

Overview of convolutional neural networks architectures for brain tumor segmentation

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ABSTRACT

Due to the paramount importance of the medical field in the lives of people, researchers and experts exploited advancements in computer techniques to solve many diagnostic and analytical medical problems. Brain tumor diagnosis is one of the most important computational problems that has been studied and focused on. The brain tumor is determined by segmentation of brain images using many techniques based on magnetic resonance imaging (MRI). Brain tumor segmentation methods have been developed since a long time and are still evolving, but the current trend is to use deep convolutional neural networks (CNNs) due to its many breakthroughs and unprecedented results that have been achieved in various applications and their capacity to learn a hierarchy of progressively complicated characteristics from input without requiring manual feature extraction. Considering these unprecedented results, we present this paper as a brief review for main CNNs architecture types used in brain tumor segmentation. Specifically, we focus on researcher works that used the well-known brain tumor segmentation (BraTS) dataset.

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1. INTRODUCTION

Medical imaging analysis has been widely used in medical diagnosis and remediation, such as diagnoses using computer-assisted methods, management of information from medical record, robotic medical devices and image-based applications [1]. Images provide a mechanism to unveil internal organs and discovering several diseases, where many types of imaging technologies are used for various medical purposes. Brain tumor segmentation is a medical problem that affects people's lives because of the moral and material effects it has on society.

The biopsy is considered as a standard mechanism that is used for tumor diagnosis, but it is a lengthy process and invasive that it may cause bleedings or injuries causing functionality loss for the brain [2]. Consequently, using non-invasive magnetic resonance imaging (MRI) can be a safer and better tool specifically if accurate and robust approaches are being used for the segmentation. Many MRI procedures can be performed such as MRI for showing different organs, MRI that study the organs functions, diffusion-

weighted imaging (DWI) and diffusion tensor imaging (DTI) where every procedure is employed for a certain specific task. Since the structural MRI visualizes wholesome brain tissues and depicts gross brain structure, vascularity system, radiation-induced microhaemorrhage and calcification, so it is proper to be used by brain tumor segmentation methods to identify aberrant from normal tissue. The structural MRI sequences incorporate T1-w, T2-w, fluid-attenuated inversion recovery (FLAIR), and contrast-enhanced T1-w [3].

Manual brain tumor segmentation problem is a slow process, prone to inter rater variability and tedious work because for every patient the MRI scan generates a large number of slices that must be delineated. Also, the different types of artifacts in images result in low quality images that prohibit specialists from the correct and accurate interpretation and diagnosis. So, researchers developed many methods to automate the process of brain tumor segmentation like region-based segmentation, supervised machine learning-based algorithms for brain tumor segmentation and deep learning-based methods for tumor segmentation [4].

During the past few years, deep learning techniques were the state-of-the-art methods with eminent results, specifically convolutional neural networks (CNNs). Many surveys have been published regarding deep learning methods in the medical field and brain tumor segmentation, but we noticed that there is not a specific study for CNNs based brain tumor segmentation methods. The closest paper to ours was presented by Bernal *et al.* [5].

Bernal *et al.* [5] presented a review that focused on the usage of deep CNNs for brain image analysis. Their work is an extended survey paper that concentrated on CNN techniques which were utilized in brain analysis using MRI focusing on their architectures. Dedicated preprocessing steps, data-preparation and post-processing techniques are also included in their work. As mentioned in [6], a brief is introduced about medical image analysis.

Akkus *et al.* [7] also presented a detailed survey that mentioned many well-known datasets, preprocessing steps and the styles of training deep learning architectures for brain tumor segmentation. Magadza and Viriri [8] also plainly clarified the building blocks of the deep learning methodologies that were considered as state-of-the-art in the task of segmenting tumors from the brain. This survey focused on the works that used CNNs variants in the field of brain tumor segmentation along with the datasets used and the results which were obtained. Magadza and Viriri [8] particularly focused on the best performing applied methods on BraTS dataset for the years 2017, 2018, and 2019. Section two presents architectural details about main CNNs components.

2. CONVOLUTIONAL NEURAL NETWORKS

CNNs are special feedforward neural networks specified to process data pixels. This type of network deals with grid-like data such as time series and images data [9]. The main layer in the CNN architecture that distinguishes it from other types of artificial neural networks (ANNs) is the persistence of the convolution layer, hence the name of this type of the network. The general architecture is mainly composed of three building block layers including convolution layer, pooling layer, and connected layer.

Figure 1 illustrates the general architecture of the CNN network. CNN models increasingly learn the features within data, such that the lower-level layers begin to learn small local patterns, whereas the higher-level layers learn larger patterns (shapes) synthesized of features from the previous layers and so forth. This ability makes them maximal choice for image analysis and different processing tasks than other usual ANNs. Brain tumor segmentation from MR images can greatly benefit from CNNs [8].

2.1. Convolution layer

In this layer, the image is convolved with many two-dimensional (2D) or sometimes three-dimensional (3D) filters (kernels), this can be determined according to the input dimensions to make automatic feature extraction. For example, the filter may have the form of (3×3) or $(3 \times 3 \times 3)$ dimensions. Since the filter convolution against the images allows weight sharing, it reduces the model complexity. Filters are spatially small patches (windows) that are moved to every possible position on the input matrix (image) to extract the specific types of features, so convolutions in CNNs can be looked as feature extractor.

The result of the convolution operation (element-wise multiplication) is a feature map which is fed to the next layer. Also, one main component of CNNs is the activation function that is used to fire the output of layer neuron, sometimes called (transfer function), it adds nonlinearity to the network. Rectified linear unit (ReLU) is a well-known and commonly used activation function which replaces the negative output values to zero.

Figure 2 illustrates the convolution operation. As noted in Figure 2, the convolution operation has two parameters: the first is the window size which is the step in which the window moves through the image being sub-sampled, it is 3×3 in this example and the second parameter is the stride which is the transition step for the window, it is 1 in this example. In the context of improving the performance of CNNs, many

enhancements were performed in the literature where conventional convolutional layers were replaced with blocks that rise the network’s capability. For example, Szegedy *et al.* [10] introduced the inception block that aided in capturing the sparse correlation patterns. Another notable improvement was the residual block which was presented by He *et al.* [11]. It facilitated the building of very deep networks that overcome the problem of vanishing gradient. Also squeeze-and-excitation (SE) block was introduced by Hu *et al.* [12] which enabled capturing the inter-dependencies between the generated feature maps of the network.

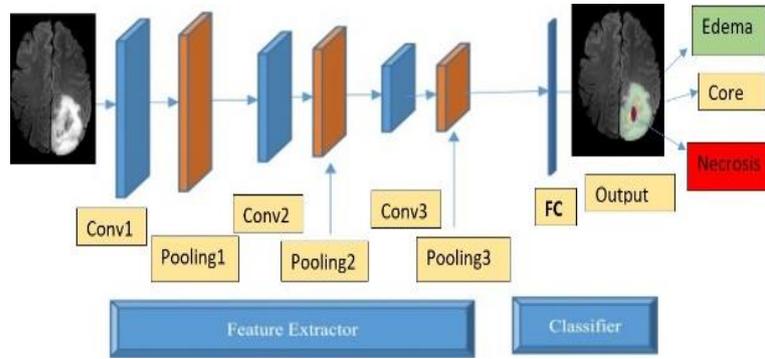


Figure 1. Convolutional neural network architecture

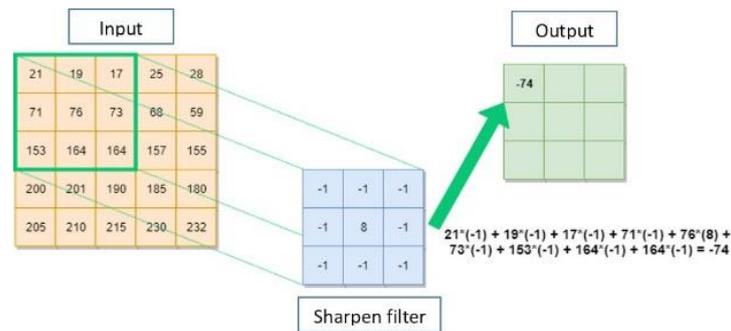


Figure 2. Convolution operation

2.2. Pooling layer

A pooling layer typically follows a convolutional layer or many consecutive existing convolutional layers in the model. Pooling layers are usually added between two convolution layers. The pooling layer aims to minify the spatial size dimensionality of feature map representation. Feature map passes through the pooling layer to generate pooled (compressed) feature map or activation map. Many pooling operations can be used in the pooling layer, the most common are the max pooling and the average pooling. The maximum value is returned by max pooling when applying the window filter while the average pooling returns the average of the values covered by the filter. Max pooling is illustrated in Figure 3.



Figure 3. Max pooling operation

2.3. Fully connected layer (FC)

After convolution and pooling of the input data, the resultant output must be flattened and fed into a regular artificial neural network layer (fully connected layer) where every layer neuron is connected with every neuron in the preceding layer. There may be more than one dense or fully connected layer (FC), but the last one (output layer) must contain many neurons equal to the number of classes in the data for the prediction. It computes the class probability scores and determines input data affiliation to which class. Additionally, different layers are added to prevent the problem of overfitting, such as dropout layers and normalization layer that keeps the mean close to 0 and the standard deviation close to 1 for the output. This layer will hence accelerate training [13].

The main problem with using FC layers is the needing for extravagant number of parameters comparatively to other types of layers, which will decrease the efficiency of the network and increase the network computational cost. Another problem with using FC layers is the necessity for a unified size for an input image. As a good solution to this problem, Shelhamer *et al.* [14] proposed replacing FC layers by 1×1 convolutional layers, this will transform the network to be a fully convolutional network (FCN). By this modification, the network has the capability to receive arbitrary sizes of the inputs and produces classification maps.

3. CONVOLUTIONAL NEURAL NETWORKS VARIANTS

Designing effective modules and network architectures have become one of the important factors for achieving accurate segmentation performance [1]. So different updates in CNNs architecture have been innovated, these improvements comprise the optimization of parameters, regularizing the network, reforming network structure. It was obviously noticed that the essential reason for increasing the performance of CNN comes from restructuring of processing units and the designing of new blocks [15]. So many variants of CNNs were utilized by researchers for brain tumor segmentation. According to the characteristics of network structures, this paper divides CNNs for brain tumor segmentation into single/multiple path networks. In the next subsections, these types will be elaborated with many examples from the literature.

3.1. Single/multiple path networks

Single and multiple path networks are used to extract features and classify the center pixels of the input patch, which is a part of the image. In single path networks, data stream happens from the input layer to the classification layer through a single path. Pereira *et al.* [16] proposed a fully automatic brain tumor segmentation based on CNN with kernels of 3×3 and used the ReLU as an activation function. The architecture of their CNN consisted of 11 layers. They used normalization as a preprocessing step and data augmentation (rotation) in their method, which were effective for brain tumor segmentation in MRI as they stated in their work. The method was performed using the BraTS dataset for training and validation and achieved the first position for the complete, core and enhancing regions in the dice similarity coefficient (DSC) metric with 88%, 83%, and 77% respectively for the challenge 2013 dataset. They also took place in the on-site BraTS 2015 competition using the same suggested model achieving the rank two with a DSC metric of 78%, 65%, and 75% for the complete, core and enhancing regions, respectively. The data comprised four sequences for every patient: T1, T1c, T2 and FLAIR. In comparison to single path networks, existence of several paths for the networks can elicit various features from these paths with multiple scales. A large-scale path (path with a large kernel size or input) allows CNN to learn global features, while small scale paths (paths with a small kernel size or input) allow CNN to learn features known as local features or descriptors. The usage of bigger sizes of kernels produces global features which tend to supply global informative view for example: tumor location, size and shape, while local features present more descriptive details such as tumor texture and boundary.

Zikic *et al.* [17] investigated deep learning CNN in the segmentation of brain tumor tissues. Their work was inspired and motivated by the good results achieved by Krizhevsky who used CNNs for object recognition on 2D images of the LSVRC-2010 ImageNet. For each point to be segmented, they used information from the surrounding patch. The CNN was trained to make a class prediction for the central patch point x . They used a standard CNN that contains just 5 layers and stochastic gradient descent with momentum (SGD) to perform the segmentation on the BraTS dataset of four sequences T1, T2, T1c and FLAIR. They stated that preliminary results indicate that even the unoptimized CNN architecture is capable of achieving acceptable segmentation results.

The work of Havaei *et al.* [18] is one of the early multipath CNNs. They proposed a CNN that was utilized to exploit simultaneously local features and global contextual features, and uses a fully convolutional final layer instead of fully connected layer hence decreases network complexity and increases the speed of training. Two types of architectures were explored in their work. The first is Two-pathway architecture in which there are two paths, one with 7×7 receptive fields and another with larger 13×13 receptive fields.

Havaei *et al.* [18] called these paths as local pathway and global pathway, this allowed the pixel label classification to be affected by the region around the pixel and also with larger context where the patch in the brain. The feature maps of both paths then were concatenated to be the input for the final layer for classification. Two-pathway architecture achieved a DSC accuracy 85%, 78%, 73% for complete, core, enhancing tumor regions, respectively with dataset BraTS 2013. The second type of architectures used by Havaei is Cascaded architectures that aimed to model the direct dependencies between the close labels that have adjacency. The authors suggested and explored three cascaded architectures versions namely, input concatenation (InputCascadeCNN), Local pathway concatenation (LocalCascadeCNN), Pre-out concatenation (MFCascadeCNN). The best version was Input concatenation (InputCascadeCNN) which achieved DSC accuracy 88%, 79%, 73% for complete tumor region, core tumor region, enhancing tumor region, respectively.

Rao *et al.* [19] also used CNN to segment tumors from a large dataset of brain tumor MR images supplied by BraTS 2015. They used four sequences of T1, T2, T1c and FLAIR. Every sequence was trained by a CNN architecture and the output of each CNN version was taken as the representation for that sequence. Then, these representations were concatenated to be the input to a random classifier, which achieved an accuracy of 67%. Iqbal *et al.* [20] presented deep learning models utilizing long-short-term memory (LSTM) and CNN to exact brain tumor delineation (segmentation) from benchmark medical images. LSTM and ConvNet were trained on the same data and then merged to get an ensemble method for more improvement. The authors used BraTS 2015 which contains (274 subject data) for four modalities: T1, T1c, T2 and FLAIR. The authors divided the 3D data into ratios of 60:20:20 for training, evaluation and testing respectively and converted them to 2D images (slices) then extracted patches of size 25×25. The authors tried to solve the problem of class imbalance by using some methods such as weight-based balancing. Experiments showed the usefulness of using LSTM in segmentation. The DSC obtained was 82%, 79% and 77% for complete tumor region, core tumor region and enhancing tumor region respectively.

Hoseini *et al.* [21] proposed the so-called AdaptAhead as new optimization algorithm for CNN learning. It is based on merging of two optimization algorithms: Nesterov and RMSProp. The proposed model had eight layers and used 3×3 filters. The data was used from BraTS 2015 and BraTS 2016. When comparing the results of their introduced optimization algorithm against some existing related works for tumor segmentation from MRI, they found that their algorithm is more accurate about the metric of DSC, as they obtained 89% and 85% in BraTS 2015 and BraTS 2016, respectively.

Zhao *et al.* [22] suggested a novelty paradigm for brain tumor segmentation by the integration of fully convolutional neural networks (FCNNs) with conditional random fields (CRFs) into a single conjoined framework. FCNNs are used to train data in a 2D patch-wise way and CRF-RNNs are used to train 2D image slices. Through the integration of them as one network, the model achieved 84%, 73% and 62% for the complete tumor region, core tumor region and enhancing tumor region, respectively. Experiments were performed on BraTS 2013 dataset.

Liu *et al.* [23] presented a novel two-task approach for the segmentation of brainstem tumors and to make a prediction for the genotype (H3 K27M) mutation status based on 3D magnetic resonance (MR) images. They proposed and trained a 3D multiscale CNN model with 55 manually labeled patient datasets of the T1c sequence. Their proposed network consists of two components: the first is a multiscale feature fusion convolutional network that aims to obtain the tumor mask from input images and the second component is the H3 K27M-mutation-status-prediction network which is a CNN to extract features from the tumor mask and then using a SVM classifier to gain high accuracy prediction for the genotype. The experiment results of their two-task proposed method gave a DSC of 77% in the task of brainstem segmentation and accuracy of 96% in genotype prediction.

Razzak *et al.* [24] described a Two-PathwayGroup CNN architecture for brain tumor segmentation where local features and global contextual features were exploited simultaneously. The applied filters performed and exploited many transformations like translation, rotations and reflections processes. Experiments were performed on BraTS2015, the results obtained were 89.2%, 79.1%, and 75.1% for complete tumor region, core tumor region and enhancing tumor region, respectively. Also, Cui *et al.* [25] presented a fully automatic segmentation method from MRI data, based on cascaded CNN. The method aimed to localize the tumor region and then accurately segment the intratumor structure by using two subnetworks: a tumor localization network (TLN) and an intratumor classification network (ITCN). The TLN subnet was used to localize the brain tumor and then, the ITCN subnet was applied for further classification of tumor sub-regions. The BraTS 2015 dataset of 274 patients was used for training and testing their method and four sequences for the images T1, T1c, T2 and FLAIR were used. This method gained DSC of 90%, 81%, 81% for the complete tumor, core tumor, enhancing tumor regions, respectively.

Naceur *et al.* [26] suggested end-to-end deep CNN architectures for fully automated brain tumor segmentation. Their three architectures which follow incremental approach in their building differ from the

usual CNN-based models which use a trial-and-error technique to find the optimal hyper-parameters. Instead, a new training strategy was proposed that consider the most influential hyper-parameters where a roof setting was bounded over these hyper-parameters to speed up the training process. The main concept behind the incremental deep CNN strategy is to add a new block at the end of each training phase (a block is composed of several convolutions and pooling layers). So, creating a CNN model to give a high prediction performance at the same time as designing a network architecture that is optimized in terms of layers. Three models of CNN were utilized, the results of their models were competitive in terms of DSC metric on the public dataset BraTS 2017. In terms of DSC metric, the authors obtained 88%, 87% and 89% for the three models that were used in discovering the whole tumor.

Wang *et al.* [27] proposed a cascade of many CNNs to perform segmentation with hierarchical sub-regions from MR images and introduced a 2.5D network that is a trade-off between consumption of memory and complexity of the model. Three networks (WNet, TNet, and ENet) were used to segment the whole, core and enhanced tumor core structures, respectively. The pipeline work for this approach consists of three stages. First, segment the whole tumor from the image, then the input is being cropped with respect to the bounding box of the segmented whole tumor. Second, the tumor core is segmented by TNet from the cropped image region, and the image is cropped again with respect to the bounding box of the segmented core region. Eventually, ENet used to segment the enhancing core from the second cropped image. The proposed method was validated with 3D BraTS 2017 and BraTS 2018. The average DSC achieved by their method for enhancing tumor core, whole tumor and tumor core was 78.6%, 90.5% and 83.8%, respectively with BraTS 2017 and the average DSC achieved for desired enhancing, whole and core was 73.4%, 86.4% and 76.6%, respectively with BraTS 2018.

3.2. Encoder-decoder architecture

This is also one of the most used CNNs variants in brain tumor segmentation. This network usually divided into a contracting path well-known as (encoder) and an expanding path well-known as (decoder), this what cause the architecture to be a u-shaped [1], [8]. The contracting path (part) consists of the frequent implementation of many convolutional layers followed by the activation function ReLU and max-pooling layer such that a reduction in spacial information is performed and the feature information is enlarged. The expansive path consists of a sequence of many corresponding up-sampling operations merged with different features taken from encoder part through the usage of skip connections. Getting a high accuracy of mapping from the patch level to the category label is difficult because of effect of input patch size and quality. Also, the mapping is mostly directed by the last fully connected layer. So, FCN and encoder-decoder CNNs solve and overcome these problems by establishing an end-to-end fashion from the input image to the output segmentation map.

Kao *et al.* [28] presented a technique that integrates location information with neural networks by using the brain parcellation atlas found in the Montreal Neurological Institute (MNI) and mapping this atlas to the individual subject data. They integrated the atlas with MR image data and used patches to enhance the brain tumor segmentation. Two different CNN architectures were used, DeepMedic and 3D U-Net. They are frequently used for image segmentation. They used data from four modalities (T1, T1c, T2, and FLAIR) from BraTS 2017 and BraTS 2018 datasets with using normalization. To clarify the advantage of their proposed location fusion strategy, they performed several experiments that showed improvements in brain tumor segmentation performance. Their measures were DSC and Hausdorff distance. Wang *et al.* [29] segmented brain tumor into different regions by using cascaded fully CNNs. They converted the tumor segmentation process into three sequential binary segmentation stages. First, they segmented whole tumor and then used the result to segment the tumor core and finally, the enhancing core was segmented from the tumor core result. First experiment was conducted on BraTS 2017 validation dataset with Dice scores of 78%, 90%, 83% for enhancing core, whole tumor and tumor core, respectively. The second experiment was conducted on BraTS 2017 testing dataset with Dice scores of 78.5%, 90%, 83% for enhancing core, whole tumor and tumor core, respectively. The corresponding values for BraTS 2017 testing set were 78%, 87% and 77%, respectively. A modified version of U-Net for segmenting tumors was used by Isensee *et al.* [30], a dice loss function was used and substantial data augmentation was performed to restrain overfitting. They achieved very good DSCs on the testing part of BraTS 2017: 85.8% for whole, 77.5% for core, and 64.7% for enhancing tumor regions

Sun *et al.* [31] presented a deep learning-based pipeline for brain tumor segmentation and prediction of survivability for glioma patients using MRI scans. They used an ensemble of three deep CNN architectures for tumor segmentation. The first network they used was cascaded anisotropic convolutional neural network (CA-CNN) which was presented previously by Wang *et al.* [29]. The second employed network was DFKZ Net, which was suggested by Isensee *et al.* [30] of the German Cancer Research Center (DFKZ). The third network used was the well-known U-Net which is a classical network for segmenting biomedical images tasks. After they obtained the results of segmentation, they extracted features from

different tumor sub-regions and used a random forest regression model to predict the survivability. The BraTS 2018 dataset was used in this work including the modalities T1, T1c, T2 and FLAIR. By using the ensemble method, the approach achieved an average DSC of 77%, 90%, 85% for enhancing tumor, whole tumor, core tumor regions, respectively.

Wang *et al.* [32] presented the nested dilation networks (NDNs) as 3-dimensional multimodal segmentation method which is a modification of U-Net architecture. To enrich the low-level features, residual blocks nested with dilations (RnD) were used in the contracting part while SE blocks were used in both the encoding and decoding paths to boost significant features. SE blocks allow enhancing the features representations derived by a convolutional network, while RnD can enlarge the receptive fields without reducing the resolution or increasing the number of parameters. Their method obtained DSC results of 66.5%, 58.8% and 66.8% for edema, non-enhancing and enhancing tumors, respectively.

Li *et al.* [33] used a modification of the U-Net architecture. They utilized an end-to-end cascaded pipeline for segmentation task. They used to skip up connections between the encoding path and the decoding path in order to improve information flow, and an inception module was adopted in each block to help their network pick up richer information representations. The experiments were conducted on 2D slices of four sequences: T1, T1c, T2 and FLAIR of BraTS 2015. Their cascaded end-to-end method achieved DSC performances of 84.5%, 69.8% and 60.0% for the complete tumor region, core tumor region and enhancing tumor region, respectively.

Jiang *et al.* [34] participated in segmentation task of BraTS 2019 contest. BraTS consisted of 335 patients as a training set. By using a two-stage cascaded 3D U-Net to segment the substructures of brain tumors, they were the first-class winners in the challenge among more than 70 teams participated in the contest. Very good results in the terms of DSC were obtained on the testing data of BraTS 2019, which comprises 125 patient cases. Intensity normalization and three types of augmentation were performed on the data during the preprocessing step. The DSC for their method was 88.7%, 83.6%, and 83.2% for the whole, core and enhancing tumor regions, respectively.

In another work, Kao *et al.* [35] used a methodology to make integration between the existing brain parcellation atlas in the MNI152 into each subject in the dataset. The experiments were conducted using BraTS 2018. Using brain parcellation masks as extra inputs to this neural network which used patches improved the network in brain tumor segmentation. Using DeepMedic with brain parcellation (BP) gave 76.6%, 89.4%, and 80.4% for enhancing tumor regions, whole tumor regions and core tumor regions, respectively. Also, using 3D U-Net with BP gave 76.4%, 89.4%, and 77.5% for enhancing tumor region, whole tumor region, core tumor region, respectively.

Kermi *et al.* [36] used modifications of the 2D U-net architecture; for example, WCE and GDL were employed as loss functions to reduce the class imbalance issue in the brain tumor datasets. Experiments were conducted on both the BraTS 2018 dataset for testing and evaluation. They trained the model on the training dataset of BraTS 2018 with 285 patients and validation data of 66 patients. The results obtained in terms of DSC were 78.3%, 86.8%, and 80.5% for enhancing tumor region, whole tumor region and core tumor region.

Tseng *et al.* [37] presented an architecture of encoder-decoder. They used multi-modal encoder where every MRI modality were trained by a different CNN. They conducted experiment on BraTS 2015 training dataset where 244 subjects were used for training and testing the model on 30 subjects. A DSC scores of 85.22%, 68.35%, and 68.77% were achieved. Myronenko [38] proposed a CNN that is encoder-decoder architecture and added a variational auto-encoder (VAE) as extra branch at the end of encoder to reconstruct the original image. VAE is added as a regularization for the encoder in the lack of data case and the model was trained on BraTS 2018 training dataset. The model was tested on BraTS 2018 validation dataset which is 66 subjects with a DSC scores of 81.45%, 90.42%, 85.96% for enhancing, whole, core tumors, respectively. Also, it was tested on BraTS 2018 testing dataset which is 191 subjects with a DSC of 76.64%, 88.39%, 81.54% for enhancing, whole, core tumors, respectively.

Peng *et al.* [39] proposed a 3D multi-scale encoder-decoder that uses several U-Net blocks. These blocks enable the model to the get spatial information at different resolutions in the encoder part. Also, feature maps were upsampled at different resolutions where, 3D separable convolutions were used as an alternative to the ordinary convolutions. They achieved a DSC scores of 85%, 72%, and 61% for the whole, core and enhancing tumors, respectively on BraTS 2015 dataset.

Hua *et al.* [40] proposed a cascaded V nets version that has encoder and decoder to segment tumor in two stages. The same model was used in two stages where first, whole tumor was segmented then, it was divided into other substructures (edema, core, enhancing). They trained their model on BraTS 2018 training dataset and tested many other datasets. They achieved a DSC of 87.61%, 79.53%, and 73.64% for edema, core and enhancing, respectively for the testing set of BraTS 2018. A dice scores of 90.48%, 83.64%, and 77.68% were achieved for the same regions mentioned above for BraTS 2018 validation dataset which is

68 subjects. Also, they tested the performance of their model on a special dataset of 56 subjects where they achieved a DSC of 86.35%, 80.36%, and 72.17% for whole, core and enhancing tumor regions, respectively.

Wang *et al.* [41] used the transformer with 3D CNN for brain tumor segmentation. They used encoder-decoder model where the encoder extracts the spatial feature maps then, these are fed into the transformer to model the global context and finally, decoder uses transformer output to get the prediction map. They trained and tested their model on BraTS 2019 validation dataset where they achieved a DSC of 78.93%, 90%, and 81.94% for edema, whole tumor, core tumor respectively. Also, the DSC results were 78.73%, 90.09%, and 81.73% for edema, whole tumor, core tumor, respectively on BraTS 2020 validation dataset.

Zhou *et al.* [42] proposed a model that has different encoders for each MRI modality. Then, the resultant feature maps were concatenated by a fusion block. Finally, the concatenated feature maps were passed to the decoder to obtain the final segmentation results. Experiments were performed on BraTS 2017 with a DSC scores of 87.7%, 79.1%, and 73.9% for whole, core, enhancing tumors, respectively.

Khan *et al.* [43] presented pyramidal encoder-decoder model that has six cascaded levels to extract the segmentation predictions at different image scales. At each level, encoder-decoder model, predicts the segmentation maps from the input images. The input images then, doubled and the prediction maps are sub-sampled to fit the size of the images. Then, predictions and images with new size are concatenated and used as inputs for next level. They performed experiments on many medical datasets, one of them was the TCIA brain tumor dataset, where they achieved intersection over union (IoU) of 83.39%.

Rehman *et al.* [44] proposed the BrainSeg-Net encoder-decoder network which uses a new block called feature enhancer (FE). The feature maps of each encoder block are passed to the (FE) to extract middle-level features from the shallow layers and propagate them with the dense layers in the decoder. This model achieved a DSC scores of 90.3%, 87.2%, 84.9% for whole core, enhancing regions, respectively.

Chen *et al.* [45] proposed CSU-Net encoder-decoder model that consists of two branches in the encoder part, a CNN and transformer, and the decoder is based on dual Swin transformer. They achieved a DSC scores of 81.88%, 88.57%, and 89.27% for enhancing, core, whole tumor regions, respectively on BraTS 2020 dataset. Zhang *et al.* [46] proposed multi-scale mesh aggregation network (MSMANet). In the encoder part, they used modified Res-Inception and SE modules for feature extraction. the decoder was replaced by aggregation block. BraTS 2018 dataset was used to evaluate their model which achieved a DSC scores of 75.8%, 89%, 81.1 % for enhancing, whole, core tumors, respectively.

Maji *et al.* [47] proposed attention Res-UNet with guided decoder (ARU-GD), that is a modified version of Res-Unet, with attention gates and guided decoder. In this model, each decoder layer was trained individually and the prediction result was upsampled to the original size of the input image to be compared with ground truth of the image. Attention gates were used instead of skip connection to pass only the relevant spatial and contextual features between encoder and decoder. This model was trained on 6,700 images from BraTS 2019 and achieved a DSC scores of 91.1%, 87.6% and 80.1% for whole, core and enhancing tumors, respectively.

Shan *et al.* [48] proposed 3D CNN based on U-net architecture. Their model comprised three main units: improved depth-wise convolution (IDWC) unit which uses separable convolution instead of conventional convolution to extract feature maps and computationally saving resources. Multi-channel convolution (MCC unit), which makes convolution with different kernel sizes, enabling the network to get features from different receptive fields. SE unit to obtain the final tumor prediction. The model was trained on training set of BraTS 2019 and tested on validation set of BraTS 2019 with DSC scores of 90.53%, 83.73%, and 78.47% for whole, core, enhancing regions, respectively.

Aghalari *et al.* [49] proposed a modification on U-net architecture, by the addition of two-pathway residual blocks (TPR), where this block has two streams: one as local path consists of (3×3) convolutional layer then residual block to capture local information while the second stream is (5×5) convolutional layer to capture global information. Experiments were performed on training set of BraTS dataset that contains 285 patients. Data was divided as 70% for training, 15% for validation and 15% for testing. Average DSC of 89.76% was obtained.

Rehman *et al.* [50] proposed 2D segmentation method (BU-Net) based on U-net model. They added two blocks: Residual extended skip (RES) and wide context (WC) block to U-net model. The network is still encoder-decoder model with using RES block to derive middle features from low features and WC block is used in the transition between contracting and expansive path. They conducted their experiments on BraTS 2017 with DSC scores of 89.2%, 78.3%, 73.6% for whole, core, enhancing tumor regions, respectively and also on BraTS 2018 with DSC scores of 90.1%, 83.7%, 78.8% for whole, core, enhancing tumor regions, respectively.

Zhang *et al.* [51] proposed 2D attention residual U-Net (AResU-Net) for brain tumor segmentation which is a U-Net based. This model is conventional encoder-decoder that includes three residual blocks in the encoder path and the decoder path also, includes three upsampling residual blocks. Finally, attention and

squeeze and excitation block (ASE) was utilized between upsampling and downsampling paths. To evaluate their system, they performed many experiments on subsets data of BraTS 2017 and 2018. HGG cases from BraTS 2017 which are 168 patients were divided into training and testing with ratio of 80:20, they achieved DSC scores of 89.2%, 85.3%, 82.5% for whole, core, enhancing tumors, respectively. Also, they performed another experiment on BraTS 2018 dataset where they used the training data of 285 subjects and tested the system on validation set which is 66 subjects with DSC scores of 87.6%, 81%, 77.3%.

4. CONCLUSION AND FUTURE WORK

Deep CNNs have been remarkably developed and many architectures have been utilized in many applications. Brain tumor segmentation process, is a task regarding the medical field that benefited from CNNs technology where, several research works are being continuously conducted to improve the efficiency of CNNs for segmentation. The updated improvements in CNNs can be classified according to different ways, comprising activation and loss functions, optimization, regularization techniques, the novelties in the learning algorithms architectures. In this paper, we review CNN variants that were used in brain tumor segmentation having a focus on the architectural taxonomy of the networks. we noticed from the existing works that the most used CNN variants are: conventional CNN (either single, multiple or cascaded paths) and encoder-decoder frameworks. Also, we focused on the works, which used the well-known BraTS dataset with four modalities (T1, T1C, T2, FLAIR) and considered a DSC metric for result evaluation, as this metric is widely used in segmentation evaluation tasks. Unlike some reviews, researcher's results were included in our overview. In the Future, this survey will be extended to contain most brain tumor segmentation works that relied on using CNNs. A detailed study of different CNNs variants that explains their architectures techniques and articulate advantages and disadvantages, listing the datasets and including different augmentation and preprocessing techniques also is required and would enrich the study to be a comprehensive reference in this field.

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