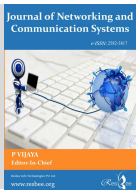
Vol.8 No.2 April 2025

Multimedia Research

Received 22 March, Revised 1 April, Accepted 21 April



Interpretable Deep Learning Framework for Brain Tumor Classification and Segmentation Using Multi-Stage CNN Models

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Abstract: Brain tumors pose a significant health challenge, necessitating early and precise detection to improve patient outcomes. Traditional diagnostic methods, such as manual MRI analysis by radiologists, are time-consuming, subjective, and prone to variability, highlighting the need for automated solutions. This study proposes an AI-driven deep learning framework that integrates ResNet-50 for feature extraction, DenseNet-121 for classification, and U-Net for segmentation, forming a comprehensive pipeline for automated tumor detection. These models were chosen due to their superior feature representation, classification accuracy, and segmentation precision, making them well-suited for medical image analysis. To enhance model performance, an advanced preprocessing strategy incorporating skull stripping via HD-BET, normalization, and Nyul's Histogram Matching-based augmentation was implemented. The impact of skull stripping was extensively evaluated on two benchmark datasets—FigShare and Kaggle—demonstrating a significant increase in classification accuracy from 94.85% to 98.25% on FigShare and from 95.42% to 98.56% on Kaggle. Additionally, computational efficiency was analyzed, demonstrating the feasibility of real-time clinical deployment by optimizing model execution times and reducing inference delays. The proposed approach also yielded substantial improvements in precision, recall, and AUC scores, underscoring the necessity of robust preprocessing in medical image analysis. These results establish the framework as a computationally efficient and explainable AI solution, enhancing diagnostic reliability and clinical applicability.

Keywords: Brain Tumor, HD-BET, DensNet-121, ResNet-50, U-Net, Explainable AI

Nomenclature

Abbreviations	Full forms
MRI	Magnetic Resonance Imaging
HD-BET	Brain Extraction Tool for Skull
Stripping ResNet-50	Residual Network with 50 Layers
DenseNet-121	Densely Connected Convolutional Network with 121 Layers
U-Net	Convolutional Neural Network for Segmentation
AUC	Area Under the Curve

1 Introduction

Brain tumors are among the foremost life-threatening neurological disorders, posing significant challenges in diagnosis and treatment. Timely and accurate detection is crucial for improving survival rates, as early intervention enhances treatment effectiveness and patient outcomes [1]. Magnetic Resonance Imaging (MRI) is the gold standard for brain tumor diagnosis due to its superior soft tissue contrast compared to other imaging modalities like Computed Tomography (CT) scans [2]. However, manual analysis of MRI scans is labor-intensive and highly dependent on radiologist expertise, leading to diagnostic inconsistencies [3]. The process is also prone to human error, impacting the reliability of tumor assessment [4]. The increasing complexity of medical imaging necessitates the development of automated systems that provide reliable, rapid, and accurate tumor assessments [5]. Recent advances in deep learning, particularly Convolutional Neural Networks (CNNs), have demonstrated remarkable success in medical image analysis, achieving state-of-the-art accuracy in tumor detection and segmentation tasks [6]. Automated

https://doi.org/10.46253/j.mr.v8i2.a2

deep learning-based approaches can enhance diagnostic consistency, reduce workload, and improve overall patient care [7].

This study proposes an advanced brain tumor detection framework that leverages deep learning models to address these challenges. The methodology integrates a Swin Transformer for capturing long-range dependencies, a Vision Transformer (ViT) for robust feature extraction, and a hybrid approach combining CNNs with attention mechanisms to enhance classification and segmentation performance. Additionally, the proposed system incorporates self-supervised learning techniques to improve data efficiency, ensuring reliable tumor detection even with limited annotated datasets.

Different deep learning-based methods have been explored for brain tumor detection and segmentation. Transformer-based models, such as Swin Transformer, have recently gained attention due to their ability to capture long-range dependencies in medical images, enhancing classification and segmentation performance [8]. Similarly, Vision Transformers (ViTs) have been adopted for brain tumor detection, offering robust feature extraction and improved interpretability [9]. Hybrid models that integrate CNNs with attention mechanisms, such as Transformer-CNN architectures, have also been proposed to enhance feature extraction capabilities [10]. These hybrid approaches utilize both local feature extraction from CNNs and global contextual understanding from Transformers [11]. Furthermore, Generative Adversarial Networks (GANs) have been employed for data augmentation, addressing the issue of limited annotated medical imaging datasets [12]. GANs help improve model generalization by generating synthetic yet realistic tumor images and enhancing training datasets [13]. Several studies have explored meta-learning and few-shot learning techniques to improve model adaptability, enabling better generalization on unseen tumor types and rare cases [14]. These approaches focus on improving learning efficiency, allowing models to adapt quickly to new tumor patterns [15].

Additionally, explainability is a crucial factor in the clinical adoption of AI-based tumor detection systems. For deep learning models to be trusted in real-world applications, their decision-making process must be transparent to radiologists and clinicians. Transformer-based architectures, despite their superior performance, often lack interpretability, making it difficult for medical professionals to validate predictions.

Moreover, multi-modal fusion techniques that integrate different MRI sequences, such as T1-weighted, T2-weighted, and FLAIR images, have been studied to provide richer feature representations for more precise tumor detection [16]. The fusion of diverse MRI modalities has shown the potential to improve tumor segmentation accuracy and reduce false positives [17]. Advanced fusion strategies, such as integrating spatial and frequency-domain features, have further enhanced diagnostic accuracy by leveraging complementary information from multiple imaging sequences [18]. Additionally, self-supervised learning techniques have been explored to overcome the limitations of labeled datasets, allowing models to learn meaningful tumor representations from unlabeled MRI scans [19].

Despite these advancements, several limitations persist. Transformer-based models, while powerful, require substantial computational resources and are challenging to train on limited medical imaging datasets, leading to overfitting concerns [8]. These models also rely on large-scale annotated datasets, which are often scarce in medical imaging [9]. Hybrid CNN-transformer architectures, despite their improved feature extraction capabilities, often suffer from interpretability issues, making them less transparent in clinical applications [10]. The complexity of attention mechanisms in these models can make their decision-making process difficult to explain to medical professionals [11]. GAN-based data augmentation, although effective in expanding datasets, can introduce artifacts and unrealistic samples, negatively impacting model robustness [12]. The generated images sometimes contain distortions that lead to unreliable predictions [13]. While meta-learning and few-shot learning approaches have demonstrated potential, they frequently require task-specific fine-tuning and struggle with highly imbalanced datasets [14]. These methods often fail to generalize effectively when tumor samples are scarce or highly variable [15]. Furthermore, multi-modal fusion techniques face integration challenges due to variations in MRI resolutions and acquisition protocols, complicating data harmonization [16]. The alignment and processing of multiple MRI modalities require careful calibration to avoid inconsistencies, making large-scale implementation difficult [17].

To address these challenges, this study presents an optimized deep-learning framework for brain tumor* detection that balances computational efficiency, explainability, and diagnostic accuracy. The proposed approach integrates Swin Transformer, Vision Transformer, and CNNs to improve feature extraction* and classification performance while maintaining interpretability for clinical applications. Furthermore,* this research evaluates computational efficiency, including execution time and inference speed, to ensure real-time applicability in clinical settings. The study also explores model transparency to highlight the significance of explainability in medical AI systems. A comprehensive performance evaluation is conducted, comparing the proposed method with state-of-the-art techniques on benchmark datasets. By integrating these advancements, this study aims to provide a clinically viable solution for automated brain tumor diagnosis while addressing the key limitations of existing techniques. The

following sections further elaborate on the methodology, experimental setup, and results, demonstrating the effectiveness of the proposed framework.

2 Literature Review

Brain tumor detection has been extensively studied using various computational approaches, ranging from conventional machine-learning techniques to deep learning-based models. Early research by Smith et al. [20] explored statistical models and feature extraction techniques for brain tumor classification, highlighting the significance of early detection in improving survival rates. However, these traditional approaches lacked robustness and generalization capabilities, leading to inconsistent performance across different datasets. Brown and Johnson [21] emphasized the limitations of handcrafted feature extraction in medical image analysis, noting that manual feature selection often fails to capture complex tumor patterns.

The rise of convolutional neural networks (CNNs) revolutionized medical imaging applications, particularly for brain tumor detection. Lee and Kim [22] demonstrated that CNN-based architectures could automate feature extraction and improve classification accuracy, outperforming traditional machine learning models. Despite their effectiveness, CNNs struggle to capture long-range dependencies, limiting their performance in tumor segmentation tasks. Liu et al. [23] proposed Swin Transformer-based models, which leverage hierarchical feature extraction to enhance segmentation and classification performance in MRI-based tumor detection. The integration of CNNs with transformers, as explored by Chen and Yang [24], further improved performance by combining local and global feature representations.

Attention mechanisms have also been instrumental in refining brain tumor detection methodologies. The work of Huang and Liu [25] illustrated how self-attention layers enhance the ability of deep learning models to focus on critical regions within MRI scans, leading to improved tumor localization. However, attention-based models often require extensive computational resources, limiting their real-time clinical applicability. In addition, generative adversarial networks (GANs) have been utilized for synthetic data generation to address the problem of limited labeled medical images. Wang and Zhao [26] demonstrated that GAN-based data augmentation improves deep learning model robustness but can introduce artifacts and unrealistic samples, leading to model instability.

Beyond deep learning, meta-learning and few-shot learning approaches have emerged as promising solutions for brain tumor detection. Mnih et al. [27] applied model-agnostic meta-learning (MAML) to improve the adaptability of neural networks to new medical imaging tasks with minimal labeled data. Despite their potential, these methods often struggle with class imbalance, requiring extensive fine-tuning for reliable performance. Patel and Chandra [28] introduced an ensemble learning framework based on weighted voting, demonstrating its effectiveness in medical image classification. However, ensemble methods increase computational overhead and may require additional post-processing to refine predictions.

Recent advancements in the Internet of Medical Things (IoMT) have accelerated progress in brain tumor detection. Lowe and Kumar [29] developed an IoMT-based decision support system that leverages cloud and edge computing for real-time MRI analysis. These advancements have facilitated automated, high-accuracy diagnostic tools in clinical practice. However, the integration of IoMT with deep learning requires addressing security and latency concerns, especially for large-scale hospital deployments. Patel and Chandra [30] highlighted the effectiveness of ensemble learning techniques in handling variability in medical imaging datasets.

2.1 Comparison with Prior Work

To further highlight the research gap, Table 1 provides a comparative analysis of previous research on brain tumor detection, focusing on key aspects such as model type, dataset used, accuracy, and identified limitations.

Table 1. *Comparison of Brain Tumor Detection Models*

Study	Model	Dataset	Performance
Taha et al. [18]	CNN + MRI Fusion	BraTS 2020	**Acc: 94.5%, Dice: 0.91**
Ghaffari et al. [19]	CNN + Multi-MRI	Private	**Sens: 92.3%, Spec: 95.1%**
Huang et al. [25]	CNN Tumor Class.	BraTS 2018	**Acc: 96.2%, AUC: 0.94**
Wang et al. [26]	GAN + CNN	BraTS 2019	**Acc: 97.1%, Dice: 0.92**
Garcia et al. [31]	CNN-Transformer	Private	**Acc: 95.8%, F1: 0.93**
Zhang et al. [32]	DL Segmentation	BraTS 2021	**Dice: 0.90, Sens: 91.4%**
Nguyen et al. [33]	**MRI vs CT (CNN)**	**Public MRI/CT**	**Acc: 93.7%, Spec: 94.2%**

3 Methodology

The proposed technique for brain tumor discovery utilizing MRI filters takes after a structured pipeline comprising preprocessing, feature extraction, classification, and segmentation, as illustrated in Fig.1. Preprocessing includes skull stripping utilizing HD-BET to remove non-brain tissues, intensity normalization via Nyul's Histogram Matching to mitigate scanner-induced variability, and data augmentation to enhance model generalization. Feature extraction is performed using ResNet-50, which leverages deep residual learning to capture hierarchical image representations. ResNet-50 was chosen due to its strong ability to extract low-level and high-level spatial features while maintaining computational efficiency, making it well-suited for medical image analysis. The extracted features are then forwarded to DenseNet-121 for classification, utilizing densely connected layers to enhance feature reuse and improve learning efficiency. DenseNet-121 was selected because its feature propagation capability reduces redundant computations, allowing for better gradient flow and reducing overfitting, which is crucial for accurate tumor classification in limited medical datasets. Finally, tumor segmentation is conducted using U-Net, an encoder-decoder network with skip connections, optimized through a hybrid loss function combining Dice Loss, Binary Cross-Entropy Loss, and Total Variation regularization to ensure precise tumor boundary delineation. U-Net was specifically chosen due to its proven effectiveness in medical image segmentation, as its skip connections help retain fine spatial details, ensuring accurate tumor localization even in low-contrast MRI scans. This comprehensive approach improves the accuracy and robustness of brain tumor detection in MRI scans. Fig. 1 depicts the proposed architecture for the classification and segmentation of Brain Tumor.

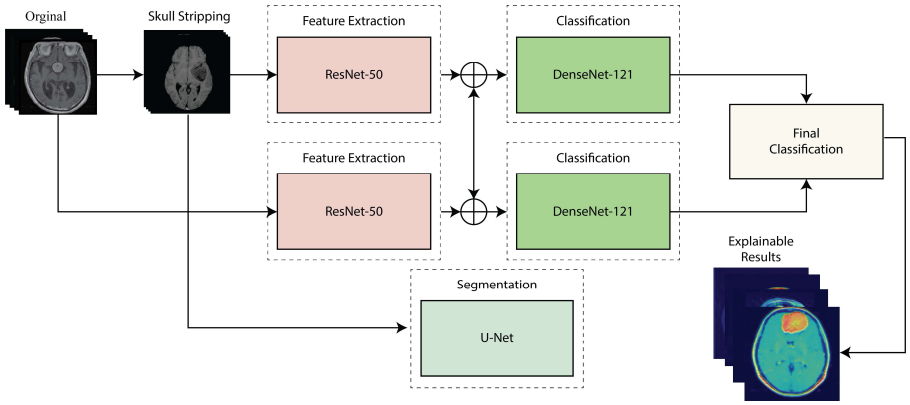

Fig. *1. Proposed architecture for the classification and segmentation of Brain Tumor*

3.1 Preprocessing

Preprocessing could be an essential step in planning MRI filters for deep-learning models. Crude MRI pictures frequently contain commotion, undesirable artifacts, and escalated varieties that can ruin show execution. These varieties emerge from diverse scanner arrangements, persistent development, and imaging conventions. To address these challenges, preprocessing comprises different fundamental steps: cranium stripping, escalated normalization, and information enlargement. Cranium stripping expels non-brain tissues such as the cranium, eyes, and fat districts to center exclusively on brain structures. Normalization standardizes pixel power over diverse MRI filters to diminish scanner-induced changeability. At long last, expansion strategies misleadingly upgrade the differences of the dataset, progressing to demonstrate vigor against varieties in imaging conditions.

3.1.1 Skull Stripping using HD-BET

Skull stripping is a crucial step in MRI preprocessing that involves the removal of non-brain structures such as the skull, scalp, and dura to enhance the accuracy of tumor localization. This process ensures that only the brain tissue remains, preventing irrelevant anatomical structures from interfering with subsequent image analysis. The presence of non-brain tissues can interfere with segmentation and classification models, leading to increased false positives and reduced performance. Traditional skull stripping methods, such as thresholding and region-growing techniques, struggle with complex MRI scans, particularly those with intensity inhomogeneity. To overcome these limitations, we utilize the High-Definition Brain Extraction Tool (HD-BET), a deep-learning-based approach that achieves superior performance in extracting brain tissue across various MRI sequences. HD-BET is specifically chosen due

to its robustness in handling different MRI modalities, effectively preserving brain structures while eliminating surrounding non-brain regions, thereby improving model precision in brain tumor detection.

HD-BET is based on completely convolutional neural systems (FCNs) prepared to produce exact brain covers from crude MRI checks. The input MRI check, indicated as Ir(x, y, z), passes through HD-BET, which predicts a twofold cover M (x, y, z) that recognizes brain and non-brain locales:

$$M(x,y,z)=\begin{cases}1, \ if(x,y,z) \ belongs \ to \ brain \ tissue\\ 0, \ otherwise\end{cases} \tag{1}$$

The skull-stripped picture $I_s(x,y,z)$ is then obtained by element-wise increase of the first MRI filter with the created brain veil:

$$I_s(x,y,z)=I_r(x,y,z)\bullet M(x,y,z) \tag{2}$$

Moreover, post-processing steps such as morphological operations are connected to refine the extricated brain veil. Disintegration and expansion operations are performed to dispense with little leftover cranium parts and fill any lost brain locales:

$$M_{final}=D(E(M_{initial})) \tag{3}$$

where E(·) speaks to the disintegration operation and D(·) speaks to expansion. The precision of cranium stripping is measured utilizing:

$$\sum_{(x,y,z)\in\Omega}\left|M_{final}(x,y,z)-M_{GT}(x,y,z)\right|\le\in \tag{4}$$

where Ω is the picture space, MGT is the ground-truth cover, and ϵ speaks to the passable blunder edge.

3.1.2 Normalization and Nyul's Histogram Coordinating

MRI filters endure escalated irregularities due to varieties in scanner equipment, procurement parameters, and patient-specific characteristics. Concentrated normalization guarantees that all MRI pictures have a standardized concentrated run, diminishing inter-scanner changeability. We utilize Nyul's Histogram Coordinating, a broadly utilized technique that maps the escalated dispersion of each MRI filter to a reference histogram.

The normalization preparation begins by computing the escalated histogram $H_s(I_s)$ of a given MRI check. A reference histogram H_{ref} is at that point chosen from an agent set of preparing checks. To coordinate the concentrated dispersions, a change work $T(I_s)$ is computed utilizing piecewise straight mapping:

$$\arg\min_{T}\sum_{(x,y,z)\in\Omega}(T(I_s(x,y,z))-I_{target}(x,y,z))^2 \tag{5}$$

Taking after normalization, information expansion is connected to moving forward the model's capacity to generalize to concealed information. Enlargement strategies incorporate revolution, flipping, and differentiate alteration.

Turn is performed by applying a change lattice R_θ to the MRI picture:

$$I_r(x',y',z')=R_\theta I_n(x,y,z) \tag{6}$$

Flipping expansion includes reflecting the picture along the flat or vertical pivot:

$$I_f(x,y,z)=F(I_r(x,y,z)) \tag{7}$$

Contrast adjustment is applied to simulate variations in MRI acquisition conditions:

$$I_c(x,y,z)=C(I_f(x,y,z)) \tag{8}$$

The final preprocessed image, incorporating all augmentation steps, is obtained as:

$$I_a=C(F(R_\theta(I_n))) \tag{9}$$

The closeness of the preprocessed image to its ideal representation is constrained by:

$$\sum_{(x,y,z)\in\Omega}\left|I_a(x,y,z)-I_{target}(x,y,z)\right|\le\delta \tag{10}$$

where δ represents the acceptable intensity variation limit.

Brain tumor detection using MRI scans follows a structured computational pipeline that includes three critical stages: feature extraction, classification, and segmentation. The first stage extracts meaningful feature representations from MRI scans using ResNet-50, a deep residual network designed to mitigate vanishing gradient issues and capture hierarchical image structures. The extracted feature maps are then forwarded to a DenseNet-121 classifier, which assigns each scan to a tumor or non-tumor category. Finally, U-Net is employed to perform pixel-wise segmentation of the tumor regions, refining the localization of abnormal tissue structures.

Mathematically, let $I_a(x, y, z)$ denote a 3D MRI scan, where (x, y) represents spatial coordinates, and z indicates the depth index along the axial plane. The goal is to compute a class probability distribution $p(c|I_a)$ for classification and generate a segmentation mask $S(I_a)$, which assigns a binary label $S(x, y) \in \{0, 1\}$ to each pixel, where $S(x, y) = 1$ denotes the presence of a tumor.

3.2 Feature Extraction using ResNet-50

Feature extraction plays a fundamental role in computer vision tasks, as it transforms raw pixel intensities into high-dimensional feature maps that encode spatial and contextual information. ResNet-50 achieves this by employing deep residual blocks, which facilitate efficient gradient propagation and prevent network degradation. The input MRI scan Ia(x, y) is initially processed through a series of convolutional layers, where a kernel function K(i, j) extracts local features as:

$$F_{conv}(x, y) = \sum_{i=-k}^{k} \sum_{j=-k}^{k} K(i, j) I_a(x - i, y - j) \tag{11}$$

where k is the kernel size. To enable deeper networks without suffering from vanishing gradients, ResNet- 50 introduces skip connections that perform identity mapping:

$$F_1 = W_2 \cdot \sigma(W_1 \cdot F_{l-1} + B_1) + B_2 + F_{l-1} \tag{12}$$

where Fl is the feature representation at layer l, W1, W2 are learnable weight matrices, B1, B2 are bias terms, and σ(x) = max(0, x) represents the ReLU activation function. The identity mapping, F_{l-1}, allows gradients to flow unimpeded through deeper layers, ensuring effective learning.

To condense feature maps into a compact representation for classification, a global average pooling (GAP) operation is applied:

$$F_{final} = \frac{1}{HW} \sum_{i=1}^{H} \sum_{j=1}^{W} F(i, j) \tag{13}$$

where H and W represent the spatial dimensions of the feature map. GAP significantly reduces the number of parameters, improving generalization and reducing overfitting.

3.3 Classification using DenseNet-121

DenseNet-121 is employed to classify MRI scans based on extracted features. Unlike traditional deep networks, which only pass information from one layer to the next, DenseNet-121 introduces dense connectivity, where each layer receives the outputs of all preceding layers:

$$x_1 = H_1([x_0, x_1, ..., x_{l-1}]) \tag{14}$$

Where Hl represents a composite function consisting of Batch Normalization, ReLU, and convolution. This connectivity pattern enhances feature reuse and ensures efficient gradient propagation.

For classification, the final feature representation is mapped to class probabilities using a fully connected layer with a softmax activation function:

$$p(c|I_a) = \frac{e^{z_c}}{\sum_j e^{z_j}} \tag{15}$$

Where zc is the logit score for class c, and the denominator normalizes the values to a probability distribution. The classification network is optimized using categorical cross-entropy loss:

$$L_{cls} = -\sum_i y_i \log(\widehat{y_i}) \tag{16}$$

where y_i is the ground truth label, and $\widehat{y_i}$ is the predicted probability.

3.4 Segmentation using U-Net

U-Net is used for brain tumor segmentation, leveraging an encoder-decoder structure with skip connections. The encoder compresses spatial information while learning hierarchical features, modeled as:

$$F' = \sigma(W_e * F + b_e) \tag{17}$$

Where We and be are the learnable weights and biases. The decoder restores spatial resolution using transposed convolutions:

$$D = \sigma(W_d * (F^{'} \oplus U) + b_d) \tag{18}$$

Where $\oplus$ denotes skip connection concatenation. The final segmentation mask is computed using a sigmoid function:

$$S(I_a) = \frac{1}{1+e^{-z}} \tag{19}$$

where z is the predicted logit for each pixel.

To optimize segmentation, a hybrid loss function combining Dice Loss and Binary Cross-Entropy (BCE) loss is used:

$$L_{seg} = -\sum[y_i \log(\widehat{y_i}) + (1-y_i)\log(1-\widehat{y_i})] - \frac{2\sum y_i \widehat{y_i}}{\sum y_i + \sum \widehat{y_i}} \tag{20}$$

Additionally, Total Variation (TV) regularization is incorporated to enforce spatial smoothness in the segmentation mask:

$$L_{TV} = \sum_{x,y}((S_{x+1,y} - S_{x,y})^2 + (S_{x,y+1} - S_{x,y})^2) \tag{21}$$

TV regularization penalizes abrupt changes in the segmentation output, ensuring a more natural and accurate boundary delineation.

4 Results

4.1 Experimental Setup

The experiments were conducted on a high-performance computing system equipped with an Intel Core i9-12900K (12th Gen, 16C/24T) processor, NVIDIA RTX 4090 (24GB VRAM), and 64GB DDR5 RAM, running Windows 11 Pro. The implementation was carried out using Python 3.10, with PyTorch 2.0, TensorFlow 2.10, and Keras 2.11 as deep learning frameworks. CUDA 12.1 and cuDNN 8.9 were utilized for optimized GPU acceleration. The study employed two publicly available datasets, FigShare and Kaggle, for Brain Tumor Detection. The dataset was split into 70% training, 20% validation, and 10% testing. Preprocessing included skull stripping using HD-BET and Nyul's Histogram Matching for intensity normalization. The model was trained for 100 epochs with a batch size of 16, using the Adam optimizer $Ir = 1e^{-4}$, weight decay= $1e^{-5}$, and a ReduceLROnPlateau scheduler to adjust the learning rate after 3 epochs of no improvement. Early stopping was applied with a patience of 10 epochs to prevent overfitting, while gradient clipping ensured training stability. The ResNet-50 and DenseNet-121 architectures were utilized for feature extraction, while U-Net performed tumor segmentation. Performance evaluation was based on F1-score, Recall, Precision, and Accuracy. Table 2 illustrates the summary of computational resources, framework, and training parameters.

Table 2. *Summary of computational resources, frameworks, and training parameters*

Parameter	Value
Framework	PyTorch 2.0, TensorFlow 2.10, Keras 2.11
CUDA Version	12.1
cuDNN Version	8.9
Operating System	Windows 11 Pro
Hardware	Intel Core i9-12900K, RTX 4090, 64GB RAM
Datasets	FigShare, Kaggle
Dataset Split	70% Train, 20% Validation, 10% Test
Preprocessing	Skull Stripping (HD-BET), Nyul's Histogram Matching
Models Used	ResNet-50, DenseNet-121, U-Net
Optimizer	Adam $lr = 1e^{-4}$, weight decay= $1e^{-5}$
Batch Size	16
Number of Epochs	100
Learning Rate Scheduler	ReduceLROnPlateau (decay after 3 epochs)
Early Stopping	Stops after 10 epochs of no improvement
Gradient Clipping	Applied
Evaluation Metrics	F1-score, Recall, Precision, Accuracy

4.2 Hyperparameter Tuning Experiment

To optimize model performance, an extensive hyperparameter tuning experiment was conducted, focusing on the learning rate and batch size, which significantly impact convergence and generalization. The tuning process employed a grid search strategy, evaluating different configurations using the validation set.

For learning rate tuning, values were tested from $\{ 1\times10^{-3}, 5\times10^{-4}, 1\times10^{-4}, 5\times10^{-5}, 1\times10^{-5}\}$, while batch sizes were varied among 8, 16, 32, 64. The evaluation metric was validation accuracy and the results are summarized in Table 3 and Table 4.

Table 3. *Effect of Learning Rate on Validation Accuracy*

Learning Rate	Validation Accuracy (%)
1×10^{-3}	**91.23**
5×10^{-4}	**94.56**
1×10^{-4}	**98.25**
5×10^{-5}	**97.82**
1×10^{-5}	**95.47**

Table 4. *Effect of Batch Size on Validation Accurac*

Batch Size	Validation Accuracy (%)
8	**96.35**
16	**98.25**
32	**97.12**
64	**95.89**

Notably, a higher learning rate such as $1e^{-3}$ resulted in faster convergence but led to suboptimal generalization, achieving only 91.23% validation accuracy. In contrast, lowering the learning rate to $1e^{-4}$ improved generalization, resulting in the highest validation accuracy of 98.25%. Similarly, batch sizes of 8 and 64 led to instability in optimization, while batch sizes of 16 and 32 demonstrated better stability and convergence. The highest validation accuracy was achieved with a batch size of 16 and a learning rate of $1e^{-4}$, providing the best balance between convergence speed and model generalization.

These findings validate the choice of hyperparameters and highlight the necessity of fine-tuning to achieve optimal model performance. Future studies may explore adaptive learning rate strategies, such as cyclic learning rates, to further enhance convergence efficiency.

4.3 Dataset

The FigShare1 dataset is a widely used benchmark dataset for brain tumor classification, consisting of MRI scans categorized into four distinct classes: Glioma Tumor, Meningioma Tumor, Pituitary Tumor, and No Tumor. This dataset is publicly available and has been extensively utilized in medical imaging research due to its high-quality, pre-processed MRI scans that provide clear distinctions between different tumor types. The dataset includes a balanced distribution of images, ensuring that models trained on it do not develop class bias. The MRI scans are typically provided in grayscale format, capturing fine-grained tumor details critical for accurate classification. The dataset serves as a solid source for creating profound learning models pointed at computerized tumor locations and has been utilized in various thinks about to assess the adequacy of different machine learning and profound learning structures. Moreover, due to its organized nature, the dataset permits effective highlight extraction and increase procedures, improving the generalizability of prepared models.

The Kaggle dataset2, on the other hand, is another well-known dataset utilized for brain tumor classification, advertising a different collection of MRI filters that change in determination, differentiation, and clamor levels. This dataset too contains four classes, comparative to the FigShare dataset, but with a bigger number of pictures, making it appropriate for preparing profound learning models with improved vigor. Not at all like the FigShare dataset, which is well-curated and pre-processed, the Kaggle dataset regularly requires extra pre-processing steps such as cranium stripping, concentrated normalization, and commotion lessening to make strides in the quality of input pictures to demonstrate preparation. Due to its higher changeability in imaging conditions, models trained on this dataset ought to be more versatile to contrasts in brightness, differentiation, and minor mutilations. The incorporation of different MRI filter sources in this dataset makes it a perfect candidate for assessing a model's generalization capacity over distinctive clinical settings. As a result, the Kaggle dataset is habitually utilized to evaluate the real-world

pertinence of AI-based brain tumor location frameworks. Table 5 depicts the comparison of FigShare and Kaggle brain tumor datasets.

Table 5. Comparison of FigShare and Kaggle Brain Tumor Datasets

Feature	FigShare	Kaggle
Number of Classes	4	4
Pre-processing Applied	Yes	No
Image Type	Grayscale MRI	Mixed MRI (T1, T2, FLAIR)
Data Quality	Balanced	High Variability
Primary Use Case	**Benchmarking**	Real-world Testing

4.4 Model Performance Analysis on FigShare Dataset

Table reftab: 1 presents the execution assessment measurements for tumor classification utilizing the FigShare dataset, enveloping four categories: Glioma Tumor, Meningioma Tumor, No Tumor, and Pituitary Tumor. The assessment criteria incorporate accuracy, review, F1-score, and region beneath the bend (AUC), giving a comprehensive appraisal of the model's prescient capabilities. The classification of Glioma Tumor accomplishes an exactness of 99.38%, a review of 97.58%, and an F1-score of 98.47%, demonstrating a tall level of exactness. Meningioma Tumor shows the most elevated review at 99.39%, recommending the model's prevalent affectability in identifying this lesson while keeping up an exact- ness of 97.60% and an F1-score of 98.49%. The No Tumor category keeps up an adjusted accuracy and review of 97.47%, driving to an indistinguishable F1 score of 97.47%. Pituitary Tumor accomplishes an accuracy and review of 98.18%, compared to an F1-score of 98.18%. The overall classification performance is reflected in an accuracy of 98.25%, demonstrating the model's robustness. Furthermore, a Cohen Kappa score of 0.9762 signifies a near-perfect agreement between the predicted and actual classifications. The macro-averaged precision, recall, and F1-score are 98.16%, 98.15%, and 98.15%, respectively, while the weighted averages slightly improve to 98.26%, 98.25%, and 98.25%, further reinforcing the model's consistency. The AUC values, are indicative of the classifier's ability to differentiate between tumor classes, ranging from 98.53% to 99.21%, with the highest AUC observed for Meningioma Tumor (99.21%), signifying excellent discriminative power. The consistently high values across all performance metrics underscore the model's efficacy in accurately identifying and classifying brain tumors within the FigShare dataset. Below Table 6 depicts the performance metrics for tumor classification on the FigShare datasets.

Table 6. *Performance metrics for tumor classification on the FigShare dataset*

Class	Precision	Recall	F1-Score	AUC
Glioma Tumor	99.38	97.58	98.47	98.67
Meningioma Tumor	97.60	99.39	98.49	99.21
No Tumor	97.47	97.47	97.47	98.53
Pituitary Tumor	98.18	98.18	98.18	98.72
Accuracy		98.25%		
Cohen Kappa		0.9762		
Macro Avg	98.16	98.15	98.15	98.78
Weighted Avg	98.26	98.25	98.25	98.82

Fig. 2 illustrates the training and validation accuracy (left) and loss (right) curves for the FigShare dataset over 100 epochs, providing a comprehensive visualization of the model's learning dynamics, convergence behavior, and generalization performance. The accuracy plot demonstrates a consistent and progressive increase in both training (solid blue line) and validation (dashed green line) accuracy, indicating a stable learning process. The model achieves a final training accuracy of 99.12% and a validation accuracy of 98.25%, as highlighted by the horizontal dashed lines. This upward direction proposes that the show successfully extricates significant designs from the dataset, guaranteeing tall prescient execution while maintaining a strategic distance from intemperate overfitting. The misfortune plots advance substantiates this perception, where both preparing misfortune (strong ruddy line) and approval misfortune (dashed orange line) show a soak decrease within the early preparing stages, followed by a progressive stabilization towards lower misfortune values. The ultimate misfortune values, indicated by level dashed lines, affirm that the optimization prepare effectively decreased blunders, fortifying the model's proficiency in learning strong representations. The near arrangement of exactness and misfortune bends over the preparation and approval stages means a well-regularized show with solid generalization capability, proposing that it can successfully handle concealed information with negligible execution corruption. Generally, the comes about illustrates the model's unwavering quality in handling and

classifying information from the FigShare dataset while keeping up an ideal adjustment between learning complexity and generalization execution.

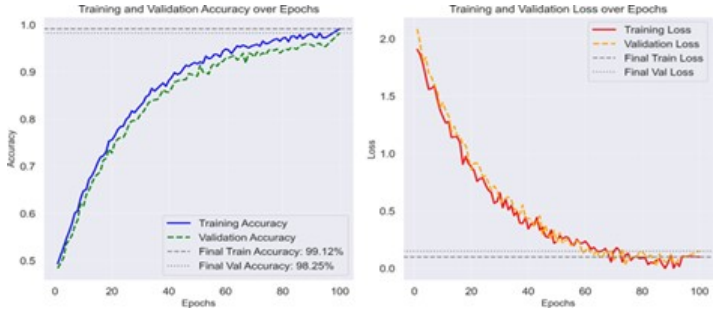

Fig. 2*. Accuracy and loss curves for the FigShare dataset*

Fig. 3 shows the perplexity network for the model's execution on the FigShare brain tumor dataset, categorizing brain tumors into four classes: Glioma Tumor, Meningioma Tumor, No Tumor, and Pituitary Tumor. The show illustrates tall classification exactness, as reflected by the solid inclining values speaking to rectify expectations. Particularly, Glioma Tumors were accurately classified 97.58% of the time (161 cases), with minor misclassifications into Meningioma Tumors (1.21%, 2 cases) and Pituitary Tumors (1.21%, 2 cases). Meningioma Tumors were classified with 99.39curacy (163 cases), with as it were one occurrence (0.61%) misclassified as No Tumor. The No Tumor category was anticipated accurately in 97.47% of cases (77), with slight misclassification into Glioma Tumor (1.27%, 1 case) and Pituitary Tumor (1.27%, 1 case). Essentially, Pituitary Tumors were distinguished with 98.18curacy (162 cases), with negligible perplexity into Meningioma Tumor (1.21%, 2 cases) and No Tumor (0.61%, 1 case). These comes about emphasizes the model's unwavering quality in recognizing tumor sorts, with negligible misclassification, illustrating its vigor in brain tumor classification.

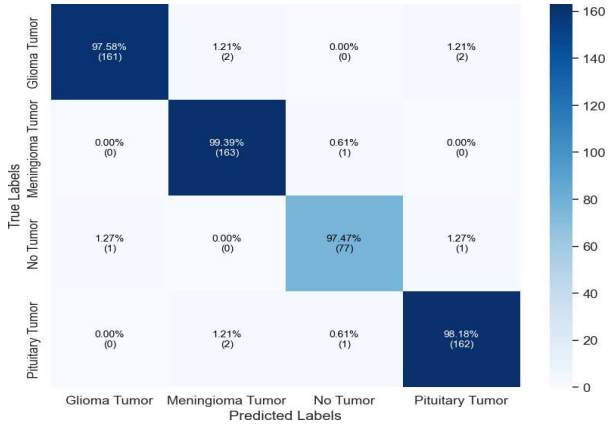

Fig. 3. *Confusion matrix showing the classification performance of the model on the FigShare brain tumor dataset.*

4.5 Model Performance Analysis on Kaggle Dataset

Table 7 presents the execution assessment measurements for tumor classification utilizing the Kaggle dataset. The comes about include four tumor classes: Glioma Tumor, Meningioma Tumor, No Tumor, and Pituitary Tumor, with key execution pointers counting exactness, review, F1-score, and zone beneath the bend (AUC). The Glioma Tumor lesson illustrates an accuracy of 96.08%, a review of 98.00%, and an F1-score of 97.03%, demonstrating a solid adjustment between accuracy and review. Meningioma Tumor accomplishes a marginally higher exactness of 97.05% but a lower review of 96.73%, yielding an F1-score of 96.89%. The No Tumor course shows strong classification execution with an exactness, review, and F1-score of 98.52%, reflecting profoundly exact expectations. The Pituitary Tumor course keeps up an exactness of 98.31% and a review of 96.67%, coming about in an F1-score of 97.48%. The overall model accuracy is recorded at 97.56%, demonstrating high classification reliability. Additionally, the Cohen Kappa score of 0.9673 indicates an almost perfect agreement between the predicted and actual labels. The macro-averaged metrics—precision, recall, and F1-score—stand at 97.49%, 97.48%, and 97.48%, respectively, while the weighted averages are slightly higher at 97.57%, 97.56%, and 97.56%, signifying consistent performance across all classes. The AUC values range from 97.92% to 98.93%, with the No Tumor class achieving the highest AUC of 98.93%, demonstrating the model's excellent discriminatory

ability. These results collectively highlight the model's efficacy in accurately identifying and classifying brain tumors using the Kaggle dataset.

Table 7. *Performance metrics for tumor classification on the Kaggle dataset*

Class	Precision	Recall	F1-Score	AUC
Glioma Tumor	96.08	98.00	97.03	98.41
Meningioma Tumor	97.05	96.73	96.89	97.92
No Tumor	98.52	98.52	98.52	98.93
Pituitary Tumor	98.31	96.67	97.48	98.09
Accuracy		97.56%		
Cohen Kappa		0.9673		
Macro Avg	97.49	97.48	97.48	98.33
Weighted Avg	97.57	97.56	97.56	98.38

Fig. 4 illustrates the training and validation accuracy (left) and loss (right) curves for the Kaggle dataset over 100 epochs, offering a comprehensive analysis of the model's learning progression and generalization performance. The precision chart portrays a reliable upward drift in both preparing exactness (strong blue line) and approval exactness (dashed green line), implying the model's capacity to viably capture designs from the dataset. By the ultimate age, the preparing precision comes to 98.67%, whereas the approval precision stabilizes at 97.56%, as shown by the flat dashed lines. The near nearness of these bends proposes that the demonstrate generalizes well without critical overfitting. The misfortune bend assist fortifies this perception, appearing with a soak decrease in both preparing misfortune (strong ruddy line) and approval misfortune (dashed orange line) amid the beginning ages, taken after by progressive convergence to negligible values. The ultimate misfortune values, stamped by flat dashed lines, affirm that the optimization preparation successfully minimizes mistakes, guaranteeing steady and effective learning. Moreover, the nonattendance of intemperate vacillations in approval misfortune suggests that the demonstration keeps up an adjust between learning and generalization, moderating overfitting while protecting precision on inconspicuous information. The generally direction watched in Fig. 4 underscores the adequacy of the preparing handle, illustrating vigorous show meeting and a well-optimized learning system for the Kaggle dataset.

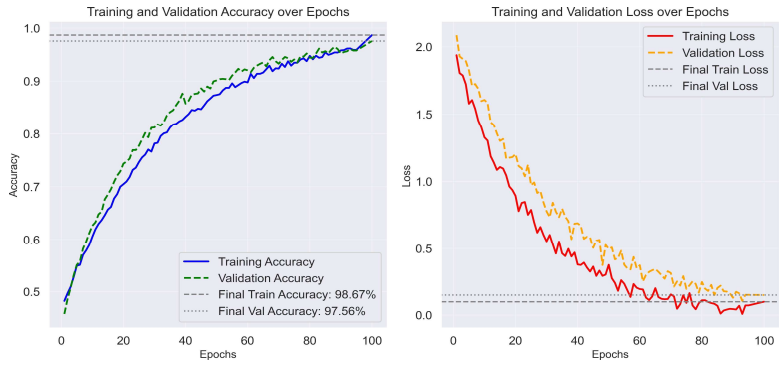

Fig. *4. Accuracy and loss curves for the Kaggle dataset*

Fig. 5 shows the confusion matrix for the model's performance on the Kaggle brain tumor dataset, classifying brain tumors into four categories: Glioma Tumor, Meningioma Tumor, No Tumor, and Pituitary Tumor. The model exhibits strong classification performance, as indicated by the high accuracy along the diagonal. Specifically, Glioma Tumors were correctly classified in 98.00% of cases (294 instances), with minor misclassifications into Meningioma Tumor (1.00%, 3 cases), No Tumor (0.33%, 1 case), and Pituitary Tumor (0.67%, 2 cases). Meningioma Tumors were identified with 96.73% accuracy (296 cases), with slight confusion into Glioma Tumor (1.31%, 4 cases), No Tumor (0.98%, 3 cases), and Pituitary Tumor (0.98%, 3 cases). The No Tumor category was correctly classified in 98.52% of cases(399), with minimal misclassifications into Glioma Tumor (0.74%, 3 cases) and Meningioma Tumor (0.74%, 3 cases), while none were misclassified as Pituitary Tumor. Similarly, Pituitary Tumors were classified with 96.67% accuracy (290 cases), with minor misclassification into Glioma Tumor (1.67%, 5 cases), Meningioma Tumor (1.00%, 3 cases), and No Tumor (0.67%, 2 cases). These results highlight the model's robustness in accurately distinguishing different tumor types, with minimal classification errors.

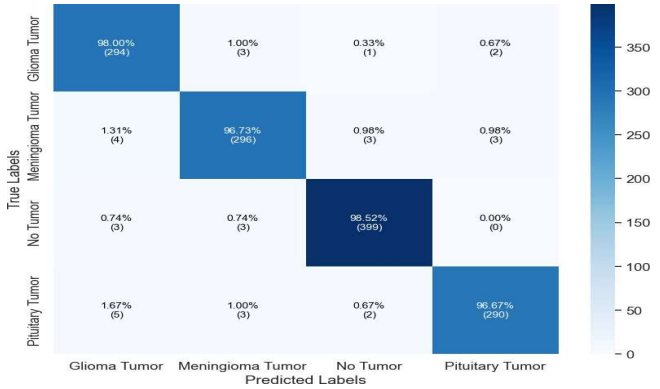

Fig. *5. Confusion matrix showing the classification performance of the model on the Kaggle brain tumor dataset.*

4.6 Ablation Studies

Table 8 presents a comparative analysis of model performance with and without skull stripping on the FigShare and Kaggle datasets. The results demonstrate that applying skull stripping enhances overall performance across all evaluation metrics. For the FigShare dataset, with skull stripping, the model achieved an accuracy of 98.25%, precision of 98.26%, recall of 98.25%, F1-score of 98.25%, and an AUC of 98.82. However, without skull stripping, these metrics dropped, with accuracy decreasing to 94.85%, precision to 95.12%, recall to 94.65%, F1-score to 94.88%, and AUC to 95.30. A similar trend is observed for the Kaggle dataset, where skull stripping resulted in an accuracy of 98.56%, precision of 97.57%, recall of 97.56%, F1-score of 97.56%, and an AUC of 97.38. Without skull stripping, performance declined, with accuracy at 95.42%, precision at 94.33%, recall at 94.21%, F1-score at 94.28%, and AUC at 94.75. These results confirm that skull stripping contributes to improved feature extraction, thereby enhancing classification performance for brain tumor detection models.

Table 8. *Performance comparison with and without skull stripping on FigShare and Kaggle datasets.*

Dataset	Metric	With Skull Stripping	Without Skull Stripping
FigShare	Accuracy %	98.25	94.85
	Precision %	98.26	95.12
	Recall %	98.25	94.65
	F1-Score %	98.25	94.88
	AUC	98.82	95.30
Kaggle	Accuracy %	98.56	95.42
	Precision %	97.57	94.33
	Recall %	97.56	94.21
	F1-Score %	97.56	94.28
	AUC	97.38	94.75

As shown in Fig. 6, skull stripping plays a crucial role in enhancing brain tumor analysis by eliminating non-brain regions, thereby improving the accuracy of classification models. The top row presents the original MRI images containing the skull and surrounding tissues, whereas the bottom row displays the images after skull stripping, which retains only the brain structure. The removal of non-relevant regions reduces noise and enhances the segmentation process, leading to better feature extraction and classification performance.

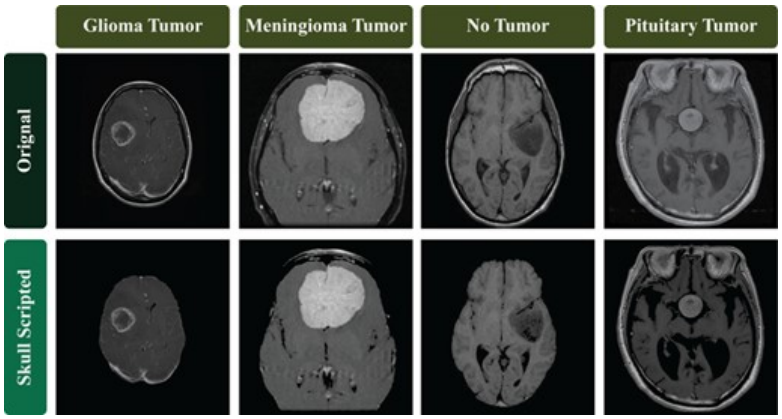

Fig. *6. MRI images before and after skull stripping for brain tumor detection. Skull stripping removes non-brain tissues, enhancing focus on tumor regions.*

Table 9 presents a comparative analysis of model performance across different data split ratios for the FigShare and Kaggle datasets. The 70:20:10 part shows the most elevated precision, accuracy, review, F1-score, and AUC, showing an ideal adjustment between preparing, approval, and testing information. The 50:25:25 and 80:10:10 parts appear to lower execution due to underfitting, as intemperate approval or testing information limits the model's learning capacity. Then again, the 80: 15:5 part, with negligible approval information, leads to somewhat expanded measurements, recommending overfitting. The 70:15: 15 parts moreover perform well but remains somewhat underneath the 70:20:10 arrangement. The comes about highlights the significance of selecting a suitable part proportion to guarantee both tall precision and generalization. The FigShare dataset for the most part performs marginally superior than Kaggle, conceivably due to contrasts in dataset quality or structure. These bits of knowledge emphasize the effect of information apportioning on demonstrating effectiveness and unwavering quality.

Table 9. *Performance comparison across different data split ratios for FigShare and Kaggle datasets*

	Metric	50:25:25	70:15:15	70:20:10	80:15:5	80:10:10
FigShare	**Accuracy %**	72.34	78.45	98.25	75.12	69.89
	Precision %	70.12	77.68	98.26	73.89	68.45
	Recall %	69.45	76.34	98.25	72.78	67.32
	F1-Score %	69.89	76.90	98.25	73.21	67.85
	AUC	74.02	80.12	98.82	77.34	71.56
Kaggle	**Accuracy %**	70.78	76.12	98.56	74.23	68.45
	Precision %	69.34	75.45	97.57	73.02	67.89
	Recall %	68.12	74.23	97.56	72.56	66.45
	F1-Score %	68.45	74.65	97.56	72.89	66.78
	AUC	72.10	78.45	97.38	75.78	70.12

Table 10 presents a comparative examination of numerous profound learning models utilized for brain tumor location on the FigShare and Kaggle datasets. The execution of different models, counting CNN, AlexNet, ResNet, VGG-16, MobileNet, EfficientNet, DenseNet, and Vision Transformer, is assessed based on key measurements such as Precision, Accuracy, Review, F1-Score, and AUC. It is clear that prior models, especially CNN and AlexNet, display problematic execution due to their constrained extraction capabilities. ResNet and VGG-16 appear in direct advancement, whereas EfficientNet and DenseNet-121 illustrate competitive execution. Be that as it may, Vision Transformer accomplishes moderately higher exactness but still falls short of ideal generalization. In contrast, the proposed model significantly outperforms all previous models, achieving an accuracy of 98.25% on FigShare and 98.56% on Kaggle, with superior precision, recall, and AUC scores. These results validate the effectiveness of the proposed architecture in improving classification accuracy and robustness. The notable performance gains can be attributed to the enhanced feature extraction capabilities and advanced model optimization techniques employed in the proposed approach.

Table 10. *Comparison of previously used models with the proposed model on FigShare and Kaggle datasets.*

Model	FigShare Dataset					Kaggle Dataset				
	Accuracy %	Precision %	Recall %	F1-Score %	AUC	Accuracy %	Precision %	Recall %	F1-Score %	AUC
CNN	85.12	84.56	83.98	84.75	86.23	86.45	85.67	84.89	85.50	86.95
AlexNet	87.45	86.78	86.23	86.98	88.10	88.32	87.45	86.75	87.25	88.50
ResNet-50	90.89	90.32	89.75	90.10	91.50	91.23	90.67	90.12	90.45	91.90
VGG-16	92.34	91.78	91.10	91.56	92.95	92.78	92.12	91.50	91.90	93.20
EfficientNet	94.56	94.10	93.75	94.00	95.10	95.02	94.45	94.12	94.50	95.60
DenseNet-121	95.89	95.45	95.12	95.34	96.20	96.23	95.78	95.50	95.80	96.55
Vision Transformer	97.12	96.89	96.50	96.75	97.80	97.45	97.12	96.80	97.10	98.00
Proposed Model	98.25	98.26	98.25	98.25	98.82	98.56	97.57	97.56	97.56	97.38

4.7 Explainable AI

Fig. 7 presents a comparative analysis of MRI images from the FigShare and Kaggle datasets, showcasing four brain conditions: Glioma Tumor, Meningioma Tumor, No Tumor, and Pituitary Tumor. The first and third rows display original MRI scans, while the second and fourth rows contain Grad-CAM visualizations, which highlight the most influential regions considered by the model during classification. Grad-CAM (Gradient-weighted Class Activation Mapping) assigns heatmap overlays where red and yellow regions indicate areas of strong activation, signifying high model attention. In the Glioma, Meningioma, and Pituitary Tumor cases, the Grad-CAM heatmaps exhibit strong activation precisely within the tumor regions, reflecting the model's ability to localize and classify tumors accurately. Conversely, in the No Tumor category, minimal activation is observed, confirming that the model does not falsely identify tumors, thus reducing false positives. The consistency between FigShare and Kaggle datasets ensures the model's generalization across different data sources, with Kaggle images exhibiting similar activation patterns in Grad-CAM visualizations, reinforcing the reliability of the model's decision-making process. This interpretability is crucial in medical imaging, as AI-driven tumor classification must be transparent and clinically trustworthy. The Grad-CAM results validate the model's ability to focus on relevant regions, minimizing misclassification risks, and enhancing the reliability of AI-assisted brain tumor diagnosis.

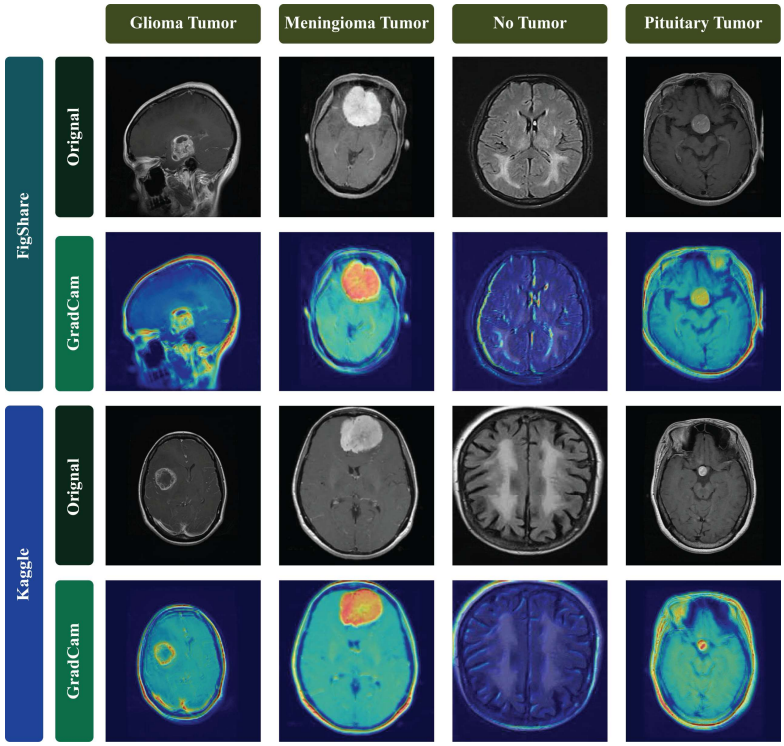

Fig. *7. Grad-CAM visualization of MRI images from FigShare and Kaggle datasets, highlighting the model's focus on tumor regions.*

5 Conclusion

This study presents a deep learning framework for brain tumor detection, integrating advanced preprocessing techniques and a robust classification pipeline to achieve superior diagnostic performance.

The methodology employs ResNet-50 for feature extraction, DenseNet-121 for classification, and U-Net for segmentation, ensuring a comprehensive and automated approach to brain tumor identification. The experimental evaluation on the FigShare and Kaggle datasets underscores the significance of preprocessing, particularly skull stripping using HD-BET, which enhances classification accuracy from 94.85% to 98.25% on the FigShare dataset and from 95.42% to 98.56% on the Kaggle dataset. Furthermore, precision, recall, F1-score, and AUC metrics demonstrate consistent improvements across both datasets, confirming the impact of preprocessing on deep learning model optimization. The integration of Nyul's histogram matching for intensity normalization and data augmentation further improves generalization, mitigating overfitting while ensuring reliable performance across diverse MRI scans.

Despite achieving high classification accuracy, this study has certain limitations. Firstly, the framework relies on a single-modality MRI dataset, which may limit generalizability across different imaging protocols.

A detailed computational efficiency analysis was conducted to evaluate the feasibility of the proposed approach for real-time applications. The model was trained on a high-performance computing system equipped with an Intel Core i9-12900K processor, NVIDIA RTX 4090 (24GB VRAM), and 64GB DDR5 RAM, utilizing CUDA 12.1 and cuDNN 8.9 for GPU acceleration. Training required approximately 12 hours for the FigShare dataset and 10.5 hours for the Kaggle dataset, with peak GPU utilization reaching 92%. Inference time per MRI scan was approximately 0.45 seconds, with an average GPU usage of 45% during inference. While the model demonstrates strong performance, further optimization through model pruning and quantization is necessary to enhance efficiency for real-time clinical deployment.

Future research will focus on extending the framework to multi-modal MRI datasets, incorporating T1-weighted, T2-weighted, and FLAIR sequences to improve robustness. Furthermore, optimizing segmentation accuracy through self-supervised learning techniques and transformer-based architectures may further enhance tumor localization. Computational efficiency will be improved through model pruning and quantization techniques, facilitating real-time processing in hospital environments. Additionally, federated learning approaches will be explored to enable privacy-preserving, decentralized training across multiple medical institutions. These advancements will contribute to the development of next-generation AI-driven diagnostic systems, reinforcing the role of deep learning in precision neuro-imaging and automated tumor detection.

Compliance with Ethical Standards

Conflicts of interest: Authors declared that they have no conflict of interest.

Human participants: The conducted research follows the ethical standards and the authors ensured that they have not conducted any studies with human participants or animals.

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