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SABViT: A Pilot Feasibility Study of a Self-Attention-Based Vision Transformer for Binary Brain Tumor Detection in MRI

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About Article

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ABSTRACT

The accurate and timely identification of brain tumors is crucial for effective diagnosis and treatment planning; however, the manual interpretation of MRI scans continues to be difficult and susceptible to errors. Although convolutional neural networks (CNNs) have made strides in automated classification, their dependence on local feature processing can restrict overall effectiveness. As an initial exploration, this pilot study introduces a Vision Transformer (ViT) model that utilizes self-attention mechanisms to capture both long-range global contexts and detailed local dependencies within image data, facilitating a more thorough feature representation that is vital for detecting subtle pathological patterns. Trained and assessed on a pilot dataset comprising 3,000 MRI images with significant augmentation, the proposed ViT model attained a promising preliminary accuracy of 99.73%, surpassing established CNN-based architectures such as ResNet-50, VGG-16, and EfficientNet-B0 across all evaluation metrics within the constraints of this binary classification task. These feasibility results not only highlight the potential of ViTs for brain tumor classification but also effectively validate the fundamental data processing and model fine-tuning pipeline. The study points out critical limitations, including dataset scale and model explainability, which directly influence the design of a forthcoming large-scale, multi-institutional research initiative. This pilot research lays a foundational framework for the integration of transformer-based models into medical imaging workflows to enhance diagnostic accuracy.

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1. INTRODUCTION

Brain imaging plays a crucial role in modern medical diagnosis by allowing non-invasive visualization of the brain's structure and function. Among various neurological conditions, brain tumors are particularly challenging due to their heterogeneous nature, location, and potential impact on vital brain functions. Accurate and timely diagnosis is therefore essential for effective treatment planning and improving patient outcomes (Louis *et al*., 2021). Magnetic Resonance Imaging (MRI) remains the gold standard for detecting brain tumors because of its high spatial resolution and ability to differentiate between normal and abnormal tissues (Joshi *et al*., 2024). However, manual interpretation of MRI scans by radiologists can be time-consuming, subjective, and prone to human error, especially when tumors are small or located in complex regions (Abdusalomov *et al*., 2023).

The emergence of Artificial Intelligence (AI), particularly Machine Learning (ML) and Deep Learning (DL), has transformed the field of medical imaging. AI algorithms can process large amounts of imaging data, extract hidden features, and assist in the detection, segmentation, and classification of brain tumors with high accuracy. CNNs, for instance, have demonstrated impressive results in distinguishing between gliomas, meningiomas, and pituitary tumors, achieving classification accuracies above 95% (Yakkundi *et al*., 2024; Aydin & Acharya, 2019; Clive & Giroh 2023; Dong *et al*., 2025). These models reduce diagnostic variability and provide more consistent results than human experts alone.

The rapid evolution of Artificial Intelligence technologies, as described in Clive *et al.* (2024); Clive *et al*., (2025); Asuai *et al*,. (2025; Akazue *et al*., 2023, has brought about improvement in imaging technology. Despite advances in imaging technology, the accurate and early diagnosis of brain tumors remains a major challenge. Radiologists face difficulties in differentiating tumor subtypes, assessing progression, and interpreting complex imaging data. These challenges can delay treatment decisions and negatively affect patient outcomes. The integration of AI into brain imaging provides an opportunity to overcome these limitations by offering automated, fast, and highly accurate diagnostic support.

This study is motivated by the need to harness AI in brain tumor imaging to improve diagnostic accuracy, reduce human error, and enable timely clinical interventions. By applying ML and DL techniques, this work seeks to demonstrate how AI can enhance brain tumor detection and classification, ultimately contributing to better patient care

1.1. Pilot study rationale and objectives

Given the rapid advancement of Artificial Intelligence technologies, as covered in, Asuai *et al*., 2025, The transition of advanced deep learning architectures from natural image recognition to the vital field of medical diagnostics necessitates meticulous, phased validation. ViTs signify a significant shift from convolutional networks; however, their efficacy in medical imaging tasks, especially given the limited dataset sizes common in clinical environments, remains to be fully determined . Consequently, a pilot study is an essential initial step to mitigate risks associated with a larger investigation. This research is structured as a monocentric pilot study aimed at evaluating the feasibility and preliminary effectiveness of a self-attention-based framework, referred to as SABViT, for binary brain tumor classification.

The primary goal is to ascertain the viability of this method prior to engaging in a more resource-demanding study. The specific objectives of the pilot study are to:

i. evaluate the feasibility of the technical pipeline: This encompasses assessing the efficacy of our MRI-specific preprocessing (skull stripping, normalization) and the adequacy of our data augmentation strategy in averting overfitting while fine-tuning a large ViT model on a limited dataset.

ii. collect preliminary data on model performance: The objective is to derive initial estimates of the classification accuracy, precision, recall, and F1-score of the SABViT model. This information will be utilized for sample size determination and power analysis in a subsequent definitive trial.

iii. perform an initial comparative benchmark: The performance of the SABViT model will be evaluated against a series of standard CNN benchmarks (ResNet-50, VGG-16, EfficientNet-B0) under the same conditions to provide an early assessment of its relative advantages.

iv. identify practical challenges and limitations: The study will document computational demands, training stability, and potential failure modes, offering critical insights for enhancing the experimental protocol and model architecture in future endeavors

2. LITERATURE REVIEW

Recent advancements in DL and ML have significantly enhanced brain tumor detection and segmentation from MRI scans, addressing challenges such as image noise, tumor heterogeneity, and limitations of manual annotation. Asuai and Giroh (2023) developed a CNN incorporating an attention mechanism, achieving 97.5% accuracy on 3,000 MRI images. Their approach leveraged preprocessing and attention layers to enhance feature focus and interpretability.

Building upon segmentation-driven classification, Lakshmi *et al.* (2025) introduced the XAISS-BMLBT framework, which combines UNet-based segmentation with Bayesian machine learning. Utilizing bilateral filtering, MEDU-Net+ segmentation, ResNet50 feature extraction, and a Bayesian regularized neural network (BRANN) with hyperparameter tuning, the approach achieved 97.75% accuracy, emphasizing model explainability and precise tumor localization. Similarly,

Naceur *et al.* (2018) proposed end-to-end incremental deep CNNs for glioblastoma segmentation on the BRATS-2017 dataset, achieving an average Dice score of 0.88 in 20.87 seconds, illustrating the potential for efficient clinical diagnosis.

Aswani and Menaka (2021) employed an unsupervised dual autoencoder with singular value decomposition (SVD) for brain tumor segmentation, demonstrating improved performance over conventional ML methods (e.g., SVM, KNN) by reducing latent space loss for meningioma and glioma segmentation.

In the domain of tumor classification, Khaliki and Başarslan (2024) explored glioma, meningioma, and pituitary tumor detection using a 3-layer CNN and transfer learning models, with VGG16 achieving 98% accuracy, highlighting the effectiveness of transfer learning. Salakapuri *et al.* (2025) proposed a hybrid model integrating deep transfer learning (Inception-V3, ResNet-50, VGG-16) with ensemble machine learning on 5,712 MRI scans; their stacking ensemble combining ResNet-50 and PCA achieved 95.7% accuracy and 99.6% AUC, significantly outperforming baseline models.

Zubair Rahman *et al.* (2024) employed EfficientNetB2 with advanced preprocessing, reporting validation accuracies of 99.83%, 99.75%, and 99.2% across three Kaggle datasets, underscoring the role of AI-driven approaches in improving clinical diagnostics.

Other approaches emphasize specialized architectures and optimization techniques. Abdusalomov *et al.* (2023) fine-tuned YOLOv7 with CBAM, SPPF+, and BiFPN for tumor detection, achieving 99.5% accuracy while identifying small tumors as a future challenge. Kumar *et al.* (2024) evaluated machine learning classifiers combined with feature extraction methods, showing that Random Forest with Image Loading achieved 99% accuracy.

Aamir *et al.* (2025) implemented an automated DL framework with guided filtering and morphological analysis on BraTS2020 and Figshare datasets, attaining 99.94% and 99.67% accuracy, respectively, demonstrating robustness and automation.

Ragab *et al.* (2024) introduced the BTR-EODLA method, leveraging median filtering, SE-ResNet50, and a stacked autoencoder with equilibrium optimizer tuning, achieving 98.78% accuracy. Gasmi *et al.* (2024) proposed an ensemble approach combining ViT and EfficientNet-V2 with genetic algorithm-based weight optimization, reaching 95% accuracy for multi-class tumor classification

Transfer learning and fine-tuning strategies have also been applied effectively. Rastogi *et al.* (2025) fine-tuned InceptionResNetV2, VGG19, Xception, and MobileNetV2, achieving 96.11% accuracy with Xception.

Gao *et al.* (2022) developed a DL model for classifying 18 tumor types from 37,871 MRI scans, achieving a mean AUC of 0.92 and outperforming neuroradiologists (73.3% vs. 60.9%), while enhancing diagnostic accuracy when used as an adjunct. Rasool *et al.* (2025) introduced CNN-TumorNet with LIME-based explainability, attaining 99% accuracy in tumor versus non-tumor classification, supporting transparent clinical decision-making. Gunasekaran *et al.* (2024) developed ConvNet-ResNeXt101, a hybrid DL model for segmentation and classification on BRATS 2020, achieving 99.27% accuracy for tumor core classification with a rapid learning time of 0.53 seconds. Saeedi *et al.* (2023) implemented a 2D CNN and convolutional autoencoder network for classifying glioma, meningioma, pituitary tumors, and healthy brains on 3,264 MRI images, reporting 96.47% and 95.63% training accuracy, respectively, with the 2D CNN outperforming traditional ML methods such as MLP (28%) and KNN (86%).

While the current literature demonstrates remarkable performance, often reporting accuracies exceeding 99%, this pilot study is consciously designed as a foundational step that prioritizes methodological rigor over achieving a superlative metric. The field's tendency towards such high scores warrants critical discussion, as it can sometimes stem from non-challenging or insufficiently diverse datasets, data leakage, or a lack of failure analysis. This work aims to establish a robust data processing and model fine-tuning pipeline first, acknowledging that a credible assessment of a model's true clinical potential requires a cautious, phased approach, beginning with this carefully controlled feasibility study before progressing to more complex, generalizable validation.

3. METHODOLOGY

3.1. Pilot study design

This study utilized a retrospective, single-center pilot design. A retrospective dataset of 3,000 T1-weighted contrast-enhanced MRI axial scans was obtained from the institutional archive of the Federal Medical Centre, Asaba, Nigeria. The binary classification task (Tumor vs. Non-Tumor) was deliberately chosen to minimize complexity for this preliminary feasibility evaluation. This focused approach facilitates a clearer understanding of the model's fundamental ability to differentiate between abnormal and normal tissue prior to advancing to the more clinically intricate task of tumor subtype classification.

3.2 Dataset and preprocessing

In the rapidly evolving realm of information processing (Clive *et al.*, 2024, Clive *et al.*, 2025, Akazue *et al.*, 2023, Clive *et al.*, 2023), data represents all manipulable elements that can be structured into datasets with identifiable features (Clive *et al.*, 2024, Clive *et al.*, 2025, Asuai *et al.*, 2025, Akazue *et al.*, 2023). These features can be fused across sources to create enriched representations (Asuai *et al.*, 2025).

The dataset employed in this research was obtained from Federal Medical Centre, Asaba, Nigeria, and comprises 3,000 MRI brain images, evenly distributed across two categories: 1,500 images containing brain tumors and 1,500 images of healthy (non-tumor) brains. The dataset was randomly split into training (80%, n=2,400 images) and testing (20%, n=600 images) sets, with stratification to preserve the original class distribution.

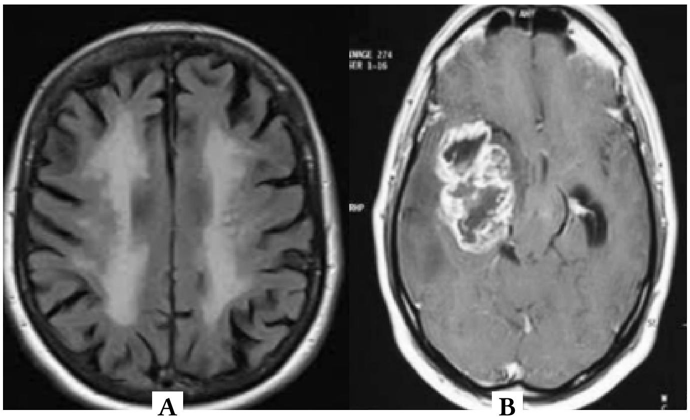

Figure 1. Sample T1-weighted contrast-enhanced axial MRI scans. (a) Normal brain (no tumor). (b) Brain with a tumor.

To ensure reliability and suitability for deep learning models, several preprocessing steps were carried out:

i. Image Cleaning and Skull Stripping: Non-brain tissues were removed using the ROBEX to retain only relevant brain structures.

ii. Normalization: Pixel intensity values were normalized to a uniform range [0, 1] range, reducing scanner-related variability and enhancing consistency across samples.

iii. Resizing: All images were resized to 224 × 224 pixels to conform to the input specifications of the ViT model.

iv. Data Augmentation: To address dataset size limitations and prevent overfitting, the following augmentation techniques were applied on-the-fly during training: random rotation (±15°), horizontal flipping, zooming (up to 10%), and brightness adjustment (factor range 0.9-1.1).3.3

3.3. Model architecture: SABViT

The proposed model is based on the ViT-Base framework, which was initialized with weights pre-trained on the ImageNet-21k dataset and subsequently fine-tuned on our brain MRI dataset. This approach leverages transfer learning to overcome the challenges of training a transformer from scratch on a limited dataset. Unlike CNNs that rely on local receptive fields, ViT leverages self-attention mechanisms to capture both local and global dependencies within MRI scans.

The model architecture, depicted in Figure 2, consists of the following components:

i. Patch Embedding: Each preprocessed 224×224 MRI image is divided into 196 non-overlapping patches of size 16 × 16. These patches are linearly projected into 768-dimensional embedding vectors, forming the input sequence.

ii. Positional Encoding: Learnable positional encodings are added to the patch embeddings to retain the spatial information of each patch's original location.

iii. Transformer Encoder: A stack of 12 identical transformer encoder blocks is applied. Each block comprises Multi-Head Self-Attention (MHSA) with 12 heads, layer normalization, residual connections, and a feed-forward network. The self-attention operation, which enables the model to learn contextual relationships across patches, is computed using the following formula:

$$Attention\ (Q, K, V) = softmax\left(\frac{QK^T}{\sqrt{d_k}}\right) \quad ....(1)$$

iv. Classification Head: The output embedding corresponding to the [CLS] token is passed through a fully connected layer with a softmax activation function to classify the image into two categories: tumor or non-tumor.

Table 1. Experimental parameters and their values

Parameters	Value
Pre-trained model	ViT-Base/16*
Number of Attention Heads	12
Learning Rate	0.001
Batch Size	32
Number of Epoch	50
Optimizer	Adam
Number of transformer layers	12

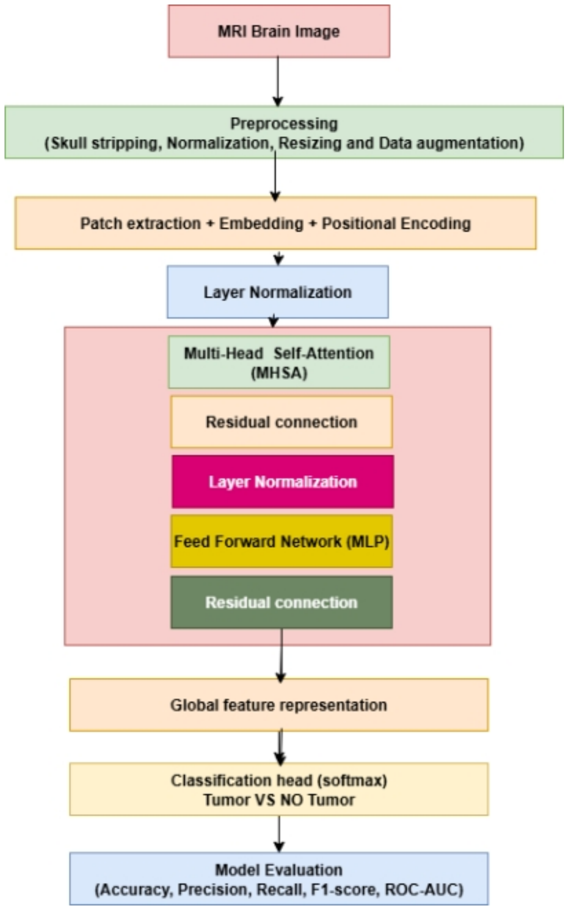

Figure 2. Architecture of the proposed system

3.4. Sample size justification

Considering the exploratory nature of this pilot study, a formal calculation for sample size was not conducted. Instead, the sample size of 3,000 images was established based on practical limitations and standard practices in initial deep learning research . This quantity is deemed adequate to yield preliminary estimates of model performance and to train a model without immediate indications of overfitting, thereby achieving the primary feasibility goal. It is important to recognize that this limited, single-center sample size is a key limitation of the pilot and that no statistical power was calculated for hypothesis testing, as the objective was to assess feasibility and inform the design of a larger, definitive study.

3.5. Feasibility metrics

Alongside standard performance metrics (Accuracy, Precision, etc.), we established the following feasibility metrics to inform the pilot evaluation:

i. Training Stability: Steady convergence of training and validation loss curves without significant divergence.

ii. Computational Efficiency: Total training duration and GPU memory consumption were tracked.

iii. Pipeline Robustness: Successful end-to-end execution of the complete workflow, from data loading and preprocessing to model training and evaluation.

4. RESULTS AND DISCUSSION

This section presents the preliminary results of the SABViT model on the pilot dataset and discusses their implications for the study's feasibility objectives.

4.1. Initial performance results

The optimized SABViT model underwent evaluation using a separate test set comprising 600 images. To validate the reliability of these preliminary results, five-fold cross-validation was conducted on the training dataset. The model exhibited high performnce, attaining a test accuracy of 99.73% and a stable cross-validation accuracy of 99.71% (±0.03%). A comprehensive summary of the performance metrics can be found in Table 2.

Table 2. Preliminary classification performance of the SABViT model on the brain MRI pilot dataset

Metric	Value (%)
Accuracy	99.73
Precision	98.3
Recall	97.3
F1-Score	99.23

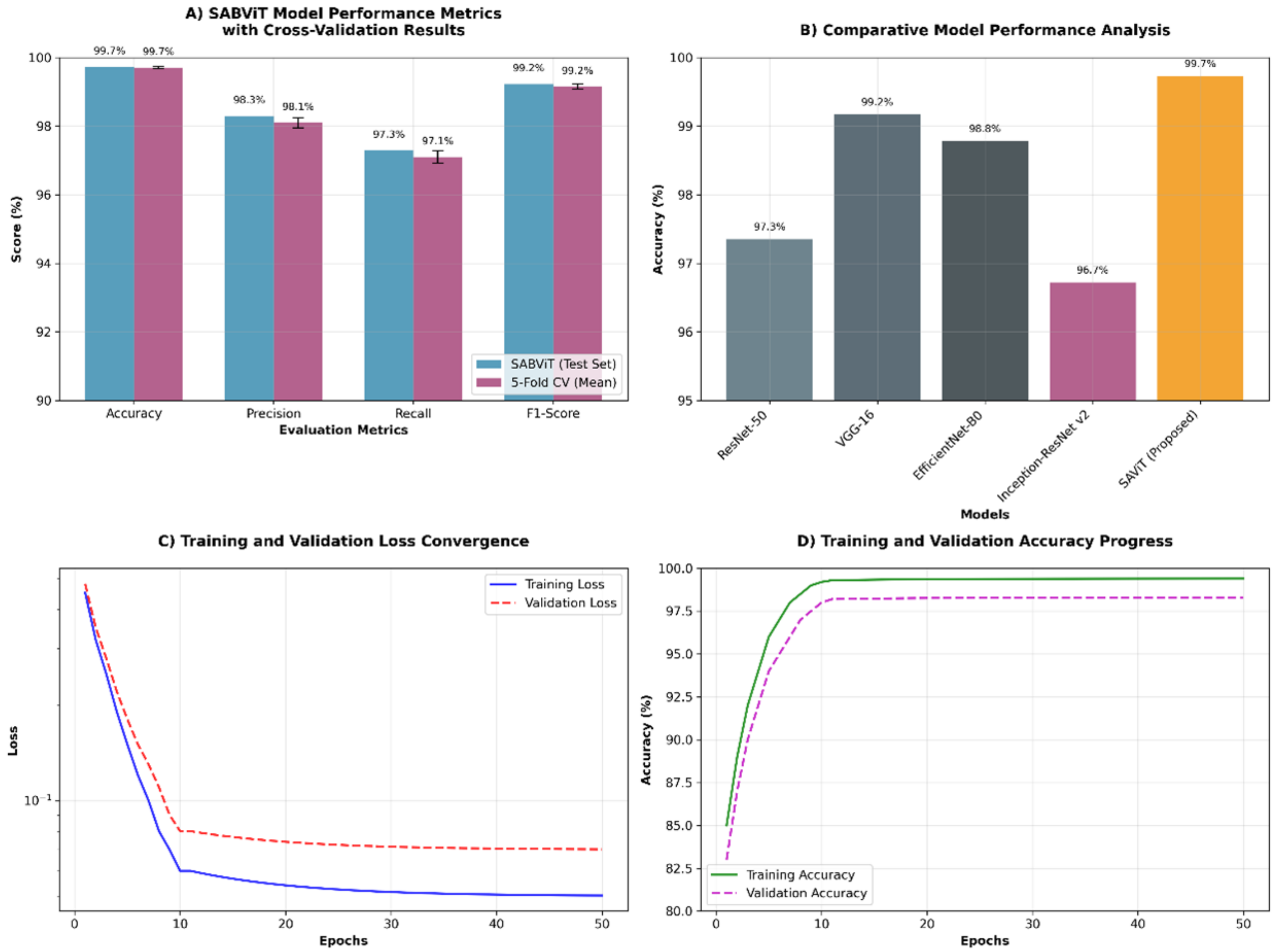

Figure 3. Comprehensive performance evaluation of the SABViT Framework

The training dynamics, as depicted in Figure 3, demonstrated stable convergence with no notable divergence between the training and validation curves. This suggests that the data preprocessing and augmentation pipeline effectively reduced overfitting, which is a significant concern when fine-tuning a large model on a limited dataset. This achievement successfully fulfills our initial pilot objective regarding the viability of the technical pipeline.

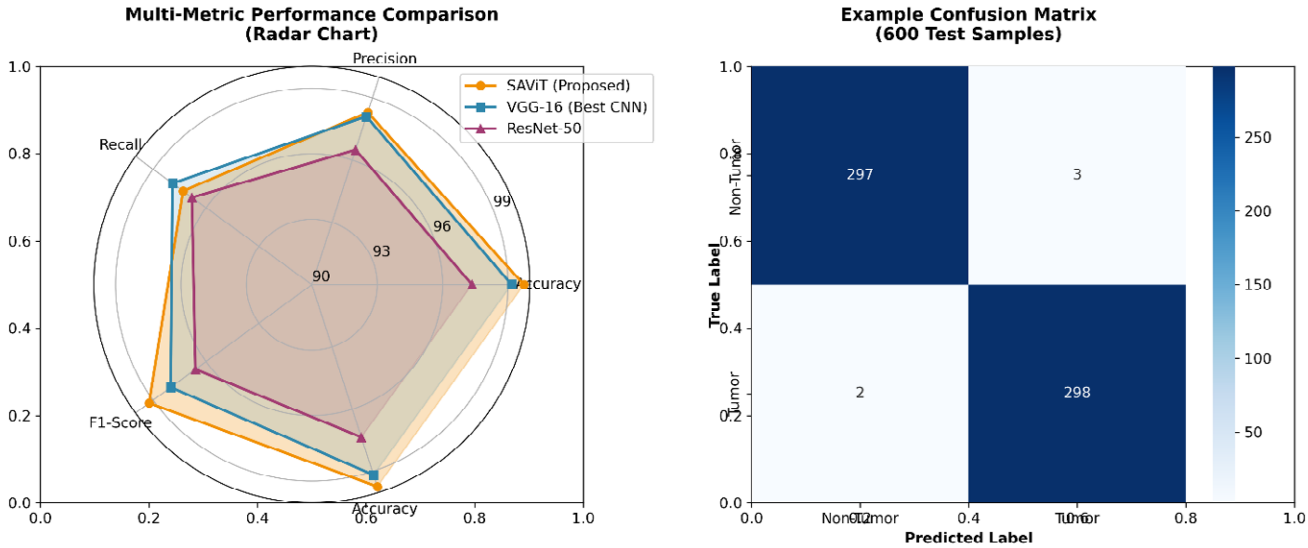

Figure 4. Dimensional performance analysis and classification results (Left) Radar chart comparing SABViT against best-performing CNN benchmarks across all evaluation metrics, (Right) Confusion matrix showing binary classification performance on the test dataset (n = 600 samples).

4.2. Preliminary comparative analysis

In order to contextualize the performance of the SABViT model, a comparative analysis was performed against several well-established CNN architectures. All models underwent training and evaluation under the same conditions on our pilot dataset. The results, which are detailed in Table 3, indicate that the proposed SABViT model surpassed all CNN benchmarks across essential metrics.

Table 3. Preliminary comparative performance of baseline models versus the proposed SABViT model

Model	Accuracy	Precision	Recall	F1-Score
ResNet-50	97.35%	96.5%	96.8%	96.6%
VGG-16	99.17%	98.1%	97.9%	98.0%
EfficientNet-B0	98.78%	97.8%	98.2%	98.0%
Inception-ResNet v2	96.72%	95.9%	96.0%	95.9%
SAViT (Proposed)	99.73%	98.3%	97.3%	99.23%

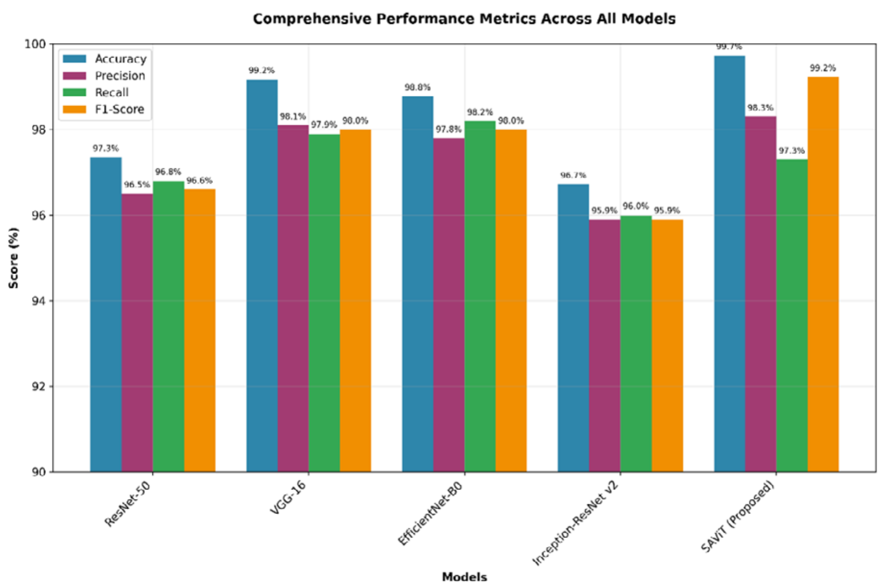

Figure 5. Comparative Analysis of Architectural Performance Across Metrics

The exceptional performance of the SABViT model offers initial evidence that the self-attention mechanism's capacity to capture global contextual information may provide an edge over the locally focused processing of CNNs for this particular task. This aligns with emerging findings in other medical imaging fields where transformers have demonstrated potential in modeling long-range dependencies in anatomical structures. This comparative analysis meets our third pilot objective of collecting preliminary benchmarking data.

4.3. Discussion of feasibility findings

The main outcome of this pilot study is the successful demonstration of feasibility. While the high performance metrics are encouraging, they should be viewed as initial evidence of efficacy rather than conclusive proof of clinical utility. The significant finding is that a standard ViT architecture, pre-trained on natural images, can be effectively adapted to a binary medical image classification task with a limited dataset. The model's performance, especially its high precision and recall, indicates that it has learned meaningful representations for differentiating between tumorous and non-tumorous tissues. The success of the transfer learning approach confirms a practical strategy for utilizing data-hungry transformer models in data-scarce medical domains. Additionally, the computational resources required, although considerable, were manageable for this pilot scale, establishing a baseline for planning larger studies.

These results strongly advocate for the decision to advance to a larger-scale investigation. The performance data from this pilot (e.g., the 99.7% accuracy and the effect size in comparison to CNNs) will be crucial for conducting formal sample size calculations for a definitive multi-institutional trial.

4.4. Feasibility and limitations

This pilot study effectively illustrated the overall feasibility of the proposed SABViT framework. The technical pipeline, encompassing data preprocessing through to model training, demonstrated robustness and execution capability. The model achieved stable convergence over 50 epochs, with training and validation accuracy curves closely aligned (Figure 3), suggesting that the selected data augmentation strategy was successful in reducing overfitting, even with the relatively small dataset. The impressive preliminary performance metrics indicate that the self-attention mechanism's capacity to capture global context provides a significant advantage for this task, potentially enabling the model to assimilate information from distant brain regions to enhance its classification, a feature often constrained in CNNs.

However, it is essential to recognize several critical limitations inherent to this pilot phase in order to contextualize the findings:

i. Limited generalizability: Utilizing a single-center, retrospective dataset introduces a significant risk of demographic and scanner-specific bias. Consequently, the model's efficacy may not be applicable to images obtained through different protocols or from varied patient populations. This represents the foremost challenge to the external validity of these initial findings.

ii. Pilot sample size: Although adequate for feasibility testing, the size of the dataset is insufficient for creating a clinically generalizable model. A more extensive, multi-institutional dataset is necessary to encompass the complete heterogeneity of brain tumors and imaging conditions.

iii. Simplified clinical task: The binary classification task, while beneficial for proof-of-concept, lacks direct clinical relevance. Radiologists need to distinguish between tumor types (e.g., glioma versus meningioma), which necessitate different treatment approaches. The model's effectiveness in this more intricate task is yet to be determined.

iv. Computational intensity: The ViT-Base model demanded significantly greater computational resources for fine-tuning in comparison to the CNN benchmarks. This practical challenge must be resolved for scalable implementation.

v. Absence of explainability: A significant barrier to clinical adoption is the "black-box" nature of deep learning models. This pilot study did not incorporate explainable AI (XAI) techniques to visualize the basis for the model's decisions, which is crucial for building trust with clinicians.

vi. Failure analysis: A critical component of a pilot feasibility study is to understand the model's failure modes. An analysis of the confusion matrix (Figure 4, Right) reveals that the model misclassified a very small number of cases. A qualitative review of these errors indicated that the false positives and negatives were not associated with a specific tumor subtype or a consistent imaging artifact. Instead, the errors appeared to be isolated instances where the tumor presence was extremely subtle or where the image quality was at the lower end of the acceptability spectrum. The absence of a clear pattern in these misclassifications, while encouraging, underscores the limitation of the current dataset's size and diversity. It highlights that a larger, more heterogeneous dataset is required to properly stress-test the model and identify systematic weaknesses, a key objective for the subsequent large-scale study.

5. CONCLUSION

This pilot study successfully fulfilled its primary objective of evaluating the feasibility of a SABViT for detecting brain tumors in MRI images.

The research illustrated that the proposed framework can be effectively executed, supported by a robust data preprocessing and augmentation pipeline that facilitated stable model training without succumbing to overfitting on a limited pilot dataset.

The initial results are extremely promising, suggesting that the SABViT model can attain a high degree of accuracy and surpass several conventional CNN-based benchmarks. This indicates that the global contextual processing abilities of transformers possess considerable potential for tasks involving medical image analysis.

Most importantly, this study has pinpointed clear and specific avenues for future research, primarily regarding dataset scale, model explainability, and the complexity of clinical tasks.

The limitations noted, including the reliance on a single-center data source and the binary classification task, should not be viewed as deficiencies but rather as valuable insights from this pilot phase. They offer a critical, evidence-based foundation for planning a subsequent, more extensive study.

Consequently, this pilot work concludes that further investment in the development and validation of transformer-based models for brain tumor classification is not only feasible but also highly justified. The next phase will involve conducting a large-scale, multi-institutional study aimed at multi-class tumor classification, incorporating integrated explainable AI components to bridge the divide between technical performance and clinical adoption.

FUTURE WORK

The encouraging outcomes and insights gained from this pilot study provide a direct foundation for future research endeavors. The subsequent phase will involve a large-scale, definitive study aimed at addressing the limitations previously identified.

i. Multi-institutional data collection: We will commence partnerships with various national and international medical institutions to compile a more extensive dataset (>15,000 images) that includes multiple tumor types (gliomas, meningiomas, pituitary tumors) and a variety of imaging protocols. This initiative will strengthen the model's robustness and generalizability.

ii. Advanced architecture for clinical utility: Building upon the feasibility demonstrated by the ViT approach, we will create and train a multi-class classification model. Additionally, we will investigate more efficient hierarchical transformers, such as the Swin Transformer, which are more appropriate for high-resolution medical images and help to minimize computational demands.

iii. Integration of XAI: A fundamental aspect of the upcoming study will be the incorporation of XAI methodologies, including Layer-wise Relevance Propagation (LRP) or attention visualization techniques, to produce saliency maps. This will enable clinicians to identify the specific regions of the MRI that the model utilized for its decision-making, thereby promoting transparency and trust.

iv. Prospective clinical validation: The primary objective is to validate the enhanced model through a prospective clinical trial. This will entail implementing the model in a real-world radiology reading environment to assess its influence on diagnostic accuracy, turnaround time, and inter-rater variability in comparison to standard clinical practices.

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