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D-UNET: Dilated-UNET for Brain Tumor Sub-Region Segmentation Using MRI Images

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ABSTRACT

The precise diagnosis and treatment planning of brain tumors significantly rely on the accurate segmentation of sub-regions from Magnetic Resonance Imaging (MRI) data. In this research, we propose a framework, D-UNET (Dilated-UNET), which enhances the traditional UNET architecture by incorporating dilated convolutions. UNET is the deep CNN architecture widely adopted for biomedical image segmentation tasks. D-UNET is specifically designed for brain tumor sub-region segmentation from multi-modal (T1, T2, T1ce, Flair) MRI images in nifti file format, each comprising 155 slices. The framework comprises of four distinct steps viz. data collection, data preprocessing, model training, and outcome evaluation. D-UNET employs two key modules during training, the dilated encoding module and the dilated decoding module. These modules enable the model to efficiently capture multi-scale contextual information, facilitating better representation learning for complex and varied tumor sub-regions. We evaluated the performance of D-UNET using Intersection over Union and Dice Coefficient metrics. The experimental results demonstrate that D-UNET outperforms the traditional UNET and other benchmark models in terms of segmentation accuracy. Notably, D-UNET excels in capturing finer details and intricate shapes of tumor sub-regions, contributing to its superiority in brain tumor segmentation. The ability to precisely delineate tumor sub-regions from different modalities provides crucial insights for medical professionals in treatment planning and decision-making.

Keywords: Medical image segmentation; Deep learning; CNN; UNET; Medical diagnosis; MRI

1. INTRODUCTION

In diagnostic imaging, brain tumor segmentation plays a pivotal role in aiding diagnosis and therapy planning[1]. The precise delineation of tumor sub-regions, namely, Tumor Core (TC), edema (including the entire tumor), and Enhancing Tumor (ET) regions, offers doctors valuable insights into the structural and characteristic aspects of the tumor[2,3]. These insights facilitate accurate treatment decisions and the development of personalized therapy plans[4]. Given that tumors consist of abnormal cell masses that can be life-threatening, identifying and separating cancerous cells through segmentation is a fundamental procedure for diagnosis and monitoring[5]. However, traditional manual segmentation by expert radiologists is resource-intensive and time-consuming[6]. To overcome these limitations and expedite the diagnostic process, the development of automated segmentation models is highly desirable. By leveraging automated segmentation, medical professionals can achieve accurate, rapid, and reliable diagnoses, leading to improved patient outcomes[7]. Moreover, automated segmentation has diverse applications, including radiotherapy planning, disease progression monitoring, and treatment evaluation.

Deep Learning[8] (DL) techniques, particularly Convolutional Neural Network[9] (CNN), has gained remarkable success in biomedical image segmentation, particularly in cases where distinguishing complex features is a major challenge. CNNs are designed to automatically learn and extract relevant features from input data, making them highly suitable for analysing complex medical images. The fundamental architecture of CNNs is inspired by the visual processing mechanisms of the human brain. Convolutional layers, comprise of interconnected neurons, being present in numerous layers within the structure, captures the local patterns and features from the input images. The convolutional layers are subsequently accompanied with non-linear activation functions, such as ReLU, which introduces non-linearity into the network and enable it to effectively capture intricate correlations among image features.

U-Net[10] is an example of deep CNN architecture which has been widely adopted for biomedical image classification and segmentation tasks. The U-Net architecture, characterized by its U-shaped structure comprising contraction and expansion blocks, has

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gained significant popularity due to its efficacy in accurately delineating object boundaries and segmentation masks. The contraction path of the U-Net, also known as the encoder, captures and encodes image features at multiple spatial resolutions. On the other hand, the expansion path, or decoder, employs transposed convolutions to upsample and produce dense feature maps, facilitating precise segmentation. This unique architecture of U-Net allows it to capture both local and global context information effectively, contributing to its superiority in biomedical image segmentation tasks.

Several brain tumor segmentation techniques have been proposed in the literature to address specific limitations and enhance segmentation performance in the domain. Zhao, *et al.* presented a correlation model capable of accommodating missing modalities by estimating modality-independent parameters and fusing correlation representations using an attention mechanism[11]. Ru, *et al.* introduced a multi-scale convolution module-based approach to enhance feature extraction using the M-UNet network[12], resulting in improved segmentation results compared to the original U-Net network. Qiu, et al. proposed a 3D EMSU-Net model with an effective multi-scale feature extraction component, focusing on regions affected by brain tumors to enhance segmentation performance[13].

Soltaninejad, *et al.* developed a fully automated encoder-decoder network capable of processing images of any size as input and achieving mean dice scores of 78 %, 70 %, and 66 % for WT, TC, and ET, respectively[14]. Ali, *et al.* combined 2D and 3D UNET models to extract radiomic characteristics from MRI volumes, maximizing the advantages of both models[15]. Qamar, *et al.* suggested a unique Hyperdense Inception 3D U-Net design achieving high dice coefficients for different tumor sub-regions[16].

C. Zhao et al. proposed multiple deep architectures to learn contextual information and integrate model estimations for accurate segmentation results[17]. Ding, *et al.* improved U-Net's topology to address information loss and excessive parameter stacking in deeper networks, striking a balance between segmentation accuracy and efficiency[18].

While many studies have focused on enhancing segmentation performance through U-Net modifications, it remains essential to consider the trade-off between accuracy and computational efficiency. These diverse approaches contribute to the advancement of brain tumor segmentation techniques, addressing various limitations and enhancing the overall reliability and performance of the models.

In-spite of the success of U-Net, there remains a room for its improvement, particularly in handling multi-modal MRI images and capturing extensive contextual information. To address these challenges, this work proposes a DL framework called D-UNET for brain tumor sub-region segmentation from MRI images. The D-UNET model is an enhancement of the traditional UNET architecture, incorporating dilated convolutions to improve the model's ability to capture multi-scale contextual information. This enables the model to better comprehend the intricate and diverse characteristics of tumor sub-regions, resulting in more accurate and comprehensive segmentation.

The challenge of brain tumor sub-region segmentation is further compounded by the presence of MRI images acquired from multiple modalities, including T1, T2, T1ce, and Flair. The integration of information from these distinct modalities can provide a more comprehensive view of the tumor, enabling a more robust and informative segmentation. The proposed D-UNET framework addresses this multi-modal segmentation task, providing a unified solution for efficient and precise delineation of tumor sub-regions across different imaging modalities.

Following is a summary of the contributions made by this study:

- Proposed a D-UNET (Dilated-UNET) framework for brain tumor sub-region segmentation, incorporating dilated convolutions to capture multi-scale contextual information effectively.
- Implementation and evaluation of the D-UNET model on the standard BraTS 2020 dataset, showcasing better segmentation performance compared to other state-of-the-art models.
- Comparison of D-UNET with S-UNET, 3D Unet, MTAUnet, and 3D CNN, highlighting the advantages of dilated convolutions in improving segmentation accuracy.

The subsequent sections of this research paper are organized in the following ways: Section 2 provides a comprehensive account of the suggested approach, encompassing the description of the dataset, the design and implementation specifics of the D-UNET model, and the assessment metrics employed. Section 3 presents the experimental result evaluation. Section 4 presents a comprehensive discussion and comparison with existing models. Finally, Section 5 concludes the paper by summarizing the contributions of the proposed D-UNET model and outlining future directions for potential enhancements.

2. MATERIAL AND METHODS

The research methodology for the proposed D-UNET is structured into four main phases. The first phase involves the collection of MRI dataset containing brain tumor images from multiple modalities. The second phase encompasses preprocessing steps, including data normalization and augmentation, to enhance the model's generalization and adaptability to diverse MRI data. The third phase focuses on the training of the D-UNET model, incorporating two key modules: the Dilated Encoding Block (DEB) and the Dilated Decoding Block (DDB).

These modules are tailored to exploit the strengths of dilated convolutions, enabling D-UNET to effectively capture context and spatial information at various scales. In the fourth phase, we evaluate the performance of the D-UNET model using two widely used metrics, Intersection Over Union (IOU)[19] and Dice Coefficient (DC)[20]. The IOU metric quantifies the overlap between predicted and ground truth masks, while the DC measures the similarity between these masks. By employing these metrics, the aim is objectively asses the accuracy and robustness of the proposed D-UNET model in segmenting brain tumor sub-regions. An analysis and interpretation of the experimental results is done by comparing the performance of D-UNET against traditional UNET and other state-of-the-art models on BraTS2020 dataset.

2.1 Data Collection

The BraTS 2020 dataset employed in this research is known as the Multimodal Brain Tumor Image Segmentation Benchmark dataset[21-22]. The dataset is publicly available on Kaggle (https://www.kaggle.com) and constitutes a valuable resource for brain tumor image analysis. It comprises MRI images from four distinct modalities which includes T1, T2, T1ce, and Flair. Each modality is represented as a three-dimensional volume, consisting of 155 slices and are in nifty file format. The brain MRI images in the BraTS dataset are annotated and categorised into four regions: the enhancing tumor, necrotic core, and edema region. Accurate segmentation of these regions is essential for precise diagnosis and treatment planning. In total, the dataset encompasses 368 files, out of which 265 files are allocated for model training, 74 files for validation, and 30 files for testing the proposed model's performance.

2.2 Data Pre Processing

Before model training, data pre-processing is performed to ensure cleanliness and uniformity. For the data processing and manipulation, two essential tools, Nilearn and Nibabel, have been utilized to preprocess the MRI data files that are available in nifti file formats. Nilearn offers an approachable and versatile platform for conducting analyses on brain volumes, enabling efficient handling and processing of the MRI data. On the other hand, Nibabel provides essential functionalities for reading and writing various medical and neuroimaging file formats, further facilitating data preparation and model training. The original dataset is structured into 369 directories, each containing five files. One file was discarded from the dataset due to an improperly formatted name. Each nifti file, consists of five files corresponding to each MRI modality, along with an additional file for the image mask. To facilitate data manipulation and analysis, the images were implemented in the nifti file format.

Further, the MRI images are standardized to have a consistent dimension, and all input pixel values are normalized. This step is crucial for achieving uniformity in data representation and facilitating model convergence during training. There are four channels in the images, depending on the four MRI modality used during training. The batch size for model training is set to one, and a data generator is employed to generate additional image data for training purposes, improving the model's capacity to generalize and effectively manage a wide range of variances present in MRI images. No post processing step has been employed in this study. By leveraging the BraTS 2020 dataset and employing rigorous data pre-processing, the proposed D-UNET model aims to achieve accurate and robust brain tumor sub-region segmentation.

2.3 Model Training

During the model training phase, two UNET architectures, namely S-UNET (Standard UNET) and D-UNET (Dilated-UNET) were implemented. S-UNET represents the traditional UNET architecture being referred, as the standard UNET in this paper. However, D-UNET incorporates dilated convolutions, also known as atrous convolutions, into the UNET architecture. Figure 1 presents the DEB, DDB and employed dilation rate for the model training. Figure 2 depicts the flow diagram of the proposed framework and the D-UNET architecture. Further, the pseudo code for the implemented D-UNET method has been presented in Fig. 3.

Dilated convolutions in D-UNET have demonstrated the ability to capture spatial features effectively from a wide receptive window without significantly increasing the model's parameter count. These convolutions introduce gaps or dilations between the kernel elements, enabling a larger receptive field while maintaining the same number of parameters as traditional convolutions. Both S-UNET and D-UNET architectures have an equal number of layers and hyper-parameters, with the primary difference being the integration of dilated convolutions in some convolutional layers of D-UNET. Both models are trained separately on the BraTS2020 dataset. As shown in Fig. 2, each image modality consists of a volume of slices. For model training, the input image shape is set to (128, 128, 4), where 4 denotes the number of channels, representing the different MRI modalities. Each channel corresponds to an MRI modality, containing 100 slices. Out of the total 155 slices, 100 slices per modality are selected for the training process.

The D-UNET design comprises a contracting path and an expanding path. The former includes four blocks, each containing two Dilated Encoding Blocks (DEBs) that incorporate dilated convolutions with a dilation rate of 2, along with one normal convolutional layer. In block 5, one DEB and one normal convolutional layer are employed. The corresponding numbers of filters for each block are as follows: block 1 (32, 32, 32), block 2 (64, 64, 64), block 3 (128, 128, 128), block 4 (256, 256, 256), and block 5 (512, 512), facilitating feature extraction, followed by ReLU activation. In each block of the contracting path, the feature maps are down-sampled using max-pooling of size (2, 2). The expanding path consists of four blocks, each incorporating one up-convolution with filter sizes of (2, 2). The numbers of

filters for the up-convolutions are 256, 128, 64, and 32, respectively. A concatenation operation is performed with the corresponding feature map cropped from the encoder path, followed by two Dilated Decoding Blocks (DDBs) having two dilated convolutional layers with a dilation rate of 2, followed by one normal convolutional layer. The numbers of filters for the decoding blocks in block 1, block 2, block 3, and block 4 are (256, 256, 256), (128, 128, 128), (64, 64, 64), and (32, 32, 32) respectively, each with ReLU activation.

Finally, a convolutional layer of size (1, 1) is employed which maps 32-component feature vector to four output labels (edema, enhancing tumor, necrotic core and no tumor region), representing the tumor sub-regions. The model training process employs the categorical cross-entropy loss function, while model optimization is performed using the Adam optimizer with a learning rate of 0.001. The model is trained for 100 epochs, allowing it to iteratively update its parameters and learn to accurately segment brain tumor sub-regions from the MRI images.

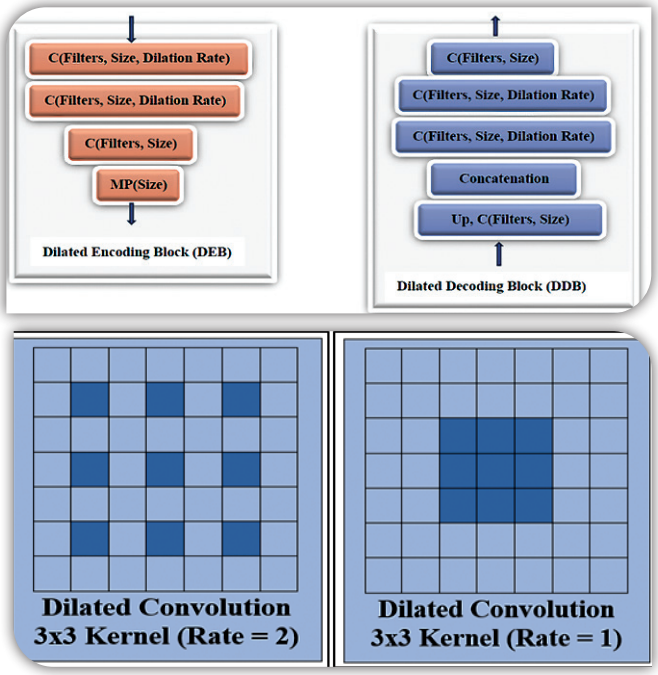

Figure 1. Proposed DEB, DDB and dilation rate.

2.4 Evaluation Metrics

As part of the model evaluation, two crucial metrics are employed to assess the segmentation performance: IOU and DC.

The DC is calculated separately for each tumor region, providing valuable insights into the accuracy and consistency of the segmentation results.

IOU reflects the amount of overlap considering the ground truth and the predicted segmentation mask for each tumor region and is calculated as the ratio between the intersection of two masks and their union, quantifying the degree of spatial alignment between the predicted and true segmentations.

DC serves as an indicator of segmentation accuracy and is calculated for each tumor region. The computation involves the multiplication of the intersection between the predicted and ground truth masks by a factor of two, followed by division by the sum of the volumes of the two masks. The range of DC is between 0 and 1, where the latter signifies a complete alignment between the two masks. By evaluating both the IOU and DC for each tumor region, a comprehensive understanding of the model's performance in accurately segmenting brain tumor sub-regions is achieved. The IOU and DC scores for each tumor region signify precise delineation of the tumor boundaries and overall segmentation performance.

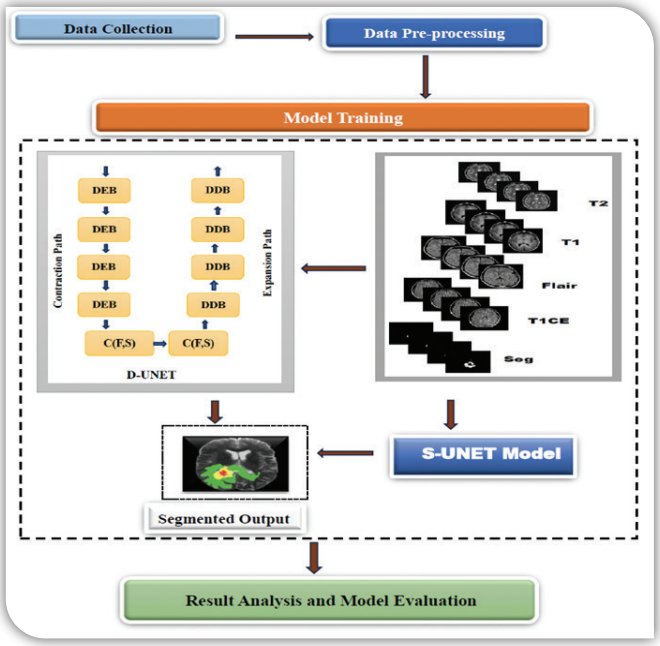

Figure 2. Flow diagram of the D-UNET framework.

3. RESULTS

This section presents the results observed from the simulation study. The segmentation performance of the proposed model is evaluated using the two popular measures: mean IOU and DC. Moreover, DC is also measured for specific tumor sub-regions viz. DC for Necrotic Core (NC), edema/WT and ET.

Table 1 presents the results of the D-UNET model on three different sets: train, validation, and test. The model achieved IOU scores of 87.32 % for train, 0.8831 for validation, and 0.8797 for test datasets. The model achieved DC of 75.77 % for train, 66.43 % for validation, and 69.27 % for test datasets.

DC (NC): This metric quantifies the accuracy of segmenting the NC within the tumor region. The proposed model achieved DC scores of 78.31 % for training, 59.36 % for validation, and 65.52 % for the test set in accurately delineating the necrotic core.

DC (WT) and DC (ET): These metrics specifically assess the accuracy of segmenting the WT and ET regions, respectively. In the training set, the model achieved DC of 89.10 % for WT and 78.97 % for ET. For the validation set, the DC scores were 74.21 % for WT and 70.13 % for ET. Lastly, in the test set, the model achieved DC of 78.10 % for WT and 72.69 % for ET. These results

show the effectiveness of the proposed approach in accurately segmenting the WT and ET regions. Overall, the D-UNET model achieved good segmentation accuracy as indicated by relatively high IOU and DC for train, validation, and test sets. However, there is some variability in performance across different tumor regions, with lower scores observed for NC in particular.

Pseudo code for proposed D-UNET model

```
Define the function DUNET_Model(inputs):
DEB1 ← Conv2D(32, 3,dilation_rate=2)(inputs)
DEB1 ← Conv2D(32, 3, dilation_rate=2)(DEB1)
C1 ← Conv2D(32, 3)(DEB2)
P1 ←MaxPooling2D(pool_size=(2, 2))(C1)

DEB2 ← Conv2D(64, 3,dilation_rate=2)(P1)
DEB2 ← Conv2D(64, 3, dilation_rate=2)(DEB1)
C2 ← Conv2D(64, 3)(DEB2)
P2 ← MaxPooling2D(pool_size=(2, 2))(C2)

DEB3 ← Conv2D(128, 3,dilation_rate=2)(P2)
DEB3 ← Conv2D(128, 3, dilation_rate=2)(DEB3)
C3←Conv2D(128, 3)(DEB3)
P3 ←MaxPooling2D(pool_size=(2, 2))(C3)

DEB4 ← Conv2D(256, 3,dilation_rate=2)(P3)
DEB4 ← Conv2D(256, 3, dilation_rate=2)(DEB4)
C4←Conv2D(256, 3)(DEB4)
P4 ← MaxPooling2D(pool_size=(2, 2))(C3)

 C5 ← Conv2D(512, 3, dilation_rate=2)(P4)
 C5 ← Conv2D(512, 3)(C5)

 Up6 ← Conv2D(256, 2)(UpSampling2D(size=(2, 2))(C5))
 Merge6 ← concatenate([C4, Up6], axis=3)
 DDB6 ← Conv2D(256, 3, dilation_rate=2)(Merge6)
 DDB6 ← Conv2D(256, 3, dilation_rate=2)(DDB6)
 C6 ← Conv2D(256, 3)(DDB6)

 Up7 ← Conv2D(256, 2)(UpSampling2D(size=(2, 2))(C6))
 Merge7 ← concatenate([C3, Up7], axis=3)
DDB7 ← Conv2D(256, 3, dilation_rate=2)(Merge7)
DDB7 ← Conv2D(256, 3, dilation_rate=2)(DDB7)
C7 ← Conv2D(256, 3)(DDB7)

Up8 ← Conv2D(256, 2)(UpSampling2D(size=(2, 2))(C7))
Merge8 ← concatenate([C2, Up8], axis=3)
DDB8 ← Conv2D(256, 3, dilation_rate=2)(Merge8)
DDB8 ← Conv2D(256, 3, dilation_rate=2)(DDB8)
C8 ← Conv2D(256, 3)(DDB8)

Up9 ← Conv2D(256, 2)(UpSampling2D(size=(2, 2))(C8))
Merge9 ← concatenate([C1, Up9], axis=3)
DDB9←Conv2D(256, 3, dilation_rate=2)(Merge9)
DDB9 ← Conv2D(256, 3, dilation_rate=2)(DDB9)
C9 ← Conv2D(256, 3)(DDB9)
C10 ← Conv2D(4,(1,1), activation='softmax')(C9)


    Return DUNET_Model(inputs=inputs, outputs=C10)
```

Figure 3. Pseudo code for the proposed D-UNET method.

Table 1. Performance measures for D-UNET model

Measures	Train	Validation	Test
IOU	0.8732	0.8831	0.8797
Dice Coefficient	0.7577	0.6643	0.6927
Dice Coefficient (Necrotic Core)	0.7831	0.5936	0.6552
Dice Coefficient (Edema)	0.8910	0.7421	0.7810
Dice Coefficient (Enhancing Tumor)	0.7897	0.7013	0.7269

The findings of using the S-UNET model to analyse the train, validation, and test datasets are shown in Table 2. DC (Edema) and DC (ET): The model achieved DC scores of 67.73 % for edema and 63.60 % for ET in the train set, and on the validation set, 65.57 % for Edema and 58.06 % for ET. Finally, for the test set, the dice scores are 69.33 % for edema and 61.53 % for enhancing tumor. It is important to note that there is some variability in performance observed across different tumor regions. Specifically, lower scores were observed for the NC and ET regions.

Table 2. Performance measures for S-UNET model

Measures	Train	Validation	Test
IOU	0.8330	0.8319	0.8339
Dice Coefficient	0.5782	0.5635	0.5868
Dice Coefficient (Necrotic Core)	0.5394	0.4825	0.5164
Dice Coefficient (Edema)	0.6773	0.6557	0.6933
Dice Coefficient (Enhancing Tumor)	0.6360	0.5806	0.6153

Fig. 4 depicts the segmented brain tumor sub-regions utilising the D-UNET and S-UNET architectures. The test set results indicate the DC scores obtained using the D-UNET model. The results indicate that the NC achieved a percentage of 65.52 %, the edema achieved a percentage of 78.10 %, and the ET achieved a percentage of 72.69 %. The second row displays the equivalent predicted images generated by the D-UNET model. The measured metrics for the D-UNET model can be referred from Table 1.

On the other hand, the S-UNET model exhibited a segmentation performance on the test data, with dice coefficient scores of 51.64 % for the necrotic core, 69.33 % for the WT, and 61.53 % for the ET. The measured metrics can be seen from the table 2, for the S-UNET model. Significantly, the first row of Figure 4 illustrates the predicted segmented images derived from

the S-UNET model, so suggesting a relatively imprecise segmentation. In contrast, the evaluation metrics clearly demonstrate the higher performance of the D-UNET model, as observed in the second row. The results of this study clearly indicate that the D-UNET model outperforms the S-UNET model in terms of segmentation performance, as evidenced by the measured performance metrics.

4. DISCUSSION

This section discusses the effectiveness of the DL models for brain tumor sub-region segmentation based on IOU and DC metrics. The comparison includes the proposed D-UNET model, S-UNET, 3D CNN[23], MTA-Unet[24], and 3D Unet[25] method. The evaluations were conducted using the BraTS 2020 dataset. Table 3 represents the comparison of our proposed model with other models. The D-UNET model, an enhancement of the traditional UNET architecture with dilated convolutions, demonstrated superior segmentation results compared to the other models. It achieved an IOU score of 87 % and a DC score of 78 % on the whole tumor region.

On the other hand, the S-UNET model, representing the traditional UNET architecture without dilated convolutions, yielded reasonable results but fell short compared to D-UNET. It achieved an IOU of 83 % and a DC of 57 % on the whole tumor, with lower values on tumor subregions. The 3D Unet proposed by Sohail et al. and MTAUnet proposed by Avasthi et al., both models have lower performance, achieving DC score of 72 % on the whole tumor region. However, specific results for other tumor subregions were not reported in their evaluation. 3D CNN proposed by Chen et al., also has DC score of 72 % which again is lower that the D-UNET. Moreover, IOU scores were not reported in the compared models as their evaluation metric. The significant advantage of the D-UNET model lies in its ability to leverage dilated convolutions, enabling it to capture multi-scale contextual information efficiently. This results in better representation learning for brain tumor sub-region segmentation. The incorporation of dilated convolutions allows D-UNET to capture finer details and intricate shapes of tumor sub-regions, contributing to its superior performance compared to the S-UNET.

Overall, the proposed D-UNET model outperforms its peers under comparison, making it a promising and effective tool for brain tumor sub-region segmentation. Although, D-UNET exhibits robustness and accuracy on the BraTS2020 dataset, still further investigations and validations on larger datasets and diverse populations can ascertain its general applicability and scalability.

5. CONCLUSIONS

This work presents a deep learning framework called D-UNET for brain tumor sub-region segmentation from MRI images. This enhancement allows D-UNET to achieve better performance in accurately delineating tumor sub-regions, demonstrating its potential as a valuable tool for brain tumor diagnosis. Through comprehensive evaluations on the BraTS2020 dataset, the D-UNET model was compared with S-UNET, 3D Unet, MTAUnet, and 3D CNN. The results reveal that D-UNET consistently outperformed the other models, achieving higher IOU and Dice Coefficient scores across various tumor sub-regions. The D-UNET model, an extension of the traditional UNET architecture, incorporates dilated convolutions to capture multi-scale contextual information effectively. Further, its ability to capture finer details and intricate shapes of tumor regions contributes to its superior segmentation accuracy.

This work can be extended with further research and validation initiated on larger datasets. Moreover, clinical settings can be warranted to confirm the efficacy and generalizability of the same.

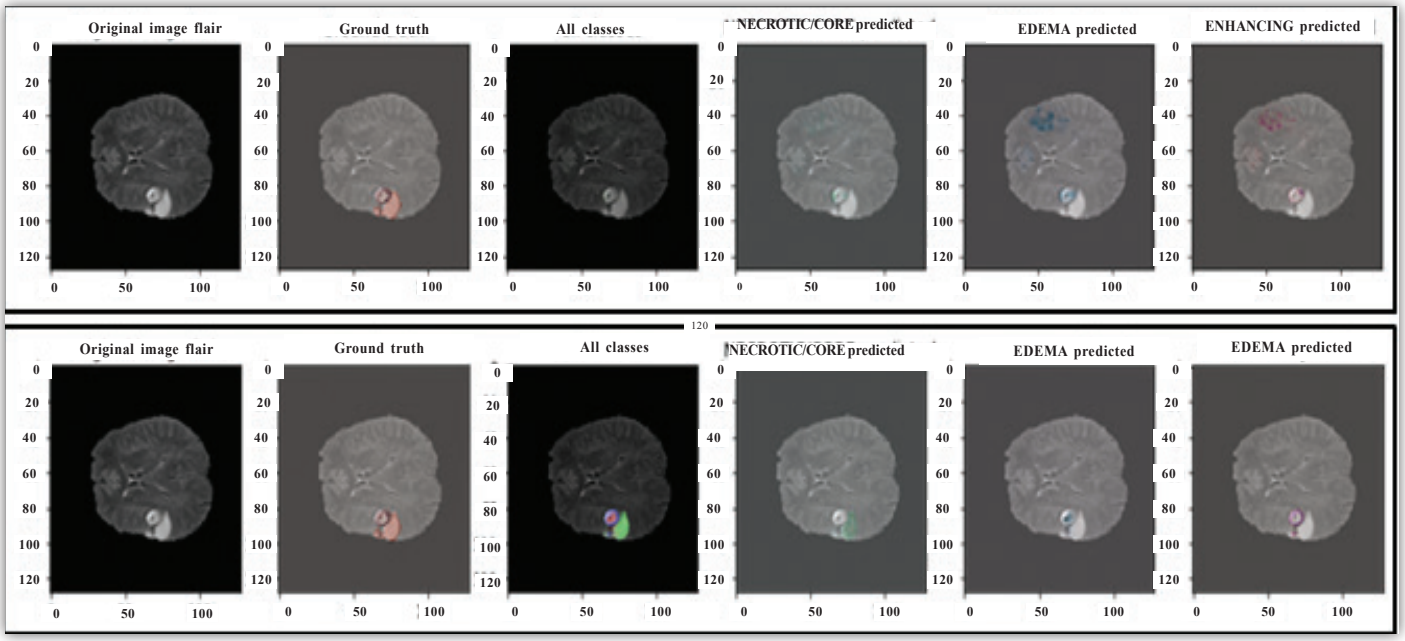

Figure 4. Predicted output of brain tumor sub-regions from S-UNET (first row) and D-UNET (second row).

Table 3. Comparison of D-UNET with peers.

Model	Dataset	IOU	DC	DC for tumor sub regions		
				NC	EDMA	ET
D-UNET	Brats2020	**87%**	**78%**	**65%**	**78%**	**72%**
S-UNET	Brats2020	83%	57%	51%	69%	61%
3D CNN (Chen et al.)[23]	Brats2020	-	72%	-	-	-
MTAUnet (Avasthi et al.)[24]	Brats2020	-	72%	59%	72%	61%
3D Unet (Sohail et al.)[25]	Brats2020	-	72%	-	-	-

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