

Transfer Learning-Driven Brain Tumor Classification from MRI: A Comprehensive Multi-Class and Binary Evaluation

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Abstract

This research investigates data-driven approaches for identifying brain tumors in magnetic resonance imaging (MRI) scans. Using deep learning (DL) methodologies, we develop and optimize two advanced convolutional neural network architectures—ResNet 50 and Inception V3—adapted for categorizing brain MRI images. Building on the proven performance of these models in other medical imaging applications, the present study examines their effectiveness across datasets that differ in complexity, including a four-class dataset and a binary-class dataset. The main contribution of this work stems from the systematic assembly and preparation of these paired datasets. To improve training efficiency, we applied key callback mechanisms such as Early Stopping and ReduceLROnPlateau, along with comprehensive hyperparameter tuning. This involved adding layers, testing multiple loss functions and learning rates, and implementing dropout regularization to support reliable model convergence. Moreover, introducing specialized pooling layers and refined regularization techniques markedly boosted classification performance. Notably, pairing ResNet 50 with the Nadam optimizer produced exceptional results, with class-specific accuracies reaching 99.34% for gliomas, 93.52% for meningiomas, 98.68% for non-tumorous cases, and 97.70% for pituitary tumors. These findings demonstrate the strength of our customized framework, yielding an overall test accuracy of 97.68% across the four categories. In the two-class scenario, ResNet 50 combined with the Adam optimizer achieved superior precision, recall, and F1 scores, along with an overall accuracy of 99.84%. It further delivered per-class accuracies of 99.62% for ‘Tumor Positive’ and 100% for ‘Tumor Negative’, marking a substantial improvement in automated brain tumor detection. This study highlights the potential of optimized DL architectures and targeted training strategies to advance non-invasive brain cancer diagnosis using MRI data.

Keywords: Brain tumor, MRI, Transfer learning, Inception Net, ResNet 50, Convolution layer

Introduction

Humans are susceptible to around 200 varieties of abnormal tissue proliferations, among which tumors—either malignant or benign—represent a significant

category. Brain tumors constitute a particularly serious pathology marked by uncontrolled cellular growth within brain tissue that interferes with essential neurological processes. Evidence of a 300 percent increase in mortality rates from brain tumors over the last three decades highlights the pressing necessity for effective therapeutic solutions. Without prompt intervention, these tumors can become life-threatening, which stresses the importance of timely identification and management to improve survival prospects. Given the challenges of performing biopsies in the intricate environment of the

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brain, magnetic resonance imaging (MRI) is a widely adopted non-invasive diagnostic technique [1-10].

Gliomas, which arise from glial cells, constitute the predominant form of brain tumor. They represent nearly 30 percent of all neoplasms in the brain and central nervous system and approximately 80 percent of malignant cases [11]. The World Health Organization (WHO) grading system divides gliomas into four categories (grades I through IV). Grade I lesions are benign and histologically similar to normal glial tissue, whereas grade II tumors display only modest deviations. Grade III tumors are malignant with noticeable cellular atypia, and grade IV represents the most aggressive variant, exhibiting marked histopathological abnormalities [11, 12].

Meningiomas, by comparison, originate from the meningeal layers enveloping the brain and spinal cord. They generally grow slowly and are mostly benign. Pituitary adenomas develop in the pituitary gland, which regulates hormones and systemic physiological functions. These may be benign, associated with bony overgrowth, or malignant, and can cause persistent hormonal imbalances and visual deficits [13].

In light of these factors, prompt detection and accurate classification of brain tumors are vital for establishing a correct diagnosis and implementing appropriate treatment strategies to safeguard patient lives. In complex cases, determining tumor grade can be laborious and time-consuming for medical professionals. This process often requires detailed assessment of tumor location, comparison of cellular morphology with adjacent regions, application of enhancement filters to improve image interpretability, and final determination of tumor presence, type, and grade. Such manual workflows are time-intensive, thereby underscoring the need for computer-aided diagnosis (CAD) systems that enable early tumor identification, streamline the diagnostic timeline, and reduce dependence on human expertise [11, 12].

Advancements in machine learning (ML), and particularly deep learning (DL), have revolutionized the detection and categorization of patterns in medical imagery. These technologies have demonstrated strong potential in multiple clinical applications, ranging from disease forecasting and diagnosis to image classification and tissue segmentation. Convolutional Neural Networks (CNNs) have proven especially effective for medical image analysis, delivering high diagnostic accuracy when trained on large-scale datasets. Unsupervised

techniques such as autoencoders have likewise contributed to feature representation learning. While numerous investigations have examined various approaches for brain tumor detection, several exhibit shortcomings, including insufficient benchmarking against traditional ML methods and high computational demands. Diagnosing tumors from X-ray or CT images still depends heavily on radiologists' expertise, leaving room for interpretive errors. Computational intelligence and computer-assisted tools can augment clinical decision-making by providing more objective and precise tumor identification and characterization. DL and ML methodologies are especially advantageous for analyzing, segmenting, and classifying cancer-related images, including brain tumors. These techniques support consistent, accurate tumor detection and help differentiate tumors from mimicking conditions. Despite existing research on DL approaches for brain tumor diagnosis, the reviewed literature shows inconsistent performance across datasets and highlights opportunities to improve current frameworks.

This work proposes an integrated framework that leverages a robust, automated deep learning classification model. The system is designed to determine whether a brain MRI scan contains a tumor and, if so, to categorize it as one of three common types: glioma, meningioma, or pituitary tumor. Contemporary DL architectures have attained impressive results in image classification. Through hierarchical feature extraction, these models autonomously learn discriminative characteristics of target objects, thereby facilitating more effective differentiation by the classification layer.

The key contributions of this study are outlined below:

- a. Selection of the ResNet-50 and Inception V3 CNN architectures to evaluate their suitability and performance in brain tumor classification from MRI scans, capitalizing on their proven capabilities in image recognition tasks.
- b. Comprehensive performance assessment using two distinct datasets: one containing 3459 MRI scans distributed across four classes, and another comprising 3000 MRI images divided into two classes.
- c. Application of multiple optimization strategies—including Early Stopping and ReduceLROnPlateau—to boost model performance. Extensive hyperparameter tuning was performed by adding layers, testing alternative loss functions and learning rates, and incorporating dropout and regularization techniques to

address overfitting. These efforts yielded leading-edge results on both datasets.

The remainder of this paper is structured as follows: Section 2 offers a thorough literature review. Section 3 briefly describes the datasets used. Section 5 presents the theoretical foundations of the employed models. Section 6 details the research methodology and the proposed system architecture. Section 7 examines the experimental results in depth. Section 8 concludes the paper with a summary of findings and their broader implications.

The literature review

Ghosal *et al.* [14] introduced a deep neural network model using a squeeze-and-excitation variant of ResNet-101 to automatically classify brain tumors from MR images. Their work concentrated on distinguishing glioma, meningioma, and pituitary tumors. The authors implemented zero-centering normalization and data augmentation strategies, which led to marked enhancements in precision, specificity, and sensitivity when benchmarked against other recent classification approaches.

Krishnapriya *et al.* [15] examined the potential of several established pre-trained deep convolutional neural network (DCNN) architectures—namely VGG-19, VGG-16, ResNet-50, and Inception V3—for sorting brain MR images into categories. Data augmentation and transfer learning improved the models' classification performance.

Díaz-Pernas *et al.* [16] developed a fully automated procedure for segmenting and classifying brain tumors in MRI data, including meningioma, glioma, and pituitary cases. Employing CNNs, the method adopted a multi-scale processing paradigm modeled after human perceptual mechanisms. When tested on 3064 image slices from 233 patients, the system achieved 97% precision.

In a separate investigation [17], researchers designed a CNN with 16 convolutional layers, supported by pooling and normalization operations, and added a dropout layer before the fully connected layer. The model delivered 96% precision using 68% of the images for training and the rest for validation and testing.

Abd *et al.* [18] processed a large collection of 25,000 brain MRI scans through a differential convolutional neural network (DCNN) to detect multiple brain tumor categories. Their framework produced exceptional results, recording a training precision of 99.25%.

Sajja and colleagues [19] applied the VGG16 architecture to differentiate malignant from benign tumors on the BraTS dataset, which contains 577 T1-weighted images. The reported accuracy rate for this classification reached 96.70.

A CNN-based solution outlined in Ref. [20] targeted the classification of glioma, meningioma, and pituitary tumors. The model was trained on 3064 T1-weighted contrast-enhanced MRI scans using various convolutional and pooling operations with filters of different sizes, ultimately attaining 94% accuracy.

Abiwinanda *et al.* [21] constructed a network featuring two convolutional layers and 64 neurons in the fully connected stage. To ensure balanced representation, they extracted 700 images per tumor type instead of using the complete dataset. Training involved 500 images per class, while testing used 200 images per class, without data augmentation. The achieved classification accuracy stood at 84.1%.

Pashaei *et al.* [22] presented a CNN structure that included four convolutional and normalization layers, three max-pooling layers, and one fully connected layer at the end. They trained the model on 70% of the data without augmentation, reserving the remaining 30% for testing under 10-fold cross-validation, yielding an overall accuracy of 81.0%.

Afshar *et al.* [23] explored the use of Capsule Networks (CapsNet) for brain tumor categorization. They refined the convolutional layer's feature mappings to boost performance. With 64 feature maps and one convolutional layer, the modified CapsNet reached a peak accuracy of 86.56 percent.

Ibrokhiov *et al.* [24] responded to the growing burden of pneumonia, especially after the COVID-19 outbreak, by devising a sophisticated deep learning computer-aided diagnosis platform. The system combined transfer learning and parallel processing using VGG19 and ResNet-50, obtaining an average classification accuracy of 96.6% on the COVID-QU-Ex dataset.

Edgar M *et al.* [25] focused on enhancing the interpretability of machine learning models for medical imaging analysis, with specific application to brain tumor survival prediction from MRI data. By integrating explainable AI tools such as Shapley overlays with CNNs and the BraTS 2020 dataset, the study improved the clarity of key predictive elements, aiding expert review and strengthening outcome evaluation.

Shokouhifar *et al.* [26] proposed THENDEL, a three-phase deep learning system incorporated into a camera

scanning device for quick, non-invasive assessment of arm volume in lymphedema patients. The architecture merged diverse feature extractors and regressors, with parameters fine-tuned through swarm intelligence optimization. Testing on 730 arms from 365 female participants confirmed strong reliability, evidenced by a mean absolute error of 36.65 mL, a mean percentage error of 1.69%, and a 0.992 correlation with ground-truth measurements.

Veeraiah *et al.* [27] presented MayGAN, a model for leukemia classification that achieved 99.8% accuracy.

Aryai *et al.* [28] introduced MDML-RP, an approach for effective health monitoring in wireless body area networks (WBANs) that delivered notable performance gains.

Ibtisum *et al.* [29] compared multiple Big Data processing tools, contributing to ongoing developments in data analytics.

Table 1 shows a comparative overview of related state-of-the-art studies.

Table 1. Comparative overview of related state-of-the-art studies.

Reference	Classification model	Dataset characteristics	Accuracy	Recall
[7]	ResNet-101	2762 MRI images, 3 categories (glioma, meningioma, pituitary)	74.09%	67.23%
	DenseNet201	Same dataset	68.71%	67.46%
	MobileNetV2	Same dataset	82.61%	80.32%
[14]	CNN with Squeeze-and-Excitation ResNet	3064 MRI images, 3 categories (glioma, meningioma, pituitary)	93.83%	—
[20]	Convolutional Neural Network (CNN)	3064 MRI images, 3 categories (glioma, meningioma, pituitary)	94.39%	93%
[30]	ResNet-50	3064 MRI images, 3 categories (glioma, meningioma, pituitary)	95.33%	—
[31]	SqueezeNet	Dataset not specified	92.08%	—
[32]	CNN	Total images: 253; Binary classes (155 tumor, 98 non-tumor)	91.6%	—
[33]	CNN	OASIS dataset; Binary classification	97.75%	96%
[14]	Inception V3	Total images: 253; Binary classes (155 tumor, 98 non-tumor)	81.25%	63.25%
	ResNet-50	Same dataset	97.92%	87.7%
[34]	CNN	Total images: 253; Binary classes (155 tumor, 98 non-tumor)	96%	89.5%
	VGG-16	Same dataset	98.15%	94.4%
[16]	Multi-scale CNN	3064 MRI images, 3 categories (glioma, meningioma, pituitary)	97.3%	—
[17]	CNN	3064 MRI images, 3 categories (glioma, meningioma, pituitary)	96.13%	—
[19]	CNN	BRATS dataset; Binary classification; 577 images	96.15%	97.05%
	VGG-16	Same dataset	96.70%	97.05%
[20]	CNN	3064 MRI images, 3 categories (glioma, meningioma, pituitary)	94.39%	93%
[21]	CNN	3064 MRI images, 3 categories (glioma, meningioma, pituitary)	84.1%	—
[22]	CNN	3064 MRI images, 3 categories (glioma, meningioma, pituitary)	81.0%	—
[23]	Capsule Network (CapsNet)	Three-class dataset (glioma, meningioma, pituitary)	86.56%	—

Description of the dataset

This study on brain tumor detection used two independent datasets acquired from publicly available online sources: figshare.com (accessed on 1 April 2023) [35] and Kaggle (accessed on 1 April 2023) [36]. Cheng *et al.* [4] were among the first to address the three-class brain tumor classification problem using T1-weighted MRI scans, with their work representing an early prominent application of the figshare collection. A four-class combined dataset was additionally sourced from a

GitHub repository [37]. MRI scans served as the fundamental data modality for this research, owing to their recognized superiority in identifying brain tumors. The initial dataset was divided into four categories corresponding to distinct tumor conditions: glioma, meningioma, no tumor, and pituitary tumor. Overall, it contained 3459 MRI scans, broken down as 1426 glioma cases, 708 meningioma cases, 395 cases without tumors, and 930 pituitary cases. The entire collection was split

into training, validation, and testing portions according to a 60%, 20%, and 20% allocation, respectively.

Figure 1 shows representative samples from the four-class dataset. **Figure 2** shows the distribution bar plot of the tumor dataset across the four classes: training, testing, and validation. **Table 2** presents the breakdown of the tumor images across the four classes (glioma, meningioma, no tumor, and pituitary) for each data split.

The training portion consisted of 2213 images, including 901 glioma, 449 meningioma, 258 no-tumor, and 605 pituitary images. The validation portion included 554 images (222 glioma, 120 meningioma, 61 no-tumor, and 151 pituitary), and the testing portion comprised 692 images (303 glioma, 139 meningioma, 76 no-tumor, and 174 pituitary).

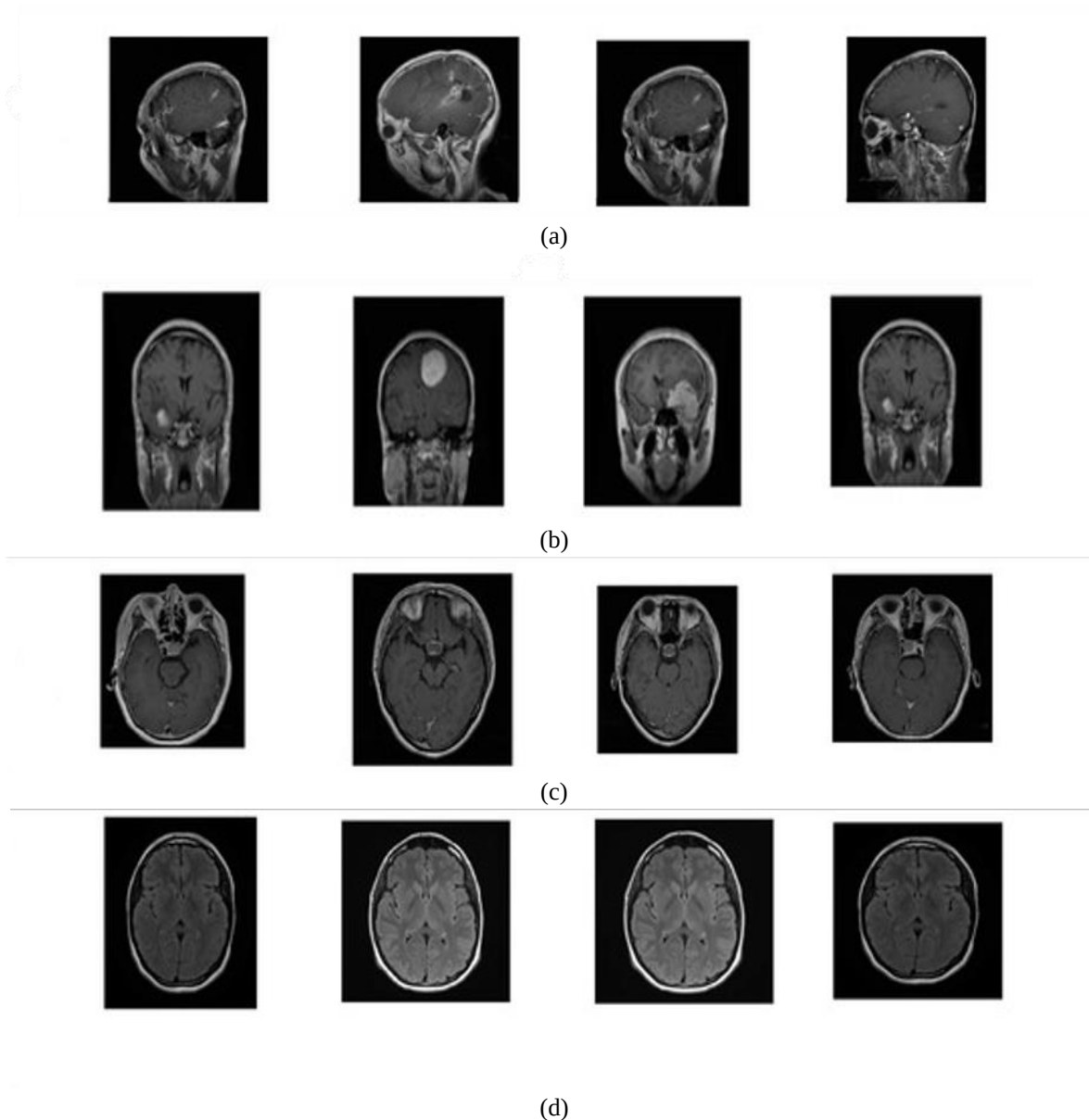


Figure 1. Visual representation of the four-class brain tumor dataset—(a) glioma, (b) meningioma, (c) pituitary, and (d) no tumor.

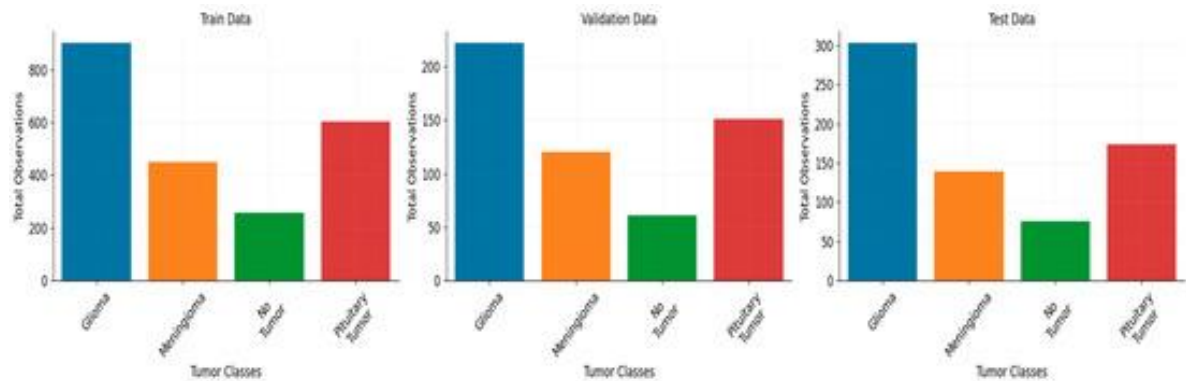


Figure 2. Distribution bar plot of the tumor dataset among four classes: training, testing, and validation.

Table 2. Distribution table of the tumor dataset among four classes: training, testing, and validation.

Dataset split	Glioma category	Meningioma category	Non-Tumor category	Pituitary category	Overall count
Training set	901	449	258	605	2213
Validation set	222	120	61	151	554
Testing set	303	139	76	174	692
Complete dataset	1426	708	395	930	3459

Conversely, the second dataset was structured as a binary classification problem with two groups: presence of tumor and absence of tumor. This collection totaled 3000 MRI scans, evenly divided into 1500 images depicting tumors and 1500 images without tumors. The same

proportional split (60:20:20) was used for training, validation, and testing sets.

Figure 3 displays example MRI scans from the two-class dataset.

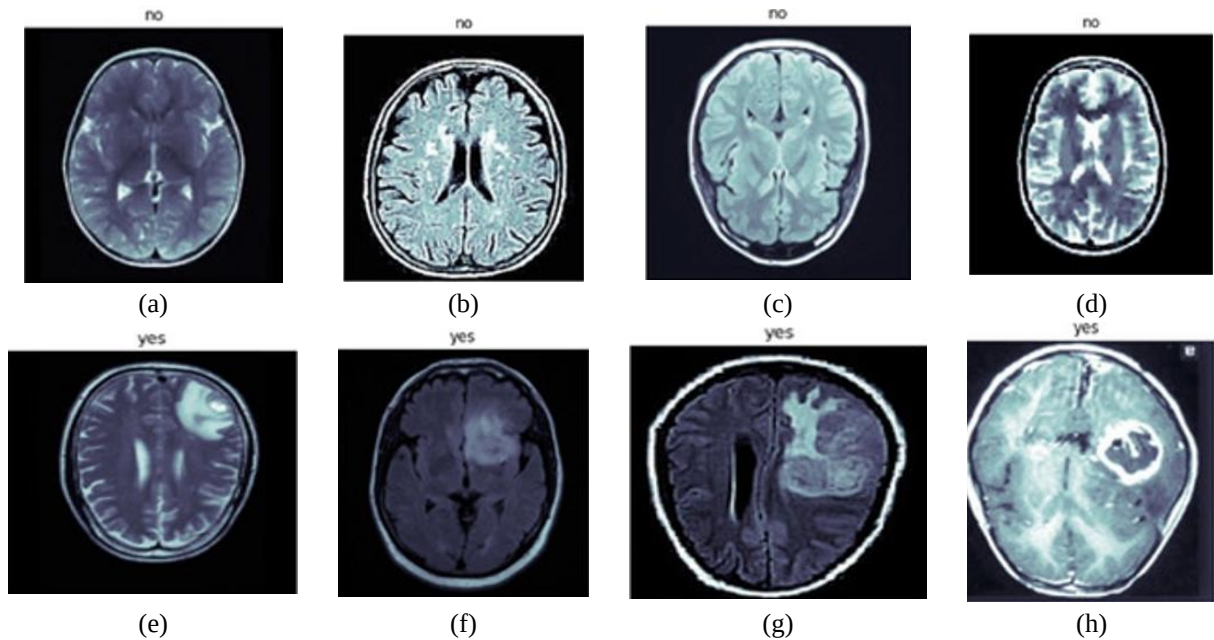


Figure 3. A sample of the two-class brain tumor dataset.

Table 3 details the distribution of images for the two classes (tumor present and tumor absent) across the respective subsets. **Figure 4** illustrates the allocation of

training, validation, and testing data for this binary dataset. More precisely, the training set had 1920 images (940 tumor-present and 980 tumor-absent), the validation

set contained 534 images (247 tumor-present and 287 tumor-absent), and the testing set included 546 images (313 tumor-present and 233 tumor-absent).

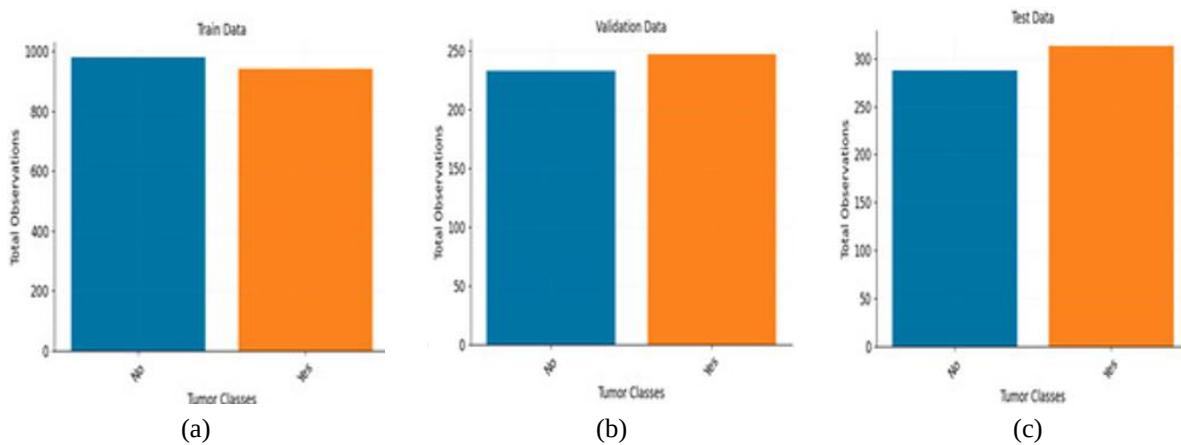


Figure 4. Distribution bar plot of the tumor dataset among two classes: training, testing, and validation.

Table 3. Distribution table of the tumor dataset among two classes: training, testing, and validation.

Data partition	Tumor present class	Tumor absent class	Total samples
Training phase	940	980	1920
Validation phase	247	287	534
Testing phase	313	233	546
Entire dataset	1500	1500	3000

Deep learning framework

The application of transfer learning has proven particularly beneficial for the multi-class classification of brain MRI tumors for several key reasons:

Limited data availability represents a major constraint. Collecting and accurately labeling large volumes of brain MRI tumor images across individual categories is often challenging and highly time-intensive. Transfer learning addresses this issue by allowing researchers to leverage existing models pre-trained on massive datasets from related domains or tasks. This strategy mitigates data scarcity and streamlines model training.

Pre-trained models, especially those trained on large-scale image collections such as ImageNet, have already learned rich and generalizable feature representations that are valuable across a wide range of visual recognition tasks. These learned features capture universal visual patterns that transfer effectively to specialized applications, including brain MRI tumor classification. By adopting transfer learning, the model can build on these robust features, reducing the need for labor-intensive manual feature engineering and leading to more efficient, effective outcomes.

Transfer learning enables favorable model initialization by incorporating weights optimized on vast amounts of data from pre-trained networks. This provides a strong starting point for subsequent training on the specific brain MRI tumor dataset. This initialization allows the model to readily use both low-level and high-level feature representations, accelerating learning and promoting faster convergence during training.

Furthermore, transfer learning improves model generalization by transferring knowledge acquired from a source domain to the target domain of brain MRI tumor classification. The pre-trained model has developed comprehensive image representations from diverse visual inputs, and this accumulated knowledge can be effectively adapted to tumor categorization. As a result, the model better identifies relevant patterns and characteristics associated with different tumor types, leading to superior performance on unseen data.

Overfitting is a common concern when training with small datasets. In such scenarios, models risk memorizing specific training instances instead of learning generalizable patterns. Transfer learning helps counteract this tendency by utilizing the regularization effects, learned weights, and strong generalization

properties of pre-trained models. This approach enables the network to generalize more effectively to new tumor images even when the number of available training samples is restricted.

Inception V3 and ResNet 50

Inception V3

Inception V3 represents an advanced evolution of the original Inception architecture, integrating several refinements designed to boost overall effectiveness and efficiency. A key innovation lies in the incorporation of factorized convolutions. The Inception V3 architecture comprises multiple convolutional layers. Each layer

applies a series of trainable filters to the input brain MRI scan and executes a convolution operation. This process involves sliding the filters across the input image and calculating the dot product between the filter weights and the corresponding input regions. The discrete-time convolution can be formally expressed as shown in Eq. (1):

$$r(t) = (y * w)(t) = \sum_{a=-\infty}^{\infty} y(a)w(t - a) \quad (1)$$

Here, w denotes the kernel filter, x represents the input, t indicates time, and r corresponds to the output. For two-dimensional input data, the operation follows Eq. (2):

$$R(i, j) = (I * K)(i, j) = \sum_m \sum_n I(i, j) * K(i - m, j - n) \quad (2)$$

The indices i and j refer to the spatial positions in the output matrix resulting from the deep learning convolution process.

Inception V3 utilizes factorized convolutions that decompose larger 3×3 and 5×5 filters into smaller asymmetric operations, such as successive 1×3 and 3×1 convolutions, rather than applying the full-sized kernels directly. This factorization strategy substantially decreases the number of parameters in the network while maintaining its expressive power. Consequently, it supports more efficient training and inference, improving computational performance.

Another important advancement in Inception V3 is the inclusion of batch normalization. This technique normalizes the activations of each layer across a mini-batch of training examples, reducing internal covariate shift and accelerating training dynamics. Batch normalization helps stabilize and speed up the optimization of deep networks such as Inception V3 [33, 34].

The batch normalization procedure can be mathematically described by the following equations [10]:

$$Q_i = \frac{P_i - \mu_B}{\sqrt{\sigma_B^2 + \epsilon}} \quad (3)$$

$$\alpha_\beta = \frac{1}{M} \sum_{i=M}^M (P_i - u_\beta)^2 \quad (4)$$

$$\mu_\beta = \frac{1}{N} \sum_{i=1}^M P_i \quad (5)$$

Where N represents the total number of input samples, $P_i = 1, \dots, N$, μ_β is the mean of the mini-batch, σ_β denotes the standard deviation of the mini-batch, and Q_i indicates the normalized values.

In addition, Inception V3 incorporates label smoothing as a regularization strategy during training. Label smoothing replaces hard binary targets (0 or 1) with softer probabilistic labels that are slightly less than 1 for the correct class and slightly greater than 0 for incorrect classes. This approach discourages the model from becoming overconfident in its predictions and can improve generalization to new data.

The output layer of Inception V3 consists of a softmax classifier that generates probability distributions over the possible brain tumor categories. These categories typically include glioma, meningioma, and pituitary tumors, and may also include different malignancy levels. Training the Inception V3 model for brain tumor classification requires a large collection of labeled MRI images. The network learns to minimize a loss function, commonly cross-entropy, through backpropagation. During optimization, the model parameters are iteratively adjusted to maximize the accuracy of tumor type predictions.

ResNet 50

ResNet-50 constitutes a 50-layer residual network containing around 26 million trainable parameters. Developed by Kaiming He and collaborators at Microsoft Research in 2015 [35], this architecture introduced residual learning. Rather than forcing each layer to learn entirely new feature mappings, the network learns

residual functions by subtracting features from each layer's input. This design significantly eases the training of very deep networks compared to standard convolutional neural networks (CNNs). For the current research, the ResNet-50 model was initialized with weights pre-trained on the large-scale ImageNet dataset, which is commonly used to develop robust deep learning systems.

The inclusion of skip connections, often described as identity mappings or shortcut connections, enables ResNet-50 to address diminishing accuracy in deeper

networks. These connections link the input of one layer directly to a later layer (specifically the n th to the $(n + x)$ th layer), facilitating the construction of more complex architectures without degradation [36-39]. Moreover, ResNet-50 has lower computational demands than architectures such as VGG16 and VGG19. In this study, we adapted and fine-tuned the pre-trained ResNet-50 to meet the specific requirements of the brain MRI dataset.

Figure 5 depicts the architecture of the pretrained Inception V3 and ResNet 50 models.

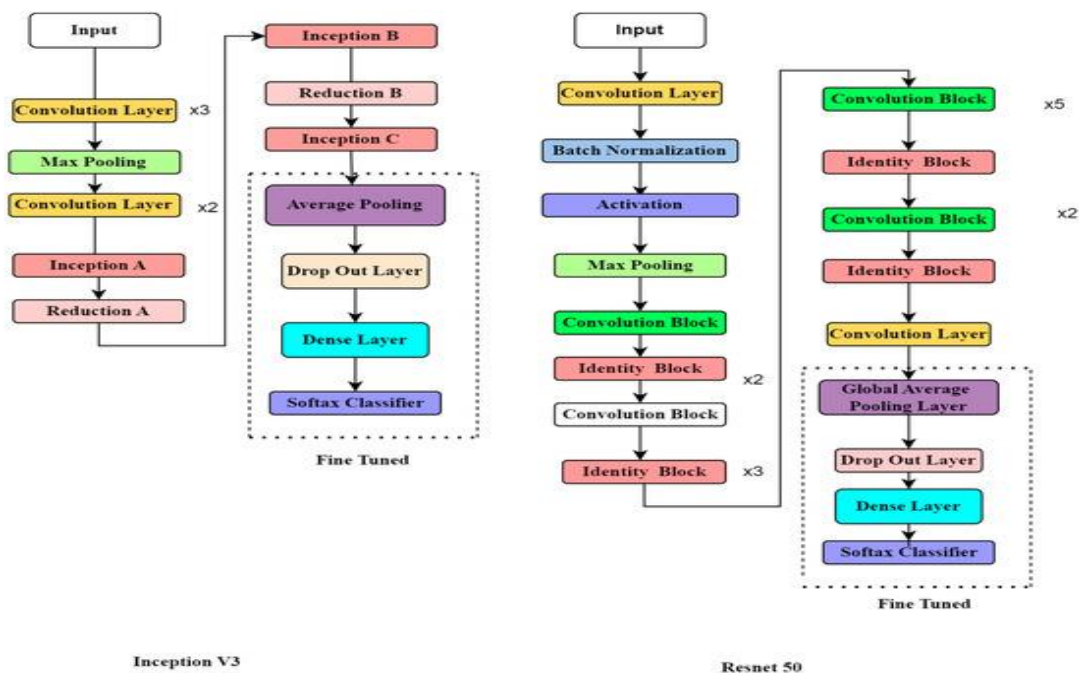


Figure 5. Fine-tuned ResNet 50 and Inception V3 architectures for brain tumor detection.

2D global average pooling layer

To bridge the convolutional stages and the subsequent fully connected components within a deep learning model, feature maps are typically transformed into vectors. In this work, 2D global average pooling replaces simple flattening. This technique calculates the mean value across the entire spatial extent of each feature map. By doing so, it maintains important spatial context while effectively reducing dimensionality. Compared to traditional pooling methods that aggressively downsample, global average pooling helps retain salient information, supports better generalization, and mitigates overfitting risks.

Dropout layer

Dropout is a widely adopted regularization strategy that helps prevent overfitting in deep neural networks. It achieves this by randomly zeroing out a subset of input units during each training iteration. This random deactivation introduces variability that forces the network to develop more independent and resilient feature representations. Consequently, it reduces reliance between neurons and encourages the learning of broadly applicable characteristics. Dropout layers can be inserted after convolutional or dense layers and have consistently improved the generalization ability of deep architectures.

Dense layer

Commonly referred to as the fully connected layer, this component ensures that every neuron is connected to all activations from the previous layer. These layers excel at

capturing intricate nonlinear patterns and relationships in the extracted features. In brain MRI classification, dense layers are generally placed toward the final stages of the model to generate class predictions. The number of neurons can be tailored based on the complexity of the specific classification objective. Nonlinear activation functions, such as rectified linear unit (ReLU) or sigmoid, are typically applied to the outputs of these layers to enhance the model's expressive capacity.

L2 regularization

L2 regularization differs from dropout by adding a penalty term to the loss function rather than randomly disabling neurons. This penalty discourages excessively large weight values, thereby controlling model complexity. By constraining weight magnitudes, it prevents any single parameter from disproportionately influencing learning. The result is a more balanced weight distribution that typically translates into stronger

performance on previously unseen data. L2 regularization is often employed alongside other methods to optimize the trade-off between learning meaningful features and achieving robust generalization in deep neural networks.

Methodology and proposed architecture

Figure 6 presents the overall structure of the proposed framework, outlining the sequential stages involved in the experimental workflow. Following dataset acquisition, all images were resized to a uniform dimension of 224×224 pixels. To manage memory limitations, the data in the training, validation, and testing directories were partitioned according to the ratios specified earlier. Data generators were configured to apply a variety of augmentation methods, which help prevent model overfitting. After evaluating multiple batch sizes during data loading, a batch size of 16 was selected for optimal results.

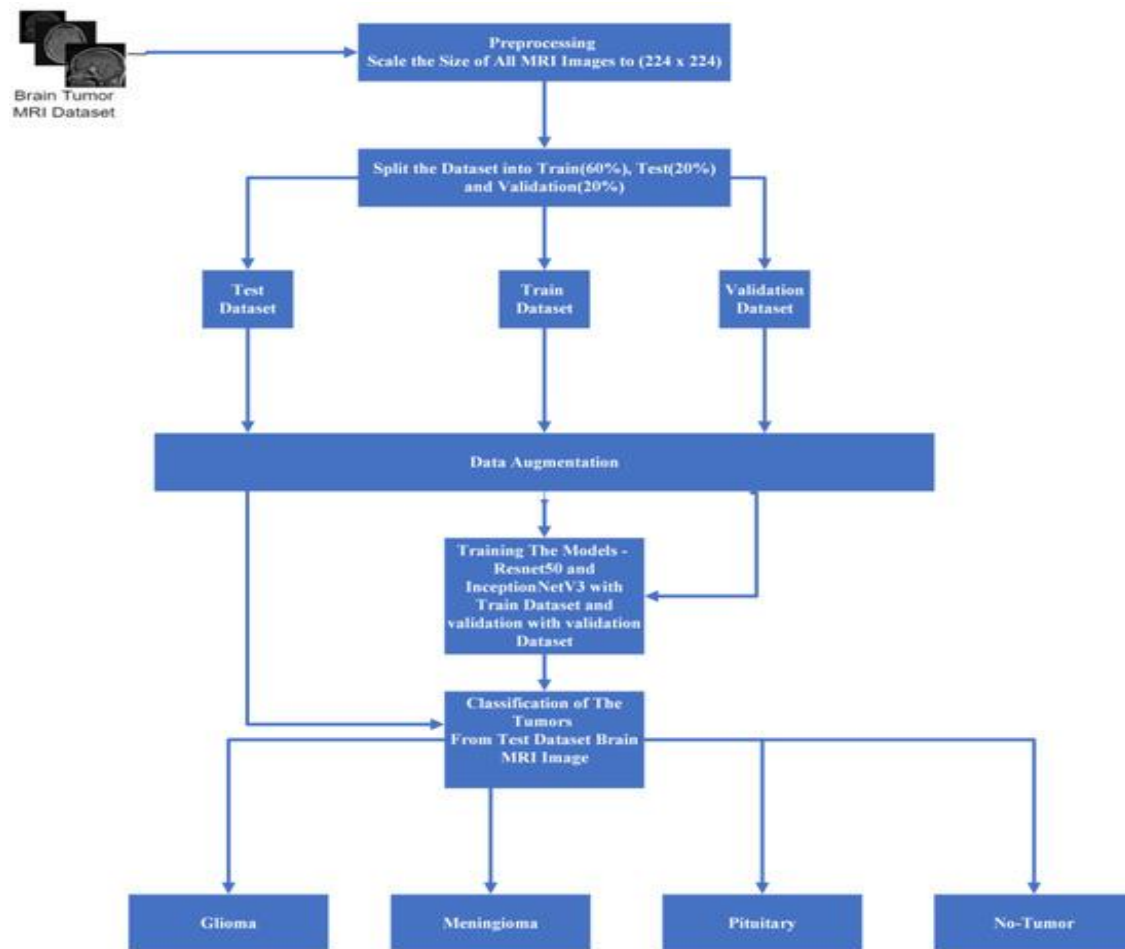


Figure 6. Step-by-step pipeline for brain tumor detection: data preprocessing to model selection.

The prepared data were used to train and optimize both the ResNet-50 and Inception V3 architectures. For experimental evaluation, models were trained for up to 30 epochs. A comprehensive set of performance metrics was used to assess the system's overall effectiveness.

Each model (ResNet-50 and Inception V3) underwent training for up to 30 epochs. During this process, three optimizers—Adam, Nadam, and RMSprop—were tested, and categorical cross-entropy served as the loss function. Notably, the ResNet-50 model reached its peak accuracy within the first 12 epochs. Multiple evaluation metrics were applied to provide a thorough analysis of the system's capabilities and reliability.

During training, the base pre-trained model weights were kept frozen, with training focused on the newly added layers. The architecture was progressively enhanced by first adding a global average pooling layer, followed by dropout layers. Extensive testing of dropout rates between 0.1 and 0.9 led to selecting 0.4 as the optimal value for stable convergence.

To further refine the models, a fully connected layer with 1024 neurons was added, succeeded by another dropout layer. This was followed by a second fully connected layer with 512 neurons and another dropout layer. The final layer consisted of a Softmax classifier designed to assign input images to their appropriate categories. Model performance on the validation set was continuously monitored, allowing for dynamic refinement of the fine-tuning strategy when required.

In conclusion, hyperparameter optimization for the ResNet-50 and Inception V3 models focused primarily on the custom top layers. The original base weights remained unchanged, while dropout rates were systematically explored from 0.1 to 0.9, resulting in the adoption of a 0.4 rate. The classification head consisted of two dense layers with 1024 and 512 neurons, respectively, each paired with dropout regularization to minimize overfitting. Training used Adam, Nadam, and RMSprop optimizers to leverage their strengths in convergence speed and stability, paired with categorical cross-entropy loss. This setup was iteratively adjusted based on validation performance to achieve strong results while avoiding overfitting.

Experimental results

This section details the experimental setup and presents the obtained findings. All simulations were executed in JupyterLab on a workstation featuring an Intel(R)

Xeon(R) E5-2680 v4 CPU running at 2.40 GHz with 32 GB RAM. JupyterLab offers a flexible, browser-based interactive computing platform suitable for notebooks, code execution, and data management. Its adaptable interface facilitates complex workflows across data science, scientific computation, machine learning, and related fields. The implementation utilized essential libraries such as Scikit-learn, NumPy, TensorFlow, and Matplotlib.

Two distinct transfer learning strategies were explored. The first extracted fixed feature representations from intermediate layers for model training. The second involved fine-tuning the pre-trained ResNet-50 and Inception V3 networks by substituting the terminal fully connected layer and appending custom dense and regularization components.

The central aim of the developed system was reliable brain tumor identification and categorization. The four-class task focused on separating glioma, meningioma, no-tumor, and pituitary cases. Evaluation relied on a 4×4 confusion matrix to derive counts of true positives, false positives, true negatives, and false negatives. These statistics enabled detailed assessment of the system's capacity to correctly recognize tumor presence and distinguish pathological cases.

The models achieved highly favorable outcomes during testing. The Adam optimizer proved especially effective, enabling fast, stable convergence despite substantial memory demands. Comparisons were performed between Adam and Nadam optimizers, both starting with a learning rate of 0.001. Learning rate scheduling was managed dynamically through the ReduceLROnPlateau callback (factor = 0.3, patience = 5), which adjusted rates according to validation loss trends.

An early stopping criterion based on validation loss (patience = 10 epochs) was implemented to avoid overfitting. Training was limited to a maximum of 50 epochs with a batch size of 20, and each run required approximately 35 minutes. Categorical cross-entropy served as the loss function for the multi-class setting.

The subsequent tables report classification performance for the deep learning models across different optimizers (Adam, Nadam, and RMSprop). **Table 4** summarizes outcomes using the Adam optimizer. ResNet-50 showed superior metrics, maintaining accuracy above 97% across all categories. For gliomas, it recorded 98.97% precision, 97.69% recall, and an F1-score of 98.33%. Meningioma performance was also strong, with all metrics exceeding

93%. The no-tumor category reached 100% precision, and pituitary tumors achieved an F1-score of 97.14% with 97.70% accuracy. InceptionV3 delivered reliable,

though slightly lower, results, with per-class accuracies between 93.52% and 97.36%.

Table 4. Evaluating brain tumor classification with adam optimizer: four-class test dataset performance metrics.

Model	Class	Precision (%)	Recall (%)	F1 Score (%)	Accuracy (%)
ResNet 50	Glioma	98.97	97.69	98.33	97.69
	Meningioma	93.79	97.84	95.77	97.84
	Non-Tumor	100	94.73	97.29	94.43
	Pituitary	96.59	97.70	97.14	97.70
Inception V3	Glioma	97.03	97.03	97.03	97.03
	Meningioma	93.52	93.52	93.52	93.52
	Non-tumor	100	98.66	98.66	97.36
	Pituitary	96.02	96.57	96.57	97.12

Table 5 provides metrics for the Nadam optimizer. ResNet-50 again led, attaining 97.09% precision, 99.33% recall, 98.20% F1-score, and 99.34% accuracy on gliomas. Meningioma results surpassed 93% across

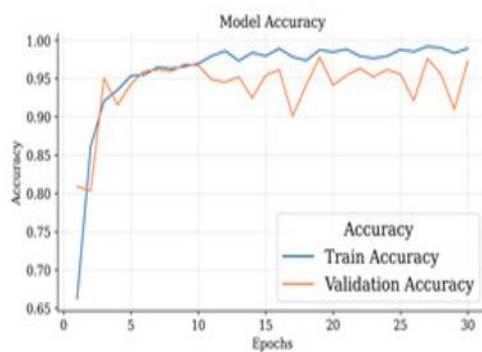
metrics, and no-tumor cases maintained perfect precision. Inception V3 showed competitive glioma performance with 96.70% accuracy and a 97.50% F1-score.

Table 5. Evaluating brain tumor classification with nadam optimizer: four-class test dataset performance metrics.

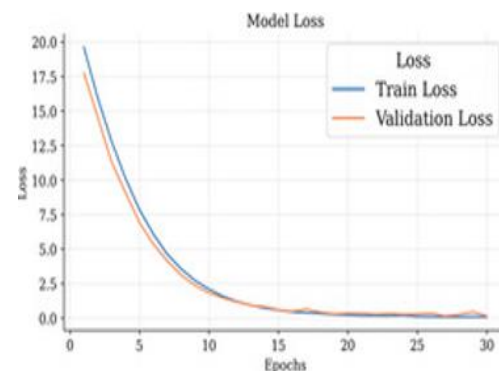
Model	Class	Precision (%)	Recall (%)	F1 Score (%)	Accuracy (%)
ResNet 50	Glioma	97.09	99.33	98.20	99.34
	Meningioma	97.74	93.52	95.58	93.52
	Non-Tumor	100	98.68	99.33	98.68
	Pituitary	97.70	97.70	97.70	97.70
Inception V3	Glioma	98.32	96.70	97.50	96.70
	Meningioma	91.11	96.40	93.70	96.40
	Non-Tumor	100	97.36	98.66	97.36
	Pituitary	98.26	97.70	97.98	97.70

Table 6 outlines results under the RMSprop optimizer. ResNet-50 sustained excellent glioma classification with precision, recall, and F1-scores above 98%. Meningioma achieved near 95% precision and recall, while the no-tumor class retained 100% precision. Inception V3

performed notably well on gliomas, with an F1-score of 98.33%, and showed strong recall and F1 values for pituitary cases. **Figures 7-9** visualize the training dynamics for the four-class models.



(a)



(b)

Figure 7. Accuracy and loss curves for InceptionV3 training with the Adam optimizer.

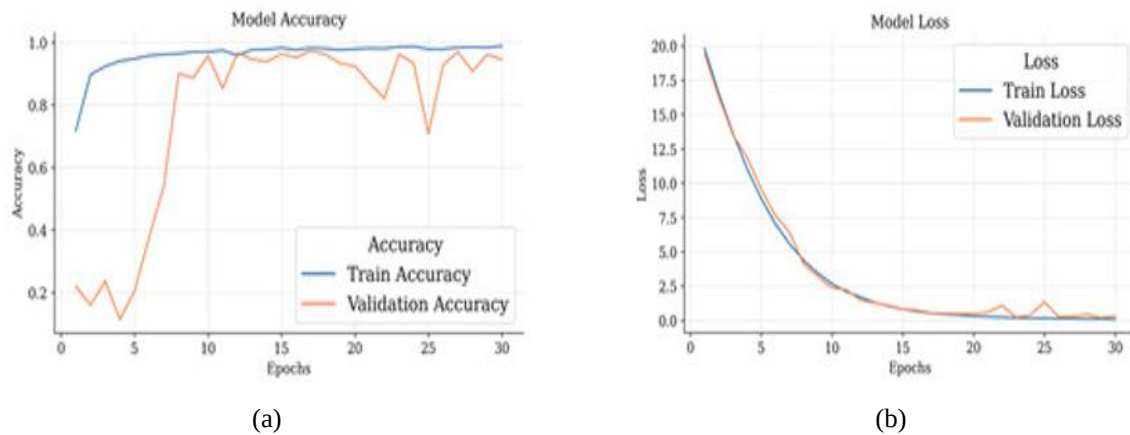


Figure 8. Accuracy and loss curves of ResNet-50 training with the Adam optimizer.

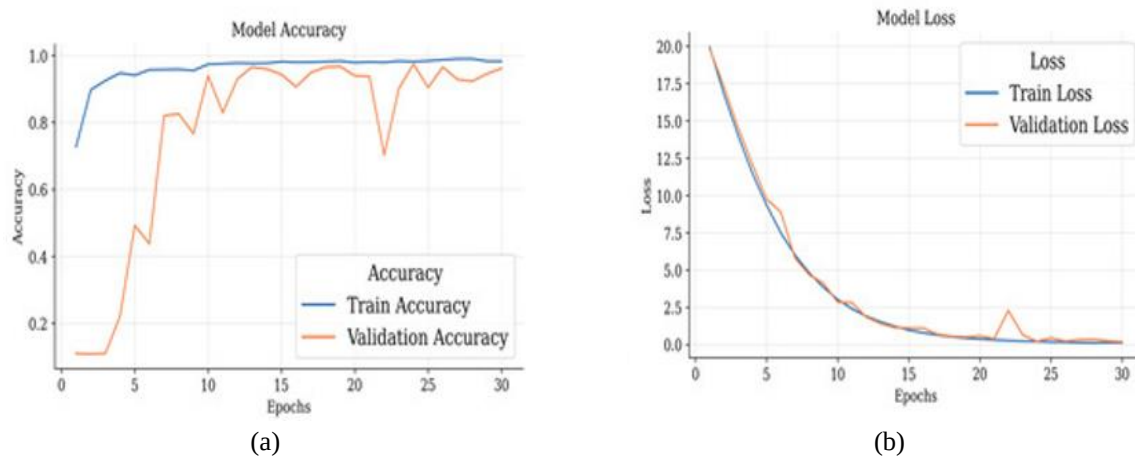


Figure 9. Accuracy and loss curve of ResNet-50 training with nadam optimizer.

Table 6. Evaluating brain tumor classification with RMSprop optimizer: four-class test dataset performance metrics.

Model	Class	Precision (%)	Recall (%)	F1 Score (%)	Accuracy (%)
ResNet 50	Glioma	98.67	98.35	98.51	98.35
	Meningioma	95.65	94.96	95.30	94.96
	Non-tumor	100	97.36	98.66	97.36
	Pituitary	95.50	97.70	96.59	97.70
Inception V3	Glioma	98.03	99.01	98.52	99.01
	Meningioma	95.55	92.81	94.32	95.68
	Non-tumor	100	96.05	97.98	96.05
	Pituitary	96.61	98.27	97.43	98.27

The presented curves capture the progression of model behavior across training epochs. Accuracy trends reveal steady gains in predictive quality as the network processes training examples, while loss trends indicate the progressive minimization of the objective function. Such visualizations are instrumental for assessing convergence patterns and detecting signs of overfitting or

underfitting, thereby supporting targeted adjustments and enhancements to the brain tumor detection framework.

Table 7 compiles aggregate performance indicators for several deep learning architectures and optimization strategies on the four-class dataset. Among these, ResNet-50 combined with Nadam achieved the most notable outcome, attaining 97.68% accuracy and 98.13%

precision. Inception V3 paired with RMSprop also performed competitively, reaching 97.25% accuracy and a 97.02% F1-score. The observed variations underscore

how optimizer selection can meaningfully influence results on this dataset, offering useful direction for identifying optimal pairings.

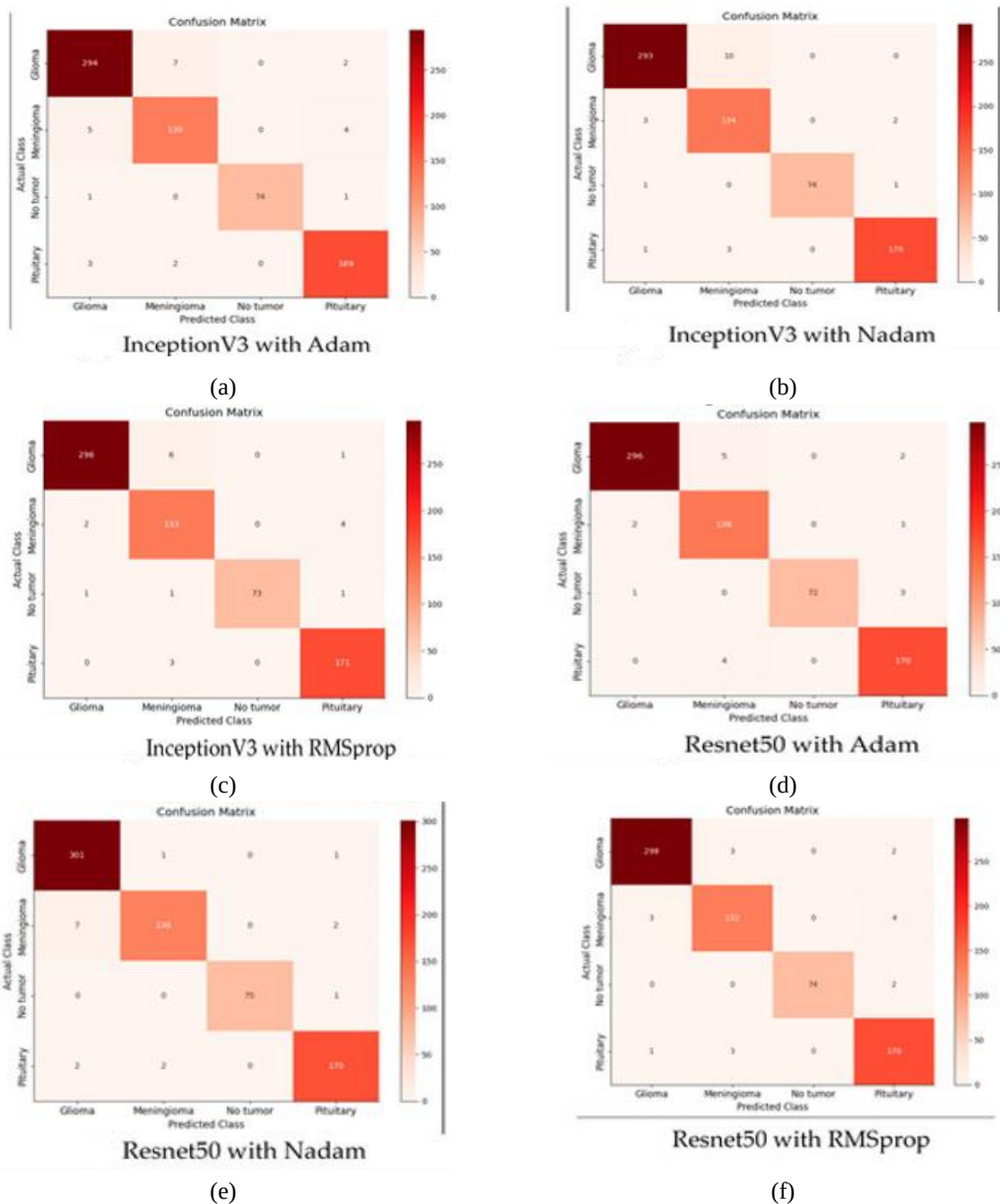


Figure 10. Confusion matrix evaluation of different DL models.

Table 7. Overall test evaluation on a four-class dataset with various models and optimizers.

Model	Optimizer	Loss	MAE	Precision	Recall	F1-Score	Accuracy
Inception V3	Adam	15.01	6.06	96.64	96.26	96.44	96.38
	Nadam	11.83	4.19	96.93	97.04	96.96	96.96
	RMSprop	14.60	4.19	97.15	96.92	97.02	97.25

Resnet 50	Adam	7.33	4.04	97.37	96.99	97.11	97.39
	Nadam	10.78	3.75	98.13	97.31	97.70	97.68
	RMSprop	13.03	4.47	97.45	97.09	97.26	97.39

Given ResNet-50's superior results, we further tested this architecture—equipped with the same supplementary layers—on the binary classification dataset. **Table 8** details the classification outcomes for ResNet-50 under

different optimizers on the two-class test set. With the Adam optimizer, the model secured 100% precision, 99.65% recall, a 99.82% F1-score, and 99.62% accuracy on tumor-positive instances.

Table 8. Performance metrics of ResNet-50 models with different optimizers for tumor classification on a two-class tumor test dataset.

Model	Optimizer	Class	Precision (%)	Recall (%)	F1 Score (%)	Accuracy (%)
ResNet50	Adam	Tumor Positive	100	99.65	99.82	99.62
		Tumor Negative	99.68	100	99.81	100
	Nadam	Tumor Positive	99.65	99.30	99.47	99.30
		Tumor Negative	99.36	99.68	99.52	99.68
	RMSprop	Tumor Positive	99.50	98.06	98.78	98.06
		Tumor Negative	98.37	99.95	98.97	99.58

For tumor-negative instances, it recorded 99.68% precision, 100% recall, a 99.81% F1-score, and perfect 100% accuracy. Using Nadam, ResNet-50 produced 99.65% precision, 99.30% recall, and a 99.47% F1-score for positive cases (99.30% accuracy), along with 99.36% precision, 99.68% recall, and a 99.52% F1-score for negative cases (99.68% accuracy). Under RMSprop, the model achieved 98.96% precision, 99.65% recall, and a 99.30% F1-score for positive samples (99.65% accuracy), and 99.67% precision, 99.04% recall, and a 99.35% F1-score for negative samples (99.04% accuracy). ResNet-50 exhibited consistently strong results regardless of optimizer, establishing it as a dependable option for binary tumor identification.

Table 9 offers an in-depth breakdown of Inception V3 performance across multiple optimization methods on the two-class dataset. Metrics are provided separately for tumor-positive and tumor-negative categories. Precision remained exceptionally high (frequently above 98%), signifying reliable positive predictions. Recall values were likewise robust (generally exceeding 97%), demonstrating effective detection of true positive cases. The F1-score confirmed balanced and accurate classification, while overall accuracy regularly surpassed 98%. These outcomes affirm the capability and stability of Inception V3 for binary tumor classification under varying optimizers.

Table 9. Performance metrics of the Inception V3 model with different optimizers for tumor classification on the two-class tumor test dataset.

Model	Optimizer	Class	Precision (%)	Recall (%)	F1 Score (%)	Accuracy (%)
InceptionV3	Adam	Tumor Positive	98.06	98.06	98.06	98.62
		Tumor Negative	98.68	99.25	98.81	98.35
	Nadam	Tumor Positive	98.56	97.61	97.08	96.61
		Tumor Negative	97.14	97.94	97.54	97.94
	RMSprop	Tumor Positive	98.96	99.65	99.30	99.65
		Tumor Negative	99.67	99.04	99.35	99.04

Figures 11 and 12 visualize key aspects of model behavior on the two-class brain MRI dataset. **Figure 11** presents accuracy and loss curves that track learning

dynamics and convergence. **Figure 12** contains confusion matrices that detail prediction patterns for the tumor-present and tumor-absent categories.

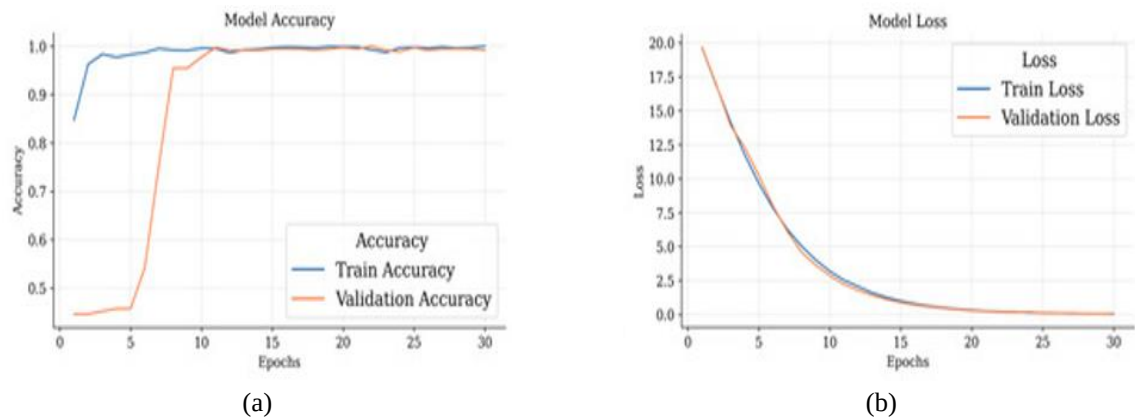


Figure 11. Accuracy and loss curves of ResNet-50 with Adam for a two-class brain tumor dataset.

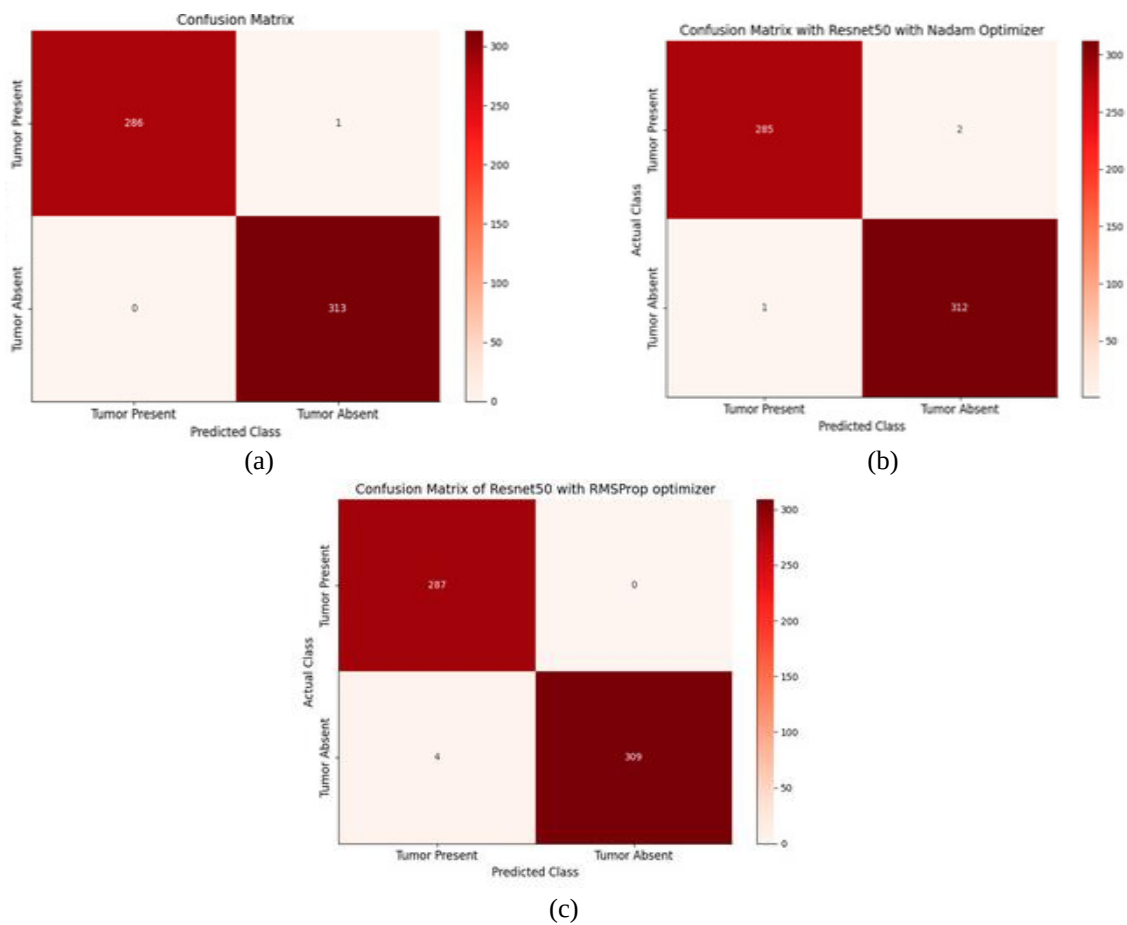


Figure 12. Confusion matrix with different optimizers tested on the test dataset for ResNet-50 for a two-class dataset: (a) confusion matrix of ResNet-50 model with Adam optimizer, (b) confusion matrix of ResNet-50 model with Adam optimizer, and (c) confusion matrix of ResNet-50 model with RMSprop optimizer.

Table 10 compares the overall test performance of ResNet-50 and Inception V3 using different optimizers on the two-class tumor dataset. For ResNet-50 with Adam, the model recorded a low MAE of 1.6 and

maintained precision, recall, F1-score, and accuracy values above 99%, highlighting its superior ability to separate the two classes.

Table 10. Performance comparison of the overall test evaluation of ResNet50 and InceptionV3 models with different optimizers on a two-class tumor dataset.

Model	Optimizer	Loss	MAE	Precision	Recall	F1-Score	Accuracy
ResNet-50	Adam	8.83	1.6	99.84	99.82	99.82	99.83
	Nadam	1.82	0.53	99.50	99.49	99.49	99.50
	RMSprop	2.91	0.16	99.84	99.82	99.83	99.33
Inception V3	Adam	8.94	1.17	98.21	98.21	98.21	98.22
	Nadam	10.86	2.67	97.35	97.28	97.31	97.33
	RMSprop	5.49	1.11	98.94	98.82	99.88	98.88

ResNet-50 continued to deliver excellent metrics with Nadam and RMSprop, though slight differences in loss emerged depending on the optimizer. In contrast, Inception V3 achieved good but comparatively lower scores across precision, recall, F1-score, and accuracy, accompanied by higher MAE values. These comparisons illustrate the value of strategically matching model architecture and optimizer to the requirements of tumor classification tasks.

Conclusion

In summary, this research developed two deep learning frameworks based on ResNet-50 and Inception V3 architectures for classifying brain MRI scans. The models demonstrated strong capabilities in identifying different tumor types, consistent with advancements reported in other areas of medical image analysis. Evaluation was conducted on publicly accessible datasets, where the systems achieved high levels of accuracy and precision across multiple tumor categories. Optimization involved three prominent algorithms: Adam, Nadam, and RMSprop. The multi-class classification task reached 97.68% accuracy, while the binary classification task attained an outstanding 99.84% accuracy. These outcomes represent a meaningful step forward in the automated detection of brain tumors from MRI data. Incorporating techniques such as global average pooling, customized fully connected layers, and L2 regularization proved instrumental in improving model performance for this application.

Several promising directions for future investigation have been identified. Expanding evaluations to include larger and more varied datasets will be crucial for validating the robustness and generalizability of the proposed approaches. Further exploration of advanced convolutional architectures, such as MobileNet, SqueezeNet, and Vision Transformers, along with ensemble methods and alternative loss functions, may

yield additional performance gains. Future efforts could also address fine-grained tumor grading and apply swarm intelligence for hyperparameter optimization. Enhancing training efficiency and conducting clinical validation in collaboration with healthcare professionals represent important next steps. It is equally essential to consider practical challenges in real-world deployment, including data privacy concerns, regulatory requirements, and seamless integration into existing clinical systems. Approaches such as federated learning may offer viable solutions to these issues and warrant dedicated attention in subsequent studies.

Through continued research along these lines, the objective is to further refine brain MRI analysis techniques and support the development of more precise, efficient, and reliable tools for brain tumor diagnosis in clinical settings.

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References

1. Kavitha AR, Chitra L, Kanaga R. Brain tumor segmentation using genetic algorithm with SVM classifier. *Int J Adv Res Electr Electron Instrum Eng*. 2016;5:1468–71.
2. Logeswari T, Karnan M. An improved implementation of brain tumor detection using segmentation based on hierarchical self organizing map. *Int J Comput Theory Eng*. 2010;2:591. doi:10.7763/IJCTE.2010.V2.217
3. Badran EF, Mahmoud EG, Hamdy N. An algorithm for detecting brain tumors in MRI images. In:

- Proceedings of the 2010 International Conference on Computer Engineering & Systems; 2010; Cairo, Egypt. New York: IEEE; 2010. p. 368–73.
4. Cheng J, Huang W, Cao S, Yang R, Yang W, Yun Z, et al. Enhanced performance of brain tumor classification via tumor region augmentation and partition. *PLoS ONE*. 2015;10(10):e0140381. doi:10.1371/journal.pone.0140381
 5. Swathi B, Kannan KS, Chakravarthi SS, Ruthvik G, Avanija J, Reddy CCM. Skin cancer detection using VGG16, Inception V3 and ResUNet. In: Proceedings of the 2023 4th International Conference on Electronics and Sustainable Communication Systems (ICESC); 2023; Coimbatore, India; 2023. p. 812–8.
 6. Khambhata KG, Panchal SR. Multi-class classification of brain tumor in MR images. *Int J Innov Res Comput Commun Eng*. 2016;4:8982–92.
 7. Ullah N, Khan JA, Khan MS, Khan W, Hassan I, Obayya M, et al. An effective approach to detect and identify brain tumors using transfer learning. *Appl Sci*. 2022;12(11):5645. doi:10.3390/app12115645
 8. Podder P, Alam FB, Mondal MRH, Hasan MJ, Rohan A, Bharati S. Rethinking densely connected convolutional networks for diagnosing infectious diseases. *Computers*. 2023;12(5):95. doi:10.3390/computers12050095
 9. Podder P, Das SR, Mondal MRH, Bharati S, Maliha A, Hasan MJ, et al. LDDNet: A deep learning framework for the diagnosis of infectious lung diseases. *Sensors*. 2023;23(1):480. doi:10.3390/s23010480
 10. Raza A, Ayub H, Khan JA, Ahmad I, Salama AS, Daradkeh YI, et al. A hybrid deep learning-based approach for brain tumor classification. *Electronics*. 2022;11(7):1146. doi:10.3390/electronics11071146
 11. Goodenberger ML, Jenkins RB. Genetics of adult glioma. *Cancer Genet*. 2012;205(12):613–21. doi:10.1016/j.cancergen.2012.10.009
 12. Louis DN, Perry A, Reifenberger G, von Deimling A, Figarella-Branger D, Cavenee WK, et al. The 2016 World Health Organization classification of tumors of the central nervous system: a summary. *Acta Neuropathol*. 2016;131(6):803–20. doi:10.1007/s00401-016-1545-1
 13. Mahmud MI, Mamun M, Abdelgawad A. A deep analysis of brain tumor detection from MR images using deep learning networks. *Algorithms*. 2023;16(4):176. doi:10.3390/a16040176
 14. Ghosal P, Nandanwar L, Kanchan S, Bhadra A, Chakraborty J, Nandi D. Brain tumor classification using ResNet-101 based squeeze and excitation deep neural network. In: Proceedings of the 2019 Second International Conference on Advanced Computational and Communication Paradigms (ICACCP); 2019; Gangtok, India; 2019. p. 6.
 15. Krishnapriya S, Karuna Y. Pre-trained deep learning models for brain MRI image classification. *Front Hum Neurosci*. 2023;17:1150120. doi:10.3389/fnhum.2023.1150120
 16. Díaz-Pernas FJ, Martínez-Zarzuela M, Antón-Rodríguez M, González-Ortega D. A deep learning approach for brain tumor classification and segmentation using a multiscale convolutional neural network. *Healthcare*. 2021;9(2):153. doi:10.3390/healthcare9020153
 17. Sultan HH, Salem NM, Al-Atabany W. Multi-classification of brain tumor images using deep neural network. *IEEE Access*. 2019;7:69215–25. doi:10.1109/ACCESS.2019.2919122
 18. Abd El Kader I, Xu G, Shuai Z, Saminu S, Javaid I, Salim Ahmad I. Differential deep convolutional neural network model for brain tumor classification. *Brain Sci*. 2021;11(3):352. doi:10.3390/brainsci11030352
 19. Sajja VR, Al E. Classification of brain tumors using fuzzy C-means and VGG16. *Turk J Comput Math Educ (TURCOMAT)*. 2021;12:2103–13.
 20. Das S, Aranya OFMRR, Labiba NN. Brain tumor classification using convolutional neural network. In: Proceedings of the 2019 1st International Conference on Advances in Science, Engineering and Robotics Technology (ICASERT); 2019; Dhaka, Bangladesh; 2019. p. 1–5.
 21. Abiwinanda N, Hanif M, Hesaputra ST, Handayani A, Mengko TR. Brain tumor classification using convolutional neural network. In: Lhotska L, Sukupova L, Lacković I, Ibbott GS, editors. *World Congress on Medical Physics and Biomedical Engineering 2018*. Singapore: Springer; 2019. p. 183–9.
 22. Pashaei A, Sajedi H, Jazayeri N. Brain tumor classification via convolutional neural network and extreme learning machines. In: Proceedings of the 2018 8th International Conference on Computer and Knowledge Engineering (ICCCKE); 2018; Mashhad, Iran; 2018. p. 314–9.

23. Afshar P, Mohammadi A, Plataniotis KN. Brain tumor type classification via capsule networks. In: Proceedings of the 2018 25th IEEE International Conference on Image Processing (ICIP); 2018; Athens, Greece. 2018. p. 3129–33.
24. Ibromkhimov B, Kang JY. Deep learning model for COVID-19-infected pneumonia diagnosis using chest radiography images. *BioMedInformatics*. 2022;2(4):654–70. doi:10.3390/biomedinformatics2040044
25. Eder M, Moser E, Holzinger A, Jean-Quartier C, Jeanquartier F. Interpretable machine learning with brain image and survival data. *BioMedInformatics*. 2022;2(4):492–510. doi:10.3390/biomedinformatics2040032
26. Shokouhifar A, Shokouhifar M, Sabbaghian M, Soltanian-Zadeh H. Swarm intelligence empowered three-stage ensemble deep learning for arm volume measurement in patients with lymphedema. *Biomed Signal Process Control*. 2023;85:105027. doi:10.1016/j.bspc.2023.105027
27. Veeraiah N, Alotaibi Y, Subahi A. MayGAN: Mayfly optimization with generative adversarial network-based deep learning method to classify leukemia from blood smear images. *Comput Syst Sci Eng*. 2023;46(2):2039–58. doi:10.32604/csse.2023.036562
28. Aryai P, Khademzadeh A, Jafarali Jassbi S, Hosseinzadeh M, Hashemzadeh O, Shokouhifar M. Real-time health monitoring in WBANs using hybrid metaheuristic-driven machine learning routing protocol (MDML-RP). *AEU-Int J Electron Commun*. 2023;168:154723. doi:10.1016/j.aeue.2023.154723
29. Ibtisum S. A comparative study on different big data tools [thesis]. Fargo (ND): North Dakota State University; 2020.
30. Divya S, Padma Suresh L, John A. A deep transfer learning framework for multi class brain tumor classification using MRI. In: Proceedings of the 2020 2nd International Conference on Advances in Computing, Communication Control and Networking (ICACCCN); 2020; Greater Noida, India; 2020. p. 283–90.
31. Shah A, Chavan P, Jadhav D. Classification of brain tumor MRI scans using transfer learning with a comparative analysis on pre-trained networks. In: Proceedings of the 2022 International Conference for Advancement in Technology (ICONAT); 2022; Goa, India; 2022. p. 1–7.
32. Brain tumor detection using deep learning models [Internet]. IEEE Xplore; 2020 [cited 2023 Sep 24]. Available from: <https://ieeexplore.ieee.org/abstract/document/9344555/>
33. Hussain E, Hasan M, Hassan SZ, Hassan Azmi T, Rahman MA, Zavid Parvez M. Deep learning based binary classification for Alzheimer's disease detection using brain MRI images. In: Proceedings of the 2020 15th IEEE Conference on Industrial Electronics and Applications (ICIEA); 2020; Kristiansand, Norway; 2020. p. 1115–20.
34. Younis A, Qiang L, Nyatega CO, Adamu MJ, Kawuwa HB. Brain tumor analysis using deep learning and VGG-16 ensembling learning approaches. *Appl Sci*. 2022;12(14):7282. doi:10.3390/app12147282
35. Cheng J. Brain tumor dataset [Internet]. Figshare; 2017 [cited 2023 Apr 1]. Available from: https://figshare.com/articles/dataset/brain_tumor_dataset/1512427
36. Br35H:: Brain tumor detection 2020 [Internet]. Kaggle; 2020 [cited 2023 Aug 18]. Available from: <https://www.kaggle.com/datasets/ahmedhama da0/brain-tumor-detection>
37. Brain-MRI-Image-Classification-Using-Deep-Learning [Internet]. GitHub; [cited 2023 Sep 25]. Available from: <https://github.com/strikersps/Brain-MRI-Image-Classification-Using-Deep-Learning/tree/main/Brain-Tumor-Dataset/Training>
38. Gheisari M, Ebrahimzadeh F, Rahimi M, Moazzamigodardi M, Liu Y, Dutta Pramanik PK, et al. Deep learning: applications, architectures, models, tools, and frameworks: a comprehensive survey. *CAAI Trans Intell Technol*. 2023;8(3):581–606. doi:10.1049/cit2.12180
39. Ghaderzadeh M, Aria M, Hosseini A, Asadi F, Bashash D, Abolghasemi H. A fast and efficient CNN model for B-ALL diagnosis and its subtypes classification using peripheral blood smear images. *Int J Intell Syst*. 2022;37(8):5113–33. doi:10.1002/int.22770