SSRG International Journal of Computer Science and Engineering
ISSN: 2348–8387 / https://doi.org/10.14445/23488387/IJCSE-V11I11P101

Volume 11 Issue 11, 1-10, November 2024

Original Article

An Advanced Brain Tumor Segmentation using Integrated Deep Learning Approach

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Received: 24 September 2024 Revised: 21 October 2024 Accepted: 08 November 2024 Published: 22 November 2024

Abstract *- Accurate segmentation of brain tumors from medical imaging are essential for diagnosis and treatment planning. Deep learning has shown promise in automating this task, but challenges remain in achieving robust results. Several conventional models, like ANN, CNN, and fuzzy C-means, are used to segment the regions of the brain. However, most models face over-segmentation due to sensitive region data appearing in the MRI brain tumor image slices. The proposed models present a novel hybrid deep learning framework by integrating U-Net with DeeplabV3 to achieve better-segmented brain tumour segmentation accuracy, advancing the current state of the art. The experiment results showed better improvement than the conventional model in terms of accuracy and dice coefficients.*

Keywords *- U-net, Deeplab V3, Data Augmentation, Fine tuning*.

1. Introduction

Brain tumors are abnormal growths of cells in the brain. The World Health Organization (WHO) categorizes brain tumors (BTs) into four grades (I-IV) based on their level of malignancy or benignity. Currently, the standard imaging modalities for detecting and analysing BTs are Magnetic Resonance Imaging (MRI) and Computed Tomography (CT) scans, which provide valuable information for diagnosis and treatment planning [8]. There are over 120 types, including Gliomas, Meningiomas, Acoustic Neuromas, Pituitary Tumors, Medulloblastoma, and Craniopharyngiomas. Gliomas, accounting for 70% of all brain tumors, arise from glial cells and can be aggressive, like Glioblastoma, or benign, like Astrocytoma. The primary obstacles in brain tumor segmentation are the variability in tumor shape, size, and location throughout the brain, as well as the subtle contrast between the tumor and adjacent brain tissue, making it difficult to accurately distinguish and isolate the tumor [9].

Meningiomas, arising from the meninges, are mostly benign, while Acoustic Neuromas, developing on the nerve between the inner ear and brain, can cause hearing loss and balance issues. Pituitary Tumors, occurring in the pituitary gland, can affect hormone production, and Medulloblastoma, typically found in children, is a malignant tumor in the cerebellum. Craniopharyngiomas, benign tumors near the pituitary gland, can impact hormone production and vision. Detecting, segmenting, and classifying brain tumors using MRI images is an active area of development aimed at improving diagnosis and treatment [1].

Segmenting brain tumors from MRI images is a challenging task due to the intricate structure and appearance of tumors, whose fuzzy borders often blend with surrounding brain tissue, making it difficult to distinguish affected tissue from healthy tissue [2]. Brain tumor classification remains a formidable task due to the variability in tumor morphology, complex appearance in images, and inconsistent illumination effects. To support radiologists' diagnoses, effective techniques are essential for accurate brain tumor classification. Fortunately, new methodologies are being developed and refined every year, offering improved diagnostic capabilities and enhanced patient outcomes [11].

Despite ongoing research, predicting brain tumors and patient survival remains an unsolved challenge. However, advances in MRI technology have opened up new avenues for brain cancer research, including predictive modelling, tumor segmentation, and segmentation analysis. Brain tumors can be broadly classified into two categories: benign and malignant. By leveraging MRI data, it is possible to differentiate and categorize specific tumor types, such as gliomas, meningiomas, and pituitary tumors. This can aid physicians in diagnosis and treatment planning, potentially reducing the need for risky histology procedures [2]. Among primary brain tumors, meningioma, glioma, and pituitary tumors are particularly aggressive and pose significant challenges to early detection and effective treatment, making them the most critical types of brain tumors to diagnose and manage [14]. The proposed method leverages a CapsNet architecture to capture rotational invariance and spatial hierarchies in brain

features, enabling robust and spatially informed analysis of brain characteristics [3]. Techniques like Generative Adversarial Networks (GANs) and Variation Auto encoders (VAEs) are used to generate realistic brain images with tumors.

Convolutional Neural Networks (CNNs), a type of Deep Learning algorithm, are commonly used for visual data analysis. Designed to require minimal pre-processing, CNNs draws inspiration from the human brain's biological processes, mimicking its efficient visual information processing [4]. Pituitary brain tumors are benign growths that develop in the pituitary gland, a small endocrine gland located at the base of the brain, beneath the hypothalamus. This gland is vital in producing and regulating essential hormones that govern various bodily functions [11]. A computer-aided diagnosis (CADx) system is crucial for addressing this challenge. By implementing CADx, the workload of radiologists and doctors can be significantly reduced, and medical image analysis can be facilitated. In recent years, numerous researchers have developed various robust and accurate solutions to automate the detection and classification of brain tumors, demonstrating the potential for improved diagnostic efficiency and accuracy [14].

Abnormal cells in the body proliferate uncontrollably, multiplying rapidly and spreading, which leads to the development and growth of tumors [13]. Gliomas, a type of brain tumor that arises from glial cells, are the primary focus of current research in brain tumor segmentation. These tumors are the most common type of brain tumor, and researchers are working to develop more accurate and efficient methods for segmenting and diagnosing gliomas using imaging techniques like MRI [10]. Additionally, segmentation informs radiation therapy plans, reducing radiation exposure to healthy brain tissue and surgical planning, reducing the risk of complications. Diagnosing brain tumors typically involves a combination of physical and neurological exams. However, the most definitive method is the biopsy, which entails surgically removing a tissue sample and examining it under a microscope using various histological techniques to confirm the diagnosis [5].

The DWA mechanism integrates tumor and brain centroid information into the model. Experiments on the BRATS 2018 dataset demonstrate the model's competitive performance, yielding mean Dice scores of 0.9203 (whole tumor), 0.9113 (enhancing tumor), and 0.8726 (tumor core). Additional quantitative and qualitative results are presented, further validating the model's effectiveness [12]. Furthermore, we investigate the effect of data augmentation on the model's test accuracy and utilize Grad-CAM visualization to gain insights into the decision-making process of the optimal model. This approach effectively highlights tumor locations within brain images, providing valuable information. Our results demonstrate that employing EfficientNetB2 as the underlying framework yields significant performance enhancements, with an overall test accuracy of 99.06%, precision of 98.73%, recall of 99.13%, and F1-score of 98.79% [13]. The cerebellum coordinates balance, posture, and movement; tumors in this area can cause coordination and balance problems. Segmenting brain tumors is a crucial step involving isolating the tumor from surrounding normal tissues like cerebrospinal fluid, white matter, and grey matter. While manual segmentation is possible, automated software-aided segmentation is preferred, as computer analysis is more accurate and efficient than human judgment, which can be unreliable and time-consuming [6].

Certain factors can increase a person's risk of developing a brain tumor. Age is a significant risk factor, with most brain tumors occurring in people over 55. A family history of brain tumors or other cancers also raises the risk. Deep learning techniques can facilitate the efficient processing and objective evaluation of vast amounts of MRI-based image data. While several review papers have addressed traditional methods for segmenting brain tumor images from MRI data, deep learning approaches offer a promising alternative for improving the accuracy and efficiency of this process [10].

Consequently, a robust and automatic brain tumor segmentation technique will have a profound impact on the diagnosis and treatment of brain tumors. Additionally, it may also facilitate timely diagnosis and treatment of neurological disorders, such as Alzheimer's disease, schizophrenia, and dementia. An automatic lesion segmentation technique can provide radiologists with crucial information regarding tumor volume, localization, and shape, including enhancing tumor core and whole tumor regions, thereby enabling more effective and informed therapy decisions [12]. Moreover, underdiagnosing brain tumors can have serious consequences, including reduced treatment effectiveness and lower survival rates. Accurate diagnoses, on the other hand, enable targeted treatments and significantly improve patient outcomes and long-term survival [7].

2. Literature Review

Dinthisrang Daimary et al. [1] presented a unique method for brain tumor segmentation—hybrid SegNet, ResNet, and U-Net. It solves the issue of tiny brain tumors being segmented improperly. They each attained mean accuracy scores of 91.6%, 93.3%, and 93.1%. By using cutting-edge hybrid designs, they seek to strike a compromise between accuracy and computing efficiency. Implementation complexity and possible computing demands are limitations. Experimental findings on the BraTS dataset demonstrate improved accuracy over conventional CNNs.

T. Balamurugan et al. [2] present a hybrid Deep Convolutional Neural Network (DCNN) classifier with a LuNet classifier for brain tumor diagnosis. The primary intention of this work is to determine the area of the tumor site

and classify brain tumors as benign or malignant. It can correctly diagnose both high and low-grade Tumors compared to previous techniques. It shows better accuracy results, 99.7% compared to the other CNN techniques. So, the proposed method outperforms the existing techniques.

Ayesha Jabbar et al. [3] introduce a hybrid model, Caps-VGGNet, to improve brain tumour detection and classification. By automating feature extraction and classification, the hybrid model tackles the problem of high dataset requirements. The study seeks to increase diagnostic accuracy, specificity, and sensitivity compared to conventional models. The accuracy obtained for this model is 99%. However, limitations include potential interpretability issues due to the model's complex architectures and the need for comprehensive validation across diverse medical conditions beyond the datasets used.

Parasa Rishi Kumar et al. [4] introduced a hybrid model, HDLN (Hybrid Deep Learning Network), and uses mask RCNN to classify brain tumor. This model's primary goal is to categorize the different kinds of brain tumours. Compared to the current categorization algorithms, it attained a remarkable accuracy of 98.53%. The study does, however, identify many limitations that could have an impact on its effectiveness, including dataset bias, generalizability to a variety of patient demographics, and potential difficulties in actual clinical settings.

Jose Dixon et al. [5] propose an improved AI-based architecture that is a major step forward in the categorization of brain tumours. The ViT (vision transform) and CNNs are combined into a hybrid ensemble framework to improve the model's robustness and accuracy for identifying brain tumours from MRI scans. The potential of AI-driven technologies in medical imaging and healthcare applications is highlighted by the overall gains in terms of diagnostic efficiency and reliability, even with certain constraints like computational complexity and interpretability. It has limitations, such as reliance solely on MRI images for predictions, limited explainability of machine decisions, and the use of a single ML classifier. These constraints provide motivation for future enhancements and refinements in our approach.

Annapareddy V. N. Reddy et al. [6] developed a novel brain tumor classification system using a comprehensive approach. Tumour borders are first identified through preprocessing with an enhanced median filter and then segmentation using a U-net model. For tumour classification, the hybrid DBN (Deep Belief Network) and Bi-LSTM (Bidirectional Long Short-Term Memory) model is used, and weights are optimized using the cutting-edge BMEBEO (Blue Monkey Extended Bald Eagle Optimisation) method. The study's significant F-measure was 96.16%. However, limitations can include computational complexity and susceptibility to changes in image quality, pointing out areas that need to be improved in the future.

Ebrahim Mohammed Senan et al. [7] proposed a novel approach integrating deep learning and traditional machine learning techniques for brain tumour diagnosis. Its goal is to improve medical diagnosis, essential to raising patient survival rates by making them timelier and more accurate. However, generalizability is impacted by restrictions such as dataset size and unpredictability. Despite difficulties, the AlexNet with SVM hybrid performs admirably, exhibiting 95.10% accuracy in the classification of MRI images of brain tumours, indicating encouraging advancements in medical diagnostic systems.

Asaf Raza et al. [8] proposed a hybrid deep learning model based on a modified GoogLeNet architecture to accurately classify three types of brain tumors. The model achieves exceptional performance metrics by enhancing GoogLeNet with additional layers and integrating a leaky ReLU activation function: 99.67% accuracy. Compared to various state-of-the-art models like AlexNet, ResNet50, and others, DeepTumorNet demonstrates superior classification accuracy, highlighting its potential for robust brain tumor classification. However, the limitation is the potential dataset bias with few malignant MRI images, impacting generalization to real-world scenarios where malignancies are rarer.

Nagwa M. Aboelenein et al. [9] propose the Hybrid Two-Track U-Net (HTTU-Net) architecture for brain tumor segmentation. By utilising batch normalisation, Leaky ReLU activation, and two separate tracks with differing layer counts and kernel sizes combined for final segmentation, it seeks to improve automated diagnosis performance and accuracy. Class imbalance is addressed by applying generalised Dice loss and targeted loss, which produce encouraging results with average Dice similarity coefficients. The paper highlights its potential to speed diagnostic processes while discussing quantitative and qualitative evaluations and displaying high accuracy comparable to expert human-level performance. The limitation here is that each epoch's training stage is time-consuming.

Ali Isin et al. [10] explores recent progress in MRI-based brain tumor segmentation, focusing on deep learning methods. Its objective is to assess the efficiency of these techniques in automating segmentation, thereby enhancing diagnostic precision and reducing manual workload. The scope includes an overview of brain tumors, traditional segmentation methods, and a detailed examination of cutting-edge deep learning algorithms. They considered a limited dataset, potentially influencing the model's performance. Future directions emphasize the integration of these advancements into everyday clinical workflows to advance patient care through timely and precise tumor detection.

Shaimaa E. Nassar et al. [11] examine the difficulties in classifying brain tumours in medical image analysis, highlighting the critical role that artificial intelligence—specifically, deep learning—plays in improving precision and effectiveness. Using a system that combines five different models, the suggested methodology uses a dataset of 3064 T1-weighted contrast-enhanced MRI scans from 233 patients. This method seeks to efficiently automate the classification of tumours, assisting radiologists in making quicker and more accurate diagnoses. The study recognises limitations in generalizability and the need for additional validation across varied patient populations despite attaining an outstanding overall accuracy of 99.31%. The limitation highlighted here is the scarcity of patient data, particularly for the meningioma class.

Ramin Ranjbarzadeh et al. [12] proposed a methodology to enhance brain tumor localization and segmentation from MRI by addressing computational complexity and overfitting. It introduces a preprocessing step focusing on relevant image regions to reduce computational load and mitigate overfitting with a Cascade Deep Learning model. A Cascade Convolutional Neural Network (C-CNN) efficiently extracts local and global features, complemented by a novel Distance-Wise Attention (DWA) mechanism improving segmentation accuracy by considering tumor and brain center locations. It achieves mean dice scores of 0.9203 for the whole tumor. The limitation here is related to the handling of large tumor volumes.

Using MRI images, Baiju Babu Vimala et al. [13] utilize transfer learning with five EfcientNets for multi-class brain tumor classification. Models are initialized with ImageNet weights and enhanced with convolution, dropout, and fully connected layers. Evaluation of the CE-MRI Figshare dataset includes fine-tuning for each EfcientNet variant. EfcientNetB2 demonstrates superior performance through rigorous testing and cross-dataset validation, achieving an accuracy of 99.06%, surpassing existing methods. Limitations involve dataset biases and reliance on high-quality MRI scans.

Mirza Mumtaz Zahoor et al. [14] proposed a two-phase deep learning framework for brain tumor analysis using MRIs. The first phase employs DBFS-EC for accurate tumor detection, achieving high performance metrics. The second phase combines HOG and BRAIN-RENet CNN features to classify tumors, aiming to enhance detection accuracy across glioma, meningioma, pituitary, and normal images. However, challenges include dataset variability, generalizability across clinical scenarios, and computational complexity for real-time use. T. Balamurugan et al. [2] designed a hybrid DCNN classifier using an enhanced LuNet algorithm for MRI brain tumor analysis. It aims to boost diagnostic accuracy by assessing tumor areas and classifying tumors as benign or malignant. Leveraging GLCM and VGG16 for feature extraction and LOG for preprocessing, the method achieves 99.7% accuracy. However, challenges persist with dataset size and computational complexity, suggesting avenues for further improvements in automated brain tumor diagnosis. Most conventional deep learning models face the problem of handling large tumor regions in high-dimensional MRI scans and potential interpretability issues due to heavy and complex architectures.

3. Materials and Methods

3.1. Imaging Analysis of BraTs

The assessment of cutting-edge techniques for segmenting brain tumors in multimodal MRI scans has always been the main emphasis of BraTS. BraTS 2020 is a multi-institution pre-operative magnetic resonance imaging system that is primarily used for the segmentation of brain tumors that are biologically heterogeneous, such as gliomas and meningioma. Additionally, employing integrative analyses of radiomic aspects and machine learning approaches, BraTS'20 focuses on the prediction of patient overall survival and the differentiation between pseudoprogression and actual tumor recurrence to identify the clinical importance of this segmentation task. Lastly, evaluating algorithmic uncertainty in tumor segmentation is the goal of BraTS'20.

3.2. Proposed Hybrid DLV-Unet Model

To overcome the Conventional issues of computational complexity and limited computing demands over Machine learning and deep learning architectures, an advanced deep learning-based brain tumor segmentation was proposed using a hybrid DLV3-Unet model. Initially, the data augmentation will be performed along the required features, and the train samples' mask images will be prepared. Build the fine-tuned hybrid DLV3-Unet model architecture by integrating enhanced Deep lab V3 and U-net models to further validate the proposed model using test data. The concept of the model architecture decorates in Figure 3.1.

- Pre-processing and augmentation through the invention of features.
- Build Fine-tuned hybrid DLV3-Unet model.
- Validate the model using test data.

3.2.1. Pre-Processing and Augmentation through the Invention of Features

The proposed model uses the Brats-2020 data set to segment the brain tumor regions. It holds 42.8 Gb of High dimensional NIfTI files (.nii.gz) related to all brain tumors multimodal MRI scans, and these offer the details about the following brain tumor MRI slices. Majorly Native (T1), post-contrast T1-weighted, T2-weighted, T2-FLAIR volumes. Before being fed into the proposed model network, the resolution of the dataset was first resized to 512 × 512 resolution because the original 1024 × 1024 resolution consumed too much GPU memory. Then, the image was normalized by dividing the pixel value by 128.

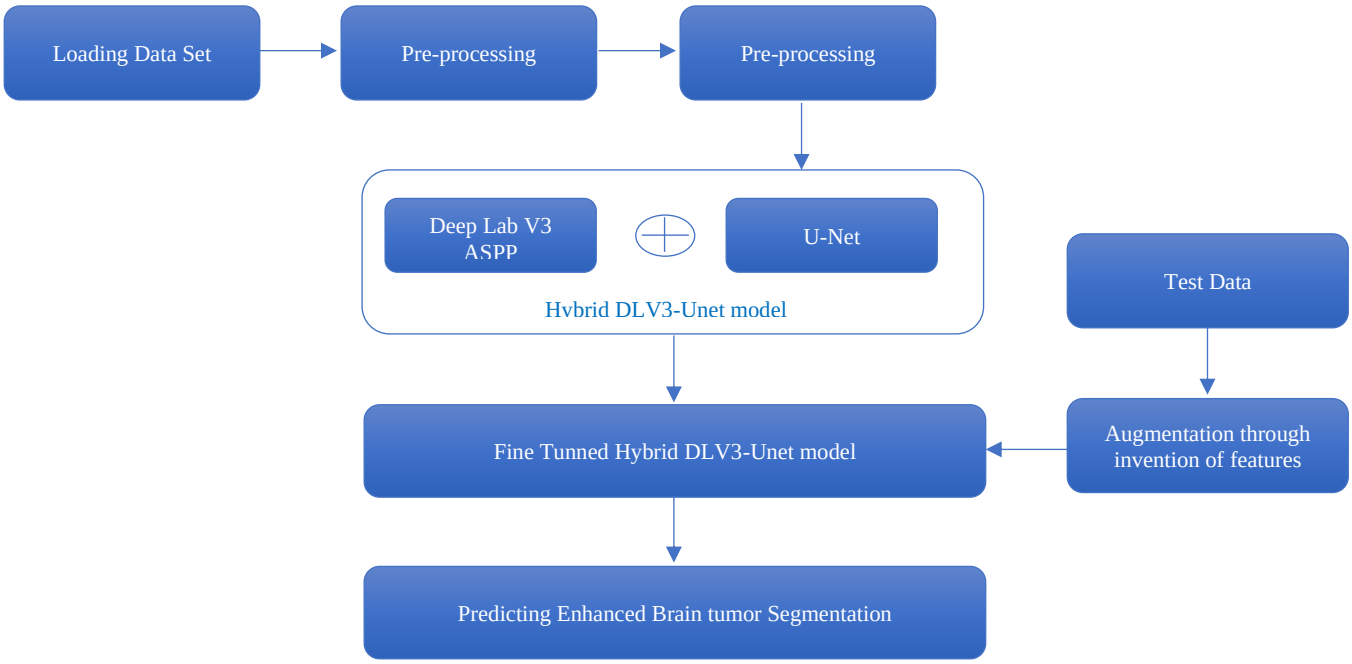

Fig. 1 Proposed hybrid model for brain tumor segmentation

Step 1: Consider dtrain, dtest, and dval and load the train, test, and validate data.
Step 2: Resize the images once they are cropped in the Train data.
Step 3: Convert the mask data to prepare the mask image XXY.
Step 4: To resize, images in the Mask image are cropped.

3.2.2. Build Fine-Tuned Hybrid DLV3-Unet Model Architecture

The major ideology behind the hybrid model architecture is to improve the detection rate in both the spalling class and the crack class. U-net has an improved detection rate for the spalling class and the crack class, but while combining U-net architecture with Deep Lab v3, the missed crack class is also detected in a better manner. U-Net's U-formed design and conjunction at each convolution level are among its key characteristics.

Initial Phase

The altered, aligned atrous spatial pyramid pooling, which forms the core of the expanded architecture, is the primary characteristic of DeepLabV3. In the altered Deeplabv3, additional layers, additional batch normalization, and ReLu are applied at strides of 4, 8, and 16 following each depthwise separable convolution operation. Utilizing three X three conventional layers at varying stride rates of eighteen, apply Atrous Spatial Pyramid Pooling (ASPP) and concatenate the conventional layer after picture pooling. A depth-wise convolution and a point-wise convolution make up an ASPP convolution. Every channel in the depthwise convolution process uses a distinct filter to carry out the convolution function. While the single-pixel dot product is all that the point-wise convolution does, The ASPP module uses point-wise convolution and depthwise atrous separable convolution of various rates. After two convolution operations in the deep lab v3, the feature map was upsampled and transferred to the encoder phase in U-net architecture.

Phase of Encoder

U-Net's encoder section employs four convolution blocks before moving on to 2D max-pooling operations. The number of channels with special features begins at 32 and increases by two, with each max-pooling until 512 channels are reached.

Phase of Decoder

After transposing convolution operations, the decoder section has four convolution blocks identical to the encoder section. Convolution in reverse, or inverted convolution, is also referred to as deconvolution techniques. Transpose convolution uses a flexible kernel that may be taught to compensate for data loss throughout the upsampling process, in contrast to bilinear upsampling, which uses a fixed kernel to upsample a feature map. Transpose convolution has the benefit of potentially being a non-linear technique that can efficiently remove extraneous information.

Phase of Deployment

Data from the decoder's previous layer was further concatenated with the feature map. Lastly, bilinear upsampling and a straightforward two-times convolution were put into practice.

Figure 2 is an illustration for DeepLabV3 + Unet. This is quite effective in a big network like the DLV3-Unet and lowers the computing cost compared to standard convolution.

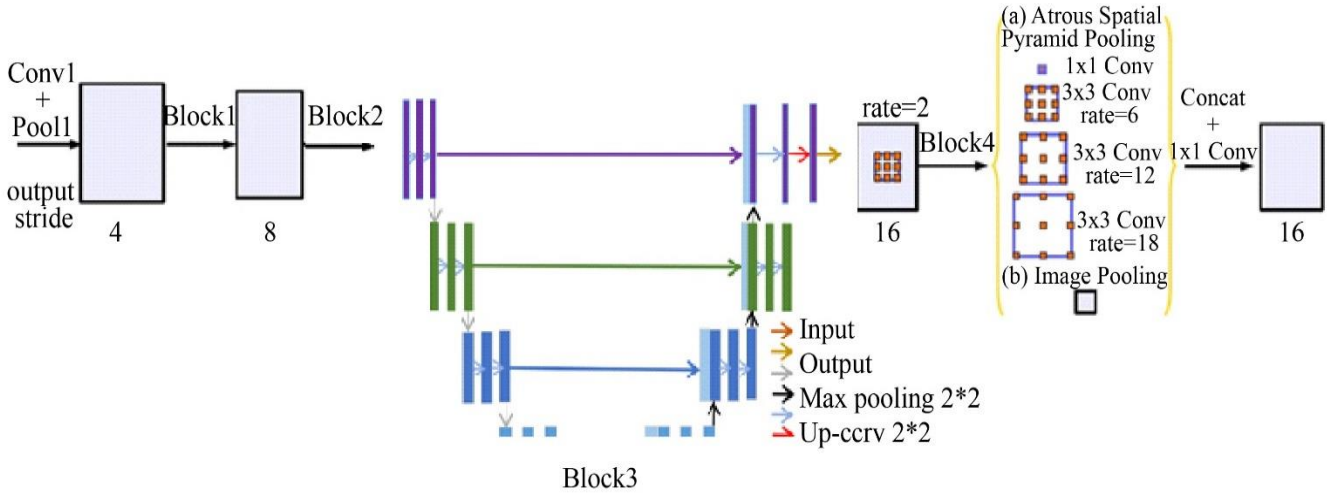

Fig. 2 Proposed Hybrid DLV3-Unet model architecture for Brain Tumor segmentation

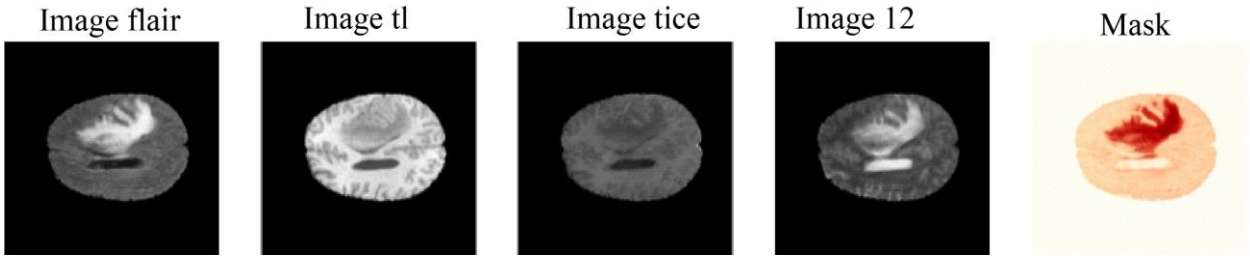

Fig. 3 Outcome of the mask brain tumor image using data augmentation

4. Results and Discussion

The quality of the segmented results is always determined by the quality of the input data. Pre-processing is the first step to improving the quality of unprocessed MRI brain tumor images. Data augmentation is a method that uses previously collected information to create modified copies of a dataset, thereby artificially expanding the training set. Data augmentation during ML model training helps avoid overfitting.

In order to increase the applicability and robustness of the model, artificial data variations are created using data augmentation for feature invention. It can manage data variability, build the mask data by learning new features, and avoid overfitting. Nonetheless, augmentation must be balanced to preserve segmented data quality and prevent excessive computational expenses.

In this stage, raw images are available in xx. nii file format with a total of 155 slices, which are converted into a grayscale image and resized to 240 x 240. The data augmentation is used to fit raw data to the learning model during the pre-processing stage. This strategy is useful for improving model performance, particularly when working with varied data. Figure 3 describes the outcomes of data pre-processing and generating mask data for the raw data using data augmentation. The experimental results show enhanced contrast with the raw data. The pre-processed images are driven by a hybrid deep learning-based fine-tuned hybrid DLV3-Unet model approach, which is an integrated model of U-Net with deep lab version 3 for brain tumor segmentation.

The proposed model is built with a learning rate of 0.0010 and a total of 8,855,293 (33.78 MB) parameters, which contain 8,821,181 (33.65 MB) trainable parameters and 34,112 (133.25 KB) non-trainable parameters to achieve better segmentation accuracy. Table 1 below refers to the total summary of the hybrid DLV3-Unet model.

A maximum of 352 runs, each run having 5 epochs, are performed to fit the fine-tuned hybrid DLV3-Unet model until it reaches the convergence state. At the 5th epoch of the 249th run, the model achieved a better training and validation accuracy of 98.74 and 98.26. It is clearly noticed that the proposed model takes 384 ms for each epoch and 96 sec for each run.

Compared with traditional models, the proposed experimental results show better results regarding Dice coefficients, precision, sensitivity, and specificity for training and validation data. Table 2 refers to model performance in terms of training and validation data.

Table 1. Summary of the proposed hybrid DLV3-Unet model

Layer (type)	Output Shape	Param #	Connected to
input_layer_2 (InputLayer)	(None, 128, 128, 2)	0	-
conv2d_14 (Conv2D)	(None, 128, 128, 3)	57	input_layer_2[0]…
mobilenetv2_1.00_1… (Functional)	(None, 4, 4, 1280)	2,257,984	conv2d_14[0][0]
up_sampling2d_2 (UpSampling2D)	(None, 16, 16, 1280)	0	mobilenetv2_1.00…
conv2d_15 (Conv2D)	(None, 16, 16, 32)	368,672	up_sampling2d_2[…
max_pooling2d_4 (MaxPooling2D)	(None, 8, 8, 32)	0	conv2d_15[0][0]
conv2d_16 (Conv2D)	(None, 8, 8, 64)	18,496	max_pooling2d_4[…
max_pooling2d_5 (MaxPooling2D)	(None, 4, 4, 64)	0	conv2d_16[0][0]
conv2d_17 (Conv2D)	(None, 4, 4, 128)	73,856	max_pooling2d_5[…
max_pooling2d_6 (MaxPooling2D)	(None, 2, 2, 128)	0	conv2d_17[0][0]
conv2d_18 (Conv2D)	(None, 2, 2, 256)	295,168	max_pooling2d_6[…
max_pooling2d_7 (MaxPooling2D)	(None, 1, 1, 256)	0	conv2d_18[0][0]
conv2d_19 (Conv2D)	(None, 1, 1, 512)	1,180,160	max_pooling2d_7[…
conv2d_20 (Conv2D)	(None, 1, 1, 512)	2,359,808	conv2d_19[0][0]
conv2d_transpose_4 (Conv2DTranspose)	(None, 2, 2, 256)	524,544	conv2d_20[0][0]
concatenate_4 (Concatenate)	(None, 2, 2, 512)	0	conv2d_transpose… conv2d_18[0][0]
conv2d_21 (Conv2D)	(None, 2, 2, 256)	1,179,904	concatenate_4[0]…
conv2d_transpose_5 (Conv2DTranspose)	(None, 2, 2, 128)	131,200	conv2d_21[0][0]
concatenate_5 (Concatenate)	(None, 4, 4, 256)	0	conv2d_transpose… conv2d_17[0][0]
conv2d_22 (Conv2D)	(None, 4, 4, 128)	295,040	concatenate_5[0]…
conv2d_transpose_6 (Conv2DTranspose)	(None, 8, 8, 64)	32,832	conv2d_22[0][0]
concatenate_6(Concatenate)	(None, 8, 8, 128)	0	conv2d_transpose… conv2d_16[0][0]
conv2d_23 (Conv2D)	(None, 8, 8, 64)	73,792	concatenate_6[0]…
conv2d_transpose_7 (Conv2DTranspose)	(None, 16, 16, 32)	8,224	conv2d_23[0][0]
concatenate_7 (Concatenate)	(None, 16,16, 64)	0	conv2d_transpose… conv2d_15[0][0]
conv2d_24 (Conv2D)	(None, 16, 16, 32)	18,464	concatenate_7[0]…
up_sampling2d_3 (UpSampling2D)	(None, 128, 128, 32)	0	conv2d_24[0][0]
conv2d_25 (Conv2D)	(None, 128, 128, 64)	18,496	up_sampling2d_3[…
conv2d_26 (Conv2D)	(None, 128, 128, 32)	18,464	conv2d_25[0][0]
conv2d_27 (Conv2D)	(None, 128, 128, 4)	132	conv2d_26[0][0]

Table 2. Performance of the hybrid DLV3-Unet model on training and validation data

Training performance	Validation performances
accuracy: 0.9874	val_accuracy: 0.9826
dice_coef: 0.3859	val_dice_coef: 0.2618
dice_coef_edema: 0.4061	val_dice_coef_edema: 0.0486
dice_coef_enhancing: 0.2640	val_dice_coef_enhancing: 0.0100
dice_coef_necrotic: 0.3231	val_dice_coef_necrotic: 0.0122
loss: 0.0330	val_loss: 0.2179
mean_io_u: 0.5102	val_mean_io_u: 0.4969
precision: 0.9942	val_precision: 0.9828
sensitivity: 0.9827	val_sensitivity: 0.9823
specificity: 0.9979	val_specificity: 0.9943

	Epoch	Accuracy	Loss	Sensitivity	Specificity	Precision
0	1	0.981940	0.075013	0.977179	0.995378	0.985908
1	2	0.983329	0.052263	0.979582	0.996600	0.989992
2	3	0.983684	0.044084	0.979006	0.997299	0.992289
3	4	0.984644	0.041712	0.979557	0.997327	0.992409
4	5	0.986651	0.034793	0.981534	0.997753	0.993801

Fig. 4 Evaluation report of the proposed model

Figure 4 refers to the performance of the test data in terms of accuracy, precision, and loss.

The loss and precision prove accurate segmentation of the brain tumor images using the proposed model.

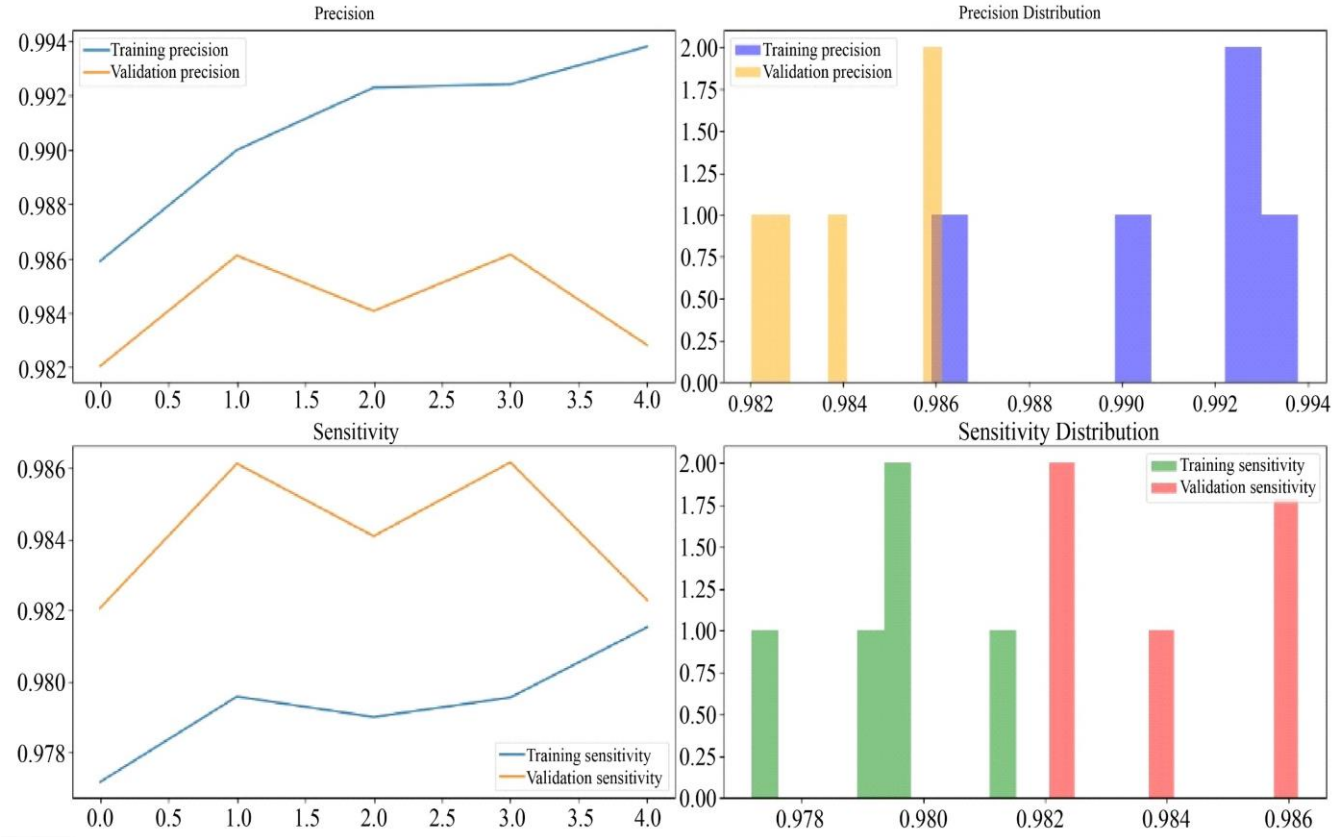

Fig. 5 Histogram-based visualization of the proposed model in terms of sensitivity and precision

Plot the training precision and validation precision across each epoch value to know how well the model is learning. The y-axis represents the accuracy, and the x-axis represents the epoch values, as shown in Figure 5. The precision of the training data gradually increases with each epoch, and the validation precision decreases after 3 epochs. Figure 5 visualizes the performance of precision and sensitivity on each epoch using a plot and histogram.

The training loss rapidly decreases initially, and then both training and validation losses gradually decrease, indicating that the model is improving at making predictions without overfitting, which leads to strong performance on the training and validation sets. Figure 6(a) refers to a plot visualization of the loss and accuracy for both training and validation precision across each epoch value to know how well the model is learning. The y-axis represents the loss, and the x-axis represents the epoch values, as shown in Figure 5. The results plot visualization refers to the growth rate of the validation loss from 0.24891 to 0.21790. The Dice coefficient of the proposed model gradually increases with each epoch, and the plotted results prove the similarity between the predicted segmented image and ground truth values of the brain tumor images using pixel-wise comparison. Fig. 6(b) refers to a plot visualization of the mean IOU and dice coefficient for both training and validation precision across each epoch value to know how well the model is learning.

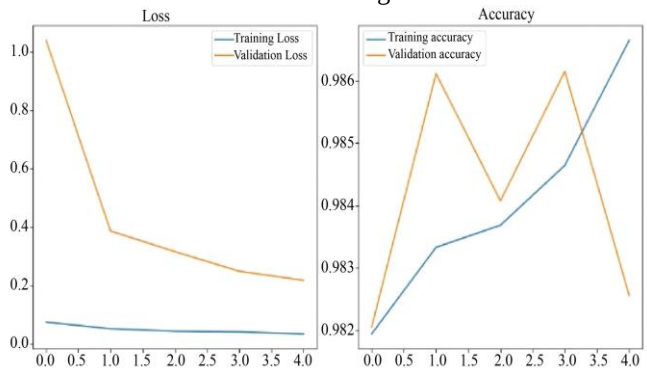

Fig. 6 (a) Plot visualization of the proposed model in terms of loss and accuracy

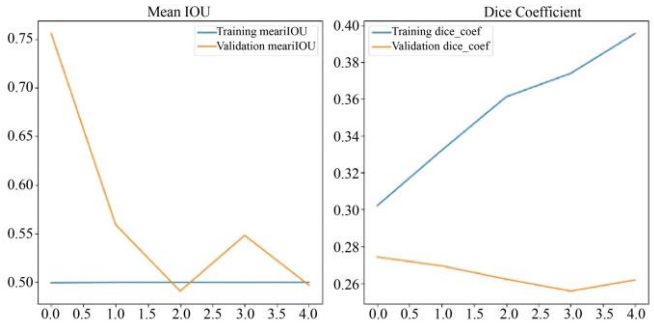

Fig. 6(b) plot visualization of the proposed model in terms of mean IOU and dice similarity coefficient

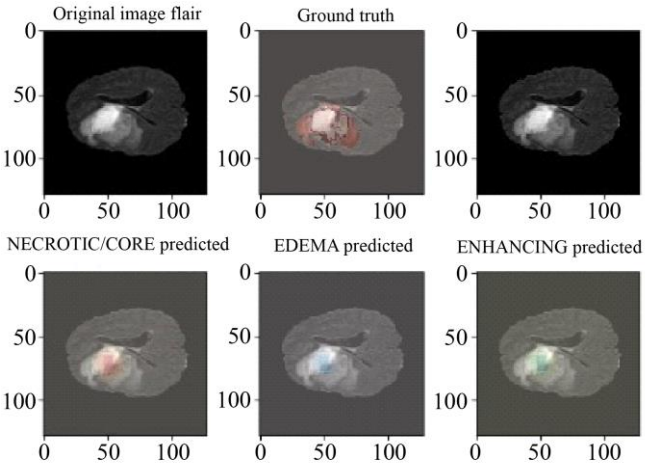

Fig. 7(a) prediction of segmented brain tumor regions on the test image

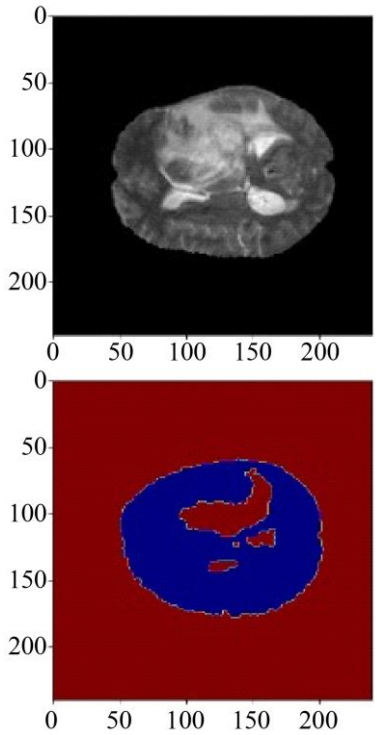

Fig. 7(b) Prediction of segmented brain tumor regions on the dynamic samples

After evaluating the performance of the trained model, assess the test accuracy using test data and prediction segments of brain tumors. The proposed hybrid DLV3-Unet model obtains a test accuracy of 98.6. Figures 7(a) and 7(b) refer to the model prediction of segmented regions of brain tumor images.

The current approaches use a variety of strategies. Nevertheless, the proposed model shows enhanced accuracy over existing approaches and can be utilized to overcome some of the shortcomings of traditional methodologies. Table 3 compares the accuracy values of the proposed and current models. The bar chart for the existing model accuracy values in relation to the suggested model accuracy is displayed in Figure 8. It demonstrates greater accuracy than the methods currently in use. The methods employed are represented by the x-axis, and their accuracy is indicated by the y-axis. Compared to the existing methods, which yield 98.64% accuracy, the suggested model's accuracy is higher than that of the existing techniques.

Table 3. Comparison of the proposed model with the conventional model

SNo	Author	Techniques Used	Accuracy
1	Dinthisrang daimary [1]	SegNet, ResNet and U-Net	93.3%
2	T.Balamurugan [2]	Hybrid Deep CNN, LuNet classifier	98.60%
3	Ayesha Jabbar [3]	Caps-VGG Net model	98%
4	Parasa Rishi Kumar [4]	Mask RCNN, Hybrid Deep CNN	98.53%
5	Annapareddy V.N. Reddy [6]	Deep Belief Network and bidirectional long short-term memory	96.16%
6	Ebrahim Mohammad Senan [7]	AlexNet, SVM	95.10%
7	Proposed Model	Proposed Fine-tuned hybrid DLV3-Unet Model	98.64%

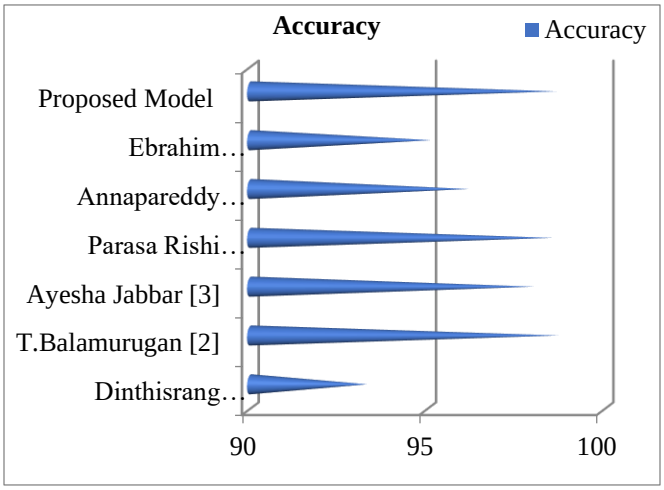

Fig. 8 Comparison graph

5. Conclusion

The proposed hybrid DLV3-Unet model is capable of handling large and sensitive tumor regions in high dimensional MRI images. The integrated architecture interprets the results well and greatly segments the brain tumor regions accurately. It is well-known for its resilience in semantic segmentation tasks. The proposed model produced remarkable results, with an accuracy of 98.6%. The reason for its excellent performance could have been its capacity to record fine-grained features while maintaining spatial information. The proposed deep learning-based hybrid architecture proved to be effective in segmentation and improved the detection rate of both the spalling class and the crack class. However, the DLV3-Unet model, tuned for image segmentation, showed its versatility and effectiveness in accurately segmenting sensitive brain tumour regions. The exceptional precision achieved by the model highlights their potential in medical imaging applications, providing physicians with useful instruments for accurate treatment and diagnostic planning. Furthermore, to improve the model's efficiency, modified kernels with multiple optimizers for detecting multiple sensitive brain tumor regions are used.

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