https://doi.org/ 10.33472/AFJBS.6.10.2024. 5515-5526

African Journal of Biological Sciences

Customized Deep Neural Network for Brain Tumor Identification and Segmentation Using Biomedical Images

[1]Tarun kumar juluru, [2]E.Kumaraswamy, [3]Sridevi Chitti, [4]Teja Sirapu, [5]Kommabatla Mahender

[1,3] Department of ECE, Kakatiya Institute of Technology and Science, Warangal

[2,5] Department of ECE, Sumathi Reddy Institute of Technology for Women

[4]Sapthagiri NPS University,Bengaluru-560057

Corresponding Author email:kommabatlasharma@gmail.com

Article History
Volume 6, Issue 10, 2024
Received: 22 Jun 2024
Accepted: 29 Jun 2024
doi: ***10.33472/AFJBS.6.10.2024. 5515-5526***

ABSTRACT:

Brain tumor segmentation plays a crucial role in medical image analysis for diagnosis, treatment planning, and monitoring of brain tumor patients, and it is quite complex. To address this, we are introducing a new method for identifying brain tumors using powerful computer techniques called deep neural networks. Deep neural networks (DNNs) have demonstrated remarkable performance in various medical image identification and segmentation tasks. We employ a customized convolutional neural network architecture tailored specifically for the task of brain tumor identification and segmentation. The proposed network is designed to effectively capture spatial information and hierarchical features from the input images. Moreover, we integrate advanced techniques such as residual connections and attention mechanisms to enhance the network's performance. To train the network, we utilize a large dataset of annotated brain MRI scans to learn the complex patterns associated with different types and sizes of brain tumors. The proposed approach offers a reliable and efficient solution for precise delineation of brain tumors from MRI images, potentially aiding clinicians in treatment planning and patient care.

Keywords: Biomedical images, Brain Tumor, Image Segmentation, Convolutional Neural Networks

1. Introduction

A tumor is an abnormal mass of tissue formed when cells grow and divide at rates that are faster than usual, or when cells don't die when they should. A brain tumor is a growth of cells in or near the brain. Brain tumors can occur in the brain tissue itself or in nearby locations such as nerves, the pituitary gland, the pineal gland, and the membranes that cover the surface of the brain. Brain tumors can originate in the brain, and these are called primary brain tumors. Sometimes, cancer spreads to the brain from other parts of the body, forming secondary brain tumors, also known as metastatic brain tumors. Many different types of primary brain tumors exist. Some brain tumors are not cancerous; these are called noncancerous or benign brain tumors. Noncancerous brain tumors may grow over time and press on the brain tissue. Other brain tumors are brain cancers, also called malignant brain tumors. Brain cancers may grow quickly, and the cancer cells can invade and destroy the brain tissue. Brain tumors range in size from very small to very large. Some brain tumors are found when they are very small because they cause symptoms that you notice right away [1]. Other brain tumors grow very large before they are discovered.Brain tumors also can happen in nerves, the pituitary gland and the pineal gland.Brain tumors happen when cells in or near the brain get changes in their DNA. A cell's DNA holds the instructions that tell the cell what to do. The changes tell the cells to grow quickly and continue living when healthy cells would die as part of their natural life cycle. This makes a lot of extra cells in the brain. The cells can form a growth called a tumor.It's not clear what causes the DNA changes that lead to brain tumors. For many people with brain tumors, the cause is never known. Sometimes parents pass DNA changes to their children. The changes can increase the risk of having a brain tumor. These hereditary brain tumors are rare. If you have a family history of brain tumors, talk about it with your health care provider. You might consider meeting with a health care provider trained in genetics to understand whether your family history increases your risk of having a brain tumor.

There is no way to prevent brain tumors, and developing one is not caused by anything you did. People at increased risk of brain tumors might consider screening tests. While screening doesn't prevent brain tumors, it can help detect them when they are small and more treatable. Diagnosing a brain tumor starts with a physical exam and a review of your medical history. The exam includes a detailed neurological evaluation, during which your doctor will test the integrity of your cranial nerves, which originate in your brain. Your doctor will use an ophthalmoscope to look inside your eyes, shining a light through your pupils onto your retinas. This allows your doctor to observe how your pupils react to light and to check for any

swelling of the optic nerve. Increased pressure inside the skull can cause changes in the optic nerve.

Various approaches are used for diagnosing brain tumors using different imaging modalities. CT scans provide a more detailed image of your body than X-rays and can be done with or without contrast. Contrast in a CT scan of the head is achieved using a special dye that helps doctors see certain structures, like blood vessels, more clearly. MRI scans can also use a special dye to help detect tumors. Unlike CT scans, MRIs do not use radiation and generally provide more detailed images of the brain's structures. During an MRI, a dye is injected into an artery, usually in the groin area, and travels to the brain's arteries. This allows doctors to see the blood supply to the tumors, which is useful during surgery. Brain tumors can cause breaks or fractures in the bones of the skull, and specific X-rays can detect these occurrences. X-rays can also identify calcium deposits within a tumor, which may appear in the bloodstream if the cancer has spread to the bones. A biopsy involves obtaining a small piece of the tumor, which a neuropathologist examines to determine whether the tumor cells are benign or malignant and whether the cancer originated in the brain or another part of the body [2].

2. Materials and Methods

In the process of identification and segmentation of brain tumor is an essential to reduce the mortality rate and increase the life span of the patients. In this connection, we proposed a customized deep CNN to identify and segment the brain tumor. For this work, the BraTS-PEDs 2023 dataset includes a retrospective multi-institutional cohort of conventional/structural magnetic resonance imaging (MRI) sequences, including pre- and post-gadolinium T1-weighted (labeled as T1 and T1CE), T2-weighted (T2), and T2-weighted fluid attenuated inversion recovery (T2-FLAIR) images, from 228 pediatric high-grade glioma [3]. These conventional multiparametric MRI (mpMRI) sequences are commonly acquired as part of standard clinical imaging for brain tumors as shown in Figure 1.

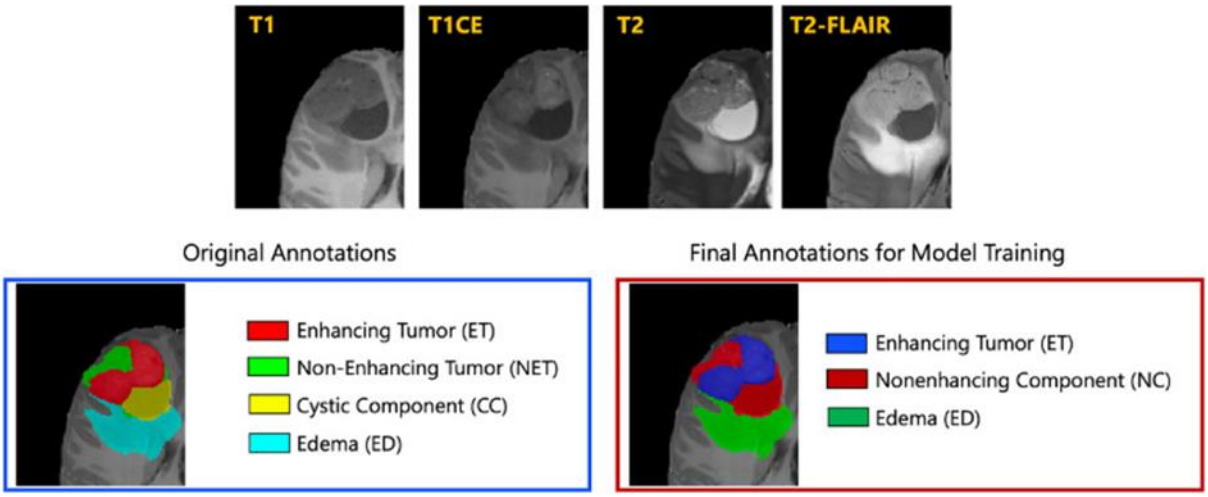


Figure 1. Illustrative example of tumor subregions in pediatric brain tumors.

Image panels with the annotated tumor subregions along with mpMRI structural scans (T1, T1CE, T2, and T2-FLAIR). The left-most side image on the bottom panel with the overlaid annotations showcases the original tumor subregions, i.e., enhancing tumor (ET - red), non-enhancing tumor (NET - green), cystic component (CC - yellow), and edema (ED - teal). The image on the right-hand side of the bottom panel with the overlaid annotations on the T2 sequence demonstrates the tumor subregions provided to the BraTS-PEDs 2023 participants: enhancing tumor (ET), no enhancing component (NC), and edema (ED).

2.1 Relevant studies

In 2019, J. Nalepa, M. Marcinkiewicz, and M. Kawulok [4] discussed data augmentation techniques for brain tumor segmentation, specifically focusing on advancements in MRI data augmentation using the BraTS 2018 dataset. Their work highlights the potential to enhance supervised learning algorithms through various data augmentation strategies and identifies exciting future research areas for creating high-quality synthetic brain tumor instances to improve the generalization skills of deep learning models. The study, centered on the BraTS dataset, explores the promising possibilities of the proposed techniques and includes published image information.The study examines which data augmentation approaches were used and their impact on the performance of supervised learning models. Finally, it highlights the most promising research directions for synthesizing high-quality artificial brain tumor examples to enhance the generalization abilities of deep learning models.

In 2019, MK Abd-Ellah, AI Awad, and AAM Khalaf [5] discussed the diagnosis of brain tumors from MRI images and assessed both conventional and deep machine-learning techniques for diagnosing brain tumors and examined the significant accomplishments based on performance measurement metrics of the implemented algorithms in the three diagnostic stages. The review highlighted the acquired knowledge as a guide for future investigations

using the BraTS 2018 dataset. The presented work consists a two-stage CAD system developed for the automatic detection and classification of brain tumors using magnetic resonance images (MRIs).In the first stage, the system classifies brain tumor MRIs into normal and abnormal images. In the second stage, it classifies the type of tumor as benign (noncancerous) or malignant (cancerous) from the abnormal MRIs.The proposed CAD system combines several computational methods: MRI image segmentation using K-means clustering, feature extraction with discrete wavelet transforms (DWT), and feature reduction through principal component analysis (PCA).The two-stage classification is conducted using a support vector machine (SVM). Performance evaluation of the proposed CAD system has shown promising results using a non-standard MRI database.

In the 2023, Ranjbarzadeh et al. [6] analyzed recent developments in data augmentation methods used for brain tumor magnetic resonance images (MRIs). They examined papers submitted to the Multimodal Brain Tumor Segmentation Challenge (BraTS 2018 edition) to determine which data augmentation approaches were employed and how they affected the performance of supervised learning models. Brain tumors have become a significant medical concern in recent years due to their high fatality rate. Radiologists typically segment tumors manually, a process that is time-consuming, prone to errors, and expensive.

In 2022, S Das L Saba, JS Suri, S Saxena et al [7] employed a PRISMA methodology to classify 75 pertinent research works into four categories, namely convolutionalneuralnetwork (CNN), encoder-decoder (ED), transferlearning (TL), and hybrid DL (HDL)-based architectures. This study analyzed 32 attributesrelated to artificialintelligence. It established a threshold for bias detection to categorize studies as having low, moderate, or high levels of bias. According to the performance ranking, TL architecture is superior, followed by ED, CNN, and HDL in descendingorder.

Ghaffari et al. [8], 2020conducted a comprehensive analysis of the development of automated models utilized for brain tumor segmentation through the integration of multimodal MR images. The study involved a comparison of various methods, and the proposed models were evaluated through their application to the well-known benchmark BraTS 2012–2018 challenges. Reliable brain tumor segmentation is essential for accurate diagnosis and treatment planning. Since manual segmentation of brain tumors is a highly time-consuming, expensive and subjective task, practical automated methods for this purpose are greatly appreciated. But since brain tumors are highly heterogeneous in terms of location, shape, and size, developing automatic segmentation methods has remained a challenging task over

decades. This method aims to review the evolution of automated models for brain tumor segmentation using multimodal MR images.

In 2017, Kapoor and Thakur [9] focused on summarizing conventional techniques for brain tumor segmentation. However, they did not provide a comprehensive technical analysis or discussion on segmentation techniques based on deep learning. Biomedical Image Processing is a rapidly growing and demanding field, encompassing various imaging methods such as CT scans, X-rays, and MRI. These techniques enable the detection of even the smallest abnormalities in the human body.

In the year 2022, E.S. Biratu [10] provided an overview of segmentation and classification algorithms, discussing three major techniques (region growing, shallow machine learning, and deep learning) and various technical aspects such as their strengths and weaknesses, as well as pre- and post-processing techniques.A brain Magnetic Resonance Imaging (MRI) scan of a single individual consists of several slices across the 3D anatomical view. Therefore, manually segmenting brain tumors from MR images is a challenging and time-consuming task.Consequently, there is extensive literature on segmentation using region growing, traditional machine learning, and deep learning methods.Numerous tasks have also been performed in the area of brain tumor classification into their respective histological types, yielding impressive performance results**.**

2.2 Proposed System

There are two main parts to a CNN architecture as shown in Figure 2.

- A convolution tool that separates and identifies the various features of the image for analysis in a process called as Feature Extraction.
- The network of feature extraction consists of many pairs of convolutional or pooling layers.
- A fully connected layer that utilizes the output from the convolution process and predicts the class of the image based on the features extracted in previous stages [11].
- This CNN model of feature extraction aims to reduce the number of features present in a dataset. It creates new features which summarises the existing features contained in an original set of features. There are many CNN layers as shown in the CNN architecture diagram.

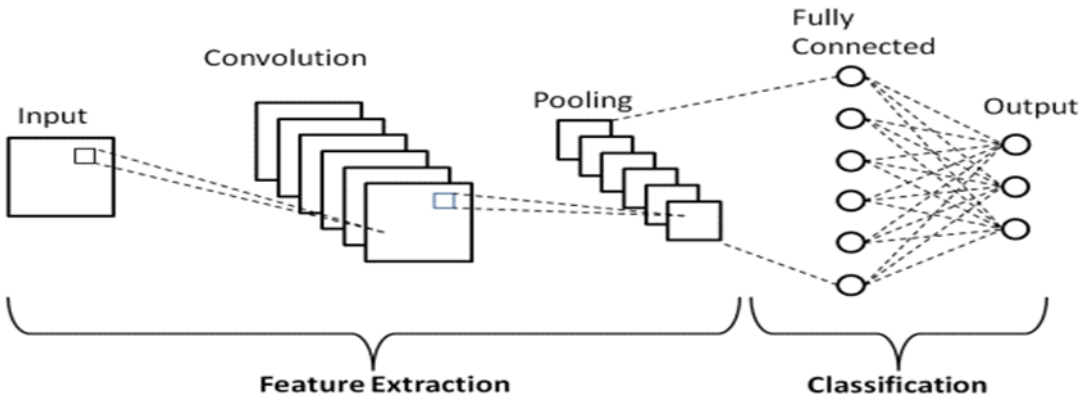


Figure 2. Architecture Of CNN

There are three types of layers that make up the CNN which are the convolutional layers, pooling layers, and fully-connected (FC) layers. When these layers are stacked, a CNN architecture will be formed. In addition to these three layers, there are two more important parameters which are the dropout layer and the activation function which are defined below.

This layer is the first layer that is used to extract the various features from the input images. In this layer, the mathematical operation of convolution is performed between the input image and a filter of a particular size MxM. By sliding the filter over the input image, the dot product is taken between the filter and the parts of the input image with respect to the size of the filter (MxM). The output is termed as the Feature map which gives us information about the image such as the corners and edges. Later, this feature map is fed to other layers to learn several other features of the input image.The convolution layer in CNN passes the result to the next layer once applying the convolution operation in the input. Convolutional layers in CNN benefit a lot as they ensure the spatial relationship between the pixels is intact.

In most cases, a Convolutional Layer is followed by a Pooling Layer [12]. The primary aim of this layer is to decrease the size of the convolved feature map to reduce the computational costs. This is performed by decreasing the connections between layers and independently operates on each feature map. Depending upon method used, there are several types of Pooling operations. It basically summarises the features generated by a convolution layer.In Max Pooling, the largest element is taken from feature map. Average Pooling calculates the average of the elements in a predefined sized Image section. The total sum of the elements in the predefined section is computed in Sum Pooling. The Pooling Layer usually serves as a bridge between the Convolutional Layer and the FC Layer.This CNN model generalises the features extracted by the convolution layer, and helps the networks to

recognise the features independently. With the help of this, the computations are also reduced in a network.

The Fully Connected (FC) layer consists of the weights and biases along with the neurons and is used to connect the neurons between two different layers. These layers are usually placed before the output layer and form the last few layers of a CNN Architecture. In this, the input image from the previous layers is flattened and fed to the FC layer. The flattened vector then undergoes few more FC layers where the mathematical functions operations usually take place. In this stage, the classification process begins to take place. The reason two layers are connected is that two fully connected layers will perform better than a single connected layer. These layers in CNN reduce the human supervision.

Usually, when all the features are connected to the FC layer, it can cause overfitting in the training dataset. Overfitting occurs when a particular model works so well on the training data causing a negative impact in the model's performance when used on a new data. To overcome this problem, a dropout layer is utilised wherein a few neurons are dropped from the neural network during training process resulting in reduced size of the model. On passing a dropout of 0.3, 30% of the nodes are dropped out randomly from the neural network.Dropout results in improving the performance of a machine learning model as it prevents overfitting by making the network simpler. It drops neurons from the neural networks during training.

Finally, one of the most important parameters of the CNN model is the activation function. They are used to learn and approximate any kind of continuous and complex relationship between variables of the network. In simple words, it decides which information of the model should fire in the forward direction and which ones should not at the end of the network. It adds non-linearity to the network. There are several commonly used activation functions such as the ReLU, SoftMax, tan and the Sigmoid functions. Each of these functions have a specific usage. For a binary classification CNN model, sigmoid and SoftMax functions are preferred an for a multi-class classification, generally SoftMax us used. In simple terms, activation functions in a CNN model determine whether a neuron should be activated or not. It decides whether the input to the work is important or not to predict using mathematical operations.

Deep neural networks (DNNs), particularly convolutional neural networks (CNNs), have demonstrated superior accuracy in identifying and segmenting brain tumors compared to traditional image processing techniques. They can capture complex patterns and features in medical images, leading to precise delineation of tumor boundaries.DNNs enable the

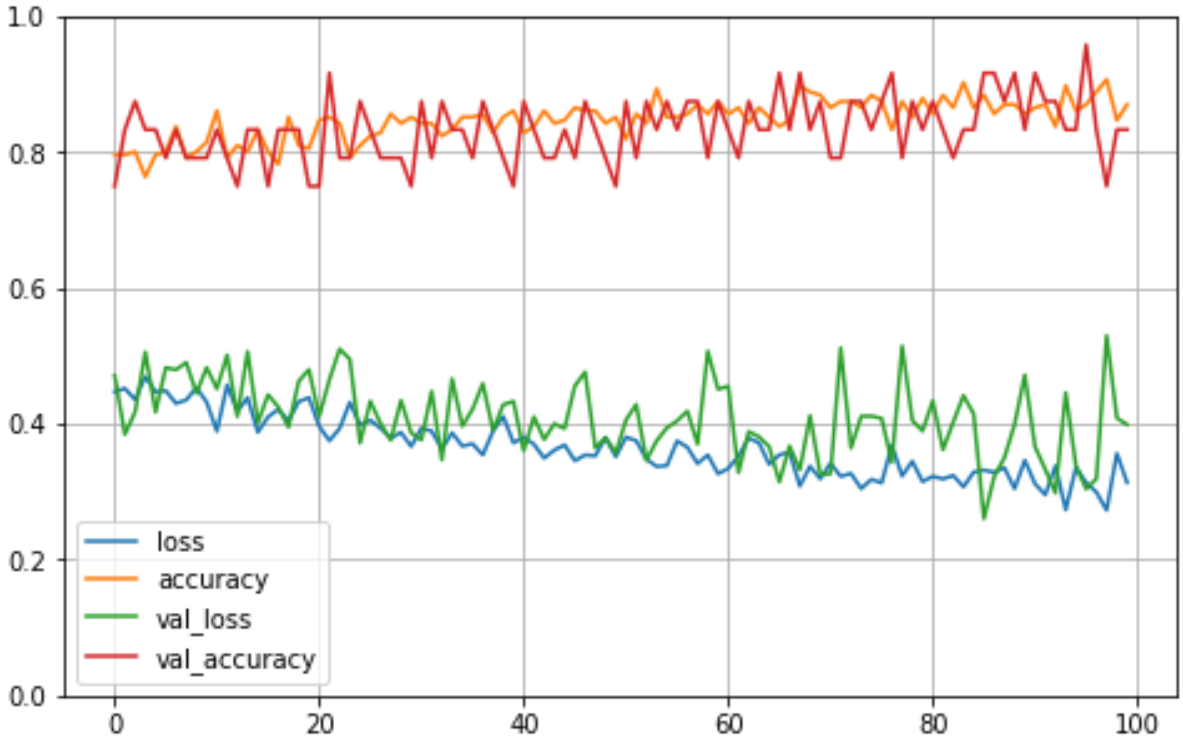
automation of the segmentation process, reducing the need for manual intervention by radiologists and clinicians. This can save significant time and reduce the likelihood of human error.Automated segmentation using DNNs provides consistent results. Unlike human experts, whose performance may vary, DNNs offer uniform performance across different datasets and conditions.Once trained, DNNs can process large volumes of medical images quickly, making them scalable for use in hospitals and research institutions dealing with numerous patient scans.Deep learning models can be adapted and fine-tuned to different types of imaging modalities (such as MRI, CT scans) and different types of tumors, enhancing their versatility.DNNs can integrate imaging data with other clinical information (like genetic data, patient history), potentially providing a more comprehensive analysis and aiding in personalized treatment planning.Deep neural networks improve the accuracy and speed of brain tumor detection in MRI And CT scans, aiding early diagnosis.Segmentation provides detailed tumor maps, assisting surgeons and radiotherapists in precise treatment planning.Regular scans with automated segmentation track tumor growth and treatment response over time.Segmentation data supports tailored treatment plans based on individual tumor characteristics and patient data.Segmented tumor datasets enable extensive research on tumor behavior, treatment outcomes, and the development of new therapies.Segmented images serve as educational tools for medical students and simulation models for surgical training.

3. Results and Discussion

For brain tumor segmentation, we employed a tailored deep convolutional neural network and conducted the experiment using the Google Colab platform. The experimental setup involved several steps:

- Initializing the libraries and authorizing access to Google Drive.
- Carrying out the segmentation task, which included data loading, preprocessing, model creation (a customized CNN), as well as training, validation, and testing.
- Executing the code cells to train the model on the provided dataset.
- Assessing the model's performance using evaluation metrics such as accuracy, precision, recall, and F1 score.
- Testing the trained model on new MRI images to evaluate its effectiveness in detecting brain tumors.
- If the model performs satisfactorily, it can be deployed for practical use, such as in a healthcare setting for automated tumor detection.

- Following these procedures in Google Colab enables the creation and execution of



code for brain tumor detection using Python and deep learning techniques

Figure 3. Training loss and accuracy curves along with the validation loss and accuracy curves.

In Figure 3, the plot shows the relationship between the number of epochs and both loss and accuracy. The x-axis represents the number of epochs, ranging from 0 to 100, where an epoch is a complete pass through the entire training dataset. The y-axis, ranging from 0.4 to 1.0, measures two key performance metrics: loss and accuracy.Lower loss values are preferable, and the blue line indicates that loss decreases over time, which is a positive outcome. Higher accuracy values are better, and the orange line shows that accuracy increases over time, which is also favorable. The green ('val loss') and red ('val accuracy') lines represent these metrics on a validation dataset, which is a separate set of data not used for training. These lines illustrate how well the model is expected to perform on new, unseen data.The fluctuations in the 'val loss' and 'val accuracy' lines suggest that the model's performance on the validation set is less stable than on the training set. This could indicate overfitting if the validation metrics are worse than the training metrics, meaning the model might be learning the training data too well and not generalizing effectively to new data.Overall, the graph serves as a tool to monitor and improve the training process of a machine learning model,

ensuring it learns effectively and can make accurate predictions on new data which nearly 90 to 95%.

4. Conclusion

We propose an ensemble of a Convolutional Neural Network (CNN) for the task of brain tumor segmentation on multimodal MRI data. By combining the outputs of two networks through variable ensemble. we achieve competitive classification accuracy on the BraTS 2019 validation set. Our method outperforms state-of-the-art techniques, yielding mean Dice scores of 0.750, 0.906, and 0.846 on enhancing tumor, whole tumor, and tumor core, respectively. We explored various networks and their combinations before opting for the CNN architecture. Additionally, we experimented with different CNN variants by altering the employed layers, but this did not lead to performance improvement. While our approach demonstrates favorable performance for whole tumor and tumor core classes, enhancing tumor segmentation accuracy requires enhancement.

However, certain limitations persist in our current work. Firstly, our proposed segmentation ensemble is solely evaluated on the official validation set of the challenge. Further validation of the method's robustness can be achieved by testing on separate clinical MRI data, independent of the challenge. Secondly, we did not extensively preprocess the dataset or postprocess the results. Postprocessing methods, such as utilizing conditional random fields, have been demonstrated to enhance segmentation accuracy. Nevertheless, our proposed ensemble demonstrates efficient and robust tumor segmentation across multiple regions. In future work, we aim to incorporate image processing (both pre- and postprocessing) into the ensemble, along with further hyperparameter tuning

REFERENCE

1. McFaline-Figueroa, J. Ricardo, and Eudocia Q. Lee. "Brain tumors." The American journal of medicine 131.8 (2018): 874-882.
2. Zhang, Dingwen, et al. "Cross-modality deep feature learning for brain tumor segmentation." Pattern Recognition 110 (2021): 107562.
3. Kazerooni, Anahita Fathi, et al. "The Brain Tumor Segmentation in Pediatrics (BraTS-PEDs) Challenge: Focus on Pediatrics (CBTN-CONNECT-DIPGR-ASNR-MICCAI BraTS-PEDs)." arXiv preprint arXiv:2404.15009 (2024).
4. Nalepa, Jakub, Michal Marcinkiewicz, and Michal Kawulok. "Data augmentation for brain-tumor segmentation: a review." Frontiers in computational neuroscience 13 (2019): 83.

5. Abd-Ellah, Mahmoud Khaled, et al. "A review on brain tumor diagnosis from MRI images: Practical implications, key achievements, and lessons learned." Magnetic resonance imaging 61 (2019): 300-318.
6. Ranjbarzadeh, Ramin, et al. "Brain tumor segmentation of MRI images: A comprehensive review on the application of artificial intelligence tools." Computers in biology and medicine 152 (2023): 106405.
7. Das, Suchismita, et al. "An artificial intelligence framework and its bias for brain tumor segmentation: A narrative review." Computers in biology and medicine 143 (2022): 105273.
8. Ghaffari, Mina, Arcot Sowmya, and Ruth Oliver. "Automated brain tumor segmentation using multimodal brain scans: a survey based on models submitted to the BraTS 2012–2018 challenges." IEEE reviews in biomedical engineering 13 (2019): 156-168.
9. Kapoor, Luxit, and Sanjeev Thakur. "A survey on brain tumor detection using image processing techniques." 2017 7th international conference on cloud computing, data science & engineering-confluence. IEEE, 2017.
10. Biratu, Erena Siyoum, et al. "A survey of brain tumor segmentation and classification algorithms." Journal of Imaging 7.9 (2021): 179.
11. Kumaraswamy, Eelandula, Sumit Kumar, and Manoj Sharma. "An invasive ductal carcinomas Breast Cancer Grade classification using an ensemble of convolutional neural networks." Diagnostics 13.11 (2023): 1977.
12. Sharma, Shallu, Rajesh Mehra, and Sumit Kumar. "Optimised CNN in conjunction with efficient pooling strategy for the multi-classification of breast cancer." IET Image Processing 15.4 (2021): 936-946.