency, commercial, or not-for-profit sectors.

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