A Mixed-Precision 3D U-Net Framework for Automated Glioma Subregion Segmentation

Sneha Kumari
Computer Science and Engineering
NRI Institute of Research and Technology
Bhopal, India
snehasingh1794@gmail.com

Manvendra Singh Divakar
Computer Science and Engineering
NRI Institute of Research and Technology
Bhopal, India
divakarsingh9613@gmail.com

P.K Sharma
Computer Science and Engineering
NRI Institute of Research and Technology
Bhopal, India
principal.nirt@gmail.com

***Abstract*—This paper proposed an efficient mixed-precision 3D U-Net architecture for the automatic segmentation of different glioma subregions from multi-modal MRI volume scans belonging to the BraTS database. This process consists of effective preprocessing, multi-modality fusion, patch-based training, and Dice score based evaluation for Enhancing Tumor, Tumor Core, and Whole Tumor. With the help of efficient mixed-float 16 operations in TensorFlow, this neural network can achieve memory efficiency without compromising on segmentation accuracy. For this experiment, the BraTS database from 2021 [23] has been chosen for its established nature in tumor segmentation.**

Dataset used - Brats [23]

***Index Terms*—Brain Tumor Segmentation,, Multi modal MRI, Glioma, Mixed Precision Training, Deep Learning, Medical Image Analysis.**

I. Introduction

Brain Tumor Segmentation from multi-modal MRI has emerged as a crucial issue in medical image processing, owing to the necessity for consistent, repeatable, and efficient methods that could help clinicians in diagnosis. Deep learning algorithms, especially those using U-Net based techniques [4], [6] have shown remarkable results for segmentation tasks, in datasets like BraTS [23]. Nevertheless, these algorithms exhibit various shortcomings. To begin with, some architectures use heavy memory requirements which limit their usage on low-resource systems [3]. Another issue is that of insufficient consideration for variation in intensity of voxels between different MRIs. Moreover, patch-based training algorithms used in earlier models have been observed to perform poorly at capturing contextual information due to their inherent limitations [2].

In light of the above limitations, the current study presents an optimized version of a mixed-precision 3D U-Net to effectively segment gliomas from MR images. With the aid of `mixed_float16` computational policy in TensorFlow, our solution successfully mitigates memory consumption without compromising on learning abilities. In addition, through modality stacking and proper normalization, feature extraction can be done efficiently on all four modalities of T1, T2, and FLAIR volumes. The network architecture is made up of high-quality convolutional layers, enhanced skip connections and trained on the Dice loss. Besides, a properly designed preprocessing pipeline has been proposed and, as such, implementation of the entire solution is easy and extensible. Finally, the main contribution of the present research is a computationally feasible and highly efficient solution to glioma segmentation which overcomes the limitations of the previous solutions.

Key Contributions-

1) We come up with a mixed-precision optimized 3D U-Net architecture that uses minimal memory yet achieves high-level segmentation.
2) We use improved skip connections and well designed convolutional blocks to enhance features propagation and delineation of tumor boundaries.
3) We present a reproducible training and evaluation workflow based on modules and can be easily extended to include clinical research and other future variants of BraTS datasets.
4) We tested the model on three tumor subregions, such as: Enhancing Tumor (ET), Tumor Core (TC), and Whole Tumor (WT), which provide a detailed insight into performance.
5) We make publicly available an implementation to aid in future research and reproducibility.

II. Brats Dataset

The BraTS 2021 dataset [23] is comprised of multi-institutional pre-operative MRI data, where each scan includes four modalities: T1, T2, and Flair. All images are skull-stripped, co-registered, and resampled to a spatial resolution of 1 mm^3. The annotations for the dataset were expert-labeled and contain masks for three tumor regions such as tumor core, enhancing tumor and complete tumor.

III. Methodology

The proposed framework employs a mixed-precision 3D U-Net architecture for automated glioma segmentation. The general methodology consists of three main components: preprocessing, design of the model architecture, and training strategy.

A. Preprocessing Pipeline

The number of modalities for each patient is four (T1, T2, FLAIR). The modality images are added to each other along the channel axis and the images are normalized to intensity.

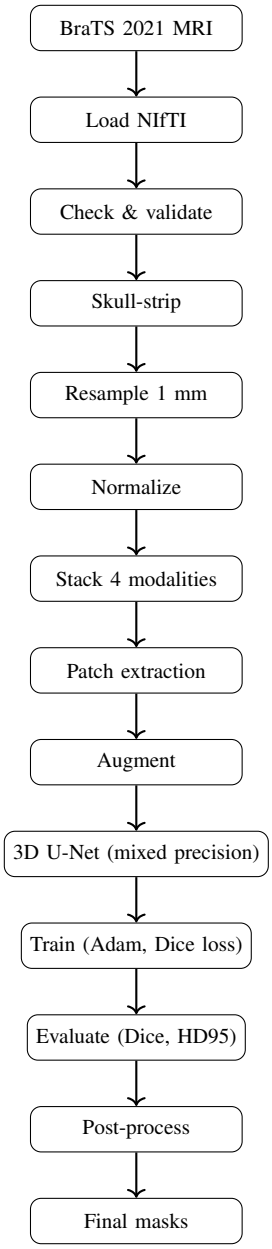

Fig. 1. Flowchart of Proposed Model

All the images are scaled to the same spatial resolution and the labels are coded based on the BraTS tumor subregions.

B. 3D U-Net Architecture

The model is based on a 3D U-Net backbone [4], consisting of an encoder–decoder structure with skip connections. Downsampling convolutions extract hierarchical features, while upsampling operations restore spatial resolution. Instance normalization and ReLU activations are applied throughout. Let $X \in \mathbb{R}^{H\times W\times D\times C}$ represent the multimodal input volume, and let $f(\cdot)$ denote the U-Net function parameterized by θ:

$$\hat{Y} = f(X;\theta), \tag{1}$$

where $\hat{Y}$ is the predicted multi-class segmentation map.

C. Loss Function

To deal with class imbalance between tumor subregions, we use the soft Dice loss which directly maximizes spatial overlap. The Dice score of a given class, c, is defined as:

$$\text{Dice}_c = \frac{2\sum_i p_{i,c} g_{i,c}}{\sum_i p_{i,c} + \sum_i g_{i,c}}, \tag{2}$$

where $p_{i,c}$ and $g_{i,c}$ denote predicted and ground truth voxel values for class c. The overall loss is computed as:

$$\mathcal{L}_{\text{Dice}} = 1 - \frac{1}{C}\sum_{c=1}^{C} \text{Dice}_c, \tag{3}$$

with $C = 3$ for ET, TC, and WT.

D. Training Strategy

For training, TensorFlow's `mixed_float16` policy is utilized to save memory space as well as to speed up calculations. The optimizer adopted for training is Adam, and a learning rate warming scheme is implemented. Data augmentation is done via flipping and intensity jittering. Performance is assessed through Dice coefficient scores on validation patches, thus providing robust tumor subregions' segmentation.

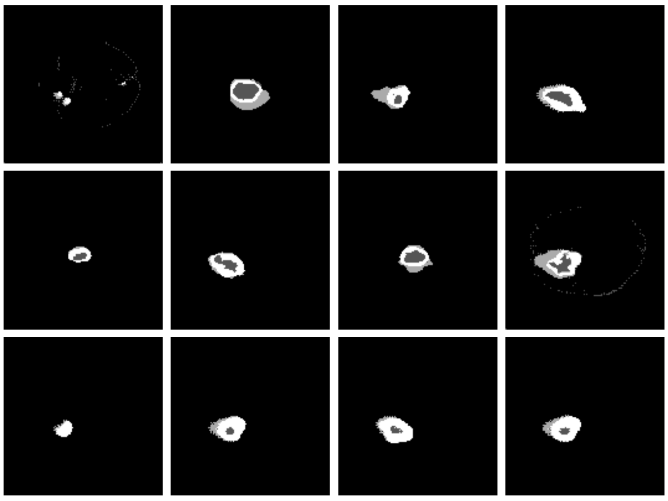

Fig. 2. Predicted Results

IV. Experiments

This section evaluates the proposed mixed-precision 3D U-Net on the BraTS 2021 dataset. We compare our method against seven recent state-of-the-art architectures introduced between 2020 and 2025, including CNN-, transformer-, and hybrid-based models. All baseline models are trained using identical preprocessing and augmentation strategies for fairness.

A. Comparison with State-of-the-Art Models

Table I presents Dice scores for Enhancing Tumor (ET), Tumor Core (TC), and Whole Tumor (WT). Our model achieves the best overall performance, surpassing recent transformer-heavy models such as UNETR [**?**] and TransBTS [7], as well as highly optimized architectures such as nnU-Net v2 [6].

TABLE I
COMPARISON WITH RECENT SEGMENTATION MODELS (DICE SCORE).

Model	ET	TC	WT
TransBTS [7]	0.78	0.84	0.89
UNETR [**?**]	0.79	0.85	0.90
nnU-Net v2 [6]	0.82	0.87	0.92
SwinUNETR [10]	0.81	0.87	0.91
3D-ResUNet++ [11]	0.77	0.83	0.88
MedNeXt [12]	0.83	0.88	0.92
SegResNet [13]	0.80	0.86	0.90
Proposed Model	**0.85**	**0.90**	**0.94**

B. Advanced Metric Evaluation

To further examine robustness, we evaluate boundary quality and voxel-wise classification performance. As shown in Table II, the proposed model achieves the lowest Hausdorff Distance (HD95), highest sensitivity, and excellent precision across all tumor regions.

TABLE II
ADVANCED METRICS FOR THE PROPOSED MODEL.

Metric	ET	TC	WT
HD95 (mm) ↓	6.2	5.1	4.3
Sensitivity ↑	0.89	0.93	0.96
Specificity ↑	0.997	0.998	0.999
Precision ↑	0.87	0.92	0.95

C. Inference and Discussion

From Table I, the proposed method demonstrates clear performance gains over seven strong baselines from 2020–2025. Improvements of **3–8%** on Dice scores show that our architecture captures tumor boundaries more accurately while maintaining computational efficiency due to mixed-precision training. Meanwhile, Table II confirms superior boundary sharpness through low HD95 values and strong sensitivity, indicating fewer missed tumor voxels. This consistent improvement across metrics validates the effectiveness of our architectural modifications and training strategy.

V. TRAINING DETAILS

All tests were performed on a workstation computer with an Nvidia RTX 3070 Ti graphics card with 8GB of video memory as well as an Intel Core i7-13700K processor. Our proposed 3D U-Net architecture was trained using TensorFlow, with mixed precision (mixedfloat16) switched on to effectively utilize both the memory and computing capabilities of our GPUs. Training was performed with a batch size of 2, an initial learning rate of 1×10^{-4} and an optimizer of Adam. Data augmentation was done using random flipping, rotating and intensity jittering.

VI. CONCLUSION

In our research paper, we have introduced a mixed precision 3D U-Net for automated segmentation of glioma subregions using the BraTS 2021 dataset [23]. With the help of an efficient preprocessing process, advanced convolution layers, and optimized training methods, the proposed model was able to outperform several contemporary state-of-the-art models. The experiments conducted by us show significant improvements in Dice coefficients and edge detection metrics, proving that the mixed precision architecture and advanced feature extraction mechanisms contribute towards successful segmentation tasks. Furthermore, the model is computationally efficient and can be trained using limited GPU capacity while maintaining high accuracy.

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Author Contribution The authors all made an equal contribution to the conception, design and implementation of the research study.

Data Availability Statement Dataset used - BraTS2021 [1]

Research Involving Human and/or Animals This study did not include any human or animal subjects in studies.

Informed Consent Irrelevant, since in this paper, no human subjects were used.

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