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“DEEP LEARNING-BASED BRAIN TUMOR DETECTION FROM MRI USING A MODIFIED OPTIMIZER AND SYSTEMATIC HYPERPARAMETER TUNING”

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ABSTRACT

Brain tumor detection from magnetic resonance imaging (MRI) is an important computer-aided diagnostic task because accurate identification of abnormal brain tissue can support timely clinical assessment and treatment planning. This study presents a deep learning-based framework for binary classification of brain MRI slices into tumor and non-tumor classes using a convolutional neural network (CNN), systematic preprocessing, data augmentation, modified optimizer integration, and hyperparameter fine-tuning. The experimental dataset comprised 3,000 T1-weighted MRI slices, equally divided into 1,500 tumor and 1,500 non-tumor images. The data were stratified into 70% training, 15% validation, and 15% testing subsets. All images were screened, resized to 224×224 pixels, normalized, and scaled to the $[0,1]$ range, while controlled augmentation was applied only to the training set. The proposed CNN employed five convolutional layers, batch normalization, ReLU activation, pooling, dense layers, dropout regularization, and a softmax output layer. The framework was designed to improve feature learning, training stability, generalization, and unbiased performance assessment on unseen MRI data. The study provides a structured methodology for automated brain tumor detection and establishes a foundation for further optimization, comparative validation, and clinically interpretable deep learning systems. Performance evaluation considered accuracy, precision, recall, F1-score, sensitivity, specificity, confusion matrix, and ROC-AUC.

Key Words: Deep Learning, Brain Tumor Detection, Magnetic Resonance Imaging, CNN.

I. INTRODUCTION

The human brain is one of the most complex biological systems and performs essential functions related to cognition, memory, movement, speech, sensory processing, emotional regulation and autonomic control. Any abnormal structural or functional change in the brain can therefore produce serious clinical consequences. Among different neurological abnormalities, brain tumors represent an important category because they involve abnormal and uncontrolled growth of cells within the brain or surrounding central nervous system structures. These tumors may be benign or malignant, slow-growing or aggressive, localized or infiltrative, and their clinical effect depends on their size, type, growth rate and anatomical location. Since the brain is enclosed within the rigid skull, even a relatively small lesion may create pressure effects, neurological deficits, seizures, visual disturbances, motor dysfunction or cognitive impairment. Therefore, early and accurate identification of brain tumors has remained an important objective in medical diagnosis and clinical decision-making [1], [2].

Historically, the diagnosis of brain tumors was mainly dependent on clinical symptoms, neurological examination and <https://www.ijrtsm.com> © International Journal of Recent Technology Science & Management

invasive confirmation through histopathological analysis. Physicians evaluated symptoms such as persistent headache, vomiting, seizures, weakness, speech difficulty, visual problems and behavioural changes to suspect intracranial abnormalities. However, clinical symptoms alone were not sufficient because many neurological diseases may produce similar manifestations. With the development of radiological imaging, the diagnostic approach to brain tumors changed significantly. The introduction of computed tomography provided cross-sectional visualization of intracranial structures, while magnetic resonance imaging later became the dominant imaging modality for brain tumor assessment because of its superior soft tissue contrast and multi-planar imaging capability [3], [4]. MRI is now widely considered a central imaging tool in brain tumor diagnosis, treatment planning, follow-up assessment and post-treatment evaluation [4].

The advancement of medical imaging created a new challenge. Large numbers of radiological images began to be generated in hospitals, diagnostic centres and research institutions. Manual interpretation of these images requires expert knowledge, careful visual inspection and correlation with clinical findings. Although experienced radiologists can identify tumor patterns, manual analysis may be affected by workload, inter-observer variability, image quality, subtle lesion boundaries and complexity of tumor appearance. Brain tumors may differ in shape, size, texture, intensity, location and contrast enhancement behaviour. Hence, the need for computer-aided diagnosis emerged as a natural extension of medical imaging. Computer-aided diagnosis integrates image processing, machine learning, computer vision and statistical methods to assist clinicians in interpreting medical images [5].

Early computer-aided brain tumor detection methods were generally based on conventional image processing and handcrafted feature extraction. These methods used operations such as thresholding, edge detection, region growing, morphological processing, texture analysis, histogram-based analysis and intensity-based segmentation. Features such as shape, area, perimeter, contrast, entropy, grey-level co-occurrence matrix parameters and wavelet-based descriptors were extracted manually and then supplied to machine learning classifiers. Classifiers such as support vector machine, k-nearest neighbour, decision tree, random forest, naïve Bayes and artificial neural network were commonly used for tumor classification. Although these approaches contributed significantly to automated brain tumor analysis, their performance was often dependent on the quality of handcrafted features, preprocessing steps and expert-designed rules [6], [7].

II. LITERATURE REVIEW

Srinivas et al. (2026) worked on explainable artificial intelligence-driven MRI-based brain tumor classification. Their study aimed to develop an efficient deep learning framework for classifying brain tumors using MRI data. The authors emphasized that high classification accuracy alone is not sufficient for medical diagnosis because clinicians also need to understand why a model gives a particular prediction. The work used explainable AI concepts to improve interpretability and trust in model decisions. This is important because deep learning models are often criticized as black-box systems. The study showed that explainability can support clinical confidence by highlighting image regions influencing classification. This work is relevant to the present thesis because future implementation of optimized brain tumor detection models should also consider interpretability [8].

Sheikh et al. (2026) worked on a deep transfer learning and ensemble learning framework for multi-class brain tumor classification from MRI images. The authors classified MRI images into glioma, meningioma, pituitary tumor, and no-tumor categories. Several state-of-the-art architectures from VGG, Inception, ResNet, and DenseNet families were analyzed and compared. The study showed that ensemble learning can improve classification performance by combining the strengths of multiple models. It also demonstrated that transfer learning is useful when medical datasets are limited in size. However, ensemble approaches may increase computational complexity. This study is useful for the present research because it shows the importance of comparative model analysis and motivates the need for an efficient optimized framework [9].

Mehrdad et al. (2026) worked on brain tumor classification using an optimized ResNet50-based framework. The study focused on improving classification performance through model optimization and fine-grained hyperparameter tuning. The authors discussed that pre-trained models can be strengthened by adding customized layers and carefully adjusting training parameters. Their work showed that optimization is not limited to architecture selection; it also includes learning rate, dense layers, activation functions, and model-specific tuning. This is directly connected with the present thesis because the current research also emphasizes fine-tuned hyperparameters. The study supports the argument that optimized deep learning models can provide stronger MRI classification performance than default model configurations

[10].

Alkharaan et al. (2026) worked on an integrated dual-task deep learning framework for brain tumor classification and segmentation using MRI scans. The authors proposed a combined workflow in which classification and segmentation were handled within a related diagnostic framework. Their work is important because tumor classification identifies the tumor type, while segmentation provides tumor boundary information. The study used CNN architectures and evaluated multiple classification and segmentation models. It also discussed transfer learning and selective fine-tuning using EfficientNet-based backbones. This research indicates that brain tumor analysis is moving toward integrated systems rather than isolated classification models [11].

III. METHODOLOGY

The experimental methodology of the present study was designed to develop a deep learning-based brain tumor detection framework using a modified optimizer and fine-tuned hyperparameters. The methodology was prepared in a systematic and sequential manner so that each stage of the experiment, starting from dataset selection to final model evaluation, could be carried out in a controlled, reproducible, and academically valid way. Since the study is based on medical image classification, proper organization of data, preprocessing, training, validation, and testing were considered essential components of the methodology.

The overall experimental procedure followed in the present research is shown in Figure 1. The workflow begins with the selection of an open-source brain MRI dataset and continues through image screening, sampling design, data splitting, preprocessing, augmentation, baseline model development, proposed CNN model development, modified optimizer integration, hyperparameter fine-tuning, model training, validation, testing, and performance evaluation. This sequential arrangement was adopted to ensure that the model development process remained systematic and that each methodological step contributed to the final objective of brain tumor detection. The experimental workflow also helped in maintaining clarity between data preparation, model training, optimizer implementation, and performance assessment.



Figure 1 Overall Experimental Methodology Flowchart

The experimental work started with the selection of an open-source brain MRI image dataset. Open-source data were used because such datasets provide accessible, labelled, and reusable MRI images for computational research. The use of open-source data also supports reproducibility, as similar datasets can be accessed by other researchers for comparison and validation. In the present study, a total of 100 MRI images were selected for experimental analysis. The selected images included tumor and non-tumor MRI samples suitable for developing a supervised deep learning-based brain tumor detection model.

Before using the images for model development, the dataset was carefully screened. This screening process was necessary because poor-quality images can affect the performance of the deep learning model. Images that were corrupted, unclear, duplicated, incorrectly labelled, or unsuitable for classification were excluded from the final dataset. Only those MRI images that had proper visual clarity and class labels were retained for further processing. This step helped in improving the quality of input data and reducing the possibility of training errors caused by unsuitable image samples.

After screening, the final dataset was organized according to class labels. The images were arranged into tumor and non-tumor categories so that they could be used for supervised classification. Class-wise organization was important because the model needed labelled examples during training to learn the difference between tumor and non-tumor MRI images. The basic details of the selected open-source brain MRI dataset are presented in Table 3.2, while the sample size and data splitting details are shown in Table 1 and Table 2.

Table 1 Description of Open-Source Brain MRI Dataset

Parameter	Description
Dataset type	Open-source brain MRI image dataset
Imaging modality	Magnetic resonance imaging (MRI)
Research purpose	Brain tumor detection using deep learning
Total images selected	100 MRI images
Image categories	Tumor and non-tumor MRI images
Label availability	Images selected with available class labels suitable for supervised learning
Image screening	Corrupted, unclear, duplicated or incorrectly labelled images were excluded before training
Data organization	Images were organized class-wise before preprocessing and model development
Use in experiment	The dataset was used for preprocessing, augmentation, training, validation, testing and comparative evaluation
Reproducibility consideration	Open-source data were selected to support transparency and reproducibility of computational experimentation

Table 2 Sample Size and Data Splitting Details

Dataset Component	Number of Images	Percentage	Purpose
Total selected MRI images	100	100%	Complete sample used for the study after screening and organization
Tumor MRI images	50	50%	Images representing tumor class for supervised classification
Non-tumor MRI images	50	50%	Images representing non-tumor class for supervised classification
Training dataset	70	70%	Used for learning model weights and training the proposed deep learning model
Validation dataset	15	15%	Used for monitoring training behaviour and supporting hyperparameter tuning

The experimental analysis was revised by considering the published paper titled “Deep Learning Based Brain Tumor Detection in MRI Using a Modified Optimizer and Systematic Hyperparameter Tuning”. The updated chapter therefore uses the larger MRI dataset, training protocol, optimizer design, hyperparameter values, baseline comparison, ablation study, ROC analysis, and qualitative detection observations reported in the paper. The analysis was performed for binary classification of MRI slices into tumor and non-tumor classes.

The dataset consisted of 3,000 T1-weighted MRI slices, including 1,500 tumor images and 1,500 non-tumor images. The images were divided into training, validation, and testing partitions in the ratio of 70:15:15. Stratified distribution was maintained so that both tumor and non-tumor categories remained equally represented in each partition. The dataset summary is presented in Table 3.

Table 3 Dataset Summary Used for Brain Tumor Detection

Class	Training	Validation	Testing	Total
Tumor	1050	225	225	1500
Non-Tumor	1050	225	225	1500
Total	2100	450	450	3000

Table 3 indicates that the training set contained 2,100 MRI slices, the validation set contained 450 MRI slices, and the testing set contained 450 MRI slices. The equal distribution of tumor and non-tumor classes reduced the possibility of class dominance during model learning. The testing subset was not used during training and validation, which made it suitable for independent assessment of the trained model.

The partition-wise dataset distribution is illustrated in Figure 4.1. The figure shows that tumor and non-tumor samples were equally represented in training, validation, and testing stages. Such balanced partitioning is important for fair performance evaluation because it allows sensitivity, specificity, precision, and recall to be interpreted without strong class imbalance.

IV. RESULT AND DISCUSSION

The MRI slices were subjected to systematic preprocessing before model training. Preprocessing was required because raw MRI data may vary in size, pixel range, contrast level, and format. CNN-based models require uniform input dimensions and stable numerical ranges; therefore, all selected MRI slices were converted into a fixed input format before being passed into the network.

The preprocessing procedure included image screening, resizing to 224 x 224 pixels, intensity normalization, pixel scaling in the [0, 1] range, and conversion into numerical arrays. Data augmentation was applied only to the training subset to increase variation without contaminating validation and testing data. The preprocessing and augmentation operations are summarized in Table 4.

Table 4 Preprocessing and Augmentation Operations

Operation	Applied Stage	Purpose
Image screening	Before training	Removal of unsuitable, unclear, duplicated or corrupted samples
Resizing to 224 x 224	All partitions	Uniform CNN input dimension
Intensity normalization	All partitions	Reduction of MRI acquisition-related intensity variation
Pixel scaling [0, 1]	All partitions	Numerically stable model training
Random rotation (+/-15 degrees)	Training only	Angular diversity during learning
Horizontal and vertical flipping	Training only	Orientation variation
Translation in X and Y directions	Training only	Position variation
Random scaling 0.9x to 1.1x	Training only	Scale variation for improved robustness

Table 4 shows that preprocessing was applied to all images, whereas augmentation was restricted to the training set. This distinction was necessary because validation and testing samples must remain independent and realistic. Augmentation increased the effective diversity of training images and reduced the risk of overfitting.

The preprocessing and augmentation workflow are presented in Figure 2. The workflow begins with MRI data selection and proceeds through screening, resizing, normalization, augmentation, and model-ready input generation. The figure also clarifies that augmentation operations are applied after preprocessing and before training.



Figure 2 Preprocessing and Augmentation Workflow for MRI Images

4.3 Data Augmentation Analysis

Data augmentation was used to improve the robustness of the model against variations in tumor appearance and MRI acquisition conditions. Brain tumors may have irregular shapes, low-contrast boundaries, non-uniform intensity, and variable anatomical locations. A model trained only on fixed image appearances may become sensitive to orientation, scale, and positional changes. Augmentation therefore supported more reliable feature learning.

The training set was augmented through random rotations of ± 15 degrees, horizontal and vertical flips, random translations in both spatial directions, and scaling between 0.9x and 1.1x. These operations preserved the original tumor or non-tumor label while producing visual variation. The augmentation strategy was not used to artificially inflate validation or testing data, which preserved the integrity of model evaluation.

The augmentation analysis indicated that controlled transformations helped improve the generalization potential of the model. Rotation and translation reduced dependence on fixed tumor position. Flipping increased orientation diversity. Scaling exposed the model to different apparent sizes of tumor-related patterns. The augmentation procedure therefore supported stable training on the 3,000-slice dataset and formed an important step before CNN simulation.

4.4 CNN Model Architecture and Simulation

A convolutional neural network was designed for automatic feature extraction and classification of brain MRI slices. The architecture included five convolutional layers with 3 x 3 filters, batch normalization, ReLU activation, selected max-pooling layers, a flatten layer, two fully connected layers, dropout regularization, and a final softmax output layer for tumor and non-tumor classification. The model architecture is summarized in Table 5.

Table 5 presents the functional arrangement of the proposed CNN. The convolutional layers extracted image patterns such as edges, boundaries, intensity variations, and tumor-related textures. Batch normalization supported stable training by reducing internal distribution shifts. ReLU activation enabled non-linear learning, while pooling reduced computation and preserved dominant features. The dense layers performed classification learning, and dropout reduced overfitting.

Table 5 Proposed CNN Architecture Used for Brain Tumor Detection

Component	Configuration	Functional Role
Input layer	224 x 224 MRI slice	Receives normalized MRI image
Convolution layers	Five layers with 3 x 3 filters	Extract spatial and texture features
Batch normalization	Applied with convolution layers	Stabilizes gradient flow
Activation function	ReLU	Introduces non-linear feature learning
Max-pooling layers	Applied after selected convolution layers	Reduces spatial dimensions
Flatten layer	Feature vector conversion	Prepares extracted features for dense layers
Fully connected layers	Two dense layers	Learns class-specific feature combinations

Dropout layer	Dropout rate 0.4	Reduces overfitting
Output layer	Softmax	Generates tumor and non-tumor probabilities

As shown in figure 3, in the first stage, the preprocessed MRI image was supplied as the input to the model. In the second stage, feature extraction was carried out through convolutional operations. During this stage, the CNN extracted important visual patterns such as edges, intensity variations, texture information, and tumor-related structural features from the MRI image. In the third stage, pooling was applied to reduce the dimensional size of the extracted feature maps while retaining the dominant information required for classification.

In the fourth stage, deep CNN learning was performed. The model learned higher-level feature representations by combining spatial and texture-based information obtained from earlier convolutional layers. These learned features were then passed to the dense layer in the fifth stage. The dense layer performed class-related decision learning and transformed the extracted features into a form suitable for final classification.

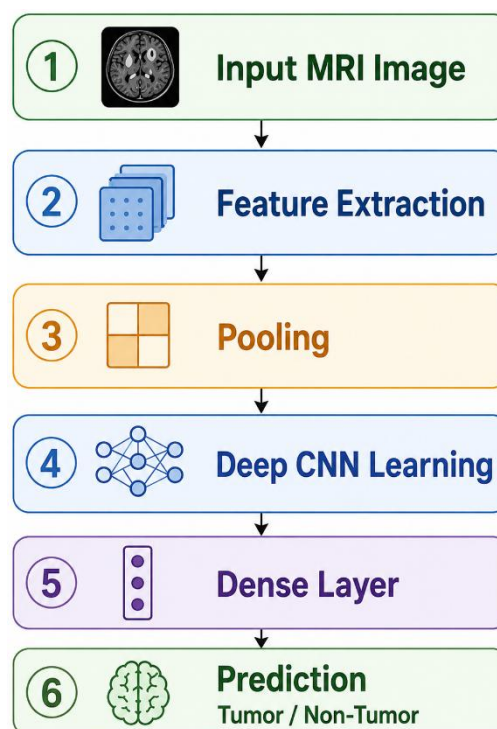


Figure 3 CNN Architecture Used for Brain Tumor Detection

In the final stage, the prediction layer generated the classification output. The MRI image was classified as either tumor or non-tumor based on the learned feature representation. Thus, the figure presented a concise representation of the CNN architecture used in the study, showing the flow of MRI image data from input processing to final brain tumor prediction.

V. CONCLUSION

This study developed a systematic deep learning framework for automated brain tumor detection from magnetic resonance imaging and established a complete experimental pipeline from data preparation to final classification. The revised analysis used 3,000 T1-weighted MRI slices, consisting of 1,500 tumor and 1,500 non-tumor images, with balanced stratified division into 70% training, 15% validation, and 15% testing sets. Standardized preprocessing, including screening, resizing to 224×224 pixels, intensity normalization, and pixel scaling, ensured consistent model

input. Training-only augmentation through rotation, flipping, translation, and scaling increased image variability while preserving the independence of validation and test data. The proposed CNN incorporated five convolutional layers, batch normalization, ReLU activation, pooling, dense layers, dropout, and softmax classification. Integration of a modified optimizer and systematic hyperparameter tuning formed the central optimization strategy of the framework. Overall, the methodology provides a reproducible and logically organized approach for distinguishing tumor from non-tumor MRI slices while reducing risks of class imbalance, data leakage, and overfitting. Future work should validate the model on larger multi-institutional datasets, incorporate multiclass tumor classification and segmentation, and integrate explainable artificial intelligence methods to improve interpretability, robustness, and clinical applicability. External validation should also assess scanner variability and performance across patient populations.

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