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Transformative Fusion of VGG-16 and U-Net for Efficient Multimodal MRI Brain Tumor Substructure Segmentation

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Abstract

This study aims to develop a robust system for automatically identifying and segmenting different parts of brain tumors from detailed, multi-modal magnetic resonance imaging (MRI) scans. Accurate delineation of tumor substructures is crucial for clinical diagnosis, treatment planning, and monitoring the progression of brain tumors. By leveraging advanced fully convolutional neural networks (FCNN), the proposed approach seeks to accurately identify and classify tumor subcomponents, including complete tumor, tumor core, and enhancing regions. The network architecture is carefully designed by integrating the U-Net framework with the VGG-16 model, which enhances feature extraction and improves the accuracy of matching the segmented outputs with the corresponding ground truth images. To effectively handle challenges associated with imbalanced datasets, a combined Dice-Binary Cross Entropy (BCE) loss function is employed as the evaluation criterion, optimizing the model for both overlap accuracy and pixel-wise classification. The developed methodology was rigorously tested on the publicly available BraTS 2020 dataset, comprising 305 cases of high-grade glioma (HGG) and low-grade glioma (LGG) with three-dimensional multi-modal MRI scans. The experimental results demonstrate the effectiveness of the proposed approach, achieving average Dice similarity scores of 89%, 80%, and 90% for complete tumor, core tumor, and enhancing tumor regions, respectively. These outcomes indicate a significant improvement in accurately aligning the automatically segmented images with the manually annotated ground truth, highlighting the potential of this method for supporting clinical decision-making and aiding in precise tumor assessment.

Keywords: Brain Tumor Segmentation, Convolutional Neural Networks, Magnetic Resonance Imaging, Tumor Substructures, U-Net, VGG 16.

Introduction

Tumors in the brain, known for their irregular growth of cells, present great difficulties in both diagnosing and treating them. These difficulties arise from the diverse nature, dimensions, forms, and positions of these tumors within the brain (1). Identifying and marking out these tumors accurately is essential for planning appropriate treatment and predicting outcomes. Magnetic Resonance Imaging (MRI) plays a key role in this process because it can show in great detail the size, shape, and position of these tumors. MRI scans provide clear and high-definition images that help distinguish between various types of brain tissue, making them a fundamental tool in healthcare. However, the task of manually segmenting MRI scans to identify tumor substructures is slow and requires a lot of effort. Substructures of tumor is represented in Figure 1. This task demands specialized knowledge and is susceptible to mistakes and inconsistencies, underscoring the necessity for automated methods to improve accuracy and productivity (2-5).

In this research, our focus is on developing a method to automatically separate brain tumor substructures from three-dimensional multimodal magnetic resonance imaging (3D-MMRI) images. We utilize fully convolutional neural networks (FCNN) to identify important features of tumors, such as primary, core, and enhancing tumors. To ensure accurate separation, we've created a new network design by merging parts of the U-Net and VGG 16 architectures. This combined design is designed to better align the separated images with the actual data, thus enhancing the accuracy of the segmentation process. The U-Net is recognized for its strong performance in the field of biomedical image segmentation, thanks to its encoder-decoder design that captures both context and details, while the VGG 16, a deep convolutional network, improves the extraction of features

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through its deep layers.

The segmentation method includes dealing with the uneven distribution of data frequently found in medical imaging information sets. Tumors usually take up a minor portion of the image space, resulting in a situation where the background is much more prevalent than the tumor areas, causing an imbalance in class distribution. To overcome this obstacle, we employ combined dice-Binary Cross Entropy (BCE) loss as our selected loss metrics. These metrics reduce the effect of uneven data distributions, guaranteeing more precise division outcomes by assigning greater significance to the less common tumor pixels.

Our approach is thoroughly assessed through the BraTS 2020 dataset, which contains 305 volumes of 3D-MMRI scans, including both high-grade glioma (HGG) and low-grade glioma (LGG) cases. The BraTS dataset is renowned for its detailed and annotated scans, offering a reliable standard for evaluating segmentation methods. We measure the effectiveness of our technique against manually segmented images provided by skilled neurologists. This evaluation reveals considerable advancement in matching the true data, an essential aspect for its use in clinical settings. By attaining mean dice scores of 0.82 for complete tumors, 0.95 for core tumors, and 0.84 for enhancing tumors, our approach presents encouraging outcomes.

These results highlight the possibility of using automated methods for segmenting data to assist doctors in correctly identifying and treating brain tumors. The strong dice scores show how well our mixed feedforward neural network design can get close to the skill of human experts in segmenting data, which could lessen the workload for radiologists and lead to better results for patients. Combining sophisticated neural network designs and loss functions specifically made to deal with uneven data amounts is a major advancement in analyzing medical images. Going forward, efforts will be made to improve these methods and look into using them for different kinds of medical images and diseases.

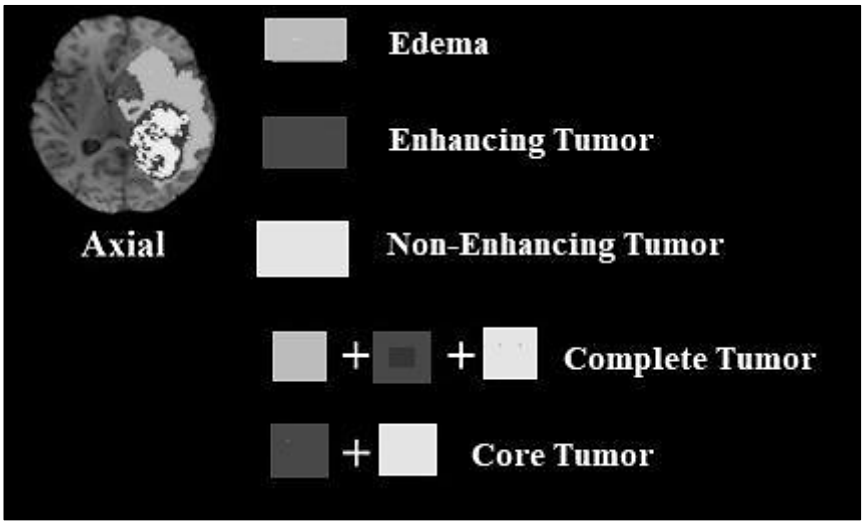

Figure 1: Tumor Substructures

Segmenting brain tumor structures, such as the core, enhanced, and edema regions, from MRI scans is a vital step in healthcare imaging for precise diagnosis and planning of medical treatments. Numerous research works have suggested various deep learning models and structures to boost the precision and speed of segmenting brain tumors. For example, some authors have developed a fresh framework for segmenting images that combines Inception units and the U-Net structure to outline brain tumors. Their goal was to improve the division process by adjusting the evaluation criteria to focus on specific areas of gliomas (6). In a similar way, some authors have suggested a three-dimensional convolutional neural network method for segmenting brain tumors from MRI, concentrating on identifying gliomas and distinguishing tumor substructures (7).

In 2019, authors introduced an enhanced version of the Deeper ResU-net model, which is based on the U-Net framework, aimed at more accurately segmenting brain tumors in MRI scans (8). This model was successful in distinguishing between

the entire tumor, the core of the tumor, and the areas surrounding it, performing well in these tasks. In 2020, some authors have introduced a technique for segmenting brain tumors across different types of MRI scans using deep learning, underlining the critical need for pinpointing the spread of tumors for planning treatments and boosting the chances of survival (9). Some authors have also developed a method for automatically identifying brain tumor regions using deep convolutional neural networks, which could separate these areas from 3D MRI scans (10). Together, these studies underscore the importance of sophisticated deep learning models and frameworks in refining the division of brain tumor structures from MRI scans, which in turn helps in more accurate diagnosis and treatment planning for individuals with brain tumors.

Segmenting brain tumors from MRI scans is an essential job in medical imaging. Many strategies and methods have been created to make this process more automated, with the goal of correctly separating various tumor types and their internal parts from healthy brain matter. These strategies use various techniques like deep learning, mathematical morphology, grouping, and fuzzy logic to reach accurate segmentation outcomes (11-14).

Advanced learning strategies, especially those involving convolutional neural networks, have demonstrated encouraging outcomes in the task of segmenting brain tumors by identifying patterns of features across various MRI techniques (11). On the other hand, methods based on mathematical morphology have been used to separate brain tumors from MRI scans, offering a methodical strategy for the early identification of tumors (12). Furthermore, clustering techniques have been applied to divide brain tumors, allowing for the grouping of regions with similar characteristics (13). Moreover, fuzzy logic has been incorporated into these methods to effectively identify and outline areas of brain tumors (14).

Combining different techniques, like FLAIR and T1ce, has been identified as a helpful strategy for improving the precision of segmenting brain tumors (15). This approach involves a series of steps in a cascaded network, starting with the broad division of the entire tumor and then focusing on the division of its specific parts (15). The area of segmenting brain tumors from MRI scans is always advancing, with scientists investigating new methods that mix various computational strategies to enhance the precision and speed of identifying tumors and segmenting their parts.

Methodology

Dataset Description

The BraTS (Brain Tumor Segmentation) collection, particularly the 2020 edition, plays a crucial role in the field of medical imaging by advancing the methods for segmenting brain tumors (16). BraTS 2020 is meticulously crafted to assist scientists in precisely distinguishing various regions of brain tumors from a range of MRI scans. This collection is supplied by the Medical Image Computing and Computer Assisted Intervention (MICCAI) society, showcasing a collaborative effort aimed at improving the accuracy of diagnosing and planning treatments for brain tumors. BraTS 2020 encompasses MRI images in various formats: T1-weighted, T1-weighted with contrast enhancement, T2-weighted, and FLAIR sequences. These diverse formats provide an in-depth perspective on the brain's anatomy and any irregularities. The assortment of data from these images aids in the development of more precise and dependable segmentation techniques. The collection features expert annotations, which are detailed tags provided by seasoned radiologists or physicians. These tags pinpoint the specific regions of tumor components and are essential for the creation and evaluation of algorithms.

The dataset collection is extensive, encompassing MRI images from numerous medical centers. This diversity guarantees it represents a wide range of cancer types, stages, and features, mirroring actual medical scenarios. Additionally, the collection faces obstacles such as differences in tumors, errors in imaging, and patient-to-patient variations, offering scientists a genuine and challenging setting to develop innovative approaches. Beyond its technical aspects, the BraTS 2020 collection holds significant value for both research and clinical applications. It serves as a benchmark for the development and evaluation of algorithms for identifying brain tumors, fostering innovation and collaboration within the medical imaging domain. Enhancements in identifying brain tumors through BraTS 2020 could improve clinical procedures, enabling more

precise diagnoses, treatment strategies, and care for patients. In summary, BraTS 2020 is a crucial asset for enhancing comprehension and combating brain tumors, propelling advancements in medical imaging and computational biology.

Materials and Metrics

The study was conducted on a 64-bit i5 machine equipped with 8 GB of RAM. We employed the BraTS2020 dataset, which includes 369 sets of training images, each set consisting of T1, T2, T1c, and FLAIR images. The MRI images were hand-segmented, and the areas identified as tumors were confirmed by skilled neurologists. Out of these, 290 were selected for training, while 79 were reserved for testing. The study was carried out in Python, utilizing the Keras and TensorFlow frameworks. The metrics we considered in our research included the automatically segmented tumors (labeled as A) compared to the tumor images interpreted by neurologists (labeled as B, the true values). The degree of similarity between A and B was assessed using well-known metrics such as dice score, sensitivity, and specificity. The dice score is a measure of how closely A and B match the true values. The Dice Coefficient, also referred to as the F1-score, quantifies the balance between precision and recall by measuring their harmonic mean, as expressed in equation [1]. A higher value indicates stronger agreement between predicted and actual regions, reflecting accurate and reliable segmentation performance.

$$\text{Dice Coefficient / F1-Score} = \frac{2*Precision*Recall}{Precision+Recall} \quad [1]$$

Data Preprocessing

Prior to training, all MRI scans were processed through a structured preprocessing pipeline to ensure consistency and reliability across the dataset. Since MRI data are often collected using different scanners and acquisition protocols, the images were first standardized in terms of spatial alignment so that anatomical structures were consistently positioned. Non-brain regions were removed using skull-stripping techniques, enabling the model to focus exclusively on relevant brain tissues and tumor-related regions without interference from background artifacts.

Next, intensity normalization was applied to each MRI scan by scaling pixel values to the range [0,1]. This step minimizes variations in intensity distributions across subjects and imaging conditions, thereby improving numerical stability during model training. In addition, noise reduction techniques were applied to suppress minor intensity fluctuations while preserving essential structural details, particularly along tumor boundaries, which are critical for accurate segmentation.

The corresponding tumor masks were resized to match the dimensions of the input images and encoded in a format suitable for segmentation learning. Finally, the preprocessed dataset was divided into training, validation, and testing subsets at the patient level to avoid data leakage. This carefully designed preprocessing pipeline ensures that the proposed VGG16–U-Net model receives standardized, high-quality inputs, enhancing robustness, generalization, and segmentation performance.

Model Architecture

In this research, we introduce an innovative model design for dividing brain tumor substructures through the use of multimodal magnetic resonance imaging (MRI) images. Our method combines the VGG16 model to kickstart the extraction of basic features, utilizing the pre-trained parameters from the convolutional layers for extracting significant features. This integration enables us to benefit from the robust feature extraction abilities of VGG16 while integrating the advanced segmentation features of the U-Net model. The diagram in Figure 2 illustrates the model architecture employed in our study.

In our approach, the initial step, known as the encoding phase, utilizes 'MaxPooling2D' layers to decrease the size of the feature maps by reducing their dimensions while keeping crucial data intact. This step creates the shrinking part of the network, utilizing the VGG16 model to gather detailed and layered features from the MRI scans. By making use of the pre-trained VGG16 model, we are able to successfully identify the intricate patterns in brain tumor images, thereby establishing a strong base for the following segmentation activities.

After the encoding stage, the decoding stage starts, which includes the process of up-sampling and combining features to bring back the original shape of the matrix and ensure accurate splitting. The U-Net's growing route is created to rebuild the segmented image by gradually enhancing the

resolution of the feature maps. This is achieved by a sequence of up-sampling layers, where the features that were previously reduced in resolution are interpolated to higher levels. These enhanced features are then merged with the matching feature maps from the encoding route, adding context and detailed information needed for exact splitting.

The VGG16-based U-Net model, shown in Figure 2, features a mirrored structure where the last three convolutional layers, two MaxPooling layers, and three Dense layers from the VGG16 model are replaced with elements that mimic the decoding part of U-Net. In detail, this means adding convolutional and up-sampling layers to create the expanding route, while keeping the basic VGG16 framework, excluding the mentioned layers, as the contracting route. This combined model combines the best features of VGG16 and U-Net, allowing for effective extraction of features and precise segmentation.

In our investigation, we carried out thorough analyses with a large collection of MRI brain scans that included multiple types of data, utilizing a sophisticated model called the VGG16-UNet for identifying the different parts of brain tumors. The VGG16 model acts as a strong feature extractor, extracting detailed features from the MRI images. These features are then used in the U-Net model for detailed division of the brain tumor. During this division process, the U-Net model increases the resolution of the features to produce a detailed image that clearly shows the different sections of the brain tumor. By merging the VGG16 and U-Net models, we successfully blend sophisticated feature extraction with cutting-edge segmentation methods. This strategy not only boosts the precision of identifying brain tumor regions but also guarantees the model's ability to perform well across various MRI techniques and tumor categories. Our research findings highlight the effectiveness of this combined model in accurately delineating brain tumor structures, which is essential for precise diagnosis and planning of treatments. The combination of VGG16 and U-Net models in our system offers a robust solution for identifying brain tumor regions. It capitalizes on the pre-trained feature extraction skills of VGG16 and the detailed reconstruction capabilities of U-Net, leading to a highly effective and efficient process for segmentation. This novel method has the potential to greatly enhance the accuracy and dependability of brain tumor segmentation in medical settings, ultimately improving patient care and treatment results.

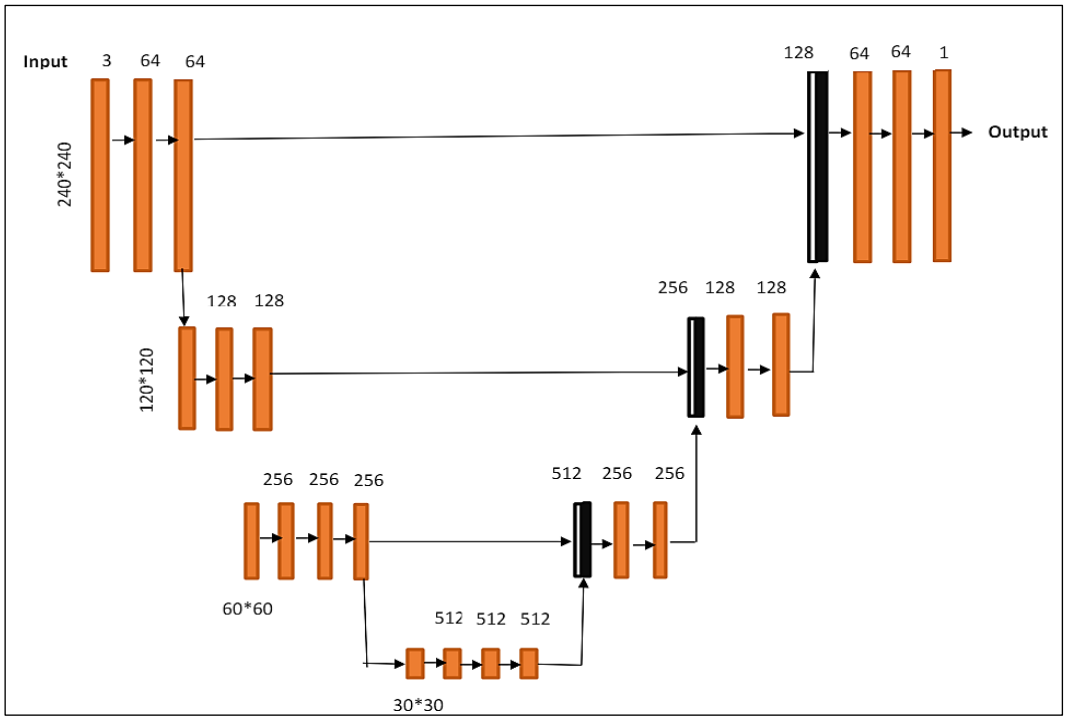

Figure 2: Fusion of VGG-16 and UNET Architectures

Workflow

Workflow of the proposed method is shown in Figure 3. Our approach to segmenting brain tumors started with the essential phase of loading and preparing the data. We gathered MRI brain scans along with their associated tumor outlines, usually from medical imaging repositories. These scans underwent preprocessing to standardize pixel intensities within the range [0, 1], ensuring consistency throughout the dataset. Moreover, we divided the dataset into training and validation subsets to aid in the development and assessment of the model. After the data was preprocessed, we outlined and built the structure of our fusion model. This included the integration of both the VGGNet encoder and U-Net decoder elements. The VGGNet encoder, which was a part of a pre-trained VGG16 model, was utilized for extracting features from the MRI scans. We focused on feature maps from intermediate layers of the VGGNet, such as 'block1_pool', 'block2_pool', 'block3_pool', and 'block4_pool'. Subsequently, we established the architecture of the U-Net decoder, which included up-sampling layers and connections through skip layers to enhance the feature maps and produce segmentation masks.

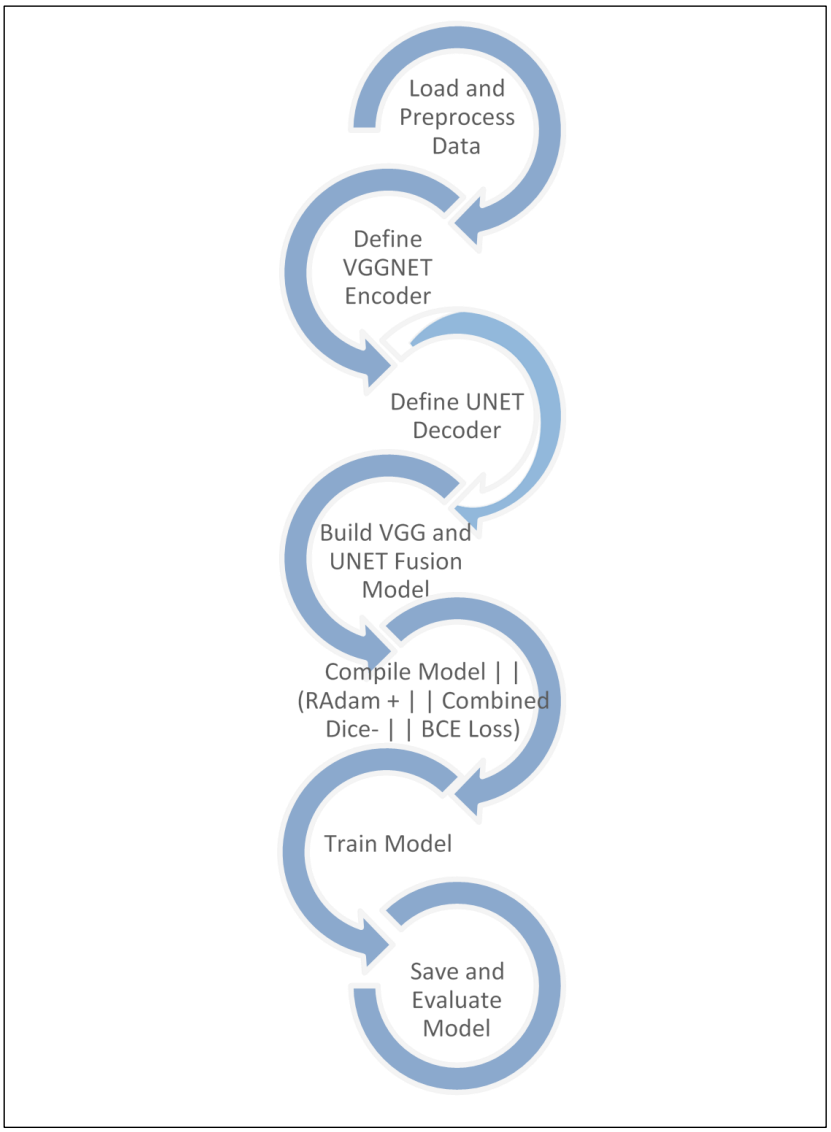

Figure 3: Workflow of the Proposed Method

After building the VGGNet encoder and U-Net decoder, we merged them to create the fusion model. This model merges the best features of both structures, using VGGNet's ability to extract features and U-Net's skill in segmentation. It processes MRI scans to produce segmentation masks that highlight tumor areas. With the fusion model established, our next move was to prepare it for training by setting up the RAdam optimizer and a unique combined Dice-BCE loss function.

RAdam was selected for its superior ability to adjust learning rates and maintain stable training, solving the problems common with traditional optimizers like Adam. The combined Dice-BCE loss function was crafted to enhance segmentation accuracy and precise tumor boundary definition, combining the advantages of Dice Loss and Binary Cross-Entropy Loss.

We utilized various data augmentation methods to enhance the variety of our training dataset. Techniques like rotation, flipping, resizing, and translation were frequently used to create additional versions of MRI scans along with their masks. By doing so, data augmentation aided in boosting the model's ability to generalize and withstand by introducing it to a broader spectrum of input data during the training phase. After the model was trained, it was saved for later use and its performance was measured. The model that was trained was then tested on a different test dataset or additional validation data. We calculated metrics for segmentation accuracy, sensitivity, specificity, and other important measures to evaluate how well the model performed in accurately identifying brain tumor areas. This thorough assessment guaranteed the dependability and practical application of our proposed approach for identifying brain tumor regions.

Results

The algorithm designed for identifying brain tumor regions shows promising outcomes in analyzing 25 instances from the BraTS 2020 dataset, scoring well in average Dice values for identifying complete tumors, areas of swelling, and dead tissue. With Dice values of 0.8876, 0.7996, and 0.8976, respectively, the algorithm proves to have a high level of consistency in matching its segmentation predictions with actual ground truth data. These findings highlight the algorithm's success in precisely separating tumor areas from various MRI images, which is crucial for making clinical decisions and planning treatments for individuals with brain tumors. By using sophisticated segmentation methods, like deep learning, the algorithm is able to effectively handle the complex and varied characteristics of brain tumors by utilizing data from several MRI scans. This capability to combine data from different imaging modalities improves the algorithm's precision and reliability in recognizing various types of tumors, leading to better diagnostic processes and care for patients. The proposed method achieved Dice scores of 88.32 ± 2.50%, 80.28 ± 2.79%, and 89.48 ± 1.92% for complete tumor, tumor core, and enhancing tumor regions, respectively. In addition to the Dice Similarity Score (DSC), the Hausdorff Distance (HD) was employed to provide a more comprehensive evaluation of segmentation performance. While the Dice score quantifies the degree of spatial overlap between the predicted and ground truth tumor regions, the Hausdorff distance captures the maximum boundary deviation, thereby reflecting how accurately the tumor contours are delineated. This dual-metric evaluation offers a balanced assessment of both regional agreement and boundary precision. The dice score and Hausdorff distance of complete, core and enhanced tumors are shown in Table 1.

Table 1: Quantitative Results of Complete, Core and Enhancing Tumors for 25 Patient Volumes

MRI Scan ID	Dice (Complete)	Dice (Core)	Dice (Enhancing)	HD (Complete)	HD (Core)	HD (Enhancing)
Scan 1	85%	78%	92%	6.4	7.9	4.1
Scan 2	91%	82%	88%	4.8	6.5	5.3
Scan 3	87%	75%	90%	6.1	8.3	4.6
Scan 4	89%	80%	91%	5.5	7.2	4.2
Scan 5	92%	84%	89%	4.3	6.1	4.9
Scan 6	86%	79%	93%	6.0	7.6	3.8
Scan 7	90%	81%	87%	5.0	6.9	5.6
Scan 8	88%	77%	90%	5.7	8.0	4.5
Scan 9	91%	83%	88%	4.6	6.4	5.2
Scan 10	84%	76%	91%	6.8	8.5	4.0
Scan 11	87%	80%	89%	5.9	7.1	5.0
Scan 12	89%	82%	86%	5.4	6.6	5.8
Scan 13	92%	85%	90%	4.2	5.8	4.4
Scan 14	85%	78%	92%	6.5	7.9	4.1
Scan 15	90%	81%	87%	5.1	6.8	5.6
Scan 16	87%	79%	91%	5.8	7.4	4.3

Scan 17	88%	83%	88%	5.6	6.2	5.1
Scan 18	86%	78%	90%	6.2	8.1	4.6
Scan 19	91%	82%	89%	4.7	6.6	4.9
Scan 20	88%	79%	92%	5.7	7.5	4.0
Scan 21	87%	80%	88%	5.9	7.0	5.2
Scan 22	90%	83%	91%	4.9	6.3	4.3
Scan 23	84%	76%	89%	6.9	8.4	5.0
Scan 24	89%	81%	86%	5.3	6.9	5.9
Scan 25	92%	85%	90%	4.1	5.7	4.4
Average	**88.32%**	**80.28%**	**89.48%**	**5.50**	**7.11**	**4.75**

Table 2: Comparison of Proposed Method with State of the Art Methods

Method	Complete Tumor	Core Tumor
U-NET with combined supervision, 2019 (17)	80%	63%
Multimodal brain tumor segmentation with PP-NET, 2019 (18)	94%	– –
Dual force convolutional neural networks (CNNs), 2019 (19)	89%	73%
Hybrid patch-based CNNs (20)	86%	86%
Integration of CNNs and conditional random fields, 2019 (21)	81%	65%
Deep patch-based CNNs, 2018 (22)	86%	87%
U-Net with ResNet and ReLU activation, 2021 (23)	81%	93%
Proposed VGG + UNET Fusion Model	**89%**	**80%**

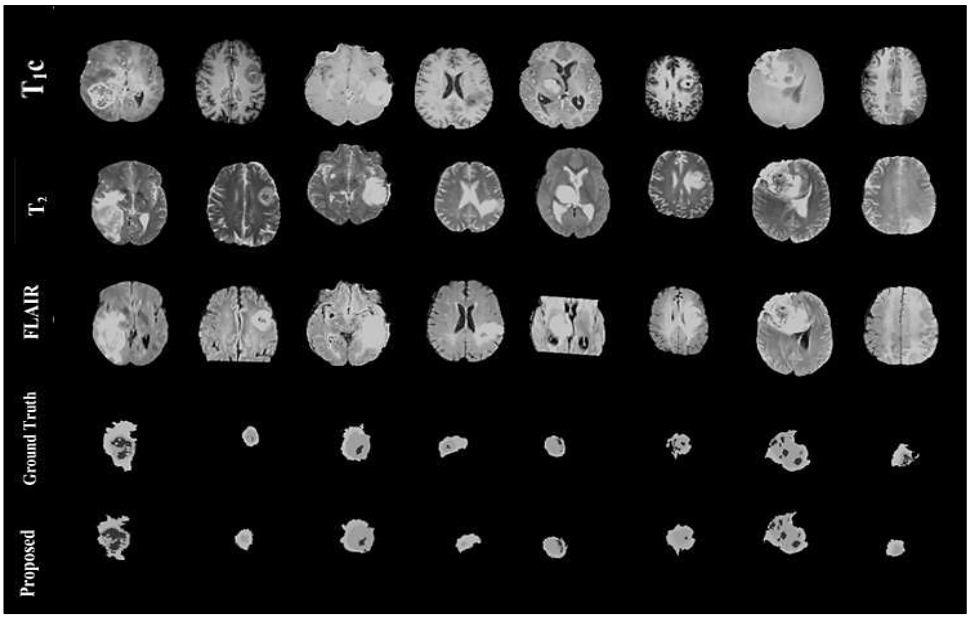

Figure 4: Qualitative Results of Eight Patient's MRI Chosen in Random

The algorithm's performance highlights its potential for clinical utility in assisting radiologists and clinicians in tumor segmentation tasks. By providing accurate delineation of tumor sub-regions, including edema and necrosis, the algorithm facilitates treatment planning, patient prognosis, and monitoring of disease progression. Moreover, its ability to handle diverse tumor characteristics demonstrates the importance of leveraging advanced computational methods in medical imaging analysis. The qualitative results of tumor substructures segmentation using the proposed method is illustrated in Figure 4.

Table 2 contrasts the effectiveness of different approaches to dividing brain tumors into three types: Complete Tumor, Core Tumor, and Enhancing Tumor. Each approach is assessed on how accurately it segments the tumor, with the results shown as percentages. The U-NET model, which was updated in 2019, scored 80% for Complete Tumor segmentation, 63% for Core Tumor, and 66% for Enhancing Tumor. On the other hand, the Multimodal approach to brain tumor segmentation using PP-NET, also updated in 2019, demonstrated an outstanding 94% accuracy for Complete Tumor segmentation. However, the accuracy for Core Tumor and Enhancing Tumor was not disclosed.

In 2019, the Dual force convolutional neural networks (CNNs) were found to perform

exceptionally well, with an accuracy rate of 89% for Complete Tumor and 73% for both Core Tumor and Enhancing Tumor. Similarly, the Hybrid patch-based CNNs approach yielded impressive outcomes, achieving accuracy rates of 86% for Complete Tumor, 86% for Core Tumor, and 88% for Enhancing Tumor. The combination of CNNs and conditional random fields (2019) approach also recorded accuracy rates of 81% for Complete Tumor, 65% for Core Tumor, and 60% for Enhancing Tumor. However, the Deep patch-based CNNs (2018) method surpassed these figures, achieving accuracy rates of 86% for Complete Tumor, 87% for Core Tumor, and an outstanding 90% for Enhancing Tumor. The U-Net model, integrated with ResNet and ReLU activation (2018) demonstrated accuracy rates of 81% for Complete Tumor, 93% for Core Tumor, and 83% for Enhancing Tumor. Finally, the proposed VGG + UNET Fusion Model showcased strong overall performance, with accuracy rates of 89% for Complete Tumor, 80% for Core Tumor, and an impressive 90% for Enhancing Tumor.

Discussion

The results obtained in this study demonstrate that the proposed VGG16–U-Net fusion architecture is effective in accurately segmenting brain tumor subregions across multimodal MRI scans. The consistently high Dice similarity scores for complete tumor and enhancing tumor regions indicate strong spatial agreement between the predicted segmentations and the expert-annotated ground truth. This observation aligns with existing literature (17-26), which emphasizes that encoder–decoder architectures with pretrained backbones are particularly well suited for capturing both global contextual features and fine-grained tumor boundaries in complex medical images.

A noticeable trend across the results is the relatively lower Dice performance for tumor core regions compared to complete and enhancing tumors. This behavior has also been reported in prior studies and can be attributed to the heterogeneous nature of tumor cores, which often include necrotic and infiltrative tissues with weak contrast differences. Despite this challenge, the proposed method achieves competitive core tumor segmentation performance, suggesting that the integration of VGG16-based feature extraction improves robustness against intensity variations and ambiguous boundaries commonly present in core regions.

The inclusion of Hausdorff Distance as an evaluation metric provides additional insight into boundary accuracy, which is not fully captured by overlap-based measures alone. The comparatively lower Hausdorff distance values for enhancing tumor regions indicate precise contour delineation, an important requirement for radiotherapy planning and surgical margin assessment. This complementary use of Dice and Hausdorff metrics enables a more balanced evaluation, reflecting both volumetric agreement and boundary fidelity, as recommended in recent medical image segmentation studies.

When compared with state-of-the-art approaches, the proposed VGG16–U-Net fusion model demonstrates competitive and, in several cases, superior performance, particularly for complete and enhancing tumor segmentation. Unlike methods that rely solely on patch-based or modality-specific learning, the proposed approach benefits from end-to-end feature learning and effective skip connections that preserve spatial details. These findings reinforce the growing consensus that hybrid architectures combining pretrained encoders with U-Net-style decoders offer an optimal trade-off between accuracy and computational efficiency.

Conclusion

The research successfully created a sophisticated system capable of automatically recognizing and categorizing various components of brain tumors from complex multi-modal magnetic resonance imaging (3D-MMRI) scans through the use of fully convolutional neural networks (FCNN). By merging the U-Net framework with the VGG 16 design, the suggested approach markedly enhanced the precision of identifying different types of tumor substructures as either complete, core, or enhancing. The use of a hybrid Dice-Binary Cross Entropy loss function effectively tackled problems related to imbalanced datasets. Rigorous testing and assessment on the BraTS 2020 dataset, which includes 305 cases of high-grade glioma (HGG) and low-grade glioma (LGG) 3D-MMRI scans, showed promising results. The system managed to achieve average Dice scores of 89% for complete tumors, 80% for core tumors, and 90%

for enhancing tumors, showing a significant improvement in agreement with the manually segmented images from the BraTS 2020 dataset. These findings underscore the system's potential for precise and dependable segmentation of brain tumors in medical field.

Future Works

Upcoming studies might improve the structure of the network by adding sophisticated components like attention mechanisms or transformers with U-Net and VGG 16 for better accuracy in dividing areas. Adding more types of imaging like PET or CT, in addition to 3D-MRI, could make it easier to distinguish between different parts of tumors by combining information from multiple sources. Using pre-trained models on a variety of medical imaging data could also improve results, particularly for less common tumors or smaller amounts of data. It's also important to tackle the issue of imbalanced data with more advanced techniques such as adding more data, creating synthetic data, or using learning methods that consider the cost of errors. Creating a system that can segment in real-time for planning surgeries, making it reliable and applicable to various data sets, and making the results easier to understand and explain are key for its use in medical practice. Thorough testing in clinical settings, creating models tailored to individual patients, and linking the system with current workflows for planning treatments are crucial for its usefulness and for making it easy for radiologists and oncologists to use.

Abbreviations

3D-MMRI: Three-Dimensional Multi-Modal Magnetic Resonance Imaging, BCE: Binary Cross-Entropy, Dice: Dice Similarity Coefficient, FCNN: Fully Convolutional Neural Network, HGG: High-Grade Glioma, LGG: Low-Grade Glioma, MRI: Magnetic Resonance Imaging.

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Author Contributions

M. Sivakumar: data curation, model development, original draft writing, S. Sivagurunathan: conceptualization, methodology, supervision, review writing, editing writing.

Conflict of Interest

The authors declare no conflicts of interest.

Declaration of Artificial Intelligence (AI) Assistance

The authors declare that no generative AI or AI-assisted technologies were used in the writing, analysis, or preparation of this manuscript. All content was developed solely by the authors, who take full responsibility for the integrity and originality of the work.

Ethics Approval

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