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Research Article

DEEP LEARNING IN NEUROLOGICAL IMAGING: A NOVEL CNN-BASED MODEL FOR BRAIN TUMOR CLASSIFICATION TÜRKİYE AND HEALTH RISK ASSESSMENT

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ABSTRACT

Brain tumors can cause serious neurological damage and death by putting pressure on critical brain regions that manage vital functions. Given the complex structures in the brain, human error in the evaluation of radiological images can create difficulties in the detection of these tumors. Convolutional neural networks (CNNs) are type of deep learning (DL) and are widely used, especially for analyzing visual data. The advantage of CNNs in detecting brain tumors is that they can automatically learn features from images and minimize human error by increasing the classification accuracy. In this study, a unique CNN-based model is proposed for brain tumor diagnosis using magnetic resonance imaging (MRI) images. A high classification score was obtained using a dataset consisting of 3096 MRI images divided into four categories: glioma, meningioma, normal brain, and pituitary tumor. The model achieved an overall 93% accuracy rate in tumor detection. In particular, great success was seen for the detection of pituitary tumors with 96% precision and a 95% F1 score. This study demonstrates that DL has significant potential in medical image analysis. The novelty of our approach lies in designing a lightweight CNN architecture from scratch that achieves high accuracy without relying on transfer learning, while requiring significantly fewer computational resources than traditional deep architectures.

INTRODUCTION

Intracranial neoplasms, commonly referred to as brain tumors, pose a considerable challenge in the fields of neurology and oncology due to their complex pathophysiology and potential to cause severe neurological disorders. Characterized by abnormal proliferation of cells within the cranial cavity, these neoplasms can be categorized as either benign or malignant with varying invasiveness and growth rates. Accurate and timely diagnosis of brain tumors is of paramount importance for optimal patient outcomes as it directly affects treatment strategies and prognosis (Louis et al., 2016).

Traditional diagnostic methods based primarily on radiological interpretation and histopathological examination are often time-consuming and subject to inter-observer variability. This limitation has prompted the search for advanced computational methods to

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support the diagnostic process. In recent years, the emergence of artificial intelligence (AI) and especially deep learning (DL) techniques has revolutionized medical image analysis (Litjens et al., 2017).

Machine learning (ML) approaches are widely used in various fields, such as medical diagnosis and preventive medicine (Adlung, Cohen, Mor & Elinav, 2021). However, the challenges of limited medical imaging data pose a major challenge for these approaches. The limited data is usually trained and tested on magnetic resonance imaging (MRI) data using traditional ML algorithms. Recently, some approaches have started to use DL methods for brain disease diagnosis. Convolutional neural networks (CNNs), a class of DL algorithms, have shown exceptional effectiveness in image classification and object detection tasks (Zhao, Zheng, Xu & Wu, 2019). Their ability to automatically learn hierarchical feature representations from raw image data makes them particularly well suited for analyzing complex medical images such as MRI scans (Hammernik et al., 2019).

CNN-based methods have been successful in detecting many brain diseases, such as epilepsy (Dutta, Manohar & Krishnappa, 2024), Alzheimer's disease (Çelebi & Emiroğlu, 2023), and stroke (Zhang, Xu, Tan, Wang & Meng, 2021). Rehman et al. (Rehman, Naz, Razzak, Akram & Imran, 2020) proposed a framework for the classification of different types of tumors using a model called triple architecture CNN. As a result of their research, they achieved an accuracy of 98.69% using the VGG16 architecture to improve classification and diagnosis. Çinar and Yildirim (2020) introduced a hybrid CNN architecture aimed at computed tomography detection via the adaptation of a deep learning model. Their integrated ResNet50 architecture attained an accuracy of 97.2%, in contrast to the standalone ResNet50 model, which recorded an accuracy of 92.53%. Banerjee et al. (Banerjee, Mitra, Masulli & Rovetta, 2019) proposed new ConvNet models to improve MRI image classification using multiple MRI images. By combining existing ConvNet and VGGNet models, the study achieved 97% accuracy of the proposed models. Furthermore, a multi-level feature extraction method was developed to overcome the differences between medical images and natural images. Pashaei et al. (Pashaei, Sajedi & Jazayeri, 2018) introduced two distinct methodologies: the first methodology used a CNN model for the classification task, while the subsequent methodology used the features derived from the CNN as inputs for a kernel extreme learning machine approach. The methodology represents a learning algorithm that is composed of multiple layers of hidden nodes. Abiwinanda et al. (Abiwinanda, Hanif, Hesaputra, Handayani & Mengko, 2019) introduced a CNN architecture characterized by a dual-layer configuration. Hashemzehi et al. (Hashemzehi, Mahdavi, Kheirabadi & Kamel, 2020) proposed a hybrid CNN-NADE model that effectively detected brain tumors from MRI images, even with limited medical image availability. Pereira et al. (Pereira, Meier, Alves, Reyes & Silva, 2018) suggested a 3D CNN that automatically grades glioma using MRI in conventional multiple sequences. The proposed system provides two functionalities, which are automatically extracting regions of interest and predicting glioma grade. Evaluated on the BRATS 2017 training set, the system achieved 89.5% accuracy, and tumor prediction based on regions of interest was performed with 92.98% accuracy. In another study, Tiwari et al. (Tiwari et al., 2022) used a CNN to classify brain tumors into four different classes (ie, non-tumor, glioma, meningioma, and pituitary tumor) and achieved 99% accuracy. Ozdemir (2023) developed a novel CNN architecture for classifying three types of brain tumors (meningioma, glioma, and pituitary) from brain MR images that is simple, fast, and computationally efficient, achieving a high accuracy rate of 98.69%. This model presented an architecture requiring less computational power, with greater flexibility and reduced complexity, particularly by utilizing high kernel size and stride values in the first convolutional layers.

This study aimed to investigate the effectiveness of CNNs in detecting and classifying brain tumors using a comprehensive dataset of MRI scans. Our research focused on four different categories: gliomas, meningiomas, pituitary tumors, and normal brain tissue. By the end of the study, we aimed to develop a highly accurate classification model to help clinicians in the diagnostic process with DL. The performance of the model was evaluated using various metrics, including precision, sensitivity, and F1-score, with special attention paid to its ability to discriminate between different tumor types.

The success of published studies in detecting brain tumor types inspired us to select a DL -based approach to improve its accuracy and performance. We evaluated our proposed approach on a publicly available dataset. The research contributes to the burgeoning literature on DL-assisted medical image analysis and explores the potential of DL techniques in improving the speed and accuracy of brain tumor diagnosis. By demonstrating the capabilities of CNNs in this context, we aimed to lay the groundwork for the development of more efficient and reliable diagnostic tools that can complement traditional clinical methods. Furthermore, with our proposed work, we aimed to answer the following research question: To what extent does the DL algorithm demonstrate efficiency and precision in the identification and classification of various tumor types?

The study provided three main contributions. (1) We presented an innovative DL model designed for the classification of four distinct categories of MRI scans. The introduced DL classification methodology demonstrated superior performance compared with prevailing state-of-the-art techniques by attaining the highest accuracy on the MRI dataset. (2) Especially limited datasets pose a major problem in medical image processing. For this reason, high-accuracy studies in the literature are usually based on transfer learning (Ozdemir, 2024) models. However, in this paper, we showed that our proposed novel CNN-based method can achieve as high accuracy as transfer learning. (3) Traditional ML methods require feature extraction. However, DL-based methods eliminate this need thanks to their ability to automatically learn features. Therefore, the superior classification performance of our CNN-based method becomes more evident when compared with traditional ML methods. In this paper, we evaluated the effectiveness of a CNN-based architecture.

The novelty of the CNN architecture proposed in this work lies in several key aspects. First, unlike many recent approaches, our model is designed from scratch to specifically adapt to the unique characteristics of brain tumor MRI images, rather than using pre-trained architectures. Second, our model achieves high accuracy (93%) with only 1.8 million parameters, using significantly less computational resources compared to complex deep architectures (e.g., VGG, ResNet). Third, the proposed architecture has shown superior performance, especially in the detection of pituitary tumors (96% accuracy), thanks to its layer configuration specifically designed to capture the morphological features of different tumor types. In these aspects, our work provides the literature with a lightweight and effective brain tumor classification model that can be used in clinical applications. Although existing studies have achieved high accuracy, they typically rely on transfer learning and large-scale pretrained models that require substantial computational resources. Our work addresses this gap by developing a lightweight CNN architecture from scratch that achieves comparable accuracy with significantly fewer parameters, making it more suitable for deployment in resource-constrained clinical settings.

With this work, we aimed to advance the field of neuro-oncology and contribute to the ongoing efforts to improve patient care with innovative technological solutions.

MATERIAL AND METHOD

In this study, a novel CNN architecture was developed to detect and classify brain tumors.

Dataset

The dataset used in the study provides a large collection of MRIs for brain tumor classification (Chitnis, Hosseini & Xie, 2022). The dataset consists of a total of 3096 images and was divided into four categories: glioma tumor, meningioma tumor, pituitary tumor, and normal brain scans. The dataset includes images acquired in the axial, coronal, and sagittal planes. Each image was labelled for medical image processing and DL model development. Figure 1 shows example images of the dataset from four different classes.

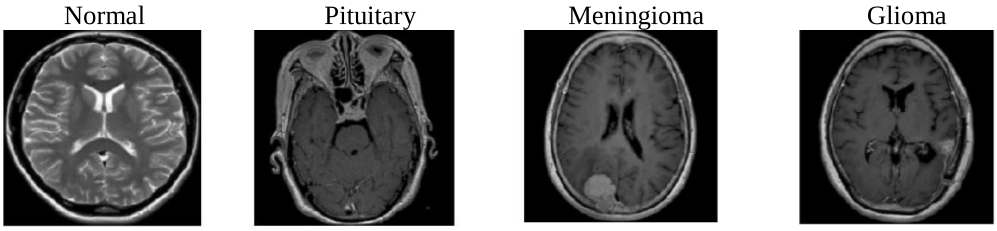

Figure 1: Dataset sample images

The images were standardized to 224x224 pixels and RGB format. The dataset was divided into groups with approximately 70% for training, 10% for validation, and 20% for model training and testing. The pixel intensity values were adjusted by the min–max normalization method and measured as a value between 0 and 1. The distribution of the dataset is shown in Table 1.

Table 1: Dataset classes

Class name	Train (n)	Validation (n)	Test (n)	Total images (n)
Glioma tumors	633	90	178	901
Meningioma tumors	640	92	182	913
Normal brain images	305	44	89	438
Pituitary tumors	588	85	171	844

Model architecture

The DL model used in the study was developed for the classification of brain tumors and was built using the Keras library. The model was specifically designed and structured for brain tumor classification. Figure 2 shows the process of the proposed method for brain tumor diagnosis. For model training, categorical_crossentropy was used as the loss function as it is suitable for multi-class classification problems. Adam Optimizer was selected as the optimization algorithm.

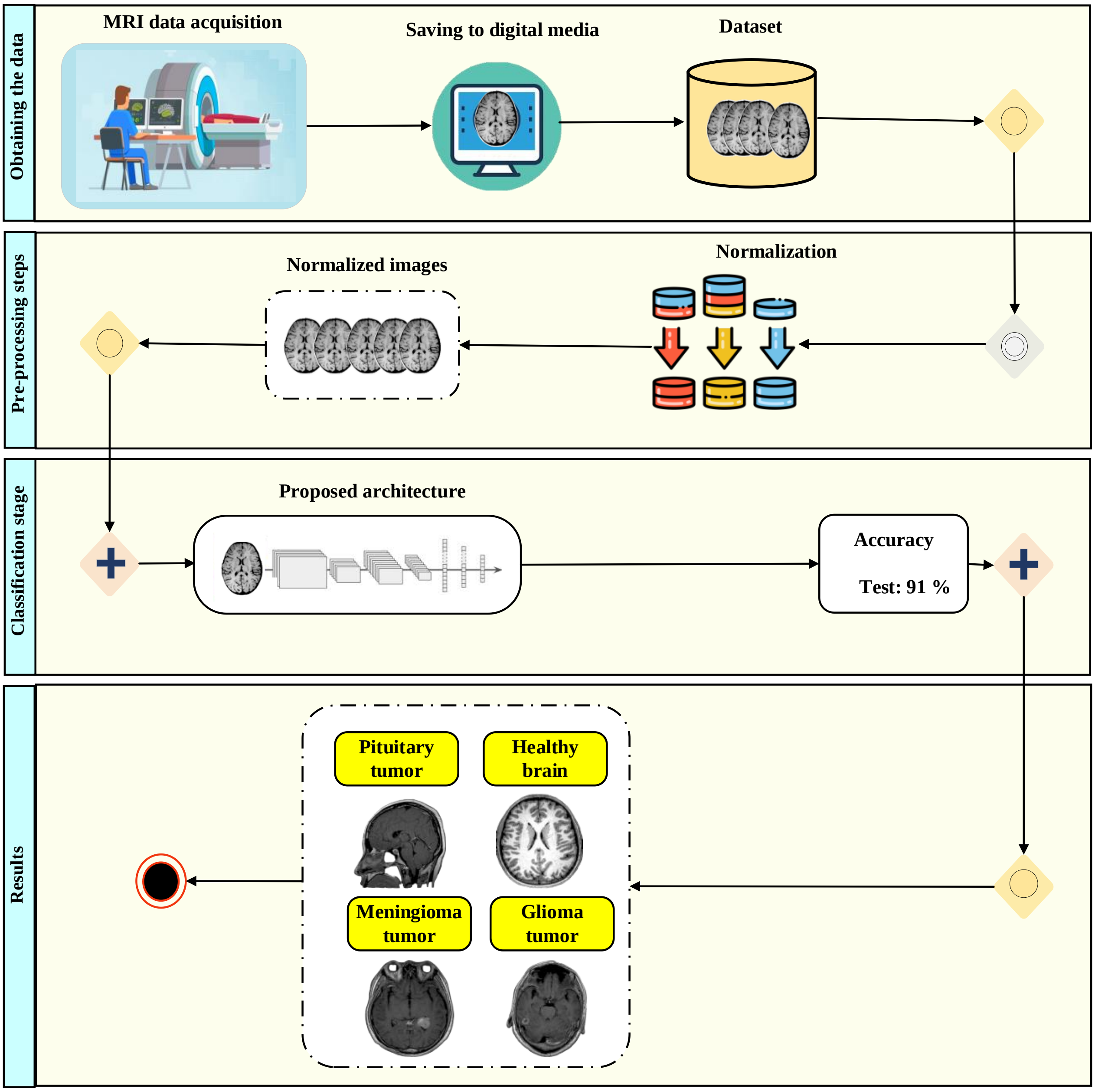

Figure 2: Proposed DL model

Adam is a gradient-based stochastic optimization method and is widely used in large-scale DL models. In our study, the accuracy metric was used to evaluate the performance of the model. The hyperparameters used for the architecture of the model designed in this study are given in Table 2.

Table 2: Model architecture details

Parameters	Value
Learning rate	1e-3
Batch size	128
Optimizer	Adam
Loss function	Categorical Crossentropy
Number of epochs	30

Rescaling	1/255
Metrics	Accuracy

The model consists of a series of convolutional (Conv2D) and maximum pooling (MaxPooling2D) layers and followed by flattening (flatten), fully connected (dense), and dropout layers. The final layer is dense and consists of four neurons. The total number of parameters in the model was 1,846,916, which suggests that the model was sufficiently complex and has the potential to discriminate various types of brain tumors. The architecture of the proposed CNN-based classifier is detailed in Table 3.

Table 3: CNN architecture

Layer	**Output shape**	**Parameter**
Conv2D	(,222, 222,64)	1,792
MaxPooling2D	(,111, 111, 64)	0
Conv2D	(,111, 111, 128)	204,928
MaxPooling2D	(,37, 37, 128)	0
Conv2D	(,37, 37, 128)	802,944
MaxPooling2D	(,18, 18, 128)	0
Conv2D	(,18, 18, 128)	409,728
MaxPooling2D	(,9, 9, 128)	0
Conv2D	(,9, 9, 128)	147,584
MaxPooling2D	(,4, 4, 128)	0
Conv2D	(,4, 4, 128)	147,584
MaxPooling2D	(,2, 2, 128)	0
Flatten	(,512)	0
Dense	(,256)	131,328
Dropout	(,256)	0
Dense	(,4)	1,028
Total parameters		1,846,916

Deep learning

Artificial neural networks (ANNs) are used to model learning processes in computer systems (Göçmen, Çıbuk & Akin, 2024). These networks have the potential to provide effective solutions in complex problem domains where traditional methods fall short. ANNs have important applications in various fields, such as for financial transactions (Havishya, Lakshmi & Aishwarya, 2024), marketing (Aslan & Çelebi, 2022), forecasting (Birecikli, Karaman, Çelebi & Turgut, 2020), and health applications (Yaşar, 2025). ANNs are used for processing and analyzing complex datasets (Aslan & Çelebi, 2024).

ANNs are a subclass of ML, and deep neural networks (DNNs) are a subclass of ANN. DNNs can process complex data structures more efficiently due to the inclusion of more layers and neurons. Following this development, CNNs emerged with the addition of the convolution process. CNNs have led to significant advances, especially in the field of image processing (Hayıt & Çınarer, 2022; Özcan & Acar, 2024). DL, thanks to its multilayer structure, has been used for image processing, natural language processing, and voice recognition. This technology offers effective applications in the healthcare, computer vision, and finance sectors. The processing and analysis of complex datasets in these fields is made more efficient with DL techniques (Shlezinger, Whang, Eldar & Dimakis, 2020).

ANN and DL techniques play a crucial role in modern AI applications, given their success in data analysis and modeling processes. These technologies offer new opportunities for future research and applications and bring innovative solutions to problems in various disciplines. As a result, ANNs and DL are leading revolutionary developments in computer science and AI and shaping the future of these fields.

Development environment

Google Colaboratory (Colab) is a widely used platform for cloud-based scientific computing and ML applications. Built on Google's infrastructure, Colab allows users to work with the Python programming language and facilitates project management with Google Drive integration. The platform is specially optimized for training DL models with high-performance computing resources, such as the Tesla K80 GPU and Tensor Processing Unit (TPU), which are available for free. Due to its web-based interface, Colab allows users access from a variety of devices without requiring any local installation, which allows researchers and developers to continue their work from different platforms, including mobile devices. The platform offers a comprehensive ecosystem for researchers working with data science, ML, and DL. Users can easily upload shared scientific and ML libraries and collaborate on their projects. Colab provides a powerful, flexible, and accessible platform for researchers and developers working in scientific computing and ML. With its free computational resources, user-friendly interface, and extensive library support, Colab plays an important role in the development of academic and industrial research projects (Sukhdeve & Sukhdeve, 2023).

Performance metrics

The key metrics used for the performance evaluation of classification models are crucial for analyzing various aspects of the model. Accuracy (ACC) is a performance metric that expresses the ratio of a model's correct predictions to total predictions. Accuracy is calculated by the equation:

$$ACC = \frac{TP + TN}{TP + TN + FP + FN} \tag{1}$$

True positive (TP) refers to the number of samples correctly predicted as positive and true negative (TN) indicates the number of samples correctly predicted as negative. False positive

(FP) represents samples that were incorrectly predicted as positive and false negative (FN) represents samples that were incorrectly predicted as negative. However, accuracy can be misleading in unbalanced datasets. Therefore, this metric is usually evaluated together with other metrics, such as precision, recall, and F1 score. In this study, the performance of the model was analyzed with four different metrics.

Precision (PRE) measures how accurate the model's positive class predictions are and is especially crucial in areas where false positives are costly, such as clinical diagnosis or risk assessment (equation 2):

$$PRE = \frac{TP}{TP + FP} \tag{2}$$

Recall indicates the model's ability to detect true positive examples. This metric is particularly important in scenarios, such as cancer diagnosis, where false negatives can have consequences (equation 3):

$$Recall = \frac{TP}{TP + FN} \tag{3}$$

The F1-score (F1-SCR) represents the harmonic mean of the precision and recall metrics and provides a balance between these two metrics. The F1-score is considered an effective metric for evaluating the overall performance of the model, especially in imbalanced datasets (equation 4):

$$F1 - SCR = \frac{2 * PRE * Recall}{PRE + Recall} \tag{4}$$

The support metric shows the number of instances of each class in the test set. This information provides a contextual framework for interpreting the other metrics and provides important information about the class distribution of the dataset.

Combining these metrics allows for a more comprehensive and versatile evaluation of the classification model's performance. Each metric indicates a different performance dimension of the model. In this way, researchers and practitioners can analyze the strengths and weaknesses of the model in more depth (Chicco & Jurman, 2020; Erenel & Altınçay, 2012; Henderi, Wahyuningsih & Rahwanto, 2021; Powers, 2020).

Data normalization

Data normalization is the process of rescaling values in a dataset within a given scale or range. This process is especially important in ML and DL applications because it helps algorithms perform better and learn faster. Min–max normalization adjusts data to a defined interval (typically ranging from 0 to 1; equation 5):

$$X' = \frac{X - min(X)}{max(X) - min(X)} \tag{5}$$

In equation 5, X^' is the normalized value, X is the input variable, and min(X) and max(X) refers to the minimum and maximum values in the series (Chicco & Jurman, 2020; Erenel & Altınçay, 2012; Henderi vd., 2021; Powers, 2020).

Receiver operating characteristic curve

A receiver operating characteristic (ROC) curve shows the relationship between the model’s true positive rate (TPR) and false positive rate (FPR) in binary classification problems, and were calculated using equations 6 and 7, respectively:

$$TPR = \frac{TP}{TP + FN} \tag{6}$$

$$FPR = \frac{FP}{FP + TN} \tag{7}$$

The ROC curve helps to evaluate the classification performance of the model. A larger area under the curve (AUC) indicates better performance of the model (Nahm, 2022).

RESULTS AND DISCUSSION

The developed DL model showed considerable performance during the training process. Although the accuracy rate was 30% at the beginning, it reached 99% in the last phase of training. The performance on the validation dataset stabilized around 92%. These results show that the model has a high learning capacity on the training data while maintaining its generalization capability. The accuracy output of the model is shown in Figure 3.

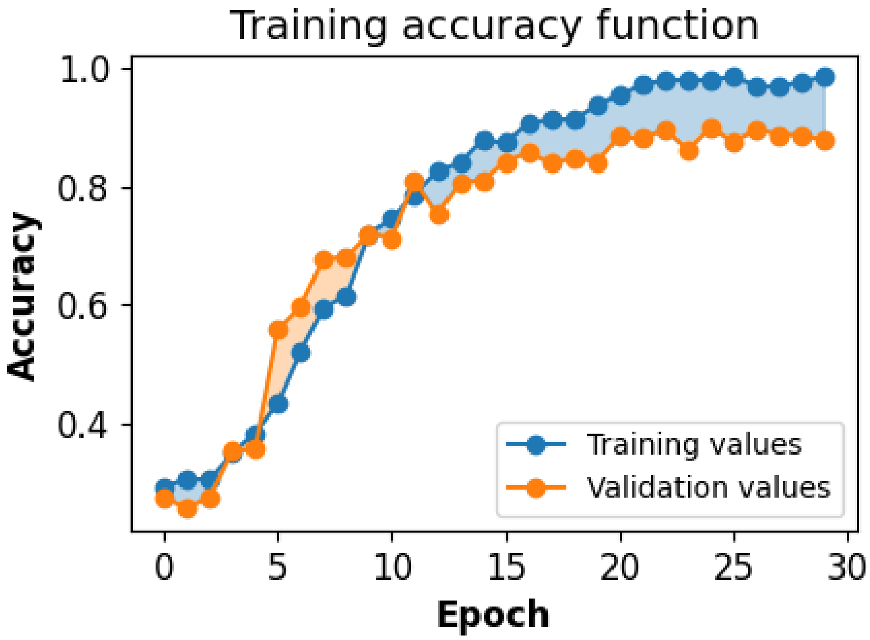

Figure 3: Training and validation accuracy of the model

The dataset was unbalanced; therefore, other performance metrics are presented in Table 4. The performance of the model in four different classes is described along with precision, recall, F1-score, and support values. The model classified brain tumors with high accuracy in the four different classes.

Table 4: Model performance results

Class	Precision	Recall	F1-Score	Support
Glioma	0.87	0.92	0.89	177
Meningioma	0.89	0.87	0.88	182
Normal	0.93	0.93	0.93	89
Pituitary	0.96	0.94	0.95	171
Accuracy	–	–	0.95	619
Macro average	0.93	0.93	0.93	619
Weighted average	0.93	0.93	0.93	619

Analyzing Table 4, the architectural pituitary tumor class had the highest F1-Score (0.95) and precision (0.96), meaning that the model can predict this tumor accurately. The normal class model performed well with an F1-Score of 0.93 and precision of 0.93. The overall accuracy was 93%, which shows that the model performed strongly overall. However, the model's prediction results in the glioma and meningioma classes showed slightly lower performance than the other classes. Especially in the glioma class, precision was lower than the other classes with a score of 0.87.

The confusion matrix shows the relationship between a model's predictions and the actual labels (figure 4).

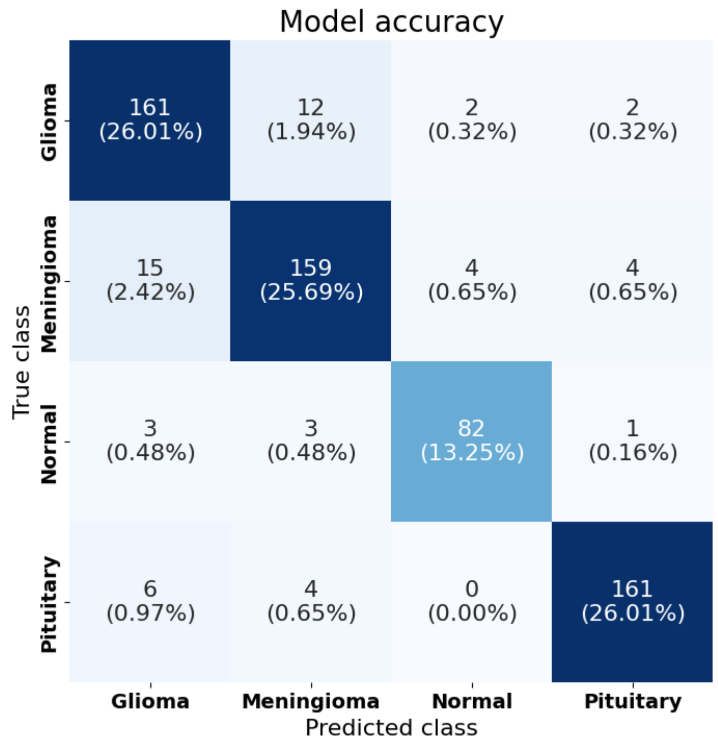

Figure 4: Confusion matrix

While 161 correct predictions were made for glioma tumors, 12 meningiomas, two normal, and two pituitary tumors were misclassified. In the meningioma tumor class, 159 correct predictions were made; 15 gliomas, four normal, and four pituitary tumors were misclassified. In the normal class, 82 correct predictions were made, while three were misclassified as glioma, three as meningioma, and one as a pituitary tumor. Lastly, in the pituitary tumor class, 161 correct predictions were made, while six gliomas and four meningiomas were misclassified. The proposed model showed success in classifying tumor classes; however, there was more confusion between the glioma and meningioma classes. The true classification rate was high in normal and pituitary tumor classes. In particular, in the pituitary and glioma tumor classes, the performance of the model was very strong.

The ROC curve presented in Figure 5 shows the performance of the classification of our proposed model for the four different classes. The ROC curve had an AUC of 0.97 for the glioma class. The model was successful at discriminating between the glioma class. The curve is almost close to the upper left corner, which implies both high accuracy of positive classification and a low false positive rate. For the meningioma class, the AUC was 0.96. Similarly, the model performed very well for meningioma. Given the AUC value of 0.96, the model was also very successful at recognizing the meningioma class. For the normal class, the model achieved an AUC score of 1.00, perfectly classifying the MRI images of normal individuals. The curve completely converges to the upper left corner, and the model worked without errors. The model achieved an AUC score of 0.99 for the pituitary class. Thus, the model performed almost perfectly and was successfully classified with high accuracy.

In general, the ROC curves for all classes are close to the upper left corner, and the AUC ranges between 0.96 and 1.00. Accordingly, our proposed model performed well in all classes. The high AUC values, especially in class imbalances or in distinguishing different classes, indicate that the model is reliable.

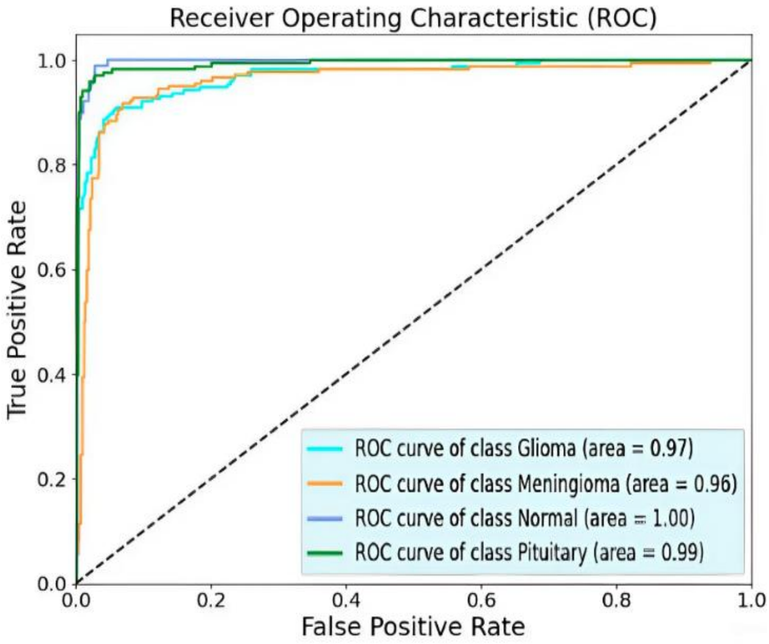

Figure 5: ROC curves and the AUC

Our high-performing model was evaluated with test images. Accordingly, the model's predictions and actual visual output are shown in Figure 6, which shows that the model is able to accurately distinguish tumor types.

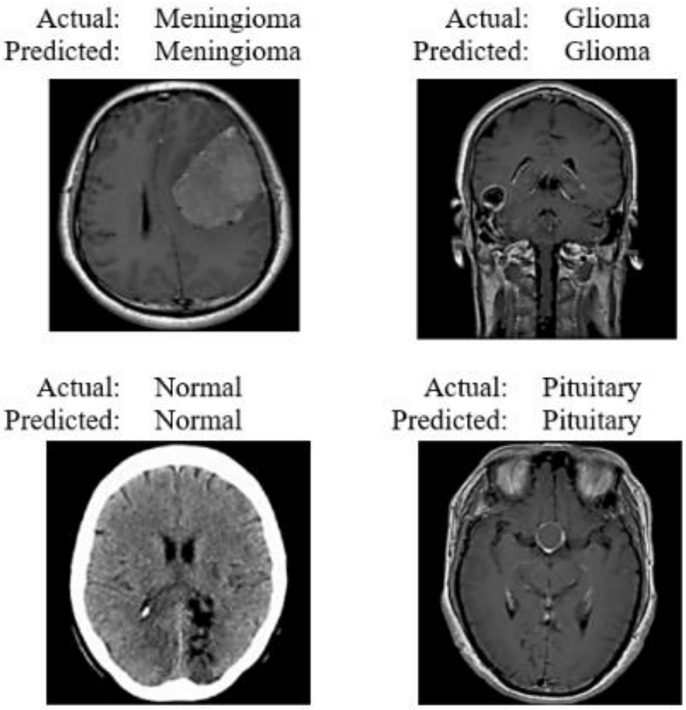

Figure 6: Actual and predicted output

These results show that the model performed very well at brain tumor classification in general. In particular, pituitary tumor detection was outstanding. However, there is potential room for improvement in meningioma tumor classification.

To determine the performance of our proposed CNN architecture, we compared it with established deep learning models that are widely used in medical image analysis. Table 5 presents the comparison of our model with popular architectures such as VGG16, ResNet50 and EfficientNetB0 on the same dataset.

Table 5: Performance comparison with standard deep learning models

Model	Accuracy	F1-Score	AUC	Parameters(millions)
Proposed CNN	93%	0.95	0.96-1.00	1.85
VGG16	90%	0.89	0.95	138
ResNet50	92%	0.92	0.94	25.6
EfficientNetB0	89%	0.88	0.93	5.3

As shown in Table 5, our proposed CNN model exhibits similar or superior performance despite requiring significantly fewer parameters compared to commonly used architectures. This computational efficiency is critical, especially in clinical settings with limited computing resources. However, while transfer learning approaches require extensive pre-training on large datasets such as ImageNet, our model is trained directly on the MRI dataset. This results in a more specialized performance on the brain tumor classification task.

This study successfully demonstrated the effectiveness of CNN in brain tumor classification. The ability of the developed model to discriminate between four different intracranial conditions with 90% accuracy emphasizes the effectiveness of this model and system for neuroradiological diagnosis. The findings of this study align with previous research, highlighting the considerable potential of using DL for medical diagnostics. Our model's high precision in detecting pituitary tumors (96%) suggests that these tumors have distinct and easily identifiable features on MRI scans. However, the comparatively lower performance in classifying gliomas (87%) might reflect the inherent heterogeneity of these tumors, which presents a greater challenge for accurate classification. These results underscore the varying complexity of different tumor types and suggest that further model refinement is necessary for better handling of more heterogeneous conditions such as glioma. The strength of our study was the use of a large and diverse dataset, which suggests that working with data can increase the overall validity of the model. However, important limitations include the fact that the model was trained with only four categories and that the data was obtained from a single center. The performance of the model can be further improved with larger datasets obtained from different health centers.

CONCLUSION

In this study, a classification system was developed to categorize brain tumors into four different classes (ie, glioma tumor, meningioma tumor, normal brain state, and pituitary tumor) using a DL-based model. The proposed model showed high performance in brain tumor classification. When the class-wise performance metrics were analyzed, the model was particularly successful in pituitary tumor and normal brain tissue classifications. Although lower performance was observed in meningioma tumor classification compared with the other categories, While the model demonstrates high diagnostic accuracy, real-world clinical validation across multiple centers remains a necessary step before deployment in clinical settings. However, the performance of the model can be improved with additional optimization approaches, such as data augmentation techniques, the use of larger datasets, and methods to address class imbalance.

The results of this study indicate that DL methods can be used as a reliable and effective tool for brain tumor classification. The widespread use of the developed model in the healthcare sector can make major contributions to accelerate diagnostic processes and increase its accuracy. In future studies, it is recommended to test the model in real clinical settings and validate it on different patient populations.

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