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Improvements in Brain Tumor Segmentation Methods Based on Convolutional Neural Networks

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Abstract

Convolutional Neural Networks (CNNs) have emerged as a prominent research area in deep learning in recent years. U-Net, an essential model within CNNs, has gradually become a research focus in the field of medical image segmentation due to its remarkable segmentation performance. This paper presents a comprehensive overview of brain tumor segmentation methods based on CNNs. Firstly, it introduces common medical image datasets in the field of brain tumor segmentation. Secondly, it offers detailed reviews on the common improvements to 2D U-Net, 3D U-Net, and improvements based on other CNNs for brain tumor segmentation. Finally, it discusses the future development directions of CNNs for brain tumor segmentation.

Keywords: brain tumor images, image segmentation, deep learning, convolutional neural network, network architecture.

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1. Introduction

In the past decade, brain tumors have posed a serious threat to human life and health, with a high risk of mortality, earning them the moniker "brain killers." According to the Global Cancer Statistics 2022 report (GLOBOCAN 2022), although the global incidence of brain tumors was only about 1.6% in 2022, the mortality rate was as high as 2.6% [1]. The primary purpose of brain tumor segmentation is to accurately determine the location and shape of tumor regions, aiding in early diagnosis and treatment planning, which is crucial for effective treatment of brain tumors. However, manual segmentation by doctors lacks objective consistency and is prone to errors due to the complex and variable edge structures of brain tumors and their subregions, as well as individual patient factors, tumor staging, and imaging equipment variations [2]. Researchers are dedicated to developing more sophisticated and accurate automated segmentation methods to address these challenges. Nowadays, deep learning-based methods, particularly those based on Convolutional Neural Network (CNN), have been widely applied and developed in the field of brain tumor segmentation. The basic flowchart for brain tumor segmentation is shown in Figure 1, this framework mainly consists of two major parts: image preprocessing and model training.

This paper offers a detailed review of brain tumor segmentation methods based on CNN. Firstly, common medical image datasets in the field of brain tumor segmentation are introduced. Secondly, improvement methods for brain tumor segmentation based on 2D U-Net are discussed, with a focus on four aspects: encoder, decoder, skip connections, and others. Thirdly, improvement methods for brain tumor segmentation based on 3D U-Net are presented, covering encoder, decoder, skip connections, and others. Fourthly, improvement methods for brain tumor segmentation based on other CNNs are shown. Finally, challenges faced by current CNN-based brain tumor segmentation methods and future research directions are analyzed.

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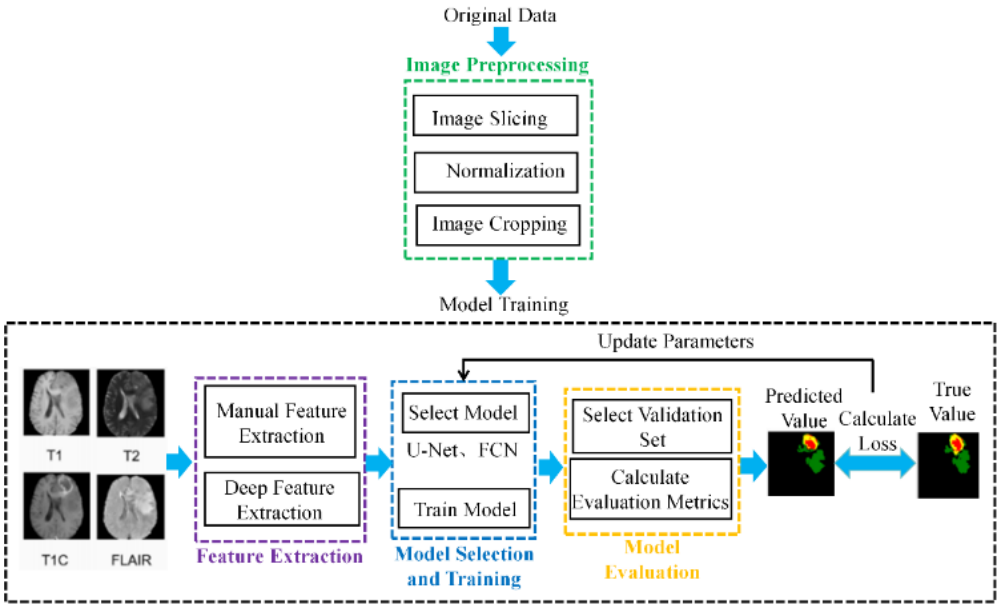

Figure 1. Basic flowchart for brain tumor segmentation

2. Brain tumor datasets

In the field of medical imaging, brain tumor segmentation is a challenging task, and the selection of datasets is crucial for the research and evaluation of algorithms. Datasets such as ISBI, ISLES, IBSR, LPBA Dataset, and BraTS (Brain Tumor Segmentation) cover different types of tumors and imaging modalities, providing rich resources and benchmarks for research in the medical imaging field. Among them, the BraTS dataset is an important member, widely used in the research of brain tumor segmentation due to its high resolution, multimodal, multicenter, and rich annotation information. The brain tumors in the BraTS dataset samples include Whole Tumor (WT), Tumor Core (TC), and Enhanced Tumor (ET) regions. The BraTS dataset, maintained by the Medical Image Computing and Computer Assisted Intervention (MICCAI) Society, consists of multimodal MRI scan images, including T1, T1ce, T2, and FLAIR images. Table 1 presents specific information about the BraTS datasets and several other datasets over the years.

Table 1. Detailed information of the BraTS 2012-2021 datasets and several other datasets.

Dataset	Modality	Samples and Resolution	Link
BraTS 2012	T1, T1ce, T2, and FLAIR	80, 130×170×170	https://www.smir.ch/BRATS/Start2012
BraTS 2013	T1, T1ce, T2, and FLAIR	30, 240×240×155	https://www.smir.ch/BRATS/Start2013
BraTS 2014	T1, T1ce, T2, and FLAIR	166, 240×240×155	https://www.smir.ch/BRATS/Start2014
BraTS 2015	T1, T1ce, T2, and FLAIR	274, 240×240×155	https://www.smir.ch/BRATS/Start2015
BraTS 2016	T1, T1ce, T2, and FLAIR	274, 240×240×155	https://www.smir.ch/BRATS/Start2016
BraTS 2017	T1, T1ce, T2, and FLAIR	285, 240×240×155	https://www.smir.ch/ISLES/Start2017
BraTS 2018	T1, T1ce, T2, and FLAIR	285, 240×240×155	https://www.smir.ch/ISLES/Start2018

BraTS 2019	T1, T1ce, T2, and FLAIR	335, 240×240×155	https://www.med.upenn.edu/cbica/brats-2019/
BraTS 2020	T1, T1ce, T2, and FLAIR	369, 240×240×155	https://www.med.upenn.edu/cbica/brats2020/
BraTS 2021	T1, T1ce, T2, and FLAIR	1251, 240×240×155	https://www.med.upenn.edu/cbica/brats2021/
ISBI 2015	T1-w MPRAGE, T2-w, PD-w, and FLAIR	21, 182×256×182	http://iacl.ece.jhu.edu/index.php?title=MSChallenge/data
ISLES 2018	Diffusion maps and Perfusion maps	103, 256×256	https://www.smir.ch/ISLES/Start2018
IBSR18	T1	18, 256×128×256	https://www.nitrc.org/projects/ibsr
IBSR20	T1	20, 256×63×256	https://www.nitrc.org/projects/ibsr
LPBA40	T1	40, 220×220×220	https://www.nitrc.org/projects/ibsr

To evaluate the segmentation performance of the network model on the brain tumor dataset, researchers usually use several commonly employed evaluation metrics in the field of brain tumor segmentation, including Dice Similarity Coefficient (DSC), Hausdorff Distance (HD), Sensitivity (Sens), and Precision (Prec).

The DSC is a measure of set similarity commonly used to calculate the similarity between two samples. It has a range of values between 0 and 1, where a value closer to 1 indicates a higher similarity between segmentation contours. The DSC can be expressed as:

$$DSC = \frac{2|A \cap B|}{|A| + |B|} = \frac{2TP}{FP + 2TP + FN} \quad (1)$$

Where A is the set of predicted labels and B is the set of true labels. TP is the true positive voxel count, FP is the false positive voxel count, TN is the true negative voxel count, and FN is the false negative voxel count.

HD is the maximum distance from a set to the nearest point in another set. It is often used in image segmentation tasks because it is sensitive to the segmented boundaries. A smaller HD indicates greater similarity between two sets. The HD can be expressed as:

$$hd(A,B) = \max_{a \in A} \min_{b \in B} \|a - b\| \quad (2)$$

$$hd(B,A) = \max_{b \in B} \min_{a \in A} \|b - a\| \quad (3)$$

$$HD(A,B) = max(hd(A,B), hd(B,A)) \quad (4)$$

Where $hd(A,B)$ is the one-way HD from set A to B, and $hd(B,A)$ is the one-way HD from set B to A. The longest distance between $hd(A,B)$ and $hd(B,A)$ is selected, which represents the HD between set A and set B.

Sens refers to the proportion of actual positive samples that the model successfully identifies as positive, also known as the true positive rate or recall. It measures the model's ability to correctly identify positive samples. The value of Sens ranges between 0 and 1, with higher values indicating that the model is better at identifying positive samples. Sens can be expressed as:

$$Sens = \frac{TP}{TP + FN} \quad (5)$$

Prec is the proportion of true positive samples among those predicted as positive by the model. It measures the model's ability to correctly predict positives. Prec ranges in (0, 1), with higher values indicating that the model can more accurately identify positives. Prec can be expressed as:

$$Prec = \frac{TP}{TP + FP} \quad (6)$$

3. Improvements in brain tumor segmentation based on CNN

Improvements based on CNN mainly include improvements to 2D U-Net, improvements to 3D U-Net, and improvements to other CNNs. The utilization of CNN can meet the practical application demands of brain tumor segmentation.

3.1. Improvements in brain tumor segmentation based on 2D U-Net

Nowadays, among numerous CNN models, 2D U-Net has proven effective in learning high-dimensional discriminative features from data [3], making it one of the most popular models in the field of deep learning, widely applied in brain tumor segmentation tasks [4-7]. The overall structure of the 2D U-Net is shown in Figure 2. The 2D U-Net adopts an encoder-decoder structure. The encoder is responsible for extracting features from input images and gradually reducing their spatial resolution. Meanwhile, the decoder upsamples the feature maps and uses skip connections to pass low-level features from the encoder to the decoder, which helps preserve detailed image information and achieve more accurate results in image segmentation tasks. Common improvements to the structure of the 2D U-Net include improvements to the encoder, decoder, skip connections, and others.

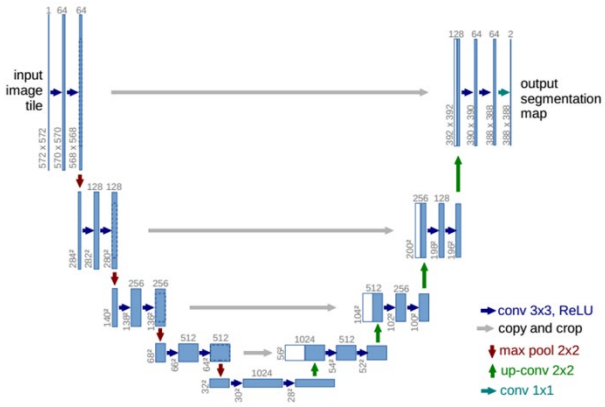

Figure 2. The overall structure of the 2D U-Net [3]

Improvements to the encoder

The encoder of the 2D U-Net is used to extract feature representations from images, gradually reducing the size and number of channels of the feature maps through successive convolution and pooling operations. Zhang et al. [8] proposed an end-to-end 2D brain tumor segmentation network, namely Attention Residual U-Net (AResU-Net), which introduces a series of residual (Res) blocks during the downsampling process of the 2D U-Net and adaptively recalibrates multi-scale features, effectively enhancing the local responses of downsampling residual features. The basic structure of the Res block is shown in Figure 3. Their method achieved DSCs of 0.892, 0.853, and 0.825 in the WT, TC, and ET regions, respectively. Huang et al. [9] proposed a Group Cross-channel Attention Residual U-Net (GCAU-Net), which fully exploits fine-grained details in the lower layers of brain tumor regions, introducing Res-blocks in the encoding path and residual-Atrous Spatial Pyramid Pooling (Res-ASPP) modules at the bottom of the encoding path, improving segmentation accuracy. Their method achieved DSCs of 0.909, 0.845, and 0.813 in the WT, TC, and ET regions, respectively. Sheng et al. [10] explored the effectiveness of second-order statistical features for brain tumor segmentation applications and proposed a Second-order Residual Network (SoResU-Net). SoResU-Net integrates residual blocks (Res Blocks) at each layer of the encoder to enhance segmentation performance, achieving DSCs of 0.876, 0.811, and 0.771 in the WT, TC, and ET regions, respectively. Ullah et al. [11] introduced a fully automatic brain tumor region segmentation method based on Multi-scale Residual Attention U-Net (MRAU-Net), which incorporates residual connections in the encoder and introduces ASPP modules at the bottom of the encoder to preserve three-dimensional sequential information as much as possible. Their method achieved DSCs of 0.901, 0.872, and 0.867 in the WT, TC, and ET regions, respectively.

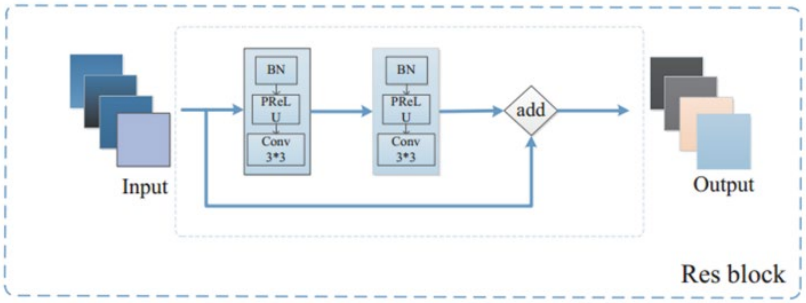

Figure 3. The basic structure of the Res block [8]

Improvements to the decoder

The decoder of 2D U-Net gradually restores the size and number of channels of the feature maps through deconvolution and conducts fine-grained segmentation. AResU-Net proposed by Zhang et al. [8] embeds Spatial Residual (SRes) modules in the decoder to accomplish feature restoration of brain tumor images. GCAU-Net proposed by Huang et al. [9] designs a cross-channel attention module from coarse to fine in the decoder, namely the Group-wise Channel Attention (GCA) module, which can emphasize important feature groups and channels in brain tumor images. The basic structure of the GCA module is shown in Figure 4. SoResU-Net proposed by Sheng et al. [10] adds residual blocks in each layer of the decoder to perform feature restoration of brain tumor images. MRAU-Net proposed by Ullah et al. [11] adds residual connections in the decoder to enhance the feature restoration performance of brain tumors.

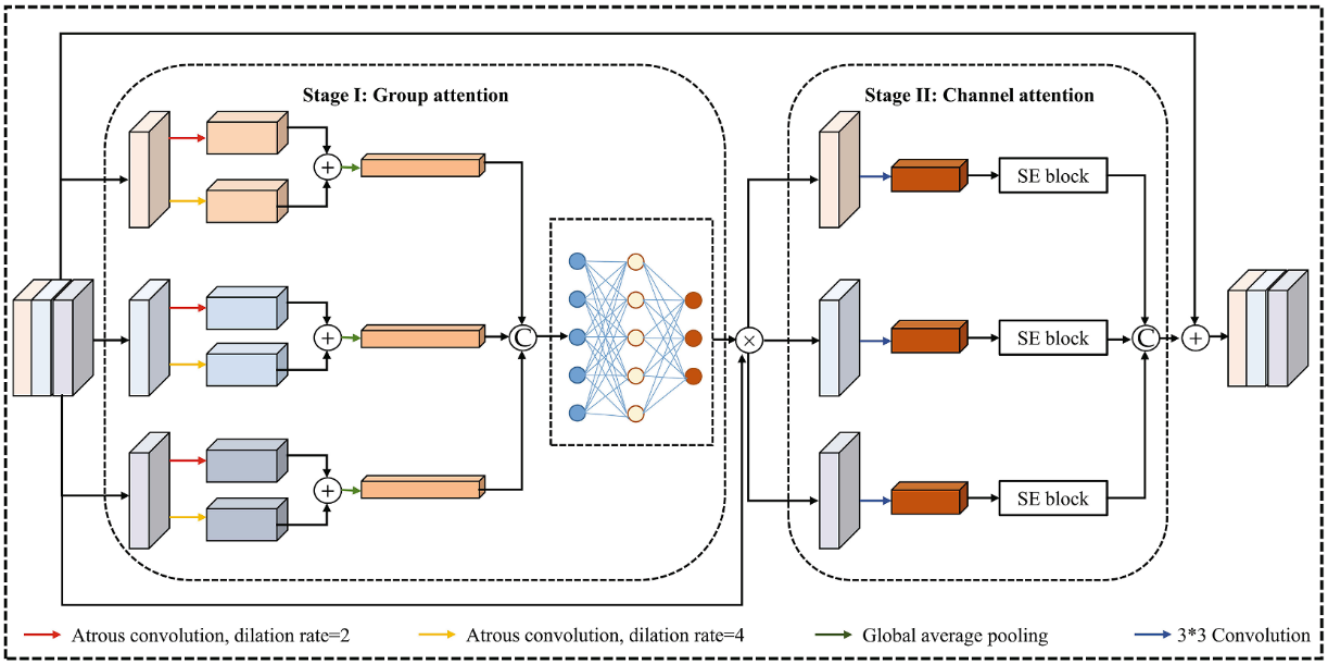

Figure 4. The structure of the GCA module [9]

Improvements to the skip connections

The skip connections of 2D U-Net connect the feature maps from the encoder to the corresponding ones in the decoder, preserving more spatial information and details. This helps alleviate the issue of information loss, enabling the network to better capture features at different scales. AResU-Net proposed by Zhang et al. [8] introduces Attention and Squeeze-Excitation (ASE) modules in the skip connections to further enhance the decoder's ability to preserve brain tumor details during feature restoration. BrainSeg-Net proposed by Rehman et al. [12] integrates Feature Enhancer (FE) modules in the skip connections, extracting intermediate features from shallow low-level features and sharing them with dense layers. This feature aggregation aids in improving brain tumor recognition performance. Their method achieved DSCs of 0.903, 0.872, and 0.849 in the WT, TC, and ET regions, respectively. GCAU-Net by Huang et al. [9] replaces skip connections with multi-scale input paths to obtain multi-scale contextual information of brain tumor images. SoResU-Net by Sheng et al. [10] replaces the original skip connection operation with multiple Second-Order (SO) modules, enhancing a series of transformation operations and increasing the nonlinearity of the brain tumor segmentation network. The basic structure of the SO module is shown in Figure 5. Sun et al. [13] introduce the Feature Pyramid Networks (FPN) structure into the 2D U-Net architecture, leveraging both the different scale information in the 2D U-Net model and the context multi-scale information from the FPN model to improve the adaptability of the model to brain tumor features at different scales. Their method achieved DSC of 0.920 in the WT region. MRAU-Net proposed by Ullah et al. [11] introduces attention gates in the skip connections, enhancing brain tumor segmentation performance.

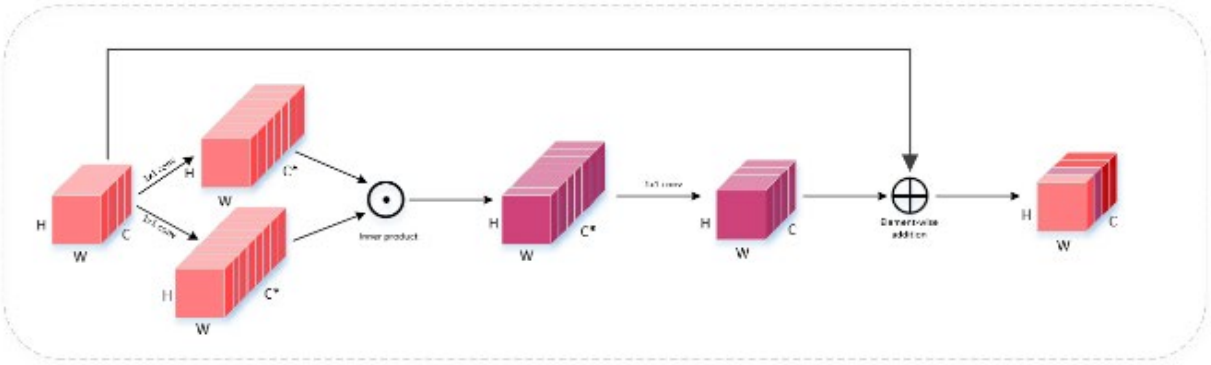

Figure 5. The structure of the SO module [10]

Other improvements

Researchers have also improved segmentation methods for brain tumor segmentation tasks using 2D U-Net from aspects such as loss functions, learning strategies, and image processing to enhance segmentation accuracy. BrainSeg-Net proposed by Rehman et al. [12] utilizes custom-designed loss functions to address issues related to class imbalance in brain tumor images. Ali et al. [14] introduce progressive growing and one-shot learning techniques into 2D U-Net to enhance the accuracy and generalization of brain tumor segmentation in MRI images. Their method achieved DSC of 0.952 in the WT region. MRA-Unet proposed by Ullah et al. [11] explores the application of post-processing techniques such as Conditional Random Fields and Test-Time Augmentation, further improving the overall segmentation performance of brain tumors.

3.2. Improvements in brain tumor segmentation based on 3D U-Net

Since 2D U-Net can only process slice information and cannot obtain the three-dimensional contextual information of medical volumetric images, researchers have proposed a 3D version of 2D U-Net, called 3D U-Net [15], and improved upon it to better handle three-dimensional brain tumor images [16-20]. Because the structural composition of 3D U-Net is similar to that of 2D U-Net, the improvement methods for 3D U-Net also include enhancements in the encoder, decoder, skip connections, and others.

Improvements to the encoder

Gammoudi et al. [21] proposed a Residual Gated 3D U-Net, which introduces newly designed ResNet 'M blocks into the encoder of 3D U-Net, achieving higher precision in brain tumor segmentation. Their method achieved DSCs of 0.879, 0.854, and 0.849 in the WT, TC, and ET regions, respectively. Sun et al. [22] presented an automatic brain tumor segmentation method based on 3D U-Net, incorporating ResNeXt blocks into the encoder of 3D U-Net to better capture contextual information. Their method achieved DSCs of 0.840, 0.720, and 0.620 in the WT, TC, and ET regions, respectively. Ngo et al. [23] suggested improving small brain tumor segmentation in the encoder part by using dilated convolutions instead of heavyweight networks with multiple resolutions or kernel sizes. Their method achieved DSCs of 0.897, 0.840, and 0.818 in the WT, TC, and ET regions, respectively. Zhang et al. [24] introduced MAU-Net, which employs Shuffle Attention (SA) modules after each convolution block in the encoder stage to enhance local details of brain tumor images. Additionally, an enhanced Transformer module is introduced at the bottom of the encoder to improve the interaction learning capability of global information in brain tumor images. Their method achieved DSCs of 0.900, 0.816, and 0.774 in the WT, TC, and ET regions, respectively. Li et al. [25] proposed an enhanced 3D U-Net, designing enhanced encoding modules to improve the extraction and utilization efficiency of brain tumor image features. Their method achieved DSCs of 0.778, 0.875, and 0.903 in the WT, TC, and ET regions, respectively. Magadza et al. [26] introduced an efficient three-dimensional brain tumor segmentation network architecture, utilizing residual modules and depthwise separable convolutions in the encoder part to reduce computational costs. Their method achieved DSCs of 0.904, 0.828, and 0.774 in the WT, TC, and ET regions, respectively. Zhang et al. [27] proposed a brain tumor image segmentation method that utilizes multimodal image feature fusion. The encoding path of this method consists of four different branches, each dedicated to extracting features from different modalities of MR images to capture their unique characteristics. Their method achieved DSCs of 0.914, 0.890, and 0.833 in the WT, TC, and ET regions, respectively. Guan et al. [28] introduced AGSE V-Net, which incorporates Squeeze Excitation (SE) modules into each encoder to automatically enhance useful information from various channels of brain tumor images and suppress irrelevant information. Their method achieved DSCs of

0.850, 0.700, and 0.680 in the WT, TC, and ET regions, respectively.

Improvements to the decoder

Gammoudi et al. [21] proposed the Res Gated 3D U-Net, which utilizes ResNet 'M blocks at each layer of the decoder for brain tumor feature restoration, achieving higher accuracy. Sun et al. [22] employed Dense Fusion (DF) modules and Refine Blocks (RB) modules in the decoder of 3D U-Net, further enhancing brain tumor segmentation performance while reducing computational overhead. Ngo et al. [23] introduced Multi-Fiber Units in the decoder section, attempting multi-task learning, with auxiliary tasks such as feature reconstruction to preserve features of small brain tumors. The Enhanced 3D U-Net proposed by Li et al. [25] designed enhanced decoding modules to improve the network's ability to recover brain tumor features. The approach by Magadza et al. [26] also utilized Depthwise Separable Convolution and Residual modules in the decoder part to preserve important details of brain tumors while reducing computational complexity. Guan et al. [28] proposed AGSE V-Net, which incorporates Attention Guide Filter (AG) modules in each decoder to utilize attention mechanisms for guiding edge information and removing the influence of noise and irrelevant information, thereby improving brain tumor segmentation accuracy.

Improvements to the skip connections

Gammoudi et al. [21] introduced the Res Gated 3D U-Net, which incorporates signal gating technology into the skip connections of the 3D U-Net, thereby improving the performance of brain tumor segmentation. Li et al. [29] trained cascaded 3D U-Net and 3D U-Net++ for brain tumor segmentation, where the feature map replication and stacking operations between the encoder and decoder are more frequent than the skip connections in 3D U-Net, extending from single-layer information transfer to cross-layer information stacking and fusion. Their method achieved DSCs of 0.890, 0.842, and 0.835 in the WT, TC, and ET regions, respectively. Sun et al. [22] replaced the simple skip connections in 3D U-Net with Encoder Adaptation (EA) blocks, enhancing the efficiency of brain tumor feature information transmission. The skip connections of the model proposed by Magadza et al. [26] rescale the brain tumor feature maps using weights learned from the attention modules, focusing the network on more crucial information.

Other improvements

The method proposed by Sun et al. [22] utilizes the Generalized Dice Loss (GDL) function and extends it to multi-class settings to train the model, addressing the issue of class imbalance in brain tumor images. The approach by Li et al. [25] combines the binary cross-entropy loss function with the Dice similarity coefficient to form a hybrid loss function, optimizing for smooth gradients and addressing class imbalance in brain tumor images, thereby speeding up the convergence of the model. Vafaeikia et al. [30] added a decoding classification branch, namely a genetic marker classifier for brain tumors, as an auxiliary task in the backbone network 3D U-Net, ultimately improving the accuracy of segmentation results. Their method achieved an average DSC of 0.830.

3.3. Improvements in brain tumor segmentation based on other CNNs

Common improvements based on CNN not only include those based on U-Net, but also some enhancements based on other models, such as Deep Convolutional Neural Network (DCNN), SegNet, Visual Geometry Group (VGG), and so on.

Chen et al. [31] proposed DeepLab, which introduces dilated convolutions (Atrous Convolution, AC), spatial pyramid pooling (SPP), and conditional random fields (CRF), enhancing the ability to preserve details of brain tumors. Myronenko et al. [32] proposed a brain tumor segmentation network based on an encoder-decoder architecture, adding a variational autoencoder branch to reconstruct the input image itself, for regularization of the shared decoder. Liu et al. [[33] proposed an "segmentation-fusion" multitask model SF-Net, using image fusion as additional regularization for feature learning, aiding in achieving more comprehensive multimodal feature fusion, beneficial for multimodal brain tumor image segmentation problems. Alqazzaz et al. [34] applied SegNet to four modalities of brain tumor MRI and integrated the four separately trained SegNets together through post-processing, generating final results by fusing machine learning feature maps from the fully convolutional layers of each trained model. Ma et al. [35] proposed R2U-Net, which combines the U-Net structure with the ResNet structure and introduces multi-task deep supervision (MTDS) and attention pre-activation residual (APR) modules to prevent overfitting and accurately locate brain tumor regions. Jakhar et al. [36] proposed the Mutli-Scale Fractal Feature Network (MFFN), which uses pixel-level segmentation based on fractal residual deep learning, improving the network's classification accuracy and sensitivity in brain tumor segmentation. Yu et al. [37] proposed HSA-Net for brain tumor segmentation, which uses shared weight dilated convolution modules (SWDC) and hybrid dense dilated convolution (HDDC) modules to capture multiscale information, effectively aggregating task-relevant information using effective multi-dimensional attention (EMA) modules and important feature attention (IFA) modules. Rehman et al. [38] proposed an approach based on Selective Deeply Supervised Multi-Scale Attention Network (SDS-MSA-Net), which utilizes a 3D input composed of five consecutive slices of brain tumor images along with a 2D slice to maintain sequential information. The method consists of two encoding units and one decoding unit, with a Selective Deep Supervision (SDS) module introduced into the intermediate layer of the decoder to enhance segmentation performance. Hu et al. [39] introduced Brain

SegNet, which employs a novel 3D refinement module capable of directly aggregating local details of brain tumors and 3D semantic contextual information within 3D convolutional layers. Liu et al. [40] proposed a new brain tumor segmentation framework comprising two networks: a segmentation backbone and a normal appearance network. This method introduces a new Feature Alignment (FA) module, aligning the feature distribution of single-modal normal brain images with multi-modal tumor brain images in normal regions while making features more distinct in tumor regions. Zheng et al. [41] proposed a serial encoder-decoder structure, employing VGG16 as the backbone and concatenating two 2D U-Nets in series, with feature concatenation and decoding module concatenation at each layer to form a tighter connection between the preceding and following encoder-decoder blocks, thereby obtaining more semantic information of brain tumors, reducing feature redundancy, and further improving the model's generalization ability. Qi et al. [42] proposed an improved knowledge distillation method, namely Coordinate Distillation (CD), which trains student networks (DeepResU-Net and U-Net++) and teacher networks (U-Net and AttU-Net) without altering the original network structures, combining channel information with spatial information to enhance brain tumor segmentation accuracy without compromising segmentation efficiency. Wu et al. [43] proposed Deep Convolutional Neural Network Fusion Support Vector Machine (DCNN-F-SVM), which integrates the Support Vector Machine (SVM) algorithm into deep convolutional neural network to address the issues of parameter abundance and significant information loss during the encoding and decoding processes in brain tumor segmentation tasks. Chen et al. [44] proposed Dilated Multi-Fiber Network (DMF Net), which significantly reduces the computational cost of brain tumor segmentation network by leveraging the idea of Group Convolution to design 3D Multi-Fiber Units. Lee et al. [45] presented a method that minimizes segmentation errors through quantification and utilization of uncertainty measures, resulting in improved performance of brain tumor segmentation, especially for small tumors.

3. Conclusions and outlook

Currently, brain tumor segmentation is confronted with challenges such as limited dataset sizes, imbalanced data categories, and low data collection quality. These challenges can directly or indirectly impact the performance of CNN in brain tumor segmentation. In the future, these issues might be resolved by adopting more efficient data augmentation techniques, devising more effective model training methods, and exploring unsupervised learning approaches.

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Conflicts of interest

The authors declare that they have no conflicts of interest.

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