BrainSegNeT: A Lightweight Brain Tumor Segmentation Model Based on U-Net and Progressive Neuron Expansion

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Abstract. Brain tumor segmentation is a critical task in medical image analysis. In recent years, several deep learning-based models have been developed for brain tumor segmentation using magnetic resonance imaging (MRI) data. To address challenges such as high computational time and the requirement of huge storage and resources, we proposed BrainSegNet, which is a lightweight extension of U-Net with progressively expanded neurons that require fewer weights and less memory space. Unlike other DL models, our proposed model has the simplest architecture and is more accurate than other state-of-the-art methods for brain tumor segmentation. The proposed approach was extensively analyzed using the BraTS2020 benchmark dataset for segmenting brain tumors. The experimental findings demonstrate the effectiveness of the proposed system, producing a 96.01% Dice score and 95.89% mean IoU for brain tumor segmentation from brain MRI images.

Keywords: Deep learning · image segmentation · U-Net · brain tumor · MRI Images

1 Introduction

Hundreds of various forms of brain tumors afflict humans, making it one of the most fatal diseases [6]. Traditional treatments, such as surgery, chemotherapy, and radiotherapy, are mainly employed to address these conditions. Artificial intelligence (AI) [4] is gaining momentum and significance as it progresses, and can play a crucial role in brain tumor diagnosis and surgical pre-assessment procedures [30]. To assist in preoperative decisions segmenting brain tumor from medical brain image is now a cutting edge research area [21,22,29]. Researchers

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around the world are vigorously making efforts to establish different kinds of solutions [34] for early detection for better diagnosis and one of the solutions can be the usage of deep learning approaches [7,9]. CNN-based segmentation methods have also achieved state-of-the-art performances in various tests [14,25]. The classical DL model improves the connection weight between the original neurons while analyzing lesion features in large medical images [28]. Consequently, the standard DL model [19], such as the convolutional neural network (CNN), the entire convolution networks (FCN) [18], the U-Net network, and the attention U-Net [24], has considerably improved brain tumor segmentation performance. Inspired by the successful use of CNNs in multiple medical image analysis tasks, we propose a novel lightweight high-performance model for brain tumor segmentation based on deep learning. Our approach aims to design a simple deep learning architecture for brain tumor segmentation. However, all the architectures proposed [5,14,17,20,23,25,33] for brain tumor segmentation have a complex structure that requires high computational time, more effective GPUs, large amounts of storage, and many resources.

Bare in mind these issues, we do straightforward modification of the U-Net developed by merging merits of convolutional blocks, progressive expansion layers, and residual network connections to obtain not only a better segmentation model but also reduce the parameters. The motivation behind this is to improve accuracy and, at the same time, maintain simplicity. The goal of this study is to construct a less complex CNN architecture for brain tumor segmentation, and our main contributions include the following:

1. We propose a simple U-Net architecture incorporating with progressive expansion layer, and residual network connection, referred to as BrainSegNet, that requires fewer weights and less memory space for brain tumor segmentation;
2. An extensive evaluation is done on two challenging datasets, then compared with the state-of-the-art architectures, and the evaluations show that the BrainSegNet results in outstanding performance compared to baselines.

The rest of this paper is organized as follows. A literature review of recent methodology 2. In Sect. 3, a description of the proposed system along with its data collection. Section 4.2 presents the experimental results and a comparative performance analysis are presented in Sect. 4.2.

2 Related Work

Manual tumor segmentation is subjective and time-consuming. In addition, the detection result is laborious and depends on the doctor's theoretical knowledge and practical ability. Therefore, designing an automatic and robust brain tumor segmentation system is essential to realize tumor diagnosis [1,8,10]. Various research studies have been suggested for segmenting brain tumors with deep learning methods. For example, Pius Kwao Gadosey et al. [1] proposed a lightweight model modifying the U-Net model named SD-UNet to obtain higher performance with fewer computational requirements. To reduce the computational complexity, they applied depthwise separable convolutions in their proposed network and achieved a 90.70% dice score for the brain segmentation task. However, their suggested architecture has 3.9M parameters, requiring 15.8 MB of disk space which can be further reduced. In the same year, Sergio Pereira et al. [25] presented a cascade-CNN system where they applied a 3×3 kernel to mitigate overfitting. Their approach could segment the brain MRI image into four areas: normal tissue, necrosis, edema, and enhancing tumor. According to the authors, two CNN architectures were used for better feature extraction, especially for low-grade and high-grade glioma. However, one drawback is that the operator needs manually determine the glioma grade in the early stage, which demands prior medical expertise. Besides these issues, the introduced system showed poor segmentation results for core areas in the BRATS 2015 dataset. Similarly, Havaei et al. [12] proposed another novel Cascading style to segment brain tumors automatically. This research utilized the cascade style of CNN to capture global and local contextual features to deal with imbalanced tumor labels. Moeskops et al. [21] suggested an automatic system incorporating a multi-scale CNN to segment white matter hyperintensities of presumed vascular origin (WMH) from MRI modalities. Chen et al. [5] introduced a model combing prior knowledge with DCNN to improve the captured motifs of DCNN for brain tumor sub-compartment identification.

In 2020, Zhang et al. [31] introduced an attention U-Net for the purpose of brain tumor segmentation. Their suggested architecture improved the local responses to down-sampling and the recovery effects of the up-sampling simultaneously. Furthermore, Wu et al. [29] introduced a CNN-based multi-features refinement and aggregation network (MRANet) for brain tumor segmentation. They adopted the feature fusion strategy to utilize hierarchical features in this system. Recently, Lee et al. [16] proposed an intelligent brain tissue segmentation method utilizing MR images. They partitioned the brain MRI image into small patches through a patch-wise U-Net model, and each patch was predicted separately. However, although the introduced model could overcome the limited disk space problem, the training stage showed higher computation complexity.

3 Research Methodology

3.1 U-Net

U-Net architecture [27] is one of the most popular deep-gaining knowledge of architectures used for medical image segmentation. This architecture is on the whole utilized through the research community due to the fact of its architectural variations with superior outcomes in the image segmentation tasks. In clinical image segmentation U-Net has established itself as well-known for recent proposed ideas including R2YU-Net, attention U-Net, and U-Net++. The place u-shape model is retained along with the two fundamental paths encoder and decoder. By incorporating more than a few strategies such as skip connections, attention modules, residual blocks or aggregate of them those u-net versions alter the encoder or the decoder blocks.

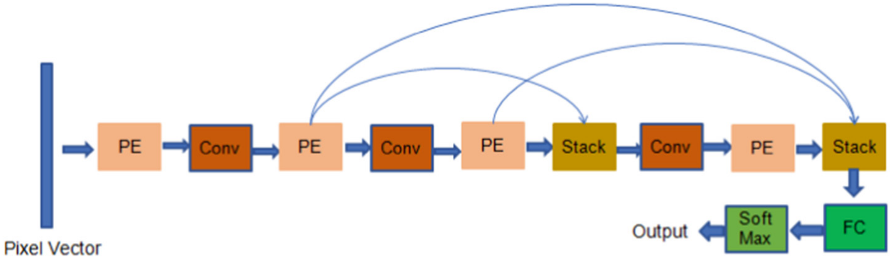

Fig. 1. Visualization of dPEN structure

3.2 dPEN: deep Progressively Expanded Network

The dPEN method takes a pixel from a multispectral image as an input vector and returns the types of objects present in the input pixel vector. Figure 1 illustrates the structure of dPEN, which is formulated as follows: four progressive expansion layers (PEL), three convolutional, three maximum-pooling, and then a fully connected layer (FC). Progressively expandable neural networks (PEN nets), developed for identifying hyperspectral images, serve as the basis of dPEN. The core idea of the dPEN paradigm is the addition of PEL, which incrementally expands each node from the input using a McClorin series expansion of a predefined nonlinear function. It is shown that the dPEN architecture is capable of extracting significant discriminative features from multispectral bands. Hence, the dPEN architecture outperforms well-known machine learning models such as random forest, support vector machine, CNN, etc.

3.3 Proposed Architecture: BrainSegNet

In this study, we propose a modified U-Net named BrainSegnet for brain tumor segmentation. BrainSegNet combines U-nets' modularity with the integration of expanded neurons using nonlinear function expansion. Our proposed architecture takes a 224 × 224 input image as input and outputs the segmented points of interest shown in Fig. 2. The U-Net's U-shape is preserved, with the encoder path on the left side and the decoder path on the right. We incorporate PEL in the encoder path only. A PEL layer, also known as PE2: progressive expansion with the first two terms in Maclaurin series expansion, is included in each residual block along with two batch normalization layers (BN), two ReLU activation layers (ReLU), two 3 * 3 2D convolutional layers (Conv 3 * 3), and a PEL layer. The enlarged area of Fig. 2 demonstrates the arrangement of the Residual PE block.

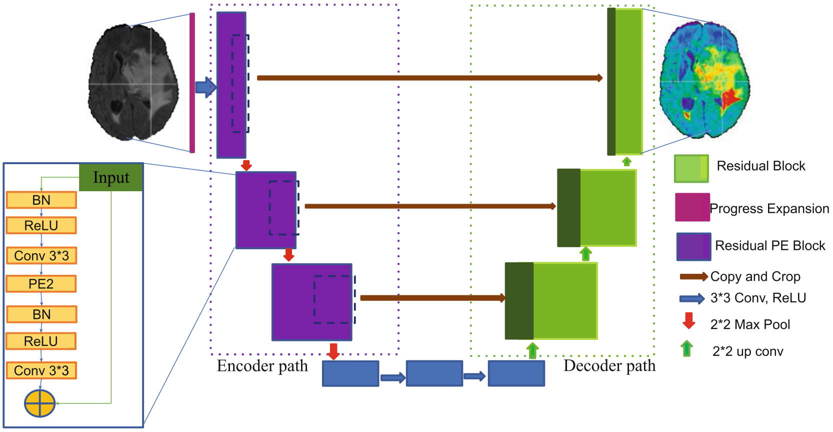

Fig. 2. The detailed illustration of the proposed BrainSegNet architecture integrated PE block with the encoder path where PE2 indicates progressive expansion with two terms.

4 Dataset and Results Evaluations

In the experiments, the training, testing, and validation datasets are all from the BraTS2020 benchmarks [2,3]. The MICCAI Brain Tumor Segmentation competition uses BraTS, a significant public dataset for multimodal brain tumor segmentation, and it is frequently utilized in research on this subject. Every year, new data are added, removed, or replaced to the dataset to enrich its scale. BraTS2020 have 369 annotated brain tumor samples for model training and 120 samples for testing. Each case includes MRI scans of four different modalities: T1-weighted (T1), T1-enhanced contrast (T1-ce), T2-weighted (T2), and T2 fluid-attenuated inversion recovery (Flair). The datasets are labeled by domain experts and contain four classes: background, necrotic and non-enhancing tumors (NCR/NET), GB-peritumoral edema (ED), and GB-enhancing tumors (ET). The evaluation is based on three different brain tumor regions:

- Whole Tumor (WT) = NCR/NET + ED + ET
- Tumor Core (TC) = NCR/NET + ET
- Enhancing Tumor (ET)

4.1 Evaluation Metrics

To verify the efficiency of the proposed model framework, two most common metrics used in medical image segmentation, mean IoU score and Dice score are used. The corresponding formulas are given:

$$\text{IoU} = \frac{(\tau\rho)}{(f\rho + \tau\rho + f\eta)}, \ \text{Dice score} = \frac{2\tau\rho}{(f\eta + 2\tau\rho + f\rho)} \tag{1}$$

where $\tau\rho$, $f\rho$, $\tau\eta$, and $f\eta$ refer to true positive, false positive, true negative, and false negative respectively.

4.2 Evaluation Results

It is essential to note that while all images are generated with 240 × 240 resolution for training, all datasets are evaluated at native resolution. No pre-processing or post-processing is done. We also train U-Net, ResU-Net, and TransUnet and keep all the settings the same.

The training and validation accuracy and loss curves are shown in Fig. 3 and Fig. 4, respectively. These Figures show that our proposed BrainSegnet and ResUnet showed almost similar accuracy and loss, while TransU-Net depicted poor performances in both cases. In BraTS2020 dataset, BrainSegNet obtained a dice score of 97.47%, 82.33%, and 90.33% for WT, ET, and TC, respectively, and the average dice score achieved 96.01%. For the sake of comparison, we also trained some state-of-the-art models with the same setup and data distribution and the experimental results are shown in Table 1 in terms of Dice score.

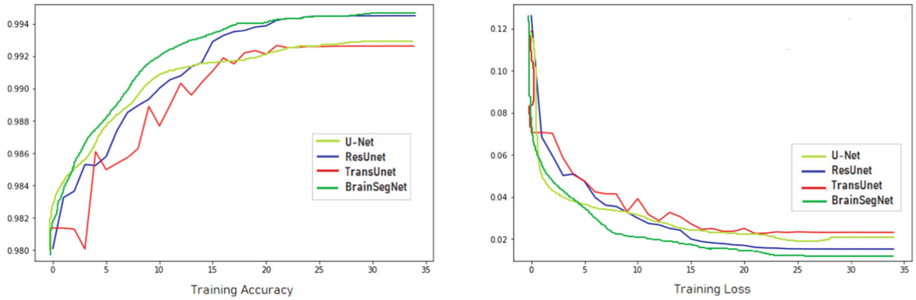

Fig. 3. Traininig accuracy and loss curves.

Generally, BrainSegNet performs well in ET, TC, and WT categories. Table 1 demonstrates that the Dice score of the BrainSegNet has a significant advantage over the conventional U-Net with less complexity. The findings indicate that the approach can segment tumors more effectively than U-Net and ResU-Net. BrainSegNet is more conducive to learning long-distance artifacts, so the effect of TC and WT category segmentation is more prominent. For ET cases, ResU-Net and Typical U-Net obtain poor results, which indicates that for brain tumor segmentation, these models cannot extract sufficient local features. However, for ET case, compared to U-Net and ResU-NeT, it performs poorly. On the other hand, Trans-Net obtains an 89.83% dice score. BrainSegNet performs exceptionally well in the ET and TC categories, demonstrating the method's superior capacity to extract both global and local features.

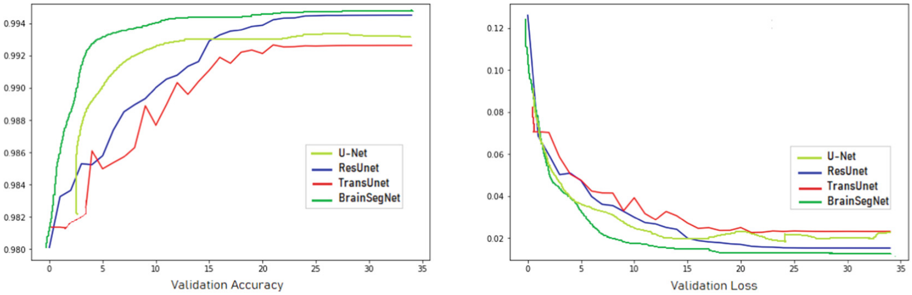

Fig. 4. Validation accuracy and loss curves.

In Table 1, the data in brackets shows the standard deviation of the proposed model segmentation outcomes. According to the table, the proposed model has a minimum classification deviation for each of the three groups. These findings suggest that the model has the best and most consistent segmentation impact and that the segmentation outcomes will not have noticeable differences. Furthermore, we can see from Table 2 that compared with U-Net and ResUet, BrainSegNet can gain 0.69% and 0.36% higher μIoU result and also has a 10.06% improvement compared to the TransU-Net model. Our model also has the minimum standard deviation among all the models mentioned in Table 2, which indicates the stability of the segmentation results of the BrainSegNet model.

Table 1. Segmentation results in terms of Dice score on BraTS 2020 dataset.

Method	Dice score (%)			
	WT	ET	TC	Avg.
U-Net [18]	96.02 (± 0.10)	78.96 (± 0.38)	89.72 (± 0.30)	95.45
ResU-Net [24]	97.06 (± 0.17)	77.85 (± 0.39)	89.73 (± 0.25)	95.23
TransU-Net [26]	92.38 (± 0.10)	72.63 (± 0.32)	79.16 (± 0.22)	89.83
BrainSegNet	97.47 (± 0.102)	82.33 (± 0.125)	90.33 (± 0.104)	96.01

Computational and Memory Requirements: The less complex methods suggested in this study are more suited for resource-constrained applications, both regarding training and deployment, for example, in portable devices. Table 3 compares the proposed architecture with three well-known architectures

Table 2. Segmentation results on the BraTS 2020 validation dataset in terms of μIoU.

Method	μIoU (%)			
	WT	ET	TC	Avg.
U-Net [18]	97.02 (± 0.11)	77.96 (± 0.20)	89.02 (± 0.30)	95.20
ResU-Net [24]	97.06 (± 0.13)	78.85 (± 0.30)	89.12 (± 0.28)	95.53
TransU-Net [26]	90.38 (± 0.10)	62.63 (± 0.32)	80.16 (± 0.22)	87.83
BrainSegNet	97.37 (± 0.10)	80.34 (± 0.10)	89.53 (± 0.10)	95.89

regarding performance vs. the volume of parameters and memory space. We can observe that our proposed BrainSegNet achieves impressive results and has the lowest memory space (18 MB) and almost ~4.8 million trainable parameters.

Table 3. Parameters and memory requirements vs performance for several brain tumor segmentation models on BraTS2020 datset.

Model	# Params (Million)	Memory Size	μIoU (%)	Dice score (%)
U-Net	~10.6	37.5 MB	95.45	95.20
ResU-Net	~4.7	17.5 MB	95.23	95.53
TransU-Net	~8.6	26 MB	89.83	87.83
BrainSegNet	~4.8	18 MB	95.89	96.01

Visualization of Tumor Segmentation Result: In Fig. 5, a visualization of the brain tumor segmentation results is made for the BrainSegNet method. The original flair images, ground truth, all class predicted, necrotic/core, edema, and enhancing tumor are shown in the first to sixth columns, respectively. Figure 5 illustrates that the segmentation result for the WT area is the best for all the models, and the segmentation results for the two complicated edges of ET and TC are pretty different. Our model shows more accurate outcomes compared with Ground Truth for detail segmentation.

4.3 Comparison with Existing State-of-the-Art

Table 4 presents the comparative insights of few recent similar research based on DL methods. Based on this performance metrics in the comparative analysis, BrainSegNet method is the most suitable for a image segmentation of Brain tumor.

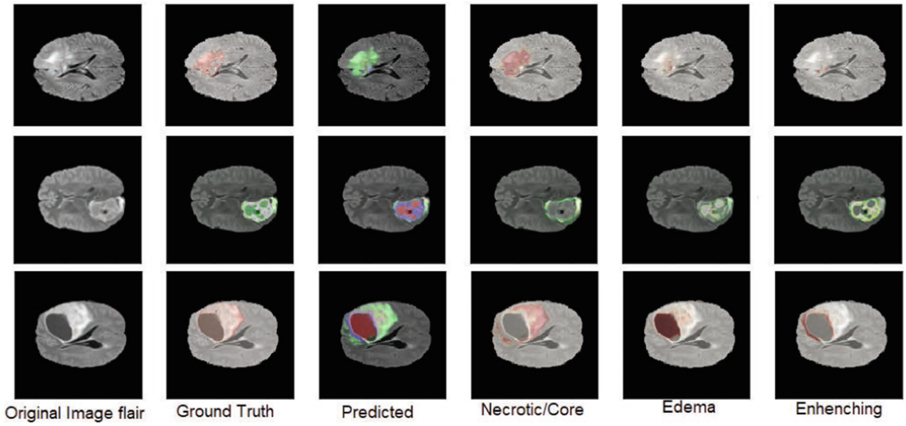

Fig. 5. Visualization of MRI Brain tumor image segmentation results of the proposed model.

Table 4. Comparison with recent state-of-the-art on brain tumor segmentation based on DL methods. For comparisons, we used μIoU and Dice score as performance metrics. Here ET = Enhancing tumor; WT = Whole tumor; TC = Tumor core.

Author	architecture	Dataset	Mean IoU (%)			Dice score (%)		
			WT	TC	ET	WT	TC	ET
Ranjbarzadeh et al. [26]	Cascade CNN model and distance-wise attention	BraTS2013	NA	NA	NA	92	87	91
Jiang et al. [15]	Multi-resolution fusion network based on inception U-Net (MRF-IUNet)	BraTS 2019	89.98	74.12	88.05	90.04	76.96	92.22
Zhang et al. [32]	Multi-encoder net (ME-Net)	BraTS 2020	NA	NA	NA	88	73	70
Guan et al. [11]	Encoder-decoder(AGSE-VNet)	BraTS 2020	NA	NA	NA	85	69	78
Huang et al. [13]	multi-depth fusion module based on V-Net structure	BraTS 2018	NA	NA	NA	80.0	75.0	71.0
Lee et al. [16]	DCNN (sparse-multi-OCM and dense-multi-OCM)	BraTS 2015,2017	NA	NA	NA	92	92	93
Proposed Method	BrainSegNet	BraTS2020	96.84	97.78	89.53	97.76	95.30	90.36

5 Conclusion

In this study, we proposed a novel segmentation system, a new variant of the U-Net architecture named BrainSegNet, which can automatically segment diseased tissues in brain MRI images. The model efficiently combines U-Net with PEN to accurately and efficiently segment tumors from brain MRI. Experimental outcomes demonstrate that our proposed system performs better in brain tumor MRI image segmentation than state-of-the-art methods (such as U-Net, ResU-

Net, and TransBTS). Furthermore, the visualization results show that the proposed system has a good segmentation performance for all three lesion regions of brain tumors. Comparisons with recent research on brain tumor area segmentation also demonstrate that our method achieves promising results on BraTs2020 datasets, indicating its potential for practical applications in auxiliary diagnostic procedures.

Further research may analyze the efficacy of additional distinctive features for segmenting brain tumors and explore the suggested method for other semantic segmentation issues.

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