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Brain tumor detection and classification in MRI using hybrid ViT and GRU model with explainable AI in Southern Bangladesh

Md. Mahfuz Ahmed^{1,2,3}, Md. Maruf Hossain^{2,3}, Md. Rakibul Islam^{3,4,7}, Md. Shahin Ali^{2,3}, Abdullah Al Noman Nafi⁴, Md. Faisal Ahmed⁵, Kazi Mowdud Ahmed⁴, Md. Sipon Miah^{1,4,6}, Md. Mahbubur Rahman⁴, Mingbo Niu^{1✉} & Md. Khairul Islam^{2,3}

Brain tumor, a leading cause of uncontrolled cell growth in the central nervous system, presents substantial challenges in medical diagnosis and treatment. Early and accurate detection is essential for effective intervention. This study aims to enhance the detection and classification of brain tumors in Magnetic Resonance Imaging (MRI) scans using an innovative framework combining Vision Transformer (ViT) and Gated Recurrent Unit (GRU) models. We utilized primary MRI data from Bangabandhu Sheikh Mujib Medical College Hospital (BSMMCH) in Faridpur, Bangladesh. Our hybrid ViT-GRU model extracts essential features via ViT and identifies relationships between these features using GRU, addressing class imbalance and outperforming existing diagnostic methods. We extensively processed the dataset, and then trained the model using various optimizers (SGD, Adam, AdamW) and evaluated through rigorous 10-fold cross-validation. Additionally, we incorporated Explainable Artificial Intelligence (XAI) techniques-Attention Map, SHAP, and LIME-to enhance the interpretability of the model's predictions. For the primary dataset BrTMHD-2023, the ViT-GRU model achieved precision, recall, and F1-score metrics of 97%. The highest accuracies obtained with SGD, Adam, and AdamW optimizers were 81.66%, 96.56%, and 98.97%, respectively. Our model outperformed existing Transfer Learning models by 1.26%, as validated through comparative analysis and cross-validation. The proposed model also shows excellent performances with another Brain Tumor Kaggle Dataset outperforming the existing research done on the same dataset with 96.08% accuracy. The proposed ViT-GRU framework significantly improves the detection and classification of brain tumors in MRI scans. The integration of XAI techniques enhances the model's transparency and reliability, fostering trust among clinicians and facilitating clinical application. Future work will expand the dataset and apply findings to real-time diagnostic devices, advancing the field.

Keywords Brain tumor, Deep learning, Pre-processing, ViT-GRU, Explainable Artificial Intelligence, Attention map

The human brain consists of billions of neurons, synapses, and nerve cells that control many essential bodily functions. Like other bodily organs, some problems may arise in the brain, such as growths known as brain tumor. These tumors occur when cells grow abnormally in various regions of the brain and can lead to significant neurological complications and have significant consequences on a patient's quality of life¹. Brain tumors are widely

¹Shaanxi Int'l Innovation Center for Transportation-Energy-Information Fusion and Sustainability, Chang'an University, Xi'an 710064, China. ²Department of Biomedical Engineering, Islamic University, 7003 Kushtia, Bangladesh. ³Bio-Imaging Research Lab, Islamic University, 7003 Kushtia, Bangladesh. ⁴Department of Information and Communication Technology, Islamic University, 7003 Kushtia, Bangladesh. ⁵Ship International Hospital, 1230 Uttara, Dhaka, Bangladesh. ⁶Wireless Communications with Machine Learning (WCML) Laboratory, Islamic University, 7003 Kushtia, Bangladesh. ⁷Department of Computer Science and Engineering, Northern University Bangladesh, 1230 Dhaka, Bangladesh. ✉email: ivr.niu@chd.edu.cn

acknowledged as among the most lethal diseases on a global scale, imposing considerable impact on mortality rates across all age groups. This condition brings challenges in terms of medical diagnosis and treatment². These tumors manifest in various forms, including glioma, meningioma, pituitary, and cases with no tumor. With almost 120 varieties of tumors found to date, their diverse characteristics and dimensions make them difficult to detect, complicated by the intricate structure of the brain³. The identification and exact segmentation of tumorous areas, which include edema, necrotic centers, and tumorous tissues, is critical for accurate diagnosis and therapy planning⁴. The significance of the automatic detection and classification of medical images, particularly in brain tumor diagnosis, cannot be overstated. Early detection and categorization of brain tumors are critical for rapid treatment and improved patient outcomes. Traditional manual procedures for locating and classifying brain tumors in large medical image databases are time-consuming and resource-intensive⁵. Medical imaging modalities, including Magnetic Resonance Imaging (MRI), Computed Tomography (CT), and Positron Emission Tomography (PET) scans, are indispensable in the detection of brain tumors. MRI is the approach that is most frequently utilized in the investigation of brain structures. Therefore, MRI was selected as the preferred modality for our study due to its widespread utilization and efficacy in examining brain structures. Despite its ability to effectively model regions of interest, MRI has difficulties in accurately distinguishing tumors due to the volatility in intensity levels caused by varying machine settings. Multimodal MRI scans, including T1-weighted, T2-weighted, T5-weighted, and Fluid Attenuation Inversion Recovery (FLAIR) images, provide supplementary profiles for various glioma sub-regions, allowing for more accurate information extraction^{6,7}. The manual segmentation of 3D MRI images conducted by health care professionals relies on the expertise as well as the experience of the physician. Even with the advancement in medical imaging approaches, automatically dividing brain tumors in multimodal MRI scans remained among the hardest issues in medical image processing. To prevent user-based difficulties, automatic classification techniques can be employed in medical images due to their measurable nature and ability to deliver dependable outcomes⁸. Brain tumor identification has been explored utilizing many machine-learning approaches and imaging types throughout the years^{9,10}. In this context, Deep Learning (DL) approaches are up-and-coming brain tumor classification and segmentation tools. Their application in computer-aided systems for diagnosing brain tumors aims to provide accurate and reliable information regarding tumor presence, location, and type.

Existing brain tumor identification models face significant challenges, including performance issues, data handling inefficiencies, and limitations in model robustness and interpretability. Encouraged by these drawbacks, this study aims to develop an innovative approach for brain tumor identification using a combination of Vision Transformer (ViT) and Gated Recurrent Unit (GRU) models¹¹. Our proposed ViT-GRU model addresses these issues by achieving higher accuracy, balancing data representation, and enhancing interpretability with Explainable Artificial Intelligence (XAI) techniques such as Shapley Additive Explanations (SHAP), Local Interpretable Model-Agnostic Explanations (LIME), and Attention mapping¹². Additionally, it processes diverse data sources, which improves adaptability and relevance across various demographics and imaging methods. Thus, the hybrid ViT-GRU model addresses the limitations of previous models by utilizing the spatial attention mechanisms of ViTs and the temporal modeling capabilities of GRUs, providing a more robust and effective solution for brain tumor identification.

This study is motivated by the severe consequences of brain tumors, including death and costly, risky treatments. In Southern Bangladesh, particularly Faridpur, patients endure significant pain and adverse outcomes, highlighting the urgent need for improved detection and classification methods. To make a meaningful impact, the focus is on primary data collection, engaging directly with the community and healthcare providers to obtain specific information about brain tumor cases. The objective of this study is to implement a hybrid DL approach to enhance precision in detection and classification, addressing the challenges in brain tumor management. This comprehensive approach seeks to increase performance accuracy, facilitate early interventions, and improve the quality of life for individuals affected by brain tumors in Faridpur and similar regions.

In this research, the study tried to fulfill some research questions, including, How to increase the detection and classification accuracy of brain tumors?, How to enhance the overall performance of the proposed model?, How to reduce the training approach or model training time without compromising accuracy?, and How to make the model's decision-making process more transparent and reliable?

In this system, the model's structure incorporates multiple layers and adjustable parameters. Each MRI image goes through a series of ViT layers first, then through GRU layers for processing^{13,14}. By integrating these components, we aim to improve feature representation and temporal modeling for robust decision-making in the final stage, making it a comprehensive and effective tool for accurate brain tumor detection and classification in medical imaging.

In this research, we achieved the following major contributions:

- Our study uses hospital-based primary MRI data to analyze brain tumor patients and improve diagnosis.
- We developed a hybrid ViT-GRU model that demonstrated superior results on our dataset, thereby enhancing the effectiveness of brain tumor diagnosis.
- Additionally, we applied several preprocessing techniques on our primary dataset to optimize the performance of our proposed ViT-GRU model.
- Finally, we employed three XAI techniques-Attention Map, SHAP, and LIME to offer interpretable and understandable explanations for the predictions made by the proposed model.

The structure of the rest of the paper is organized as follows: Section “[Challenges of brain tumor disease detection with AI](#)” describes the challenges associated with the identification of neurodegenerative diseases using AI. Section “[Literature review](#)” represents a thorough review of the most recent studies on identifying and classifying

brain tumor disease. The comprehensive description of the materials and method employed in this study is presented in reference section “[Materials and method](#)”. Sections “[Results](#)” and “[Discussion](#)” provide an in-depth evaluation of the outcomes and findings in our study described as results and discussion. Section “[Conclusion and future work](#)” provides an extensive summary of the entire study.

Challenges of brain tumor disease detection with AI

The efficient integration of Artificial Intelligence (AI) into healthcare necessitates both transparency and efficacy, despite its immense potential. The utilization of primary MRI data in conjunction with Machine Learning (ML) and DL algorithms to detect brain tumors poses several challenges. Here are important considerations for brain tumor detection and classification associated with our whole research procedure.

- *Complexity of Diverse Data:* Multi-modal MRI datasets contain DWI, FLAIR, T1, T2, and T1 Fat-Sat images for brain information. Integrating these data types is complicated and requires study.
- *Data Preprocessing and Feature Extraction:* In the case of preprocessing of primary MRI data, we face obstacles, including the need to standardize imaging protocols, mitigate artifacts, and reduce inter-subject variability. Feature extraction itself is challenging, requiring cautious selection to capture meaningful tumor characteristics.
- *Limited Availability of Annotated MRI data:* Annotating primary MRI scans is a laborious and time-intensive technique. The lack of well-annotated data for training models may limit the development of robust algorithms for MRI datasets.
- *Class Imbalance and Tumor Rarity:* The rarity of brain tumors in comparison to normal brain tissue within MRI datasets leads to class imbalance. This imbalance might result in biased models struggling to effectively detect the minority class (tumors), impacting overall performance.
- *Ethical and Legal Considerations in MRI Studies:* The implementation of AI-based medical diagnostic systems employing MRI scans poses ethical and legal problems, including difficulties relating to patient privacy, permission, and potential biases in the algorithms. These concerns demand cautious attention and resolution.

Literature review

Early and precise identification of brain tumors is essential for optimal treatment. MRI scans play a crucial part in this procedure, however this might present challenges to interpret. DL has emerged as an efficient tool for brain tumor detection, and recent advances in the desire to automate and enhance the accuracy of brain tumor diagnosis are mentioned below.

An innovative Internet of Things (IoT) computational system in Ref.¹⁵ integrates a hybrid Convolutional Neural Network (CNN) and Long Short Term Memory (LSTM) approach for brain tumor detection and classification in MRI images which outperforms traditional CNN models, demonstrating superior accuracy in experiments conducted on a Kaggle dataset with 3264 MRI scans. Minimizing a lengthy training approach can increase the efficacy of this study. The authors¹⁶, introduce an innovative real-time intraoperative brain tumor diagnosis using stimulated Raman histology (SRH) and CNNs, obtaining a notable 94.6% accuracy, significantly reducing diagnosis time to under 150 seconds. The study suggests incorporating spectroscopic detection and investigating SRH’s role in molecular diagnosis. Researchers in Ref.¹⁷ proposed a cutting-edge, entirely automatic brain tumor segmentation and classification approach employing a multiscale Deep Convolutional Neural Network. Achieving a remarkable 97.3% accuracy on a dataset of 3064 MRI slices, which outperforms existing methods. However, dataset diversity, alternative architecture, and assessing the model may improve the results. According to the concept of Ref.¹⁸ this study represents a DL-based semantic segmentation method for automatic brain tumor segmentation on 3D BraTS datasets. Achieving a mean prediction ratio of 91.718% and excellent scores in IoU and BF metrics, the method exhibits accurate tumor prediction and 3D imaging. The authors in Ref.¹⁹ have comprehensively reviewed 147 recent studies on ML and DL approaches for detecting Alzheimer’s, brain lesions, epilepsy, and Parkinson’s. Analyzing 22 datasets, the study offers insights into effective methods of diagnosis, emphasizing future research directions and unresolved issues in brain disease diagnostics. This study highlights significant results, offering a foundational framework for future developments in the discipline. The author of the study²⁰ explored glioma utilizing multimodal MRI scans, employing three 3D CNN architectures. This study obtained 5th place for segmentation and 2nd place for survival prediction in the 2018 MICCAI BraTS challenge among 60+ teams, obtaining a significant 61.0% accuracy in classifying survival categories. Diverse network architectures and training strategies may affect the further refinement of this study. The study²¹ employed a DL CNN model to automatically detect brain tumors using augmented MRI data from the Br35H dataset, achieving 98.99% accuracy. Future research could explore advanced architectures and integrate multimodal data to improve the interpretability of this study for more robust clinical applications in brain tumor diagnostics.

In Ref.²², the author of this study employs artificial intelligence (AI) techniques and pre-trained models (Xception, ResNet50, InceptionV3, VGG16, MobileNet) to enhance MRI-based brain tumor classification, accomplishing F1-scores ranging from 97.25% to 98.75%. Investigating biases, fine-tuning strategies, investigating hyperparameters, and expanding datasets may improve the efficiency of the study. The author of this paper²³ proposed a CNN-based DL model for brain tumor classification using MRI images, achieving high accuracies of 96.13% and 98.7% across two studies. Improving model generalizability, benchmarking against existing methods, and enhancing interpretability for clinical applications may increase the efficacy of this study. Researchers introduce a strategy²⁴ employing 3D U-Net Design and ResNet50 models for accurate brain tumor segmentation in MRI and CT scans, achieving high accuracies of 98.96% and 97.99%. Future work in this paper suggests that model enhancement, real-time training, and addressing class imbalance scenarios may yield better results. The paper¹ presents a hybrid model for precise brain tumor classification in MRI images, integrating a novel CNN model

with optimized ML algorithms. Achieving an exceptional mean accuracy of 97.15%, the proposed hybrid model outperforms advanced CNN models, exhibiting higher time efficiency. Exploring diverse ML algorithms and DL models and validating the hybrid model on larger and more diverse datasets may lead to better performance. In Ref.²⁵, the author represented a modified U-Net structure for accurate brain tumor segmentation in MRI images, incorporating shuffling and sub-pixel convolution. Achieving notable accuracy of 93.40% and 92.20% on BraTS Challenge datasets, the proposed model outperforms existing approaches. Larger datasets and smooth computational assessment may assist in investigating the model's generalizability and may become more efficient for diverse medical image segmentation tasks. The author of this paper²⁶ utilized feature fusion and majority voting by introducing a class-weighted focal loss and working on imbalanced brain tumor classification datasets, yielding substantial improvements over conventional CNNs. Alternative fusion techniques and computational efficiency can overcome challenges in class weight determination and increase accuracy. In study⁷, the authors presented a robust brain tumor segmentation framework utilizing four MRI sequence images and an optimized CNN model. Demonstrating superior performance on the BRATS 2018 dataset with notable precision, recall, and Dice Score, the proposed method underscores its efficacy. Addressing additional pre-processing strategy exploration, scalability issues, and clinical challenges may contribute to an improvement in the model's performance. The author of the study²⁷ presented a DL fusion model for brain tumor classification, leveraging MRI images with a notable accuracy of 98.98%. The model incorporates features extracted from VGG16, ResNet50, and convolutional deep belief networks (CDBNs). However, enhancing data augmentation strategies and evaluating the model's applicability across various clinical datasets and imaging techniques could further enhance its efficacy. In this paper²⁸, the authors utilized the FPCIFHSS model to assess brain tumor susceptibility with complex intuitionistic fuzzy numbers (CIFNs), offering a versatile approach for managing diagnostic uncertainties, especially beneficial in resource-limited settings. Future studies should simplify the model for practical clinical application and validate its effectiveness through thorough comparative analyses with established diagnostic methods. The paper²⁹ proposed two models: XGBoost achieved 98.620% accuracy in differentiating cancer stages using multi-omics data from the Cancer Genome Atlas, while a cascading Deep Forest ensemble accurately identified cancer subtypes from the METABRIC dataset (83.45% for five subtypes, 77.55% for ten). These advancements highlight the potential of AI in omics data analysis. However, future research should focus on refining AI algorithms, improving preprocessing techniques, validating models across diverse datasets, and conducting rigorous clinical trials for robust validation.

Previous models for identifying brain tumors have challenges such as low accuracy, class imbalance, large computing demands, poor interpretability, and limited generalizability. Our ViT-GRU model overcomes these difficulties, delivering greater accuracy and addressing class imbalance while enhancing interpretability using XAI techniques like LIME, SHAP, and Attention mapping. It also handles data from diverse sources, making it more adaptable and relevant across varied demographics and imaging methods.

Materials and method

The methodology employed in this research consists of a meticulous and methodical process, which is depicted in Fig. 1, which provides a comprehensive description of the research methodology utilized in this study.

Dataset collection

In this research, we compiled a dataset named Brain Tumor MRI Hospital Data 2023 (BrTMHD-2023), consisting of 1166 MRI scans collected at Bangabandhu Sheikh Mujib Medical College Hospital (BSMMCH) in Faridpur, Bangladesh, over the period from January 1, 2023, to December 30, 2023. Our BrTMHD-2023 dataset contains different kinds of tumors and normal conditions, with images acquired from a Siemens Magnetom



Fig. 1. Flowchart of the proposed methodology illustrating the distinct phases involved in the research approach.

Skyra MR scanner for clarity and quality across Diffusion-Weighted Imaging (DWI), FLAIR, T1-weighted (T1), T2-weighted (T2), and T1 Fat-Sat categories. Legal regulations were followed, and informed consent was obtained from patients. Though the sharing of data is restricted for privacy, it is available upon request with ethical approval to assist in advancing brain tumor diagnosis and treatment. Furthermore, we confirm that all data collection and analysis methods adhered to the Declaration of Helsinki and Bangladesh Medical Research Council (BMRC) ethical guidelines.

A few samples of each category DWI, FLAIR, T1, T2-weighted, and T1 Fat-Sat from the dataset are shown in Fig. 2. This research also utilized an additional publicly available [Brain Tumor Kaggle Dataset](#) consisting 256 MRI images to evaluate the proposed model.

The dataset specifications are shown in Table 1.

The dataset employs multimodal imaging protocol MRI scans, which ensures a consistent and standardized data acquisition approach. This makes the data in this research more reliable and trustworthy.

Data preparation

After acquiring MRI data from the medical facility, the samples were assembled using image reconstruction approaches and then optimized acquisition parameters for T1, T2-weighted, and other multimodal images³⁰. We transformed DICOM files to JPG using MicroDicom for compatibility with image-processing tools and then performed enhancement and denoising³¹. Qualified radiologists classified the images into tumor and non-tumor types, ensuring high-quality data for ML training. Noise reduction techniques like filtering and advanced reconstruction were implemented to enhance the signal-to-noise ratio and image quality for accurate diagnosis^{32,33}.

Data preprocessing

Preprocessing MRI images elevates their quality for DL analysis while retaining their integrity. We employed motion correction, data resizing, data normalization, data augmentation, and conversion to numerical data³⁴. Motion artifacts were handled Utilizing retrospective and prospective motion correction approaches³⁵. Dimensionality reduction enhances the computing efficiency and our model performance³⁶. Pixel normalization between 0 and 1 improved feature extraction accuracy. To address the data imbalance caused by the unequal ratio of diseased to normal MRI images, we employed data augmentation techniques. This expanded our dataset to 2,190 MRI images, mitigating the scarcity and improving the learning and performance of our proposed model. Converting grayscale photos to RGB representation allowed us to apply pre-trained models, enhancing performance. These preprocessing methods assure the optimal results in the following image classification tasks^{37,38}.

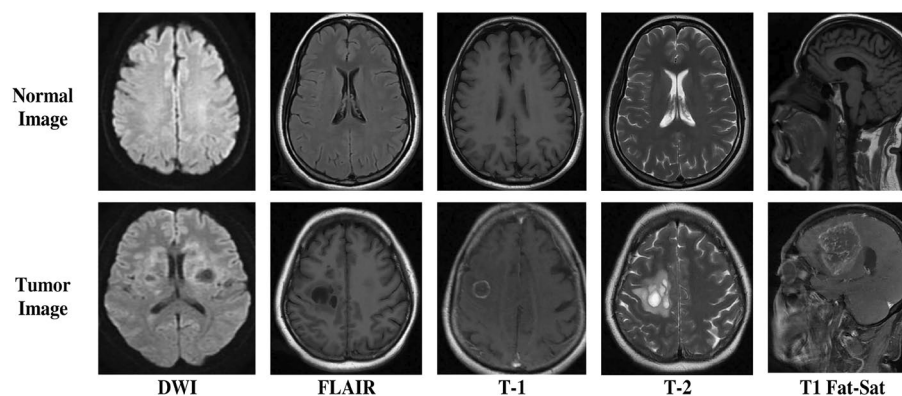


Fig. 2. Sample images of the BrTMHD-2023 Dataset.

Dataset	Label of the dataset	Number of total collected patient	No of disease patient	No of MRI image	No of MRI image after augmentation	Male tumor patient	Female tumor patient	Total MRI image	Total MRI image after augmentation
BrTMHD-2023	Normal patient	232	163	945	1210	61	102	1166	2190
	Tumor patient		69	221	980	45	24		
Brain tumor Kaggle dataset	Normal	-	-	156	-	-	-	256	-
	Tumor		-	100	-	-	-		

Table 1. Datasets of brain tumor disease utilized in this study.

Proposed ViT-GRU model

The proposed model called the hybrid ViT-GRU model, is for analyzing brain tumor detection and classification as illustrated in Fig. 3. Particularly in its utilization of ViT, this hybrid DL technique for classifying brain tumors exhibits an apparent connection to the original Transformer architecture³⁹.

ViT for feature extraction

This study builds upon the sophisticated ViT framework, which is renowned for its proficiency in acquiring visual data employing self-attention mechanisms; this architecture has been specifically fine-tuned to identify brain tumors from MRI scans. By exploiting the ViT backbone, our model excels at extracting hierarchical representations that show valuable patterns characteristic of brain tumors. Compared to traditional CNNs, the ViT utilizes self-attention mechanisms, which allow it to capture long-range dependencies and global context more effectively. To improve the ViT encoder for this purpose, we introduced strategic modifications. Firstly, we removed the Multi-Layer Perceptron (MLP) layer to increase computational efficiency and introduced layer normalization to accelerate convergence and stabilize training¹³. This adjustment contrasts with CNNs, where the dense layers are often a source of high computational load. Then, we added a dropout layer that reduces overfitting and enhances generalization. Finally, Incorporating a “flatten” layer improves the model’s ability to distinguish varied visual patterns in MRI data. These adjustments jointly increase the model’s reliability and effectiveness in brain tumor identification^{40,41}.

GRU for temporal analysis

In this approach to the temporal analysis of brain MRI images, we incorporate a GRU, a specialized form of the neural network, after the extraction of critical features from the images. GRUs, which were initially proposed by Ref.⁴², can be likened to an enhanced iteration of conventional Recurrent Neural Networks (RNNs). They are capable of recognizing patterns and establishing relationships within data sequences. GRUs have these neat features called update and reset gates that help them manage information better. By using a GRU with 1024 units in our architecture, we take advantage of its ability to comprehend changes over time in brain MRI images. This allows us to identify better and classify brain tumors. The GRU was chosen over other RNNs like LSTM for its simpler architecture and faster training while maintaining comparable performance in capturing dependencies. LSTM represents a type of RNN architecture with two crucial components: an input gate and a forget gate. These components play a vital role in regulating the flow of information within the network. The input gate determines which input information is stored in the memory cell, while the forget gate decides which information should be discarded. GRUs, which have an essential function in a variety of Natural Language Processing (NLP) operations such as recognition of speech, machine translation, and language modeling, play an indispensable part in our methodology, which allows the model to distinguish and categorize brain tumors with improved precision and efficacy⁴³.

Classification head

Once the feature extraction phase from the ViT and sequential data analysis of GRU architectures are finished, the final prediction is generated incorporating a classification head. The ViT-GRU-based process utilizes the final hidden state of the GRU unit as the input for a series of fully connected layers. The process of converting the hidden information into a probability distribution over the available categories is carried out by these layers through a sigmoid activation function. By utilizing the extracted features, the incorporation of this classification head substantially improves the model’s ability to generate precise predictions, which allows efficient classification within ViT-GRU frameworks.

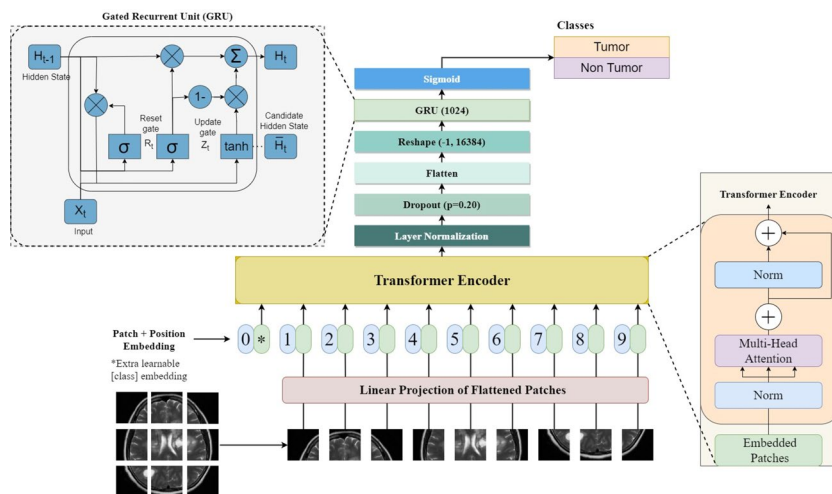


Fig. 3. Architecture of the hybrid ViT-GRU model showing the interconnected components and their functional relationship in the proposed model.

Hyperparameters settings

In this study, we trained models with various configurations that enabled us to adapt how the model works in various manners. Our main focus was on hyperparameter tuning, a crucial phase for optimizing model performance. This involved finding the best hyperparameter values for our model, using a mix of usual settings, and trying out new approaches to make our model better at evaluating and predicting things. To compare the model parameters, we initially set them sequentially, adjusting one at a time while keeping others constant. After this systematic process, we identified the best-fitting parameters based on performance metrics. These optimized parameters were then used for our final analysis. Table 2 presents a comprehensive list of all the hyperparameters that were used in our ViT-GRU model. Pre-trained transfer learning model parameters were also selected using the same procedure.

The training was carried out on Google Colab by using a GPU with 12 GB of RAM.

Evaluation metrics

The proposed model's performance is evaluated using various metrics, including accuracy, precision, recall, and F1-score. These measurements are calculated from the data provided in the confusion matrix, like True Positive, True Negative, False Positive, and False Negative, showing the model's progress. We have used the following equations for measuring the performance of our proposed ViT-GRU model:

$$\text{Precision} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Positives}} \quad (1)$$

$$\text{Recall} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Negatives}} \quad (2)$$

$$\text{F1 - Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad (3)$$

$$\text{Accuracy} = \frac{\text{True Positives} + \text{True Negatives}}{\text{Total Number of Samples}} \quad (4)$$

Explainable artificial intelligence

XAI is important for transparent and understandable AI systems and crucial in healthcare where AI judgements impact patient results⁴⁴. As a pioneer in medical image categorization, XAI facilitates human interpretation of complex AI decisions. Particularly in brain tumor detection, techniques such as LIME, SHAP, and Attention Maps improve the interpretability of DL models¹³. In our study, we integrated XAI techniques into the proposed model to enhance its interpretability and provide valuable insights into its decision-making process. This integration allows healthcare practitioners to understand how the model arrives at its predictions, thereby building trust and facilitating better diagnostic and treatment decisions.

LIME as XAI

LIME interprets ML model choices, particularly advantageous for “black box” DL architectures⁴⁵. Its fundamental function lies in providing perceptive heatmaps, emphasizing crucial locations affecting model predictions. The application of LIME resulted in intuitive heatmaps that highlighted key regions within MRI images critical for the model's predictions, thereby enhancing the interpretability of our DL model. These heatmaps enabled us to visualize significant areas influencing the model's predictions, providing valuable insights into its decision-making process. This integration facilitated a clearer understanding of the model's decisions, thereby supporting

Hyperparameters	Values
Epochs	35
Batch size	64
Image size	224×224×3
Learning rate	0.0001
Weight decay	0.0001
Optimizer	AdamW, Adam, SGD
Loss function	Categorical cross-entropy
Patch size	8
Number of patches	256
Projection dimension	64
Number of parallel self-attention heads	4
Number of transformer encoder layers	8

Table 2. Hyperparameters of our proposed ViT-GRU model with their values.

more informed clinical judgments by healthcare professionals. By assigning relevance scores to pixels or image areas, LIME delivers a thorough comprehension of the key characteristics guiding categorization necessary for grasping intricate model behavior⁴⁶. This process can be expressed by the following formula:

$$f(x) = \underset{x_i \in N(x)}{\operatorname{argmin}}_f \sum L(f, \pi(x_i)) + \Omega(f) \quad (5)$$

- $f(x)$ is the interpretable model's projection for the image instance x .
- $N(x)$ shows the immediate vicinity of the image x .
- $L(\cdot)$ is a loss function assessing the difference between the estimates of the interpretable model $f(x)$ and the original model's estimate π in the surrounding area $N(x)$.
- $\Omega(f)$ is a normalization term.

SHAP as XAI

SHAP elucidates ML model outputs, specifically applying Shapley values to clarify feature contributions. Crucial for medical image categorization, SHAP indicates critical regions within images vital for model judgments⁴⁷. We integrated SHAP into the model to calculate Shapley values for each pixel in the MRI images, identifying and visualizing the most critical regions influencing classification results. It graphically depicts essential feature values, which is helpful in predicting particular categories. Our application in brain tumor detection gave insights into critical brain areas, combining LIME explanations for a thorough comprehension of data patterns.

Attention map as XAI

Attention maps depict DL model focus areas in input pictures, boosting interpretability by illuminating key regions⁴⁸. In medical image identification, they are essential for detecting tumor-impacted brain regions. We integrated attention maps by leveraging the multi-head attention layer in the proposed model, which highlights areas with high activation that contributed to the final classification. Leveraging the last multi-head attention layer to generate attention maps provided crucial insights into the model's decision-making by highlighting key image regions and enhancing interpretability, thus emphasizing the need for further refinement to maximize patient care improvements⁴⁹. Visualizing these maps considerably bolsters comprehension of DL model operations in sophisticated AI-driven assessments in healthcare.

Results

We conducted three experiments to assess our model's performance. In experiment 1, We employed the primary BrTMHD-2023 dataset and applied a rigorous 10-fold cross-validation technique to verify the efficacy of our model during our evaluation. Experiment 2 involved a holdout analysis, on the BrTMHD-2023 dataset without k-fold validation. Finally, in experiment 3, we validated our model on an additional Brain Tumor Kaggle dataset to demonstrate its generalizability.

In experiment 1, our proposed model obtained the highest average accuracy of 98.97%, an average precision score of 97%, highlighting its accuracy in identifying positive instances. The model's efficacy in accurately distinguishing true positives and minimizing false negatives was also demonstrated by its 97% average recall rate. The model's dependable performance was affirmed by the F1-score, which achieved an exceptional average value of 97% by balancing precision and recall. Furthermore, we introduced various pre-trained transfer learning models into our study to investigate the training and performance capabilities of ML models. The results, summarized in Table 3, indicate that our model performed exceptionally well. Figure 4 illustrates the training accuracy and loss curves across various folds, highlighting the model's learning trajectory. Figure 5 depicts the

Number of fold	Precision (%)	Recall (%)	F1-score (%)	Training loss (msec)	Test loss (msec)	Training accuracy (%)	Test accuracy (%)
1	98	98	98	0.0042	0.0107	100	100
2	98	97	97	0.0082	0.0307	99.9	99.15
3	100	100	100	0.0026	0.0688	100	97.44
4	97	97	97	0.0098	0.0378	99.81	99.15
5	98	97	97	0.0021	0.0153	100	100
6	96	96	96	0.0044	0.0478	100	98.29
7	96	96	96	0.0042	0.0374	99.81	99.14
8	99	99	99	0.0034	0.0097	99.9	100
9	96	96	95	0.0035	0.0562	100	98.28
10	96	96	96	0.0139	0.0591	99.9	98.28
Average	97	97	97	0.0056	0.0374	99.93	98.97
STDEV	0.014	0.013	0.015	0.004	0.021	0.079	0.884

Table 3. Results of 10-fold cross-validation in our proposed ViT-GRU model. Significant values are in bold.

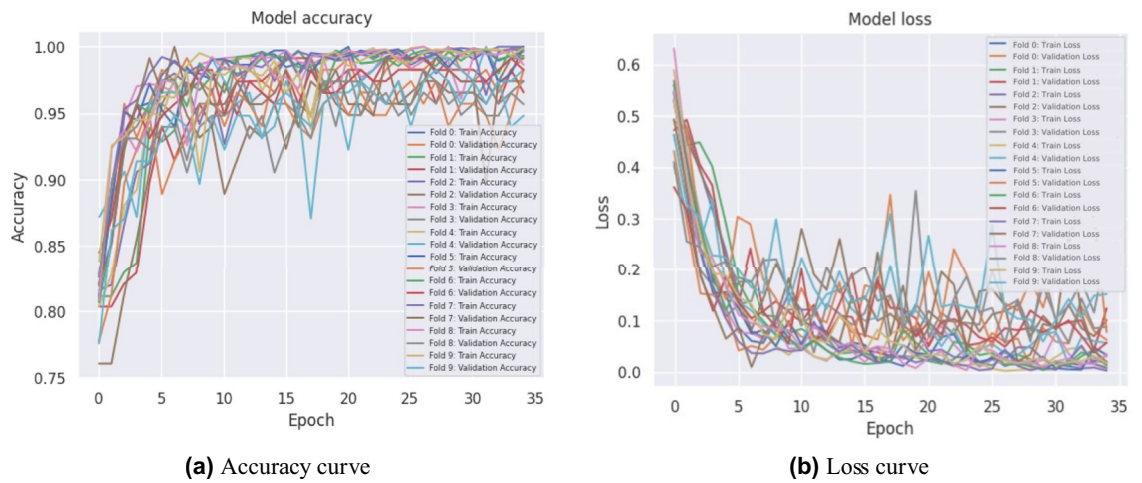


Fig. 4. Accuracy and loss curves for 10-fold cross-validation of the proposed ViT-GRU model.

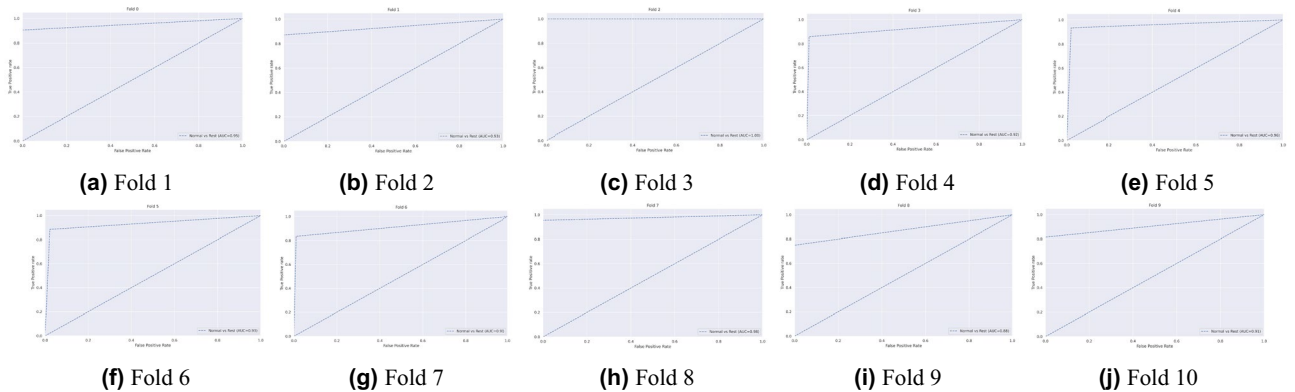


Fig. 5. AUC-ROC curves for 10-fold cross-validation of the proposed ViT-GRU model.

AUC-ROC contours for each fold, demonstrating the model’s class discrimination capability. Figure 6 presents the confusion matrices, providing a detailed analysis of each fold’s classification performance.

In experiment 2, we adopted three different optimizers into our proposed ViT-GRU model, with the AdamW optimizer attaining the highest accuracy of 98.97%. This high mean test accuracy underscores the model’s precision in classifying data. Table 4 contrasts the results of multiple models with our proposed model using distinct optimizers. Additionally, Table 5 provides a comprehensive comparison of important approaches used

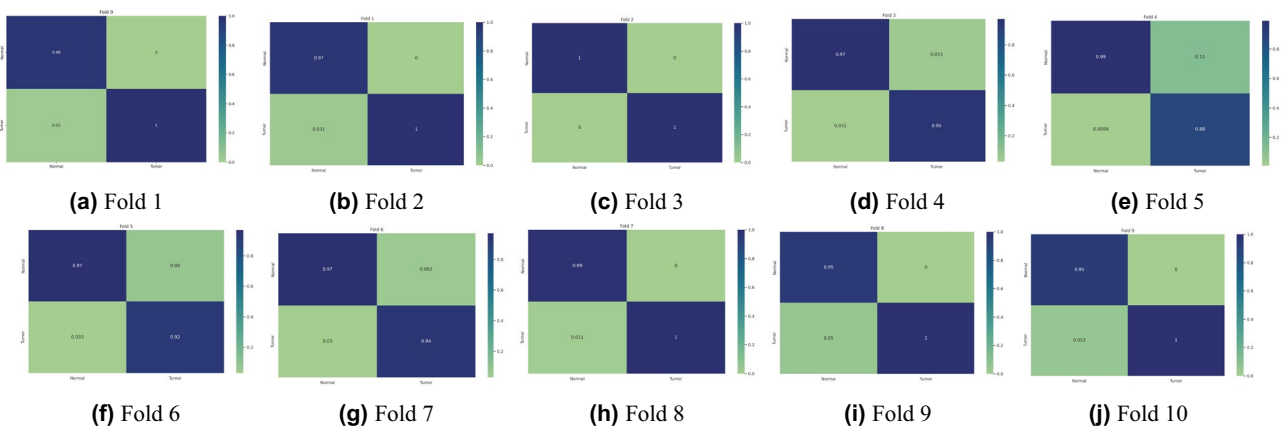


Fig. 6. Confusion matrices for 10-fold cross-validation of the proposed ViT-GRU model.

Model	Optimizer	Precision (%)	Recall (%)	F1-score (%)	Training loss	Validation loss	Trainig time (s)	Training accuracy (%)	Test accuracy (%)
ResNet18	AdamW	91	91	90	0.0113	0.1577	5.83	99.88	94.29
	Adam	94	93	93	0.0124	0.1193	6.07	99.88	96.86
	SGD	65	81	72	1.4124	1.4792	5.63	81.25	80.57
ResNet50	AdamW	91	91	91	0.0435	0.2218	12.94	98.65	91.43
	Adam	92	92	92	0.0524	0.2454	13.03	98.65	92.86
	SGD	63	79	70	0.5341	0.5443	12.64	81.74	79.43
VGG16	AdamW	91	92	91	0.0588	0.1521	18.41	97.43	93.71
	Adam	93	93	93	0.0547	0.1415	18.9	99.02	94
	SGD	72	81	75	0.5593	0.5347	17.73	78.55	81.43
VGG19	AdamW	92	91	91	0.0540	0.1755	20.92	98.28	94.29
	Adam	91	91	91	0.0540	0.1755	20.92	98.9	94.29
	SGD	72	79	73	0.5951	0.5601	20.55	78.8	78.29
EfficientNet_V2_1	AdamW	91	91	91	0.0723	0.1646	17.36	96.56	92.65
	Adam	89	89	89	0.1131	0.2954	14.61	95.83	91.71
	SGD	68	76	72	6.0248	6.0263	14.57	50.86	51.14
MobileNet_V2	AdamW	85	86	85	0.2885	0.3368	6.43	90.2	85.14
	Adam	80	83	80	0.2819	0.3643	6.54	88.97	83.71
	SGD	74	84	77	3.6244	2.5056	11.82	82.27	84.86
DenseNet121	AdamW	97	97	97	0.0182	0.0892	13.87	99.88	97.71
	Adam	93	93	93	0.0311	0.1541	13.93	99.88	96.29
	SGD	72	83	73	2.7244	2.6056	13.82	80.27	82.86
AlexNet	AdamW	86	87	86	0.1983	0.2656	4.57	92.89	89.43
	Adam	89	89	88	0.1451	0.2399	4.05	96.08	91.14
	SGD	71	84	77	6.8541	6.8497	4.29	79.78	84
ViT-GRU	AdamW	97	97	97	0.0056	0.0374	47.93	99.93	98.97
	Adam	96	95	95	0.0089	0.1025	49.28	99.75	96.56
	SGD	66	81	73	0.4695	0.4606	48.3	81.02	81.66

Table 4. Comparing the results of pre-trained transfer learning models with the proposed ViT-GRU on the AdamW, Adam, and SGD optimizer.

for classifying brain tumors that focus on important factors such as the dataset used, number of classes, classification algorithm applied, image count, and performance measures.

Here, the model we used demonstrated consistently high performance, achieving a precision, recall, and F1-score of 97% each.

Our proposed model's accuracy and loss curves are represented in Fig. 7. Visual analyses provided in Fig. 9a extend deeper into the confusion metrics details, and Fig. 9b displays the AUC-ROC curves. These visuals collectively emphasize the model's exceptional performance across diverse testing circumstances.

In experiment 3, the model demonstrated exceptional results, achieving an accuracy of 96.08%, a precision of 97%, a recall of 96%, and an F1 score of 96% on the Brain Tumor Kaggle dataset as presented in Table 5. This evaluation's accuracy and loss curves are presented in Fig. 8. Also, the confusion matrices and the AUC-ROC curve are illustrated in Fig. 10.

Discussion

This study provides a new framework combining a ViT with a GRU network for brain tumor assessment in MRI images. The hybrid ViT-GRU model employs ViT for regional feature extraction and GRU for temporal contextual assessment, increasing classification accuracy by collecting both spatial and temporal properties.

In our study, 10-fold cross-validation enhanced the model's robustness and reliability, achieving an average 98.97% accuracy due to high-quality data, effective preprocessing, hyperparameter tuning, resulting in high precision, recall, and F1-scores of 97% respectively. In experiment 2, our proposed model showed excellent classification accuracy (98.97% with AdamW, 96.56% with Adam, and 81.66% with SGD). This study also evaluates our dataset using various pre-trained transfer learning models, including DenseNet121, ResNet18, and VGG19. After completing the necessary preprocessing techniques and parameter tuning, these models achieved the highest accuracies of 97.71%, 96.86%, and 94.29%, respectively. Our proposed model beat these pre-trained models in important parameters such as precision, recall, and F1-score and significantly shows 1.26% better accuracy than the highest performed TL models. We enhanced these models with hyperparameter adjustments and layer alterations. In addition, we presented and assessed our suggested model, which performed better than any other model in every metric. Table 4 presents the comparative results for AdamW, Adam, and SGD optimizers. The impact of each optimizer on the model's performance is compared, and AdamW achieves higher accuracies

Study	Year	Model	Dataset	Image modalities	Number of classes	Number of images	Performance	XAI
Choudhury et al. ⁵⁰	2020	CNN	Brain tumor Kaggle dataset	MRI	2	–	Accuracy: 96.08% Precision: 94.87% Recall: 98.63% F1-score: 97.36%	Not used
Saleh et al. ²²	2020	Pre-trained DL models	Brain tumor Kaggle dataset	MRI	4	4480	Accuracy: 97.25-98.75% Precision: – Recall: – F1-score: 100%	Not used
Bhanothu et al. ⁵¹	2020	Faster R-CNN	Brain tumor Figshare dataset	MRI	3	2406	Accuracy: – Precision: 77.6% Recall: 80% F1-score: –	Not used
Waghmare et al. ⁵²	2021	fine-tuned VGG-16 CNN	Brain tumor Kaggle dataset	MRI	3	3664	Accuracy: 95.71% Precision: – Recall: 83.28% F1-score: –	Not used
Díaz-Pernas et al. ¹⁷	2021	DCNN	BRATS 2013	MRI	3	3064	Accuracy: 97.3% Precision: – Recall: – F1-score: –	Not used
Khairandish et al. ⁵³	2022	CNN-SVM	BRATS 2015	MRI	2	230	Accuracy: 98.49% Precision: – Recall: – F1-score: –	Not used
Mohan et al. ⁵⁴	2022	DLBTDC-MRI	BRATS2015 dataset	MRI	4	42,470	Accuracy: 98.145% Precision: 95.134% Recall: 97.348% F1-score: 96.25%	Not used
Srinivas et al. ⁵⁵	2022	VGG-16	Kaggle dataset	MRI	2	256	Accuracy: 96% Precision: 94% Recall: 100% F1-score: 98%	Not used
Montaha et al. ⁵⁶	2022	TD-CNN-LSTM	BraTS 2018, BraTS 2019 and BraTS 2020	MRI	2	978	Accuracy: 98.90% Precision: 98.95% Recall: 98.78% F1-score: 98.83%	Not used
Hossain et al. ²⁴	2022	ResNet50	TGCA-GBM dataset	MRI and CT scans	3	3064	Accuracy: 98.96% Precision: 98.67% Recall: 99.12% F1-score: 98.87%	Not used
Vankdothu et al. ¹⁵	2022	CNN-LSTM	Brain tumor kaggle dataset	MRI	4	3264	Accuracy: 92% Precision: 96% Recall: 98.5% F1-score: –	Not used
Rasheed et al. ⁵⁷	2023	CNN	Brain tumor Kaggle dataset	MRI	3	3064	Accuracy: 98.04% Precision: 98% Recall: 98% F1-score: 98%	Not used
Abdusalomov et al. ⁵⁸	2023	YOLOv7	Brain tumor Kaggle dataset	MRI	4	10,288	Accuracy: 99.5% Precision: 99.5% Recall: 99.3% F1-score: 99.4%	Not used
Meena, Gaurav, et al. ²¹	2024	InceptionV3	kaggle	–	2	228	Accuracy: 98% Precision: – Recall: – F1-score: –	Not used
			BrTMHD-2023	MRI	2	1166	Accuracy: 98.97% Precision: 97% Recall: 97% F1-score: 97%	Used
Proposed study	2024	ViT-GRU	Brain Tumor Kaggle Dataset	MRI	2	256	Accuracy: 96.08% Precision: 97% Recall: 96% F1-score: 96%	Not used

Table 5. Performance evaluation of existing state-of-the-art models and the proposed model.

by decoupling weight decay from gradient updates, enhancing model generalization, and allowing for better control over learning rates and regularization, resulting in improved overall metrics. Additionally, this study comprehensively compares existing technologies and previous work, which is shown in Table 5 with a detailed state-of-the-art comparison, highlighting how our hybrid model achieves better results across various metrics. The proposed model achieved high AUC-ROC scores of 96% on the BrTMHD-2023 dataset and 97% on the

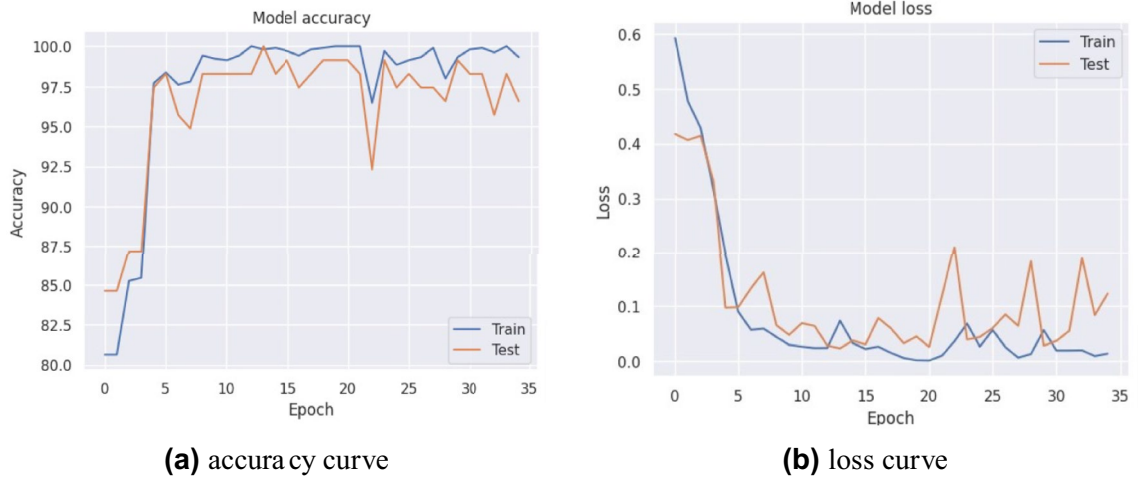


Fig. 7. Accuracy and loss curves analysis obtained from the proposed ViT-GRU model for BrTMHD-2023 dataset.

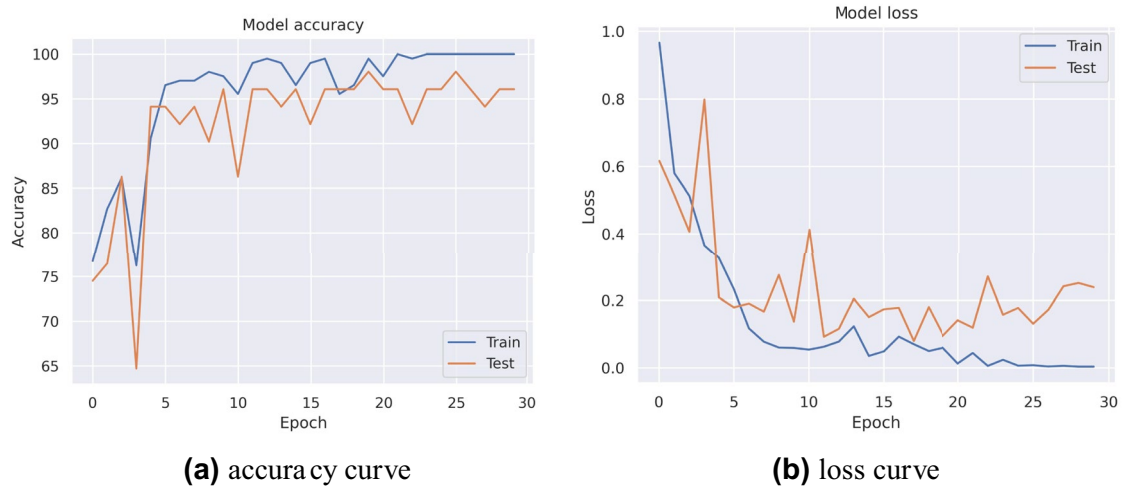


Fig. 8. Accuracy and loss curves analysis obtained from the proposed ViT-GRU model for Brain Tumor Kaggle Dataset.

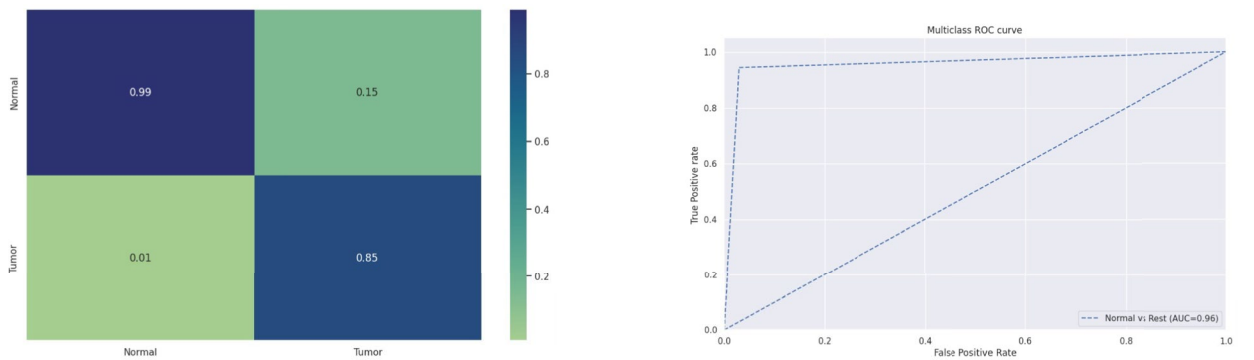


Fig. 9. Confusion matrices and AUC-ROC curves of our proposed ViT-GRU model for BrTMHD-2023 dataset.

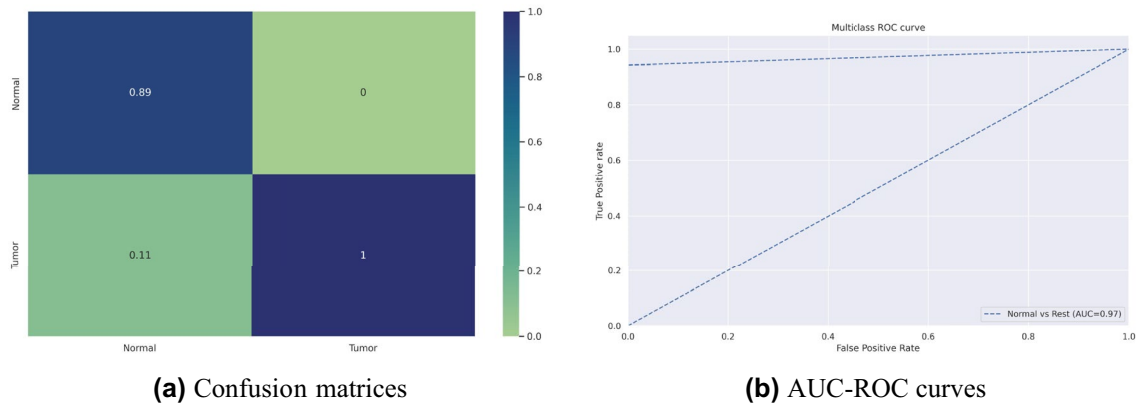


Fig. 10. Confusion matrices and AUC-ROC curves of our proposed ViT-GRU model for Brain Tumor Kaggle Dataset.

Brain Tumor Kaggle Dataset, demonstrating its robust effectiveness in brain tumor detection and classification, which is shown in Figs. 9b and 10b, respectively.

The innovativeness of this research lies in leveraging primary data with the development of the hybrid model, offering distinct advantages, including enhanced model interpretability through XAI techniques like LIME, SHAP, and Attention maps. This increased transparency supports clinicians in understanding the model's judgments, thereby aligning our model with clinical expertise and improving its applicability in healthcare settings. Using XAI approaches like LIME, SHAP, and Attention maps, we increased model interpretability, emphasizing crucial aspects like white matter lesions and cortical atrophy, thereby supporting clinicians in comprehending the model's judgments. The corresponding radiologist ensures and provides positive feedback about our model's decision-making ability with the integration of XAI, allowing them to understand and trust the process that ensures the reliability and compatibility of the model. This transparency creates confidence and assures alignment with clinical expertise, boosting real-world application in healthcare. Our results, shown in numerous figures, support the model's capacity to appropriately reflect brain tumor pathophysiology.

The results are shown in Fig. 11a, where each figure represents the LIME analytical assessment of our proposed model using sample images. Furthermore, SHAP analysis findings are shown in Fig. 11c, which again aligns with our suggested model and includes sample images. Lastly, sample images from the attention map analysis are used in Fig. 11b to demonstrate the results.

Despite the promising results, this study faces several limitations. The complexity of integrating multi-modal MRI data, challenges in data preprocessing and feature extraction, and the limited availability of well-annotated MRI scans impact the robustness of our model. Additionally, class imbalance due to the rarity of brain tumors and ethical and legal considerations related to AI implementation in medical diagnostics necessitate careful attention. Addressing these limitations in future research could further enhance the accuracy and applicability of AI-based brain tumor detection systems.

Conclusion and future work

In summary, this study introduces and examines the effectiveness of our newly developed ViT-GRU model for the detection and classification of brain tumors. We assessed our model's performance by benchmarking it against several pre-trained models employing transfer learning using three distinct optimizers. Our ViT-GRU model achieved a remarkable accuracy of 98.97% using a 10-fold cross-validation technique. When tested on the BrTMHD-2023 dataset without cross-validation, it outperformed the top transfer learning model by 1.26% in accuracy. Additionally, in another Kaggle benchmark dataset, our model achieved an accuracy of 96.08%, exceeding previous results for this dataset. These results demonstrate that our model surpasses these existing

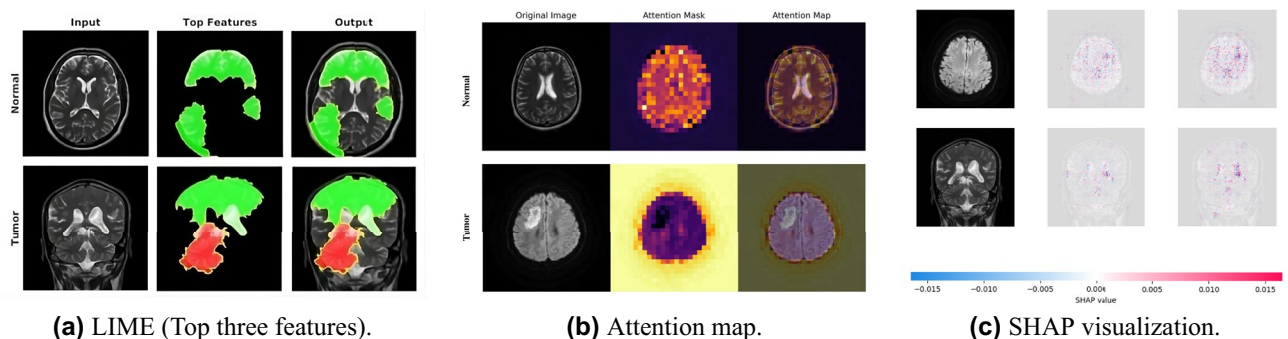


Fig. 11. Visualization of XAI Techniques.

models in accuracy, precision, recall, and F1-score metrics for MRI image analysis. The proposed model combines the regional feature extraction capabilities of ViT with the temporal contextual assessment strengths of GRU, leading to superior performance in comparison to several pre-trained models such as ResNet and VGG. Our model demonstrated exceptional accuracy, precision, recall, and F1-score metrics, particularly when optimized with the AdamW algorithm, achieving an accuracy of 98.97%. These theoretical advancements underscore the potential of hybrid models in enhancing diagnostic accuracy by integrating spatial and temporal data features. The practical implications of our research are further supported by extensive visual analyses, including accuracy and loss curves, confusion matrices, and AUC-ROC curves, which collectively highlight the model's robust performance and reliability in diverse testing scenarios. Moreover, this study utilizes XAI techniques to increase the interpretability and transparency of the ViT-GRU model. We further illustrated the performance of our proposed model through accuracy and loss curves, confusion matrices, and AUC-ROC curves. The research incorporated primary MRI data collected from a hospital, which underwent preprocessing to prepare for analysis. Our approach combines the ViT with GRU and integrates the latest developments in Graph Neural Networks to effectively categorize brain tumor, deliver clinicians with essential information, and lead the way for efficient clinical implementations. The proposed study of this research demonstrates potential in facilitating a prompt response and enhancing the quality of life through early and precise diagnosis of brain tumor.

Future research should focus on expanding the dataset to improve model performance and generalizability across diverse patient populations and clinical settings. Additionally, integrating the ViT-GRU model into real-time diagnostic devices should be investigated to assess its practical utility in clinical environments, potentially transforming diagnostic workflows. Lastly, applying the model to other medical imaging tasks can validate its versatility and robustness, extending its utility beyond brain tumor classification.

Data availability

The BrTMHD-2023 dataset used to support the findings of this study is available from the corresponding author upon request. Additionally, the study utilized the Brain Tumor Kaggle Dataset, which is publicly accessible online.

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Author contributions

Md. Mahfuz Ahmed: Conceptualization, Formal analysis, Methodology, Software, Data curation, Validation, Writing—Original Draft, Review & Editing. Md. Maruf Hossain: Methodology, Software, Validation, Writing - Review & Editing. Md Rakibul Islam: Data curation, Writing, Validation. Md. Shahin Ali: Methodology, Writing—Review & Editing. Abdullah Al Nomaan Nafi: Data curation, Writing, Validation, Visualization. Md Faisal Ahammed Data labeling, Validation. Kazi Mowdud Ahmed: Methodology, Writing—Review & Editing. Md Sipon Miah: Methodology, Writing—Review & Editing. Md Mahbubur Rahman: Methodology, Writing—Review & Editing, and Supervision. Mingbo Niu: Writing—Review & Editing, and Project Administration. Md Khairul Islam: Methodology, Formal analysis, Validation, Writing - Review & Editing, and Supervision.

Competing interests

The authors declare competing interests.

Ethical approval

The dataset utilized in this study was collected from BSMCH, Faridpur, Bangladesh. We affirm that the dataset has received approval from the approval board of the hospital. The Ethical Approval Committee of Islamic University, Bangladesh, has also approved the use of this dataset in research, with the reference number EC/FBS/2024/06. Furthermore, we confirm that all data collection and statistical analysis methods were conducted in accordance with the relevant guidelines and regulations, including the Declaration of Helsinki and the BMRC ethical guidelines.

Additional information

Correspondence and requests for materials should be addressed to M.N.

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