

# Deep learning-based automated brain tumor detection using a proposed convolutional neural network architecture

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## ABSTRACT

Brain tumors pose a critical threat to human health, often resulting in significant neurological impairments and high mortality rates. Early and accurate detection is essential for improving patient outcomes; however, conventional diagnostic methods, such as magnetic resonance imaging (MRI) interpretation by radiologists, are prone to subjectivity and inconsistency. This study proposes a deep learning (DL)-based solution to automate brain tumor detection using a customized convolutional neural network (CNN) architecture tailored for multi-class classification of glioma, meningioma, pituitary tumors, and non-tumor cases. The model incorporates residual blocks, activation functions, and batch normalization to extract and generalize complex spatial features from MRI images. A dataset of 6,000 labeled MRI images was preprocessed and augmented to enhance robustness. The model was evaluated using standard metrics: accuracy, precision, recall, and F1-score. Comparative analysis against ResNet50, InceptionV3, and MobileNetV2 demonstrated superior performance of the proposed model, achieving a classification accuracy of 99.14% and F1-scores of up to 1.00 across some tumor classes. These results validate the model's potential as a reliable and scalable diagnostic aid, offering improved accuracy and reduced diagnostic time. This work sets the foundation for intelligent, accessible, and clinically deployable brain tumor detection systems.

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## 1. INTRODUCTION

Brain tumors represent one of the most critical health challenges in the field of neuro-oncology, characterized by their diverse nature and varying degrees of severity, from benign lesions to aggressive malignancies. The complexity associated with brain tumors often results in significant neurological deficits, cognitive impairments, and notably shortened life expectancy for patients, emphasizing the critical need for timely and accurate diagnosis [1]. According to recent epidemiological reports, there has been a noticeable increase in brain tumor cases globally, reflecting the growing public health concern and underscoring the urgent necessity for innovative diagnostic techniques and treatments [2]. Conventionally, brain tumor detection has

heavily relied on imaging techniques such as magnetic resonance imaging (MRI) and computed tomography (CT) scans. Although these methods have greatly advanced medical diagnostics, they are inherently dependent upon the subjective interpretation skills of radiologists. Such reliance introduces variability and inconsistency, which could potentially result in delayed diagnosis or misdiagnosis, thereby negatively impacting patient outcomes [3]. Additionally, regions with limited healthcare resources experience exacerbated challenges due to a shortage of experienced radiologists, further increasing the risk of delayed detection and treatment initiation [4]–[6].

With the advent of artificial intelligence (AI), especially machine learning (ML) and deep learning (DL) techniques, the healthcare industry has witnessed a significant shift towards automation and computational diagnostics [7]. DL, a subset of ML, has particularly emerged as a powerful tool for medical image analysis because of its ability to automatically extract and interpret complex patterns within imaging data. Convolutional neural networks (CNNs), a specialized DL architecture, have exhibited remarkable success in medical imaging tasks, notably in the detection and classification of tumors, outperforming traditional methodologies in terms of accuracy, consistency, and efficiency [8]. Despite recent advancements, existing DL models encounter various challenges, such as computational intensity, difficulties in model interpretability, and varying effectiveness based on tumor size or type [9]–[11]. In addition, many models rely on complex architectures or are evaluated using relatively limited datasets, which may restrict their generalizability and practical applicability in real clinical environments. Furthermore, several studies focus primarily on improving classification accuracy without adequately addressing issues related to computational efficiency, model transparency, and reproducibility. These limitations highlight an important research gap in developing efficient and reliable DL architectures that can achieve high diagnostic performance while maintaining practical feasibility for real-world medical applications [9]–[11].

Addressing these limitations, our research introduces a comprehensive approach leveraging advanced CNN architecture specifically tailored for robust brain tumor detection and accurate classification. Unlike many existing approaches that rely heavily on generic DL architectures or computationally intensive models, the proposed study focuses on designing a customized CNN architecture that balances classification accuracy with architectural efficiency while ensuring transparent implementation and reproducible experimental evaluation. The primary motivation behind our study is to bridge existing gaps by developing a reliable, efficient, and user-friendly diagnostic system capable of handling the diverse presentation of brain tumors seen in clinical practice [12]–[14].

The main contributions of this research are detailed comprehensively as follows: firstly, this work introduces a novel CNN architecture specifically tailored to the challenging task of brain tumor detection and classification from MRI images. The proposed model employs an advanced CNN design featuring multiple convolutional layers integrated within residual blocks, pooling layers for efficient feature dimension reduction, and fully connected layers responsible for accurate tumor classification. By carefully combining residual connections and rectified linear unit (ReLU) activation functions, the proposed architecture significantly mitigates common training challenges such as the vanishing gradient problem, enabling deeper learning and improved recognition capabilities. Secondly, extensive experimental validation of the developed model has been meticulously conducted using a substantial dataset containing 6,000 MRI images equally distributed across four distinct classes: glioma, meningioma, pituitary tumors, and non-tumor cases. To enhance model generalization and robustness, comprehensive preprocessing and data augmentation techniques were systematically implemented. This included normalization, resizing, noise reduction, image rotation, cropping, and flipping. Thirdly, this research presents an in-depth comparative analysis against prominent CNN architectures commonly used in medical imaging applications, namely ResNet50, InceptionV3, and MobileNetV2. The experimental results conclusively demonstrate the proposed model's superior performance, achieving an exceptional accuracy rate of 99.14%, notably surpassing benchmark models in terms of precision, recall, and F1-score metrics. These comparisons underscore the robustness and effectiveness of our novel CNN-based methodology in accurately classifying complex and heterogeneous tumor types.

This research paper is systematically structured to thoroughly explore and present our findings. Following this introductory section, a comprehensive literature review in section 2 critically analyzes previous studies and highlights existing gaps in brain tumor diagnostic methods. Section 3 details the proposed methodologies, clearly outlining each phase from data collection and preprocessing to the final CNN model architecture. Section 4 discusses experimental results comprehensively, analyzing dataset characteristics, experimental setups, and performance comparisons. Lastly, section 5 summarizes our findings and draws pertinent conclusions.

## 2. LITERATURE REVIEW

Recent advances in computational methods, particularly ML and DL, have substantially reshaped medical imaging diagnostics, including brain tumor detection and classification. Numerous studies have introduced various ML and DL-based approaches for brain tumor analysis, demonstrating different

performance levels and methodological limitations in accurately detecting brain tumors from medical images, particularly MRI.

Early research explored traditional ML techniques combined with handcrafted feature extraction methods. Amin *et al.* [15] addressed early tumor detection employing statistical approaches alongside ML. Their proposed technique used noise reduction via Wiener filtering and wavelet bands, clustering algorithms to isolate tumor pixels, and fusion of features derived from local binary patterns (LBP) and Gabor wavelet transform (GWT). Although the method achieved approximately 88% accuracy, its reliance on handcrafted features and limited interpretability may reduce robustness and restrict clinical applicability.

With the emergence of DL, CNNs have become the dominant paradigm for medical image analysis. Sajid *et al.* [16] developed a hybrid CNN architecture focusing on glioma segmentation. Their framework integrated patch-based analysis alongside regularization techniques like dropout and batch normalization to reduce overfitting. Additionally, the model employed a two-phase training strategy to enhance segmentation performance. While their method demonstrated robust segmentation outcomes, achieving 0.86, 0.86, and 0.91 for dice score, sensitivity, and specificity, respectively, for the whole tumor region, the relatively limited training dataset may restrict clinical generalizability, pointing to the need for evaluation on larger datasets.

Other studies have attempted to enhance classification performance by integrating hybrid computational frameworks. Özyurt *et al.* [17] explored a hybrid approach combining neutrosophy and CNN to classify brain tumors as benign or malignant. They applied neutrosophic sets for initial segmentation, followed by CNN-based feature extraction and classification using support vector machines (SVM) and k-nearest neighbors (KNN). Their methodology achieved high accuracy (95.62%); however, the multi-stage framework increases computational complexity, posing challenges for scalability and practical clinical implementation.

Similarly, Amin *et al.* [18] presented a segmentation-based approach combined with SVM for detecting brain tumors from MRI images. Segmentation techniques were applied to identify tumor regions, followed by extraction of shape, texture, and intensity-based features. These features were then used as inputs to the SVM classifier, achieving high diagnostic performance, with accuracy of approximately 97.1%, an area under the receiver operating characteristic curve (AUC) of 0.98, a sensitivity of 91.9%, and a specificity of 98.0%. Despite these strong results, the approach faced challenges related to model interpretability, which may limit its clinical applicability.

To address feature representation limitations, more recent studies have focused on advanced CNN architectures. Toğaçar *et al.* [19] introduced BrainMRNet, a CNN-based architecture leveraging attention modules and hypercolumn techniques within a residual network design. Compared to pre-trained CNN models such as AlexNet, GoogleNet, and VGG-16, BrainMRNet demonstrated improved classification accuracy (96.05%). Although effective, the complexity inherent in their model may increase computational cost and limit practical clinical deployment, emphasizing the need for simpler and more efficient models.

Transfer learning has also been widely explored to improve performance in medical imaging tasks with limited datasets. Majib *et al.* [20] introduced VGG-SCNet, a stacked classifier using transfer learning and hybrid techniques for brain tumor classification from MRI images. Their experiments demonstrated strong performance, achieving precision, recall, and F1-scores of approximately 99%. However, the method used a limited dataset, which may affect model generalizability to diverse clinical data, highlighting the need for validation on larger datasets.

Segmentation-based frameworks have also shown promising results in tumor localization tasks. Sadad *et al.* [21] adopted the U-Net framework with ResNet50 as a backbone network to segment brain tumors. Using data augmentation and preprocessing, their model achieved an intersection-over-union (IoU) rate of 0.95, indicating accurate tumor boundary segmentation. They also evaluated several CNN architectures, including DenseNet201 and NASNet, with NASNet achieving the highest accuracy of 99.6%. Despite these results, the model's high computational complexity and limited evaluation datasets may restrict its practical use in real-time clinical environments. Rehman *et al.* [22] focused on pediatric brain tumor diagnosis using 3D CNN-based architecture and feature selection methods. While their model demonstrated good results (88% accuracy), the specificity to pediatric cases limited applicability for adult populations, representing an essential limitation. Thus, generalizing these models across diverse age groups remains an open research challenge.

Hybrid DL frameworks have also been explored to improve classification accuracy. Khairandish *et al.* [23] proposed a hybrid CNN-based framework integrated with SVM classifiers. The method used threshold-based segmentation and CNN feature extraction, followed by SVM classification. This approach yielded significant improvements, reaching an overall accuracy rate of 98.49%. Nevertheless, their model exhibited certain constraints, particularly regarding the precise localization of tumors. In clinical scenarios, accurately pinpointing tumor locations remains crucial for effective treatment planning, indicating a critical gap that needs further exploration.

More recently, Saeedi *et al.* [24] developed DL models, specifically 2D CNNs and convolutional auto-encoder networks, using an extensive MRI dataset of 3,264 images. Their study highlighted strong performance outcomes (96.47% accuracy), yet computational complexity again emerged as a significant limitation, indicating the persistent need for developing computationally efficient yet accurate methods. To provide clarity and facilitate comparative analysis, the key findings, methodologies, datasets used, achieved accuracy, and respective limitations of these important studies are summarized in Table 1.

Table 1. Summary of existing brain tumor detection and classification studies based on MRI images

| Author(s)                      | Year | Methodology                            | Key strength                                             | Limitation                                           | Evaluation metric                                                               | Key result (%) | Future work                                    |
|--------------------------------|------|----------------------------------------|----------------------------------------------------------|------------------------------------------------------|---------------------------------------------------------------------------------|----------------|------------------------------------------------|
| Amin <i>et al.</i> [15]        | 2019 | Weiner filter with wavelet bands       | Effective noise reduction and early tumor detection      | Limited Interpretability and complexity concerns     | Peak signal-to-noise ratio, mean squared error, and structured similarity index | 88             | Couple with supervised techniques              |
| Sajid <i>et al.</i> [16]       | 2019 | Hybrid CNN (patch-based method)        | Advanced regularization techniques to reduce overfitting | Small dataset size limits generalization             | Dice score, sensitivity, and specificity                                        | 86, 86, and 91 | -                                              |
| Özyurt <i>et al.</i> [17]      | 2019 | Neutrosophy-based CNN (NS-CNN)         | Effective feature extraction using CNN                   | High computational complexity and runtime            | 5-fold cross-validation                                                         | 95.62          | Investigate additional neutrosophic frameworks |
| Amin <i>et al.</i> [18]        | 2020 | SVM and lesion segmentation            | Accurate variation between benign and malignant tumors   | Limited interpretability due to handcrafted features | AUC and Accuracy                                                                | 97.1           | -                                              |
| Toğaçar <i>et al.</i> [19]     | 2020 | BrainMRNet deep CNN architecture       | Improved performance compared with pretrained CNN models | Model complexity limits clinical deployment          | Specificity, sensitivity, F-score, and accuracy                                 | 96.05          | Evaluation with other imaging modalities       |
| Majib <i>et al.</i> [20]       | 2021 | VGG-SCNet with transfer learning       | High precision, recall, and F1-scores                    | Small dataset size, limiting generalization          | Precision, recall, and F1-score                                                 | 99.2           | Detect other tumor types                       |
| Sadad <i>et al.</i> [21]       | 2021 | ResNet50 with U-Net architecture       | High segmentation and classification performance         | High computational resource requirements             | IoU and accuracy                                                                | 99.6           | Reduce complexity                              |
| Rehman <i>et al.</i> [22]      | 2021 | 3D CNN with feature selection          | Effective for pediatric brain tumor diagnosis            | Limited applicability to adult populations           | ROC-AUC                                                                         | 88             | Expand dataset diversity across age groups     |
| Khairandish <i>et al.</i> [23] | 2022 | Hybrid CNN-SVM                         | High binary classification accuracy                      | Limited tumor localization capability                | Accuracy                                                                        | 98.49          | Apply bio-inspired optimization techniques     |
| Saeedi <i>et al.</i> [24]      | 2023 | 2D CNN with convolutional auto-encoder | Large dataset used for model validation                  | High computational cost                              | Accuracy                                                                        | 96.47          | Improve efficiency through model optimization  |

Despite the substantial progress achieved in applying ML and DL techniques to brain tumor detection, several limitations still restrict their clinical applicability. Many models are developed using relatively small or single-source MRI datasets, which may not represent the diversity of real clinical environments and therefore limit generalizability. Additionally, some studies rely on highly complex DL architectures that introduce significant computational demands. Although these models often achieve high accuracy, their computational requirements may hinder deployment in routine clinical workflows. Another major concern is the limited interpretability of many DL-based systems, as they function as black-box models. This lack of transparency can reduce clinicians' confidence in adopting such systems for medical decision support. Furthermore, several approaches focus mainly on classification accuracy while overlooking important clinical aspects such as precise tumor localization and robust validation across diverse datasets. Therefore, further research is required to develop models that are accurate, computationally efficient, generalizable, and clinically interpretable.

### 3. PROPOSED METHOD

This section elaborates comprehensively on the proposed methodology adopted in this research. The methodology is systematically structured into several distinct stages, including data collection, preprocessing, augmentation, model architecture, and detailed procedures related to model training, testing, and evaluation.

#### 3.1. Data collection

The dataset utilized in this study was obtained from an openly available source hosted on Kaggle, specifically the “Brain Tumor MRI Dataset” provided by Nickparvar [25]. This dataset consists of high-quality MRI images categorized into four distinct classes: glioma, meningioma, pituitary tumors, and healthy (non-tumor) brain images. Initially, the original dataset comprised approximately 7,023 images. To ensure balanced class representation, exactly 1,500 images were selected from each category, yielding a final, balanced dataset of 6,000 MRI images, facilitating robust training and fair evaluation. It should be noted that the dataset originates from a single publicly available repository, and external or multi-institutional validation was not performed in this study. Therefore, while the experimental results demonstrate strong performance, further validation using independent clinical datasets from multiple institutions would be necessary to fully assess the model’s clinical generalizability.

#### 3.2. Data preprocessing

Data preprocessing is essential for image standardization and improving model performance. Initially, all MRI images were resized uniformly to a resolution of 150×150 pixels to facilitate computational efficiency. Subsequently, image normalization was conducted by scaling pixel intensity values from their original range (0-255) down to a normalized range of (0-1), significantly improving model convergence during training. Furthermore, noise reduction was carried out to improve image clarity using Gaussian smoothing filters, which eliminated minor artifacts and enhanced image quality. Although the input resolution (150×150) is relatively small, it was selected as a balance between computational efficiency and feature preservation. Experimental observations indicated that this resolution retains the essential structural features required for tumor classification while significantly reducing training complexity.

#### 3.3. Data augmentation

Due to the relatively limited size of available medical imaging datasets and the high likelihood of model overfitting, extensive data augmentation was implemented as a critical step in this research. Specifically, various augmentation strategies were systematically applied, including horizontal and vertical flips, rotations at incremental angles, random cropping, zooming, and shifting. These techniques generated multiple diverse variations of the original dataset images, significantly increasing the dataset’s complexity and variability, thereby improving the generalizability and robustness of the proposed CNN model. Although a separate quantitative elimination study was not conducted to isolate the individual contribution of augmentation, these techniques were applied as a standard practice in medical image classification to enhance model generalization and improve robustness to variations in MRI acquisition conditions. The use of augmentation was therefore intended to support stable training and reduce overfitting when learning from the available dataset.

#### 3.4. Convolutional neural network model architecture

The proposed CNN architecture is carefully designed to ensure robust performance in detecting and classifying brain tumors from MRI images. The model strategically integrates multiple convolutional layers, residual blocks, activation functions, pooling operations, and dense layers to extract discriminative features critical for precise classification. Initially, as illustrated in Figure 1, the network accepts input images with dimensions of 150×150 pixels, incorporating three color channels (RGB). This standardized input ensures uniformity and facilitates efficient processing by subsequent layers. The proposed CNN architecture begins with two sequential convolutional layers (Conv2D) responsible for preliminary feature extraction. The first convolutional layer uses 32 filters with a kernel size of 3×3, followed by a second convolutional layer with 64 filters and a 3×3 kernel, which are commonly used default settings in CNN-based image classification models. These convolutional layers employ multiple filters to systematically analyze and capture essential low-level features such as edges, textures, and basic structural elements inherent within the MRI scans.

To address the training challenges associated with deeper networks, such as vanishing gradients, the model introduces carefully designed residual blocks featuring skip connections (“Add” operations). Residual connections serve as a direct pathway linking earlier layers to deeper layers, thus permitting information to flow efficiently throughout the network. Specifically, these skip connections help maintain gradient magnitudes during backpropagation, ensuring deeper layers effectively capture hierarchical and abstract feature representations essential for distinguishing complex tumor types. Within the residual blocks, convolutional operations employ 64–128 filters with 3×3 kernels, which represent commonly adopted default

configurations for feature extraction in CNN architectures. After each residual block, ReLU activation functions are strategically incorporated. These activation layers impart essential non-linearities into the model, significantly enhancing its ability to learn intricate patterns from complex imaging data. ReLU activations are chosen for their computational simplicity and ability to accelerate the network's convergence, effectively mitigating issues like neuron saturation.

Interleaved with convolutional and residual layers are MaxPooling2D operations, serving a critical role in reducing the dimensionality of feature maps. Max pooling systematically extracts dominant features from local regions of the feature maps, preserving the most significant characteristics while substantially reducing computational complexity. A pooling window of  $2 \times 2$  is applied, which is a widely used default configuration for spatial down-sampling in CNN models. This step aids in improving the model's ability to generalize and reduces potential overfitting, enhancing the robustness of predictions on unseen data.

Following multiple convolutional, residual, and pooling operations, the feature maps generated are flattened into a single-dimensional feature vector. This flattened feature vector is subsequently passed into fully connected dense layers that perform high-level feature integration and complex feature-to-class mapping. Between these dense layers, dropout regularization is deliberately introduced, temporarily disabling random neuron connections during training. A dropout rate of 0.5 is applied, which represents a commonly used default regularization value in DL architectures to mitigate overfitting and improve generalization performance. The use of dropout significantly enhances the network's generalization capability by preventing excessive reliance on any subset of neurons, thereby reducing overfitting risks.

The final stage of the architecture involves a SoftMax activation function embedded in the output layer. The SoftMax function converts the final outputs into probability scores for four classes: glioma, meningioma, pituitary tumors, and non-tumor cases. Thus, the classification outcome is both interpretable and actionable, clearly indicating the most likely tumor class for the given MRI image. The carefully designed combination of convolutional layers, residual blocks, activation functions, pooling, dense layers, and regularization techniques culminates in an effective and efficient proposed CNN architecture, specifically optimized for accurate and reliable brain tumor classification. Figure 1 provides a detailed visual representation of the CNN architecture, illustrating the intricate arrangement of convolutional layers (Conv2D), residual connections ("Add"), activation layers (ReLU), pooling layers (MaxPooling2D), dense layers, dropout, flattening, and the final SoftMax classification layer.

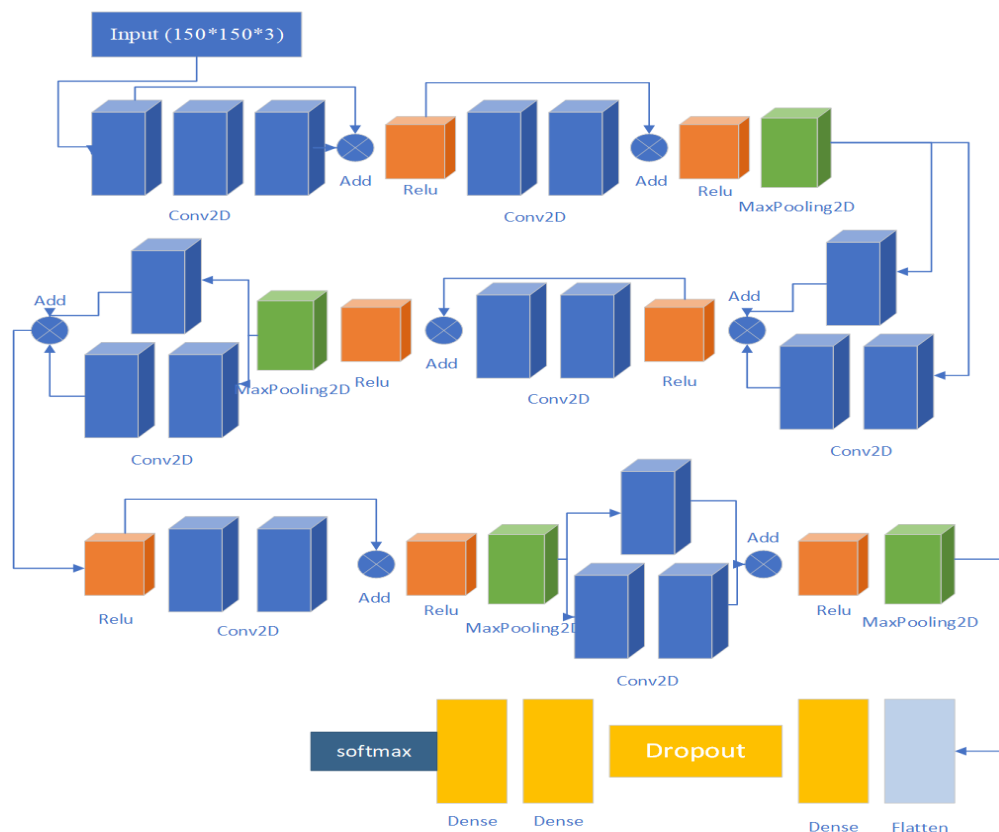


Figure 1. Schematic diagram of the proposed CNN model architecture for brain tumor classification

3.5. Model training and validation

The proposed CNN model was trained using supervised learning, with categorical cross-entropy employed as the loss function. The Adam optimizer was selected to provide an adaptive learning rate and promote efficient and stable model convergence. Training was performed using a learning rate of 0.001, a batch size of 64 and 50 epochs. The dataset was partitioned into training and validation subsets, allocating 90% (5,400 images) for model training and 10% (600 images) for validation. This division enabled continuous monitoring of model performance throughout training and facilitated the identification and mitigation of potential overfitting.

4. EXPERIMENTAL RESULTS AND DISCUSSION ANALYSIS

This section evaluates the experimental results of the proposed CNN model for brain tumor detection and classification. It outlines the experimental setup, assesses performance using accuracy, precision, recall, and F1-score, and discusses the model’s strengths and limitations in comparison with existing approaches.

4.1. Experimental setup and parameter settings

All experiments were executed on Google Colab Pro, providing access to high-performance GPU computing and adequate memory for DL tasks. Model training and validation were conducted using a Tesla P100 GPU with 16 GB of VRAM, enabling faster convergence and reduced computational time. The software environment was based on Python 3.10 and included TensorFlow 2.x, Keras, NumPy, Pandas, OpenCV, and Matplotlib for model implementation, data processing, and visualization. This study employed a publicly available brain tumor MRI dataset obtained from Kaggle, comprising 6,000 high-quality images evenly distributed among four classes: glioma, meningioma, pituitary tumor, and non-tumor. The dataset was divided into training and validation subsets, with 90% of the images (5,400 images) allocated for training and the remaining 10% (600 images) retained for validation.

The training configuration was established through empirical experimentation and standard practices in image classification. A batch size of 64 was adopted to balance computational efficiency with stable model convergence. Training was conducted over 50 epochs to provide sufficient learning while reducing the potential for overfitting. The Adam optimizer was used with an initial learning rate of 0.001, which was further evaluated against learning rates of 0.0001 and 0.00001 to examine its effect on model performance and training sensitivity. Categorical cross-entropy was selected as the loss function due to its appropriateness for multi-class classification tasks. The hyperparameters used during model training are presented in Table 2.

| Table 2. Hyperparameter settings |                             |
|----------------------------------|-----------------------------|
| Parameter                        | Value                       |
| Input image size                 | 150×150 pixels              |
| Batch size                       | 64                          |
| Epochs                           | 50                          |
| Optimizer                        | Adam                        |
| Learning rate                    | 0.001                       |
| Loss function                    | Categorical cross-entropy   |
| Dataset size                     | 6,000 images                |
| Dataset split                    | 90% training/10% validation |
| Computational environment        | Google Colab GPU (Tesla)    |

4.2. Model performance evaluation

The proposed model was systematically assessed using four standard classification metrics: accuracy, precision, recall, and F1-score. Accuracy quantified the overall percentage of correctly classified samples, while precision and recall evaluated the model’s ability to reduce false-positive and false-negative predictions, respectively. The F1-score defined as the harmonic mean of precision and recall, provided a balanced measure of the overall classification performance.

For comprehensive evaluation, our proposed CNN model was benchmarked against three well-established CNN architectures commonly used in medical image analysis: ResNet50, InceptionV3, and MobileNetV2. Training conditions and parameter settings remained consistent across all evaluated models for fair comparative analysis.

4.3. Results and analysis

The proposed brain tumor classification model was assessed through a comprehensive series of experiments. This section provides a detailed evaluation of its performance using accuracy, loss, precision,

recall, and F1-score. The results are compared with three widely adopted DL models—ResNet50, InceptionV3, and MobileNetV2—to demonstrate the proposed architecture's improved predictive performance and robustness across all tumor classes.

#### 4.3.1. Model performance across learning rates

To identify the optimal training configuration, the proposed model was tested with three different learning rates: 0.001, 0.0001, and 0.00001. The results, summarized in Table 3 show that a learning rate of 0.001 provided the highest classification accuracy (99.14%) and the lowest training loss (0.046), indicating optimal convergence and stable learning behavior.

Table 3. Proposed model performance at different learning rates

| Learning rate | Accuracy (%) | Loss  |
|---------------|--------------|-------|
| 0.001         | 99.14        | 0.046 |
| 0.0001        | 92.65        | 0.150 |
| 0.00001       | 85.40        | 0.347 |

These findings affirm that fine-tuning the learning rate significantly impacts training efficiency and model precision. A higher learning rate expedited convergence without compromising performance, while lower rates led to underfitting and slow progress.

#### 4.3.2. Impact of training/validation split ratios

The dataset was also evaluated under varying training-to-validation ratios to determine the model's generalizability. As shown in Table 4, increasing the training proportion led to higher overall accuracy and reduced validation loss. The 90/10 split delivered the best results, supporting the decision to use this configuration for final model evaluation.

Table 4. Results with different training/validation ratios

| Train/validation (%) | Accuracy (%) | Loss  |
|----------------------|--------------|-------|
| 80/20                | 95.60        | 0.143 |
| 85/15                | 96.72        | 0.101 |
| 90/10                | 99.14        | 0.046 |

#### 4.3.3. Comparison with baseline models

The proposed model was comparatively assessed against ResNet50, InceptionV3, and MobileNetV2 under identical dataset and training conditions. Table 5 presents the precision, recall, and F1-score achieved by each model for the four classification categories: glioma, meningioma, pituitary tumor, and no tumor.

The proposed model clearly outperformed all baseline architectures, achieving near-perfect scores in all categories. In particular, the glioma classification achieved a perfect F1-score of 1.00, while the other three classes also scored consistently high, indicating superior model accuracy and balance in classification.

Table 5. Precision, recall, and F1-score across models and classes

| Model          | Class      | Precision | Recall | F1-score |
|----------------|------------|-----------|--------|----------|
| ResNet50       | Glioma     | 0.99      | 0.98   | 0.98     |
|                | Meningioma | 0.95      | 0.94   | 0.95     |
|                | No Tumor   | 0.97      | 1.00   | 0.98     |
|                | Pituitary  | 0.98      | 0.97   | 0.97     |
| InceptionV3    | Glioma     | 0.95      | 0.92   | 0.93     |
|                | Meningioma | 0.87      | 0.79   | 0.83     |
|                | No Tumor   | 0.87      | 0.97   | 0.92     |
|                | Pituitary  | 0.95      | 0.95   | 0.95     |
| MobileNetV2    | Glioma     | 0.98      | 0.95   | 0.96     |
|                | Meningioma | 0.91      | 0.92   | 0.91     |
|                | No Tumor   | 0.97      | 0.95   | 0.96     |
|                | Pituitary  | 0.95      | 0.99   | 0.97     |
| Proposed model | Glioma     | 1.00      | 0.99   | 1.00     |
|                | Meningioma | 0.98      | 0.98   | 0.98     |
|                | No Tumor   | 0.99      | 0.99   | 0.99     |
|                | Pituitary  | 0.99      | 0.99   | 0.99     |

4.3.4. Overall accuracy and loss comparison

To provide a more comprehensive performance snapshot, Table 6 displays the overall accuracy and loss for each model. The proposed model again achieved the highest accuracy and the lowest loss, reinforcing its robustness and efficiency.

Table 6. Final model accuracy and loss comparison

| Model          | Accuracy (%) | Loss  |
|----------------|--------------|-------|
| ResNet50       | 97.00        | 0.086 |
| InceptionV3    | 89.17        | 0.237 |
| MobileNetV2    | 95.83        | 0.100 |
| Proposed Model | 99.14        | 0.046 |

4.4. Discussion

The findings of this study demonstrate the effectiveness of the proposed CNN-based model in accurately detecting and classifying brain tumors from MRI images. The results highlight the robustness and reliability of the proposed approach compared with established state-of-the-art architectures, including ResNet50, InceptionV3, and MobileNetV2. This discussion examines the implications of these results, emphasizes the contribution of key architectural design choices, and considers the potential relevance of the proposed model to clinical practice.

One of the most noteworthy outcomes is the exceptional classification accuracy achieved by the proposed model, peaking at 99.14% with a minimal loss value of 0.046. These results not only surpass those achieved by baseline models but also reflect a high degree of generalization, as validated across different training-validation splits and tumor categories. The ability to maintain such high performance across glioma, meningioma, pituitary tumor, and no-tumor classes confirms that the model is not biased toward specific types of tumors and can operate reliably across heterogeneous datasets. This characteristic is particularly important in practical medical settings, where diagnostic misclassification may result in delayed treatment or the implementation of inappropriate therapeutic interventions.

The strong performance of the proposed model can be attributed to several architectural and methodological innovations. Unlike conventional CNNs, this model incorporates residual connections and batch normalization, which enhance gradient flow and stabilize learning across deeper layers. Furthermore, data augmentation techniques such as rotation, flipping, and cropping played a vital role in reducing overfitting and simulating a broader variety of clinical imaging conditions. This not only strengthened the model’s generalization ability but also simulated the real-world variability found in MRI acquisitions across different machines and medical facilities.

Another critical insight derived from the analysis is the importance of hyperparameter tuning. As the experimentation with learning rates revealed, a learning rate of 0.001 was optimal, facilitating both fast convergence and high precision. Conversely, lower learning rates were associated with slower learning and lower accuracy, emphasizing the need for empirical optimization in training DL models. Similarly, evaluating the impact of training-validation splits demonstrated that increased training data substantially boosts model performance, particularly when validation data is maintained at a sufficiently representative level.

The comparison with other architectures further supports the argument for the proposed model’s superiority. While ResNet50 and MobileNetV2 achieved high performance, they fell slightly short in terms of recall and F1-score across some tumor classes, indicating potential challenges in consistent feature extraction or class imbalance sensitivity. InceptionV3, despite its proven success in general image classification tasks, lagged behind in medical image analysis, possibly due to its complex structure and greater sensitivity to preprocessing quality. The proposed model, designed specifically for medical imaging, demonstrated that domain-specific customization can yield substantial improvements over general-purpose architectures.

From a clinical perspective, the integration of this high-performing model into a web-based diagnostic platform adds a practical dimension to its utility. By providing fast and accurate results upon MRI scan upload, the system could significantly reduce diagnostic turnaround times and help alleviate the workload of radiologists. This is particularly valuable in underserved or resource-limited healthcare environments, where the shortage of trained medical personnel can lead to delayed or inconsistent diagnoses.

Nonetheless, while the results are promising, several limitations merit consideration. The experiments were conducted on a curated public dataset with balanced class distributions and high-quality imaging. In actual clinical environments, images may suffer from noise, artifacts, or incomplete metadata, potentially affecting model performance. Moreover, further external validation on multi-institutional datasets and patient populations is necessary to confirm the model’s reliability and scalability. Future work must also explore model

explainability to aid clinicians in understanding the decision-making process of AI systems, a factor that is increasingly important for regulatory approval and ethical deployment in medicine.

## 5. CONCLUSION

This study presents a DL-based diagnostic framework for brain tumor detection from MRI images, demonstrating substantial improvements over existing models. By combining a customized CNN architecture with effective preprocessing and data augmentation strategies, the proposed model achieved high accuracy, precision, recall, and F1-scores across four major tumor categories. Comparative experiments with ResNet50, InceptionV3, and MobileNetV2 demonstrated the reliability of the proposed approach, which attained a classification accuracy of 99.14% and outperformed all benchmark models. In addition, the model obtained an average precision, recall, and F1-score of 0.99 across the evaluated tumor classes. These findings demonstrate its potential for clinical applications by supporting early tumor detection and enabling radiologists to achieve more consistent and accurate diagnoses. Beyond its quantitative performance, the results demonstrate the methodological benefits of the proposed architecture, particularly the incorporation of residual connections and structured convolutional layers, which strengthen feature extraction and promote training stability. Nevertheless, several limitations must be considered. First, the experiments relied on a single publicly available dataset, potentially limiting the model's generalizability across diverse clinical settings. Second, external and multi-institutional validation was not performed, which is essential for further assessing model robustness. Future studies should therefore incorporate multi-institutional validation, explainable AI methods to enhance interpretability, and real-world clinical datasets to improve practical medical applicability.

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This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

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C : **C**onceptualization

M : **M**ethodology

So : **S**oftware

Va : **V**alidation

Fo : **F**ormal analysis

I : **I**nvestigation

R : **R**esources

D : **D**ata Curation

O : Writing - **O**riginal Draft

E : Writing - Review & **E**ditng

Vi : **V**isualization

Su : **S**upervision

P : **P**roject administration

Fu : **F**unding acquisition

## CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

## DATA AVAILABILITY

The data that support the findings of this study are openly available in [Kaggle, “Brain Tumor MRI Dataset 2021,” Available: <https://www.kaggle.com/datasets/masoudnickparvar/brain-tumor-mri-dataset> at reference number [25].

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