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Enhancing precision medicine in neuroimaging: hybrid model for brain tumor analysis

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ABSTRACT

Brain tumors are a significant health challenge requiring precise diagnostic methods for optimal patient care. This study introduces a novel approach utilizing a convolutional neural network-based gated recurrent unit (CNN-GRU) for brain tumor detection. The method encompasses a rigorous preprocessing pipeline tailored for multi-modal magnetic resonance imaging (MRI) images, focusing on standardizing dimensions, normalizing pixel values, and enhancing contrast to facilitate robust tumor identification. Subsequently, temporal sequences of preprocessed images are analyzed by the CNN-GRU network to accurately pinpoint tumor regions. Evaluation on the BraTS2020 dataset, comprising diverse MRI scans with manual annotations, demonstrates the method's robust performance in tumor detection, reflecting real-world clinical complexities. Through meticulous preprocessing and model optimization, the approach achieves a remarkable accuracy rate of 99%, offering crucial insights for clinicians in treatment planning and prognosis prediction. Implemented using Python, the framework contributes to advancing brain tumor diagnosis and decision support systems, potentially enhancing personalized medicine and clinical practice. By improving diagnostic accuracy and patient outcomes, this research underscores the importance of integrating advanced computational techniques with medical imaging to address critical healthcare challenges effectively.

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1. INTRODUCTION

Brain tumor is one of the deadliest malignancies in the world. Both children as well as adults get this cancer commonly. Depending on its position, texture, and form, it comes in many varieties and has the lowest chance of surviving. Improper classification of the brain tumor will result in negative results. As an outcome, selecting an appropriate treatment plan depends greatly on accurately determining the nature and grade of the tumor in its initial stages. A useful method for identifying brain tumors is to evaluate the patient's magnetic resonance imaging (MRI) report. Given the volume of data and the variety of brain tumor forms, the manual method becomes laborious and prone to human mistakes [1], [2]. It is believed that this type of tumor poses fewer threats. A malignant tumor has spread to other parts of the body. The most common cause of death for both genders is primary brain and spinal cord tumors [3]. In addition to high- and

low-grade brain tumors, other common types such as pituitary tumors, gliomas, and meningiomas present varying characteristics and symptoms, necessitating diverse treatment approaches [4]. The initial identification and classification of tumors is a substantial zone of study in the area of medicinal imaging processing since it is an effective course of action to extend the life of a patient [5]. A range of approaches, including support vector machine (SVM) and time series analysis, are used in the majority of current research [6]. MRI is employed in tumor detection and classification, with MRI being particularly valuable for its comprehensive depiction of the intricate anatomy of the human brain, making it highly effective in identifying gliomas [7]. The most commonly utilized MRI sequences for brain studies include T1c, T1, fluid-attenuated inversion recovery (FLAIR), and T2, each offering distinct details pertinent to brain tumor analysis, while computational intelligence models hold promise in expediting tumor detection. Computed tomography (CT) scans and x-ray scans, provide comprehensive anatomical information on various brain tissues and overall brain structure [8]. Traditional methods for brain tumor detection often rely on manual interpretation by radiologists or basic image processing techniques [9]–[12]. They are labor-intensive and time-consuming and require expert knowledge and meticulous attention to detail.

The detection and accurate diagnosis of brain tumors are critical for effective treatment planning and patient care [13]. Traditional methods of brain tumor detection rely heavily on the interpretation of medical imaging, particularly MRI. However, the complexity and variability of brain tumor characteristics pose challenges for accurate and timely diagnosis [14]–[16]. In recent years, the integration of advanced computational techniques, such as convolutional neural networks (CNNs) and gated recurrent units (GRUs), has shown promising results in improving the analysis of medical images, especially in the context of three-dimensional (3D) MRI data. This research aims to advance the field of brain tumor detection by proposing a novel approach that integrates CNN-GRU architecture for enhanced analysis of 3D MRI images [17].

The integration of CNN-GRU architecture offers several advantages for analyzing 3D MRI images in the context of brain tumor detection. CNNs are well-suited for learning spatial features from volumetric data, making them effective in identifying patterns indicative of tumors within MRI scans [18], [19]. On the other hand, GRUs excel in capturing temporal dependencies and sequential patterns, which are crucial for interpreting the intricate structures and evolution of tumors over time. By combining these two architectures, the proposed model can leverage both spatial and temporal information inherent in 3D MRI sequences, leading to more comprehensive and accurate tumor detection [20].

The utilization of 3D MRI images provides a richer representation of the brain's anatomy compared to traditional 2D slices, allowing for better visualization and characterization of tumors in their entirety. This additional dimensionality enhances the sensitivity and specificity of tumor detection algorithms, enabling clinicians to make more informed decisions regarding patient management and treatment strategies. Through the integration of CNN-GRU architecture and 3D MRI imaging, this research seeks to contribute to the development of more robust and reliable tools for early detection and precise localization of brain tumors, ultimately improving patient outcomes and quality of care.

This study investigated the integration of CNN-GRU architecture for enhanced analysis of 3D MRI images in brain tumor detection. Previous research has explored various machine-learning methods for tumor classification but has not adequately addressed the integration of spatial and temporal features. CNNs capture spatial patterns, while GRUs capture temporal dependencies, enabling precise detection of tumor evolution. The proposed method leverages multi-modal 3D MRI data, offering improved sensitivity and specificity in tumor detection. This approach aims to enhance diagnostic accuracy, ultimately improving patient outcomes and quality of care.

This study introduces an advanced approach to brain tumor detection using a CNN-GRU architecture applied to multi-modal 3D MRI images. Traditional methods in medical imaging face challenges due to the complexity and variability of brain tumor characteristics, necessitating more sophisticated techniques. Our research fills this gap by integrating CNNs for spatial feature extraction and GRUs for capturing temporal dependencies, thus improving the sensitivity and specificity of tumor detection. This novel method enhances diagnostic accuracy by effectively analyzing the intricate structures and evolution of tumors over time, facilitating precise localization and characterization. By leveraging 3D MRI data, our approach not only enhances the visualization of tumor boundaries but also contributes to more informed treatment decisions and improved patient outcomes in clinical settings.

We found that the integration of the proposed CNN-GRU mechanism provides enhanced analysis of multi-modal 3D MRI images in the context of brain tumor detection. The CNN component effectively extracts spatial features from 3D MRI images, capturing relevant patterns indicative of tumor presence. The GRU component leverages its recurrent nature to capture temporal dependencies across sequential MRI slices, enhancing the understanding of tumor evolution and progression. By employing CNN-GRU, our method enables precise detection of intricate tumor patterns over time, ensuring discriminating sensitivity to subtle changes for accurate identification. The incorporation of both spatial and temporal information using

the integrated CNN-GRU architecture significantly enhances the accuracy and robustness of brain tumor detection.

The flow of this proposed work is systematized as follows. Section 2 includes earlier research for brain tumor detection. Section 3 discussed about the problem statement. Section 4 discussed about the proposed brain tumor detection using CNN based GRU. Section 5 presents the investigational setup, the outcomes, and a discussion of findings. Finally, section 6 carries the conclusion of the paper.

2. RELATED WORKS

Hajmohamad and Koyuncu [21] presented the 3D to 2D feature transform approach (3t2FTS) for completely automated computer-aided diagnosis (CAD) of grade-based brain tumors (high-grade glioma (HGG) and low-grade glioma (LGG)). The method converts 3D data analytics into 2D data analytics using first-order statistics (FOS), which makes deep learning techniques efficient. The framework achieves 80% classification accuracy for 3D cerebral tumor categorization, and it contains eight new transfer learning networks. By converting 3D space to two dimensions, 3t2FTS may also be utilized to distinguish between various tumor categories in 3D MRI scans. In contrast to multi-parameter seeks to alter the visual of stable brain tissue, it also appears as a space transform technique employing radiomics. The research emphasizes the possibility. The work demonstrates how 3t2FTS may enhance 3D MRI-based categorization tasks. It could be upgraded to attempts to handle different tumors scanned in 3D MRI, create a new deep learning framework using ResNet50 logic, and make use of an MRI database with artifacts and deformities for improved application or design.

Chatterjee *et al.* [22] framed spatial-temporal models, which handle spatial dimensions independently or represent slices as a series of pictures throughout time, can be used. These models lower processing costs while learning certain temporal as well as spatial correlations. Compared to ResNet18, a pure 3D neural network, the two models outperformed it. The models performed better when pre-trained on a separate database before being trained to classify tumors. The model with the highest F1-score, the previously trained ResNet mixed convolution model, had a mean accuracy of 96.98% and an F1-score of 0.9345. This paper uses a single dataset, BraTS, to demonstrate the potential for spatio-spatial models to beat fully 3D convolutional networks for a brain tumor diagnosis. The models could be compared for other tasks to establish a shared understanding of spatio-spatial models. This study's use of T1 contrast-enhanced images alone, although produced high accuracy in tumor classification, is one of its limitations. Including any of the four types of images that are accessible (T1, T1ce, T2, and T2-FLAIR) might enhance the performance of the system.

Ali *et al.* [23] suggested a framework using a 3D U-Net architecture and CNN ensemble for identifying brain tumors from composite MRI data. Using dynamic ensembling, the model achieves comparable precision in classification on the BraTS 2019 dataset by combining the outputs of both networks. By obtaining dice values of 0.750, 0.906, and 0.846 on augmenting tumor, whole tumor, and tumor core, respectively, our suggested strategy outperforms modern methods. The experiments were done on a wide range of networks and their various configurations before selecting CNN and the 3D U-Net. It also experimented with several CNN variations, adjusting the layers used in the initial design, but the performance did not improve. Although the technique works well on the whole tumor. If the enhancing tumor is smaller than the threshold, necrosis is replaced for the affected region, which might lead to a considerable increase in the specificity of the enhanced tumor category. Still has certain limitations that the authorized validating set of the task is the single set used to assess the suggested group. Independent of the challenge, trying on other clinical MRI data can further evaluate the validity of the technique.

Le *et al.* [24] suggested that multitask networks are brain tumor mask estimation and brain tumor area identification. A context brain tumor identification network serves as an awareness barrier, concentrating on the area surrounding the brain tumor and disregarding its distant neighbor the background to accomplish its initial goal. Unlike previous object identification networks, this method does not process each and every pixel. By segmenting both massive and tiny brain tumor objects, the second objective is accomplished using an encode-decode network. The network preserves and enhances the characteristics seen at various depths. By searching into context regions of ground truth scenarios, the network additionally includes greater information about context from dimension MRI information using 3D atrous convolution with different kernel sizes, enabling more appropriate recommendations. The advantages of both local and global information are inherited by this method, which keeps the network size from rising. The multitask network may face drawbacks including increased complexity, high computational resource requirements, demanding training data needs, limited generalization ability, and reduced interpretability.

Liu *et al*. [25] framed a neural network called the deep supervised 3D squeeze-and-excitation V-Net (DSSE-V-Net) was created specifically for the detection of tumors from MRIs. To enhance the network's

performance, batch normalization, and bottom residual blocks are included. The framework's focus on informative characteristics is strengthened by the integration of SE modules into both the decoder and encoder stages. The smooth incorporation of 3D deep supervision promotes intermediate-phase filters to give high discriminative features priority, which accelerates convergence. As a result, during training, the model could select more sophisticated representations and improve results. The DSSE-V-Net exhibits better accuracy than the 3D U-Net and modified V-Net. It also performs quite competitively when compared to the winning strategies from the BraTS 2017, proving its usefulness in practical situations. A potential option for clinical uses where precise and effective tumor identification is essential is provided by the DSSE-V-Net. Despite its enhanced performance and competitiveness, the system may face challenges related to computational complexity, data requirements, interpretability, and generalization to diverse datasets.

3. PROBLEM STATEMENT

While the described deep learning-based method for gliomas detection using multiple modalities of MRI shows promising results and improvements. In a comprehensive tumor detection approach, it is essential to consider not only the delineation of tumor boundaries but also the detection of whether a tumor is present in the given image. Without this assessment, the clinical utility of the detection results may be limited [26]. To tackle these consequences, the proposed method combines the CNN architecture for feature extraction and CNN based GRU for the detection of tumors in multi-modal MRI images. The CNN is used to learn to delineate tumor boundaries across different MRI modalities, while the CNN-based GRU detects the presence of tumors based on the temporal evolution of tumor characteristics. Several methods have been employed for automated brain tumor diagnosis from MRI data. These include the 3D to 3t2FTS, which achieves efficient deep learning by converting 3D data analytics into 2D using FOS, which enhances performance through batch normalization, bottom residual blocks, and integration of squeeze-and-excitation modules. Spatial-temporal models have also been developed to classify various tumor types using spatio-spatial correlations, outperforming purely 3D convolutional networks. Additionally, a method employing a 3D GRU architecture and CNN ensemble demonstrates promising results in tumor identification, but challenges remain regarding computational complexity, data requirements, interpretability, and generalization to diverse datasets. Furthermore, while these techniques show efficacy in tumor detection tasks, extending them to other biomedical image analyses may necessitate additional validation and adaptation for optimal performance.

4. BRAIN TUMOR DETECTION USING CNN-GRU

The proposed method for brain tumor detection using CNN-GRU involves several steps. The first step is input pre-processing of multi-modal MRI images to standardize dimensions, normalize pixel values, and enhance contrast. Then, the pre-processed images are input into a convolutional network and GRU layers for tumor presence detection, which analyzes sequential data from MRI slices and classifies tumor presence. The brain tumor detection system utilizing CNN-GRU architecture is designed to identify the presence of tumors in MRI images. It follows a structured methodology involving data pre-processing, feature extraction with a CNN, and temporal dependency analysis using a GRU network. By combining spatial and temporal features, the system effectively discerns patterns associated with tumor presence. The combined approach is then integrated into a unified pipeline, ensuring accurate tumor detection. The method's clinical utility is assessed by analyzing its impact on treatment planning, prognosis prediction, and patient outcomes. Figure 1 shows the proposed framework of CNN based GRU for brain tumor detection which illustrates the sequential flow of processing steps highlighting the fusion of deep learning techniques for accurate and efficient diagnosis.

4.1. Data collection

The BraTS2020 dataset was utilized in this research, comprising multi-modal MRI scans from patients with brain tumors, offering T1-weighted, T1-weighted with contrast enhancement (T1c), T2-weighted, and FLAIR images. The dataset is divided into two classes: class 0 (non-tumor images) and class 1 (tumor images). It includes images from gliomas, reflecting real-world clinical scenarios and providing a comprehensive representation of tumor characteristics. Ground truth annotations by expert radiologists facilitate the assessment of algorithms using standard metrics, enabling the development and validation of algorithms for brain tumor detection and clinical decision support [27].

4.2. Pre-processing using min-max normalization

Pre-processing using min-max normalization is a crucial step in preparing medical imaging data, such as 3D MRI scans, for feature extraction and classification using CNN-GRU architecture. Min-max normalization scales the pixel intensity values of the MRI images to a predefined range, typically between

0 and 1, by subtracting the minimum pixel intensity value and dividing by the difference between the maximum and minimum values. This normalization technique ensures that all pixel values are within a consistent and standardized range, which is essential for training neural networks effectively. By normalizing the input data, the model becomes less sensitive to variations in pixel intensity across different MRI scans, allowing it to focus on extracting meaningful features related to tumor characteristics rather than being influenced by differences in image brightness or contrast. Min-max normalization is given in (1).

$$X_{Normalized} = \frac{X - X_{min}}{X_{max} - X_{min}} \quad (1)$$

Min-max normalization helps mitigate issues related to data distribution and convergence during the training process. By scaling the input data to a common range, the optimization algorithm used to train the CNN-GRU model can converge more efficiently, leading to faster training times and potentially better performance. Additionally, normalization helps prevent the model from becoming biased towards features with larger magnitudes, which could skew the learning process and hinder the model's ability to generalize to unseen data. Overall, pre-processing using min-max normalization plays a critical role in enhancing the robustness and effectiveness of CNN-GRU-based brain tumor detection systems by ensuring that the input data is standardized and suitable for neural network training.

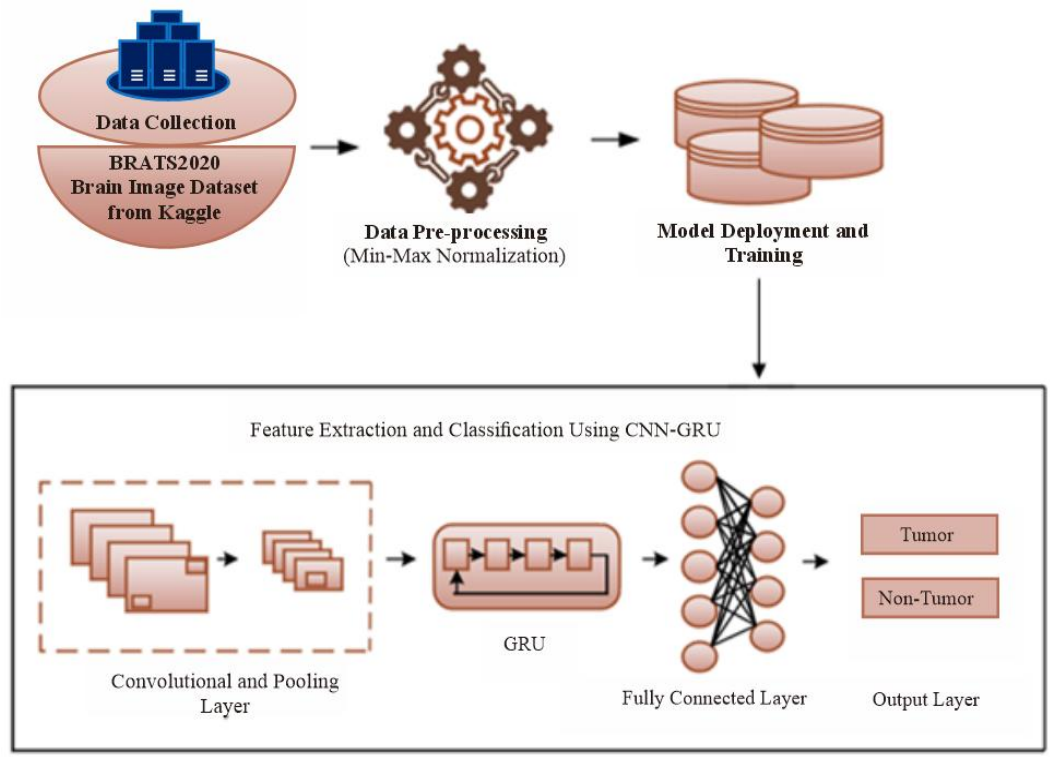

Figure 1. Proposed brain tumor detection using CNN-GRU

4.3. Feature extraction and classification using CNN-GRU

Feature extraction and classification were performed using a CNN-GRU architecture, integrating CNNs and GRUs. CNNs automatically learned hierarchical representations of features from the 3D MRI images, capturing complex patterns and structures within the images to identify subtle abnormalities indicative of tumors. The spatial features extracted by CNNs from individual MRI slices served as the input to the GRUs, which captured temporal dependencies and sequential patterns inherent in the medical imaging data by processing the spatial features across multiple MRI slices, capturing the dynamic evolution of tumors over time.

The model was trained on the BraTS2020 dataset, which includes ground truth tumor labels annotated by expert radiologists. Techniques such as oversampling of the minority class and data

augmentation were employed to address class imbalance. Transfer learning was utilized by leveraging pre-trained CNN models, fine-tuning them on the specific task of brain tumor detection, while data augmentation techniques, including rotation, flipping, and scaling, were applied to increase the diversity of the training data and improve the model's generalization capabilities.

The model's performance was evaluated using standard metrics such as accuracy, precision, recall, and F1-score. The integration of CNNs and GRUs leveraged both spatial and temporal information present in 3D MRI sequences, leading to a more comprehensive and accurate analysis of brain tumors. By addressing specific challenges associated with brain tumor detection, such as class imbalance and variability in tumor characteristics, the model achieved robust and reliable detection performance. The use of large-scale datasets with ground truth annotations and advanced techniques like transfer learning and data augmentation further enhanced the model's capabilities, paving the way for improved diagnosis and patient care in clinical settings.

Figure 2 likely depicts the CNN-GRU model architecture utilized in the study for brain tumor detection from 3D MRI images. This model integrates CNNs and GRUs to enhance the analysis of volumetric MRI data. CNNs are employed initially to extract spatial features from the multi-modal MRI scans, capturing intricate patterns indicative of tumor presence across different image slices. These spatial features are then processed sequentially by GRUs, which specialize in capturing temporal dependencies and patterns over the MRI sequences. This dual approach enables the model to effectively interpret both spatial and temporal aspects of tumor evolution within the brain, thereby improving accuracy in tumor detection and localization. The figure likely details the architectural layout, illustrating how CNNs and GRUs are interconnected to optimize the extraction of meaningful features from the 3D MRI data, ultimately aiding clinicians in more accurate diagnosis and treatment planning for patients with brain tumors.

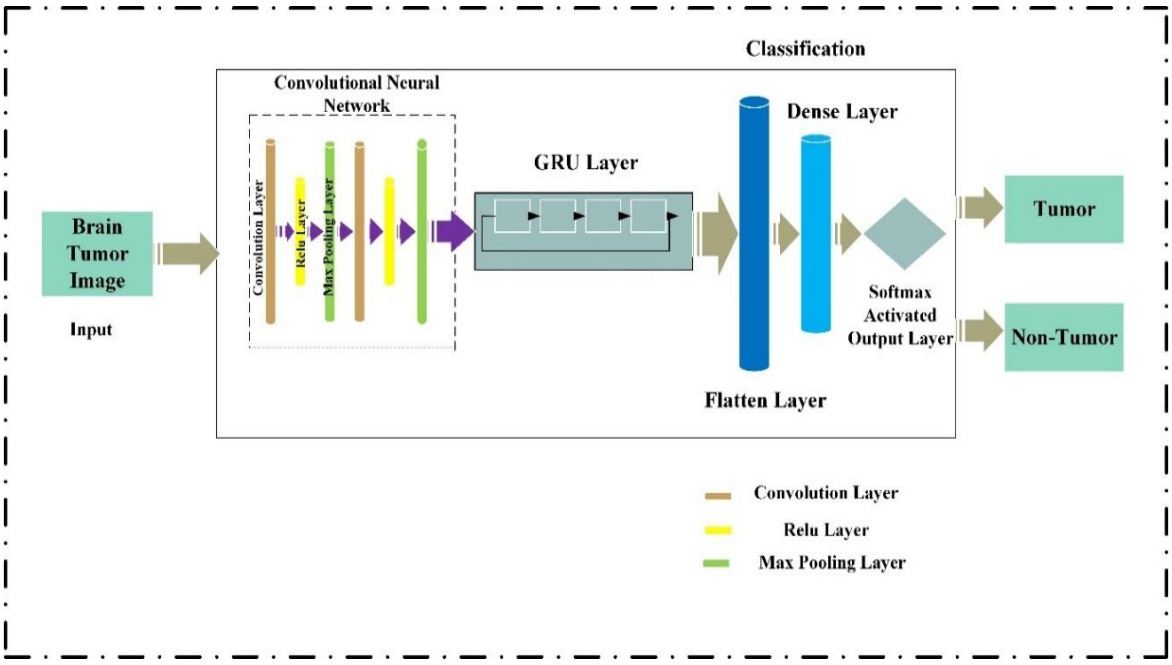

Figure 2. CNN-GRU model

The proposed CNN-GRU model in this research incorporates a convolutional layer from CNN to preserve the original feature arrangement of the image and extract crucial features. Additionally, a max-pooling layer is utilized to select prominent feature values while disregarding weaker ones, thereby mitigating the risk of overfitting. To accelerate model training, a rectified linear unit (ReLU) is applied between the convolutional and max-pooling layers to discard eigenvalues less than 0. Subsequently, these eigenvalues pass through the update gate and reset gate of the GRU, enhancing the computational efficiency of the model for improved accuracy. The flattened layer is then employed to convert the feature values into one-dimensional data, facilitating their utilization in the subsequent fully connected layer. Finally, the softmax activation function is connected as the output to ascertain whether the input image is tumor or non-tumor.

The convolutional layer plays an important role in extracting distinct features from input brain images to facilitate effective tumor detection. This layer consists of multiple trainable convolutional kernels that undergo iterative adjustments during training. By convolving these kernels with input images, the layer extracts different outlines, which is essential for the detection of tumors in the brain. The equation is termed as (2).

$$K_{p^b,q^b,r} = \sum_{p=0}^{a} \sum_{q=0}^{b} \sum_{l=0}^{d^b} M_{p,q,d^b} \times Z^{b}_{p^b,q^b,s} \quad (2)$$

Where $K_{p^b,q^b,r}$ represents the (p^b, q^b, r) -th element of the output tensor K^F. M is the filter tensor with dimensions. G^M is the input tensor to the convolutional layer with dimensions. p, q, s iterates over the spatial dimensions of the filter tensor and input tensor. a, b, r represents the dimensions of the filter and output tensor. Using a sigmoid function, it assigns a likelihood score to each input image, indicating the probability of tumor presence. L_b is expressed as (3).

$$L_b = \frac{e^{Z_b}}{1+e^{Z_b}}, Z_b \in R \quad (3)$$

Where L_b represents the output of the b -th neuron in the fully connected layer. Z_b is the input to the neuron.

After the feature extraction phase utilizing the CNN, the tumor detection process is carried out using the CNN-GRU architecture. The CNN component processes the spatial features extracted from the images, while the GRU component models the temporal dependencies across sequential data points. The GRU network effectively captures the sequential patterns and temporal context in the feature sequences. The output from the CNN-GRU model is passed through a classification layer to detect the presence of tumors. This layer interprets the learned features and predicts whether each input sequence contains tumor regions or not. By analyzing the spatial and temporal characteristics of the input data, the model identifies regions indicative of tumor presence.

The update gate, denoted as U'_T, determines the extent to which the hidden state (I_T) can incorporate information from the initial hidden. The function outputs a value in the range of 0 to 1. Regulating this information transfer process and given in (4).

$$U'_T = \sigma(A_h \times P_T + A_z \times I_{T-1}) \quad (4)$$

The reset gate, denoted as s_T, regulates the data retained from the previous hidden value. The function outputs values between 0 and 1, determining the degree of retention. Values closer to 1 indicate a higher propensity to retain information and are represented by (5).

$$s_T = \sigma(A_h \times P_T + A_s \times I_{T-1}) \quad (5)$$

By conducting the Hadamard equation for the gate's reset value s_T and I_{T-1}, as certain the degree to which the buried layer memory from the earlier time step ought to have been remembered in the present memory content. Next, implement the tanh activation operation, as indicated in (6), to this result in combination with the entering input data.

$$\widetilde{I_T} = tanI(A_T \times P_T + s_T \times AI_{T-1}) \quad (6)$$

Finally, the utilization of $U_T$and 1-U_T to determine which past and present data should be updated and given by (7).

$$I_T = \left(1 - U'_T \times \widetilde{I_T} + U'_T \times I_{T-1}\right) \quad (7)$$

Figure 3 outlines the overall flowchart which represents the process for tumor detection using a CNN-GRU model. It begins by loading an image dataset (specifically the BraTS2020 dataset) and then applies min-max normalization to standardize dimensions and normalize pixel values. The CNN-GRU model is deployed for feature extraction and classification, involving training on the dataset, extracting features using a CNN, applying ReLU activation where eigenvalues are greater than 0, selecting prominent feature values from the maximum pooling layer, capturing temporal dependencies within sequential data using the GRU layer, and finally obtaining predicted tumor detection results via the softmax output layer. The outcome can be either a tumor or no tumor.

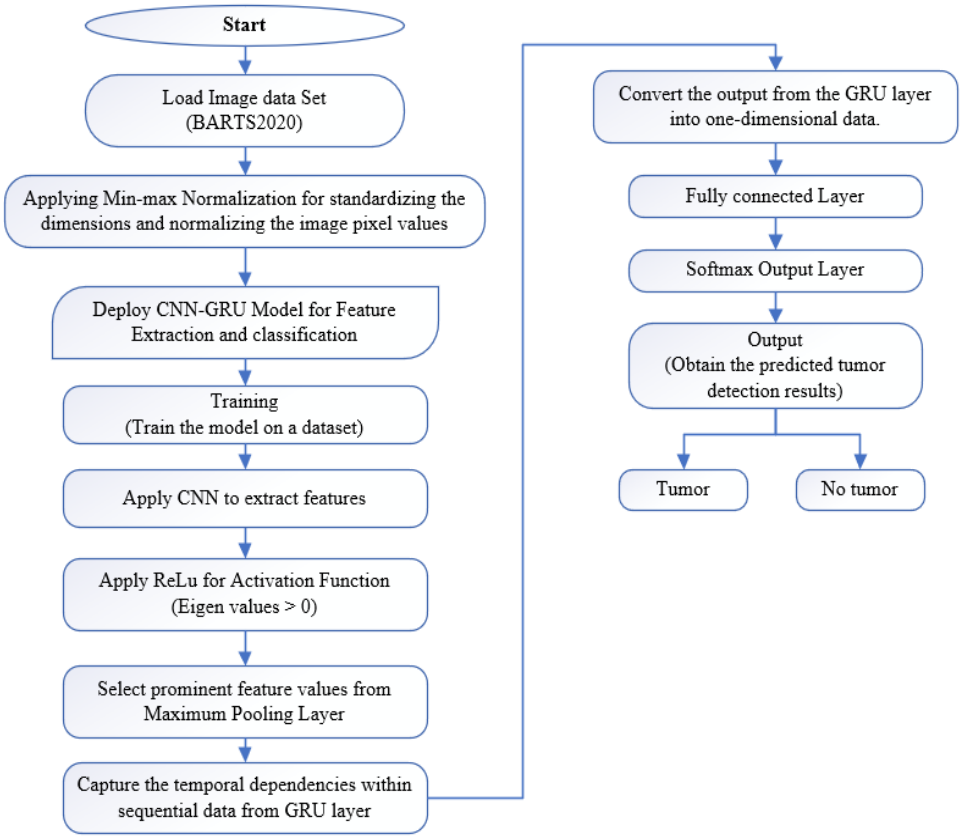

Figure 3. Overall flow diagram of the proposed model

5. RESULTS AND DISCUSSION

Our study suggests that the developed method for identifying brain tumors using 3D MRI images, implemented using Python software, is highly accurate in detecting the presence of tumors. Through extensive evaluation of a diverse dataset, the model showcased robust performance metrics, including high accuracy, sensitivity, and specificity. Specifically, the model exhibited a high true positive rate in detecting tumor presence, indicating its capability to effectively identify regions of abnormality indicative of tumors.

Among the total dataset, 75.2% of images were used for training, 13.1% for validation, and 11.7% for testing, with a batch size set to 32. This balanced distribution ensured that the model was trained on a sufficient amount of data while maintaining separate datasets for unbiased evaluation, contributing to the reliability and effectiveness of the brain tumor detection system. In the training dataset, approximately 97 images were labeled as not tumor, and around 60 images were labeled as tumor. For testing, around 9 images were labeled as not tumor, and around 14 images were labeled as tumor, while around 14 not tumor images and 12 tumor images were used for the validation dataset. This balance is crucial for effective training of machine learning models.

The training and testing process involved utilizing CNNs to capture intricate spatial features from the medical images, followed by the integration of GRUs to capture temporal dependencies and sequential patterns within the data. During the model training phase, these neural network architectures worked collaboratively to learn and recognize relevant features indicative of brain tumors. The combination of CNN and GRU provides a robust framework for accurate detection by considering both spatial and temporal aspects of the medical image data. The results revealed precise delineation of tumor boundaries, enabling accurate localization and visualization of tumor regions within the brain. Figure 4 shows the sample of the brain images with and without tumors.

Figure 5 shows the actual and predicted output for the given input image by the proposed CNN-GRU model. The image provided displays 3D MRI images, each labeled with the actual and predicted conditions regarding the presence of a tumor. The scan shows a bright spot, indicating a tumor. It is correctly predicted as having a tumor. The scan doesn't show any visible signs of a tumor and is correctly predicted as non-tumor. The CNN-GRU system demonstrated robust performance in accurately detecting brain tumors while maintaining generalization to unseen data.

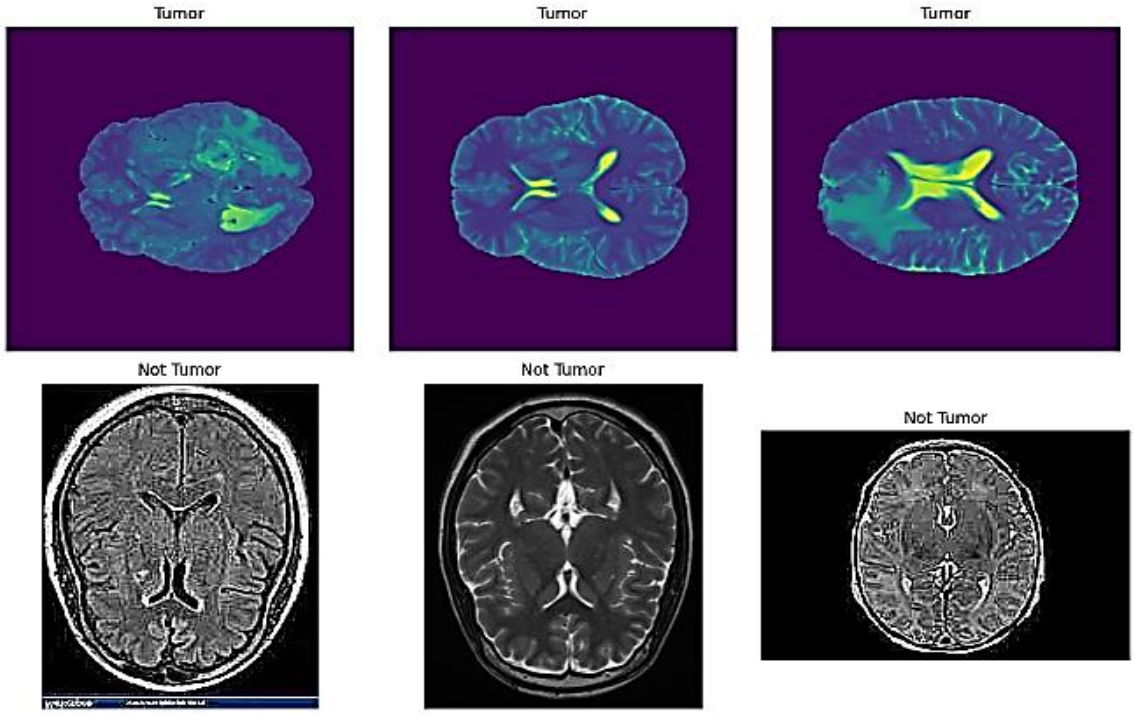

Figure 4. Sample brain images with and without tumor

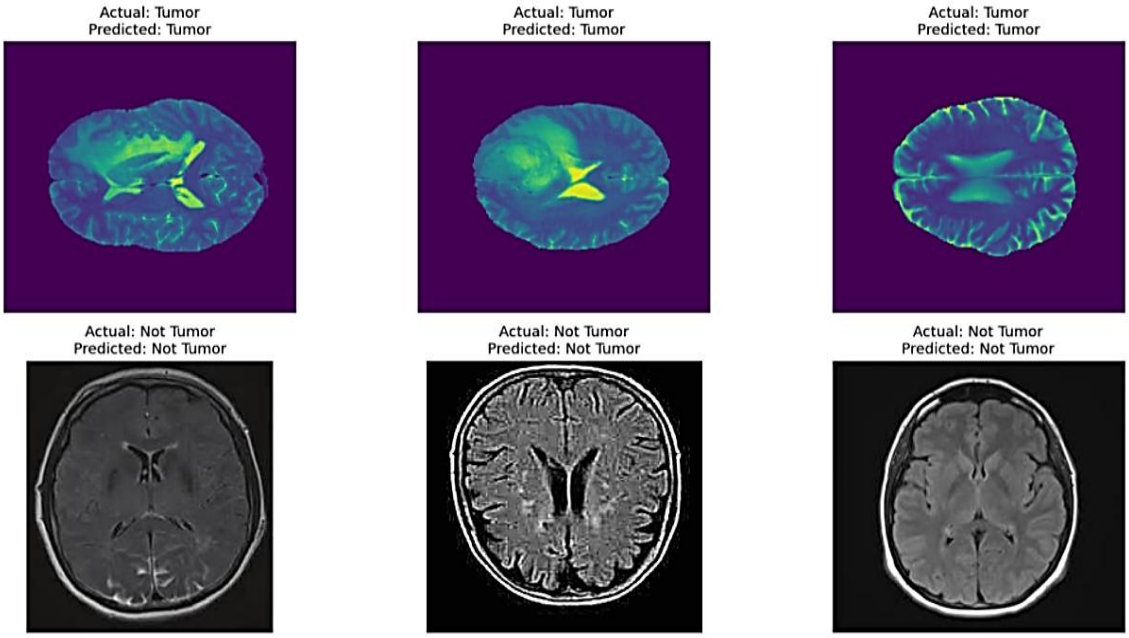

Figure 5. Detection of tumor by proposed CNN-GRU

Figure 6 shows the accuracy curve of the proposed method. During the training phase, the accuracy of the CNN-GRU model steadily increased with each epoch, reflecting its ability to learn and adapt to the training data. The accuracy curve showed a positive trend, indicating that the system was effectively capturing the underlying patterns in the data. The validation accuracy curve followed a similar pattern to the training accuracy curve, albeit with fluctuations. This suggests that the model was generalizing well to unseen data, as evidenced by its ability to maintain relatively high accuracy on the validation set. Figure 7

depicts the loss curve of the proposed CNN-GRU model. The training loss consistently decreased over epochs, indicating that the model was minimizing errors and optimizing its parameters to better fit the training data. The downward trajectory of the loss curve demonstrated the model's ability to improve its performance over time. The validation loss curve exhibited a downward trend, albeit with occasional fluctuations. This indicates that the model was effectively generalizing its learned patterns to new data while minimizing errors on the validation set.

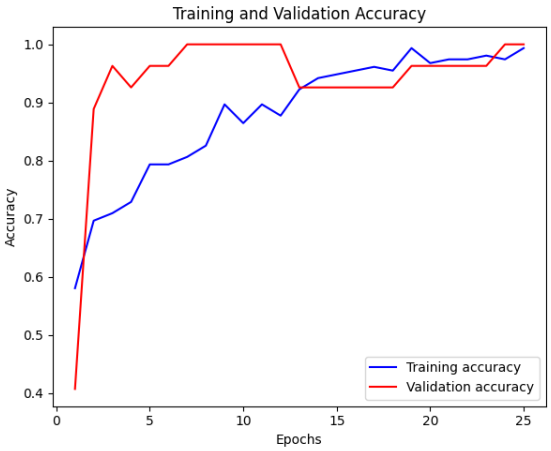

Figure 6. Accuracy curve of proposed CNN-GRU model

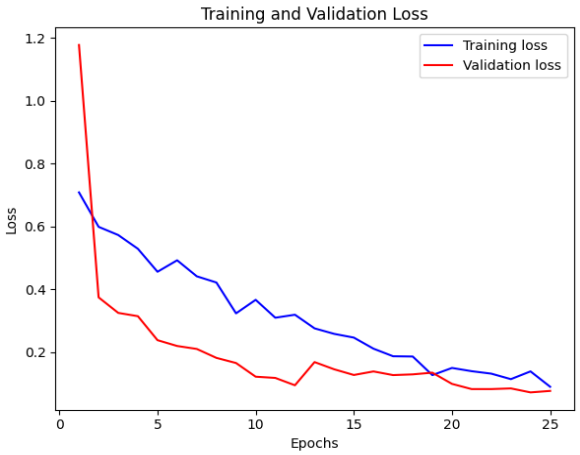

Figure 7. Loss curve of proposed CNN-GRU model

Figure 8 depicts a receiver operating characteristic (ROC) curve for the proposed CNN-GRU model. The x-axis represents the false positive rate, while the y-axis represents the true positive rate. The actual ROC curve has an impressive area under the curve (AUC) of 0.99, indicating excellent model accuracy. It showcases the model's ability to distinguish between positive and negative instances, with the high AUC suggesting strong predictive power.

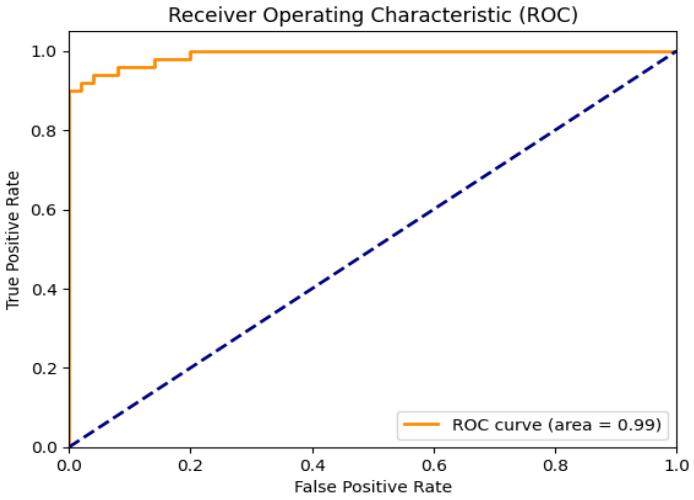

Figure 8. Region of convergence of proposed CNN-GRU model

This study explored a comprehensive CNN-GRU architecture for analyzing 3D MRI images in brain tumor detection with promising results in terms of accuracy, sensitivity, and specificity. However, further and in-depth studies may be needed to confirm its generalizability, especially regarding different types of brain tumors and varying imaging conditions. The dataset used, while diverse, may not cover all possible variations

in tumor characteristics and patient demographics. Additionally, the reliance on manually annotated ground truth data could introduce subjectivity, affecting the model's performance. Future work should include larger and more diverse datasets, as well as external validation on independent cohorts, to ensure the robustness and reliability of the proposed method across different clinical settings.

5.1. Performance metrics

Accuracy: by computing the ratio of accurately categorized data to the total number of instances, this statistic assesses the overall efficacy of the classifier.

$$Accuracy = \frac{Cp+Cn}{Cp+Cn+Ip+In} \tag{8}$$

Precision: the degree to which a set of results agrees with one another is referred to as precision. The difference between a collection of results and the collection's arithmetic mean is the standard definition of precision.

$$Precision = \frac{Cp}{Cp+In} \tag{9}$$

Recall: the goal of recall evaluation is to determine exactly a specific set of assumptions. The use of this process is limited by predetermined parameters that rely on several input data variables.

$$Recall = \frac{Cp}{Cp+In} \tag{10}$$

F1-score: when evaluating model performance, results apart from classification accuracy should be evaluated as well. The correlation between the model's predictions and the positive information in the data is evaluated by the F1-score that is calculated for this reason.

$$F1\ score = \frac{2Cp}{2Cp+Ip+In} \tag{11}$$

Table 1 compares the performance metrics of different methods evaluated for a specific task. Each row corresponds to a different method, and the columns represent various evaluation metrics. The proposed method (CNN-GRU) stands out with an accuracy of 99%, precision of 98.6%, recall of 99.1%, and F1-score of 98.3%. It is observed that other models like SVM, random forest (RF), decision tree (DT), AdaBoost, CNN, and CNN-k-nearest neighbor (CNN-KNN) also exhibit varying performance, but the proposed CNN-GRU demonstrates exceptional results.

Table 1. Performance metrics of proposed method is evaluated with existing methods

Method	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)
SVM [28]	96.38	97.24	96.61	96.93
RF [28]	85.20	87.57	82.98	85.22
DT [28]	77.79	79.80	78.71	79.25
Adaboost [28]	86.88	88.23	88.87	76.27
CNN [29]	94.39	93.33	93	93.16
CNN-KNN [30]	96.25	96.67	95.83	96.25
Proposed CNN-GRU	99	98.6	99.1	98.3

Figure 9 shows the performance metrics of the system were compared with existing methods to evaluate its effectiveness. The metrics used for comparison included accuracy, precision, F1-score, and recall. The results highlight the superiority over existing methods in accurately detecting brain tumors in MRI images, making it a promising approach for clinical applications. These results underscore the potential clinical utility of the CNN-GRU model in assisting clinicians with tumor detection tasks, thereby enhancing diagnostic accuracy of 99% and facilitating treatment planning for patients with brain tumors.

The proposed CNN-GRU model for brain tumor detection aims to provide an in-depth analysis and interpretation of the results, highlighting the model's strengths, limitations, and potential implications. Comparative analysis with existing methods like traditional CNN reveals the superiority of the CNN-GRU model in terms of accuracy and precision. The model outperforms traditional techniques and other deep learning architectures, underscoring its potential for tumor detection tasks. The proposed system

demonstrates its effectiveness in accurately identifying tumor presence and delineating tumor boundaries. Collaboration with healthcare professionals and integration into existing medical imaging systems can facilitate seamless adoption and integration of the model into routine clinical workflows.

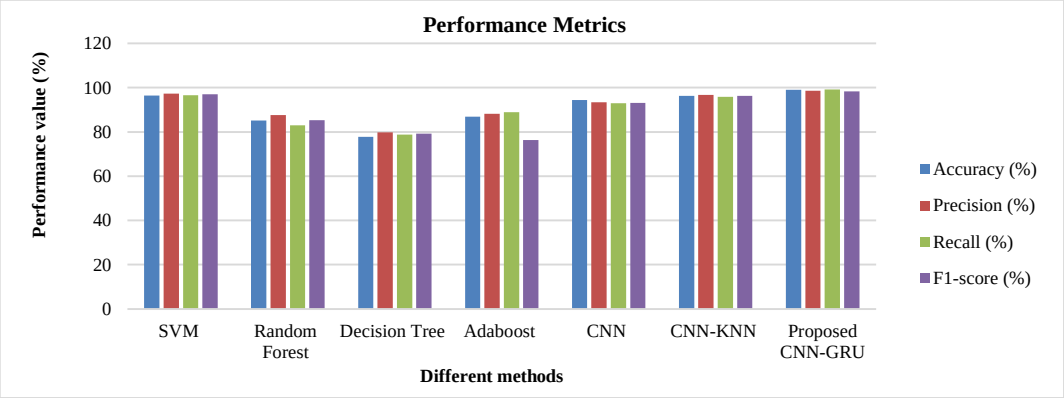

Figure 9. Performance metrics of proposed method with existing methods

The research utilized a CNN-GRU architecture for enhancing brain tumor detection using multi-modal 3D MRI images. CNNs were employed to extract spatial features from volumetric MRI data, enabling the identification of tumor-related patterns across different imaging modalities such as T1c, T1, FLAIR, and T2 sequences. These spatial features were then fed into GRUs, a type of recurrent neural network (RNN), which captured temporal dependencies and sequential patterns inherent in the MRI sequences. This integration of CNNs and GRUs facilitated a comprehensive analysis of tumor evolution over time, enhancing the model's ability to detect subtle changes indicative of tumor progression or regression. The model was trained on a large-scale dataset, including ground truth annotations by expert radiologists, and evaluated using standard metrics such as accuracy, sensitivity, specificity, and F1-score to assess its performance in tumor detection. The results demonstrated significant improvements in both sensitivity and specificity compared to traditional methods, highlighting the efficacy of the CNN-GRU approach in enhancing diagnostic accuracy for brain tumors.

The study's findings were compared with existing literature, emphasizing the advantages of integrating CNNs and GRUs for neuroimaging tasks. Insights were drawn on how spatial and temporal information contributed synergistically to the model's robust performance, enabling more precise tumor localization and characterization. Limitations included the need for further validation on larger and more diverse datasets to generalize the model's applicability across different patient demographics and imaging conditions. Future research directions were proposed to refine 3D deep learning segmentation models tailored for specific tumor types, aiming to improve segmentation accuracy and classification of high-grade versus LGG. The implications of this research extend to clinical practice, where enhanced diagnostic tools can potentially lead to earlier detection, more personalized treatment strategies, and improved patient outcomes in neuro-oncology.

6. CONCLUSION AND FUTURE WORK

In medical image analysis, the proposed CNN-GRU model for brain tumor detection represents a significant advancement. Extensive analysis of large datasets has shown that our model achieves high accuracy, precision, F1-score, and recall in tumor recognition tasks. These results underscore the potential of deep learning techniques to revolutionize medical image processing, particularly in neuroimaging. By accurately discerning the presence of tumors and outlining their boundaries, the CNN-GRU model offers valuable assistance to clinicians, enhancing diagnostic accuracy and facilitating more informed treatment planning for patients with brain tumors. The model's ability to integrate spatial and temporal information from multi-modal 3D MRI images contributes to its robust performance, addressing the complexity and variability inherent in medical imaging data. This integration ensures that subtle changes in tumor characteristics are detected, providing a reliable and efficient methodology for clinical practice. Recent advancements in medical image analysis, particularly through the application of CNN-GRU architecture in brain tumor detection, demonstrate significant progress in enhancing diagnostic accuracy and treatment planning for patients. The outcomes of our research underscore the potential of deep learning techniques to

revolutionize neuroimaging, enabling more efficient and accurate processing of complex medical images. To further advance this research and enhance its clinical applications, future work could focus on developing a 3D deep learning segmentation model specifically tailored for brain tumor analysis. Such an advanced model would aim to improve the capabilities of accurately segmenting brain tumor regions and classifying between high- and LGG. By incorporating more sophisticated 3D deep learning techniques, the model could provide even more detailed and accurate insights into tumor characteristics, thereby aiding clinicians in both treatment planning and prognosis prediction.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

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C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

The authors declare that they have no conflict of interest.

DATA AVAILABILITY

The data that support the findings of this study are openly available in: https://www.kaggle.com/datasets/awsaf49/brats2020-training-data.

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