Brain Tumor Segmentation with an Ensemble Method

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요 약

Nowadays, brain tumors are widespread, and the most prevalent brain tumors are intracranial metastases from systemic cancers, meningiomas, and gliomas, specifically, glioblastoma. Brain tumor segmentation is an excellent way to detect brain tumors at an early stage. As a non-invasive examination method, MRI has a significant guiding role in tumor clinical intervention. However, manually segmenting brain tumors from MRI requires a lot of time and energy for doctors, which affects the implementation of follow-up diagnosis and treatment plans. With the development of deep learning, medical image segmentation is gradually automated. We proposed an ensemble method from DMF-Net and HDC-Net with STAPLE algorithm to solve this problem. Our result is evaluated on the BraTS2019 dataset. The method got 0.6839, 0.7947, and 0.7039 on enhancing tumor, whole tumor, and tumor core, respectively.

Keywords: brain segmentation segmentation, ensemble, STAPLE algorithm, MRI, deep learning.

1. Introduction

Low-grade glioma and high-grade glioma are the two forms of glioma. The most frequent type of brain cancer is glioma[1]. An essential part of all brain tumor treatments is segmenting tumors and surrounding tissues precisely so that the doctors estimate tumor progression and have the correct treatment response for patients. Glioma tumors and edema are scattered, low-contrast, and have a lot of shapes that are very difficult to segment. Another problem with brain tumors is that they can occur anywhere within brain areas, in any shape and size. On the other hand, automated brain tumor segmentation in multi-modal MRI scans is a challenging task due to gliomas' heterogeneous appearance and shape.

2. Related Works

Convolution Neural Networks (CNNs) for brain tumor segmentation has been the subject of a lot of research, with promising results. Havaei et al.[2] describe a two-pathway CNN architecture that predicts the label for each pixel based on a sliding window input of a local picture patch. Ronneberger et al.[3] create U-Net, a fully convolutional network (FCN) for the dense prediction that processes the entire image. The network is trained end-to-end to provide a complete resolution.

3. Proposed Method

The target segmentation framework of the proposed ensemble model is exhibited, which is mainly composed of two parts, DMFNet [4], HDCNet [5].DMF-Net is the model which employs the multi-fiber (MF) and dilated multi-fiber (DMF) units as the building blocks. This model is a variant of encoder-decoder network architecture. The input of DMFNet is four types of brain image suchas T1, T1ce, T2, and FLAIR. Except for the first and last layers, all of the other layers in the model are controlled by a combination of DMF and MF units. To get the benefit of learning the multi-scale context of brain tumors in the encoding phase, the first six encoding units are generated based on DMF units. With the aim of preserving the information of features during learning, the model uses the concatenation operation between high-resolution features from the encoding path and the upsampled features. Note that trilinear interpolation has been used for the upsampling phase. The second model is HDC-Net, which can explore multi-scale multi-view spatial contexts with high efficiency. The second advantage is the light-weight model. After that, we used STAPLE algorithm[16] to combine two results from DMF-Net and HDC-Net. STAPLE is an expectation-maximization algorithm for simultaneous truth and performance level estimation.

4. Experimental Results

4.1.Dataset

We tried our model based on the BraTS2019 dataset. The medical images were provided in 3D volumes with four types of MR images acquired: T1-weighted (T1), post-contrast T1-weighted (T1ce), T2-weighted (T2), and Fluid Attenuated Inversion Recovery (FLAIR). The dataset consists of 335 patients for the training dataset and 125 patients for the validation dataset. Dataset

BraTS 2019 visulization is in Fig. 1.

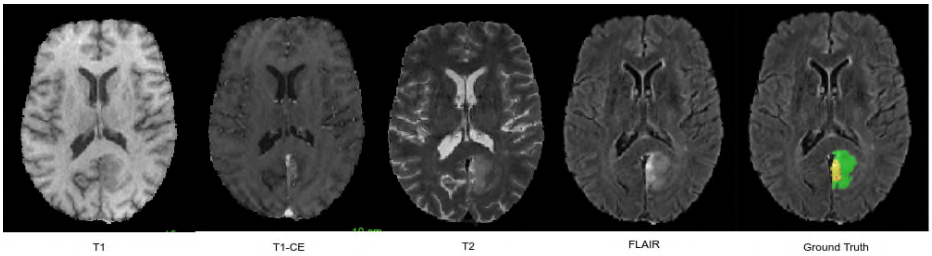

Fig. 1 BraTS 2019 dataset

4.2. Implementation

In our proposed network, we developed the proposed model on the Pytorch platform with python programming language. We trained our model with batch size is 2 and epoch is 100. We used NVIDIA GeForce RTX 1080 GPU processor.

4.3. Implementation

The brain tumor segmentation results were evaluated by the dice similarity coefficient [6]. The dice similarity coefficient is one of the commonly used evaluation metrics in segmentation models. They have a value between 0 and 1. The metric indicates the overlap level between two objects. A value of 0 means there is no overlap and a value of 1 means the two objects completely overlap each other. The formula for calculating dice similarity coefficient (DSC) is expressed in the equation:

$$DSC = \frac{2|A \cap B|}{|A| + |B|}$$

In which A and B are the predicted segmentation and ground truth, respectively.

4.4. Results

We performed the training stage on the BraTS2019 training set and then evaluated the segmentation results on the validation set. The segmentation performances of our proposed model were 0.6839, 0.7947, and 0.7039 for the enhancing tumor, whole tumor, and tumor core, respectively. We also set up a table comparing our performance with other segmentation methods such as U-Net[18], Seg-Net[18]. Our results is in Table 1.

Table 1: Our results

	Dice_ET	Dice_WT	Dice_TC
U-Net[18]	0.5264	0.8083	0.7033
Seg-Net[18]	0.4994	0.7611	0.6887
Ours	0.6839	0.7947	0.7039

5. Conclusion

In this paper, we built a 3D ensemble model with STAPLE algorithm and got good results. We proved the efficiency of our proposed brain tumor segmentation on BraTS2019 dataset. During training, we did not use any external dataset. Our model outperformed other models.

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