Multi-Class Brain Tumor Diagnosis Using a Vision Transformer with MRI Image Segmentation

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ABSTRACT

Over the last decade, brain tumors have emerged as a significant and potentially fatal medical issue. Traditional methods for detecting and classifying brain tumors using Magnetic Resonance Imaging (MRI) scans are often time-consuming and prone to inaccuracies, necessitating a precise classification method for brain tumors, effective diagnosis, and therapy planning. This study proposes the use of a Vision Transformer (ViT) model to classify brain tumors from the Brain Tumor MRI dataset available on Kaggle into four categories: no-tumor, meningioma, pituitary tumor, and glioma. Unlike conventional Convolutional Neural Networks (CNNs), the proposed ViT model leverages self-attention mechanisms, making it particularly effective for capturing global relationships and extracting complex features from medical images. The model processes images by dividing them into fixed-size patches, which are then linearly embedded and passed through a positional encoding layer. These encoded representations are input into the transformer's encoding layers, and the final classification is produced through a fully connected output layer. The performance of the ViT model is evaluated using standard multi-class classification metrics. The model achieved an impressive average accuracy of 99.3%, outperforming all other Deep Learning (DL) models previously tested on this benchmark dataset. The ViT model's auto-focusing capability enables it to capture both fine-grained and large-scale features, significantly improving the accuracy and reliability of brain tumor detection.

Keywords-brain tumor; Vision Transformers (ViT); CNN; Magnetic Resonance Imaging (MRI) images; multi-class classification; self-attention

I. INTRODUCTION

The brain is a vital organ that regulates all human behavior. Various biological factors can impair its functioning, leading to serious health risks and, in some cases, loss of life. Among such conditions, brain tumors are particularly life-threatening due to their complexity and potential impact on surrounding neural tissues. A brain tumor is characterized by the abnormal growth of cells within the brain, disrupting its normal function. Tumors are broadly classified into benign (non-cancerous) and malignant (cancerous) types, with their severity determined by location, size, and growth rate [1, 2]. Timely and precise diagnosis is essential for effective treatment planning [3]. Symptoms can be generalized (e.g., increased intracranial pressure) or focal (e.g., speech or motor impairment), depending on the tumor's type and location [4]. Although brain cancer is less common than other cancers, its complexity and treatment difficulty make it more dangerous [5]. Common types include:

- Meningiomas: Usually benign, originating from the brain's protective membranes [6].
- Gliomas: Originate from glial cells and include both brain and spinal cord cancers. High-grade gliomas, such as Glioblastoma Multiforme (GBM), are aggressive and hard to treat [7].
- Pituitary tumors: Typically non-cancerous, forming in the pituitary gland and not spreading to other parts of the body [8].

The traditional method for brain tumor diagnosis and treatment planning requires the Magnetic Resonance Imaging

(MRI). MRI images provide a high-resolution, non-invasive imaging with excellent soft tissue contrast [9, 10], allowing clinicians to assess tumor size, shape, and location without exposing patients to ionizing radiation [11]. They also support multiclass tumor classification beyond the binary determination of tumor presence; however, interpretation demands significant time and expertise from radiologists [12]. In order to reduce the time needed and to minimize bias errors, several computational methods have been implemented for brain tumor diagnosis and classification.

Traditional Machine Learning (ML) models such as K-Nearest Neighbors (KNN) and Support Vector Classifiers (SVC) have been applied to MRI-based brain tumor classification, but often fall short in accuracy [13]. More recently, Convolutional Neural Networks (CNNs) have shown superior performance in medical imaging tasks [14, 15], but they struggle with capturing global context and long-range dependencies in images, despite their excellence at extracting local features (edges, textures). Other CNN limitations include high computational requirements, long training times, and potential overfitting with smaller datasets. To address these issues, transfer learning techniques are commonly used. Pre-trained models are fine-tuned on MRI datasets, leveraging knowledge from large-scale image databases [16]. Feature extraction and fine-tuning allow CNNs to adapt effectively to new domains; however, overfitting may still occur, especially when datasets are small or task domains differ significantly.

To overcome CNN limitations, Vision Transformers (ViTs) have been introduced in medical imaging. Initially developed for Natural Language Processing (NLP), transformers were adapted to image tasks due to their global attention mechanism [17]. ViTs divide input images into patches, encode them with position embeddings, and process them via self-attention layers to learn both local and global features effectively. This makes ViTs ideal for image classification, object detection, and segmentation. In brain tumor detection, ViTs have shown promising results due to their ability to model complex spatial relationships and reduce overfitting [18].

Research on brain tumor classification has progressively advanced from binary classification (tumor vs. non-tumor) to multiclass classification (e.g., glioma, meningioma, pituitary tumor). Early investigations focused on textual data and traditional feature-based ML methods. Over time, medical imaging data, particularly MRI scans, became central to these studies, leveraging the strength of ML and DL algorithms for enhanced predictive accuracy. Initial classification efforts applied algorithms like Support Vector Machines (SVM) and Random Forest (RF) to MRI images for binary classification [19, 20]. These methods learned decision boundaries from extracted features but often lacked the capability to capture complex image patterns inherent in medical scans. While effective for basic classification, these models generally underperformed on multiclass tasks or when applied to noisy or limited datasets. For example, authors in [21] achieved high accuracy on a small dataset of 253 images, but the limited sample size raises concerns about generalizability. Authors in [22] addressed issues of overfitting and underfitting by proposing a deep encoder architecture tailored for tumor identification. Similarly, authors in [23] emphasized early-stage tumor detection, achieving 92.3% accuracy, with a focus on continuous model updates and symptom-based learning. Authors in [24] proposed a CNN-based grading system for gliomas using both whole-brain and tumor-region-focused approaches. While achieving 92% accuracy, the model lacked external validation and was potentially affected by noise from irrelevant regions. Authors in [25] used SVMs with hand-engineered features such as shape and texture, achieving only 70% accuracy due to the lack of tumor segmentation and poor performance on large datasets. On the other hand, authors in [26] combined CNNs with data augmentation to classify multi-grade tumors with 94% accuracy. However, high computational demand and segmentation errors posed limitations.

To exploit volumetric data, authors in [27] introduced a 3D CNN model using T1-Gado MRI sequences. This approach, designed for glioma classification, achieved 96.4% accuracy, outperforming 2D CNNs but requiring substantial computational resources. Authors in [28] developed a segmentation system for identifying tumor slices across volumetric scans, achieving 89% accuracy. However, the lack of Deep Learning (DL)-based segmentation and reliance on small datasets limited broader applicability. Authors in [29] improved ResNet50 by modifying its architecture, achieving 97.2% accuracy on MRI tumor classification tasks. Although effective, the model faced overfitting risks due to limited data and required substantial training data for reliable performance. Authors in [30] applied the AlexNet architecture for binary and multi-grade tumor classification, reaching 91.6% accuracy. However, the model lacked pixel-level classification and comparative analysis with other architectures. Authors in [31] compared AlexNet and GoogleNet for glioma grading using rectangular ROIs. GoogleNet, trained from scratch, achieved 93.9% accuracy. Despite promising results, the study used only 113 patient cases, increasing overfitting risk and limiting tumor localization capabilities. Authors in [32] adopted fuzzy cognitive maps for grade classification using 100 clinical cases. The approach achieved 90.2% and 93.2% accuracy for low- and high-grade tumors, respectively, but lacked integration with modern DL frameworks. Authors in [33] proposed a CNN-Genetic Algorithm (GA)-based framework achieving 90.9% accuracy for glioma grading and 94.2% for classifying three tumor types. The model demonstrated potential but required further validation on diverse datasets.

Recent advancements have made it possible to automatically identify brain tumors using 3D medical imaging techniques. Studies employing the BraTS 2018 dataset have demonstrated competitive segmentation accuracy, supporting the effectiveness of ML and DL models, particularly CNNs, for brain tumor detection [34]. A comparative study in [35] focused on CNNs for identifying and classifying brain tumors using MRI data. Their research compared several architectures, including ResNet-50, VGG16, and Inception V3, and proposed a CNN model that achieved 93.3% accuracy for early tumor detection, underscoring its utility in clinical settings [36]. Authors in [37] explored classification techniques across multiple tumor types, including meningioma, pituitary, and glioma, as well as normal brain images. They developed and

trained a 2D CNN and a convolutional autoencoder, evaluating the performance of various algorithms. Among them, KNN achieved the highest accuracy, while the Multilayer Perceptron (MLP) exhibited the lowest. These results reinforce the superior performance and reliability of CNN-based models for brain tumor classification. Lastly, authors in [38] investigated the use of ensemble learning models and ViT in the categorization and identification of brain tumors from MRI images. Additional information for several of the abovementioned studies is listed in Table I.

In this work, we propose a ViT model for brain tumor detection and classification using MRI scans across four categories: glioma, meningioma, pituitary tumor, and no tumor. The model is trained and evaluated on the publicly available Brain Tumor MRI dataset from Kaggle. Unlike conventional CNNs, the proposed ViT architecture leverages self-attention mechanisms to effectively capture global contextual relationships and extract complex features from medical images [39]. The proposed model achieved a high average accuracy of 99%, outperforming all previously tested DL models on this dataset.

II. PROPOSED FRAMEWORK

A. Dataset

The dataset used in this study is the Brain Tumor MRI dataset obtained from the Kaggle repository [40]. It consists of MRI images categorized into four classes: glioma, meningioma, pituitary tumor, and no tumor. The dataset is organized with pre-defined training and testing folders, facilitating straightforward model development and evaluation. It encompasses a diverse range of images with variations in intensity, tumor size, and anatomical location, thereby supporting robust and generalized model training. Initially, the training set included 1,321 glioma, 1,339 meningioma, 1,457 pituitary tumor, and 1,595 no-tumor images, while the test set comprised 300, 306, 300, and 405 images for the same categories, respectively. To address class imbalance and prevent overfitting or underfitting, the training data was balanced to include 1,600 images per class. This number was selected based on the largest class in the test set (405 images), maintaining an approximately 80:20 ratio between training and testing samples to ensure consistent and reliable performance evaluation.

B. Preprocessing Steps

Preprocessing MRI images is an important step before training a DL model, as it significantly enhances image quality and improves classification accuracy. The initial step involves resizing all images to a uniform dimension of 224 × 224 pixels. Since MRI scans often come in varying resolutions, standardizing their size ensures consistent input to the model, enabling the neural network to process the images efficiently. To improve the model's generalization capability, data augmentation techniques were applied. These augmentations introduce controlled variations in the training data without requiring additional images. Specifically, Random Horizontal Flip was used to flip images horizontally with a predefined probability, introducing mirror-image diversity, while Random Rotation was applied to rotate images within a range of ±10 degrees, helping the model become more robust to orientation differences. The images are then loaded into a DataLoader, which is used to handle batching and shuffling for efficient training.

TABLE I. OVERVIEW OF RELATED WORK

Ref.	Objectives	Methods used	Results
[19]	Classifying brain tumors using ML algorithms based on MRI images.	KNN, RF, SVM	Achieved an accuracy of 90%.
[20]	Evaluating and comparing the performance of multiple ML algorithms.	SVM, decision tree, RF, Naïve Bayes.	SVM outperformed other models.
[21	Classifying brain tumors using DL algorithms based on MRI images	CNN, VGG-16, ResNet-50, Inception-v3.	CNN achieved the highest accuracy among the models.
[22]	Developed a DL model using spectral augmentation for tumor identification.	Deep autoencoder	Achieved 97% accuracy.
[23]	Explored DL approaches for early detection of brain tumors using medical images.	CNN, Transfer Learning, SVM, RF	CNN demonstrated an accuracy of 92.3%.
[25]	Improving accuracy using data augmentation and DL.	CNN	Achieved 95.58% accuracy.
[27]	Developing a fully automatic 3D CNN for glioma tumor classification.	3D CNN applied on BraTS 2018 benchmark dataset	Achieved 96.49% accuracy.
[28]	Developed an automated method for tumor identification.	Feature extraction using Modified Gray-level Co-occurrence Matrix (MGLCM); feature selection using Analysis of Variance (ANOVA)	Achieved 89% ± 4.7% segmentation accuracy compared to manual segmentation.
[35]	Designed an automated system for brain tumor detection using DL and ML algorithms.	CNN compared with traditional ML methods.	Achieved 92.86% accuracy.
[36]	Developed a DL model for brain tumor detection and classification.	CNN, ResNet, VGG-16, Inception-v3	CNN achieved the best performance with 93.3% accuracy.
[37]	Compared DL models with ML models for tumor detection.	2D CNN, Convolutional Autoencoder, MLP, KNN, etc.	2D CNN achieved the highest accuracy of 96.47%; Autoencoder achieved 95.63%; ML models achieved lower accuracies.

Following augmentation, all images are converted into tensors, as DL models operate on numerical data. This step involves scaling pixel values from the original [0, 255] range to [0, 1]. Subsequently, normalization is performed using a mean

and standard deviation of 0.5 for each channel, transforming pixel values into the range [-1, 1]. This normalization facilitates a more stable and faster training process.

Another key aspect of preprocessing is dataset balancing. MRI datasets often exhibit class imbalance, where certain tumor types are overrepresented compared to others. This imbalance can bias the model toward the majority class, degrading performance on minority classes. To mitigate this, data duplication is employed for underrepresented classes until all classes have a similar number of samples. This ensures that the model learns to classify all tumor types more equitably. Finally, the dataset is loaded using the ImageFolder utility, which applies all defined transformations during data loading. This comprehensive pre-processing pipeline ensures that the model is trained on high-quality, standardized, and balanced data, thereby improving its performance and accuracy in brain tumor detection and classification.

C. Classification

The architecture of the proposed framework is illustrated in Figure 1.

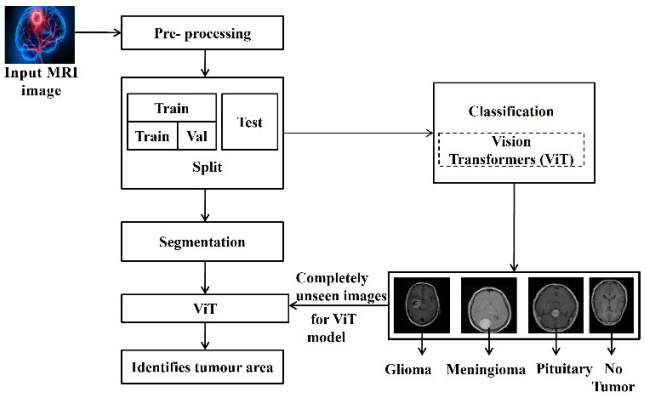


Fig. 1. Proposed framework for multi-classification of brain tumors.

This framework utilizes two distinct ViT models, both based on the same core architecture but trained with different parameter configurations and datasets. One model is dedicated to multi-class classification, while the other leverages ViT for a specialized task under a separate dataset.

A pre-trained ViT is loaded and fine-tuned to suit the specific number of output classes. For training, Cross-Entropy Loss is employed as the loss function, which is well-suited for multi-class classification tasks. The optimization is carried out using the Adam optimizer with a learning rate of 0.0001.

Following the training phase, the model is evaluated on the validation set to assess its classification performance. Key evaluation metrics such as precision, recall, and F1-score are calculated for each class using a confusion matrix and classification report. Upon completion of training, the model is saved for future deployment in automated brain tumor detection tasks. The complete workflow of the proposed model is depicted in Figure 2.

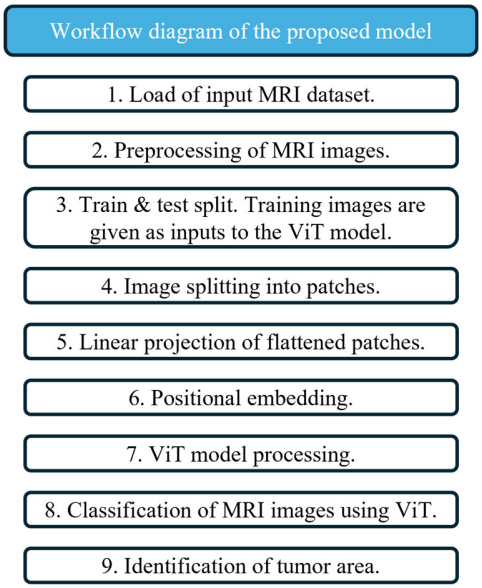


Fig. 2. Workflow of the proposed ViT model.

D. Vision Transformers (ViT)

In ViT, an input image is divided into fixed-size non-overlapping patches, each of which is flattened and projected into a high-dimensional embedding space using a linear transformation. This process is handled by the Patch Embedding Layer:

$$Z_0 = [Ex_1, Ex_2, \ldots, Ex_N] + E_{pos} \quad (1)$$

where x_i denotes the individual patch vectors, E is the linear projection, and E_{pos} is the positional embedding that provides spatial information to the model. This is necessary because, unlike CNNs, transformers are inherently permutation-invariant. The resulting sequence of patch embeddings is passed through a stack of transformer encoder layers, each consisting of: Multi-Head Self-Attention (MHSA), Layer Normalization (LN), Feed-Forward Networks (FFN), and skip connections. These layers work together to capture long-range dependencies and complex inter-patch relationships. Each patch embedding is transformed into query Q, key K, and value V matrices for the self-attention mechanism:

$$Attention\,(Q,K,V) = softmax\left(\frac{QK^T}{\sqrt{d_k}}\right)V \quad (2)$$

Multiple attention heads are concatenated and projected linearly:

$$SA\,(Z) = Concat\,(head_1, \ldots, head_h)W^O \quad (3)$$

where $head_i = Attention\,(Q_i, K_i, V_i)$. To ensure stable training, LN is applied, and skip connections are added to prevent vanishing gradients and support efficient gradient flow:

$$Z' = LN(Z + MSA(Z)) \quad (4)$$

$$Zout = LN(Z' + FFN(Z')) \quad (5)$$

The FFN in each transformer layer comprises two fully connected layers with a non-linearity in between:

$$FFN\ (Z) = W_2 \cdot \sigma(W_1 Z + b_1) + b_2 \quad (6)$$

Finally, for classification, a special [CLS] token is prepended to the patch sequence during input. This token gathers global information from all patches. After passing through the transformer encoder layers, the output corresponding to the CLS token is fed into the final classification head, which is a fully connected layer followed by a SoftMax activation:

$$y = softmax\left(W\, Z_{\{CLS\}} + b\right) \quad (7)$$

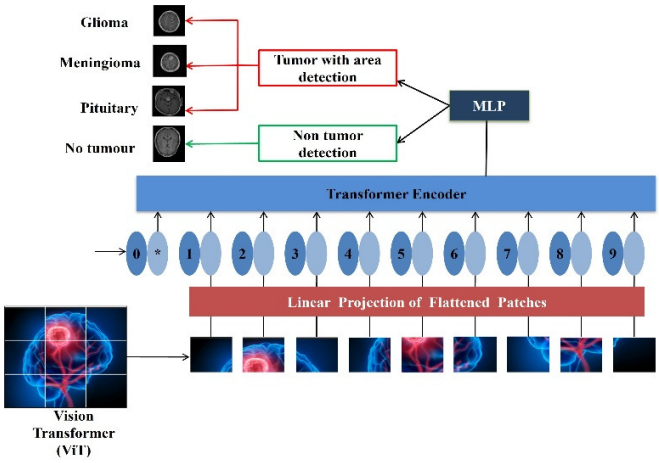


Fig. 3. ViT architecture for classifying brain tumors.

III. RESULTS AND DISCUSSION

A. Experimental Setup

The proposed model was trained and evaluated using PyTorch and relevant Python libraries within a Kaggle notebook environment, utilizing dual NVIDIA T4 GPUs.

A ViT-based model previously trained on the Br35H-Mask-RCNN dataset [41] was employed for tumor segmentation. This model, developed and published in our earlier work [42], was loaded to identify tumor regions in the MRI scans.

B. Model Evaluation

The performance of the proposed model was assessed using standard classification metrics to evaluate its ability to distinguish among four classes: glioma, meningioma, pituitary tumor, and no tumor. Precision, which indicates the proportion of correctly predicted positive cases among all predicted positives, is defined as:

$$Precision = \frac{TP}{TP+FP} \quad (8)$$

Recall, also known as sensitivity or the true positive rate, measures the proportion of actual positives correctly identified:

$$Recall = \frac{TP}{TP + FN} \quad (9)$$

The F1-score, the harmonic mean of precision and recall, provides a balanced metric that reflects both aspects of performance:

$$F1 - score = 2 \cdot \frac{Precision \cdot Recall}{Precision + Recall} \quad (10)$$

Overall model accuracy, reflecting the proportion of correct predictions among all instances, is computed as:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (11)$$

Table II summarizes the classification performance of the proposed ViT model. The model for glioma cases achieved a precision of 0.996, indicating a low false positive rate, and a recall of 0.973, suggesting that most true cases were correctly identified. For meningioma cases, it showed well-balanced performance with a precision of 0.962 and a recall of 0.993. The pituitary class had the lowest recall of 0.983 and a precision of 0.993. The no-tumor class achieved the highest F1-score of 0.997, reflecting nearly perfect classification. Overall, the model achieved a final accuracy of 99.3%, demonstrating its robustness in classifying all tumor categories.

TABLE II. METRICS-BASED PERFORMANCE ANALYSIS OF THE PROPOSED MODEL

Category	Precision	Recall	F1- Score	Accuracy
Glioma	99.6%	97.3%	98.4%	99.3%
Meningioma	96.2%	99.3%	97.7%	98.9%
Pituitary	99.3%	98.3%	98.8%	99.4%
No-tumor	99.7%	99.7%	99.7%	99.8%

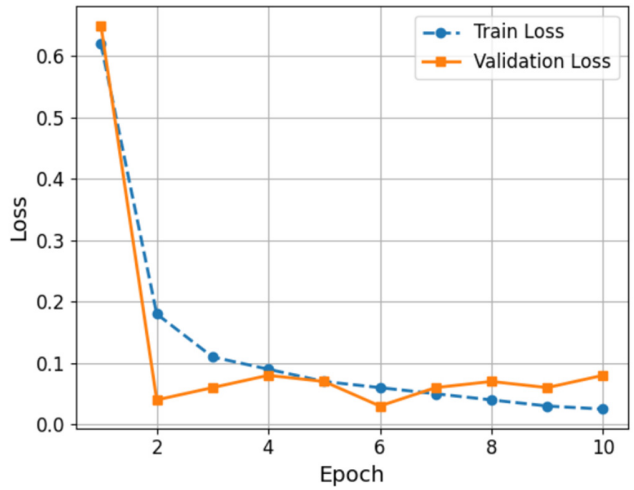
Figure 4(a) illustrates the glioma classification training and validation loss over 10 epochs. The training loss decreased from 0.65 to 0.03, indicating effective model convergence. The validation loss also dropped from 0.65 to 0.08, confirming reduced overfitting. Figure 4(b) shows the corresponding accuracy curves, where training accuracy reached 0.99 and validation accuracy 0.97 by the final epoch.

Figure 5(a) shows the meningioma classification training and validation loss. Training loss decreased from 0.65 to 0.02, and validation loss from 0.62 to 0.03, demonstrating excellent generalization. As shown in Figure 5(b), the training and validation accuracies reached 0.98 and 0.99, respectively.

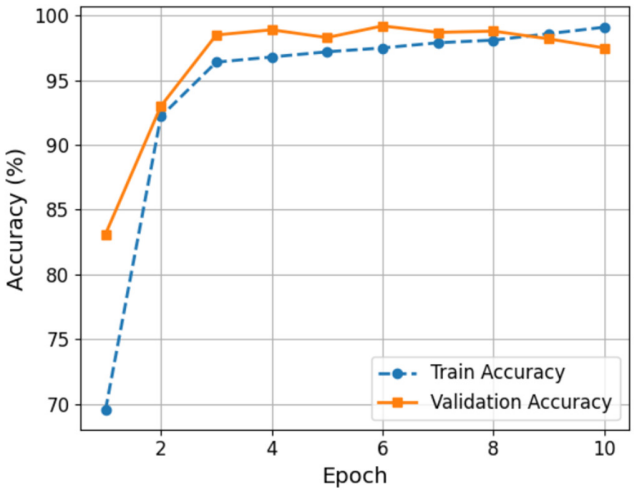
Figure 6(a) presents the pituitary tumor classification training and validation loss trends. Training loss declined from 0.66 to 0.03, while validation loss began at 0.04, briefly increased near epoch 5, then reduced again to 0.03 by the end, indicating stable performance. Figure 6(b) shows that training and validation accuracies increased to 0.98 and 0.97, respectively.

Figure 7 displays the confusion matrix of the ViT model. The Y-axis represents the true labels, while the X-axis shows the predicted labels. Diagonal elements indicate correct predictions, and off-diagonal elements represent misclassifications. The matrix shows high classification accuracy across all classes, indicating the model's strong ability to differentiate between tumor types.

Table III compares the performance of the proposed ViT model with other established classification models.

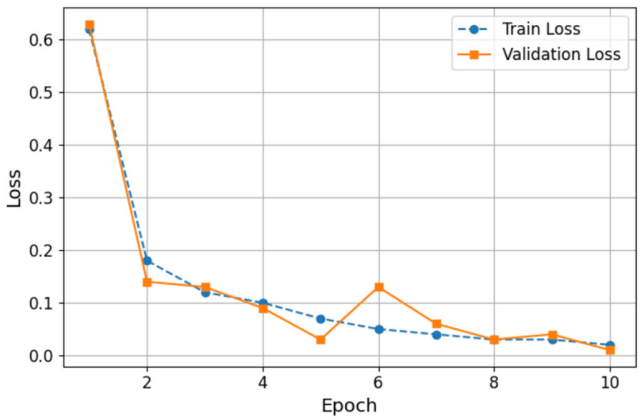


(a)

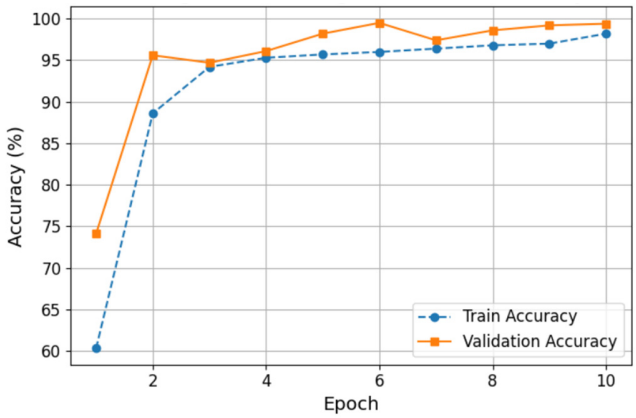


(b)

Fig. 4. Glioma training and validation (a) loss, and (b) accuracy.

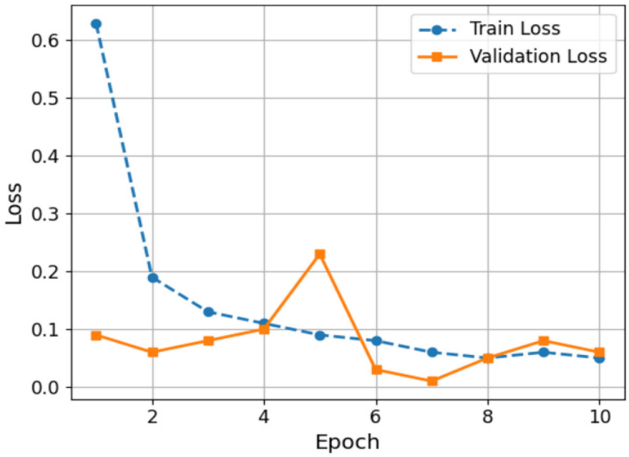


(a)

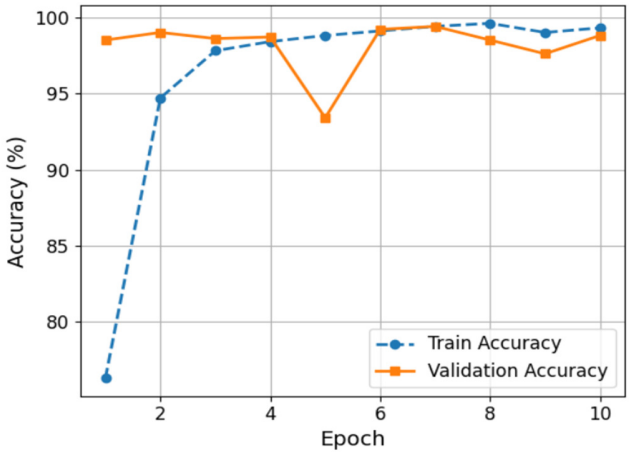


(b)

Fig. 5. Meningioma classification training and validation (a) loss and (b) accuracy.



(a)



(b)

Fig. 6. Pituitary tumor classification training and validation (a) loss and (b) accuracy.

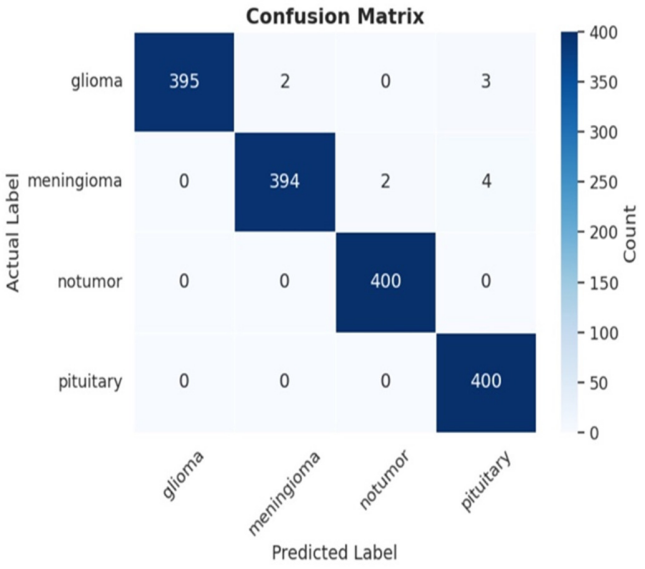


Fig. 7. ViT model confusion matrix.

The SVM in [25] achieved 70% accuracy, while GoogleNet in [31] improved this to 86%. AlexNet in [29] further increased accuracy to 91.6%. Other models, including CNN [24], ResNet101 [43], KNN [44], Deep Neural Network (DNN) [43], and ResNet50 [29], achieved accuracies of 92%, 93%, 96%, 96.9%, and 97%, respectively. The proposed ViT model outperformed all others, achieving a superior accuracy of 99.3%.

TABLE III. COMPARATIVE SUMMARY OF DIFFERENT CLASSIFIERS

Model Name	Accuracy
CNN [24]	92%
SVM [25]	70%
AlexNet [29]	91.6%
ResNet50 [29]	97%
GoogleNet [31]	86%
DNN [43]	96.9%
ResNet101 [43]	93%
KNN [44]	96%
Proposed ViT model	99.3%

IV. CONCLUSION

This study presents a Vision Transformer (ViT)-based model for the detection and classification of various brain tumor types (glioma, meningioma, pituitary tumor, and no tumor) in Magnetic Resonance Imaging (MRI) scans. The proposed approach divides input images into smaller patches and leverages attention mechanisms to capture both local features and global context. This enables the model not only to classify tumor types but also to accurately localize the affected regions within the scans, providing clinicians with a comprehensive diagnostic tool.

Experimental results show that the proposed model achieved an overall classification accuracy of 99.3%. Class-wise evaluation metrics, including precision, recall, F1-score, and accuracy, exceeded 96%, with many metrics surpassing 99%. When compared to other established classification models, the ViT-based approach demonstrated superior performance, establishing it as a highly competitive solution for brain tumor diagnosis.

Future work should include validating the model in real-world clinical settings to assess its effectiveness on patient data. Additionally, exploring semi-supervised or self-supervised learning techniques may improve its performance on limited or weakly labeled datasets. Integrating additional imaging modalities could further enhance diagnostic capabilities.

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