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Deep Learning for Precise Brain Tumor Segmentation from MRI

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Abstract : Understanding the course of a disease is greatly aided by the automated segmentation of brain tumors from multimodal MR images, especially given the complexity of gliomas. Precise segmentation methods are crucial to address this problem by classifying tumors into intratumoral classes. When compared to conventional computer vision techniques, deep learning algorithms—most notably Convolutional Neural Networks (CNNs)—have proven superior in semantic segmentation tasks. In our research, we propose employing the U-Net architecture for brain tumor segmentation, a widely acknowledged and effective approach in biomedical image analysis. To evaluate the model's effectiveness, we assessed its performance across several key metrics, including accuracy, dice score, sensitivity, specificity, Intersection over Union (IoU), among others. These metrics provide a comprehensive understanding of the model's segmentation accuracy and robustness, enabling us to gauge its capability in accurately delineating tumor sub-regions and overall performance. By leveraging the U-Net architecture, our aim is to generate precise segmentation maps that capture the spatial distribution and characteristics of brain tumors across different modalities. Our study underscores the significance of harnessing advanced deep learning techniques to improve the accuracy and reliability of brain tumor segmentation, thereby facilitating enhanced clinical decision-making and patient care.

IndexTerms **- Brain Tumor, Image Segmentation, CNN, U-Net, MRI, Deep Learning**

I. INTRODUCTION

The recent integration of deep learning and machine learning algorithms has propelled a remarkable revolution in the field of medical imaging. These developments have had a major impact on the diagnosis, classification, and prognosis of a number of illnesses, including brain tumors. Gliomas, the most prevalent kind of adult brain tumor, start out as glial cells and spread to nearby tissues. The two main subtypes of gliomas are high-grade glioblastoma (HGG) and low-grade glioblastoma (LGG). The manual analysis of magnetic resonance imaging (MRI) modalities for the purpose of producing quantitative information presents difficulties, especially when it comes to segmenting 3D modalities because of errors and variations, especially when tumors exhibit variations in size, shape, and location. For the purposes of disease diagnosis, treatment planning, monitoring, and clinical procedures, it is crucial to accurately segment brain tumors from neuroimaging modalities. But because tumor characteristics vary so much and it can be difficult to tell tumor tissue from healthy brain tissue, this task is complicated. To tackle this challenge, it is imperative to integrate data from multiple MRI modalities, including T1-weighted MRI (T1), T1-weighted MRI with contrast (T1c), T2-weighted MRI (T2), and Fluid-Attenuated Inversion Recovery (FLAIR). Various convolutional neural network (CNN) architectures have been used for automatic segmentation of MRI images.

The advent of challenges like Brain Tumor Segmentation (BraTS) has facilitated this process by providing annotated 3D MRI images. In this study, we aim to explore the efficacy of a 2D UNET model for brain tumor segmentation, leveraging the BraTS 2020 dataset. Our focus is solely on this benchmark, aiming to provide insights into the performance of our proposed model in this specific context. Moreover, the extensive application of artificial intelligence (AI) and deep learning across various domains, combined with its potential to address the challenges posed by brain tumors, underscores its significance in improving medical diagnostics.

II. LITERATURE REVIEW

In a study by Pereira et al. [1], researchers introduced a new method for automatically detecting and outlining gliomas, which are serious brain tumors, using MRI scans. They used a special type of computer system called Convolutional Neural Networks (CNNs) with small 3x3 grids to do this. The researchers explained the challenges of dealing with the different shapes and sizes of brain tumors and emphasized the importance of accurately identifying them.

Their method was tested on large MRI databases from 2013 and 2015 and performed very well. It was among the top-performing methods in identifying the different parts of tumors. In a competition called the BraTS-2015 Challenge, their method achieved high scores, particularly in a measure called the Dice Similarity Coefficient, which indicates how well it outlined the entire tumor, its core, and the parts that stand out.

Meanwhile, in another study led by Pravitasari et al. [2], researchers focused on a different aspect of brain tumor detection in MRI scans. They developed a system called UNet-VGG16, which combines two types of models and uses a technique called transfer learning to simplify the process.

Their study highlighted the importance of achieving high accuracy when dealing with brain tumors in medical procedures. They aimed to determine which parts of the MRI scans showed the tumor and which did not. Their system achieved a very high accuracy rate of 96.1% when tested on their learning data, and when validated with other data, it still showed strong performance in identifying tumor areas, with an accuracy of about 95.69%.

Both studies represent significant advancements in utilizing MRI scans to detect brain tumors. Pereira's team demonstrated the effectiveness of their CNN-based method with small grids in accurately identifying gliomas, while Pravitasari's team showcased the potential of combining different models for improved accuracy in tumor detection in MRI scans. These findings underscore the importance of leveraging advanced computer systems to enhance the diagnosis and treatment of brain tumors using MRI technology.

III. DATASET DESCRIPTION

The BraTS (Brain Tumor Segmentation) challenge, which has been held annually since, continued through the years as part of the MICCAI conference. The data used in this competition were gathered from various institutions utilizing different MRI scanners. The organizers pre-processed the data by co-registering them to an exact anatomical template, ensuring consistent resolution ($1mm^3$), and skull stripping. This study uses the BraTS 2020 dataset, like its predecessors which consists of 3D MRI brain scans focusing on a specific type of brain tumor called Glioma. The dataset included four distinct MRI modalities: native (T1), T2-weighted (T2), post-contrast T1-weighted (T1ce), and fluid-attenuated inversion recovery (FLAIR). Each MRI modality comprised 155 slices per volume. For segmentation tasks, the annotations integrated three regions: the whole tumor (labels 1, 2, and 4), the tumor core (labels 1 and 4), and the enhanced tumor (label 4). The BraTS 2020 dataset comprises a total of 369 patients, with 293 diagnosed with High-Grade Glioma (HGG) and 76 with Low-Grade Glioma (LGG). Each patient's data include multiple MRI modalities, namely native, T2-weighted, post-contrast T1-weighted, and FLAIR, with 155 slices per volume for each modality. This dataset, with its comprehensive patient representation and rich imaging data, serves as a valuable resource for advancing.

IV. SYSTEM REQUIREMENTS

A. Hardware Requirements:

1. Minimum 8GB RAM
2. Hard Disk: 512 GB or Above
3. Processor: Intel Core i5 or above
4. GPU: NVIDIA RTX 2050 or above

B. Software Requirements:

1. Operating system: Windows / Linux / Mac OS
2. Anaconda or VS Code IDE

C. Libraries:

1. Streamlit
2. Numpy
3. Pandas
4. Nibabel
5. OpenCV

V. METHODOLOGY

In this study the U-Net architecture of CNN has been used for the Brain Tumor Segmentation. The data is loaded into the main memory with the help of Data Generator. The BraTs20 dataset will be split into train, test and validation sets which will be fed to our U-Net model. This trained model will be evaluated with the performance metrics. Figure 1 will depict the flow of the model.

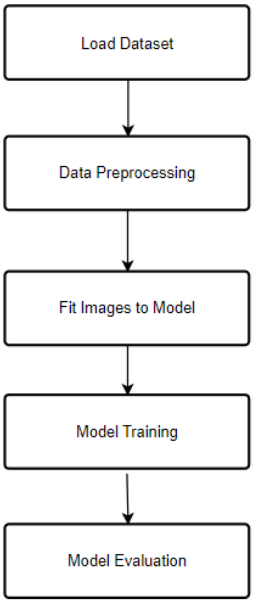

Fig. 1: Flow of the model

1. U-Net Model Layers

Figure 2 shows the model summary of the U-Net architecture for the brain tumor segmentation.

Model: "model"

Layer (type)	Output Shape	Param #	Connected to
input_1 (InputLayer)	[(None, 128, 128, 2)]	0	[]
conv2d (Conv2D)	(None, 128, 128, 32)	608	['input_1[0][0]']
conv2d_1 (Conv2D)	(None, 128, 128, 32)	9248	['conv2d[0][0]']
max_pooling2d (MaxPooling2D)	(None, 64, 64, 32)	0	['conv2d_1[0][0]']
conv2d_2 (Conv2D)	(None, 64, 64, 64)	18496	['max_pooling2d[0][0]']
conv2d_3 (Conv2D)	(None, 64, 64, 64)	36928	['conv2d_2[0][0]']
max_pooling2d_1 (MaxPooling2D)	(None, 32, 32, 64)	0	['conv2d_3[0][0]']
conv2d_4 (Conv2D)	(None, 32, 32, 128)	73856	['max_pooling2d_1[0][0]']
conv2d_5 (Conv2D)	(None, 32, 32, 128)	147584	['conv2d_4[0][0]']
max_pooling2d_2 (MaxPooling2D)	(None, 16, 16, 128)	0	['conv2d_5[0][0]']
conv2d_6 (Conv2D)	(None, 16, 16, 256)	295168	['max_pooling2d_2[0][0]']
conv2d_7 (Conv2D)	(None, 16, 16, 256)	590080	['conv2d_6[0][0]']
max_pooling2d_3 (MaxPooling2D)	(None, 8, 8, 256)	0	['conv2d_7[0][0]']
conv2d_8 (Conv2D)	(None, 8, 8, 512)	1180160	['max_pooling2d_3[0][0]']
conv2d_9 (Conv2D)	(None, 8, 8, 512)	2359808	['conv2d_8[0][0]']
dropout (Dropout)	(None, 8, 8, 512)	0	['conv2d_9[0][0]']
up_sampling2d (UpSampling2D)	(None, 16, 16, 512)	0	['dropout[0][0]']
conv2d_10 (Conv2D)	(None, 16, 16, 256)	524544	['up_sampling2d[0][0]']
concatenate (Concatenate)	(None, 16, 16, 512)	0	['conv2d_7[0][0]', 'conv2d_10[0][0]']
conv2d_11 (Conv2D)	(None, 16, 16, 256)	1179904	['concatenate[0][0]']
conv2d_12 (Conv2D)	(None, 16, 16, 256)	590080	['conv2d_11[0][0]']
up_sampling2d_1 (UpSampling2D)	(None, 32, 32, 256)	0	['conv2d_12[0][0]']
conv2d_13 (Conv2D)	(None, 32, 32, 128)	131200	['up_sampling2d_1[0][0]']
concatenate_1 (Concatenate)	(None, 32, 32, 256)	0	['conv2d_5[0][0]', 'conv2d_13[0][0]']
conv2d_14 (Conv2D)	(None, 32, 32, 128)	295040	['concatenate_1[0][0]']
conv2d_15 (Conv2D)	(None, 32, 32, 128)	147584	['conv2d_14[0][0]']
up_sampling2d_2 (UpSampling2D)	(None, 64, 64, 128)	0	['conv2d_15[0][0]']
conv2d_16 (Conv2D)	(None, 64, 64, 64)	32832	['up_sampling2d_2[0][0]']
concatenate_2 (Concatenate)	(None, 64, 64, 128)	0	['conv2d_3[0][0]', 'conv2d_16[0][0]']
conv2d_17 (Conv2D)	(None, 64, 64, 64)	73792	['concatenate_2[0][0]']
conv2d_18 (Conv2D)	(None, 64, 64, 64)	36928	['conv2d_17[0][0]']
up_sampling2d_3 (UpSampling2D)	(None, 128, 128, 64)	0	['conv2d_18[0][0]']
conv2d_19 (Conv2D)	(None, 128, 128, 32)	8224	['up_sampling2d_3[0][0]']
concatenate_3 (Concatenate)	(None, 128, 128, 64)	0	['conv2d_1[0][0]', 'conv2d_19[0][0]']
conv2d_20 (Conv2D)	(None, 128, 128, 32)	18464	['concatenate_3[0][0]']
conv2d_21 (Conv2D)	(None, 128, 128, 32)	9248	['conv2d_20[0][0]']
conv2d_22 (Conv2D)	(None, 128, 128, 4)	132	['conv2d_21[0][0]']

Total params: 7759908 (29.60 MB)
Trainable params: 7759908 (29.60 MB)
Non-trainable params: 0 (0.00 Byte)

Fig. 2: U-Net Model Summary

Two convolutional layers and a max-pooling layer come first in the network architecture, which efficiently reduces spatial dimensions while boosting the number of feature channels. Deeper layers are added as the encoding process proceeds, eventually hitting a bottleneck where the feature channels increase but the spatial dimensions are drastically decreased. After that, the decoding path starts, which consists of concatenating matching feature maps from the encoding path with layers that have been up-sampled. This procedure reduces the number of feature channels while progressively restoring spatial dimensions. The network is able to maintain fine-grained information that are essential for precise segmentation because of the skip links between the encoding and decoding paths. Ultimately, each pixel in the output layer's segmentation map is assigned to one of the four classes, and it has the same dimensions as the input image.

2. Dataset Pre-Processing

There are four different MRI modalities in the datasets. The CNN model requires a lot of processing power to train with all those modalities. As a result, the proposed U-net considers FLAIR and T1ce as input. The majority of the useful data in this collection is found in FLAIR and T1ce. However, every MRI modality has an extra black background that takes up computational resources and is not needed for the training phase. This is why the images are divided into multiple parts (100 slices for 2D U-net) in order to reduce background noise and highlight the informative areas of the pictures. Images from the input and output are both

scaled to fit the U-net model's specifications. One hot encoding was performed for the segmented images. The dataset was then divided into train, validation, and test datasets, with corresponding ratios of 68%, 20%, and 12% of the total dataset.

3. Experimental Setup

The model was developed with Keras and Tensorflow by using the Hyperparameters like the 60 Number of epochs with batch size as 1. The Adam optimizer along with the Categorical Cross Entropy as a loss function is used for the model.

4. Performance Metrics

The efficiency of the model is evaluated based on various performance metrics. The most widely used performance metrics for the medical image segmentation is the Dice Coefficient. Other metrics such as Accuracy, Precision, Sensitivity, Specificity and Mean-IoU are also computed to evaluate the performance of the model. A higher score in each of the metrics depicts the better performance of the model.

In the equations, True Positive (TP) indicates a match between the expected and real tumor. A match between the expected and actual non-tumor is indicated by a True Negative (TN). False Negative (FN) indicates that the expected non-tumor is the real tumor region, while False Positive (FP) indicates that the projected tumor area is not the actual tumor.

$$Dice\ Coefficient = \frac{2\ x\ Intersection\ (TP)}{Intersection + Union\ (TP+FP+FN)}$$

$$IoU = \frac{Intersection\ (TP)}{Union\ (TP+FP+FN)}$$

VI. RESULTS

The results demonstrate the successful implementation of a utilizing the U-Net architecture for brain tumor segmentation from MRI images, integrated with Streamlit for seamless deployment and user interaction. The proposed U-Net model achieved robust result on the BraTs20 dataset. The model has achieved accuracy (0.9891), Precision (0.9873), Specificity (0.9881), Dice Score (0. 8302), Mean IoU (0.9096), Sensitivity (0.9895) and Loss (0.0046) for the BraTs20 dataset. The segmentation predictions are showed with the help of streamlit web app. Below are the screens for the brain tumor segmentation using the U-Net model.

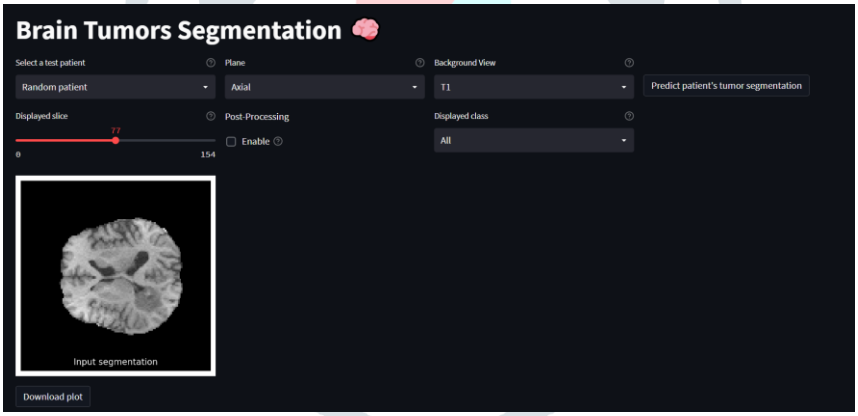

Fig. 3: Home Screen of Brain Tumor Segmentation

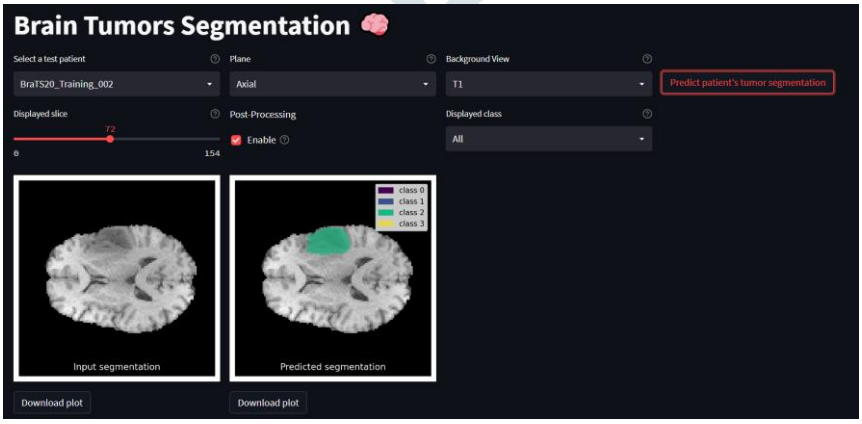

Fig. 4: Tumor Prediction of Brain Tumor on Axial Plane

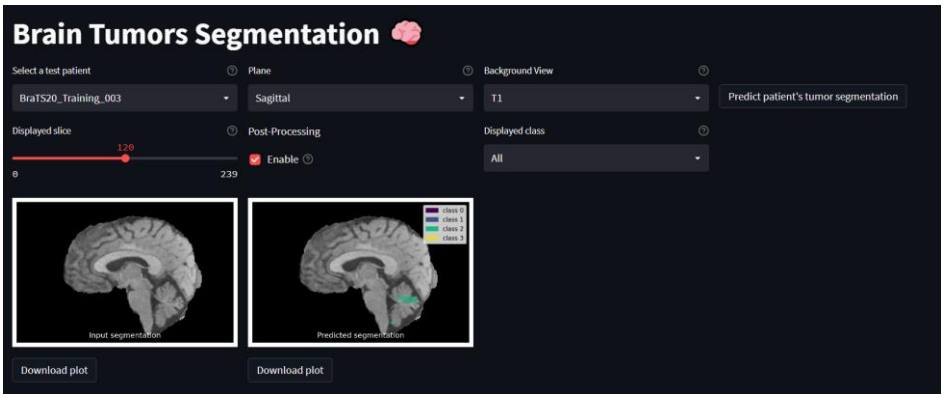

Fig. 5: Tumor Prediction of Brain Tumor on Sagittal Plane

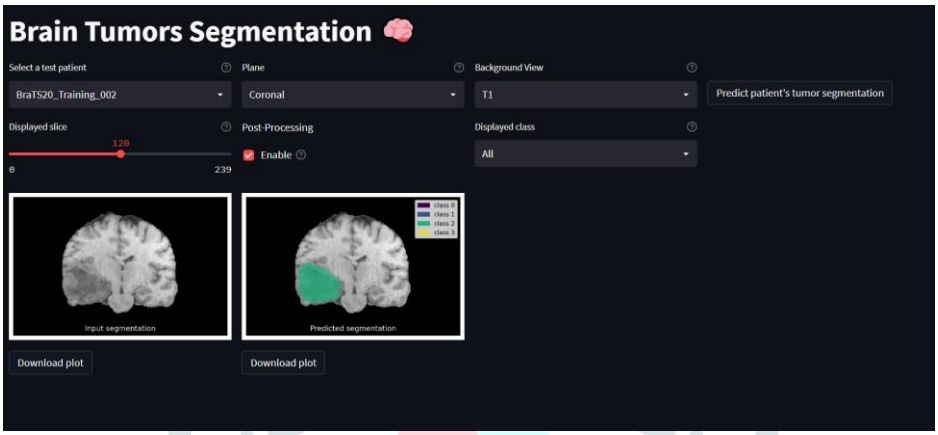

Fig. 6: Tumor Prediction of Brain Tumor on Coronal Plane

VII. CONCLUSION

In conclusion, this project focusing on advanced deep learning techniques for brain tumor segmentation holds promise for theoretical advancements. The implementation of the U-Net architecture applied to multimodal MR imaging aims to delineate enhancing tumor, whole tumor, and tumor core sub-regions. Utilizing the BraTS 2020 dataset as a benchmark establishes a solid theoretical foundation for real-world adaptability. The theoretical exploration of the U-Net architecture, supported by anticipated success in segmentation accuracy, is expected to significantly advance brain tumor segmentation methodologies. While tangible results are pending, the theoretical framework suggests substantial progress in this domain, with performance evaluations such as dice scores and comparisons with existing architectures poised to contribute significantly to the theoretical landscape. Acknowledging theoretical limitations, including challenges in segmenting heterogeneous tumors, the project maintains a theoretical focus on research and development. In essence, this anticipated outlook positions the project at the forefront of advancing theoretical methodologies for brain tumor segmentation, contributing significantly to the theoretical landscape of precise and reliable diagnostics.

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