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Research Article

Brain Tumor Segmentation and Classification Using Neural Networks Based on Selected Features

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Abstract: The human brain, a highly intricate organ, governs the entirety of physiological functions. The emergence of brain tumors, characterized by the anomalous and unregulated proliferation of brain cells, both within and outside the cranial cavity, presents a multifaceted challenge. These tumors manifest diversely in terms of their spatial distribution, morphology, and radiological attributes. Brain tumor segmentation entails the precise demarcation of pathological tumor tissue from normal brain constituents, while classification pertains to the discernment of the specific tumor subtype based on its distinctive features. The accuracy of brain tumor segmentation holds paramount significance in the realms of diagnosis, patient monitoring, and treatment strategizing, particularly for individuals afflicted by cerebral malignancies. This computational challenge is extremely complex since it lies at the intersection of computer vision and medicine. The most common method for evaluating brain malignancies is magnetic resonance imaging (MRI). Nonetheless, the manual segmentation and classification of 3D MRI images impose an arduous and time-intensive burden, contingent upon operator proficiency, leading to variable outcomes. In light of these challenges, the imperative arises for the development of a dependable, fully automated method for brain tumor segmentation and classification, offering efficiency and consistency in delineating tumor subregions. Convolutional Neural Networks (CNNs), a representative of deep learning techniques, have surpassed earlier machine learning paradigms in this endeavor by completing the challenging process of segmenting brain tumors. This paper introduced a deep learning-based framework tailored for the segmentation of brain tumors from multi-modal MRI scans. This innovative framework draws inspiration from two prominent architectural paradigms, namely the U-Net and residual network, further enhanced with attention mechanisms. The embedded attention gates facilitate automatic focalization on structures of varying dimensions and shapes while suppressing irrelevant regions. The method underwent rigorous evaluation on the BRATS 2015 dataset, comprising 220 High-Grade Glioma (HGG) cases and 54 Low-Grade Glioma (LGG) cases. The results exhibited Dice scores of 0.53, 0.73, and 0.61 for enhancing tumor, whole tumor, and tumor core segmentation, respectively, on the BRATS 2015 test data, affirming the efficacy of that approach.

Keywords: Brain Tumor Segmentation; MRI image analysis; Deep learning; Convolutional Neural Networks (CNN); Medical Image Processing;

1. Introduction

The human brain is an exceedingly complex organ, comprising approximately 100 billion distinct cell types. Within this intricate neural landscape, brain tumors manifest as aberrant masses of irregularly shaped brain tissue characterized by uncontrolled cellular proliferation. Damage to nerve cells can result in a variety of health issues for people as well as abnormalities in the human body's brain. The brain's tissues are negatively impacted by these injured cells. This issue raises the possibility of brain tumors developing in people [24]. Brain tumors fall into two distinct categories: primary and metastatic. While metastatic brain tumors form in other bodily sections of the human body, such as the breasts or lungs, and then spread to other areas of the brain, primary brain tumors originate inside the brain, including nerves, blood arteries, or different brain glands [25]. Malignant and benign tumors exist. Malignant brain tumors are malignant and grow rapidly within the body. Glioblastoma is the most prevalent malignant brain tumor [26]. The cells in benign brain tumors proliferate slowly and are not malignant. This kind of tumor doesn't spread to other bodily areas. It won't reappear in the body if surgically removed safely [27]. Approximately 120 different subtypes of brain tumors have been found via ongoing studies, highlighting the diversity of these diseased entities. The clinical presentation of brain tumors encompasses a spectrum of symptoms, including but not limited to headaches, mood fluctuations, memory impairment, seizures, disruptions in sleep patterns, and visual disturbances. These manifestations serve as indicative markers of the presence and potential impact of a brain tumor on neurological function.

Here are some figures to help you understand how brain tumors affect people's quality of life:

- Among the various malignancies, brain tumors are responsible for many deaths worldwide in both men and women [1].
- Nearly 2% of cancer cases worldwide are caused by brain tumors [2].
- Only 33% of people with brain cancer survive five years or more, compared to 90% of people with breast cancer and 65% of people with leukemia [3].

Brain tumors exhibit substantial diversity in appearance and shape, often displaying marked heterogeneity. They can emerge within the brain or extend beyond its confines, varying in size and presenting irregular, indistinct borders that pose challenges for differentiation from normal tissues. Magnetic resonance imaging (MRI) has emerged as a pivotal technique for brain tumor analysis, facilitating the critical processes of segmentation and classification within volumetric 3D data. Because it serves as the first stage in diagnosing, monitoring, and forecasting patient outcomes, this project is a significant one in the field of medical image analysis. Machine learning methods have historically been used for the segmentation and classification of brain tumors. However, contemporary advancements in deep learning have eclipsed conventional methodologies. This study exclusively explores deep learning approaches. The annual MICCAI challenge on Brain Tumor Segmentation (BRATS) serves as a standardized platform for diverse algorithms to benchmark their performance, and numerous conferences provide avenues for the dissemination of novel findings. this context presents a convolutional neural network-based model tailored for brain tumor segmentation and classification, leveraging the BRATS dataset. This ground-breaking framework takes cues from two well-known architectural paradigms: the U-Net and residual network. By incorporating attention gates and residual connections into a streamlined U-Net structure, the model autonomously learns to identify tumor structures of varying shapes and sizes while effectively suppressing irrelevant regions. The evaluation was conducted on the BRATS 2015 dataset, comprising 220 High-Grade Glioma (HGG) cases and 54 Low-Grade Glioma (LGG) cases, affirming the model's efficacy.

1.1 Problem Statement

In the realm of brain tumor segmentation and classification using MRI, numerous challenges abound. Brain tumors exhibit substantial variability in appearance and shape among patients, necessitating the capture of four distinct MRI modalities for each individual to glean comprehensive insights into these conditions. It is typical to use numerous modalities as input during the process of segmenting and classifying brain tumors since each modality may provide a clearer definition of certain tumor features.

This complex undertaking typically involves various stages, encompassing pre-processing, feature extraction, segmentation, classification, and post-processing, culminating in the generation of a segmented brain tumor with distinct classes. The utmost importance lies in ensuring the accuracy and reliability of the segmented tumor, as it directly impacts the efficacy of disease treatment.

1.2 Objectives of Research

The main objectives of this research are as follows:

Application of Deep Learning in the Medical Field: In recent times, artificial neural networks have revolutionized the medical domain, being employed in various medical applications such as classification, captioning, segmentation, and disease detection. By offering accurate illness analysis and supporting better medical decision-making, deep learning plays a crucial role in assisting medical professionals.

Literature Review: Another key objective of this research is to conduct an in-depth review of recent literature concerning deep learning methodologies in the context of brain tumor analysis. This paper tries to assess numerous factors that have a big impact on how well automatic brain tumor segmentation and classification work.

Practical Application: Utilizing the BRATS dataset, this research aims to develop a convolutional neural network (CNN) algorithm for the automated segmentation and categorization of brain tumors.

1.3 Significance of the Research

The research addresses the formidable challenges in brain tumor segmentation and classification using MRI by acknowledging the inherent variability in tumor characteristics among patients. Its emphasis on combining various MRI modalities and using deep learning techniques shows a dedication to improving precision and dependability in the intricate process of tumor analysis. By exploring the practical application of a convolutional neural network (CNN) on the BRATS dataset, the research contributes to the advancement of automated, precise, and efficient brain tumor segmentation, holding potential implications for improved medical decision-making and treatment efficacy.

2. LITERATURE REVIEW

The objective of this section is to provide a brief overview of the research conducted on the segmentation and classification of brain tumors, with a primary focus on neural network approaches.

Pereira et al. [4] introduced an advanced Convolutional Neural Network (CNN) architecture that utilizes 3x3 convolutional kernels. The network encompassed three primary stages: preprocessing, classification, and postprocessing. In preprocessing, they executed bias field correction, intensity normalization, and data augmentation. Each sequence underwent intensity normalization using the z-score approach and bias field correction using the N4ITK method. Their study demonstrated the substantial impact of data augmentation with adequate preprocessing. Notably, the HGG architecture consisted of 11 layers, surpassing the 9 layers of the LGG architecture. Both architectures comprised convolutional layers, followed by pooling layers and concluded with fully connected layers. Post-processing relied on a threshold-based technique, with the utilization of LReLU activation as an alternative to ReLU. The proposed CNN yielded the following results on the BRATS 2013 dataset: 80% for complete tumor, 83% for core tumor, and 77% for enhancing tumor regions.

In a separate study, R. Lang et al. [5] presented a CNN-based model for brain tumor segmentation across multiple modalities. This CNN architecture featured four pairs of convolutional layers with downsampling layers, culminating in a single fully connected layer. Input images were divided into three distinct patch sizes: 28x28, 12x12, and 5x5. Particularly, the model with a patch size of 28x28 showed better accuracy. The training was performed on BRATS 2013 data using the 28x28 patch size, with image segmentation into five distinct regions. The experiments highlighted the superior performance of deeper neural networks with larger patch sizes, culminating in a dice score of 0.88.

Moreover, R. Sauli and colleagues [6] introduced a novel fully automated ensemble learning approach for the segmentation and classification of brain tumors. Their methodology employed three end-to-end incremental deep Convolutional Neural Networks (CNNs) known as 2CNet, 3CNet, and EnsembleNet. The initial two networks employed parallel architecture for feature extraction, while EnsembleNet amalgamated the outcomes of both networks. An innovative training strategy was employed, monitoring hyperparameters to enhance the training process. Experiments conducted on the BRATS-2017 dataset, without post-processing, yielded an average dice score of 0.88 for the complete tumor region.

In their work [7], H. Dong et al. introduced a brain tumor segmentation approach employing a 2D UNet architecture built upon deeper convolutional networks. Each modality underwent standardization through z-score normalization, resulting in a mean of 0 and a standard deviation of 1 for the data. The methodology included the development of a unique loss function called Soft Dice, the use of cross-validation, and a wide range of data augmentation techniques. Subsequently, the proposed model underwent testing and evaluation using the BRATS 2015 dataset, focusing exclusively on two tumor subregions, namely, complete and core. Remarkably, this model achieved Dice scores of 86% for Whole Tumor (WT), 86% for Core Tumor (CT), and 65% for Enhancing Tumor (ET).

In a separate study [8], Wang et al. presented a convolutional neural network (CNN)-based cascaded architecture designed to identify brain tumor subregions through a divide-and-conquer strategy. This architecture featured three networks WNet, TNet, and Enet each structured similarly, with one dedicated to each tumor subregion. These networks were made up of many convolutional filters, each with a sizable encoder and a simple decoder. The approach utilized residual connections, multi-view fusion, and an ensemble of three networks from orthogonal viewpoints. Notably, the use of smaller convolution kernels (1x1x3) and (3x3x1) instead of (3x3x3) kernels contributed to computational efficiency and memory conservation. The output of the preceding network served as input for the subsequent one. This cascaded approach yielded Dice scores of approximately 0.7859 for ET, 0.9050 for WT, and 0.8378 for CT, as evaluated on the BRATS 2017 dataset.

Lastly, M. Havaei et al. [9] introduced a novel cascaded network architecture for segmentation. This model concurrently leveraged local and global features through two distinct pathways based on convolutional neural networks (CNNs). One pathway employed small filters to extract local features, while the other employed large filters for global features. To predict the tumor location, the outputs from both paths were combined into a single fully connected layer. Preprocessing steps encompassed normalization and bias field correction, while a two-phase training procedure was employed to address tumor label imbalance. The cascaded network's performance was assessed using the 2013 dataset from BRATS, yielding final scores of approximately 0.81 for WT, 0.72 for CT, and 0.58 for ET, respectively.

Kamnitsas et al. [10] introduced an innovative approach that aggregates various neural networks to achieve enhanced performance. Their approach combines two 3D U-Net models, three 3D Fully Connected Network (FCN) architectures, and two DeepMedic models to achieve robust and precise segmentation. Each model is trained independently, and at the end of the procedure, their individual segmented forecasts are fused. The study incorporates diverse intensity normalization and data augmentation techniques to optimize performance. As a result, this approach, termed EMMA, demonstrates superior generalization capabilities, yielding scores of 72.9, 88.6, and 78.5 for ET, WT, and CT, respectively, when applied to the BRATS 2017 dataset.

F. Chen et al. [11] introduced DU++, an innovative network architecture that combines the strengths of Half DenseNet (HDU) and UNet++. This design successfully handles a sizable number of factors, accommodating the complexities of intricate medical imaging. DU++ optimizes the architecture by reducing parameter count and implementing feature fusion. It incorporates a series of bridges at varying semantic levels, departing from UNet++'s original lengthy connections. The model achieved notable scores of 84.9 for dice score, 80.6 for positive predictive value (PPV), and 78.0 for sensitivity when evaluated on the BRATS dataset 2015.

Isensee et al. [12] demonstrated the efficacy of a well-trained UNet network with carefully selected hyperparameters. By training the baseline UNet on larger patches, they improved its ability to capture contextual data. Additionally, their approach encompassed region-based training, preprocessing techniques, additional training data utilization, postprocessing procedures, and a combination of diverse loss functions. This refined U-net yielded impressive dice scores of 77.88 for ET, 87.81 for WT, and 80.62 for CT on the testing dataset.

L. Sun et al. [13] presented a comprehensive framework employing multiple CNN architectures. They employed an ensemble learning approach, integrating three distinct 3D CNN architectures: Cascaded Anisotropic Convolutional Neural Network (CA-CNN), DFKZ Net, and U-Net. Their preprocessing steps encompassed intensity normalization and augmentation. The performance evaluation used the BRATS 2018 dataset for training, validating, and testing to show that the ensemble model outperformed individual ones.

McKinly et al. [14] introduced a group of classifiers based on the DeepSCAN structure, which is a variation of DenseNet employing dilated convolutions to extend the receptive field while managing high memory usage. These dilated convolutions were used to build a UNet framework. Despite its advantages, this architecture's substantial memory requirements limit its depth, batch size, and input dimensions. The study introduces a novel loss function, Label-Uncertainty Loss, built upon binary cross-entropy (BCE). They utilized a cascaded network for the separation of the entire tumor, combined with data augmentation techniques such as shifting, rotating, and scaling, as well as intensity standardization for preprocessing. Additionally, they applied a threshold-based post-processing approach. This architecture achieved the highest scores of 0.797, 0.903, and 0.854 for ET, WT, and CT, respectively, on the BRATS 2018 dataset.

Y. Ding and colleagues [15] introduced the Residual Dilated Network with Middle Supervision (RDM-Net), which combines the Residual Network (ResNet) and dilated convolutions. ResNet helps enable deeper networks by addressing gradient vanishing, while dilated convolutions provide an extended receptive field without spatial dimension reduction. The design consists of residual dilated blocks (RD-Blocks), a spatial fusion block, and a middle supervision block. They also introduced a new loss function called Multi-Hierarchical Loss (MHL), based on focal loss, to handle class imbalance. Z-score standardization is applied for preprocessing. This model achieved a final score of 0.86, 0.71, and 0.63 for complete, core, and enhanced tumor subregions, respectively, on BRATS 2015.

Y. Wang and colleagues [16] introduced the Wide Residual and Pyramid Pool Network (WRN-PPNet), which merges wide residual networks and pyramid pool networks (PPN). PPN encompasses three pooling paths, end-to-end without post-processing, consisting of modules, feature fusions, and scale recovery. The architecture includes a Wide Residual Network (WRN) module with convolution layers and ResNet blocks, a Pyramid Pool Network (PPNet) with three pooling layers, and a scale recovery module with convolutions and deconvolutions. Preprocessing involves intensity normalization (zero mean and unit variance) and data augmentation techniques such as flipping, rotation, shifting, and shear. This model achieved scores of 0.94 (mean dice), 0.92 (sensitivity), and 0.97 (positive predictive value) using BRATS 2015.

G. Wang and colleagues [17] presented a cascaded neural network with uncertainty estimation, which divides the multi-class problem into simpler binary sub-problems. The network comprises WNet, TNet, and ENet, which are responsible for segmenting the whole tumor, and tumor core, and enhancing the tumor, respectively. They use bounding boxes for cropping each tumor sub-region. WNet and TNet share a network structure with a larger receptive field compared to ENet. These networks incorporate residual connections, dilated convolutions, and multi-scale prediction. Test and training time augmentation, along with intensity normalization, are employed. All networks are trained in three orthogonal planes. This 2.5D neural network reduces memory consumption, model complexity, and receptive fields, resulting in improved segmentation accuracy. This method achieved mean dice scores of .786, .905, and .838 for ET, WT, and CT, respectively, on the 2017 BRATS dataset.

D. Liu et al. [18] introduced the Dilated Convolution Refine (DCR) network, comprising two components: an encoder with ResNet, a DCR module, and downsampling convolutional layers, and a

decoder with upsampling deconvolution layers. Cross-entropy and content prediction loss functions are combined to create a new loss function using the DCR structure, which includes both local and global characteristics. Their experiments were conducted using the BRATS 2015 dataset.

R. Zheng et al. [19] introduced a 3D Convolutional Neural Network (CNN) for the segmentation of brain tumors. They obtained both local and global features through two separate pathways, one using 48x48x48 patches and the other using 28x28x28 patches. Each pathway was composed of convolutional layers and two dense blocks, with each dense block containing 6 convolutional layers. The application of dropout and pooling layers reduced the characteristics of the dense blocks. Local and global features were concatenated before the final convolutional layer. Preprocessing involved Z-score normalization and N4ITK techniques, and the BRATS 2018 dataset was used for evaluation. Their achieved scores were .87, .84, and .81 for CT, CT, and ET regions, respectively.

This Paper [20] introduced a technique merging fully convolutional neural network (FCNN) and conditional random fields (CRF) implemented as a recurrent neural network (RNN) within a single deeper network with FCNN. Preprocessing included bias field correction using the N4ITK method and intensity normalization with the z-score method. A threshold-based post-processing approach was also employed. For the purpose of segmenting brain tumors, three models were trained in axial, coronal, and sagittal views. The model evaluation utilized BRATS 2013, 2015, and 2016 datasets, demonstrating competitive results across three imaging modalities (Flair, T1, and T2).

In this Research, the authors [21] proposed combining the One-Pass Multi-task Network (OM-Net) and the Model Cascade baseline (MC-baseline) and their respective variations. They developed deeper architectures to capture contextual and attentive information based on OM-Net and MC-baseline. OM-Net, a single deeper neural network, concurrently handles three sub-tasks in a single pass. Both models underwent enhancements in multiple aspects, including deeper OM-Net, the incorporation of dense connections, the addition of an attention block, and the integration of multi-scale context information. To increase segmentation accuracy, OM-Net and its variations were individually trained and then their predictions were combined. The pretreatment and post-processing phases were included in the study as well. This architecture yielded mean scores of .81, .91, and .87 for ET, WT, and CT, respectively, using the BRATS 2018 dataset.

A. Myronenko [22] introduced an automatic semantic neural network architecture based on an encoder and decoder convolutional neural network. This architecture featured an expanded encoder section to extract deeper features and a scaled-down decoder section to reconstruct the original mask. The encoder section incorporated ResNet blocks comprising convolutional layers, batch normalization layers, ReLU activations, and skip connections. The decoder block mirrored the encoder block but included a single block at each level. To reconstruct the original image, an extra encoder branch was also used. This study introduced a novel loss function that combined soft dice loss and VAE penalty. Z-score normalization was applied solely to non-zero voxels, complemented by various augmentation techniques for preprocessing, and postprocessing involving Conditional Random Fields (CRF). The final prediction was generated by averaging the outputs of 10 trained models. This architecture achieved mean dice coefficient scores of .84, .91, and .87 for ET, WT, and CT, respectively, using the BRATS 2018 dataset.

F. Isensee et al. [23] introduced a modified UNet network architecture for brain tumor segmentation. Their preprocessing steps included z-score normalization, and the architecture was designed to process large patch sizes of 128x128x128 voxels. Extensive data augmentation techniques were employed during training, including random rotations, random scaling, elastic deformation, and gamma correction. Augmentation was also applied during model testing. The evaluation was conducted using the BRATS 2015 and 2017 datasets, resulting in dice coefficient values of .90, .80, and .73 for WT, CT, and ET, respectively.

Authors	BRATS	Pre-Processing	Segmentation Technique	Post-processing	Result (DSC Score)		
					CT	ET	WT
[4]	2013 2015	-Intensity normalization -Patch normalization -Data augmentation -Bias field correction	Deeper Convolutional Neural network (CNN) with 3x3 kernel	Threshold	0.83	0.77	0.88
[5]	2013	-Intensity normalization	Convolutional Neural Network (CNN) of different scales	--	--	--	0.88
[6]	2017	--	Ensemble Net of 2CNet and 3CNETbased on CNN	--	--	--	0.88
[7]	2015	-Z-score normalization -Data augmentation	2D U-Net	--	0.86	0.65	0.86
[8]	2018	-Intensity normalization -Data augmentation	Cascade of WNet, TNet and ENet	CRF	0.84	0.77	0.91
[9]	2013	-Intensity normalization -Bias field correction	Dual path cascaded CNN	Connected components	0.72	0.58	0.81
[10]	2017	-Intensity normalization -Data augmentation	Ensemble of Multiple Models and Architectures (EMMA)	CRF	0.79	0.73	0.89
[11]	2015	-Batch normalization	DenseNet + U-Net	--	--	--	85
[12]	2018	-Intensity Normalization	Modified U-Net	Thresholding	0.81	0.78	0.88
[13]	2018	-Intensity normalization -Data augmentation	Ensemble of 3 different CNN architectures	--	0.85	0.81	0.91
[14]	2018	-Intensity normalization -Data augmentation -Skull Stripping	Ensemble of densely connected CNNs with dilated convolutions	-Thresholding	0.85	0.80	0.90
[15]	2015	-Z-score normalization	Residual networks with dilated convolutions	--	0.86	0.63	0.71
[16]	2015	-Data augmentation -Intensity normalization	Wide residual network and pyramid pool network (WRN-PPNet)	--	--	--	0.94
[17]	2017 2018	-Intensity normalization\ -Data augmentation	Triple cascade CNN with hierarchical tumor sub-regions	-Conditional random forest (CRF)	0.84	0.79	0.91
[18]	2015	-Data augmentation	Dilated Convolutional Refine (DCR) network	--	0.62	0.68	0.87
[19]	2018	-Intensity normalization -Bias field correction	Two pathway hyper-dense convolutional neural networks	--	0.84	0.81	0.87
[20]	2013 2015 2016	-Intensity normalization -Bias field correction	Integration of FCNN and CRF as Recurrent Neural Network	-Simple thresholding -3D CRF	0.87	0.83	0.78
[21]	2018	-Intensity normalization	Ensemble of OM-Net, MC-baseline and its variants	-Threshoding	0.87	0.81	0.91
[22]	2018	-Intensity normalization -Data augmentation	Ensemble of ten encoder-decoder architectures	-Conditional random field	0.87	0.82	0.90
[23]	2015 2017	-Intensity normalization	Modified U-Net with extensive augmentation	--	0.80	0.73	0.90

3. Research Methodology

This section presents the research methodology used to address the segmentation and classification of brain tumors. The approach was developed to satisfy the segmentation requirements of the BRATS competition. The approach was designed to meet the segmentation requirements of the BRATS competition, facilitating a straightforward comparison with other BRATS techniques. Figure 1 illustrates the adopted approach for addressing the challenge.

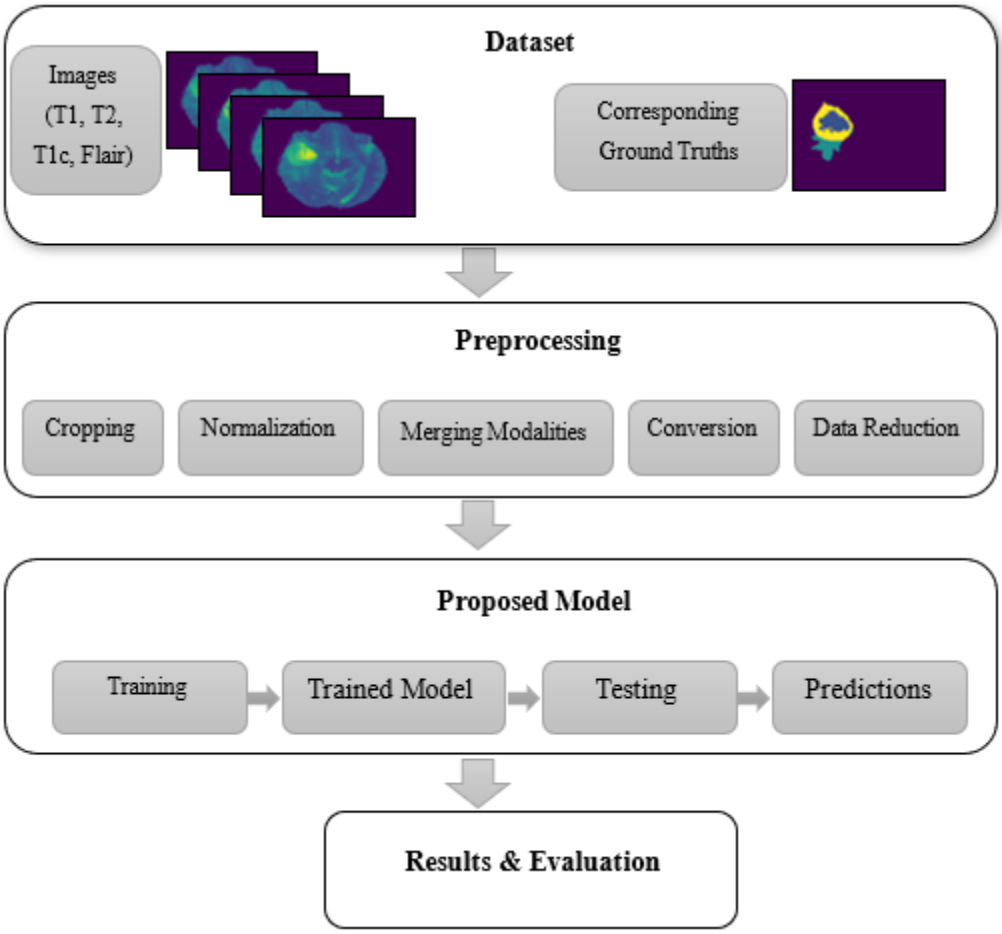

Figure 1: Research Methodology

3.1 Dataset Description

In this study, BRATS 2015 dataset is used to train, validate, and test the model. The BRATS 2015 dataset was chosen for the study because it is a commonly used benchmark in medical image analysis and provides a uniform framework for impartial assessment. The suggested brain tumor segmentation and classification algorithm is proven to be reliable and applicable in real-world scenarios by its varied collection of multimodal MRI data and incorporation of difficult instances. The are two sets of data in this dataset: train data and test data. 220 HGG patients and 54 LGG patients make up the training data. Four modalities—T1, T1c, T2, and FLAIR along with associated ground truths are available for every patient. The shape of the four modalities and their respective ground truths is 155x240x240. Except for ground truth, the testing data set consists of 110 patients across four modalities. Voxels in an image are categorized into five groups using the numbers 0, 1, 2, 3, and 4. Different parts of the brain tumor are represented by each numeric labeling.

Label 0: This label corresponds to the background portion.

Label 1: This label corresponds to the necrosis portion of the brain tumor.

Label 2: This label corresponds to the edema portion of the brain tumor.

Label 3: This label corresponds to the non-enhancing tumor.

Label 4: This label corresponds to the enhancing tumor.

The final outcomes of brain tumor segmentation and classification are evaluated in three specific subregions:

Whole Tumor: This includes all labels except label 0, representing the entire tumor.

Tumor Core: This comprises label 1 (necrosis), label 3 (non-enhancing tumor), and label 4 (enhancing tumor), representing the central tumor region.

Enhancing Tumor: This is represented by label 4 (enhancing tumor) and specifically focuses on the enhancing part of the tumor.

In this study, only HGG (High-Grade Glioma) data is used for training the proposed model.

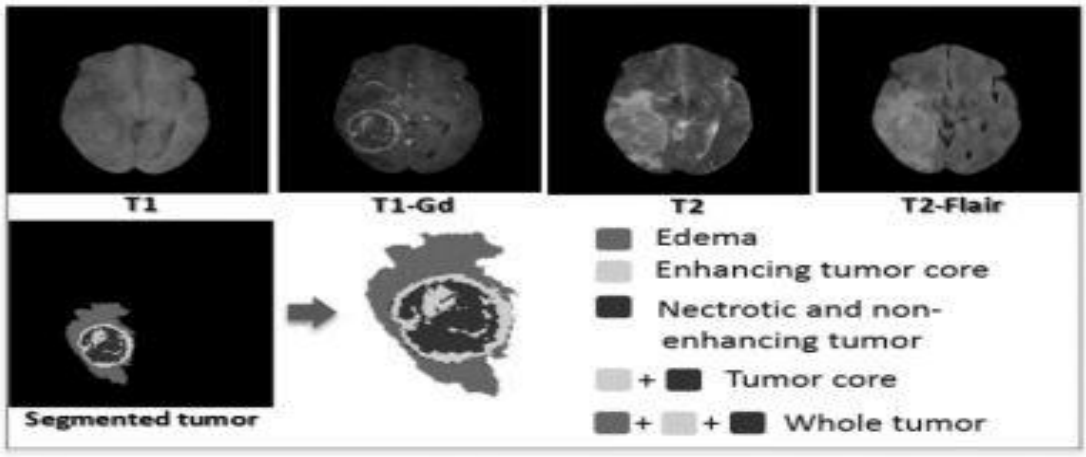

Figure 2: Four different modalities and corresponding ground truth of HGG in the BRATS dataset

3.2 Preprocessing

Preprocessing plays a pivotal role in enhancing the efficacy and competitiveness of brain MRI image segmentation model. This phase involves taking several crucial steps to prepare the data for training. Brain MRI images in MHA file format from disk using the SimpleITK library. These MRI images, which are originally 3D and sized at 155x240x240, are transformed into 2D slices of 240x240, resulting in 155 slices per image. Subsequently, each slice is further cropped to a size of 192x192. After cropping, min-max normalization is applied to handle variances in image intensities, establishing uniform pixel value ranges across the dataset. The four corresponding clipped and normalized modalities are stacked slice by slice to generate the final input form (192x192x4) for the model. Additionally, the data format is converted from MHA to numpy (npy), and the preprocessed data is saved on disk.

Furthermore, addressing the issue of empty slices in the BRATS 2015 dataset, which appear at the beginning and end of all four brain MRI sequences, as well as in the ground truth data. These empty slices not only require a lot of training time and memory, but they also lack important data. To mitigate these challenges, these empty slices were removed, resulting in a significant reduction in the dataset size by approximately 50%.

Table 1: Training and testing dataset summary

Dataset (HGG)	Total Slices	Training	Validation	Testing
Original 2D Slices	34100 (100%)	23870 (70%)	5115 (15%)	5115 (15%)
Reduced 2D slices	16105(100%) (48% of original)	11275 (70%) (33% of original)	2415 (15%) (7% of original)	2415 (15%) (7% of original)

3.3 Proposed Architecture

The proposed model leverages the principles of two well-established Convolutional Neural Network (CNN) architectures, namely the Residual Network (ResNet) and U-Net, complemented by an attention mechanism. As seen in Figure [insert figure number], this model includes a variety of blocks and layers.

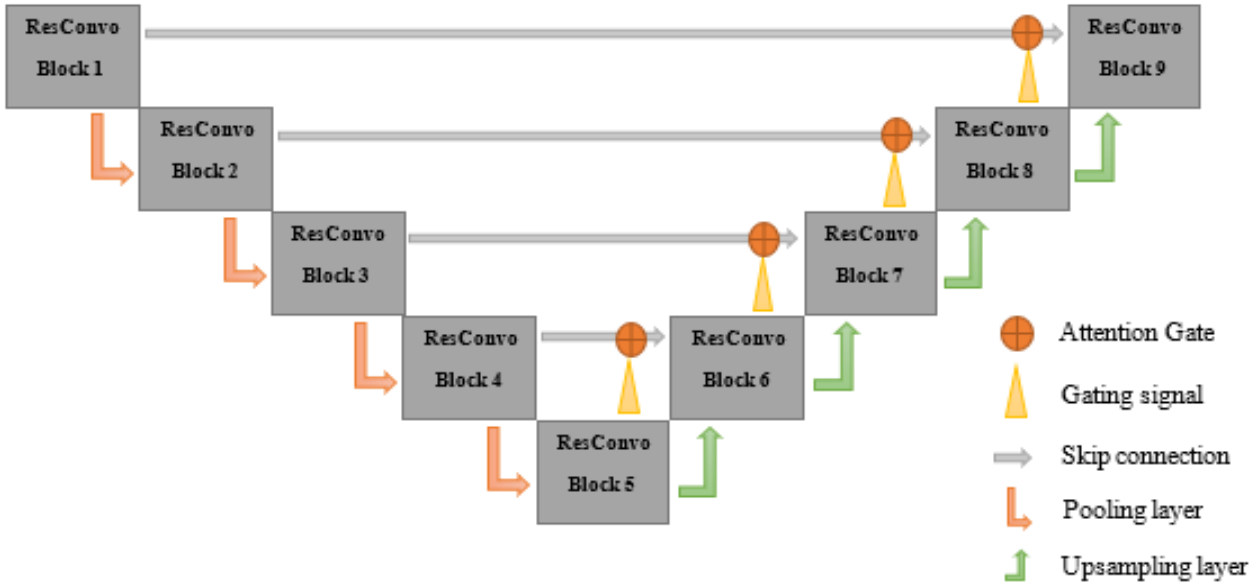

Figure 3: Proposed Model

The proposed model is divided into three parts: Downsampling path, Bottleneck and Upsampling Path

3.3.1 Downsampling Path

This pathway comprises four ResConvo Blocks (RC Blocks), denoted as block 1 through block 4, with each block being succeeded by precisely one pooling layer.

3.3.2 Bottleneck

The bottleneck section comprises a single RC Block, which is not followed by a pooling layer. Within this RC Block, the downsampling path concludes, and the upsampling path commences.

3.3.3 Upsampling Path

Similar to the downsampling path, the upsampling path comprises four RC Blocks. In addition to RC Blocks, this pathway incorporates gating signals, attention gates (AGs), upsampling layers, concatenation layers, and corresponding skip connections from the downsampling path**.**

3.4 Training Parameters

After removing empty slices, the original dataset was reduced by approximately 50%. This reduced dataset was then divided into three parts: training data, validation data, and testing data, with proportions of 70%, 15%, and 15%, respectively. The proposed model was configured with a batch size of 10 and underwent training on the training data for a total of 150 epochs. Throughout the training process, the model's performance was continuously assessed using validation loss. At the end of each epoch, only the weights of the best-performing model were saved. For optimization, the Adam optimizer was employed with a learning rate of 0.001, and categorical cross entropy was chosen as the loss function. Detailed information regarding the training hyperparameters of the proposed model can be found in Table 2**.**

Table 2: Hyperparameters of Proposed Model

Number of epochs	150
Batch size	20
Dropout	0.2
Learning Rate	0.001
Initial biases	Zeros
Patch-size	192x192
Optimizer	Adam
Loss function	categorical_crossentropy
Metrics	Dice and accuracy
Activation Function	ReLU

4. Experimental Analysis and Results

The implementation of the proposed model was carried out using the Keras and TensorFlow libraries. Throughout the development process, multiple experiments were conducted on both the training and validation datasets, aiming to identify optimal parameters that would yield the desired performance. Each experiment varied a single factor to see how it affected overall model performance. The majority of the hyperparameters included in the proposed model were chosen using recognized principles in CNN design. To gauge the effectiveness of the trained model, assessed by using various metrics, including training accuracy, validation accuracy, training loss, and validation loss. Upon completing the training process, the final model weights were saved. During the testing phase, these saved weights were loaded into the system to facilitate the prediction of tumor classes. After conducting an extensive array of experiments, the ultimate hyperparameters and their corresponding values have been compiled and are presented in Table 3

Table 3: Parameters and hyper-parameters of Proposed Model

Number of epochs	150
Batch size	20
Dropout	0.2
Learning Rate	0.001
Initial biases	Zeros
Patch-size	192x192
Optimizer	Adam
Loss function	categorical_crossentropy
Metrics	Dice and accuracy

4.1. Final loses

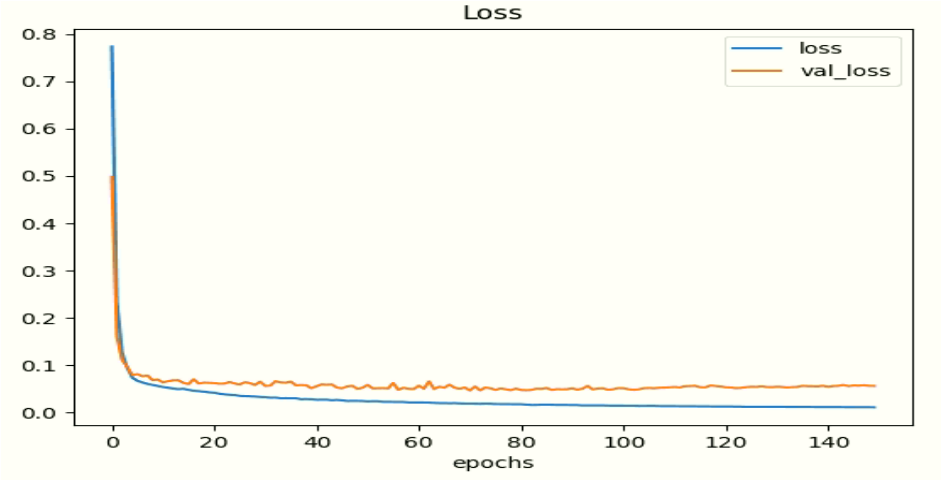

Figure 4: Training Results (Training and Validation Losses)

4.2. Final Accuracies

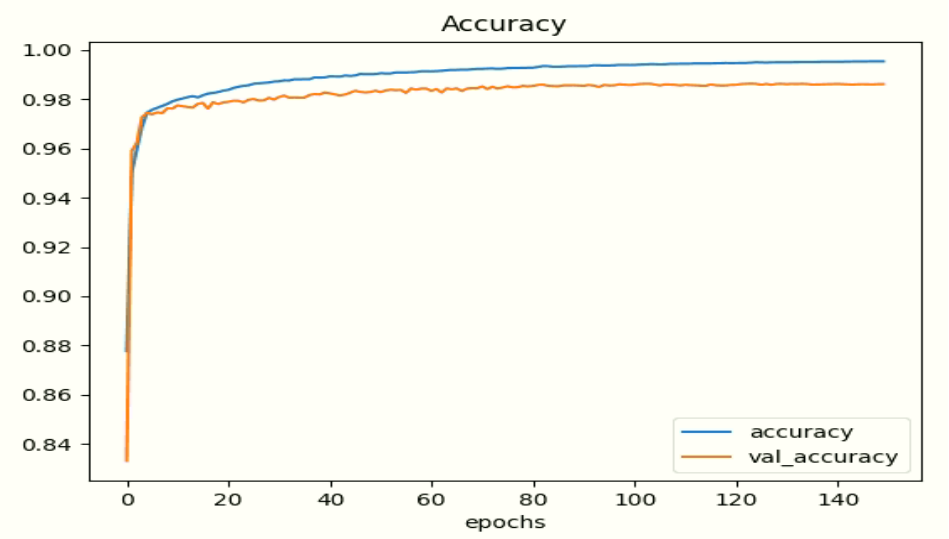

Figure 5: Training Results (Training Accuracy and Validation Accuracy)

4.3. Test Scores

Dice score, sensitivity, and positive predictive value (PPV) are metrics that span the range from 0 to 1, with a dice value of 0 signifying complete inaccuracy in the predictions made by the proposed model concerning the ground truth. A dice score of 1 indicates that the suggested model gives completely accurate predictions, matching the ground truth with 100% precision. The performance evaluation of the proposed model is conducted through online testing via the BRATS Challenge 2015 platform, and the resulting test scores are presented in Table 5.4 for reference.

Table 4: BRATS 2015 test scores

Metrics	Dice Scores			Positive Predictive Value			Sensitivity		
Tumor	Complete	Core	Enhancing	Complete	Core	Enhancing	Complete	Core	Enhancing
Testing	0.67	0.57	0.51	0.56	0.59	0.47	0.94	0.63	0.59

4.4. Some Predictions of Trained Model

Below, several predictions made by trained model for brain tumors of varying sizes. Each prediction is accompanied by the display of four input modalities and one corresponding ground truth.

4.4.1 Small-Sized Tumor Prediction

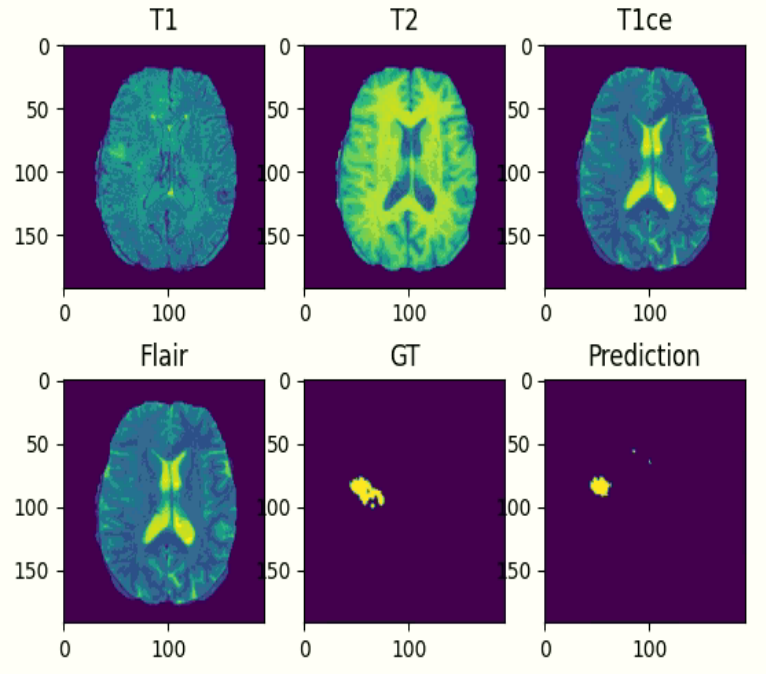

Figure 6: Small-sized tumor prediction

4.4.2 Medium-Sized Tumor Prediction

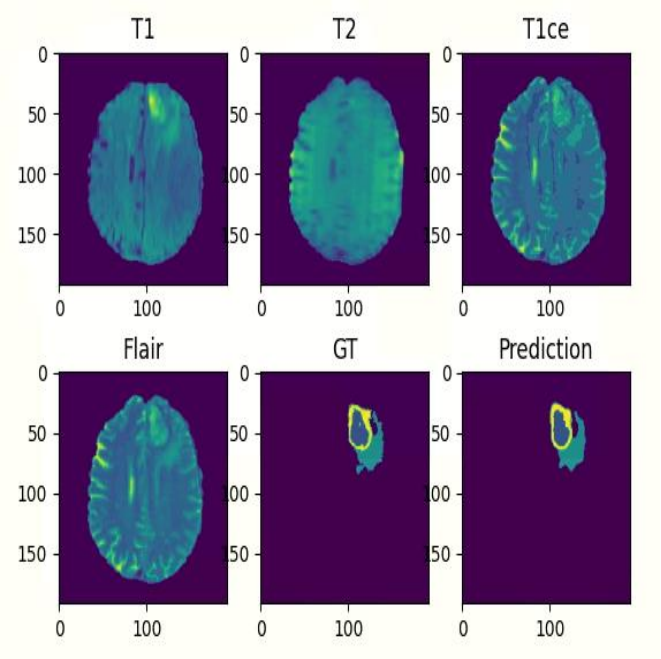

Figure 7: Medium, sized tumor prediction

4.4.3 Large-Sized Tumor Prediction

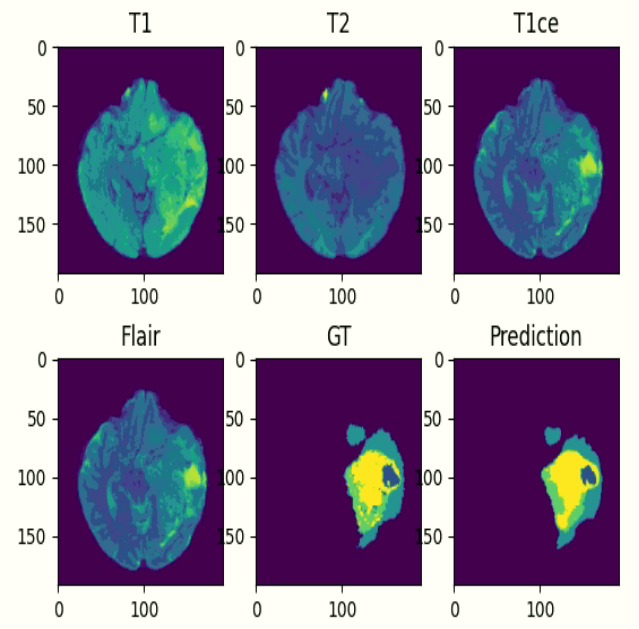

Figure 8: Large-sized tumor prediction

In this section, an in-depth examination of select outcomes generated by proposed model. The findings show that the model has significantly improved accuracy in identifying the complete boundaries of medium and large-sized tumors, as shown in Figures 7 and 8. However, it is noteworthy that the model's performance is relatively less satisfactory when tasked with precisely localizing core and enhancing tumors, primarily owing to the inherent challenge posed by their often indistinct and ambiguous boundaries.

5. Conclusion

The process of brain tumor segmentation and classification unfolds through a structured sequence of five key stages: data acquisition, preprocessing, model training, post-processing, and evaluation. Notably, this study adheres to the same pipeline but omits the post-processing step. The training dataset utilized comprises 220 High-Grade Gliomas (HGGs) extracted from the BraTS 2015 dataset, while the preprocessing phase employs the Min-Max normalization technique. This research introduces an automatic brain tumor segmentation and classification technique rooted in Convolutional Neural Networks (CNNs), drawing inspiration from UNet, ResNet, and attention gates. Extending beyond this inspiration, the study integrates elements such as skip connections, residual connections, gating signals, and attention gates to enhance information propagation. Through the judicious usage of attention gates, the primary goal is to promote focused feature propagation and augment the selection of relevant characteristics. Evaluation of the proposed model is carried out on the BraTS 2015 testing dataset, encompassing 110 Low-Grade Gliomas (LLGs). Experimental findings underscore the promising performance of the model in addressing the challenges of brain tumor segmentation and classification.

References

[1] https://www.cancer.net/cancer-types/brain-tumor/statistics

[2] https://www.brainlab.org/get-educated/brain-tumors/investigate-brain-tumors/how-common-are-brain-tumors/

[3] https://seer.cancer.gov/statfacts/html/brain.html

[4] Pereira, Sérgio, Adriano Pinto, Victor Alves, and Carlos A. Silva. "Brain tumor segmentation using convolutional neural networks in MRI images." *IEEE transactions on medical imaging* 35, no. 5 (2016): 1240-1251.

[5] Lang, R., Zhao, L. and Jia, K., 2016, “October. Brain tumor image segmentation based on convolution neural network”, *9th International Congress on Image and Signal Processing, BioMedical Engineering and Informatics (CISP-BMEI)* (pp. 1402-1406). IEEE.

[6] Saouli, Rachida, Mohamed Akil, and Rostom Kachouri. "Fully automatic brain tumor segmentation using end-to-end incremental deep neural networks in MRI images." *Computer methods and programs in biomedicine* 166 (2018): 39-49.

[7] Dong, Hao, Guang Yang, Fangde Liu, Yuanhan Mo, and Yike Guo. "Automatic brain tumor detection and segmentation using U-Net based fully convolutional networks." In *Medical Image Understanding and Analysis: 21st Annual Conference, MIUA 2017, Edinburgh, UK, July 11–13, 2017, Proceedings 21*, pp. 506-517. Springer International Publishing, 2017.

[8] Wang, Guotai, Wenqi Li, Sébastien Ourselin, and Tom Vercauteren. "Automatic brain tumor segmentation using cascaded anisotropic convolutional neural networks." In *Brainlesion: Glioma, Multiple Sclerosis, Stroke and Traumatic Brain Injuries: Third International Workshop, BrainLes 2017, Held in Conjunction with MICCAI 2017, Quebec City, QC, Canada, September 14, 2017, Revised Selected Papers 3*, pp. 178-190. Springer International Publishing, 2018.

[9] Havaei, Mohammad, Axel Davy, David Warde-Farley, Antoine Biard, Aaron Courville, Yoshua Bengio, Chris Pal, Pierre-Marc Jodoin, and Hugo Larochelle. "Brain tumor segmentation with deep neural networks." *Medical image analysis* 35 (2017): 18-31.

[10] Kamnitsas, Konstantinos, Christian Ledig, Virginia FJ Newcombe, Joanna P. Simpson, Andrew D. Kane, David K. Menon, Daniel Rueckert, and Ben Glocker. "Efficient multi-scale 3D CNN with fully connected CRF for accurate brain lesion segmentation." *Medical image analysis* 36 (2017): 61-78.

[11] Chen, Fujuan, Yi Ding, Zhixing Wu, Dongyuan Wu, and Jinmei Wen. "An improved framework called Du++ applied to brain tumor segmentation." In *2018 15th International Computer Conference on Wavelet Active Media Technology and Information Processing (ICCWAMTIP)*, pp. 85-88. IEEE, 2018.

[12] Isensee, Fabian, Philipp Kickingereder, Wolfgang Wick, Martin Bendszus, and Klaus H. Maier-Hein. "No new-net." In *Brainlesion: Glioma, Multiple Sclerosis, Stroke and Traumatic Brain Injuries: 4th International Workshop, BrainLes 2018, Held in Conjunction with MICCAI 2018, Granada, Spain, September 16, 2018, Revised Selected Papers, Part II 4*, pp. 234-244. Springer International Publishing, 2019.

[13] Sun, Li, Songtao Zhang, Hang Chen, and Lin Luo. "Brain tumor segmentation and survival prediction using multimodal MRI scans with deep learning." *Frontiers in neuroscience* 13 (2019): 810.

[14] McKinley, Richard, Raphael Meier, and Roland Wiest. "Ensembles of densely-connected CNNs with label-

uncertainty for brain tumor segmentation." In *Brainlesion: Glioma, Multiple Sclerosis, Stroke and Traumatic Brain Injuries: 4th International Workshop, BrainLes 2018, Held in Conjunction with MICCAI 2018, Granada, Spain, September 16, 2018, Revised Selected Papers, Part II 4*, pp. 456-465. Springer International Publishing, 2019.

[15] Ding, Yi, Chang Li, Qiqi Yang, Zhen Qin, and Zhiguang Qin. "How to improve the deep residual network to segment multi-modal brain tumor images." *IEEE Access* 7 (2019): 152821-152831.

[16] Wang, Yu, Changsheng Li, Ting Zhu, and Chongchong Yu. "A deep learning algorithm for fully automatic brain tumor segmentation." In *2019 international joint conference on neural networks (IJCNN)*, pp. 1-5. IEEE, 2019.

[17] Wang, Guotai, Wenqi Li, Sébastien Ourselin, and Tom Vercauteren. "Automatic brain tumor segmentation using cascaded anisotropic convolutional neural networks." In *Brainlesion: Glioma, Multiple Sclerosis, Stroke and Traumatic Brain Injuries: Third International Workshop, BrainLes 2017, Held in Conjunction with MICCAI 2017, Quebec City, QC, Canada, September 14, 2017, Revised Selected Papers 3*, pp. 178-190. Springer International Publishing, 2018.

[18] Liu, Di, Hao Zhang, Mingming Zhao, Xiaojuan Yu, Shaowen Yao, and Wei Zhou. "Brain tumor segmention based on dilated convolution refine networks." In *2018 IEEE 16th International Conference on Software Engineering Research, Management and Applications (SERA)*, pp. 113-120. IEEE, 2018.

[19] Qamar, Saqib, Hai Jin, Ran Zheng, and Parvez Ahmad. "3D hyper-dense connected convolutional neural network for brain tumor segmentation." In *2018 14th international conference on semantics, knowledge and grids (SKG)*, pp. 123-130. IEEE, 2018.

[20] Zhao, Xiaomei, Yihong Wu, Guidong Song, Zhenye Li, Yazhuo Zhang, and Yong Fan. "A deep learning model integrating FCNNs and CRFs for brain tumor segmentation." *Medical image analysis* 43 (2018): 98-111.

[21] Zhou, Chenhong, Shengcong Chen, Changxing Ding, and Dacheng Tao. "Learning contextual and attentive information for brain tumor segmentation." In *Brainlesion: Glioma, Multiple Sclerosis, Stroke and Traumatic Brain Injuries: 4th International Workshop, BrainLes 2018, Held in Conjunction with MICCAI 2018, Granada, Spain, September 16, 2018, Revised Selected Papers, Part II 4*, pp. 497-507. Springer International Publishing, 2019.

[22] Myronenko, Andriy. "3D MRI brain tumor segmentation using autoencoder regularization." In *Brainlesion: Glioma, Multiple Sclerosis, Stroke and Traumatic Brain Injuries: 4th International Workshop, BrainLes 2018, Held in Conjunction with MICCAI 2018, Granada, Spain, September 16, 2018, Revised Selected Papers, Part II 4*, pp. 311-320. Springer International Publishing, 2019.

[23] Isensee, Fabian, Philipp Kickingereder, Wolfgang Wick, Martin Bendszus, and Klaus H. Maier-Hein. "No new-net." In *Brainlesion: Glioma, Multiple Sclerosis, Stroke and Traumatic Brain Injuries: 4th International Workshop, BrainLes 2018, Held in Conjunction with MICCAI 2018, Granada, Spain, September 16, 2018, Revised Selected Papers, Part II 4*, pp. 234-244. Springer International Publishing, 2019.

[24] Sharma, Sarang, Sheifali Gupta, Deepali Gupta, Abhinav Juneja, Harsh Khatter, Sapna Malik, and Zelalem Kiros Bitsue. "Deep Learning Model for Automatic Classification and Prediction of Brain Tumor." *Journal of Sensors* 2022 (2022).

[25] Kumar, R. Lokesh, Jagadeesh Kakarla, B. Venkateswarlu Isunuri, and Munesh Singh. "Multi-class brain tumor classification using residual network and global average pooling." *Multimedia Tools and Applications* 80 (2021): 13429-13438.

[26] Rehman, Amjad, Muhammad Attique Khan, Tanzila Saba, Zahid Mehmood, Usman Tariq, and Noor Ayesha. "Microscopic brain tumor detection and classification using 3D CNN and feature selection architecture." *Microscopy Research and Technique* 84, no. 1 (2021): 133-149.

[27] Rajasree, R., C. Christopher Columbus, and C. Shilaja. "Multiscale-based multimodal image classification of brain tumor using deep learning method." *Neural Computing and Applications* 33 (2021): 5543-5553.