Dubai Medical Journal
Volume 7, Issue no. 3, DOI 10.18502/dmj.v7i3.17732
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Research Article

A New Approach for Brain Tumor Detection Using Machine Learning

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Received: August 8, 2024
Accepted: October 4, 2024
Published: December 8, 2024

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Abstract

Introduction: The abnormal brain cells consist of brain tumor which leads to severe organ dysfunction and potentially death. These tumors exhibit a wide range of sizes, textures, and locations. Diagnosing brain tumors process is a time-consuming process requiring the expertise of radiologists. Brain tumors are classified as glioma, meningioma, pituitary, and no tumor. As patient numbers and data volumes rise, traditional methods have become costly and inefficient.

Methods: Researchers have developed algorithms for detecting and classifying brain tumors and prioritizing accuracy and efficiency. Deep learning (DL) techniques are increasingly used to create automated systems capable of precisely diagnosing or segmenting brain tumors, particularly for brain cancer classification. This approach supports the use of transfer learning models in medical imaging. This proposed model is a modification to components of Xception model by adding a lot of parameters for increasing the Xception model efficiency.

Results: This proposed Xception model was applied to Masoud Nickparvar brain-tumor-mri-dataset, achieving an accuracy of 99.6%, sensitivity of 99.7%, and specificity of 99.7% with an F1 score of 99.9%.

Discussion: The efficiency parameters of the proposed model assured that it is an effective model for diagnosing brain tumor. Comparative analysis with other models shows that the proposed framework is highly reliable for the timely detection of various brain tumors.

Conclusion: The results confirm the effectiveness of our proposed model, which attains higher overall accuracy in tumor detection compared to previous models. As a result, the proposed model is considered a valuable decision-making tool for experts in diagnosing brain tumor.

Keywords: machine learning, deep learning, Xception model, brain tumor, MRI

How to cite this article: Ibrahim EH, Abo-Youssef SE, El-Bahnasy K, and Fathy KAM. A New Approach for Brain Tumor Detection Using Machine Learning. *Dubai Medical Journal*. 2024;7(3):160–176. DOI 10.18502/dmj.v7i3.17732

1. Introduction

The nervous system regulates numerous biological functions, including organizing, analyzing, decision-making, integrating information, and issuing commands to the body [1, 2]. Radiologists and neuropathologists have a difficult time making an early diagnosis of brain tumors, brought on by aberrant brain cell proliferation. Detecting brain tumors through magnetic resonance imaging (MRI) is a complex and manual procedure that is prone to errors. The aberrant proliferation of nerve cells is a characteristic of these tumors, resulting in a mass. Tumors in the brain and central nervous system can be of various kinds from extremely rare to relatively common and from benign to malignant. [3]. Image analysis and medical reporting depend on precise computer-aided diagnostic systems. Medical image evaluations done by hand are laborious, erroneous, and prone to errors.

In addition to the difficult field of brain tumor surgery, artificial intelligence (AI) is a major factor in diagnosing and detecting brain tumors. Neuropathological practices have been developed by two subsets of AI: machine learning (ML) and deep learning (DL). These methods involve preprocessing data, extracting features, selecting features, reducing features, and classification, among other steps. According to the study by Hollon et al., [4], AI has significantly enhanced confidence in neuropathologists' in diagnosing brain tumors, enabling better treatment decisions for patients. Numerous applications including speech recognition, object detection, pattern recognition, and decision-making have been made possible by recent developments in DL [5]. Therefore, AI has become a force for change in medical imaging as it enhances diagnostic precision, speed, and improves patient quality. This has been enabled by the incorporation of AI techniques, such as DL algorithms, which, in turn, have allowed more sophisticated performances of image segmentation, classification, and detection of medical images obtained from MRI, CT, and ultrasound [6-10]. Most of the AI applications in medical imaging focus on DL, specifically Convolutional Neural Network (CNN), for their outstanding features in extracting intricate features from medical images. According to the studies by Almeida, Sukegawa et al., and Barragán-Montero et al., [11-13], such algorithms are normally trained based on large datasets. The latter may rely on the digital imaging and communications in medicine standards for easy transfer and storage of these medical images. This provides the power to learn complex patterns and anomalies within images for AI systems, which has significantly improved diagnostic performance in diseases such as cancer and liver diseases.

It has been proved, for instance, that AI can contribute to the early detection and classification of tumors, both in mammography and other imaging modalities by reducing the workload for radiologists and increasing diagnostic precision [14, 15]. The benefits of AI in medical imaging are not restricted to sheer accuracy but involve efficiency in workflow management. AI systems can perform routine tasks themselves, like image acquisition and preliminary analysis, allowing health professionals to focus on the decision-making process of a higher degree of complexity. Furthermore, since an AI system can analyze large volumes of data in a minimum amount of time, it allows timely interventions that are very important in acute medical situations, as in the COVID-19 pandemic, where speed of diagnosis has a greater impact on patient outcomes. AI integration also enables personalized medicine through the extraction of high-dimensional imaging biomarkers that may guide treatment decisions in personalized medicine for individual patient profiles [16, 17]. AI is finding usage in diagnostics and treatment within oncology, cardiology, ophthalmology, and many more. For example, AI algorithms have been applied to the analysis of MRI scans for cervical cancer diagnosis [8]; in ophthalmology, AI technologies enable the detection of subtle changes within the retinal images indicative of early disease [18]. Apart from that AI in radiomics has brought up new dimensions in feature analysis of medical images for predictive modeling and treatment planning. Some recent studies involving AI in radiomics have been reported [13, 16]. AI-based medical imaging is one of the major technologies emerging in healthcare. With AI, it means enhanced diagnostic precision, improved efficiency of workflow, and ways opening for personalized treatment approaches. Medical imaging and patient care are about to change their face. AI can therefore be integrated further into clinical practice, with ongoing efforts to overcome challenges in data privacy, algorithm transparency, and regulatory issues related to AI integration. In the healthcare industry, researchers use a lot of algorithms depending on ML including Naive Bayes, (k-NN) k-nearest neighbors, decision trees, and support vector machines (SVMs), as well as brain tumor diagnosis can be aided by DL algorithms like VGGNets [19], trained CNNs, ResNets [20], and GoogleNet [21]. Research is hampered, nevertheless, by the absence of extensive medical datasets because of privacy concerns. Moreover, recall and precision are frequently lacking in current methods, leading to inefficiencies and delays in image classification, which can delay treatment initiation [22]. In this paper using an improved Xception model increased the brain tumor diagnosis accuracy and reduced the consumption time in the diagnosis process. This paper reviews previous studies using various ML algorithms on brain tumors in the following section. A thorough synopsis of our investigation including information on the suggested architecture and methodology is provided in Sections 3 and 4. The paper also presents the model training in Section 5. The Section 6 explores the findings from our evaluation of the functioning modeled by DL as well as examines the DL models and performance metrics that were applied in this study. Section 7 provides the final assessment of this study.

2. Related Works

This paper investigates how to examine brain tumors and interpret medical images using ML and DL techniques in this section. Given its wide range of applications in healthcare for the past 20 years, medical image analysis has garnered a lot of interest and research particularly in patient investigation and diagnosis. Studies have proposed employing ML strategies to categorize and examine the architecture of the brain [23]. Abd-Ellah et al., [24] compared conventional ML and DL techniques in a comprehensive analysis of the available techniques for diagnosing brain MRI scans, highlighting their, respective strengths and weaknesses. Additionally, the authors introduced a novel semi-automatic segmentation approach for brain tumor images [25]. A DL neural model was presented in a different study [26] to extract features from MRI. These features were subsequently used as input for ML classifiers including multilayer perceptrons (MLPs) SVMs and Naive Bayes. Using SVMs the suggested method produced a 96% classification accuracy. Hossain et al., [27] carried out a thorough investigation using a variety of DL and ML methods such as SVMs k-nearest neighbors MLPs Naive Bayes and random forest algorithms for brain tumor segmentation and detection. Notably with 92. 4% classification accuracy SVMs showed the best performance. In addition, the researchers developed a unique CNN architecture with five layers for MRI-based brain tumor detection and it achieved an amazing 97.2% accuracy. In the same way, Rehman et al., [28] used the VGG19 CNN architecture and K-means clustering to create a method for segmenting and classifying brain cancers in MRI images. Their method included statistically normalizing intensities and preprocessing the input MRI modality into slices. Their method reached an overall precision of 94%. Using DenseNet in classification and special three-dimension CNN architectures for multimodal image segmentation researchers, [29] presented a method for combining 2D and 3D MRI images. Their method demonstrated strong efficiency on the testing data, achieving 92% accuracy using DenseNet and 85% accuracy with the specialized 3D CNN models. Kang et al., [30] used an ensemble of deep CNN features and ML classifiers for exploring brain tumor categorization and experimenting it with datasets of varying sizes. Among the classifiers evaluated, an SVM with a radial basis function kernel performed the best. Another notable contribution [31] developed a ML network-based automated system for brain tumor classification, for telling high-grade glioma pictures from low-grade ones. The researchers employed the extreme gradient boosting model to achieve accuracies of 90% and 95% for classifying cancers in the central nervous system, including the brain. Zar Nawab et al., presented a transfer learning blockwise method based on fine tuning. Swati et al., [32] utilized a pretrained deep CNN model. They assessed this method using a benchmark dataset magnetic resonance imaging contrast-enhanced (CE-MRI) with T1-weighted. Their approach is more adaptable than traditional methods which rely on manually designed features and intensive preprocessing. An average accuracy of 94.082% was attained after five cross validations. In addition to conventional ML techniques the authors also compared the outcomes with CNN-based DL methods. The trial findings demonstrate that their proposed method effectively utilizes topical classification algorithms on the CE-MRI dataset. Mehmood et al., [33] introduced an automated method for MRI-based intracranial tumor detection, which enhanced the capacity to discriminate between areas with and without tumors by using colored images of the tumor region. Outperforming previous methods in terms of performance, the generated images had an average structure similarity index (SSIM) score of 0.92 and an average peak signal-to-noise ratio (PSNR) value of 28%. Additionally, in both the pre- and postcolorization stages the use of NASNet-Large produced quantitative improvements in classification accuracy (CA). Specifically, the method achieved classification accuracy scores of 88.5% and 92.4% respectively, as well as other metrics. For these contributions, the paper proposed an improved Xception model for increasing brain tumor diagnosis accuracy and early detection, according to the modified

Xception approach based on a new CNN architecture and transfer learning parameters as a potential improvement method for image classification tasks.

3. Materials and Methods

3.1. Dataset Collection

The paper used an MRI scan images dataset from the Kaggle website www.kaggle.com which is an openly available dataset [34, 35] to verify the validity of our findings. This collection includes MRI scan images that are considered the gold standard for diagnosing brain tumors. All dataset images were rescaled to 299 pixels in both vertical and horizontal vertices. For our analysis, 5712 MRI images were used for training (80% of the dataset) and 1311 MRI images (20% of the dataset) for testing. Table **1** details the dataset comprising four subsets, the number of images in different subsets (glioma, pituitary, meningioma, and no tumor), with different categories in sagittal, coronal, and axial views. It is crucial to remember that medical images are more complicated and call for a higher degree of skill for accurate interpretation and analysis in contrast to natural images. To ensure precision and consistency, the brain tumor dataset was labeled under the supervision of a medical specialist.

Table 1: Brain tumor dataset.

Brain tumor Types	**No. of Samples training**	**No. of Samples Testing**
Glioma	1321	300
Meningioma	1339	306
Pituitary	1457	300
No tumor	1595	405
Total	5712	1311

3.2. Dataset Preprocessing

The training data generator module specifies two preprocessing steps: data augmentation and input image normalization. For the validation and test data generators only normalization is applied, ensuring consistent evaluations aligned with the original dataset. Data augmentation includes various transformations like rotation, flipping, zooming, shifting, shearing, and adjusting image brightness to the training images. Normalization rescaled pixel values to the [0, 1] range, ensuring uniformity and aiding model convergence during training by optimizing the cost function more easily when features (pixels) are on a similar scale. To maintain consistency, validation, and test images are also normalized.

4. Proposed Methodology

The Xception model, delivered through François in 2017, is a sophisticated CNN structure that employs depthwise separable convolutions, significantly improving computational performance at the same time as retaining high accuracy in image classification tasks. This architecture includes a linear stack of depthwise separable convolution layers, taking into consideration a greener use of parameters compared to traditional convolutional layers, ensuing in superior overall performance on big datasets along with ImageNet, in which it outperformed the Inception V3 model [36]. The architecture's layout contains residual connections, which assist in schooling deeper networks with the aid of mitigating the vanishing gradient trouble, thus facilitating higher feature extraction and type competencies [37]. In the world of medical imaging, the Xception model has verified its superiority through various packages. For example, in breast cancer detection, a modified version of the Xception model has been proven to decorate mammogram analysis drastically, achieving better sensitivity and accuracy compared to conventional strategies [38, 39]. This look highlighted the model's ability to leverage transfer getting-to-know and self-attention mechanisms, which can be crucial for improving diagnostic accuracy in complex scientific pics. Moreover, the Xception structure has been correctly utilized in the analysis of COVID-19 from chest X-ray images. Research suggests that models based totally on Xception performed remarkable category accuracies, with some research reporting accuracies exceeding 90% in distinguishing COVID-19 cases from other pneumonia kinds [40]. For instance, the CoroNet version, which is based totally on the Xception structure, especially designed to aid radiologists in speeding up the identification of COVID-19 infections, demonstrating a high level of accuracy and performance [40]. Additionally, the COVID-AleXception version, which mixes functions from each AlexNet and Xception, accomplished an outstanding type accuracy of 98.68%, further underscoring the effectiveness of the Xception architecture on this essential location [41]. Furthermore, the Xception version has been implemented in numerous other scientific imaging contexts, along with the automated detection of nasal hollow space hundreds, wherein it carried out a typical accuracy of 79.2% across more than one instruction of lesions [42]. This versatility illustrates the version's robustness and flexibility to special forms of medical imaging duties, reinforcing its function as a leading architecture in the field of deep-gaining knowledge of scientific diagnostics. The Xception model stands out due to its revolutionary structure that optimizes performance even by reducing computational prices. Its software in medical imaging has yielded giant advancements in diagnostic accuracy throughout diverse diseases, especially in breast cancers and COVID-19 detection, highlighting its capability to decorate scientific choice-making and patient consequences using Xception model. It is a deep convolutional neural network architecture that improves upon the Inception model by replacing the standard Inception modules with depthwise separable convolutions. This architecture is highly efficient and has been shown to achieve superior performance in various image classification tasks. The Xception model is particularly well-suited for medical image analysis due to its ability to capture fine-grained features and patterns. Figure **1** presents the workflow of the proposed model.

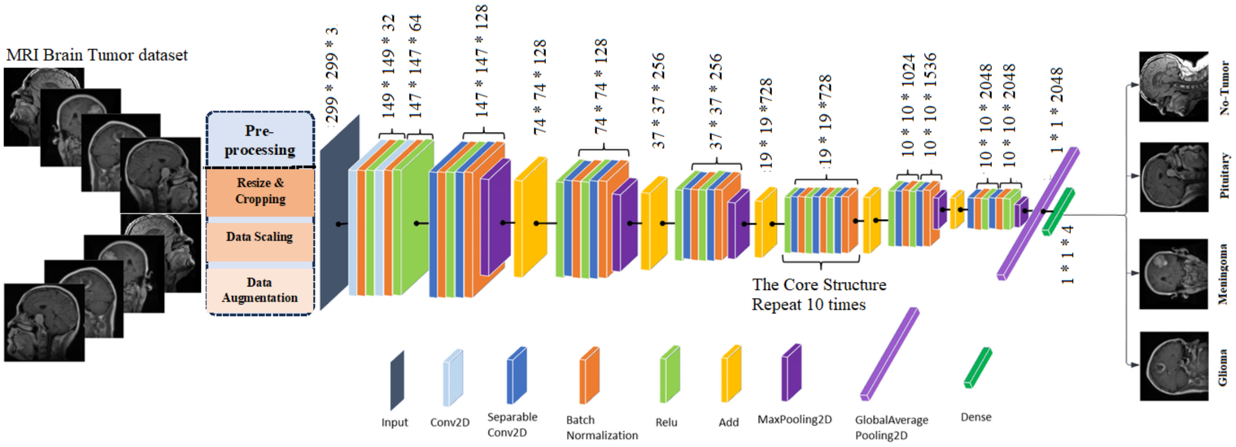

Figure 1: Work flow of the proposed Xception model. This figure illustrates the work and data flow of the proposed model for the MRI brain tumor dataset. Starting with feed MRI brain tumor dataset to the proposed model after that preprocessing the input data until detection of the brain tumor type: glioma, pituitary, meningioma, and no tumor.

4.1. Data Preparation

We utilize the brain tumor MRI dataset (Masoud Nickparvar), which contains MRI scans of brain tumors. To improve the dataset and increase the proposed model performance, different techniques for data augmentation are applied such as rotation, scaling, translation, and flipping. These augmentations help prevent overfitting and rise the diversity of the training data.

4.2. Transfer Learning with Xception

Given the limited size of medical imaging datasets, transfer learning-based models are effective in leveraging pretrained models. The Xception model pretrained on the brain tumor MRI dataset serves as a robust feature extractor. We fine-tune the model by replacing the final classification layers with layers tailored to our specific task of brain tumor detection.

4.3. Model Architecture

The modified Xception model architecture for brain tumor detection includes the following steps

4.3.1. Input Layer

Accepts MRI images resized to 299 * 299 pixels to match the input size required by Xception.

4.3.2. Base Model

Utilizes the pretrained Xception model excluding its top layers. The weights of the base model are initially frozen to retain the pretrained features.

4.3.3. Fully Connected Layers

Includes one or more dense layers with ReLU activation functions to learn complex patterns specific to brain tumors.

4.3.4. Dropout Layer

Applies dropout regularization to prevent overfitting.

4.3.5. Output Layer

Consists of an activation function softmax in a dense layer for multiclass classification.

5. The Model Training

The training process contains the following steps

5.1. Freezing and Unfreezing Layers

Initially, only the newly added fully connected layers are trained, while freezing the base model layers. After achieving initial convergence, the entire model layers are fine-tuned with a lower learning rate and the top layers of the proposed model are unfrozen.

5.2. Loss Function

For multiclass classification loss, categorical cross-entropy loss is used.

5.3. Optimizer

Adam optimizer is used for its efficiency and adaptive learning rate properties.

5.4. Performance Metrics

Model performance is evaluated using accuracy, sensitivity, specificity, and the F1 score.

6. Results and Discussion

6.1. The Proposed Model

Improving the classification model's performance for brain tumor datasets was the primary goal of this study to facilitate precise patient diagnosis. In order to start the experiments, the datasets were first split into two groups with 80% designated for training and 20% for testing. Additionally, the training dataset was further split into two parts first training with 80% of the data and second validation with 20% of the data. The model was developed using the Keras library with TensorFlow as the backend, programmed in Python. The optimized hyperparameter values were set with 0.001 for learning rate value, a maximum of 20 epochs, and a batch size of 32. The Model Accuracy: 99.62% on test data. Figure **2** shows the training and validation data accuracy according to the number of epochs. Figure **3** shows the training and validation data loss according to the number of epochs. Figure **4** represents the confusion matrix between true labels and predicted labels with a batch size of 32, and Figure **5** represents the confusion matrix between true labels and predicted labels with a batch size of 1300 using the proposed Xception model. These confusion matrices show that the model performs very well across all classes, with high precision, recall, and F1 scores for each category. The relation between the true labels and predicted labels confirms that the proposed model improved the diagnosis process the accuracy lines for both training and validation indicate an excellent training process with no signs of overfitting. After constructing the model, it was tested with the testing data. Table **2** displays the testing data set results with a batch size of 32. Table **3** displays the testing data set results with a batch size of 1300. The performance metric for each brain tumor class glioma, meningioma, pituitary, and no tumor confirms that the proposed model using an improved Xception model is the best contribution to brain tumor diagnosis. These findings demonstrate the model's ability to perform accurately.

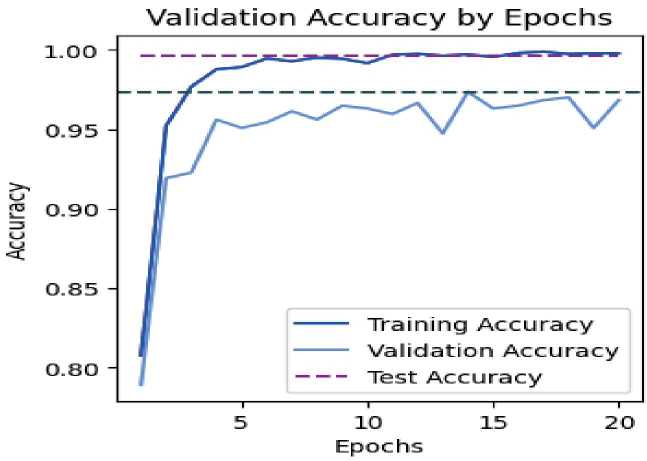

Figure 2: Validation accuracy. This figure illustrates the performance of the proposed model for the three dataset categories training, validation, and testing. Each curve represents the relation between the accuracy of proposed model according to numbers of epochs. the proposed model accuracy for training and testing data reached 100% in a small number of epochs which sure the effectivity of proposed model.

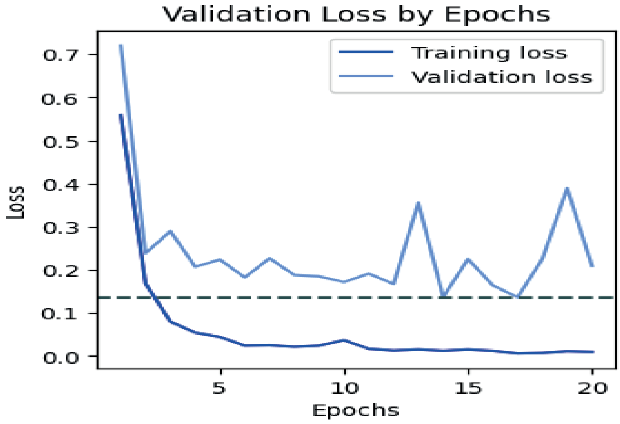

Figure 3: Validation loss. This figure illustrates the loss of the proposed model for the two dataset categories training and validation. Each curve represents the relation between the loss of proposed model according to the number of epochs. The proposed model loss for training data reached 0% in a small number of epochs, which ensures the effectiveness of the proposed model.

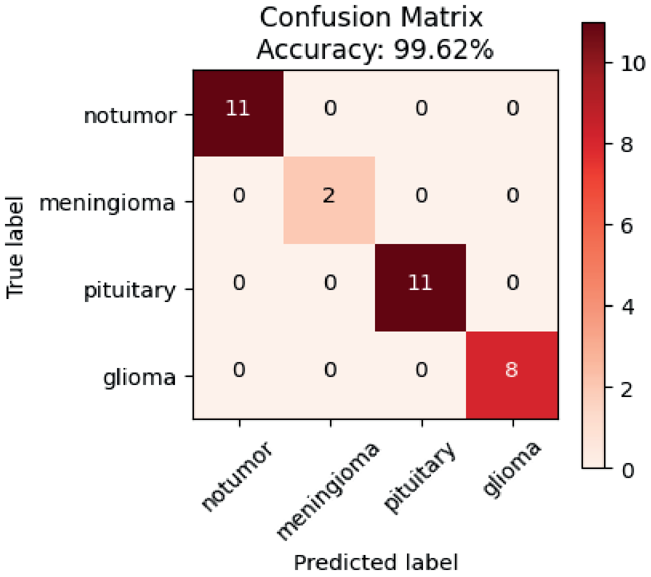

Figure 4: Confusion matrix for test data with batch size 32. This figure represents the confusion matrix of the proposed model for the testing dataset. The confusion matrix between the true labels and predicted labels for the four brain tumor categories glioma, pituitary, meningioma, and no tumor. Batch size of 32 brain tumor samples. This figure assured the efficiency of the proposed model in detecting the brain tumor type.

6.2. Comparing the Proposed Model with Other Techniques

In this section, we compared five different models with the proposed model. The different CNN architectures are InceptionV3, ResNet50, InceptionResNetV2, EfficientNet, and VGG16, as detailed in Table **4**. The number of layers differed amongst CNN designs despite the parameters remaining the same in the fully connected (FC) and convolutional layers. The proposed model accuracy rates are considered better than the accuracy rates for the other DL models, this is shown in Figure **6**.

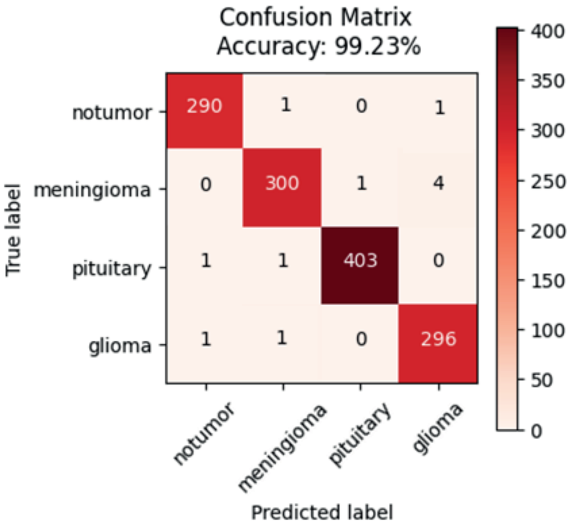

Figure 5: Confusion matrix for test data with batch size 1300. This figure represents the confusion matrix of the proposed model for the testing dataset with 1300 batch size. The confusion matrix between the true labels and predicted labels for the four brain tumor categories glioma, pituitary, meningioma, and no tumor. This figure assured the efficiency of the proposed model in detecting the brain tumor type.

Table 2: Results of test data with 32 batch size.

	Precision	**Recall**	**F1-Score**	**Support**
Glioma	1.00	1.00	1.00	8
Meningioma	1.00	1.00	1.00	2
Pituitary	1.00	1.00	1.00	11
No tumor	1.00	1.00	1.00	11
Accuracy			1.00	32
Macro avg	1.00	1.00	1.00	32
Weighted avg	1.00	1.00	1.00	32

Table 3: Results of test data with 1300 batch size.

	Precision	**Recall**	**F1-Score**	**Support**
Glioma	0.99	0.99	0.99	298
Meningioma	0.99	0.98	0.98	305
Pituitary	0.99	0.99	0.99	405
No tumor	0.99	0.99	0.99	292
Accuracy			99.23	1300
Macro avg	0.99	0.99	0.99	1300
Weighted avg	0.99	0.99	0.99	1300

Table **5** displays the validation accuracy and additional evaluation metrics for the new approach network and the other pretrained DL models. All models with the exception of InceptionResNetV2, which initially showed some overfitting, showed very small error gaps during the training stages according to the results. Conversely, the other models continuously reduced losses over time. Comparing the proposed model evaluation metric with other studies assured that the proposed model is the best in brain tumor diagnosis.

Table 4: Performance evaluation of deep learning models and the proposed model.

Models	Pr (%)	Re (%)	Se (%)	Sp (%)	Ac (%)	F1-Score (%)
InceptionV3	93.5	94.2	93.3	93.2	93.6	93.6
InceptionResNetV2	95.2	95.6	95.6	95.1	95.3	95.4
ResNet50	94.6	94.8	94.8	94.2	94.5	94.7
EfficientNet	95.3	95.5	96.0	95.1	95.4	95.4
VGG16	96.1	96.4	96.4	96.1	96.3	96.3
The proposed model	99.7	99.7	99.7	99.6	99.6	99.9

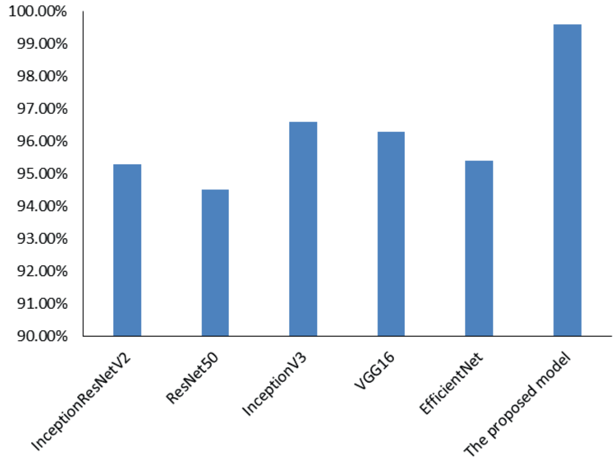

Figure 6: Accuracy of the proposed model and other DL models. This columns graph compares the accuracy of the proposed model and other DL models used with the same data set for brain tumor detection. These models are used in related works for brain tumor detection. The graph presents the efficiency of the proposed model.

Table 5: Performance evaluation of existing models and the proposed model.

Models	Pr (%)	Re (%)	Se (%)	Sp (%)	Ac (%)	F1-Score (%)
VGG19 [28]	95.3	95.4	95.4	95.0	94.9	95.2
DenseNet [29]	94.6	94.7	94.7	94.2	94.4	94.6
Hybrid ensemble [31]	95.6	96.0	96.0	95.3	95.2	95.7
CNN ensemble [43]	95.7	95.6	95.6	95.1	95.3	95.5
SVM [26]	96.3	96.5	96.5	96.2	96.5	96.3
EfficientNet [44]	97.5	97.6	97.6	97.4	97.6	97.6
YOLOv4 [45]	97.6	97.8	97.8	97.5	97.5	97.8
The proposed model	99.7	99.7	99.7	99.6	99.6	99.9

7. Conclusion

The study used a DL model with an open-source MRI scanned images dataset to enhance the early detection of brain tumors. Using the improved Xception model with transfer learning and data augmentation techniques offers a powerful approach for brain tumor diagnosis, where the proposed model accuracy reached 99.62% for the testing data. The model's robustness due to pretraining on a large dataset like a brain tumor MRI dataset and its ability to capture detailed features contribute to its high performance in disease diagnosis and other medical purposes. The modified model surpassed the previous works in brain tumor diagnosis, exhibiting higher accuracy, precision, recall, and f1-scores. Its efficiency and reliability, supported by its shorter training time, make it a valuable tool for early diagnosis and monitoring. Future work will focus on the diagnosis of other diseases such as Alzheimer's disease and further exploring interpretability tools, refining the model, and validating the approach on larger and more diverse datasets.

Acknowledgment

None.

Statement of Ethics

The researchers acquired the data for this study from publicly available data on Kaggle. Since the dataset does not include any personally identifiable information and is openly accessible to the public, it was concluded that formal ethical approval was unnecessary. Throughout the process of obtaining and analyzing the data, the researchers strictly followed Kaggle's terms of service and privacy policy.

Ethical Approval

The research passed on public data is not required.

Informed Consent Statement

None.

Conflict of Interest

The authors declare that there is no conflict of interest.

Artificial Intelligence (AI)

AI-unassisted work.

Funding

No funding received.

Author Contribution

The authors confirm their contribution to the paper as follows: study conception and design proposed model: first, third, and fourth author; data collection: second Author; analysis and interpretation of results: first Author, second Author. third Author; draft manuscript preparation: first Author, third Author, and fourth author. All authors reviewed the results and approved the final version of the manuscript.

Data Sharing Statement

Data sets are available publicly in the depository storage at https://www.kaggle.com/datasets/elsadekhussien/brain-tumor.

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