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CNN technique for brain tumor detection and classification using MRI

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Abstract
In general, an uncontrolled and sudden growth of cells poses a significant threat to human life, particularly in the brain region. Diagnosis of these tumors by classifying and dividing them to determine the location, structure, and proportion of tumors is a major challenge, despite the strenuous efforts made by researchers in this field. In this study, statistical image processing techniques and computational intelligence were used to suggest several approaches for recognizing brain tumors and cancer. In this research, the CNN algorithm was used for classifying brain cancer images into two categories: cancerous and non-cancerous. The image features are extracted by entering data through the first layer and gradually moving to the other layers until reaching the final layer. In this work, the CNN algorithm, ReLu, and Maxpool are used with three steps of filters (16,32,64), the Adam technique is used for stochastic optimization, and the SoftMax function for classification is implemented. Kaggle dataset for 7023 patient images is used, the network is trained until reach 0verall accuracy 63.74% at epoch 35, with a learning rate of 0.003.

Keywords: Brain tumor, Image preprocessing, Classification, CNN, Learning, Training, Testing

1. Introduction

Brain tumors are categorized as either malignant or benign [1], and their unchecked growth can strain the skull, significantly interfering with normal brain function. These tumors are generally categorized into four groups [2]: Grade 1 pilocytic astrocytoma, which grows gradually and is almost always surgically removable; Grade 2 tumors like oligodendroglioma, which spread over time and may go undetected even during active treatment; Grade 3 astrocytomas, which require intensive treatment as they spread more quickly than Grade 2, often making surgery alone insufficient; and Grade 4 glioblastoma multiforme, a highly aggressive and rapidly spreading tumor. Detecting these pathologies is inherently challenging because of differences in tumor shape, size, and location.

Consequently, texture analysis has become an essential term in medical image analysis for extracting features and describing image objects for classification [3]. While Magnetic Resonance Imaging (MRI) and artificial intelligence techniques are widely employed to visualize internal bodily structures [4], the increasing complexity of MRI data often prevents the human visual system from identifying subtle anomalies, thereby driving the development of computer-aided diagnosis systems that utilize machine learning to ensure accurate diagnoses [5].

2. Literature review

There have been a number of techniques that have lately been created to identify brain tumors on MRI images. These methods include neural networks as well as the conventional picture processing, which uses machine learning. A hybrid approach combining random forest (RF), K-nearest neighbor (KNN), and decision tree (DT), referred to as KNN-RF-DT, was proposed by [6] using a majority voting scheme. This method aims to identify tumor regions and classify brain tumors as either benign or malignant. For segmentation, Otsu's thresholding method is initially applied. Feature extraction is then performed using the Stationary Wavelet Transform (SWT), Principal Component Analysis (PCA), and Gray Level Co-occurrence Matrix (GLCM). In another study, N. Abiwinanda, M. Hanif, et al. [7] trained a convolutional neural network (CNN) to identify three common types of brain tumors, including pituitary adenoma, meningioma, and glioma. The model achieved a minimum validation accuracy of 84.19% and a maximum training accuracy of 98.51%.

D. Jain, A. Pandey, et al. [8] proposed a method that employs the Whale Optimization Algorithm (WOA) for effective feature selection, combined with a classification approach based on Long Short-Term Memory (LSTM) and an attentive symmetric autoencoder (ASA) for segmentation. The model was evaluated on three tumor regions: tumor core (TC), enhancing tumor (ET), and whole tumor (WT), achieving accuracies of 99.48%, 99.44%, and 99.32%, respectively.

Y. Pourasad [9] introduced a method involving preprocessing steps such as windowing, followed by the extraction of histological and statistical features from T1-weighted and FLAIR MRI brain images. Dimensionality reduction and feature training were also applied. The results demonstrated that combining symmetry-based analysis with a multi-layer clustering technique reduces processing time while improving accuracy. Finally, A. Agrawal [10] evaluated a transfer learning (TL)-based DenseNet121 model, reporting performance metrics of 98.38% accuracy, 97.33% sensitivity, 99.1% specificity, 98.23% F1-score, 98.62% precision, and 96.62% intersection over union (IoU).

The results of the brain tumor data set indicate that the proposed method is superior to the others due to the F1-score, precision, sensitivity, accuracy, specificity, and the IoU. Based on [11], a combination of two types of convolutional neural networks is applied to collect the data about the characteristics of tumors and to identify the type of tumor. The former is a new segmentation method that uses a firefly optimization (FFO) approach, where the quality of the segmentation is considered on a wide range of parameters to enhance the accuracy of the identification process, as well as the general performance of the MRI scan methodology. Testing was done with MRI scans of BBRATS2018, and the mean accuracy was 98.6.

Jeya Maria Jose Valanarasu et al. [12] published a gated axial-attention model, which introduces an additional control mechanism to the self-attention module in existing architectures. Moreover, the Local-Global training technique (LoGo) is used to improve the performance of the model to effectively train the model on medical pictures. In particular, during the acquisition of global and local properties, work with the whole image and patches. It is proven that the proposed Medical Transformer (MedT) is more effective in comparison with convolutional and other related transformer-based architectures after they are tested on three separate medical picture segmentation datasets.

3. Methodology

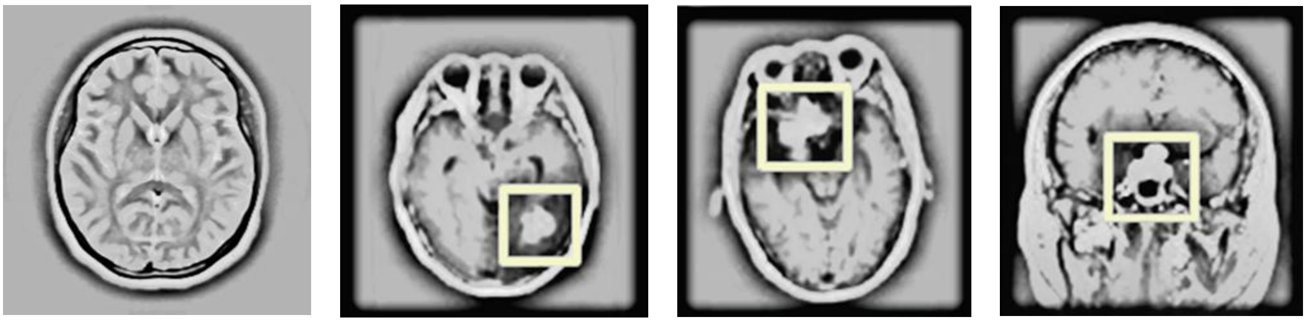
The Kaggle dataset is used, which consists of 7023 images in total for benign and malignant brain tumors. The malignant tumors include three categories of brain tumors (meningioma, glioma, and pituitary) [13]. Table 1 shows the type and number of tumor images that were used for training, and Table 2 shows the types and numbers of tumor images for testing. Figure 1 shows the kinds of brain tumors [14].

Table 1. Type and number of images of tumors for training

No.	Tumor name	No. of image
1	No Tumor	2000
2	Glioma	1621
3	Meningioma	1645
4	Pituitary	1757
Total number of images		7023

Table 2. Type and number of images of tumors for training

No.	Tumor name	No. of image
1	No Tumor	1000
2	Glioma	810
3	Meningioma	822
4	Pituitary	878
Total number of images		3510



a) Benign Tumor b) Glioma c) meningioma d) Pituitary

Figure 1. Types of brain tumors [14]

It is necessary to identify the tumor mass and segment it, then subject it to feature extraction. The segmented area is then classified into several categories [15]. Primary and secondary brain tumors are the two varieties. Secondary tumors originate in another body part and then spread to the brain [16, 17]. Brain tumors that arise in the brain itself are identified as principal brain tumors. Figure 2 shows benign brain tumors, and Figure 3 shows cancerous brain tumors.

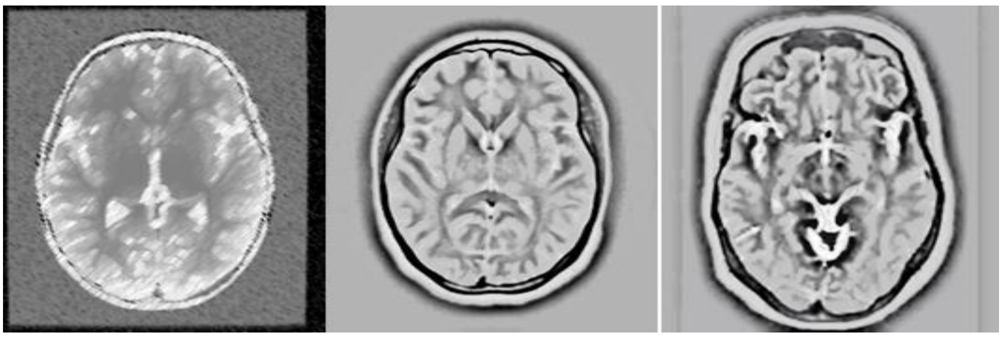


Figure 2. Benign brain tumors

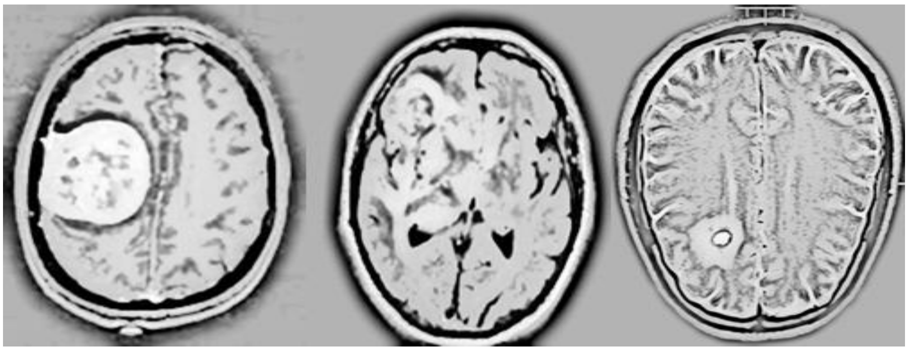


Figure 3. Malignant brain tumors

A CNN convolution layer is a network that creates feature maps by convolutionally applying filters to an image. The following convolution layer will receive these feature maps to get or extract more advanced features from the input picture. The image's dimensionality is decreased, and non-linearity is added between convolution layers using down-sampling and non-linearity functions, respectively. Because it preserves the dominating feature in the feature maps while reducing the dimension, max-pooling is frequently employed as the down-sampling method. A flattening layer is present to vectorize the feature maps immediately following the last convolution layer or before the neural network's first layer. The flattened input vector will be sent into the neural network or classification phase [18].

Convolutional neural networks perform very well in image segmentation. However, they don't comprehend the image's long-range dependencies [19]. In this work, six steps are performed to classify brain cancer images as follows:

- Step 1: Load and process the dataset:
  After obtaining the brain image data, the image size is changed to 128*128, and then the image is converted to grayscale.
- Step 2: Define CNN Architecture:
  At this stage, the image feature is extracted, and 16, 32, and 64 learnable filters make up the convolution layers parameter. Each filter is tiny in terms of (width and height), but it penetrates the input volume's fill depth. During the forward passes, we calculate the dot product between the filter's and the input's entries at any place by sliding (or convolving) each filter across the input volume's width and height. The ReLU layer adds non-linearity to the network by functioning as a non-linear activation function. Neural networks may learn intricate patterns and produce precise predictions thanks to their non-linearity. It is especially noteworthy for its capacity to manage massive data collections. After that, Max pooling is used; the purpose of the pooling layers is to gradually reduce the spatial size of the representation to reduce the number of parameters and computations in the network. In contrast, the pooling layer frequently employs the max operation to carry out the down-sampling process. If the feature map from the previous layers is not down-sampled, the output of this stage is directed to the next step as a vector.
- Step 3: Classification:
  The flattened layer typically follows the convolutional and pooling layers in a CNN structure. It connects the convolutional/pooling layers, which extract spatial data, and the fully connected layers, which perform classification tasks. The next step is a fully connected layer, which acts as a bridge between the convolutional/pooling layers, which extract spatial data, and the fully connected layers, which conduct classification tasks. The SoftMax function is used for classification tasks; it takes the exponent of each output and normalizes these values by dividing by the sum of all exponents, thereby converting raw output scores into probabilities. Four categories are used to categorize the data in this study: glioma, meningioma, pituitary, and benign tumor.

“Adam” is a technique for adaptive learning rates intended to accelerate deep neural network training and achieve convergence. "Adaptive moment estimation" refers to an iterative optimization technique that is used to minimize the loss function when neural networks are being trained. RMSprop and stochastic gradient descent with momentum are combined in this method [20]. Figure 4 shows the steps of the methodology.

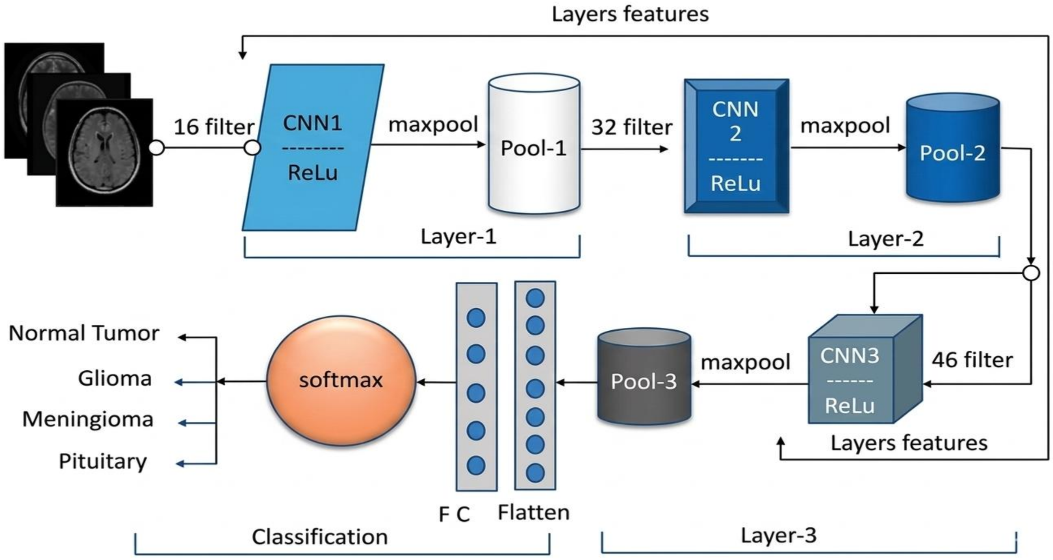


Figure 4. The steps of the methodology

- Step 4: Evaluate the Model and Results:
  In this stage, the network was trained on 7023 JPG images, including three types of brain tumors (glioma, meningioma, pituitary). The data is divided into 70% for training and 30% for testing. The best training model was at epoch 35, and the learning rate was 0.003, as shown in Figure 5. After that, augment the training data to improve normalization and create an augmented image data store for training, as well as an image data store for testing. The size of the max-pooling kernel, the number of neurons in the fully connected layers, and the number and size of filters in the convolution layers are among the hyperparameters at each layer that are held constant in our experiment.

After the training process, the network is tested, and some criteria are calculated to measure the efficiency of the network. The metrics are calculated, including F1-score, recall, and precision for every category described as follows:

Precision is calculated by dividing the number of accurate forecasts for a category by the total number of predictions made for that category, as explained in Equation 1.

$$Precision = \frac{True\ Positive}{(True\ Positive + False\ Positive)} \qquad (1)$$

Recall: The percentage of instances of a category that are properly identified, as explained in Equation 2.

$$Recall = \frac{True\ Positive}{(True\ Positive + False\ Negative)} \qquad (2)$$

F1-Score: A single metric that strikes a balance between precision and recall by taking the harmonic mean of the two. When recall and precision values are similar but not identical, it is especially helpful, as explained in Equation 3.

$$F1\ Score \frac{(2 * Precision * Recall)}{(Precision + Recall)} \qquad (3)$$

In this model, the data used in training is unbalanced; therefore, other criteria are calculated, such as precision, recall, and F1 score. These criteria have a value between 0 and 1, and the higher the value, the better the result in the classification process.

F1 Score combines precision and recall, which is a means of balancing between precision and recall. Its value ranges between 0 and 1. The higher the value, the better the result. The lower the value, the more it indicates that the model cannot balance these two criteria. Table 3 shows these criteria, and Figure 5 shows the confusion matrix for testing the data.

Table 3. The criteria that were calculated

Category	Precision	Recall	F1 Score
Glioma	0.76	0.65	0.70
Meningioma	0.51	0.44	0.47
Benign Tumor	0.88	0.85	0.86
Pituitary	0.56	0.56	56

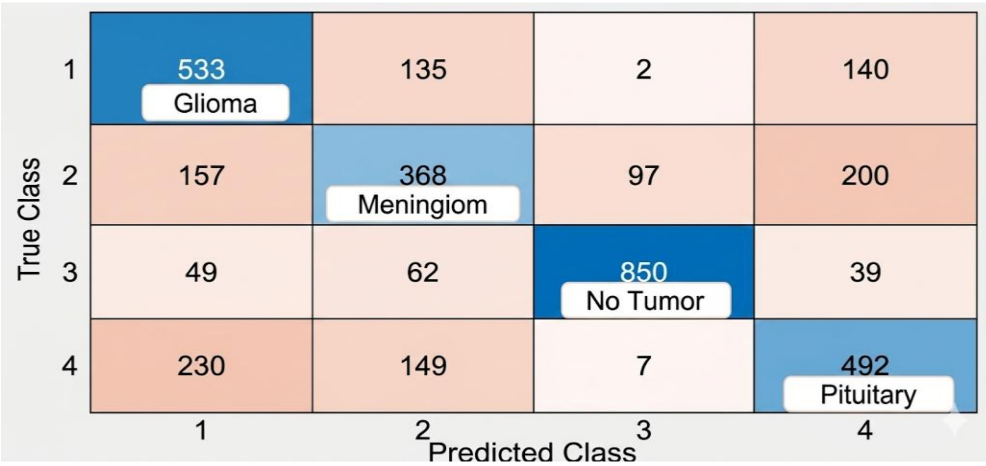


Figure 5. Confusion matrix for testing Data

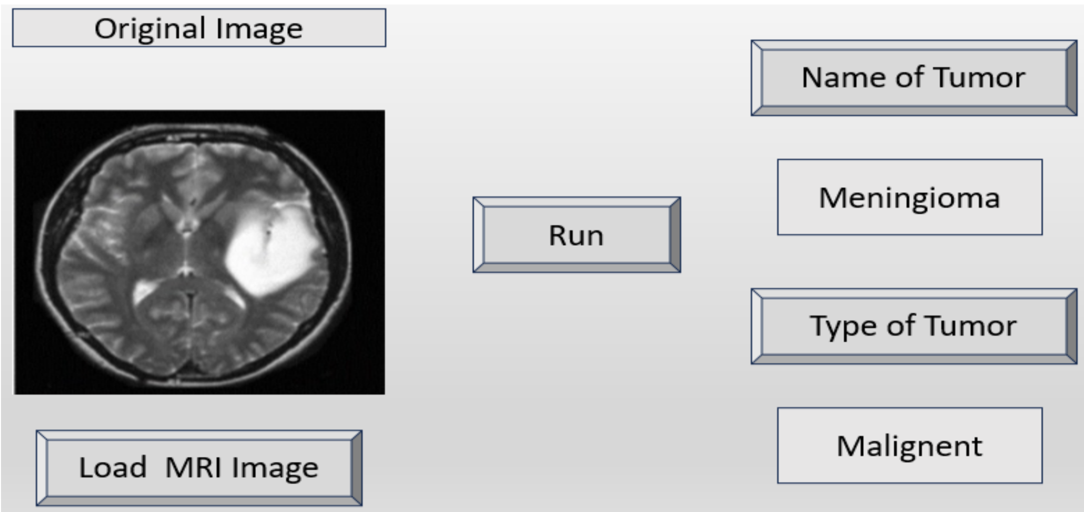


Figure 6. GUI for the proposed model in MATLAB 2020

In Figure 6, when the program is run, the image to be examined is loaded. Either the case is healthy or infected. If it is infected, the type and name of the disease are diagnosed. Accuracy percentage and loss results are depicted in Figure 7.

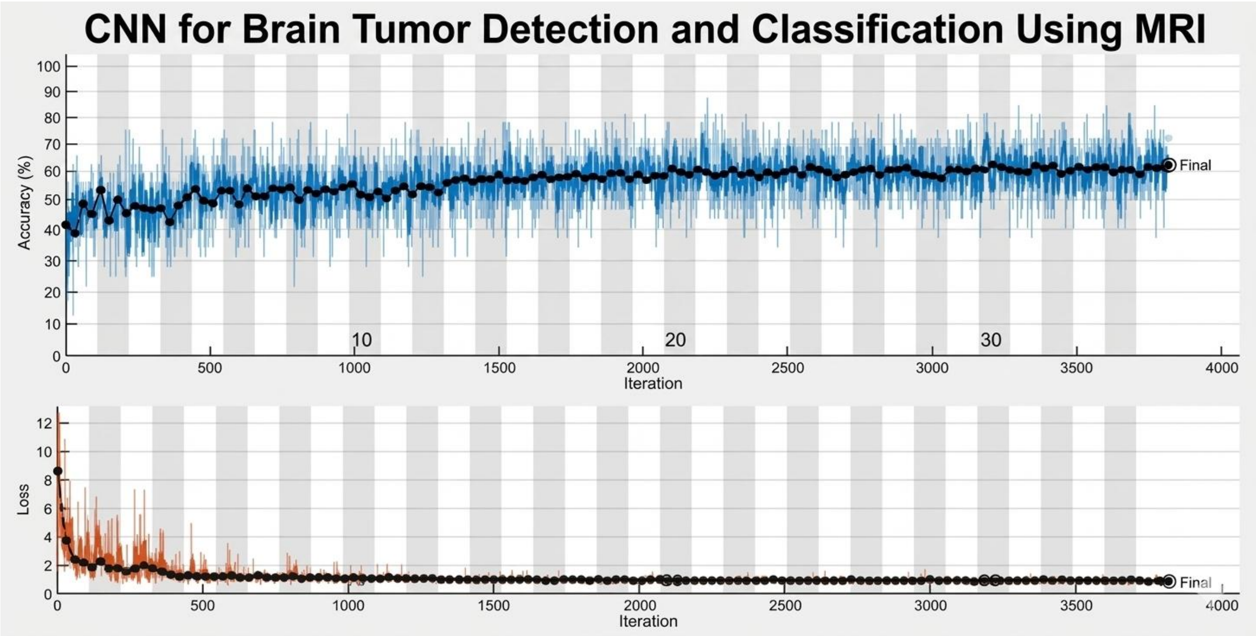


Figure 7. Accuracy and loss of the projected model

4. Conclusions

This paper presented a CNN system with three layers that can be used to prognostically differentiate between benign and malignant tumors without preprocessing procedures involving regions. We used filters (16, 32, 64) to classify the three most common types of brain cancers (glioma, meningioma, and pituitary tumor); the accuracy of the classifier is dependent on the number of filters in a convolution layer .

Experimental findings indicate that the behavior of the trained network is highly dependent on the training parameters used, especially the learning rate and number of training epochs. In this experiment, the model was trained several times with various combinations of these parameters to be able to get the best possible performance. The best configuration was achieved by the learning rate being 0.0003 and the number of epochs being 35, and hence, overall classification was about 63%. Even though this value might seem moderate, it is supposed to be considered in the framework of the dataset characteristics. The data used in this research was extremely skewed, which means that certain classes had a great number of images in comparison to others. This imbalance may lead to this model giving preference to the majority classes during the training process, and this influences the consistency of accuracy as an exclusive measure of performance.

Thus, the findings verify that the use of overall accuracy alone as a metric to assess machine learning models that have been trained on imbalanced data is deceptive. Under this, the model can potentially get an apparent satisfactory accuracy with poor performance on minority classes. In order to have a more comprehensive analysis, some other metrics of performance were taken into consideration, such as precision, recall, and F1-score. These measures provide a more balanced evaluation of model competence since they both take into account both the accuracy of positive predictions and the capacity of the model to detect all the relevant samples. The application of these evaluation measures will give an additional understanding of the actual effectiveness of the trained model and guarantee a more credible evaluation of the classification ability.

5. Future scopes

Although the performance was quite reasonable, in the future, it is possible to consider several improvements that may contribute to the further enhancement of the proposed model. Among the directions is to solve the problem of dataset imbalance with the use of data augmentation models or resampling methods like oversampling minor classes or undersampling majority classes. Such practices may be used to develop a more balanced training distribution and increase the generalization of the model across all classes. Also, it is probable that, by gathering more and more diverse data, one could enhance the strength and the generalization power of the model.

It can also be inferred in future research that more advanced deep learning architectures and optimization strategies will be used in order to further optimize classification performance. Such methods as transfer learning with pretrained convolutional neural networks, hyperparameter optimization, and ensemble learning may be potentially beneficial in terms of accuracy and stability. Moreover, automated feature extractions and attention mechanisms can be incorporated, leading to a model that can center on informative tendencies within the images. With such enhancements, further research would assist in considerably enhancing the accuracy and efficiency of the classification system, especially when operating with complex or skewed data.

Declaration of competing interest

The authors declare that they have no competing interests in this paper.

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Author contribution

Asmaa Abdul-Razzaq Al-Qaisi: Conceptualization, methodology, and writing the original draft.
Geehan Sabah Hassan: Data collection, analysis, and interpretation of results.
Enas Muzaffer Jamel: Development of the CNN model and implementation of experiments.
Raghad Abdulaali Azeez: Review and editing of the manuscript, and supervision of the research project.
All authors contributed to the final version of the manuscript and approved it for publication.

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