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Convolutional Neural Network based Tumor Classification Using Brain MRI Images

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***Abstract*—Classifying brain tumors is crucial for accurate diagnosis and treatment planning in medical imaging. In hospitals, research facilities, and AI-powered diagnostic tools, tumor classification aids in early detection, personalized treatment planning, and monitoring disease progression to improve patient care and outcomes. This study employs a convolutional neural network (CNN), specifically designed for medical imaging tasks, to classify brain MRI scans into four categories: pituitary, meningioma, glioma, and no tumor.The model achieves a validation accuracy of 95.27% after 50 epochs, with performance further assessed through the confusion matrix, precision, recall, and F1-score. This scalable approach not only enhances diagnostic speed but also supports more targeted treatments, ultimately leading to better patient outcomes and more efficient healthcare delivery.**

K*eywords - *Deep Learning* , *CNN* , *Data Augmentation* , *Image Normalization* , *Adam Optimizer* , *MRI Image Analysis

I. Introduction

Brain tumors are a serious medical issue that must be identified early in order to be effectively treated. Manual MRI analysis is one of the time-consuming and error-prone traditional diagnostic techniques [1]. In order to automatically classify brain MRI scans into four categories—pituitary tumors, gliomas, meningiomas, and non-tumorous conditions—this study suggests a (CNN)-based method.To improve accuracy, the model is trained on a carefully selected dataset using sophisticated CNN architectures, reliable data augmentation, and preprocessing methods [2]. Classification reports and confusion matrices are used for performance evaluation, which provide a thorough analysis of the system's efficacy across a range of tumor kinds.

This automated approach reduces human error while increasing accuracy, providing a dependable and affordable diagnostic tool. It paves the way for more extensive AI integration in healthcare by expediting the diagnosis procedure, which eventually improves patient care and operational effectiveness [3].This paper's remaining sections are arranged as follows: Brain tumors are introduced in Section II. The review of the literature is described in Section III. Section IV explains the dataset and data preprocessing. The topic of methodology is covered in Section V. Section VI describes the outcome, evaluates the performance, and The paper's discussion of the difficulties and potential paths for CNN-based tumor classification models is concluded in Section VII.

II. Problem Statement

It is essential to diagnose brain tumors accurately; however, due to its labor-intensive nature and susceptibility to mistakes, manual MRI analysis complicates the task of differentiating among various tumor types—gliomas, meningiomas, pituitary tumors, or the absence of a tumor. This research employs CNN for the automation of brain tumor classification, with the aim of improving both diagnostic precision and efficiency. By employing CNNs, medical practitioners gain a dependable resource for speedier and more accurate tumor detection, which in turn aids in enhanced treatment planning and contributes to improved patient outcomes.

III. Literature Review

We go over earlier studies on brain tumors using a range of deep learning methods in this part.

Deng et al. [4] divided object detection techniques into single-stage (like YOLO) and two-stage (like Faster R-CNN) approaches. They discovered that CNN-based architectures such as Fast R-CNN (70% mAP) and R-CNN (66% mAP) enhanced performance on the VOC2007 and VOC2012 datasets, demonstrating CNN's usefulness in autonomous driving and video surveillance.In order to improve feature extraction and sensitivity, Abdusalomov et al. [3] developed a YOLOv7-based model for brain tumor identification in MRI scans that integrates CBAM and BiFPN. With a 99.5% accuracy rate in detecting pituitary tumors, meningiomas, and gliomas, their model showed promise for supporting oncology diagnostic workflows.Using a hybrid Adaboost-MLP model for fire prediction and Adaboost-LBP with CNN for fire detection in surveillance images, Saeed et al. [5] created a fire detection model that combines sensor and visual data. The

model's efficacy in early fire detection was demonstrated by its above 99% accuracy and low false alarm rate.With effective preprocessing and training, Ahmed S. Musallam et al. [6] created a lightweight DCNN for detecting brain tumors in MRI images, with an accuracy of 98.22%. The model is reliable and can correctly identify pituitary tumors (97.3%), meningiomas (99.13%), and gliomas (99%).In order to detect wildfire smoke in UAV footage, Kim [7] improved YOLOv7 using SPPF+, decoupled heads, BiFPN, and CBAM. With an AP50 of 86.4%, these enhancements improved performance and outperformed competing detectors by 3.9%.

IV. DATASET DESCRIPTION AND PREPROCESSING

A. Dataset Description

Classifying brain tumors, specifically gliomas, meningiomas, pituitary tumors, and tumor-free instances, is the main goal of this study's dataset, which was obtained via Kaggle [8] .The 5712 images in the training set are made up of 1321 glioma images, 1339 meningioma images, 1457 pituitary tumor images, and 1595 non-tumor images. There are 400 pituitary tumors, 336 meningiomas, 1300 gliomas, and 300 non-tumor pictures in the testing set. The subtypes of brain tumors are visually represented in Fig. 1.

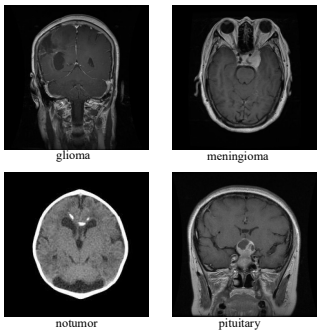

Fig. 1. Visual Representation of Brain Tumor Subtypes: (Glioma, Meningioma, Pituitary, and Non-Tumor)

B. Data Preprocessing

The dataset is organized into four subdirectories, each of which represents a class: pituitary (3), meningioma (1), glioma (0), and no tumor (2). The labels in each subdirectory match the directory index. OpenCV was used to load the images, first reading them in BGR format and then converting them to RGB. As part of the preprocessing stages, all images were resized to 224×224 pixels, and pixel values were normalized to a 0–1 range by dividing by 255. The dataset was split into 1,311 images for testing and 5,712 images for training in order to provide a thorough assessment of the model's functionality. Glioma was mapped to 0 via label encoding, meningioma to 1, no tumor to 2, and pituitary to 3.The scattered data and experimental setup are displayed in Table I,II.

V. METHODOLOGY

The process entails obtaining input images from a dataset of four tumor types (pituitary, glioma, meningioma, and non-tumor), then downsizing and normalizing them to improve accuracy. 5712 images are used to train and 1311 images are used to test a CNN model that includes convolutional layers, ReLU activation, max-pooling, dropout, and dense layers. Training is done using the Adam optimizer and sparse categorical cross-entropy loss, and accuracy, precision, recall, and F1-score are used to assess performance. The model's efficacy in tumor categorization is demonstrated by its 95.27% accuracy on the test set.The methodological steps are displayed in Fig. 2.

TABLE I
DATA DISTRIBUTION TABLE

Tumor Type	Training Data	Testing Data	Total Data
Glioma	1321	300	1621
Meningioma	1339	306	1645
Pituitary	1457	405	1862
Notumor	1595	300	1895
Total	5712	1311	7023

TABLE II
MODEL HYPERPARAMETERS AND EXPERIMENTAL SETUP

Parameter/Setup	Details
Model Type	convolutional neural network (CNN)
Optimizer	Adam (learning rate: 0.001)
Loss Function	Sparse categorical cross-entropy
Activation Functions	ReLU, Softmax
Training Epochs	50
Batch Size	32
Data Augmentation	Rotation, zoom, width/height shift, horizontal flip (no vertical)
Training Environment	Python 3.8, TensorFlow 2.x, Keras, OpenCV, scikit-learn, NumPy
Hardware	CPU: Intel i5, GPU: Nvidia Tesla P100, 8GB RAM
Operating System	Windows 10,11 / Linux

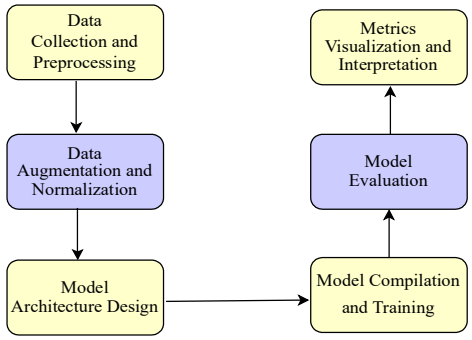

Fig. 2. Workflow of methodological steps

A. Convolutional Neural Network

This CNN model [5] uses Keras to categorize brain cancers (glioma, meningioma, pituitary, and non-tumor).Max-pooling, three convolutional layers with ReLU activations, and a 0.4 dropout layer to avoid overfitting make up this system.Here, Table. III displays the architecture's layer information. For classification, flattened feature maps are passed via a softmax output layer and a dense layer (128 units). To enhance generalization, data augmentation techniques such as rotation,

zoom, and shifts were applied. With sparse categorical cross-entropy loss and the Adam optimizer, the model's training and validation accuracy were 94.48% and 95.27%, respectively. Its potential for clinical applications is validated by a confusion matrix. The proposed architecture is shown in Fig. 3.

Convolution Operation:

$$O = I * K + B \tag{1}$$

Max-Pooling Operation:

$$P(i,j) = \max(F(i,j), F(i+1, j+1), \dots) \tag{2}$$

Loss Function (Sparse Categorical Cross-Entropy):

$$L(y, \hat{y}) = -\sum_{i=1}^{C} y_i \log(\hat{y}_i) \tag{3}$$

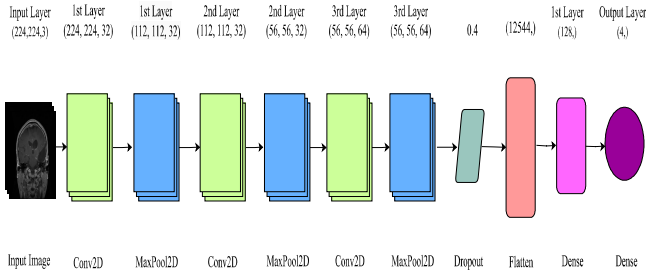

Fig. 3. Proposed CNN Architecture

B. Model Architecture

TABLE III
LAYER DETAILS OF THE CNN ARCHITECTURE WITH PARAMETERS.

Layer Type	Output Shape	Parameters
Conv2D (1st Layer)	(224, 224, 32)	896
MaxPool2D (1st Layer)	(112, 112, 32)	0
Conv2D (2nd Layer)	(112, 112, 32)	9,248
MaxPool2D (2nd Layer)	(56, 56, 32)	0
Conv2D (3rd Layer)	(56, 56, 64)	18,496
MaxPool2D (3rd Layer)	(28, 28, 64)	0
Dropout (1st Layer)	(28, 28, 64)	0
Flatten	(12544)	0
Dense (1st Layer)	(128)	1,600,576
Dense (Output Layer)	(4)	516

This architecture includes three convolutional layers combined with max-pooling layers for feature extraction and dimensionality reduction, along with a Dropout layer to mitigate overfitting. The network concludes with two Dense layers that are fully connected, and the final output layer categorizes the input into four classes.

VI. RESULTS AND PERFORMANCE ANALYSIS

The proposed model achieved a final training and validation accuracy of 94.48% and 95.27% after 50 epochs.The model was trained on 5712 images, while 1311 test images from four categories were used for evaluation. Data augmentation (flipping, zooming, and rotating) were applied to increase the model's resilience.This outcome could help medical professionals by offering an automated, dependable, and effective way to correctly diagnose brain tumors from MRI images.The training and validation summary is displayed in Table IV.

TABLE IV
MODEL TRAINING AND VALIDATION SUMMARY

Epoch No.	Loss (%)		Accuracy (%)	
	Training	Validation	Training	Validation
41	17.62%	17.19%	93.06%	94.05%
42	19.01%	16.01%	92.97%	92.98%
43	17.86%	17.43%	93.69%	92.37%
44	16.61%	13.27%	93.69%	94.89%
45	16.54%	25.05%	93.80%	91.08%
46	16.89%	12.97%	93.55%	94.28%
47	16.15%	15.32%	93.84%	93.75%
48	15.44%	13.26%	93.93%	94.74%
49	16.11%	12.01%	93.81%	95.04%
50	16.11%	12.66%	**94.48%**	**95.27%**

Fig. 4,5 vidually represents the evolution of accuracy and loss over training epochs.The graphs shed light on the convergence behavior, emphasizing any signs of overfitting or underfitting noted throughout the training process.

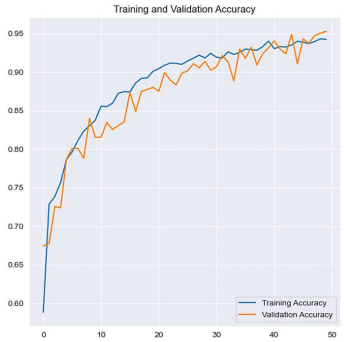

Fig. 4. Accuracy Curve

Fig. 5. Loss Curve

In fig. 6 the confusion matrix of brain tumor classification shows that it can predict pituitary, glioma, meningioma, and

non-tumor categories, accurately recognizing 292 pituitary , 399 non-tumor, 276 meningioma, and 282 gliomas as True Positives. Nevertheless, it produced false positives by misclassifying 8 non-tumor as meningioma, 17 gliomas as meningioma, 3 as non-tumor, and 4 as pituitary; 17 meningiomas as glioma, 3 as non-tumor, 4 as pituitary. False Negatives resulted from the misclassification of 17 gliomas as non-tumor, 8 meningiomas as non-tumor, and 1 pituitary as meningioma. It emphasizes the need for additional model refinement and shows where misclassifications frequently happen.

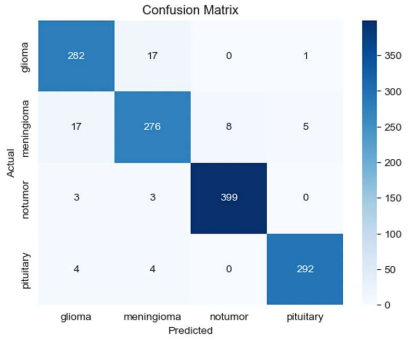

Fig. 6. Confusion Matrix

The classification report shows excellent performance with high precision, recall, F1-scores, and accuracy for all tumor types. For gliomas, the model obtains 92.02% precision, 94.01% recall, 93.04% F1-score, and 93.16% accuracy; for meningiomas, it achieves 92.08% precision, 90.01% recall, 91.00% F1-score, and 91.29% accuracy; for non-tumor, it achieves 98.02% precision, 99.05% recall, 98.01% F1-score, and 96.02% accuracy; and for pituitary tumors, it achieves 98.01% precision, 97.04% recall, 98.0% F1-score, and 98.05% accuracy. The model is a reliable option for tumor classification in medical imaging since it continuously performs well across all classes, achieving a 95.27% overall accuracy rate . The report's summary is displayed in Table V.

TABLE V
OVERVIEW OF THE CLASSIFICATION REPORT

Class	Accuracy	Precision	Recall	F1-Score	Support
glioma	**93.16%**	92.02%	94.01%	93.04%	300
meningioma	**91.29%**	92.08%	90.01%	91.00%	306
notumor	**96.02%**	98.02%	99.05%	98.01%	405
pituitary	**98.05%**	98.01%	97.04%	98.07%	300

TABLE VI
COMPARISON OF MODEL ACCURACY

Description	Accuracy/Performance
VGG16 [9]	87%
InceptionV3 [10]	91%
Proposed Model	**95.27%**

Table VI compares the accuracy of many models from several recent articles.The accuracy of VGG16 was 87.0% [9], while Inceptionv3 improved it to 91.0% [10] by capturing more intricate patterns. The suggested CNN model outperformed both of these models, reaching 95.27% thanks to sophisticated preprocessing and data augmentation, proving the importance of customized architectures for improved medical imaging diagnostics.

VII. CONCLUSION

Using image preprocessing techniques like scaling, normalization, and augmentation, this work suggests a CNN-based deep learning method for diagnosing gliomas, meningiomas, no tumor, and pituitary tumors. It achieves 94.48% training accuracy and 95.27% validation accuracy. Although the model performs well on criteria like precision, recall, and F1 scores, problems with data quality, can affect how successful the model is. The model, which is based on a CNN architecture with several layers and dropout for regularization, is highly dependent on labeled data and can produce subpar predictions when presented with insufficient or unbalanced datasets.

Two major drawbacks include the need for large, high-quality datasets and the computational expense. In resource-limited environments, the model's accuracy may decline. Additionally, its use is restricted to settings with access to high-quality medical imaging.

In conclusion, while the CNN approach is promising, future work should explore diverse architectures, larger datasets, and optimized preprocessing to enhance generalization and efficiency.Additionally, incorporating transfer learning and fine-tuning with domain-specific data could further improve model performance and adaptability.

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