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Brain Scan: Brain Tumor Detection And Classification

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Abstract:

Brain tumor detection is a critical challenge in medical imaging due to the structural complexity of the brain, wide variability in tumor morphology, and the severe consequences associated with delayed diagnosis. Magnetic Resonance Imaging (MRI) is the preferred modality for clinical assessment; however, manual interpretation is often time-consuming, subjective, and prone to inconsistencies. To address these limitations, this study proposes a deep learning–based classification framework that leverages multiple architectures—including CNN, VGG16, VGG19, ResNet50, and DenseNet121—to accurately categorize brain MRI scans into four classes: Glioma, Meningioma, Pituitary tumor, and No Tumor. The framework extensively employs transfer learning, enabling pretrained models to be fine-tuned for extracting highly discriminative MRI features, thereby reducing the reliance on large annotated medical datasets and improving model robustness. Experimental results demonstrate that DenseNet121 achieves the highest classification accuracy and superior generalization compared to other evaluated models. The findings underscore the significant role of transfer learning in enhancing the performance, efficiency, and clinical applicability of automated brain tumor detection systems. This study contributes to the advancement of intelligent diagnostic tools that can support radiologists and improve decision-making in neuro-oncology.

Keywords: Brain Tumor, Deep Learning, MRI, CNN, Transfer Learning, Medical Imaging

1. INTRODUCTION

Brain tumors are abnormal and uncontrolled proliferations of cells within the brain that disrupt normal neural functioning and may become life-threatening if not diagnosed at an early stage. Timely and accurate detection is therefore essential for selecting appropriate treatment strategies and improving patient survival outcomes [1]. Magnetic Resonance Imaging (MRI) remains the gold standard for brain tumor assessment due to its superior soft-tissue contrast, non-invasive nature, and ability to capture detailed structural information without ionizing radiation. These attributes make MRI highly suitable for tumor localization, morphological characterization, and evaluation of disease severity.

Traditional diagnostic workflows rely heavily on expert radiologists who manually examine MRI scans. However, significant variations in tumor size, shape, intensity, texture, and anatomical location make interpretation challenging, often leading to intra-observer and inter-observer inconsistencies. Moreover, manual analysis is time-consuming and susceptible to fatigue-related errors, which can delay diagnosis and adversely affect clinical decision-making. To address these limitations, deep learning–based techniques [1][2][3] have gained substantial attention in recent years as powerful tools for automated medical image analysis.

Deep learning—particularly Convolutional Neural Networks (CNNs)— offers several advantages for brain tumor detection and classification, including:

- Automated extraction of complex and discriminative features directly from MRI scans
- High classification accuracy with minimal manual pre-processing
- Strong robustness and generalization capability across diverse imaging conditions and datasets

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- Fast, consistent, and scalable diagnostic support for clinical environments

This study aims to develop and evaluate an efficient deep learning–based system for brain tumor detection and classification across four categories of MRI images:

1. Meningioma – Tumors originating from the meninges with typically well-defined boundaries
2. Pituitary Tumor – Lesions located in the sella turcica near the pituitary gland
3. Glioma – Highly aggressive tumors characterized by irregular, infiltrative growth
4. No Tumor – Normal MRI scans representing healthy brain anatomy

By employing advanced CNN architectures and optimized training strategies, the proposed framework seeks to deliver accurate and fully automated tumor classification. The overarching objective is to minimize diagnostic errors, accelerate clinical workflows, and provide reliable decision-support tools that enhance radiological assessment and improve patient outcomes in neuro-oncology.

2. Related Work

Many recent studies have successfully utilized deep learning methods for automated brain tumor detection and classification from MRI images. CNN-based classifiers have demonstrated a strong capability in learning tumor-specific spatial and textural patterns directly from the images, eliminating the need for manual feature engineering. Researchers have explored a variety of deep architectures where transfer learning [4] [5][6][7][8][9] plays a major role. Pretrained models such as VGG16 [10], VGG19 [11], ResNet50 [12] and DenseNet-121 [13]— uses transfer learning for multi-class brain tumor classification on MRI data have been widely applied because their previously learned feature representations can be fine-tuned for medical imaging tasks, helping improve diagnostic accuracy even with limited datasets.

Among these architectures, DenseNet-based models [13] have consistently outperformed others in research studies due to their dense connectivity pattern, which enables efficient feature reuse, reduced parameters, strong gradient flow, and better handling of complex MRI patterns. Studies also highlight that deeper models like ResNet [14][16] enhance classification through residual learning, whereas VGG models [14][15] effectively extract fine texture and boundary details crucial for differentiating tumors such as glioma and meningioma.

Despite significant progress, several challenges still hinder real-world applicability:

• Class imbalance in datasets, where tumor samples are more frequently available than normal images.
• MRI noise, contrast variability, and orientation differences, which reduce model generalization.
• Lack of standardized evaluation protocols, causing differences in reported accuracy across studies.
• Difficulty in distinguishing tumors with similar intensities and overlapping regions in the brain.

Therefore, this research aims to improve robustness and prediction reliability by using enhanced pre-processing, balanced dataset splitting, and advanced CNN-based architectures. The study focuses specifically on four-class brain tumor classification: Glioma, Meningioma, Pituitary, and No Tumor, ensuring a comprehensive diagnostic assistance system suitable for clinical environments.

3. Methodology

The proposed methodology presents a deep learning–based framework for automated brain tumor classification from magnetic resonance imaging (MRI) scans using pretrained convolutional neural network (CNN) models. As illustrated in the block diagram shown in Fig. 1, the workflow consists of sequential stages including pre-processing, data augmentation, transfer learning–based feature extraction, fine-tuning, and classification. The objective of the framework is to accurately categorize MRI images into four clinically significant classes: Glioma, Meningioma, Pituitary Tumor, and No Tumor. The process begins with the acquisition of brain MRI images from publicly available datasets [17][18][19]. Since MRI scans may exhibit variations in resolution, contrast, and noise due to different imaging

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conditions, all input images undergo a pre-processing stage. This includes resizing the images to meet the input requirements of the pretrained CNN architectures, intensity normalization to standardize pixel values, and basic noise removal to suppress imaging artifacts. These steps enhance visual consistency across samples and improve the reliability of feature learning.

Following pre-processing, the dataset is divided into training and test sets, as depicted in the block diagram. To mitigate overfitting caused by limited medical imaging data, data augmentation techniques are applied exclusively to the training set. Augmentation operations such as rotation, flipping, scaling, and translation artificially expand the dataset by introducing spatial variations while preserving the underlying tumor characteristics. This step significantly improves model generalization and robustness. Feature extraction and classification are performed using four state-of-the-art pretrained CNN models: VGG16, VGG19, ResNet50, and DenseNet121. These models are initialized with pretrained weights and leveraged through transfer learning to exploit their strong representational capability. The convolutional layers automatically extract hierarchical spatial and textural features from MRI images, capturing critical tumor-related patterns such as shape irregularities, boundary variations, and intensity heterogeneity, without the need for handcrafted feature engineering.

To adapt the pretrained models to the brain tumor classification task, fine-tuning is performed by modifying the final classification layers to accommodate four output classes. A partial fine-tuning strategy is employed in which early convolutional layers are kept frozen to preserve generic feature representations, while deeper layers and newly added classification layers are retrained using the MRI training data. This approach enables effective domain adaptation while preventing overfitting and excessive computational cost.

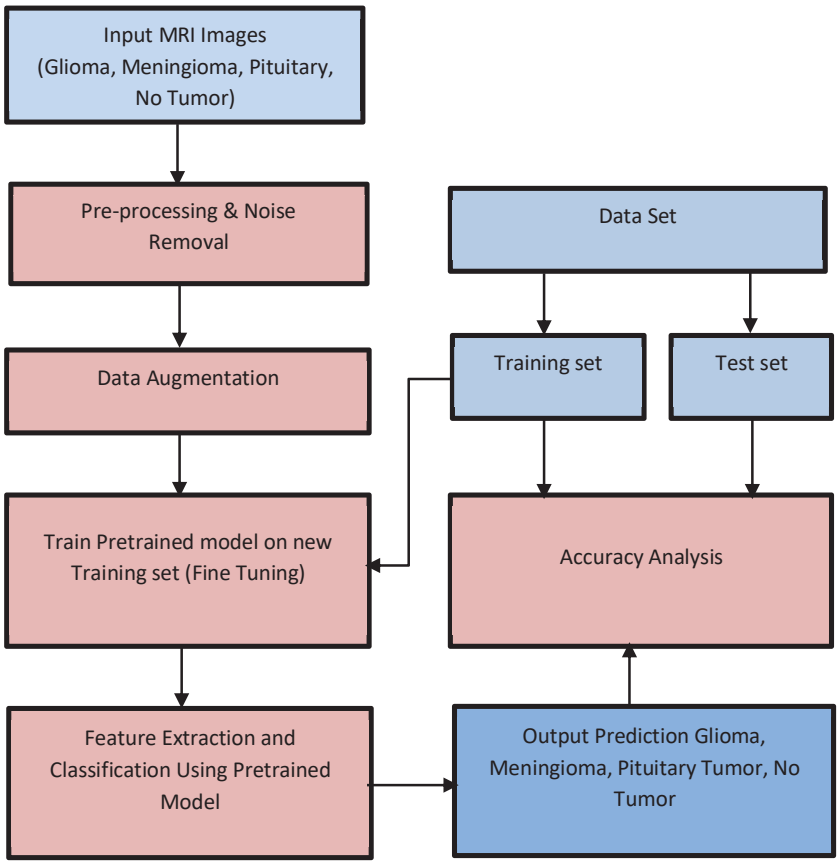

Fig. 1 Proposed Classification Scheme

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During inference, the trained models generate class probabilities for each MRI image, and the final prediction corresponds to the class with the highest confidence score. The output of the system is one of the four categories: Glioma, Meningioma, Pituitary Tumor, or No Tumor. Performance evaluation is conducted on the test set using accuracy-based analysis, enabling a comparative assessment of the effectiveness of VGG16, VGG19, ResNet50, and DenseNet121 within the proposed classification framework.

3.1 Mathematical Concepts Used

Let X be the input MRI image dataset.
Convolution Operation

$$F(i,j) = \sum_{m} \sum_{n} X(i+m, j+n) \cdot K(m,n)$$

Where K is the convolution kernel used to extract spatial features.
ReLU Activation Function

$$f(x) = \max(0, x)$$

Prevents vanishing gradients and adds non-linearity.
Softmax Classification

$$P(y = i \mid x) = \frac{e^{z_i}}{\sum_{j=1}^{c} e^{z_j}}$$

Predicts probability of each tumor class.

3.2 Evaluation Metrics: Definitions

To assess the performance of the proposed brain tumor classification framework, standard evaluation metrics are employed shown in Table 1. Accuracy measures the overall correctness of classification by computing the ratio of correctly predicted samples to the total samples. Precision evaluates the reliability of positive predictions, indicating how many predicted tumor cases are actually correct. Recall reflects the model's ability to correctly identify tumor cases, which is particularly critical in medical diagnosis to minimize false negatives. **F1-score** is a harmonic mean of Precision and Recall that provides a single, balanced measure of a model's classification performance. It is particularly useful when dealing with class imbalance, as it penalizes extreme values of either Precision or Recall. A high F1-score indicates that the model achieves both reliable positive predictions and effective detection of relevant cases. In medical image classification, the F1-score offers a robust indicator of diagnostic reliability by jointly considering false positives and false negatives.

Table 1. Evaluation Metrics

Metric	Formula	Purpose
Accuracy	$\frac{TP + TN}{TP + TN + FP + FN}$	Overall correctness
Precision	$\frac{TP}{TP + FP}$	Reliability of prediction
Recall	$\frac{TP}{TP + FN}$	Ability to detect tumors
F1-score	$\frac{2 * Precesion * Recall}{Precesion + Recall}$	Balanced evaluation

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4. Experiments and Results

The experiments were conducted using a publicly available brain MRI dataset containing four classes: Glioma, Meningioma, Pituitary Tumor, and No Tumor. All images were resized and normalized prior to training. The dataset was divided into training and test sets, with data augmentation applied only to the training data. Pretrained CNN models VGG16, VGG19, ResNet50, and DenseNet121 were fine-tuned for the classification task. Model training was performed using a standard deep learning framework on a GPU-enabled environment. Performance was evaluated on the test set using classification accuracy to compare the effectiveness of the different pretrained architectures.

4.1 Datasets

The MRI dataset consists of four categories as shown in Figure 2:
A. Glioma: Gliomas are infiltrative brain tumors that originate from glial cells. They are characterized by irregular boundaries, which makes them difficult to detect and segment accurately. Gliomas can vary in size and location, often affecting multiple regions of the brain, which presents a challenge for automated detection systems.
B. Meningioma: Meningiomas arise from the meninges, the protective layers covering the brain and spinal cord. These tumors typically have a well-defined structure and distinct edges, making them relatively easier to identify in MRI scans. However, their size and pressure effects on adjacent brain tissues can still impact diagnosis and treatment planning.
C. Pituitary Tumor: Pituitary tumors are located near the pituitary gland, specifically in the sella turcica region. Due to their proximity to critical structures such as the optic nerve and hypothalamus, accurate detection is crucial. These tumors often vary in shape and intensity, requiring precise feature extraction for effective classification.
D. No Tumor: This class contains normal MRI brain images without any detectable abnormalities. Including these images helps the model learn the difference between healthy brain structures and various types of tumors, reducing false positives during classification.

The brain tumor classification system is designed to handle all four classes of MRI images: No Tumor, Pituitary, Glioma, and Meningioma. Users can upload images of any of these types, and the model will classify them into the correct category.

The models were implemented on google colab [20] using TensorFlow/Keras libraries [21]. The Adam optimizer was used for efficient weight updates, and Categorical Cross-Entropy was employed as the loss function for multi-class classification. MRI images were preprocessed by resizing to a standard dimension, normalizing pixel intensity values, and applying data augmentation (rotation, flipping, and zooming) to improve model generalization.

The dataset was divided into 70% training, 15% validation, and 15% testing, with each split containing representative samples from all four classes. During training, the model learned features specific to each tumor type, while validation helped monitor overfitting and optimize performance. For testing, unseen MRI images from all four classes were fed into the model to evaluate its accuracy. Outcome metrics included Accuracy, Precision, Recall, and F1-score for each class. This setup ensures reliable classification for user-uploaded images, providing predictions such as whether an MRI shows No Tumor, Pituitary Tumor, Glioma, or Meningioma, along with confidence scores. The results can help in rapid diagnosis and assist radiologists in decision-making.

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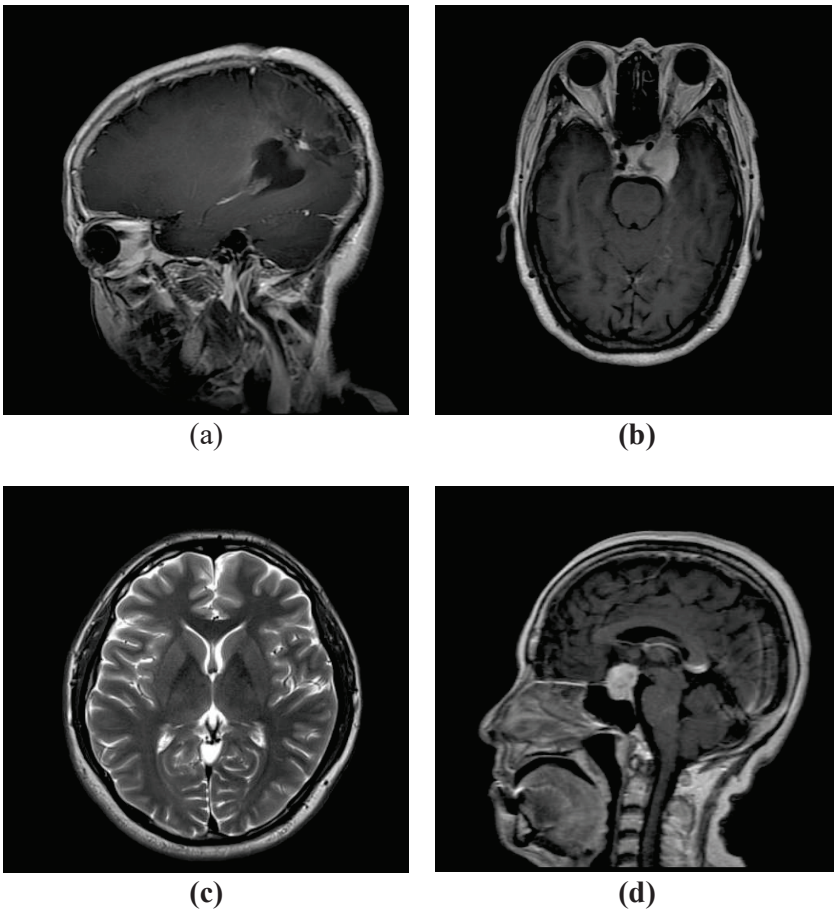

Figure 2. a). Glioma b). Meningioma c). Notumor d). Pituitary

5. Results & Analysis

The experimental results shown in Table 2, indicates that DenseNet121 delivers superior performance due to its ability to maximize feature reuse through dense connections, which is particularly beneficial for capturing complex and subtle tumor patterns in MRI images. The use of transfer learning significantly accelerated convergence and enhanced classification accuracy, demonstrating the effectiveness of leveraging pretrained knowledge for medical image analysis. In addition, data augmentation techniques played a crucial role in reducing overfitting and improving model generalization across all tumor classes. Despite the overall strong performance, most misclassifications were observed between glioma and meningioma, likely due to their similar visual characteristics and overlapping radiological features. Future work will focus on integrating tumor segmentation and attention mechanisms to enhance tumor localization and emphasize clinically relevant regions, which is expected to further improve classification robustness and interpretability.

The line chart shown in Figure 2, visually illustrates the comparative trends of Accuracy, Precision, Recall, and F1-score across the four models. It clearly shows DenseNet121 as the most robust and reliable model for brain tumor classification, followed by ResNet50, thereby validating the quantitative results reported in Table 2.

Table 2. Performance comparison between models

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Model	Test Accuracy	Precision	Recall	F1-Score
VGG16	**84.70%**	84.1%	83.8%	83.9%
VGG19	**86.10%**	85.7%	85.3%	85.5%
ResNet50	**88.90%**	88.5%	88.3%	88.4%
DenseNet121	**90.80%**	90.3%	90.1%	90.2%

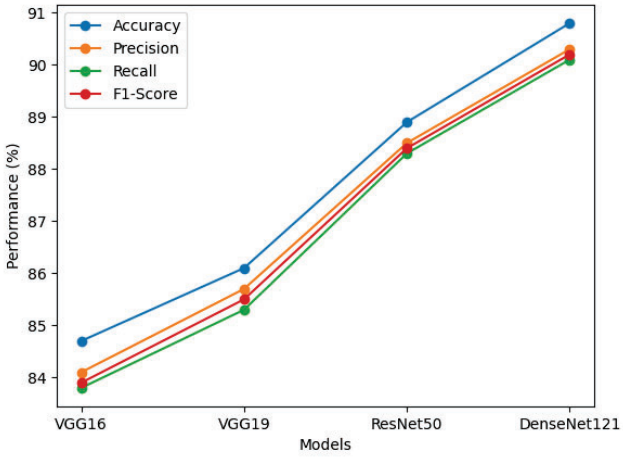

Figure 3. Performance comparison between models

6. Conclusion and Future Work

This study presented a comprehensive deep learning–based framework for automated brain tumor detection and multi-class classification using MRI images. By leveraging transfer learning with pretrained CNN architectures—VGG16, VGG19, ResNet50, and DenseNet121—the proposed system effectively classified MRI scans into four clinically relevant categories: Glioma, Meningioma, Pituitary Tumor, and No Tumor. Experimental results demonstrate that DenseNet121 outperforms the other models, achieving the highest test accuracy (90.80%) along with superior Precision, Recall, and F1-score. This performance gain can be attributed to DenseNet's dense connectivity, which promotes efficient feature reuse, improved gradient propagation, and enhanced representation of complex tumor characteristics.

The results further validate the importance of transfer learning and data augmentation in addressing challenges associated with limited medical imaging datasets, such as overfitting and poor generalization. The comparative analysis confirms that deeper and more advanced architectures, particularly DenseNet121 and ResNet50, are better suited for capturing subtle variations in brain tumor morphology. Overall, the proposed framework demonstrates strong potential as a reliable computer-aided diagnostic support system that can assist radiologists in accurate and timely decision-making.

Future work will focus on extending the framework to 3D CNNs for volumetric MRI analysis, incorporating multimodal MRI sequences (T1, T2, FLAIR) for richer feature representation, and integrating explainable AI techniques such as Grad-CAM to improve clinical interpretability. These enhancements are expected to further strengthen the robustness, transparency, and real-world applicability of automated brain tumor diagnosis systems.

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