A Survey on Brain Tumor Segmentation Using MRI Data

J. A. Sushanth[1*], G. S. Rudresh[2], K. Anuj Prabhu[3], Arif Ali[4]

[1,2,3,4]*Student, Department of Information Science & Engineering, Dayananda Sagar Academy of Technology and Management, Bengaluru, India*

Abstract: **Gliomas are the most frequent primary brain tumors, with varying degrees of aggressiveness, prognosis, and histological sub-regions, such as peritumoral edematous, necrotic core, active, and non-enhancing core. Variable intensity profiles spread throughout multi-parametric magnetic resonance imaging (mpMRI) images illustrate these sub-regions, representing diverse biological features. In longitudinal scans, the amount of resected tumor is also taken into account while evaluating the apparent tumor for possible progression diagnosis. Furthermore, there is growing evidence that accurate segmentation of multiple tumor sub-regions can provide a foundation for quantitative image analysis to predict patient overall survival. Manual segmentation of brain tumor regions is time-consuming and prone to human error, and its accuracy is determined by pathologists' experience. This study includes about 10 scientific papers that address a wide range of technical topics, including network architecture design, segmentation under imbalanced situations, and multi-modality processes. We use this survey to present a complete assessment of newly established deep learning-based brain tumor segmentation algorithms, taking into account the astonishing breakthroughs produced by state-of-the-art technology.**

Keywords: **Artificial Intelligence, Brain tumor segmentation, Deep Learning, Image segmentation, MRI scan, Neural Networks, ResNet.**

1. Introduction

Although brain tumors are uncommon, they are extremely lethal. Gliomas are the most prevalent type of brain tumor. Low-grade gliomas (LGG) and high-grade gliomas (HGG) are the two types, with the latter being more aggressive and infiltrative. Gliomas are very invasive because they grow swiftly and aggressively invading the central nervous system (CNS). Every year, approximately 18,000 Americans are diagnosed with glioma, according to the US National Cancer Institute, and many of them die within 14 months [1].

Magnetic resonance imaging (MRI) has long been used in clinical practice to assess the presence of a tumor and its dissemination to other areas, such as the CNS. In comparison to other techniques such as computed tomography (CT) and positron emission tomography (PET), it also provides soft tissue contrast [2]. Furthermore, multi-modal MRI methods are commonly used to analyze brain tumor tissues because they can differentiate distinct tissues based on tissue features using a specified sequence. T1-weighted pictures help to distinguish healthy brain regions, whereas T1ce (contrast-enhanced)

images aid to distinguish tumor boundaries, which appear brighter due to the contrast agent. T2-weighted scans detect edema around tumors effectively, while FLAIR pictures are superior for distinguishing edema from cerebrospinal fluid (CSF) [2].
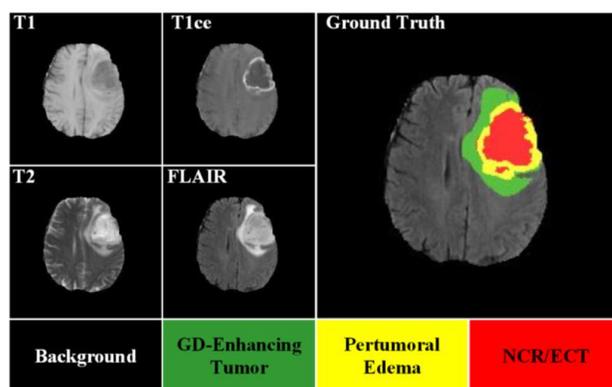

Fig. 1. Exemplar input dataset with different MRI modalities and corresponding ground truth segmentation map

Each frame represents a unique MRI modality. The last frame on the right is the ground truth with corresponding manual segmentation annotation. Different colors represent different tumor sub-regions, i.e., gadolinium (GD) enhancing tumor (green), peritumoral edema (yellow) and necrotic and non-enhancing tumor core (NCR/ECT) (red).

Manual segmentation of brain tumors is usually time-consuming and prone to human errors. Furthermore, it takes a large number of pathologists and a huge amount of time to manually segment brain tumors from all the available MRI data. Hence, the reason to implement different machine learning algorithms for the detection and segmentation of brain tumors and their sub-regions respectively. The way that the machine learning models work is that they are fed (trained) with manually labeled instances of MRI scans and this trained model is used for the automatic detection and segmentation of brain tumors and their sub-regions on the unlabeled instances. Many machine learning algorithms have been used to detect brain-tumor and segment the tumor into different sub-regions. The most notable network architecture in machine learning for segmenting tumors is U-Net, and several improved models have already been developed [8]. Other network architectures have

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Table 1
Literature survey

Reference Number	Publication Year	Author Names	Architecture Used	Dice Scores		
				WT	TC	ET
[1]	2018	Shaoguo Cui, Lei Mao, Jingfeng Jiang, Chang Liu, and Shuyu Xiong	Deep Cascaded Neural Network	0.90	0.81	0.81
[2]	2019	Salma Alqazzaz, Xianfang Sun, Xin Yang, and Len Nokes	SegNet	0.85	0.81	0.79
[3]	2020	Theophraste Henry, Alexandre Carre, Marvin Lerousseau, Theo Estienne, Charlotte Robert, Nikos Paragios, and Eric Deutsch	3D U-Net neural network	0.89	0.84	0.79
[4]	2020	Roelant S. Eijgelaar, Martin Visser et al.	DeepMedic		0.81	
[5]	2021	Lucas Fidon, Sebastien Ourselin, and Tom Vercauteren	nnUNet	0.92	0.93	0.86
[6]	2021	Syed Talha Bukhari and Hassan Mohy-ud-Din	E_1D_3 U-Net	0.92	0.86	0.82
[7]	2021	Md Mahfuzur Rahman Siddiquee and Andriy Myronenko	SegResNet	0.93	0.89	0.86
[8]	2021	Muhammad Usman Saeed, Ghulam Ali, Wang Bin, et al.	RMU-Net	0.91	0.88	0.83
[9]	2021	Li Sun, Songtao Zhang, Hang Chen, and Lin Luo	Ensemble model (CA-CNN, DFKZ Net, and 3D-UNet)	0.91	0.85	0.81
[10]	2019	Guotai Wang, Wenqi Li, Sébastien Ourselin, and Tom Vercauteren	Cascade of 3 CNNs (WNet, TNet, and ENet)	0.88	0.80	0.75

also been implemented such as SegNet and its improved model architectures, DeepMedic, etc.

2. Existing Work

Shaoguo Cui, et al. [1] have used the MRI data from the 2015 MICCAI BraTS (Brain Tumor Segmentation) dataset to train a Deep Cascaded Neural Network and have achieved a DSC score of 0.90, 0.81, and 0.81 (DSC measures the overlap between the ground truth and the automatic segmentation) for the segmentation of whole tumor, tumor core, and enhancing tumor, respectively.

Salma Alqazzaz, et al. [2] have used the MRI data from the 2017 BraTS dataset to train an improved version of the SegNet model architecture and have achieved F-measure scores of 0.85, 0.81, and 0.79 for the segmentation of whole tumor, tumor core, and enhancing tumor, respectively.

Theophraste Henry, et al. [3] have used the MRI data from the 2020 BraTS dataset to train a deeply-supervised 3D U-Net neural network and have achieved a Dice score of 0.79, 0.89, and 0.84 for the segmentation of enhancing tumor, whole tumor, and tumor core, respectively.

Roelant S. et al. [4] have used MRI data from the 2013 BraTS dataset along with the MRI data from six different hospitals to train a convolutional neural network (CNN), named DeepMedic and have achieved a median Dice score of 0.81 for segmentation on BraTS test data and only 0.49 on the clinical data.

Lucas Fidon, et al. [5] have used the MRI data from the 2020 BraTS dataset to train a 3D U-Net architecture-based pipeline of nnUNet and have achieved a median Dice score of 85.9%, 92.4%, and 92.6% for the segmentation of enhancing tumor, whole tumor, and tumor core, respectively.

Syed Talha Bukhari and Hassan Mohy-ud-Din [6] have used the BraTS Dataset to train an E1D3 U-Net architecture-based model and have achieved a Dice score of 92.4%, 86.3%, and 81.8% for segmentation of the whole tumor, tumor core, and enhancing tumor, respectively.

Md Mahfuzur Rahman Siddiquee and Andriy Myronenko [7] have used the MRI data from the 2021 BraTS dataset to train a ResNet architecture-based model named SegResNet from MONAI (deep learning framework) with an encoder-decoder based CNN architecture and have achieved a mean Dice score of 0.86, 0.89, and 0.93 for the segmentation of the enhancing tumor, tumor core, and whole tumor, respectively.

Muhammad Usman Saeed et al. [8] have used the MRI data from 2020, 2019, and 2018 BraTS datasets to train a MobileNetV2 architecture-based model called RMU-Net and have achieved the dice coefficient scores for whole tumor, tumor core, and enhancing tumor of 91.35%, 88.13%, and 83.26% on the BraTS 2020 dataset, 91.76%, 91.23%, and 83.19% on the BraTS 2019 dataset, and 90.80%, 86.75%, and 79.36% on the BraTS 2018 dataset, respectively.

Li Sun, et al. [9] have used the MRI data from the 2018 BraTS dataset to train an ensemble model comprising of Cascaded Anisotropic Convolutional Neural Network (CA-CNN), DFKZ Net, and 3D-UNet and have achieved a mean Dice score of 0.81, 0.91, and 0.85 for the segmentation of enhancing tumor, whole tumor, and tumor core, respectively.

Guotai Wang, et al. [10] have used the MRI data from the 2018 BraTS dataset to train a cascade of three CNNs (WNet, TNet, and ENet) and have achieved a Dice score of 0.75, 0.88, and 0.80 for the segmentation of enhancing tumor, whole tumor, and tumor core, respectively.

The table 1, depicts a summary of the research papers that we have referred to. The table consists of Reference numbers, Publication years, Author Names, Model Architectures used, and finally the Dice scores.

3. Conclusion

Different authors have trained different model architectures for the detection and segmentation of sub-regions of brain tumors. All of them have used a common evaluation metric called the Dice score for the evaluation of the automatically predicted segmented regions providing an overall Dice score on segmentation of brain tumors and their sub-regions ranging from 79% to 93% using MRI scan images. We can observe that the ResNet architecture-based model, SegResNet has achieved the highest Dice score on the segmentation of the Whole Tumor (WT) – 0.93, and the 3D U-Net architecture-based pipeline of nnUNet has achieved the highest Dice score on the segmentation of the Tumor Core (TC) – 0.93, and the same SegResNet model has achieved the highest Dice score on the

segmentation of Enhancing Tumor (ET) – 0.86. By seeing the above metrics, we are planning to implement the ResNet architecture-based model, ResUNet for the segmentation of brain tumors and their sub-regions and achieve a maximum Dice score in doing so.

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