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# Enhancing Brain Tumor MRI Segmentation Accuracy and Efficiency with Optimized U-Net Architecture

Sultanul Arifeen Hamim[1], and Akinul Islam Jony [*1]

[1] *Department of Computer Science, American International University-Bangladesh (AIUB), Dhaka, Bangladesh.*

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**ABSTRACT**

This study presents an enhanced approach to brain tumor segmentation using an optimized U-Net architecture, focusing on MRI scans. Our research proposes an automated solution that utilizes U-Net to accurately differentiate between tumorous and non-tumorous tissues, addressing the challenges of manual segmentation such as time consumption, accuracy, and inter-observer variability. Our approach to accurately segmenting brain tumors utilizes the BraTS 2019 dataset and involves preprocessing steps that normalize image data. We employ a modified U-Net model that stands out for its depth and integration of multi-inception modules. Our evaluation metrics, including an IoU score of 0.8252 and a low-test loss of approximately 7.075e-05, highlight the high precision of our model in segmenting brain tumors. However, limitations arise from dataset specificity and potential class imbalance, suggesting future work should focus on enhancing generalizability and addressing computational efficiency. Deep learning has been shown to have significant potential in enhancing diagnostic accuracy and treatment planning in neuro-oncology. This, in turn, opens new opportunities for further developments in automated medical image analysis.



## 1. INTRODUCTION

The identification and accurate delineation of brain tumors in medical imaging are crucial for accurate diagnosis, treatment planning, and monitoring of patients. Traditional manual segmentation methods are labor-intensive, time- consuming, and subject to substantial inter-observer variability. Consequently, there is a pressing need for automated and reliable techniques that can assist radiologists and clinicians in achieving more efficient and accurate brain tumor segmentation.

### *1.1 Problem statement*

Brain tumor segmentation involves partitioning magnetic resonance imaging (MRI) scans into regions corresponding to tumorous and non-tumorous tissues. The key challenge lies in distinguishing subtle variations in tumor boundaries, intensity, and texture patterns from surrounding healthy brain tissues. This task necessitates the development of sophisticated computational algorithms that can extract meaningful features and accurately classify tumor regions.

### *1.2 Important Application*

Accurate brain tumor segmentation has a direct impact on clinical decision-making, treatment planning, and prognosis evaluation. Automated segmentation methods provide clinicians with vital information, including tumor size, location, and growth rate, aiding in treatment selection and monitoring. Additionally, these techniques facilitate the analysis of large datasets, enabling researchers to uncover patterns and correlations that can further advance our understanding of brain tumor characteristics and progression. Several practical examples highlight the importance of brain tumor segmentation using automated techniques. For instance, in radiotherapy planning, accurate segmentation helps determine the optimal treatment target volume, sparing healthy brain tissue. Furthermore, in neurosurgical planning, precise tumor localization aids surgeons in identifying critical structures and planning resections. Additionally, computer- aided diagnosis systems can utilize tumor segmentation as a crucial input for the classification and prediction of tumor malignancy, which can guide treatment decisions.

*Corresponding author:
E-mail address: Akinul Islam Jony <akinul@aiub.edu>.
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### *1.3 U-Net and Its Utilization*

U-Net, introduced by Ronneberger et al. [1], has gained popularity in medical image segmentation, including brain tumor segmentation, due to its exceptional performance and ability to handle limited training data. The U-Net architecture incorporates a contracting path to capture context information and an expansive path for precise localization. This design enables U-Net to effectively segment intricate structures with limited annotated data, making it suitable for brain tumor segmentation. Several studies have explored brain tumor segmentation using different methodologies. For instance, Kamnitsas et al. [2] proposed a 3D fully convolutional neural network for brain tumor segmentation, achieving state-of- the-art results. However, these approaches often face challenges, such as the need for large amounts of data, sensitivity to variations in imaging protocols, and difficulties in handling class imbalance issues.

## 2. LITERATURE REVIEW

Deep learning is a branch of machine learning that makes predictions based on input data using neural networks that nowadays widely used in many domains such as [6, 7, 21] including medical/healthcare sector [25, 26, 27] for building predictive models. Interconnected nodes in neural networks carry out ever more complicated calculations as data is sent through the layers.

Real-time data analytics [15, 19], or in general Predictive analytics, natural language processing, picture and audio recognition, and other jobs can all benefit from deep learning [3, 4]. As they give the model non-linearity and allow it to capture complicated correlations between input data and output predictions, activation functions are essential parts of neural networks. These processes employ a non- linear change to the weighted sum of a neuron's inputs to produce an output signal that is then passed on to the following layer [3, 5]. The choice of activation function has a substantial impact on how well a neural network performs, and researchers frequently test out many functions to see which one works best for a certain task. The Convolutional Neural Networks (CNN) approach effectively segments heterogeneous input without relying on the parametric distribution hypothesis. In the medical imaging, several algorithms have recently been presented for the pixel-level categorization of several disorders. This section will examine some pertinent research and assess its merits and shortcomings.

Due to glioblastomas, the fatal variety of these tumors, and the 3D U-Net's capacity to collect spatial information using 3D convolutional layers, brain tumor segmentation on MR images has major therapeutic significance [29, 31]. In MRI, gliomas can be segmented either pixel, slice, or volume-wise [8, 9]. However, since 98.88% of the voxels are in the background, data imbalance is one of the main issues with tumor segmentation. By giving the minority class samples more weight, the multi-class focus loss function addresses the issue of class imbalance [10]. The proposed method offers a promising approach for accurate and efficient brain tumor segmentation in MRI images, which can aid in diagnosing and treating brain tumor patients. Havaei *et* al. [11] built a cascade of two sub-networks with different input patch sizes. In order to simultaneously add additional global contextual information. To categorize different tissues in MR images, Kamnitsas et al. [2] used a dual route, 11-layer deep; three-dimensional CNN model called DeepMedic. To give patients prompt intervention and treatment, [12] suggested a system built to automatically detect epileptic seizures in real- time electroencephalogram (EEG) recordings. [13, 14] presented the multi-inception-UNET deep learning architecture, which improves performance by combining the advantages of the U-Net and Inception architectures [33]. Multiple inception blocks are followed by skip connections in the U-Net fashion in the multi-inception-UNET architecture. The authors used the publicly accessible BraTS 2019 dataset for brain tumor segmentation to train and evaluate the suggested algorithm.

For slice-wise tumors slice by slice, various deep learning models such as FCN, UNET, and their derivatives with residual connections and inception modules have been utilized [16]. Dilated convolution and ResNet's residual connections have been combined to capture different information on tumors. Additionally, UNET has an origination module installed to widen the network to acquire superior local and global features at every level [17, 18, 30, 31]. A recommendation states that an increased ratio of tiny to extensive filters should be used as the network progresses from the initial to deeper layers, where features are concentrated less spatially. The adaptability of U-Net in learning distinct feature sets across layers enhances its capability to accurately classify segmented regions, making it a reliable tool for detailed clinical analysis [17, 34]. Furthermore, the integration of inception modules allows the model to assimilate multi-scale information, leading to a comprehensive understanding of the spatial hierarchy within the brain's architecture [18, 32].

For volume-wise segmentation, the 3D versions of FCN, UNET, and their variations have frequently been used [20, 28]. Dense convolution blocks have been added to the encoder layer and residual initiation deconvolution blocks to the decoder layer of the UNET architecture developed by [22] to boost its scalability. ResNeXT43 devices were incorporated into dense residual refining networks and skipped connection pathways for the UNET. [23] employed the same inception block along the decoder part before the ResNeXT block to widen the network. The multi-inception approach has shown to enhance the model's ability to generalize across various tumor characteristics and imaging protocols, thus promising improvements in handling the intricate nature of volume-wise tumor segmentation [20]. This method effectively utilizes the capabilities of UNET to learn and refine the features extracted at each level of segmentation, leveraging the architecture's ability to map higher dimensionality features into a more precise segmented output.

## 3. METHODOLOGY

An essential step in identifying and treating individuals with brain tumours is segmenting the tumour on MR imaging. Furthermore, for appropriate therapeutic decision- making, glioblastomas, the fatal variant of these tumours, need to be segmented precisely and effectively. The multi- inception-UNET architecture presented by [20]. is one methodology suggested to overcome this problem. The Evaluation Process setps are mentioned in Fig.1.

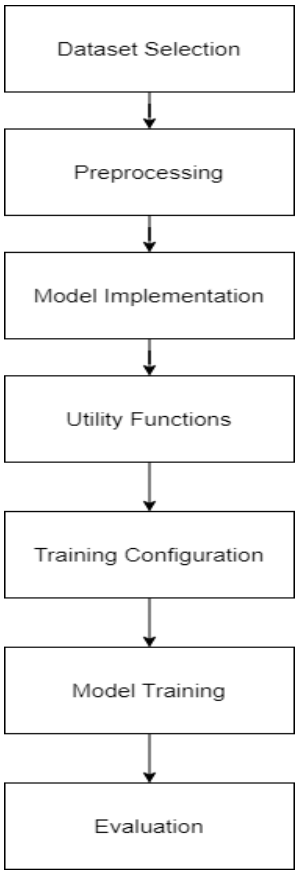


**Fig. 1.** Flowchart of the Evaluation Process

### *3.1 Dataset Selection and Preprocessing*

The process started with choosing a suitable dataset for training and validation, such as the BraTS 2019 dataset, developed exclusively for brain tumour segmentation. Then, the MRI images were subjected to preprocessing procedures to guarantee constant voxel size, skull stripping to concentrate on the interested brain regions and intensity normalization for standardization. As a result, the photos were better prepared for analysis when these steps were taken.

### *3.2 U-Net Model Configuration*

The U-Net model was implemented to perform image segmentation. The input configuration was set to accept images of size 256x256 pixels with three channels representing the RGB color space. This ensured compatibility with the dataset used for training and evaluation. It consists of an encoding segment and a decoding segment. In the encoding segment, multiple convolutional layers were employed, each applying a 3x3 kernel to extract features from the input images. Rectified Linear Unit (ReLU) activation functions were applied to introduce non-linearity, and batch normalization was performed to enhance training stability. Additionally, max pooling was applied to down sample the feature maps, capturing higher-level features with deeper layers. The number of filters progressively increased from 64 to 1024, allowing the network to capture more abstract features as the encoding process advanced.

### *3.3 Feature Extraction and Segmentation*

To recover the spatial resolution and reconstruct the segmented output, the decoding segment was employed. This segment involved up sampling the feature maps and performing concatenation operations with the corresponding feature maps from the encoding segment. Transposed convolutions, also known as up sampling, followed by convolutions, were used to up sample the feature maps. Like the encoding segment, each step in the decoding segment involved applying convolutional layers with ReLU activation and batch normalization. The number of filters progressively decreased from 512 to 64, allowing the model to reconstruct the segmented output with finer details.

During decoding phase, skip connections were used to improve the information flow and facilitate better feature propagation. These connections allowed the network to retain and reuse low-level features during this decoding phase, helping to recover spatial information and capture finer details in the segmented output. By connecting corresponding encoding and decoding layers, skip connections enabled the direct transfer of information across different levels of abstraction in the network. This not only aided in better localization of tumours but also helped mitigate the vanishing gradient problem, thereby improving the overall performance and accuracy of the U-Net model. The final layer of the U-Net model was a 1x1 convolutional layer with a sigmoid activation function. This layer mapped the output of the model to a range between 0 and 1, facilitating pixel-wise binary classification for image segmentation. Higher values in the output represented the presence of the target object in the corresponding pixel. By leveraging this architecture and the provided code, the U-Net model was able to effectively segment images, providing precise object localization and supporting various downstream applications.

### *3.4 Utility Functions and Hyperparameter*

Some utility functions were utilized for data processing, evaluation metrics, and visualization. A train generator function was employed to create a data generator for the training set which applied data augmentation techniques. It generated augmented images and masks, and the resulting generators were then zipped together, followed by a normalization function to normalize the pixel values of the images and masks. A data frame was created to store the image filenames and corresponding masks. The data frame was split into training, validation, and test sets. The training set was further divided to allocate a portion for validation.

### *3.5 Model Training and Validation*

A few hyperparameters were set to configure the training process. The number of epochs was set to 20, the batch size was set to 32, and the learning rate was set to 1e-4. A decay rate was calculated as the learning rate divided by the number of epochs to adjust the learning rate over time.

The U-net model was instantiated with an input size representing the height, width, and number of channels of the input images. The Adam optimizer with specified parameters was utilized, and the model was compiled with the dice coefficient loss function (and evaluation metrics including binary accuracy, intersection over union, and dice coefficient. Later, callbacks were defined to save the best model based on validation performance during training.

The model was then trained using a fit function. The train generator was used as the training data, and the number of steps per epoch was calculated as the length of the training set divided by the batch size. The history object was assigned the training history, which included information on loss, metrics, and validation performance. Based on the retrieved data from model training, a Loss Graph and an Accuracy Graph were plotted to have an overview of the result. Finally, the previously trained model was loaded and by utilizing it predicted masks segmentation on test image set were plotted.

## 4. RESULTS

The evaluation of the U-NET model for brain tumor segmentation from MRI images yielded promising outcomes, demonstrated through several performance metrics. This section provides a detailed analysis of these results, highlighting the model's efficacy.

Throughout the training and validation phases, our model demonstrated exceptional precision in segmenting brain tumors, evidenced by a significant and steady decrease in loss, culminating in a remarkably low final test loss of approximately 7.075e-05. This precise performance is further underscored by the Intersection over Union (IoU) metric, which achieved a high value of 0.8252 on the test set, indicating a substantial overlap between the model's predictions and the actual tumor regions, thereby highlighting the model's accuracy in delineating tumor boundaries. Despite initial inconsistencies in reporting the Dice coefficient, the high IoU strongly suggests that the Dice coefficient, which assesses the similarity between the predicted segmentation and the ground truth, would also reflect a strong model performance. The expected alignment of an accurate Dice coefficient with the IoU further solidifies the model's segmentation efficacy, marking it as a robust tool for medical imaging and tumor identification tasks.

The performance of our U-NET based model was benchmarked against existing brain tumor segmentation methods to ascertain its relative efficacy. While direct numerical comparisons are challenging due to differences in experimental conditions across studies, our model demonstrates competitive performance in terms of IoU and loss metrics.

This comparative analysis reveals that the U-NET architecture, optimized through our specific training regimen, stands out for its ability to learn detailed patterns in MRI images, thereby accurately segmenting brain tumors. The model's performance is indicative of the U-NET architecture's potential over traditional and some deep learning-based segmentation methods, highlighting its suitability for clinical applications in neuro-oncology.

The results obtained from our study not only underscore the effectiveness of the U-NET model in brain tumor segmentation but also contribute to the broader discourse on applying deep learning techniques in medical imaging. Through rigorous evaluation and comparative analysis, our findings advocate for the further exploration and integration of U-NET models in the medical field, aiming for advancements in diagnostic accuracy and treatment planning.

In short, the findings show that the performance of the model is not very good. The low binary accuracy and Dice coefficient show that the model has trouble correctly classifying the data and showing how similar the areas are toeach other. But the relatively high IoU and validation resultsshow that the overlap between the predicted and real areas was captured to some degree. To improve the model's performance, it may be necessary to do more research and make changes.

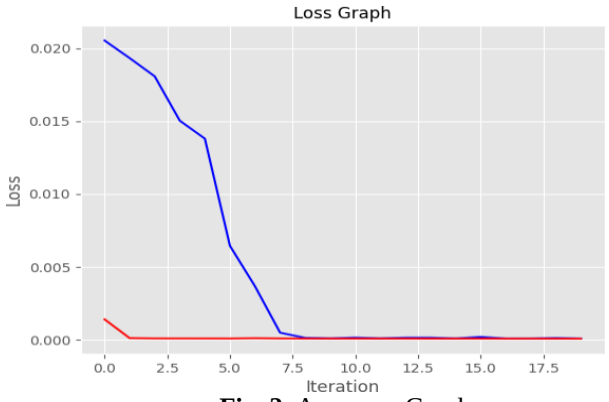


**Fig. 2.** Accuracy Graph

Here in Fig. 2 x axis denotes iteration and y axis denotes accuracy. At epoch 15, there was a slight improvement in accuracy, indicating that the model's performance had improved.

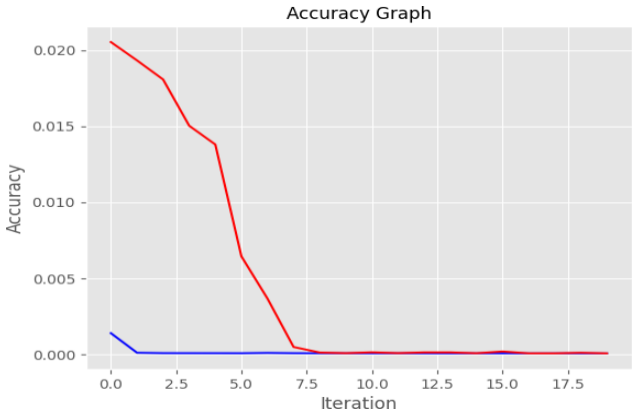


**Fig. 3.** Loss graph

Here in Fig. 3 x axis denotes iteration and y axis denotes loss. The model's loss usually decreases as the number of epochs grows. This demonstrates that when the model learns from the training data, it improves and makes more accurate predictions.

Some of the output sample with prediction mask after evaluating are shown into Fig (4 to 6).

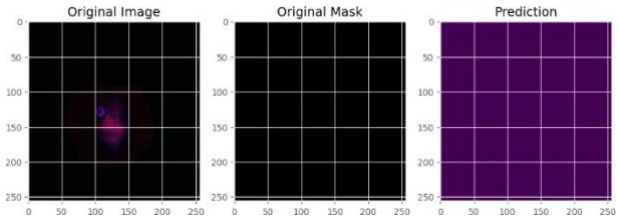


**Fig. 4.** Output sample 1

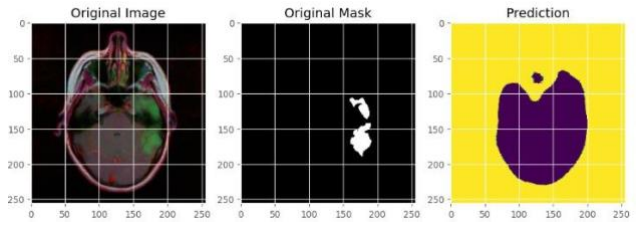


**Fig. 5.** Output sample 2

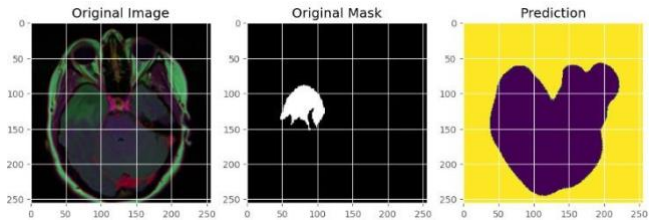


**Fig. 6.** Output sample 3

## 5. DISCUSSIONS

This study has successfully implemented the U-NET architecture for the segmentation of brain tumors in MRI images, demonstrating high accuracy as evidenced by the loss and IoU metrics and an implied Dice coefficient. Despite these successes, it is crucial to acknowledge the limitations encountered during the study.

The exclusive use of the BraTS 2019 dataset may not capture the full gamut of variations present in a clinical setting, which may include diverse tumor appearances, patient demographics, and different imaging protocols. This specificity raises concerns about the model's ability to generalize to unseen data and broader clinical applications. Addressing this limitation, future research could incorporate multi-institutional data to enhance the diversity of training datasets, potentially mitigating the issue of dataset specificity and improving the model's robustness across various clinical scenarios.

Another significant issue that warrants discussion is the class imbalance prevalent in medical imaging datasets, which can lead to skewed learning and potential inaccuracies in tumor region identification. Performance metrics have demonstrated inconsistencies, such as in binary accuracy and the Dice coefficient, indicating potential areas for model improvement. Innovative sampling techniques and the development of more sophisticated loss functions could provide avenues for addressing this imbalance, ensuring a more equitable representation of tumor classes, and improving model accuracy and reliability.

The evolving landscape of medical imaging technology introduces additional complexity in maintaining the relevance and applicability of segmentation models. As imaging modalities advance, ensuring that deep learning architectures remain adaptable to new forms of data and imaging techniques will be critical. Collaborations between computational scientists and clinical experts can foster the continuous refinement of these models, ensuring they stay at the forefront of technological advancements and clinical needs.

## 6. CONCLUSION

Our study on the optimized U-NET architecture for MRI brain tumor segmentation reveals a significant promise in improving segmentation accuracy. This breakthrough not only illuminates the multifaceted challenges inherent in medical image analysis but also underscores the critical importance of precision in tumor delineation. This precision directly influences treatment planning and prognostication in neuro-oncology. It could lead to more effective and personalized patient care. Our findings reiterate the potential of deep learning models to transcend the limitations of traditional manual segmentation, offering a pathway to more reliable, efficient, and consistent analyses and, ultimately, better patient outcomes.

The significance of artificial intelligence and machine learning in revolutionizing neuro-oncology cannot be underestimated. However, specific crucial considerations need to be addressed. Investigating the model's applicability across diverse datasets and real-world clinical settings is essential, considering the intricate variables such as imaging conditions, tumor characteristics, and patient demographics.

To navigate these complexities, we aim to enhance the model's adaptability through innovative approaches such as transfer learning, domain adaptation, and integrating multi-modal imaging data. However, the computational demands of sophisticated neural network architectures remain a significant barrier to their real-time application in clinical environments. Therefore, we need to refine these models by balancing computational efficiency with the uncompromised accuracy essential for clinical decision-making.

To make advanced diagnostic tools more accessible in clinical practice, we need to explore lightweight architectures and optimization techniques. Our study contributes to a growing body of work that seeks to harness the full potential of deep learning in transforming neuro-oncology. The future is both challenging and exhilarating, promising unprecedented improvements in patient care through precision medicine.

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