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Automated Detection and Segmentation of Heterogeneous Brain Tumor Regions Via Transformer Based Deeplabv3+

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Abstract

A tumor is one of the most dangerous diseases that affect any body part, where tumors of the brain are the most serious because of their important place. They pose an important risk to life and are an important cause of death because of their complexity and treatment challenges. This paper uses the transformer deeplabv3+ model, starting with employ data pre-processing techniques, including augmentation and resizing given images. The Gated Shape Convolutional Neural Network (GSCNN) model is trained using a training set as a base model, expanded with the pre-trained ResNet50 weight, and the predictions are then fed into the DeepLabv3+ model. The model's performance is assessed based on its F1 score, accuracy, sensitivity, precision, and specificity. As per the study's outcomes, our suggested model enhances performance and can achieve 98.87% accuracy, 98.84% sensitivity (recall), 99.49% specificity, 98.83% precision, and a 98.83% F1-score. Compared to earlier studies, our model produced beneficial results, utilizing the dataset BraTS2020.

Keywords: Classification; Magnetic resonance imaging (MRI); DeepLabv3+; Brain tumor; Segmentation; The Gated Shape CNN.

1 Introduction

Tumors are one of the most serious medical conditions that can develop in any body part; brain cancers are particularly dangerous. Of these, gliomas are particularly mortal because of their origin deep inside the brain, making them difficult to detect and treat. Unlike other tumors that may appear on the surface of the brain, glioma often develops in its inner areas. Low-grade gliomas (LGG) and high-grade gliomas (HGG) are the two major classifications for gliomas. Grades I and II are typically categorized as below LGG, whilst grades III and IV are categorized as HGG (Sekar et al., 2023; Arbane et al., 2020). Figure 1 illustrates an example of an LGG and HGG MRI.

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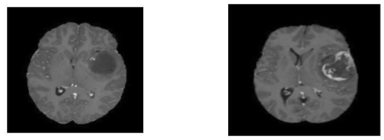

a b

Figure 1: An illustration of a) LGG), and b) HGG using MRI

The deep neural network has advanced significantly in artificial intelligence activities in recent years, such as image recognition and segmentation (Biswas & Tiwari, 2024). In particular, semantic segmentation research is enriched by incorporating relevant information at the high level. The strong performance of a fully practical CNN-based model (Stathopoulos et al., 2024) in medical image segmentation has encouraged its use in works such as brain tumor segmentation (Sargunapathi et al., 2020).

DeepLabv3+ (Harkat et al., 2020), an increased model that includes a user-friendly decoder module, improves the object area detection. It uses parallel pool mechanisms to remove features in multiple parameters and help in the segmentation of different sizes (Saritha & Gunasundari, 2024).

The semantic segmentation of brain tumors in MRI scans is the main emphasis of the suggested method (Ganesh et al., 2021). A transformer-based Deeplabv3+ architecture is created by utilizing the GSCNN's output by renewing with a pre-trained ResNet50 weight and using the GSCNN's output as an input to the Deeplabv3+ model. The BraTS2020 MRI dataset was utilized for developing this network, and a number of assessment criteria were used to assess its performance.

This paper's remaining section has been written as follows: Section 2: Reviews of MR-based images and pertinent research on deep learning techniques for tumor classification. A thorough explanation of the content and technique is given in Section 3. Experimental findings are shown in Section 4, along with a performance comparison of the suggested model, GSCNN, Deeplabv3+, and current methods for classifying medical images (Mooraki et al., 2021). Section 5 brought the study to a close, went over its shortcomings, and highlighted potential avenues for further investigation.

2 Related Work

Kokila et al., 2021, introduced a single approach to brain classification using MRI, rather than utilizing different models for every classification task. This experimental endeavor to diagnose brain malignancies with MRI includes the detection of the tumor as well as its classification according to its grade, nature, and tumor site. Numerous studies have employed a CNN-based multi-task classification for the classification and identification of tumors.

For the purpose of segmenting entire brain tumors from MR images, Ilhan et al., 2022 introduced an efficient technique that relies on improving the tumor approaches and the location using a deep learning architecture called U-Net. The suggested tumor enhancement method alters the targeted regions to improve the visibility of low-contrast or dim tumors. First, the histogram-based nonparametric tumor localization method is used to locate the tumorous areas.

Zhang et al., 2021, employed a multi-encoder architecture to segment brain tumors (Fatima et al., 2024). They also developed a new categorical loss function, also gave each split region a different weight. The BraTS2020 dataset was utilized to evaluate the method. This strategy yielded excellent results, with dice scores for the total tumor, disease core, and enhanced tumor being 70.24%, 88.26%, and 73.86%, respectively.

Messaoudi et al., 2020, trained a two-dimensional network to divide up brain tumors in three dimensions (Brainee 2025). The encoder portion of the system, called EfficientNet, produced encouraging outcomes. Bruna & Mallat, 2013, A non-feedback wavelet scattering network was suggested. This network can sustain stability in the face of slight deformations in addition to presenting the frequency domain picture energy distribution. This includes the ability to extract image boundaries and separate small objects, which somewhat compensates for the CNN model's inadequacies. Additionally, some academics have made a concerted effort to integrate the CNN model with the wavelet method. To extract features from MRI scans, the researchers use pretrained deep convolutional neural networks, particularly models such as VGG16, VGG19, ResNet50, and InceptionResNetV2, by improving these models using a dataset of MRI images of the brain. Rodriguez et al., 2020, suggested using a deep adaptive wavelet network to extract fundamental data for picture classification from the input data. Investigations using three datasets for image classification revealed that the model lowered training parameters and obtained good accuracy. Cotter, 2020, a dual-tree complex wavelet scattering network was suggested. It achieves quick inference capabilities and great accuracy in picture classification applications when paired with a CNN model. Liu et al., 2022, suggested a scattering wavelet network model for learning and presented the module for dual-tree complex wavelet scattering transform. Shoushtari et al., 2022, designed a deep neural network approach (Deep-Net) with initial ResNet18 weights that have been pre-trained and the DeepLabv3+ architecture for the glioblastoma tumors semantic segmentation in MRI images. The training package for BraTS2020 provided the MR image dataset that was utilized to train the network, involved a team of skilled neuroradiologists hand-drawing the actual labels for different tumor sub-regions (Alraddady et al., 2023).

This paper introduces many major contributions as given below:

- Suggested a new hybrid model: a transformer-based DeepLab3+ model is introduced, which has started with the pre-trained ResNet50 weight, to evaluate how well a novel deep learning method works automatic brain tumors segmentation.
- Two-phase Training Strategy: The GSCNN is first trained as a basic model, and its predictions are later used as inputs for the Deeplabv3+ model, which improves the segmentation performance.
- Comprehensive evaluation measurements: The suggested method efficiency is assessed by accuracy, specificity, sensitivity /recall, F1 score, and precision matrices.
- Superior performance: The model gets 98.87% high accuracy, 99.49% for specificity, 98.83% for precision, 98.84% for sensitivity, and 98.83% for F1 score, outperforming a pre-approach on the BraTS2020 dataset.
- Strong data preparation pipelines: We use different preprocessing and data augmentation techniques—including changing image size, rotation, width/height round, zoom, cleaning, and horizontal cutting—to increase the strengthening and generalization of the model.

3 Material and Methods

3.1 Dataset description

BraTS2020 has long been used to evaluate contemporary techniques for brain tumors segmenting in multiple-modal MRI images (BraTS2020 Dataset, 2020). The brain cancers segmentation that are inherently distinct in terms of appearance, pathology, and shape, specifically gliomas, is a focus of the multi-institution preoperative magnetic resonance imaging system BraTS2020 (Odeh & Taleb, 2023). Furthermore, BraTS2020 also highlights the distinction between true tumor recurrence and pseudo progression, as well as the overall patient survival prognosis, for the purpose to ascertain the segmentation task's therapeutic value. Finally, BraTS2020 aims to assess algorithmic uncertainty in tumor segmentation.

3.2 Data Preprocessing

The data pre-processing approaches, such as resizing the input images, and augmentation techniques like (Rotation, Width and high shift, Zoom, Shear and Horizontal flip) are utilized.

- Image Resizing: To guarantee uniformity in model input, all images were scaled to a standard dimension of 240 × 240 × 3 before the use of any preprocessing procedures.
- Dataset Splitting: three subsets were created: a test part that was used only to assess the final algorithm's generalization and accuracy, a validation set for model tuning and performance comparison, and training set for learning and updating model parameters.
- Data Augmentation: This step was utilized to artificially enlarge the training set and introduce more variability in order to improve model performance and robustness. In classification tasks, this also aids in addressing class imbalance challenges. Rotation, shear transformation, horizontal flipping, width and height shifts, and zooming were some of the augmentation techniques utilized.

3.3 Methods

3.3.1 Gated Shape Convolutional Neural Network

Gated Shape Convolutional Neural Network (GSCNN) (Takikawa et al., 2020), two streams in CNN architecture —more especially, wired form data as a separate handling stream—are used to segment semantics. i.e., a form stream that handles data concurrently with the traditional stream. A novel kind of gate was needed for this design to link the two streams' intermediate layers. To enable the shape stream to concentrate exclusively on processing the pertinent boundary-related data, they employed the higher-order classical stream activations to gate the activations at a lower level in the form stream. This effectively eliminated noise. Consequently, they were able to effectively employ the shape stream at the picture-level resolution using a comparatively shallow design. GSCNN connected the intermediate layers using gating techniques. The final step involved combining data from multiple streams using a fusion module. High-quality borders were predicted using a loss function that motivates the expected semantic segmentation masking to align with ground truth-based bounds.

3.3.2 Deeplabv3+ model

By integrating a stronger decoder module for better segmentation results, particularly near object boundaries, DeepLabv3+ is an enhanced semantically segmenting structure that builds on the capabilities of its predecessor, DeepLabv3. It efficiently integrates multiple scales of context data by fusing the advantages of spatial pyramid pooling with atrous (dilated) convolutions. Accuracy in dense prediction tasks is increased by the encoder-decoder structure, enabling the model to collect rich semantic features and then progressively recover spatial details during up-sampling. Flexibility and enhanced feature extraction are made possible by DeepLabv3+'s ability to use several backbone networks, including ResNet50 and Xception. It is a well-liked option in the field of biomedical image analysis because of its exceptional performance in medical image segmentation tasks, including diagnosing brain tumors from MRI images. Figure 2 illustrates the encoder-decoder architecture upon which the DeepLabV3+ is built.

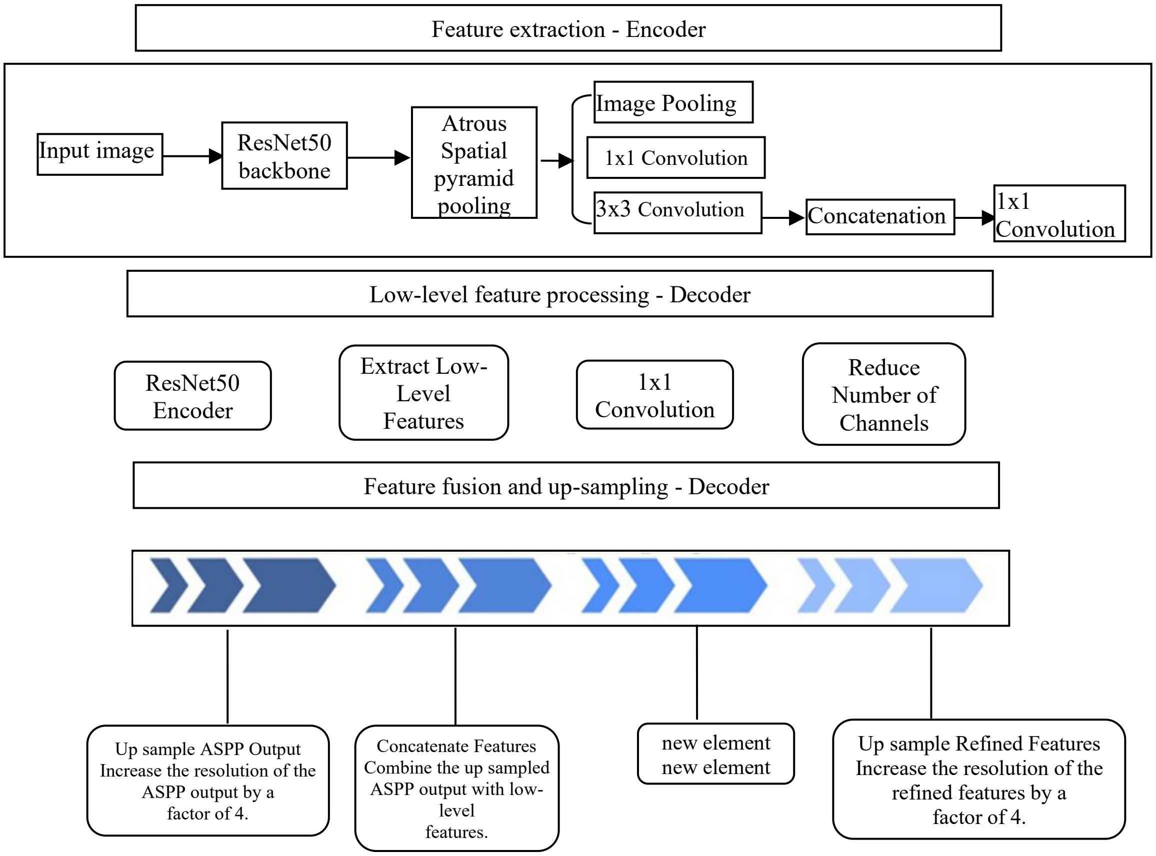

Figure 2: The architecture of the Deeplabv3+ model

In the encoder stage of this preparation, feature extraction requires a network. During the encoder stage of DeepLabV3+, trained models like ResNet18, Xception, ResNet101, ResNet50, EfficientNet, and MobileNetV2 can be utilized as extractors. Out of all the possible networks, our algorithm chose the ResNet50 weights as its initial weights.

4 The Proposed Model

Our method is aimed at the MRI image semantic segmentation of brain cancers by taking output's advantage of the GSCNN model, expanded with the pre-trained ResNet50 weight, and using this output as an input for the DeeplabV3+ model, as shown in the following algorithm.

To improve prediction accuracy, our proposed model combines two different models. The GSCNN model is initially used as the basis model and is trained via the training dataset. The proposed model, which is based on the DeepLabv3+ architecture, then uses its predictions as input. Results from this multi-layered approach are more accurate than those from conventional techniques. The outcomes of the GSCNN model are supplied into the introduced method, which is then trained and assessed, following the GSCNN model's training and saving. Common measurements include F1-score, accuracy, sensitivity, specificity, and precision, are used to evaluate the meta-model's performance. This method increases the clarity of the final segmentation results in addition to improving overall performance. In Figure 3, the suggested model is displayed.

Algorithm Proposed method for Brain Tumor Segmentation:

Start
1. Data Preprocessing:
2. Splitting Data
3. Data Augmentation
a. Resizing to (240, 240)
b. For train data do
i. Rotation
ii. Width and high shift
iii. Zoom
iv. Shear
v. Horizontal flip

End for

Model Training
c. Train the base model (GSCNN) with training data set
d. Get predictions of the base model
e. Fed that predictions as input to the meta model deeplabv3+
f. Get final predictions of the meta model deeplabv3+
4. Model Evaluation

Compute the metrics(Accuracy, Recall, Precision, Specificity, F1-score)
5. Save Model

Stop

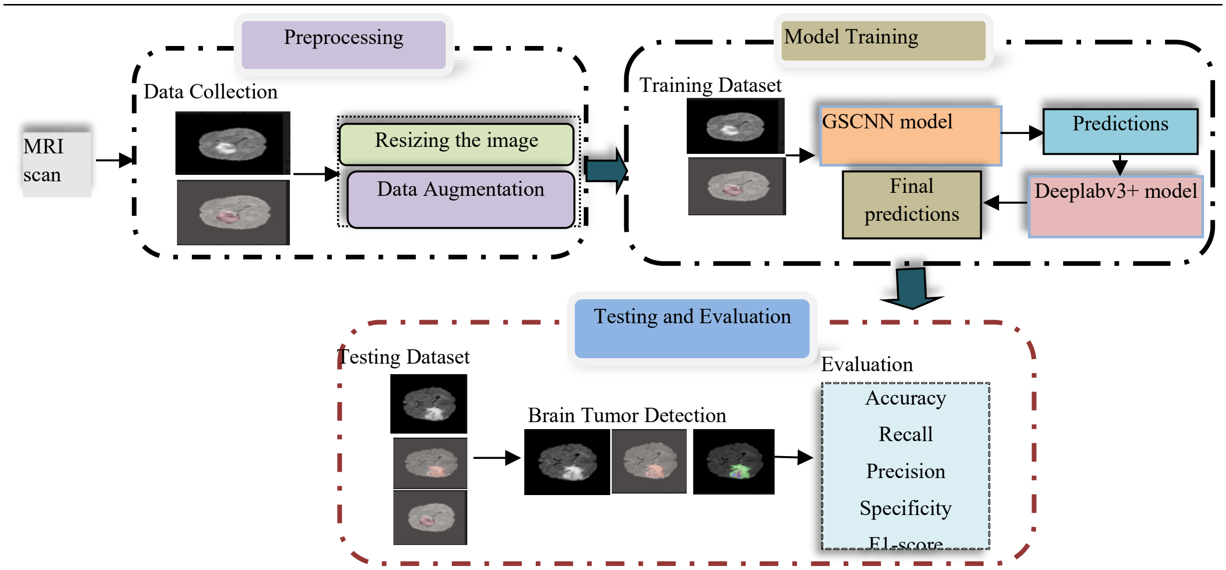

Figure 3: The Diagram of the Proposed Method

5 Evaluation Metrics

The usual measures were applied to evaluate how well different deep learning algorithms performed in segmenting the brain MR images. The following section will provide an explanation of the F1-scores, precision, recall/sensitivity, accuracy, and specificity used during this study.

Accuracy: contrasts the overall quantity of samples that match the number of samples that were correctly predicted. These samples are often pixels or voxels in image processing. However, accuracy is rarely taken into consideration on its own and is not beneficial in uneven data distributions that may develop in image processing.

Precision: contrasts all positive predictions with the quantity of accurately predicted positive examples.

Specificity: calculates the percentage of all negative samples that are accurately predicted like negative samples. When determining the quantity of false positive pixels in an image, both specificity and precision are helpful.

Recall/sensitivity: calculates the proportion of samples that tested positive and were correctly identified as such.

F1-score is often used to combine recall and precision to measure the method's overall effectiveness.

$$Accuracy = \frac{TP + TN}{TP + FP + TN + FN} \quad (1)$$

$$Precision = \frac{TP}{TP + FP} \quad (2)$$

$$\text{Sensitivity(Recall)} = \frac{\text{TP}}{\text{TP} + \text{FN}} \quad (3)$$

$$Specificity = \frac{TN}{TN + FP} \quad (4)$$

$$F1 - Score = 2\left(\frac{Precision * Sensitivity}{Precision + Sensitivity}\right) \quad (5)$$

The overlap between two sets is determined by the Dice Similarity Coefficient (DSC). It can be described as follows in relation to ground truth comparison:

$$DSC = \frac{2TP}{2TP + FP + FN} \quad (6)$$

A True Positive (TP) indicates an equation that compares the actual tumor to the expected one. A True Negative (TN) matches the expected and actual non-tumor. A False Positive (FP) indicates that the actual tumor is not in the predicted tumor region, whereas a False Negative (FN) indicates that the actual tumor region is non-tumor.

6 Experimental Results

The BraTS2020 dataset, which includes 4 distinct MRI modalities (T1-weighted contrast-enhanced (T1-CE), Fluid Attenuated Inversion Recovery (FLAIR), T2-weighted (T2), and T1-weighted (T1) images) is utilized in this work to assess the efficacy of our proposed model. Every modality captures unique brain tumor characteristics. To separate the whole tumor (WT), tumor core (TC), and enhancing tumor (ET), the tumor mask must be properly segmented. It consists of areas of necrosis, edema, and enhancement. The validation and training sets are utilized to train the underlying method, Gated Shape CNN (GSCNN). The final segmentation predictions were then produced by feeding its prediction outputs into the DeepLabv3+ model. The effectiveness of the method was validated utilized a different set of tests.

A 32 batch size, a 0.001 learning rate, and more than 35 epochs were utilized for the training process. 2,980 training photos, 340 validation images, and 370 test images compose the dataset. Resizing the raw images and using data augmentation methods like rotation, zoom, shear, width and height changes, and horizontal flipping were all part of the preprocessing procedure. Convolutional layers that recognized patterns such as textures, edges, and corners were used to extract features. The Adam optimizer was utilized during training, and the last activation layer was SoftMax function.

The suggested method's performance metrics were contrasted with those of the DeepLabv3+ and standalone GSCNN models. As shown in Table 1, the proposed method performed better than the other techniques in terms of specificity, accuracy, precision, F1-score, and sensitivity.

Table 1: The introduced method's comparison with (GSCNN and deeplabv3+) models on BraTS2020.

Model	Accuracy%	Sensitivity%	Specificity%	Precision%	F1-Score
GSCNN	94.63	94.35	98.52	95.43	94.89
Deeplabv3+	97.82	97.82	99.27	97.82	97.82
The proposed model	98.87	98.84	99.49	98.83	98.83

Table 1, offers a comparative analysis of three models — GSCNN, Deeplabv3+ and proposed model—which is based on five performance measurements: accuracy, F1 score, specificity, and sensitivity. Of the three, the introduced model consistently improves others in all assessment criteria. In particular, this achieves the highest accuracy of 98.87%, reflecting better general prediction performance. When it comes to sensitivity (98.84%) and specificity (99.49%), the proposed model shows excellent ability to identify both positive tumor regions and negative/background. In addition, the model gets an accuracy of 98.83%, reflecting a low false positive rate, and a 98.83%F1 score, which balances precision and memory accuracy. In comparison, DeePlabv3+ shows strong performance but still retires slightly, while GSCNN shows the lowest score in all matrices. These results clearly validate the better partition and classification capacity of the proposed models.

With 99.49% specificity, 98.87% accuracy, 98.83% precision, 98.83% F1-score, and 98.84% sensitivity/recall, it is obvious that the suggested model performed best across all criteria. It showed significant improvements by increasing accuracy by 1.05%, sensitivity by 1.02%, specificity by 0.22%, precision by 1.01%, and F1-score by 1.01% when compared to the DeepLabv3+ model. The enhancements are even more significant when compared to the GSCNN model: the F1 score increased by 3.94%, specificity by 0.97%, accuracy by 4.24%, sensitivity by 4.49%, and precision by 3.4%. A 2D depiction of the segmentation outcomes generated by the suggested model is shown in Figure 4. The suggested method produces more accurate and precise segmentation than the alternative, as demonstrated by a visual comparison with the ground truth.

Original Image Flair	Ground Truth	All classes	NECROTIC/CORE (TC) predicted	EDEMA (WT) predicted	ENHANCING (ET) predicted

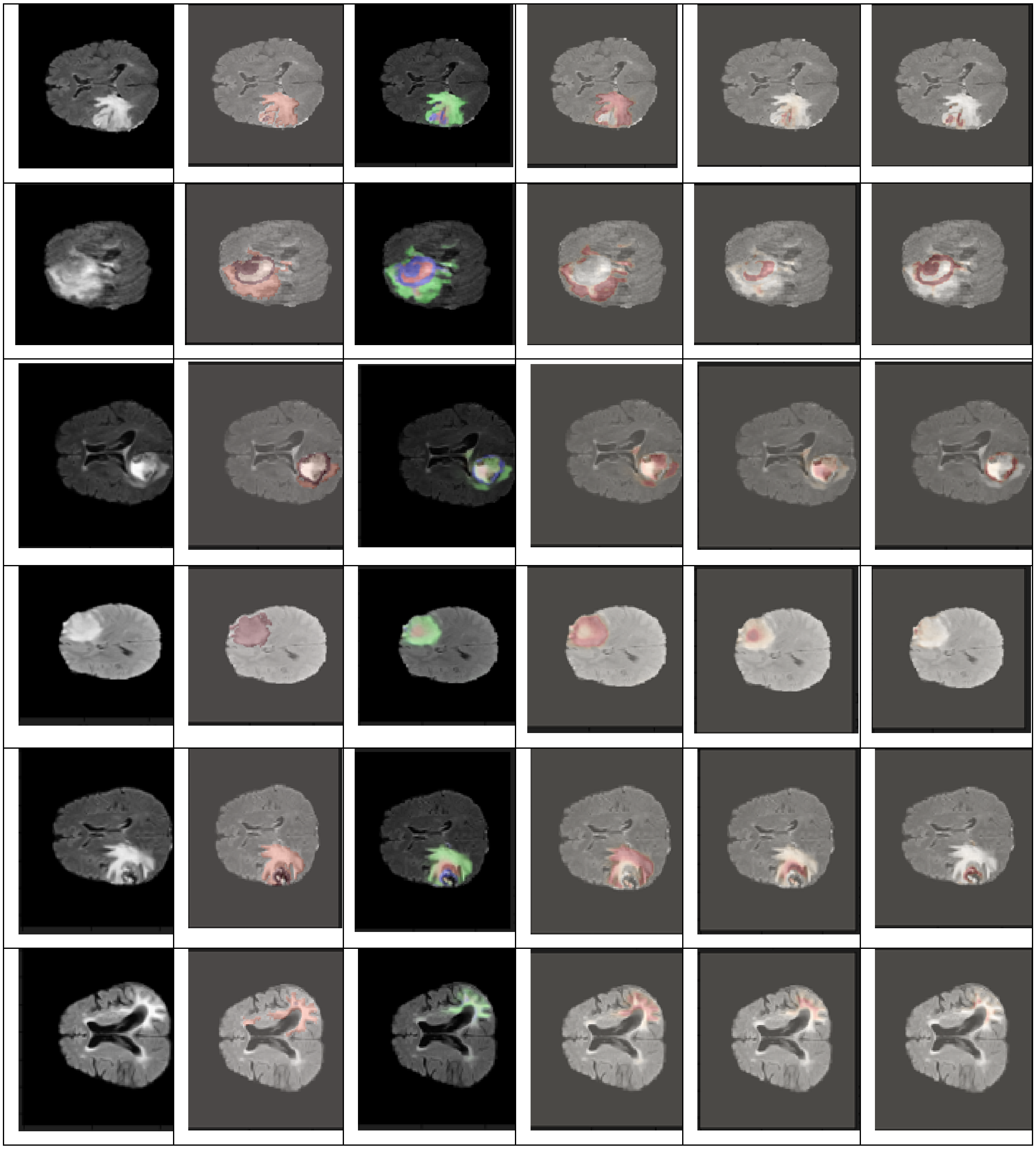

Figure 4: Shows the original image, the ground truth and the predicted mask all classes and the predicted (TC, WT, and ET) of the proposed model.

Two line graphs that show the suggested model's training performance over 35 epochs are shown in Figure 5, the model's training loss over epochs is displayed in the left plot. Rapid learning and convergence during early training are indicated by the sharp decline in the first few epochs. The loss stabilizes and keeps decreasing steadily after the fifth epoch, indicating that the model is learning efficiently and avoiding divergence or overfitting. The training accuracy over the same epochs is shown in the right plot (training accuracy). Within the first few epochs, the accuracy increases dramatically, quickly getting close to 99%. It then continuously stays high, showing that the model has perfected the art of accurately classifying the training data. These plots illustrate the stability and effectiveness of the training procedure by showing that the model converges rapidly and performs excellently with high accuracy and little training loss.

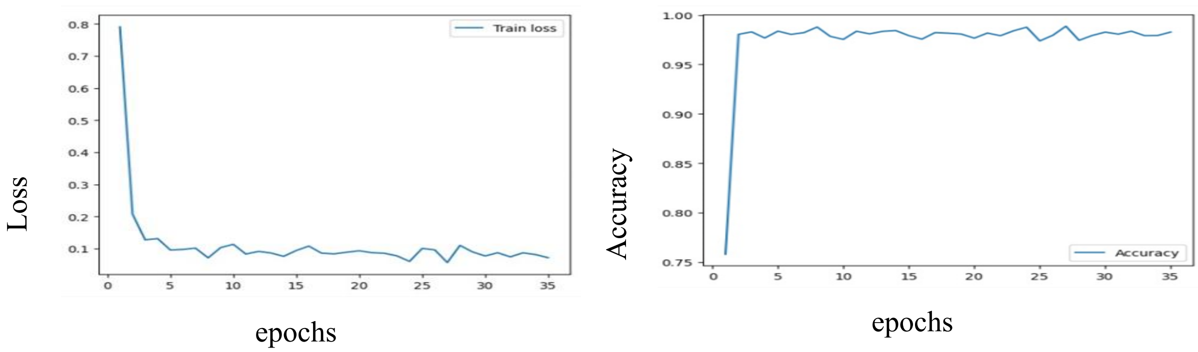

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Figure 5: a) The loss curves, and b) the accuracy of brain tumor segmentation model.

Table 2 examined various deep learning techniques applied to brain tumor segmentation across editions of BraTS2020 dataset, with a focus on high-grade glioma (HGG) cases. Each strategy provided dice scores of tumor core, tumor segmentation, and tumor enhancement using multiple MRI procedures, typically T1, FLAIR, T2, and T1c. On dice test, 3D convolutional networks (Yi et al., 2016) and U-Net (Dong et al., 2017) architectures outperformed autoencoder-based models (Vaidhya et al., 2015) and conventional CNNs (Zikic et al., 2014; Pereira et al., 2016), which did not perform as well. The Deep Cascaded Neural Network (Cui et al., 2018) produced one of the best results, scoring 90, 81, and 81 for the three tumor locations. Competitive results were also shown by more recent models like 3D U-Net with residual-dense ASPP (Alex et al., 2019) and Dense FCNs (Shaikh et al., 2017). The proposed meta Deeplabv3+ model, which combines GSCNN as a base and ResNet-50 enhanced Deeplabv3+ as a meta model, demonstrated the advantages of model stacking and deeper feature integration by slightly outperforming previous models in whole tumor segmentation (87.48%) while still achieving strong results across other regions (83.96% for tumor core and 79.27% for enhancing tumor). DeepLabv3+ with ResNet-18 (Shoushtari et al., 2022) also performed well on the BRATS2020 dataset.

Table 2: Comparison of the results of this study with previous investigations

Method	Summary of method	Database	MRI Modality	Grade	DSC		
					Whole Tumor	Tumor Core	Enhancing Tumor
Shoushtari et al., 2022	Deeplabv3+ With Resnet-18	BraTS2020 Training	T1c, Flair	HGG	87	85	78
Yi et al., 2016	3-D Convolution	BraTS2015 Training	T1, T2, T1c, Flair	HGG	89	76	80
Dong et al., 2017	U-Net Based Fully Convolutional Networks	BraTS2015 Training	T1, T2, T1c, Flair	HGG	88	87	81
Vaidhya et al., 2015	stacked denoising autoencoder (SDAE), (A deep neural network that reconstructs its input)	BraTS2015 Challenge	T1, T2, T1c, Flair	HGG	81	68	64

Zikic et al., 2014	Convolutional Neural Networks	BraTS2013 challenge	T1, T2, T1c, Flair	HGG	84	74	69
Pereira et al., 2016	A CNN with small 3 × 3 kernels	BraTS2013 Leaderboard	T1, T2, T1c, Flair	HGG	88	76	73
Cui et al., 2018	Deep Cascaded Neural Network	BraTS2015 Training	T1, T2, T1c, Flair	HGG	90	81	81
Alex et al., 2019	3D U-Net with residual-dense ASPP	BraTS2019 Training	T1, T2, T1c, Flair	HGG	87	84	78
Shaikh et al., 2017	Dense Fully Convolutional Neural Network	BraTS2017 Challenge	T1, T2, T1c, Flair	HGG	84	83	80
Pereira et al., 2016	Deep neural network	BraTS2016 Challenge	T1, T2, T1c, Flair	HGG	78	76	79
Ahmad et al., 2019	Deep Fully Convolutional	BraTS2017 Training	T1, T2, T1c, Flair	HGG	87	82	80
Proposed method	Base model (GSCNN), deeplabv3+ with Resnet50	BraTS2020 Training	T1, T2, T1c, Flair	HGG	**87.48**	**83.96**	**79.27**

Table 3 presented a comparative evaluation of different models to assess the segmentation of tumors in the brain according to the most important performance measurements: specificity, sensitivity, F1 score, and accuracy. Among the listed models, the proposed model shows the most balanced and better effectiveness, with 98.87% accuracy, a sensitivity of 98.84%, a specificity of 99.49%, and a 98.83% F1 score. These results both cross baseline models (GSCNN and Deeplabv3+) and already published methods. While Ilhan., et al. (Biswas & Tiwari, 2024) reached a slightly greater accuracy and a specificity of 99.83% with the 99.40% model, it had significantly low sensitivity (83.62%) and F1 score (88%), indicating the high probability of the lack of actual tumor regions.

Corresponding to other models such as Liu et al., 2022; Zhang et al., 2021, it offers high specificity and sensitivity but lacks complete metric coverage or demonstrated unbalanced performance. Shoushtari et al., 2022, achieved appropriate accuracy (97.5%) and sensitivity (95.43%), but were particularly less precise (79%), resulting in more false positives. Overall, the proposed model outperforms others in delivering high and consistent results in all matrices and confirms the efficiency and strength of the exact brain tumor division.

When compared to alternative research-based methods and traditional models (GSCNN, DeepLabv3+), the suggested model performs better in almost all critical areas. It provides a good compromise between limiting inaccurate predictions (high specificity and precision) and accurately recognizing tumor regions (high sensitivity).

Table 3: Comparing the suggested approach to other methods

Model	Accuracy%	Sensitivity%	Specificity%	Precision%	F1-Score
GSCNN	94.63	94.35	98.52	95.43	94.89
Deeplabv3+	97.82	97.82	99.27	97.82	97.82
Biswas & Tiwari, 2024	99.40	83.62	99.83	92.94	88
Liu et al., 2022	-	86.9	-	90.77	-
Zhang et al., 2021	-	90.5	99.9	-	-
Shoushtari et al., 2022	97.5	95.43	93.1	79	86.4
The proposed model	98.87	**98.84**	99.49	**98.83**	**98.83**

7 Conclusion

This work introduced the transformer dependent on the DeepLabV3+ model for brain tumor segmentation. The approach includes the first base model, GSCNN, and then, by using the prediction output as the input to the DeepLabv3+ model, generating the final predictions. This integration increases the total performance, an estimated 1.05% improvement in accuracy. To prepare the data, we implemented many preprocessing techniques, including image size and augmentation strategies, including zooming, rotation, cutting, width and height shift, and horizontal flipping. The proposed model demonstrated a strong segmentation performance on the BraTS2020 dataset. We assessed the efficiency using a standard evaluation matrix that included sensitivity, accuracy, F1 score, and specificity. Compared to individual GSCNN and Deeplabv3+ models, our method improved 98.87% accuracy, 99.49% specificity, 98.84% sensitivity, 98.83% F1 score, and 98.83% precision. The future work will focus on validating the model in several datasets to assess its generality.

Conflicts of Interest: The authors have no conflicts of interest to report.

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