A 3D U-Net Approach for Brain Tumor Segmentation on the BraTS2020 Dataset

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***Abstract*—Deep Learning is the state-of-the-art technology for segmenting brain tumors. However, this requires a lot of high-quality data, which is difficult to obtain, especially in the medical field. U-Nets were introduced to address this very problem. U-Net is the most widespread image segmentation architecture due to its flexibility, optimized modular design, and success in all medical image modalities. Over the years, the U-Net model has received tremendous attention from academic and industrial researchers. Several extensions of this network have been proposed to address the scale and complexity created by medical tasks. In this paper, we proposed a simple 3D U-Net model trained on the BraTS2020 dataset for the brain tumor segmentation.**

***Index Terms*—U-NET, BraTS2020, Dice loss, Focal loss, Brain Tumour segmentation**

I. Introduction

Brain tumours originate from different cell types, mainly from glialcells (astrocytes, oligodendrocytes, microglia, ependymal cells) and are then referred to as gliomas. The World Health Organization (WHO) classifies brain tumors into grades 1 to 4 based on histologic features and molecular parameters. Grade 1 tumors are typically slow-growing and benign, and grade 4 tumors, such as glioblastomas (GBMs), are the most aggressive and malignant forms. Patients diagnosed with glioblastoma now have a median survival of approximately 16 months with standard treatment (radiotherapy and temozolomide). The mortality rate of GBMs remains high and significant improvements in patient survival have been elusive. Extensive research to improve diagnosis, characterization, and treatment has been reducing the mortality rate of this disease [1]. Glioma segmentation is a critical step for tumor evolution, treatment efficacy assessment, survival prediction, and treatment planning. Multiple modalities of MRI scans (T1, T2, T1Gd, and FLAIR) are usually used to accurately segment the tumor and individual regions [2].

The Brain Tumor Segmentation Challenge (BraTS) [3] provides a large, fully annotated and publicly available dataset for model development and promotes a competition to evaluate the latest state-of-the-art approaches for brain tumor segmentation. This competition was launched in 2012 and continues to evolve every year, adding more samples and many different tasks.

II. Literature Review

U-Net, introduced by Ronneberger et al. [4] in 2015, has been a breakthrough architecture for biomedical image segmentation tasks like brain tumor segmentation. The U-Net architecture is designed to tackle the challenges of limited data by incorporating a U-shaped architecture with skip connections. These skip connections help in capturing both low-level and high-level features, enabling the model to effectively segment objects of interest even with limited training data.

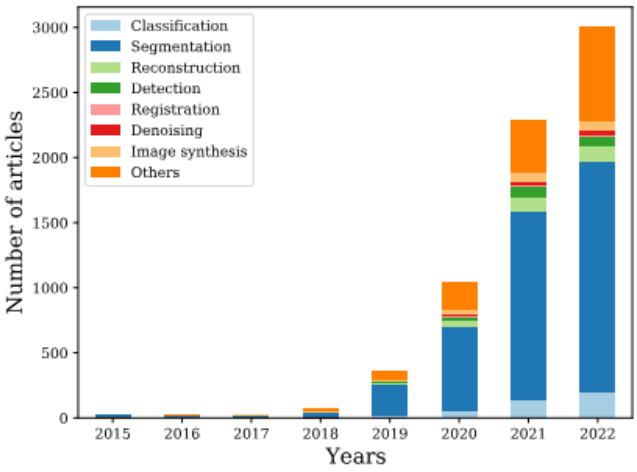

Fig. 1. The number of research works published in the past decade using the U-Net model as their baseline to address various medical image analysis challenges [11].

There are some other related studies where the authors used simple U-Net architecture with different numbers of encoder-decoder blocks and feature sizes. There is some other significant work done by the authors of [5] [6], where they used CNN to segment brain tumor on medical images. Dong et al [7] utilized 2D U-Net architecture on the BraTS 2015 dataset and gained dice scores of 0.86, 0.86, and 0.65 for whole, core, and enhancing tumors, respectively. In paper [8], the authors integrated a 3D attention module of the decoder paths of simple U-Net architecture and achieved mean dice scores of 0.704, 0.898, and 0.792, mean sensitivity of 00.751, 0.900, and 0.816, mean specificity of 0.998, 0.994, and 0.996, mean hausdorff95 of 7.05, 6.29, and 8.76 for enhancing tumor, whole, and core respectively on BraTS 2019 Dataset.

III. Dataset Description

This project uses the BraTS 2020 dataset to train, evaluate, and compare the models. These datasets contain 3D MRI brain

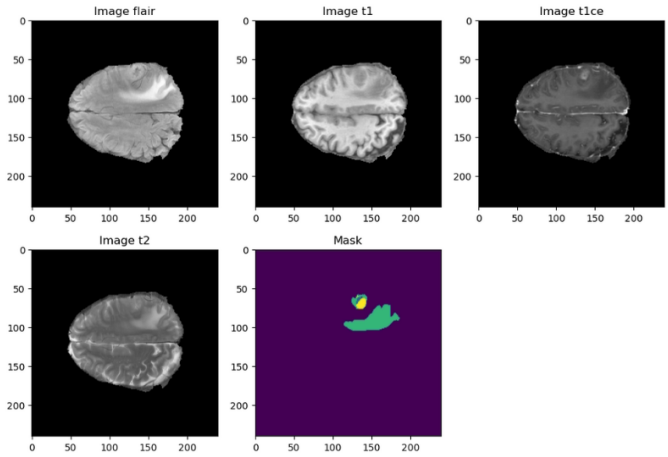

Fig. 2. A slice sample from the BraTS2020 dataset with all its channels and segmentation mask.

scans for a precise type of brain tumor, Glioma. The dataset has 369 samples for training the model and 125 samples to validate the model [9]. Expert physicians from different institutions did the annotation. All of these were provided to make a similar task, Segmentation, and Survival prediction, and all of the datasets are pre-operative MRIs. These datasets consist of 4 distinct MRI modalities, namely, native (T1), T2-weighted (T2), post-contrast T1-weighted (T1ce), and fluid-attenuated inversion recovery (FLAIR). Each MRI modality has 155 slices per volume. The enhancing tumor, the necrotic, the peritumoral edema, and the non-enhancing tumor core are the three tumor sub-regions that are annotated. 1 for necrosis and a non-enhancing tumor (NCR/NET), 2 for peritumoral edema (ED), 4 for an enhancing tumor, and 0 for background in each training patient's annotated labels. Integrating three regions—the whole tumor (also known as Whole Tumor or Whole: labels 1, 2, and 4), the tumor core (also known as Core: labels 1 and 4), and the enhanced tumor (known as Enhancing Tumor or Enhancing: label 4).

IV. Methodology

The 3D U-Net architecture of CNN has been employed for brain tumor segmentation. A data generator class has been used in this experiment to fit the dataset into the main memory. After that, the training dataset was divided into train and validation datasets with a ratio of 0.75, and 0.25 respectively. It was then fed into the U-Net model. Then, we evaluate the trained model and measure the performance based on different metrics. Figure 1 shows the workflow of the model.

A. Model Architecture

The 3D U-Net architecture is an extension of the original 2D U-Net architecture, the one shown in Figure 2. It is adapted to handle volumetric data. The architecture consists of a contracting path and an expansive path, connected by skip connections.

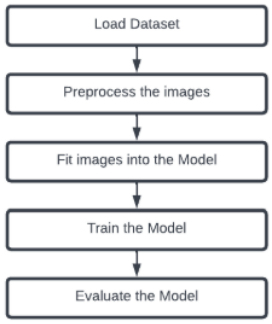

Fig. 3. Workflow of our model

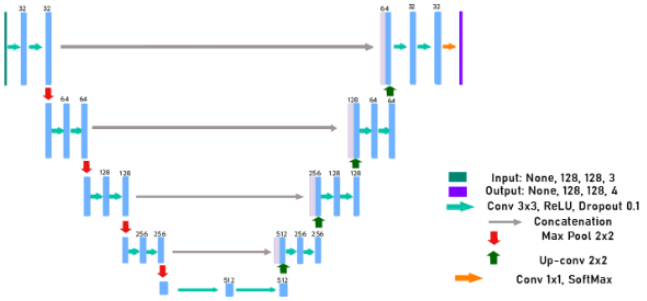

Fig. 4. U-net architecture from M. A. Nasim, et al. [10], similar to our working methodology

The contracting path begins with an input layer that takes 3D volumetric images as input. It consists of several layers of 3D convolutional (Conv3D) and max-pooling (MaxPooling3D) operations. Each convolutional layer is followed by a rectified linear unit (ReLU) activation function and a dropout layer for regularization. The number of filters in the convolutional layers increases gradually, capturing features at different scales. The contracting path downsamples the spatial dimensions of the input while increasing the number of feature maps.

The expansive path consists of several layers of 3D transposed convolutional (Conv3DTranspose) operations, which upsample the feature maps. Each transposed convolutional layer is followed by concatenation with feature maps from the corresponding contracting path, facilitating the flow of high resolution information. Similar to the contracting path, the expansive path includes convolutional layers with ReLU activation and dropout for feature extraction and regularization. The output layer consists of a convolutional layer with a softmax activation function, which produces probability maps for each class. The number of output channels corresponds to the number of classes in the segmentation task.

B. Data Preprocessing

The datasets contain 4 distinct MRI modalities. Training the CNN model with all those modalities is computationally expensive. Thus, FLAIR, T1ce, and T2 were considered as input for the 2D U-net. FLAIR and T1ce contain most of

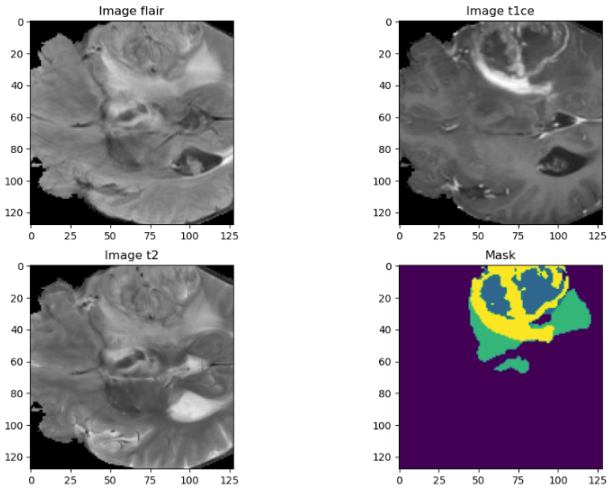

Fig. 5. Visualizing preprocessed data

the valuable information in this dataset. Each MRI modality contained an unnecessary black background, which is not required for the training phase and increased the computational time. For this reason, the images were cropped to 128x128x128x3 and 128x128x128x4 for input data and mask, respectively. Both input and output images have been resized to the required shape of the U-net model. And lastly, the input and output images are normalized using MinMaxScaler. For the Segmented images, one hot encoding has been used. After that, we split the training dataset into train and validation datasets with a ratio of 75pc and 25pc, respectively.

C. Experimental Setup

The model was created using Keras and TensorFlow. The training of the model was done on a workstation with an Nvidia RTX A2000 12GB GPU. Python version 3.11.5 and TensorFlow version 2.15 were used.

D. Evaluation Metrics

IOU Score (Intersection over Union) measures the overlap between the predicted segmentation mask and the ground truth mask. It calculates the intersection divided by the union of the predicted and ground truth regions. An IOU score closer to 1 indicates better segmentation accuracy. The loss function used for training is a combination of Dice Loss and Categorical Focal Loss. Dice Loss measures the overlap between the predicted and ground truth masks, while Categorical Focal Loss focuses on hard-to-classify examples by down-weighting easy examples and emphasizing hard examples. The combination of these loss functions aims to improve the model's segmentation performance. True Positive (TP) in the equations denotes a tumor match between the anticipated and actual tumor. True Negative (TN) indicates a match between the expected and actual non-tumor. False Positive (FP) denotes that the predicted tumor area is not the actual tumor, and False Negative (FN) means that the expected non-tumor is the actual tumor area.

$$IoU = \frac{Areaof Intersection(TP)}{AreaofUnion(TP+FP+FN)} \quad (1)$$

$$DiceCoefficient = \frac{2Intersection(TP)}{Intersection+Union(TP+FP+FN)} \quad (2)$$

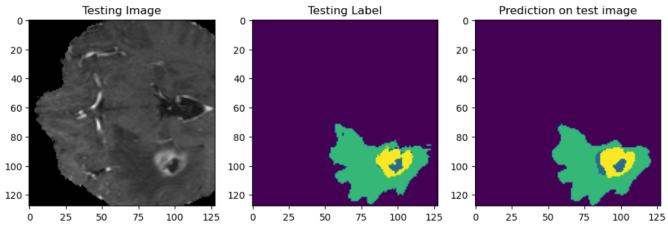

Fig. 6. Our model generating a mask

V. Experimental Results

After 100 epochs, the model achieved a training IoU score of 0.7789 and a total loss of 0.7896 and achieved a mean IoU of 0.6557 for validation.

VI. Conclusion

Brain tumors cause thousands of innocent victims to die due to failed brain surgery every year. However, thousands of individuals will have more hope knowing their operation will be successful if a model is developed to segment the data correctly. This study presents an extensive comparative analysis among the benchmark Brain Tumor Dataset and state-of-the-art models to predict brain tumor segmentation to achieve this goal. We aim to explore different kinds of other deep neural models and carry out an in-depth analysis of those models by comparing them with each other on different BraTs datasets.

Fig. 7. Model loss over epochs

Fig. 8. IoU scores over epochs. An IOU score closer to 1 indicates better segmentation accuracy

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