Multimodal MRI Brain Tumor Segmentation Using ACU-Net with Efficientnet Encoder and Uncertainty Estimation

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Abstract—**Brain tumor segmentation is necessary for accurate diagnosis, proper treatment planning, and patient monitoring. Magnetic Resonance Imaging (MRI) is widely used because it provides an ability to capture detailed images of brain structures. Manual segmentation is time consuming process, labour intensive, and prone to inconsistencies. Although deep learning models have performed well, single network architectures may not be able to accurately segment the complex tumor structures and blurred boundaries from multimodal MRI images. To overcome these challenges, this work introduces an enhanced Efficient Net based ACU-Net model for brain tumor segmentation. Multimodal MRI images are preprocessed by normalizing intensity variations to improve data consistency and then slice extraction and stacking the MRI modalities. An Efficient Net model encoder extracts rich and discriminative features which are decoded using an ACUNet style architecture to generate accurate tumor segmentation maps. A boundary aware loss function is introduced to improve edge precision and while Monte Carlo Dropout is used to estimate prediction uncertainty to know how much the model is confident about the prediction and produce the confidence map. The proposed method is evaluated on merged dataset from Brain Tumor Segmentation (BraTS) 2019, 2020, and 2021, which consists of four different MRI modalities T1, T1ce, T2, and FLAIR. The results demonstrate strong segmentation performance, achieving Dice scores of 94.2% for Whole Tumor region, 96.2% for Tumor Core region, and 86.5% for Enhancing Tumor region, along with high IoU, precision, and recall values. The proposed model outperforms the other architectures such as U-Net and ACUNet in both quantitative metrics and boundary precision. These results show the effectiveness, robustness, and clinical applicability of the proposed model for reliable brain tumor segmentation and decision support.**

Index Terms—**Brain Tumor Segmentation, MRI, ACU-Net, Efficient Net, Boundary Aware Loss, Uncertainty Estimation**

I. INTRODUCTION

Brain tumors are abnormal cell that grow in the brain that can affect the normal brain functions and neurological functions. They are classified as primary tumors and secondary tumors. Primary tumors are the arising tumors in the brain or other tissues surrounding the brain such as the meninges. Secondary tumors are the metastatic i.e., they spread from the other organs of the body, such as lungs or breast. They can be benign or malignant, where with malignant tumors being more aggressive and life threatening. The presence of the tumor in brain will affect essential functions of the brain and cause headaches, seizures, nausea and other neurological symptoms. The proper diagnosis and accurate localization of tumor is important for decision making. The accurate diagnosis will help in surgery and radiotherapy and chemotherapy for the patient. Brain tumor is diagnosed using Magnetic Resonance Imaging (MRI) as they are better to produce high resolution images of brain structures. But analyzing MRI images is a complex task, requires specialized skills, and can be time consuming and error-prone. So, there is a need for automated, reliable computational models for improved diagnosis and subsequent prognosis.

Early diagnosis and precise localization of brain tumors in effective clinical decision-making process may include surgical planning, radiotherapy, and chemotherapy. The most common types of imaging include Computed Tomography (CT) as well as Magnetic Resonance Imaging (MRI). CT is quicker to assess structural abnormalities, but is lower in soft-tissue contrast, whereas MRI is more effective at soft-tissue resolution, and, therefore, better suited to the minute analysis of brain tumors. MRI is applicable in identifying typical brain tissues as various types of

tumors such as glioma, meningioma and pituitary tumors with disproportionate strengths and distorted forms. In spite of such advantages, it is challenging to interpret manually on tumor heterogeneity and in an indistinct state because it does not have tumor boundaries. AI has been critical in enhancing medical image analysis with automatic and precise perception of a complex imaging data. In brain tumor detection, segmentation, and classification, deep learning models are trendy. These algorithms are also directly trained on MRI scans, reducing variability and improving diagnostic accuracy and helps clinicians to make effective decisions. It uses different modalities (such as T1, T1 contrast-enhanced (T1ce), T2 and FLAIR). T1-weighted MRI provides an explicit anatomy with the tumor in most cases being low contrast. Amplification of functional sites of tumor with contrast agents using T1ce enhances localisation. T2-weighted-MRI adds image edema into bright lesions indicating the tumor spreading in contrast to FLAIR, which deletes the images of cerebrospinal fluid, and of more invasive tumor regions. This form of combination makes it easier to visualize tumor better, boundaries are delimited and the extent of tumor is determined correctly.

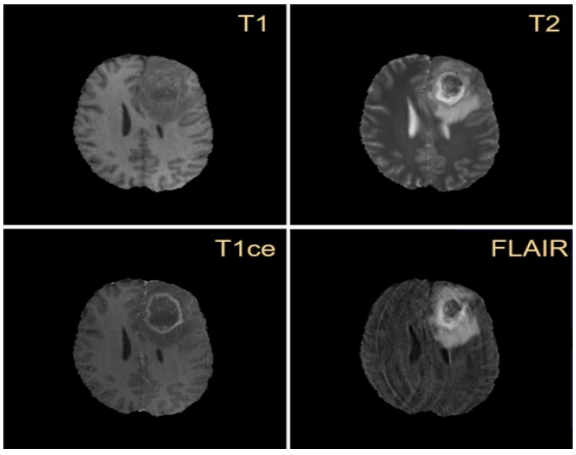


Fig. 1 Multimodal MRI sequences for brain tumor

Fig.1 presents multimodal MRI sequences i.e. T1, T2, T1ce, and FLAIR and every modality displays different tumor characteristics of a superior visualization and analysis. Segmentation in MRI scans of brain tumor is a complex and time-consuming process that requires expertise of a professional. The demerits that affect boundary identification of tumors in more than two modalities, include tumor heterogeneity, irregularity in shapes, blurred margins and variations in the intensity. The factors are likely to cause inter-observer disparity and inconsistency. Automatic brain tumor segmentation can be considered a solution to these issues because it outlines the tumor section accurately, rapidly and reliably. It enables the efficient scaling of the large multimodal MRI data to find the tumor sub-regions such as the tumor core, enhancing tumor and surrounding edema in a consistent manner. This precision plays a fundamental role in clinical practice like diagnoses, surgery planning, radiotherapy and treatment monitoring. Even as significant improvements have been attained, there are still several problems present with the existing assortment of segmentation practices. The different techniques rely on the encoder-decoder designs, such as U-Net, that might not be the most effective ones to identify complex tumor structures and blurred edges. Other models are precise, but poor when used in the multiple dataset and tumor subtypes. Also, uncertainty estimation is not used in the majority of the methods, which limits clinical reliability, and the others impose significant computational loads limiting their suitability to use.

The work introduces a refined brain tumor segmentation model used to achieve more accuracy on boundaries, feature representation, and prediction. It is these constraints that have prompted this research study. In spite of the improved results of deep learning models in segmentation, finer tumor boundaries and infiltrative regions remain hard to get right. In addition, there is no doubt wanting mechanisms, this means that there is no confidence that involves reduced advancements. So, this paper proposes a structure of brain tumor segmentation in that will result in improved accuracy in the boundaries, representation of the features and improved accuracy in prediction. The research is geared towards multimodal MRI image brain tumor segmentation using T1, T1 contrast-enhanced (T1ce), T2, and FLAIR, BraTS images. It can only be applied to segmentation, not classification and survival prediction. The main findings in this work are: (i) Efficient Net is used with ACU-Net, to obtain more precise features, (ii) loss on the boundary to obtain a coherent look at the tumor and (iii) Monte Carlo dropout to train to estimate error and make precise forecasts.

II. RELATED WORK

Brain tumor segmentation from Magnetic Resonance Imaging is a critical step for accurate diagnosis and treatment planning. Different deep learning models and image processing methods have been proposed to enhance segmentation. However, several challenges persist, such as the diverse nature of tumor characteristics, blurred edges and inter-subject and inter-scanner MRI variations. Furthermore, there are variations in network architecture, feature space, and multimodal input from MRI approaches. These methods need to be understood to compare their potential, limitations and to build more effective, efficient and clinically meaningful segmentation models. Zhang et al. (2023) presented a multimodal MRI segmentation model, using the BraTS dataset, based on the ACU-Net architecture [1]. This model uses a combination of MRI imaging types (T1, T1ce, T2 and FLAIR) to segment sub-regions of the tumor. It employs depth wise separable convolutions for efficient feature extraction and residual blocks for better information propagation throughout the network. It also uses an active contour model to segment tumor using smooth contours. The proposed model produces accurate segmentations; but its reliance on informal post-processing steps and lack of uncertainty estimates weaken its practical value. Musallam et al. (2022) proposed a lightweight, basic deep convolutional neural network for brain tumor analysis [2]. The authors apply preprocessing methods including cropping the image, denoising, and histogram equalization before performing multi-class classification with MRI scans. Although this model is lightweight and has high accuracy, it works slice by slice, without spatial detection and volumetric analysis, which reduces its effectiveness in clinical applications. Majib et al. (2021) proposed a VGG16-based stacked classifier VGG-SCNet. Their method uses transfer learning with ensemble classifiers, including Support Vector Machine (SVM), Multi-Layer Perceptron (MLP) and Random Forest to improve classification accuracy [3]. While the model demonstrates high precision and F1-score, it is highly complicated and offers only classification, with no information about tumor segmentation.

Rahman and Islam (2023) proposed a parallel deep CNN for diagnosing and classifying brain tumors based on MRI scans [4]. It combines two CNN models to capture local and global features, and then merges these features with dropout for better performance. But reducing images to low resolution grayscale results in loss of details, which makes this approach inappropriate for the segmentation task. Methil (2021) developed a deep learning model using a combination of preprocessing methods like histogram equalization, morphological operation and ResNet101v2 architecture for binary classification of the extracted features [5]. This model has high recall and accuracy on training and validation data. But its accuracy is sensitive to preprocessing and class diversity, and binary classification prevents its use to determine and segment multiple classes and edges of the detected tumor. Islam et al. (2021) proposed a machine learning model employing super pixels, Principal Component Analysis and K-means clustering for tumor detection [6]. Their approach facilitates feature dimensionality reduction and tumor identification. But the method's use of hand-crafted features and assumptions about clusters limits its scalability and adaptability, particularly with complex tumor shapes. Chattopadhyay and Maitra (2022) introduced a CNN model using the BraTS 2020 dataset, with high accuracy [7]. But their model uses 2D slices, which misses out on cross-slice interactions and is less effective for 3D segmentation.

Rizwan et al. (2022) proposed a Gaussian CNN for classifying different types of tumors and glioma grading from MRI scans [8]. Gaussian based preprocessing enhances image for feature extraction, yielding high multi-class and grading accuracy. But this may smooth the tumor's borders, making it inappropriate for segmentation tasks that need to delineate tumors accurately. Khan et al. (2022) trained deep CNNs on multiple datasets to detect and classify brain tumors [9]. They utilize a combination of custom architectures, transfer learning, and large data augmentation resulting in good performance. Nevertheless, this framework concerns classification on image-level, neglects consistency of spatial features needed in the process of tumor localization through segmentation. Asiri et al. (2024) had a two-module framework that combines image enhancement and SVM classification [10]. Although the strategy enhances detection accuracy, it is modular in fact, it does not allow end-to-end optimization, which makes it inefficient and not very adaptable to a wide range of datasets. Anaya Isaza and Mera Jiméz (2022)

examined data augmentation and transfer learning with a ResNet50 model on TCGA LGG data [11]. Though the study gives good comparative and statistical analysis, its dependency on single MRI modality inhibits the study to give multimodal feature interactions.

Asif et al. (2022) [12] have compared various deep transfer learning models, i.e., Xception, NasNet, DenseNet121, and InceptionResNetV2, on brain tumor detection. The framework combines preprocessing, data augmentation, and optimization object on two datasets in binary classification. It offers comprehensive comparisons and backbone performance comparison. Nonetheless, the investigation concentrates more on the classification accuracy and excludes the capability of learning spatial features involved in segmentation tasks. Khushi et al. (2023) [13] introduced a version of EfficientNetB7 that is trained on brain tumor MRI images and is developed to handle multiclass evaluations. The model improves the learning of features through the use of dense layers, batch normalization and dropouts which lead to high classification. Nonetheless, this deficiency impedes its capability to carry out region-wise segmentation and an in-depth analysis of the boundaries due to the lack of encoder-decoder architecture. Tariq et al. (2025) [14] developed an EfficientNetV2 with a Vision Transformer hybrid multiclass classifier. Unlike EfficientNet which bases predictions on local features or ViT which looks at global context, the method concentrates on predictions at the image level and not pixel-level segmentation. Preetha et al. (2025) [15] proposed multi-scale feature extraction hybrid CNN EfficientNetB2 structure. Though, it has good classification, the performance is hampered by the inability to perform spatial decoding which limits its use in tumor segmentation.

Shah et al. (2022) [16] suggested one of the brain tumor detection frameworks on the basis of a fine-tuned EfficientNet-B0 based on preprocessing and data augmentation. Transfer learning is better in performance with less data, reaching an efficient feature extraction with less complexity. Nonetheless, the model uses 2D data and does not consider inter-slice relationships and heterogeneity of tumors across volumes of MRI. Rajendran et al. (2023) [17] introduced a segmentation model that integrated textural features of the GLCM with U-Net and 3D CNN models. The ensemble enhances the locality of tumor sub-regions by using volumetric information. Although adequate, reliance on hand crafted features and a multistep pipeline, increase complexity and reduces flexibility, and the lack of uncertainty modeling reduces clinical reliability. Alqhtani et al. (2024) [18] have suggested a model that combines preprocessing, Fuzzy C -Means clustering, as well as SVM classification to segment and classify tumors. Image enhancement enhances the quality of MRI and then clustering based-segmentation. This structured pipeline brings about better performance, although sensitivity to variation in initializations and intensity decreases homogeneity throughout the heterogeneous tumor datasets. Jabbar et al. (2023) [19] established a hybrid Caps-VGGNet model to detect and multi-grade tumors by using multimodal MRI data. Capsule Networks maintain spatial hierarchies and enhance segmentation. The model promotes the segmentation and classification activity. Nonetheless, it comes with sophisticated architecture, preprocessing, and is not properly tested on the appropriateness of generalization on diverse datasets. Khairandesh et al. (2021) [20] came up with hybrid CNN-SVM framework by using a threshold-based segmentation to detect and classify tumors. CNN notes features and SVM classifies. In spite of improved performance in detection, segmentation relies on intensity thresholds and also on 2D slices, which is not as robust to a complex tumor structure. The 2D and 3D U-Net segmentation features integrated with machine learning classifiers were suggested by Mallampati et al. (2023) [21] as a framework. Radiomic features of segmented MRI images enhance their performance in detection. But dependence on hand-made features and inability to go end-to-end makes scale less efficient and effective with full automation of clinical systems. While deep learning methods have improved brain tumor analysis, there remain some limitations. Most approaches primarily focus on detection or classification, rather than segmentation of the tumor boundary. Encoder decoder networks like UNet have difficulty with capturing the tumor shapes and fuzzy boundaries. Moreover, the increase of hand designed post processing methods complicates the model and lower its flexibility in use. There is also under utilization of multimodal MRI data, resulting in limited feature extraction. uncertainty estimation is often ignored, reducing the reliability of these models

in clinical settings. This presents a new segmentation approach using an Efficient Net ACU-Net model to improve these limitations. The model employs a pretrained Efficient Net encoder to generate rich and informative features from MRI images. This work also uses a boundary aware loss function to enhance tumor boundary segmentation. Also, prediction uncertainty is estimated using Monte Carlo Dropout to improve segmentation performance and to determine the how confident the model is about the prediction.

III. PROPOSED WORK

The proposed study focuses on the design and implementation of the proposed brain tumor segmentation. The model processes multimodal MRI data to generate accurate pixel-wise segmentation maps of tumor regions. The overall system consists of data preprocessing, feature extraction using a deep encoder, segmentation through a decoder network, and uncertainty estimation to assess prediction confidence.

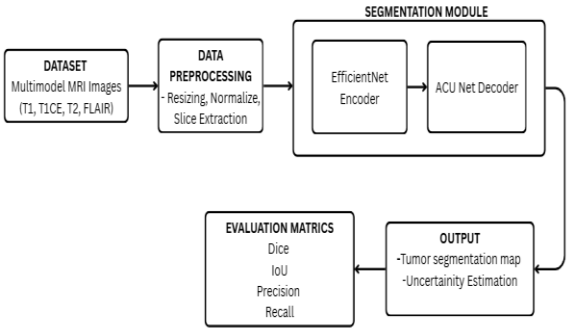


Fig. 2 Proposed Block Diagram

Fig. 2 presents the overall workflow of the proposed multimodal MRI brain tumor segmentation system. It begins with multimodal MRI inputs of T1-weighted and T1 contrast-enhanced, T2-weighted and FLAIR images that provide a complementary information of brain tumors. The images are processed first by the use of resizing to give them uniformity, enhancement of intensity and pulling out of slices. The processed output is fed to the segmentation phase that uses hierarchical features that are derived by an Efficient Net encoder that uses depth wise separable convolutions and residual links. These features are decoded using the ACU-Net style decoder with up sampling progressively and skips to generate segmentation maps. The accuracy can be increased to the boundary by a loss based on boundary awareness and Monte Carlo Dropout is employed to obtain an approximation of the probability of a prediction. Dice coefficient, IoU, precision and recall are used to analyze the final results.

A. Data Preprocessing

Data preprocessing plays a crucial role in preparing multimodal MRI images for accurate and stable brain tumor segmentation. The BraTS datasets offer a three-dimensional image of MRI volume at a resolution of 240 × 240 × 155 of each modality. All the MRI volumes are down-sampled to a uniform spatial resolution to maintain consistency across samples. Normalization of the intensity of each modality is performed to decrease variances between scanners and other imager conditions, which helps in enhancing the stability of training and convergence. Modalities (T1, T1ce, T2, and FLAIR) are applied to each patient, and they are spatially aligned and combined to create one multimodal input. The 3D MRI volumes are converted to slice wise representations by removing slices of the axial dimensions as the proposed model requires two-dimensional entries, resulting in grid based two-dimensional data. The method of slicing is preservative of anatomical structure, and offers clear visualization of tumor localizations in consecutive sections. The ground truth masks are resized and fitted to the respective slices to allow one to be able to have pixel level accuracy. In order to enhance a higher level of computational efficiency and minimize redundancy, slices that contain little brain substance or lack regions of tumors are eliminated. This is to achieve the model concentrating on clinically relevant areas of training. Validation and testing sets are not augmented with data to ensure unbiased evaluation. Lastly, channel-wise stacking of the slices extracted of all four modalities is done to construct a single multi-channel input of size (H × W × 4) to enable the model to be effectively trained in complementary anatomical and pathological structures.

Fig. 3 Axial slice extraction from 3D MRI volume

Fig. 3 represents the axial slices (240 × 240 × 155) of a 3D BraTS MRI volume. It illustrates the way in which 3D structure is preserved to yield 2D cross-sectional images for the training of slice-wise deep learning models while also preserving anatomical structure and tumor shape. MRI volumes are stepped through along the depth index, with the slice obtained at each step. From a volume V of size H × W × D, a 2D slice is extracted by selecting a specific depth index d and retrieving the corresponding matrix. The aligned modalities (T1, T1ce, T2, FLAIR) are extracted at the same depth index for all channels. The corresponding segment will have the same index to ensure pixel-to-pixel correspondence between the input. Multimodal data is stacked to combine valuable information from various MRI sequences into a single input. The extracted and normalized slice is stacked to form a multi-channel input tensor by combining the four registered modalities (T1, T1ce, T2, and FLAIR). Given the registration between models, the same anatomical region is represented in each channel. This leads to a four-channel (H × W × 4) input to the EfficientNet ACU-Net, allowing it to effectively learn multi-modality anatomical and pathological features.

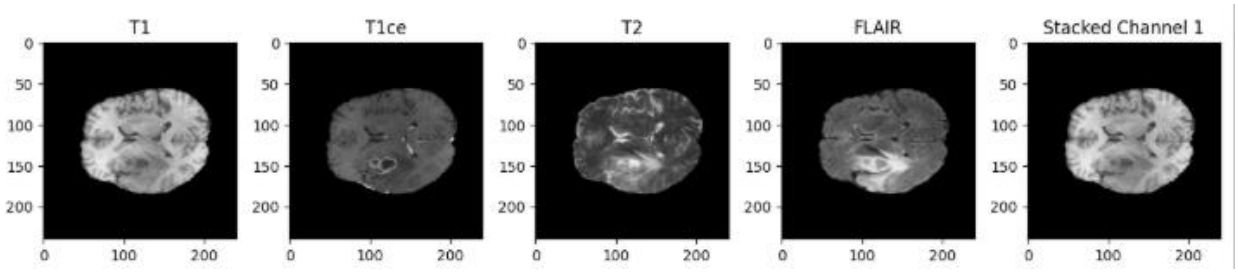


Fig. 4 Channel-wise stacking of multimodal MRI slices

Figure 4 illustrates the way in which the T1, T1ce, T2 and FLAIR images are combined to form a four-channel input tensor in a channel-wise fashion. The MRI images are aligned together thus; the corresponding slices represent the same anatomical region. The input shape of (240 × 240 × 4) enables the network to learn multi-modal information about the tumor regions, such as the shape and structure information from T1, enhancing core information from T1ce, and edema information from T2 and FLAIR.

B. Model Architecture

The proposed segmentation framework is based on a hybrid EfficientNet ACU-Net architecture designed to accurately segment brain tumor regions from multimodal MRI inputs. The architecture consists of an encoder which extracts features at multiple resolutions, and a decoder which maps those features to output pixel-wise segmentation masks. The model takes a four-channel image tensor, which is obtained by concatenation of T1, T1ce, T2, and FLAIR modalities, to capture diverse anatomical and pathological features. The encoder is a pretrained EfficientNet model that uses compound scaling for efficient high-performance models with fewer parameters. It employs depth wise separable convolutions and scaling of width, depth, and resolution to capture informative features. In this study, the EfficientNet encoder provides multi-scale features that contain both low-level information (edges, textures) and high-level semantic features of the tumor regions. Pretrained weights enhance feature generalization and speed up training.

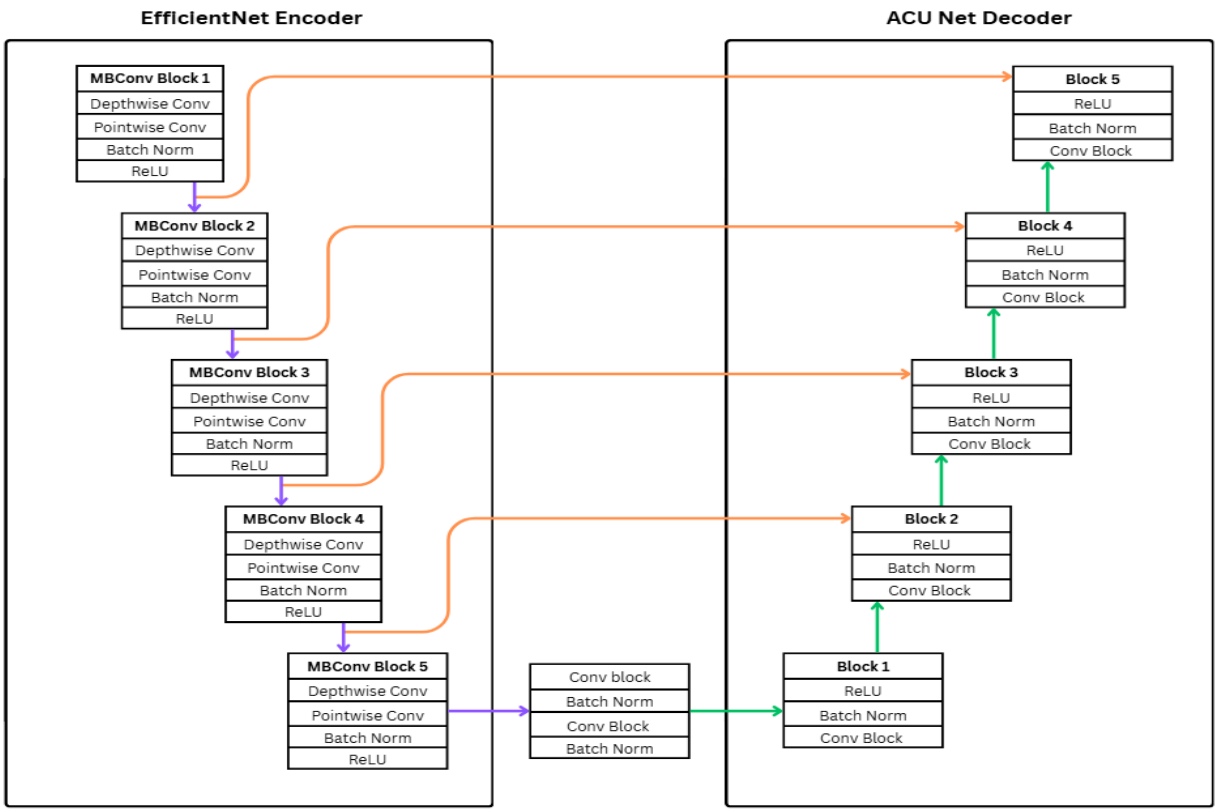


Fig. 5 Architecture of the proposed EfficientNet ACU-Net segmentation model

Fig. 5 illustrates the architecture of the proposed model. The encoder learns feature maps at various resolutions, provided to the decoder via skip connections to retain spatial information and improve segmentation boundaries The decoder, based on ACU-Net, gradually upscales the extracted features to produce fine segmentation masks. The decoder incorporates multi-scale contextual information to improve segmentation accuracy, especially in areas with complex tumor shapes. The model gives predictions for different sub-regions of tumor on slice basis. The model is trained with a supervised learning approach, using multimodal MRI slices as input volumes and segmentation masks as ground truth. The model is trained in a mini batch fashion with a batch size of typically between 8 and 16 to make efficient use of the GPU and to reduce gradient update noise. Data is shuffled for each epoch during training to enhance generalization, and not shuffled to ensure consistency for validation and testing. To mitigate class imbalance and enhance segmentation performance, a custom loss function is used that combines Dice loss and a boundary component. Dice loss ensures better region overlap between predicted and ground truth masks, with edge sharpening and increased accuracy achieved through the boundary component. The boundary component is scaled to prioritize both region-based and boundary-based learning. The model is trained using AdamW optimizer with an initial learning rate of 1 × 10-4 to allow adaptive updates of the network parameters and provide regularization. Mixed precision training is used to save memory and accelerate training. In addition, learning rate scheduling may be applied during training to stabilize convergence.

During training, forward propagation generates segmentation predictions, and the computed loss is backpropagated to update network parameters. To avoid exploding gradients, gradient clipping may be used. The model is trained for 100 epochs with early stopping based on validation performance to prevent overfitting. In the validation phase, the model is in inference mode with no gradients computed. The metrics used for judging the performance are Dice coefficient, Intersection over Union (IoU), precision and recall. The model with the highest validation Dice

is chosen to minimize overfitting. Uncertainty estimation using Monte Carlo Dropout is adopted to improve prediction accuracy. Dropout layers are enabled at inference time and multiple probability samples (e.g., 10-20 samples) are generated. The ensemble prediction is generated by averaging, and an uncertainty map is computed from the variance. This results in higher variance around areas of lower confidence, such as tumor boundaries and intricacies.

IV. RESULTS AND DISCUSSION

The dataset used in this study is obtained by combining the BraTS 2019, BraTS 2020, and BraTS 2021 datasets, forming a comprehensive collection of multimodal brain MRI scans with corresponding segmentation masks. The combined data comprises 1955 cases of patients, with 335, 369, and 1251 as BraTS 2019, BraTS 2020, and BraTS 2021, respectively. Every patient report includes four MRI modalities such as T1, T1 contrast-enhanced (T1ce), T2 and FLAIR that gives supplementary anatomical and pathological data about the precise tumor segmentation. A patient-wise splitting design is used with a 70:15:15 proportion to guarantee strong training and unbiased testing. In this regard, 1368 are trained, 293 are validated and 294 are tested. The dataset includes 89,635 training images, 19,178 validation images, and 19,196 testing images, each labeled with a segmentation mask. The organized data set includes sufficient diversity and can avoid the data leakage, thereby enabling the assessment of the proposed segmentation model. This large-scale dataset provides diverse tumor characteristics across different patients, improving the robustness and generalization capability of the proposed model. The designed EfficientNet ACU-Net model is optimized by mini batch optimization and a batch size of 8-16 and optimized by AdamW optimizer with a 1 × 10-4 learning rate. Training occurs with the help of GPU acceleration and the validation is made after every epoch to evaluate performance and avoid overfitting. Standard measures are used to assess the performance of the segmentation, which comprise Dice coefficient, Intersection over Union (IoU), precision and recall, which determine the overlap of tumor region prediction across classes, along with the accuracy of the prediction.

Table 1 Training Performance of the Proposed Model

Tumor Regions	Dice	IoU	Precision	Recall
Whole Tumor	94.5%	89.6%	92.5%	87.5%
Tumor Core	97.0%	94.2%	97.5%	95.5%
Enhancing Tumor	89.0%	80.3%	94%	83.1%
Mean	93.5%	88%	94.7%	88.7%

The proposed EfficientNet ACU-Net model shows high results in terms of segmentation of tumor regions. Table 1 demonstrates that the model has a mean Dice score of 93.5% and IoU of 88%, which means a high overlap with the ground truth. The Tumor Core receives the highest Dice score of 97%, while Enhancing Tumor shows a relatively low score due to complex structures. The model successfully learns with significant features from multimodal MRI. The model performed relatively well in the Enhancing Tumor volume because it is small, has variable intensity, and multiple shapes, which causes difficulty in segmenting them accurately.

Table 2 Validation Performance of the Proposed Model

Tumor Regions	Dice	IoU	Precision	Recall
Whole Tumor	93.8%	88.4%	92.10%	87.4%
Tumor Core	96.5%	93.2%	96.9%	95.6%
Enhancing Tumor	87.5%	77.8%	93.1%	82.9%
Mean	92.6%	86.5%	94.3%	88.6%

The validation outcomes demonstrate the capacity of the model to generalize well on unobserved MRI data. The results of Table 2 demonstrate that the mean Dice score is 92.6% with an IoU of 86.5%, which corresponds to stable performance. The Tumor Core has the maximum Dice score of 96.5% and the Enhancing Tumor has a comparatively lower score of 87.5% due to its irregular structure and high variability. These findings ensure that there is uniform performance in segmentation across validation samples. The consistency between training and validation results indicates that the model does not overfit and maintains strong generalization across unseen data.

Table 3 Testing Performance of the Proposed Model

Tumor Regions	Dice	IoU	Precision	Recall
Whole Tumor	94.2%	89.1%	92.10%	90.5%
Tumor Core	96.2%	92.7%	96.98%	95.10%
Enhancing Tumor	86.5%	76.2%	93.5%	80.10%
Mean	92.3%	86%	94.1%	88.56%

The results on the test set indicate the effectiveness of our model in previously unseen MRI images. Table 3 demonstrates that the average Dice score of 92.3% and IoU 86.0% are achieved, therefore the results are very accurate. The Tumor Core has the highest Dice score of 96.2%, and the Enhancing Tumor is less accurate with complex boundaries. This shows reliable segmentation between all of the tumor regions. The results show that the developed model is able to perform accurately on unseen data, which makes it applicable in clinical practice.

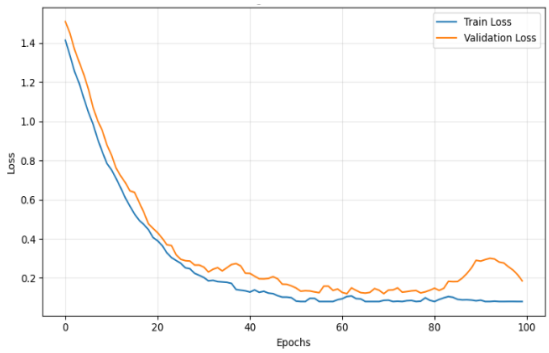


Fig. 6 Training and Validation Loss Curve

Fig. 6 shows the training and validation loss curves, which illustrates the convergence of the proposed model during the training stages. As the training loss is consistently decreasing, it indicates good feature learning. The validity loss is also decreasing in the same way, which means a good generalization. The decrease in the last epochs suggests a little overfitting but the overall trend shows that there is stable convergence and good segmentation loss. The stable descent of both training and validation curves also shows stable and effective optimization with the learning of features.

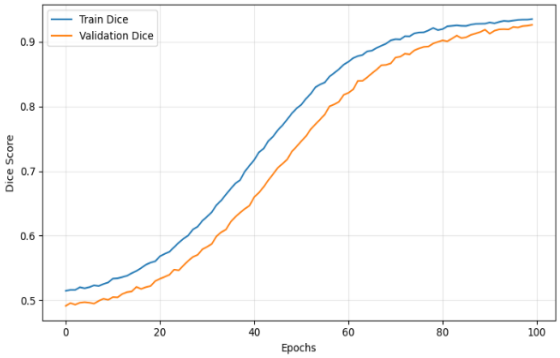
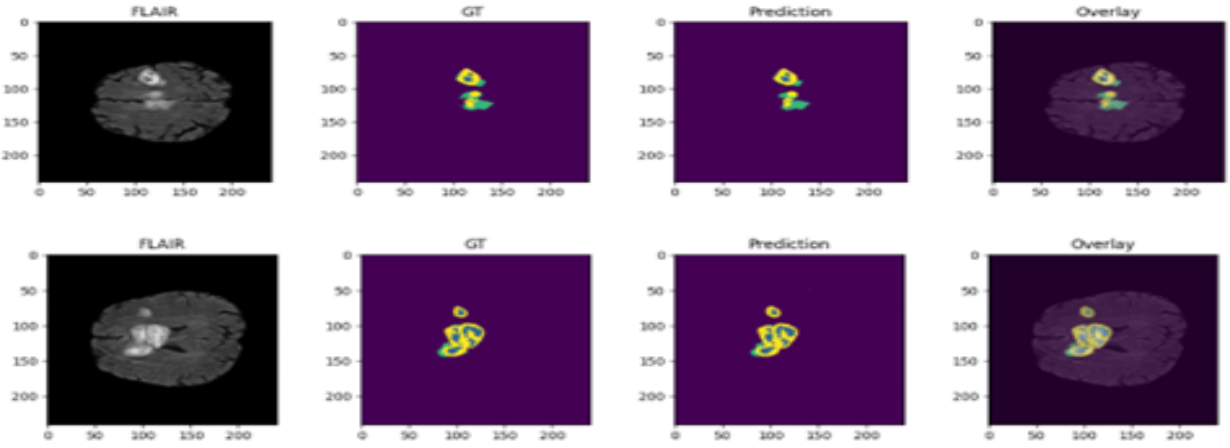


Fig. 7 Training and Validation Dice Curve

Fig. 7 illustrates training and validation Dice curves with respect to epochs, where the segmentation accuracy is improved. The Dice value is increasing because the region of overlap of the predicted mask and the ground truth mask is increasing. The validation curve is relatively close to the training curve, which suggests the strong generalization capability. The gap between curves is small and shows stable learning process and confirms reliable and accurate segmentation results. The similarity of training and validation Dice curves also demonstrate that overfitting is avoided. The qualitative analysis is performed to determine the effectiveness of the proposed model in identifying the regions of the brain tumor in the MRI images. The results of the segmentation masks, can be compared with the ground truth masks to check the spatial accuracy of the tumor detection. This visual analysis highlights how well the model can capture the shape, boundary and variance in the different sub-tumors of the brain tumor.



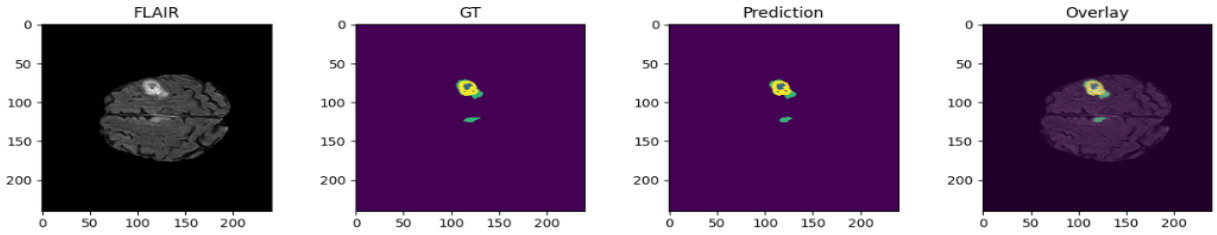


Fig. 8 Visualization of Predicted Tumor Segmentation

Fig. 8 shows a qualitative segmentation output of the proposed model. The initial picture is the FLAIR MRI slice which indicates the tumor areas. The second image is the ground truth mask, which is Whole Tumor (Class 1) in yellow, Tumor Core (Class 2) in green and Enhancing Tumor (Class 3) in blue, with the background in violet. The third image shows the predicted segmentation with a high agreement with the reference. The last overlay shows overlap of predicted tumor areas with underlying brain structures. Uncertainty estimation helps to further understand the credibility of deep learning-based segmentation models. Prediction confidence can also be unevenly distributed in different parts of an MRI scan, even where the performance of segmentation is good, especially around the complex boundaries of tumors. In order to assess the confidence of the proposed framework, the Monte Carlo dropout technique is used to estimate uncertainty. The model allows stochastic forward passes to make inferences, producing many segmentation predictions. The differences between these predictions are taken to calculate an uncertainty map, which identifies less certain areas.

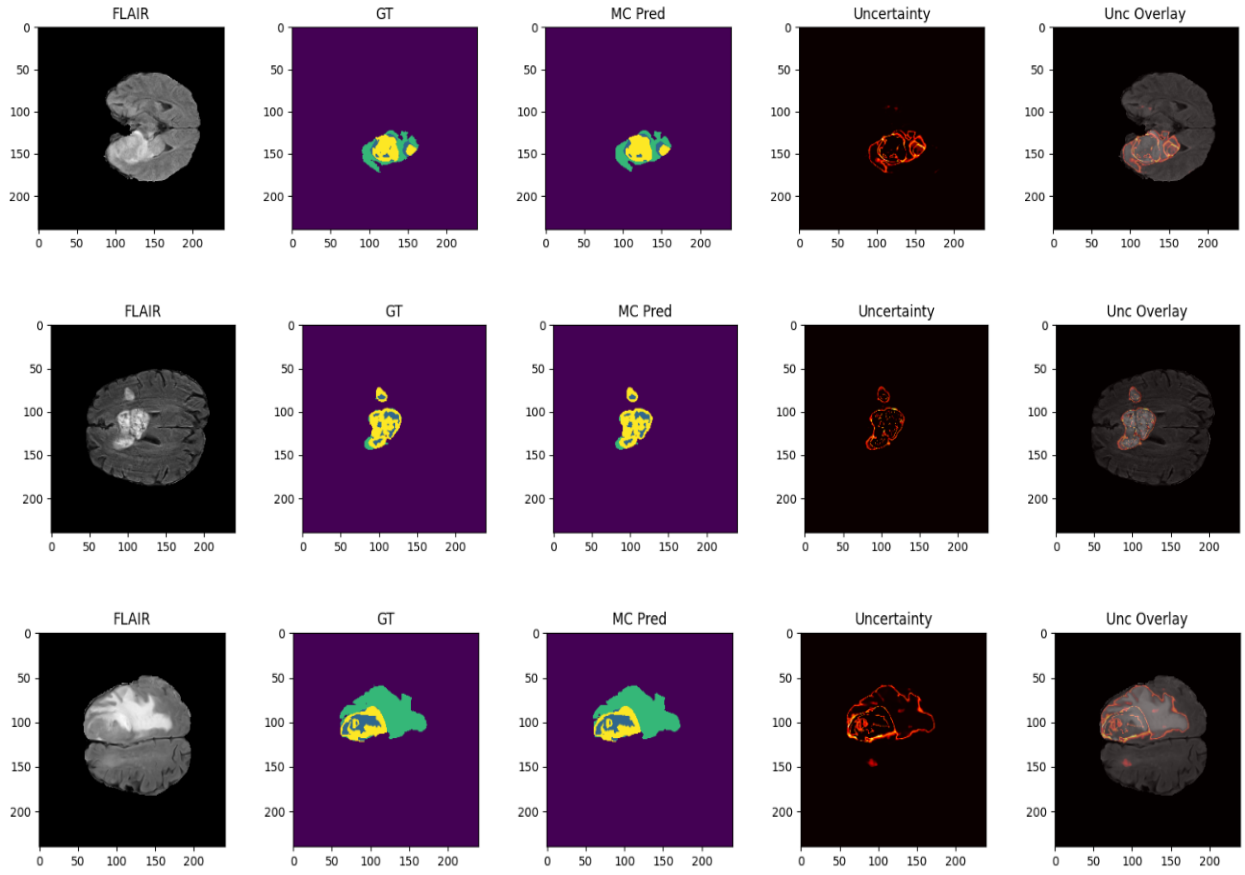


Fig. 9 Uncertainty Map Visualization

Fig. 9 illustrates the uncertainty estimation of the proposed segmentation model. The first image is an input FLAIR MRI slice where the tumor region can be observed with a high contrast. The second picture shows the mask of ground truth segmentation and the third one is the prediction with Monte Carlo inference. The fourth image is the overlay image, in which the position of the tumor is shown. The final image is the uncertainty map which shows the uncertainty in the prediction. To demonstrate the effectiveness of the EfficientNet-ACU-Net model, it is compared with other well-known segmentation algorithms, such as U-Net and ACU-Net. This allows us to assess the efficiency and viability of the proposed model in delineating the brain tumor regions in multimodal MRI images. It is evaluated in terms of Dice, Intersection over Union (IoU), precision and recall in the sub-regions associated with the tumor. These metrics are visually presented and the improvements are observed against the existing approaches.

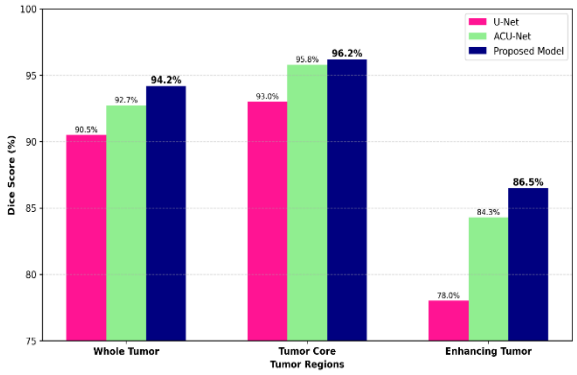


Fig. 10 Comparison of Dice Scores Across Segmentation Models

Fig. 10 shows the comparison of Dice scores for the proposed model, and U-Net and ACU-Net for various tumor regions. The Dice score is a measure of overlap between the predicted segmentation and the actual ground truth, with higher scores reflecting more accurate segmentation. With the proposed model, the Dice scores for Whole Tumor are 94.20%, Tumor Core are 96.20% and Enhancing Tumor are 86.50%. This is an improvement over U-Net and ACU-Net, implying that the model can better extract areas of the tumor. This can be attributed to the model's capacity to capture spatial details, resulting in better segmentation accuracy aligned with the tumor boundary.

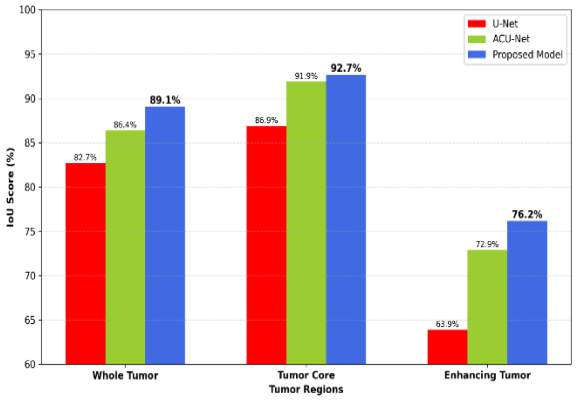


Fig. 11 Comparison of IoU Across Segmentation Models

Fig. 11 shows the Intersection over Union (IoU) values for U-Net, ACU-Net, and the proposed model in various regions of the tumor. IoU represents the ratio of the intersection of the predicted mask and the ground truth to the sum of the union of the segmentation and the ground truth, thus it is a more stringent measure. The proposed model's IoU values are 89.01% for Whole Tumor, 92.70% for Tumor Core, and 76.20% for Enhancing Tumor. The proposed model achieves higher IoU values than the other models, meaning better overlap between the predicted segmentation and the ground truth. The outcomes demonstrate more accurate segmentation with improved spatial delineation in the proposed model than current techniques.

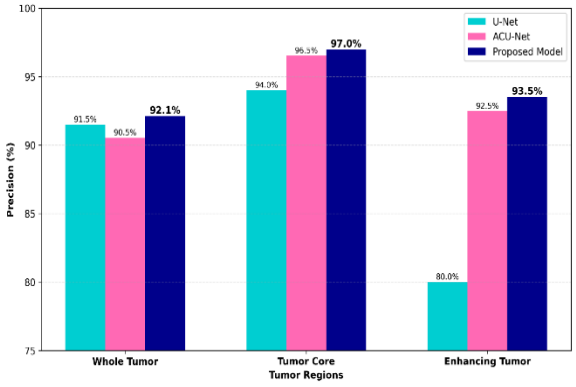


Fig. 12 Comparison of Precision Across Segmentation Models

The comparison of precision values for the three models (U-Net, ACU-Net, and proposed) across different tumor types is depicted in Fig. 12. It is clear that the proposed Efficient Net-based ACU-Net model

attains higher precision values of 92.10% for Whole Tumor, 96.98% for Tumor Core, and 93.50% for Enhancing Tumor than other models. Precision indicates how effectively the model identifies the tumor regions while avoiding non-tumor regions. Overall, these results demonstrate the ability of the proposed model to do precise segmentation of the tumor.

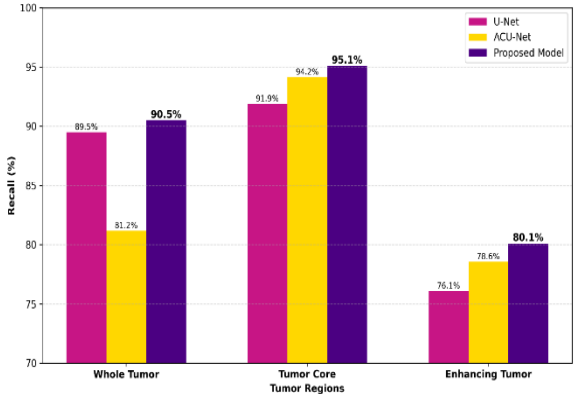
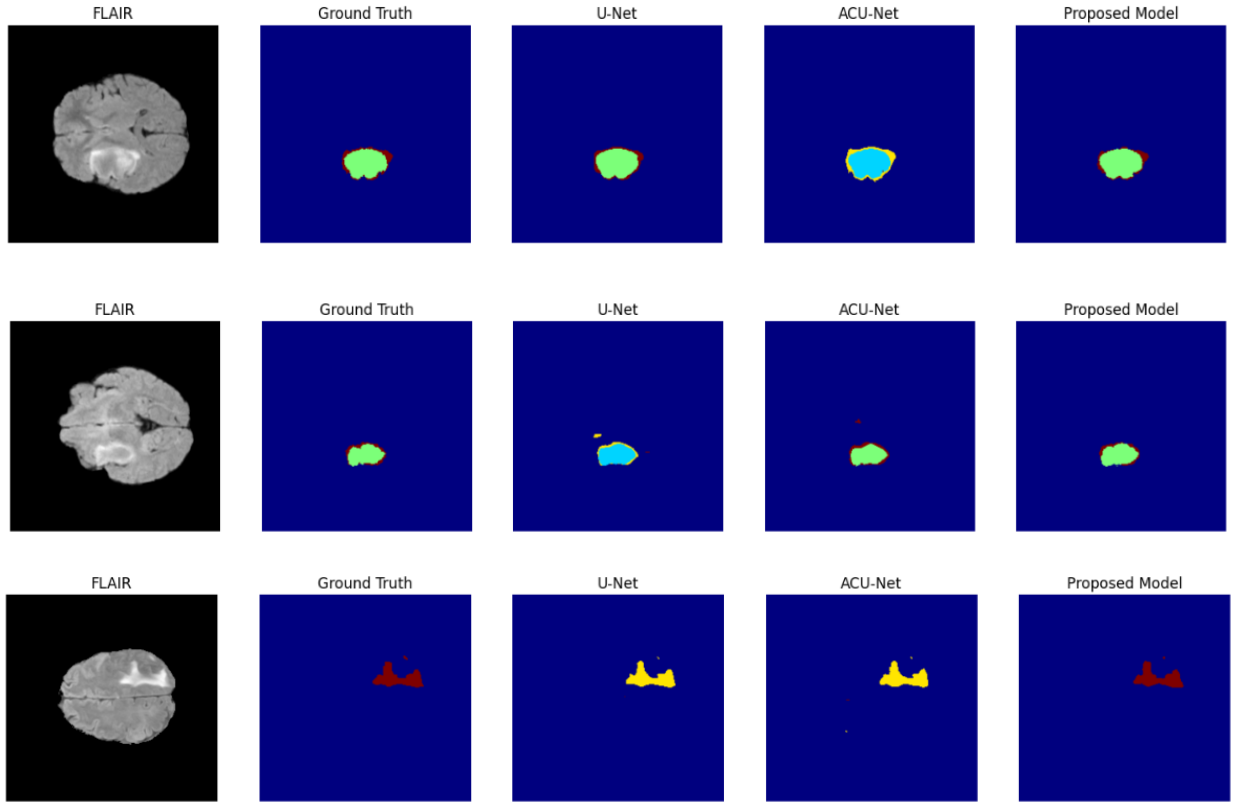


Fig. 13 Comparison of Recall Across Segmentation Models

Fig. 13 shows the recall comparison between U-Net, ACU-Net and proposed model for various tumor regions. It is evident that the EfficientNet-based ACU-Net model proposed in this paper has a recall value of 90.50% for Whole Tumor, 95.10% for Tumor Core and 80.10% for Enhancing Tumor. Recall is a measure of the model's ability to identify all of the true regions of the tumors in the MRI scans. While the recall value for Enhancing Tumor is comparatively low, this is justified because of its irregular structure and size. The improvement in all evaluation measures confirms the success of using EfficientNet based feature learning and ACU-Net decoding and boundary learning. A qualitative analysis using visual segmentation comparisons is conducted to assess the ability of various models to segment brain tumor regions. The segmentation results of U-Net, ACU-Net, and the proposed EfficientNet based ACU-Net model are compared using sample MRI slices. This helps to understand their segmentation accuracy in terms of identifying the location of the tumor regions and determining boundaries between different tumor sub-regions, and therefore, different segmentation accuracy and stability.



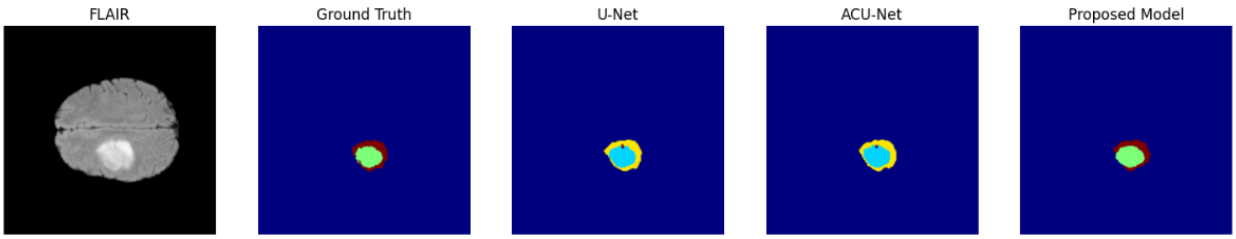


Fig. 14 Visual Comparison of Segmentation Outputs for Different Models

Fig. 14 illustrates a qualitative comparison of model segmentation. The FLAIR images highlight the tumor regions and the ground truth masks are the references. These are shown in the maps using the following color codes: Tumor whole area (cyan), Tumor core (yellow), Enhancing Tumor (red), background (dark blue). The proposed model is closer to the ground truth because it segments better the shape and tumor boundaries. U-Net and ACU-Net have missed regions and less accurate boundaries, which indicates they have less accurate segmentations. Overall, the proposed Efficient Net ACU-Net model demonstrates strong and consistent performance across training, validation, and testing datasets. The combination of multimodal features, boundary-aware loss, and uncertainty has enhanced segmentation performance and confidence and therefore has potential for clinical applications.

V. CONCLUSION AND FUTURE WORK

This study proposes a robust deep learning model for brain tumor segmentation using a modified ACU-Net with Efficient Net encoder. The proposed approach addresses the challenges of multimodal MRI segmentation in terms of tumor heterogeneity and lack of clear boundaries by improving features representation and boundary delineation. The multimodal MRI images are used to extract complementary anatomical and pathological information that enables accurate sub-regions identification. The evaluation results show that high accuracy with Dice scores of 94.2% Whole Tumor, 96.2% Tumor Core and 86.5% Enhancing Tumor, high IoU, precision and recall are obtained. These results show higher accuracy and robustness than other conventional models such as U-Net and ACU-Net. Qualitative analysis also shows improved representation of boundaries and correlation with the ground truth masks. Additionally, Monte Carlo Dropout is used to evaluate uncertainty of decisions, which in turn leads to confidence maps, which highlight uncertain regions and contribute to better model confidence. Overall, the proposed model is a promising solution to the task of brain tumor segmentation and has high potential for clinical decision support. The proposed model shows strong potential for real-time clinical applications and automated decision support systems.

Future research could involve developing more sophisticated methods to enhance the performance of segmentation and clinical usefulness. Transformers and CNN-transformer hybrid models can enhance the capacity for capturing long range spatial interactions in brain tumor segmentation. Volumetric segmentation can also improve the consistency across slices and yield better segmentation results. Unsupervised and semi supervised learning can help overcome the requirement for large labeled datasets. Adversarial and other domain adaptation methods can address variations in imaging. Federated learning can allow for training models without sharing the data. Further advances can be made to uncertainty estimation using probabilistic deep learning techniques, for more reliable segmentation results and better fit for clinical use and realistic medical images.

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