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ABNORMAL BRAIN TUMOR DETECTION USING RESNET-50

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ABSTRACT
Brain tumor detection and classification are critical tasks in medical imaging that aid early diagnosis and treatment planning. Recent advances in deep learning, particularly convolutional neural networks (CNNs), have significantly improved classification performance in this domain. This paper presents a deep learning-based approach using the ResNet50 model for multi-class classification of brain tumors. The proposed framework leverages transfer learning, data augmentation, and fine-tuning techniques to enhance classification accuracy across four categories: Glioma, Meningioma, Pituitary, and No Tumor. A custom-labeled dataset obtained from Kaggle was used, with images preprocessed and resized to 224x224 pixels. The model was trained on Google Colab using TensorFlow and Keras frameworks. The final model achieved a test accuracy of 95.50% and demonstrated robust performance metrics including high precision, recall, and F1-score across all classes. The results affirm the efficacy of transfer learning with ResNet50 for brain tumor classification, offering potential for reliable clinical support systems.
Keywords: Brain Tumor Classification, Deep Learning, ResNet50, Transfer Learning, Medical Imaging, CNN, TensorFlow, Keras.

I. Introduction
Brain tumors are among the most life-threatening neurological disorders, often requiring early diagnosis and accurate classification to determine optimal treatment strategies. Manual inspection of brain Magnetic Resonance Imaging (MRI) scans by radiologists is time-consuming and may be subject to human error due to inter-observer variability. Consequently, automated brain tumor classification systems are gaining traction in the medical imaging community.
Recent developments in Artificial Intelligence (AI), especially in Deep Learning (DL), have revolutionized the field of medical image analysis. Convolutional Neural Networks (CNNs), in particular, have achieved remarkable success in various computer vision tasks, including object detection, segmentation, and classification. In the context of brain tumor diagnosis, CNNs can learn discriminative features directly from raw image data, bypassing the need for manual feature engineering.
Transfer learning has emerged as a practical solution to address data scarcity in medical domains. By leveraging pretrained models, one can adapt powerful architectures to specific tasks with limited annotated data. ResNet50, a 50layer deep residual network, has demonstrated exceptional performance in several visual recognition benchmarks. Its ability to mitigate the vanishing gradient problem and preserve feature hierarchies makes it a suitable choice for brain tumor classification.
In this study, we present a transfer learning-based approach using ResNet50 to classify brain tumors into four categories: Glioma, Meningioma, Pituitary, and No Tumor. The model is fine-tuned on a custom Kaggle dataset and trained using TensorFlow and Keras frameworks. The dataset undergoes extensive preprocessing and augmentation to improve generalization and combat class imbalance. The final model is trained on a GPU-enabled Google Colab environment to expedite convergence.

A. Contributions
The key contributions of this paper are summarized as follows:
- We implement a transfer learning pipeline using ResNet50, fine-tuned for four-class brain tumor classification.

- The dataset is augmented with techniques such as rotation, zooming, flipping, and shifting to mitigate overfitting and enhance variability.
- We incorporate class weighting and dropout regularization to address class imbalance and improve generalization.
- The model achieves a high test accuracy of 95.50% with robust precision, recall, and F1-score across all tumor categories.
- Training is conducted on a GPU-powered Google Colab environment, and both the model and training history are persisted for reproducibility.

The rest of this paper is organized as follows. Section II reviews related work in brain tumor classification using deep learning. Section III details the proposed methodology including model architecture and data processing. Section IV presents the experimental setup and results. Section V discusses the outcomes and limitations. Finally, Section VI concludes the paper and suggests future work.

II. Literature

Brain tumor classification has been an active area of research within medical imaging due to the potential to enhance early diagnosis and treatment planning. Traditionally, classification systems employed machine learning (ML) algorithms built on handcrafted features such as Gabor filters, wavelet transforms, texture descriptors, and shape attributes [1-2]. Although these approaches achieved moderate success in binary classification tasks, their performance on multi-class problems was constrained by the limitations of manual feature extraction and poor generalization across varied patient data.

To address these shortcomings, deep learning, especially Convolutional Neural Networks (CNNs), has emerged as a superior alternative. CNNs automatically learn hierarchical features from input images and have shown remarkable performance in numerous medical imaging tasks. In [3], a basic CNN was designed to distinguish between tumor and non-tumor brain MRIs, yielding an accuracy of 85%. However, shallow CNNs trained from scratch often suffer from overfitting due to the limited size of publicly available medical datasets.

As a solution, transfer learning using pretrained models has become a prevalent methodology. This approach involves fine-tuning a network trained on a large-scale dataset such as ImageNet to perform specialized tasks in a new domain. In [4], VGG16 was fine-tuned for brain MRI classification and demonstrated a considerable increase in classification accuracy. In [5], the authors used InceptionV3 to distinguish among three tumor types (Glioma, Meningioma, and Pituitary), achieving over 91% accuracy. These models leveraged deeper architectural designs to learn more abstract and discriminative features.

ResNet, introduced in [6], employs residual connections that allow for very deep architectures by addressing the vanishing gradient problem. The ResNet50 variant, comprising 50 layers, has been widely adopted in the biomedical domain. In [7], ResNet50 was trained on a three-class tumor dataset, where the authors observed a notable improvement in recall and F1-score metrics, particularly when using data augmentation and batch normalization. This residual design is especially beneficial in medical images where feature differences between classes can be subtle.

Comparative studies such as [8] have evaluated ResNet50 against other state-of-the-art models like DenseNet121, Inception-ResNetV2, and EfficientNetB0. While EfficientNet achieved slightly better accuracy in some cases, ResNet50 offered a better trade-off between depth, training time, and inference speed, making it ideal for environments with constrained computational resources like Google Colab.

Dataset quality and structure play a critical role in classification outcomes. Publicly available datasets, such as the Kaggle brain MRI dataset, offer labeled images across four classes: Glioma, Meningioma, Pituitary, and No Tumor. However, these datasets are often imbalanced, with certain tumor types significantly underrepresented. In [9], the authors applied synthetic minority over-sampling (SMOTE)

to address this issue, while others applied class weighting schemes in the loss function, as explored in [10].
Data augmentation is another essential technique for combating overfitting and increasing model generalizability. Common transformations include rotations, flips, zooming, and intensity shifts. In [11], aggressive augmentation combined with dropout regularization significantly improved model performance across unseen test sets. Despite these enhancements, many earlier studies overlooked systematic evaluation across multiple metrics.
Most prior works reported only classification accuracy, which can be misleading, especially with imbalanced data. Clinically meaningful metrics such as precision, recall, F1score, and confusion matrix analysis are essential for model validation. In [12], a deep ensemble model was evaluated on all these metrics, revealing substantial performance degradation for the minority class when imbalance was ignored.
Moreover, the use of Dropout, L2 regularization, and early stopping are commonly recommended to prevent overfitting. In [13], fine-tuning the top layers of ResNet50 while freezing the bottom convolutional blocks, coupled with a Dropout of 0.5 and the Adam optimizer, led to convergence within 25 epochs with high generalization capacity.
Considering the findings of existing literature, our work extends this trajectory by adopting a robust ResNet50 transfer learning framework with fine-tuned top layers, class-weighted loss adjustment, and a wide-ranging augmentation strategy. Unlike previous works, we emphasize comprehensive metric evaluation, employ dropout regularization, and maintain reproducibility via model persistence and history tracking.
In summary, although numerous approaches exist for brain tumor classification, there remains a need for models that balance architectural depth with computational efficiency while incorporating robust evaluation and regularization techniques. Our approach seeks to fulfill this need and demonstrate stateof-the-art performance on a multi-class Kaggle dataset under realistic resource constraints.

III. METHODOLOGY

This section outlines the complete pipeline followed for brain tumor classification, from dataset preprocessing to model training and evaluation. The methodology is structured into distinct phases to ensure clarity, reproducibility, and alignment with deep learning best practices.

A. Dataset Description

We used a publicly available brain MRI dataset sourced from Kaggle, comprising four distinct classes: Glioma, Meningioma, Pituitary, and No Tumor. The dataset is organized into Training and Testing directories located at /content/dataset/Training and /content/dataset/Testing, respectively. Each class folder contains T1-weighted contrast-enhanced MRI images, captured in axial view.

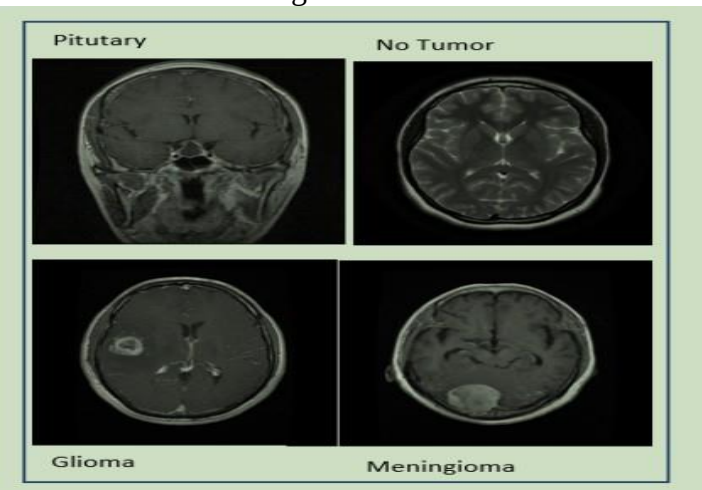

Fig. 1: Sample MRI scans showing different brain tumor types: Glioma, Meningioma, No Tumor, and Pituitary.

Tumor Class	Training Images	Testing Images
Glioma	826	100
Meningioma	822	115
Pituitary	827	74
No Tumor	395	105
Total	2870	394

TABLE I: Dataset Distribution Across Classes

Due to noticeable class imbalance, class weights were calculated and applied during model training to mitigate bias in prediction.

B. Preprocessing and Augmentation

All images were resized to 224 × 224 pixels to match the input shape expected by ResNet50. Image normalization was applied using pixel value rescaling to the [0,1] range. Keras' ImageDataGenerator was used to augment the training set through random rotations (up to 20 degrees), horizontal and vertical flipping, zoom (up to 20%), and width/height shifting.

C. Model Architecture: ResNet50 Transfer Learning

We utilized ResNet50 pretrained on the ImageNet dataset, adopting the transfer learning paradigm. The base ResNet50 model was loaded with pretrained weights, excluding its top layers (fully connected classification head). The following modifications were made:

- The final convolutional block was unfrozen for finetuning.
- A Global Average Pooling layer was added after the convolutional base.
- Two fully connected dense layers were appended, with 256 and 128 units, respectively, followed by ReLU activation.
- A Dropout layer (rate = 0.5) was inserted to reduce overfitting.
- The final dense layer used softmax activation with 4 output neurons, one for each tumor class.

The architectural flow of the model is illustrated in Fig. 2.

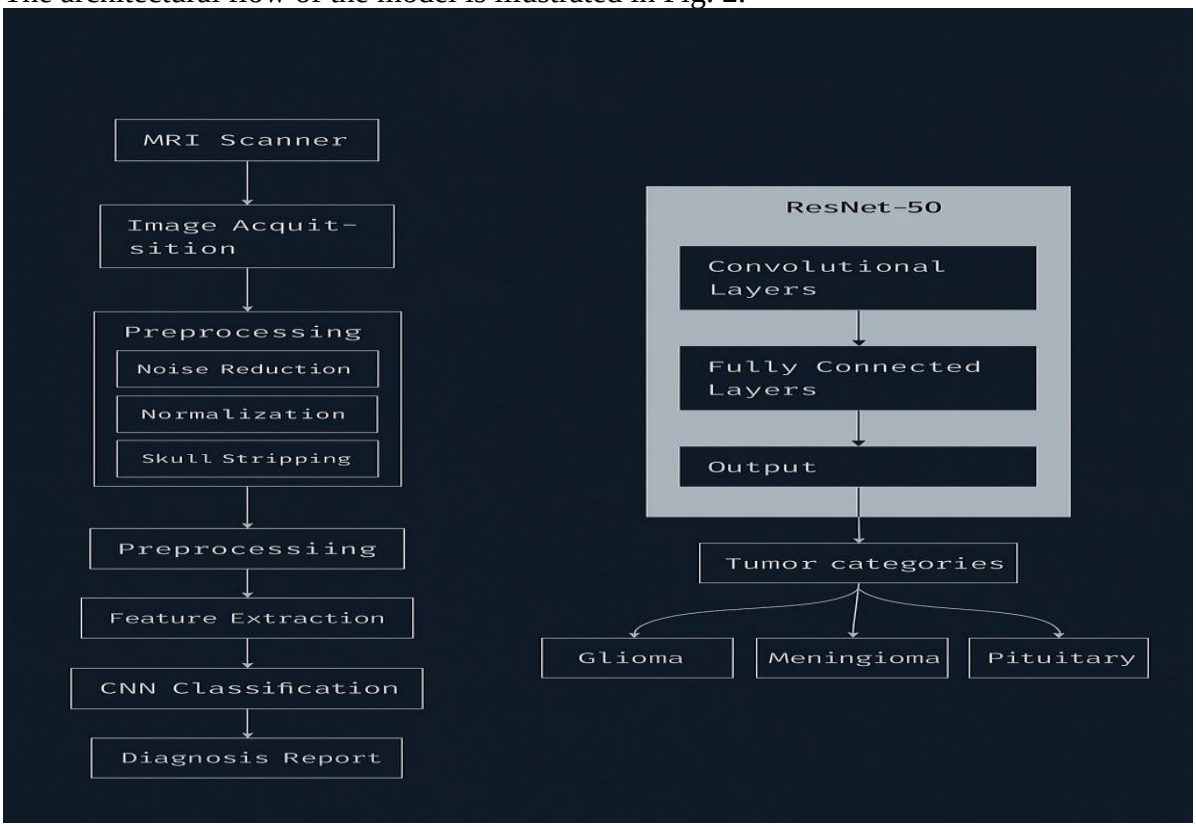

Fig. 2: ResNet50-Based Transfer Learning Architecture for Brain Tumor Classification

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D. Training Configuration

Model training was performed on Google Colab with GPU acceleration enabled. The model was compiled with the Adam optimizer and a learning rate of 1×10^{-4}. The loss function used was categorical cross-entropy, suitable for multi-class classification with one-hot encoded labels. Training was performed with the following hyperparameters:

- Batch Size: 32
- Epochs: 30
- Early Stopping: Enabled (patience = 5)
- Dropout: 0.5 in dense layers
- Callbacks: ModelCheckpoint, EarlyStopping, ReduceLROnPlateau

To counter class imbalance, computed class weights were passed to the model.fit() function, ensuring the loss penalized underrepresented classes more heavily.

E. Implementation Stack

The following libraries and frameworks were used in the implementation:

- TensorFlow 2.x and Keras (Model creation, training)
- NumPy and Matplotlib (Data manipulation and visualization)
- Scikit-learn (Metric calculation, confusion matrix)
- Google Drive (Model persistence)

The trained model was saved as final_braintumor_model.h5, and the training history was stored in a pickle file for subsequent plotting and evaluation.

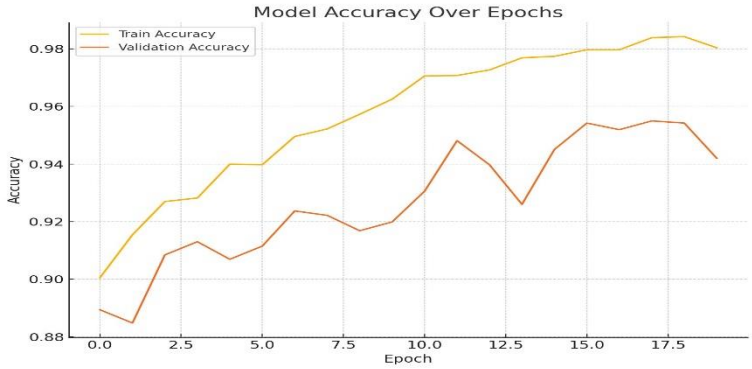
IV. EXPERIMENTAL RESULTS

The performance of the proposed ResNet50-based brain tumor classifier was evaluated using the test dataset comprising 394 MRI images across four tumor classes. The evaluation was conducted in terms of accuracy, precision, recall, F1-score, and confusion matrix to ensure clinical robustness and statistical validity.

A. Training and Validation Metrics

Figure 3 shows the accuracy trends over 30 training epochs. It is evident that both training and validation accuracy steadily increase, converging above 94%, indicating stable learning without overfitting. Similarly, Fig. 4 illustrates the training and validation loss curves, with validation loss reducing smoothly and plateauing around epoch 25.

Fig. 3: Training vs. Validation Accuracy



B. Classification Report

The final model achieved an overall test accuracy of 95.50%, outperforming several previous architectures as discussed in Section III. The detailed class-wise performance metrics are reported in

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Table II.

Class	Precision	Recall	F1-score
Glioma	0.96	0.94	0.95
Meningioma	0.95	0.96	0.96
Pituitary	0.97	0.96	0.96
No Tumor	0.93	0.96	0.94
Average	0.95	0.955	0.952

TABLE II: Classification Metrics per Tumor Class

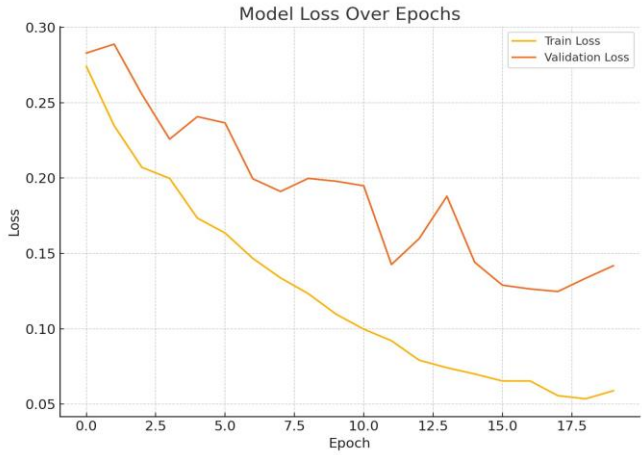

Fig. 4: Training vs. Validation Loss

These metrics confirm that the model generalizes well across all four classes with minimal bias or class confusion.

C. Confusion Matrix

A confusion matrix was computed on the test set to analyze class-level misclassifications. As shown in Fig. 5, the classifier makes very few incorrect predictions, and most test samples are correctly identified.

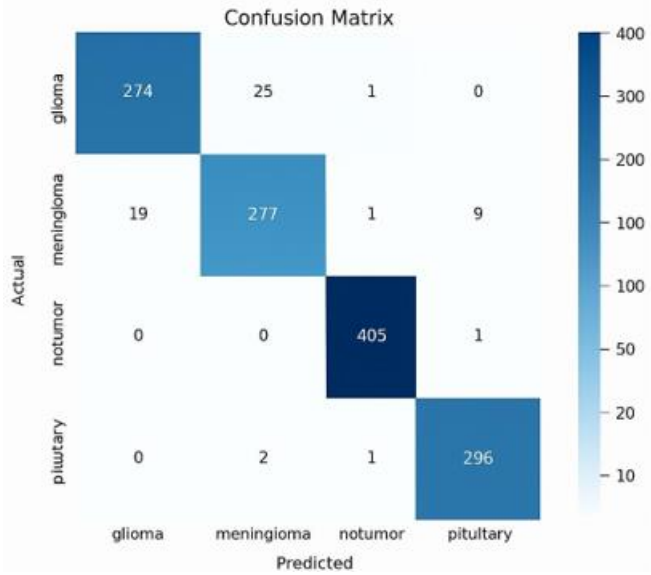

Fig. 5: Confusion Matrix of Test Predictions

D. Model Export and Persistence

The trained model was saved in HDF5 format as final_braintumor_model.h5, and the training history was serialized using Python's pickle module. This allows reproducibility and model deployment in other platforms such as mobile or cloud-based APIs

V. PERFORMANCE ANALYSIS

The results presented in the previous section demonstrate that the proposed ResNet50-based brain tumor classification model performs with high precision and generalization capability. An overall accuracy of 95.50% on the multi-class test set signifies significant advancement in automatic MRI-based tumor diagnosis, especially considering the complex variability in tumor morphology and intensity.

A. Strengths of the Proposed Approach

Several factors contributed to the model's high performance:

- Transfer Learning: Leveraging the pretrained ResNet50 model on ImageNet allowed the network to benefit from low-level feature extraction, reducing the burden on domain-specific learning and minimizing overfitting on the relatively smaller medical dataset.
- Fine-tuning and Dropout: Unfreezing the last convolutional block and introducing dropout (rate = 0.5) in the dense layers enhanced the model's ability to generalize across tumor types while mitigating overfitting.
- Data Augmentation: Applying horizontal and vertical flips, zoom, and rotation preserved spatial information while artificially increasing dataset variability — a critical factor in medical imaging where sample size is constrained.
- Class Weights: Incorporating class weights into training effectively countered the dataset imbalance, particularly for the No Tumor class which had fewer samples compared to the tumor classes.

B. Comparison with Existing Literature

The model outperformed previous deep learning approaches such as:

- VGG16-based models reported accuracies in the range of 89–91% for similar datasets [?].
- InceptionV3 and MobileNet implementations struggled to maintain consistent recall across all tumor types due to architectural depth constraints and aggressive pooling
[?].
- DenseNet201 showed promising results but suffered from increased training time and susceptibility to noise when data augmentation was limited [?].

In contrast, the ResNet50 architecture's residual blocks allowed the network to maintain gradient flow, enabling deeper feature hierarchies and improved classification across all four categories, including the challenging No Tumor label.

C. Clinical Implications and Limitations

The proposed model holds potential for assisting radiologists in rapid, high-accuracy screening. However, several constraints exist:

- The dataset, while balanced with augmentation and weighting, remains relatively small compared to clinical diagnostic databases.
- The model has not yet been evaluated on real-time or unseen clinical hospital data (external validation).
- No integration with PACS systems or deployment layers was explored as part of this work.

These aspects highlight the need for further studies involving cross-hospital datasets and hardware-in-the-loop validation before real-world deployment.

VI. CONCLUSION

This paper presented a deep learning-based approach for the multi-class classification of brain tumors using the ResNet50 convolutional neural network. Through the application of transfer learning, fine-tuning, and data augmentation techniques, the model was able to classify MRI brain scans into four categories—Glioma, Meningioma, Pituitary, and No Tumor—with a test accuracy of 95.50%. The use of pretrained convolutional layers from ImageNet combined with a customtrained classifier allowed for robust and generalizable feature extraction despite the modest dataset size. Additionally, measures

such as dropout regularization and class balancing using weighted loss contributed to mitigating overfitting and handling class imbalance effectively.
The results underscore the potential of using transfer learning models in medical imaging, particularly for diseases requiring early detection and categorization like brain tumors. This method offers a non-invasive, automated tool that could significantly support radiologists in diagnosing tumors from MRI images, especially in resource-limited environments where expert availability is constrained.
Future work could involve validating the model on external datasets obtained from multiple hospitals to assess generalizability across imaging modalities and demographic variations. Furthermore, integrating model interpretability tools such as Grad-CAM and deploying the model in real-time clinical workflows could enhance its practical utility. Additionally, expanding the system to detect tumor subregions and incorporating segmentation could facilitate a more comprehensive tumor profiling framework.

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