Journal of Information Systems Engineering and Management
2025, 10(34s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

Early Diagnosis of Brain Tumor Using Machine Learning Approaches

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ARTICLE INFO

Received: 28 Dec 2024
Revised: 18 Feb 2025
Accepted: 26 Feb 2025

ABSTRACT

Introduction: The brain tumor is formed by abnormal brain cells, leading to serious organ dysfunction and potentially death. These tumors vary widely in size, texture, and location. Diagnosing brain tumors is a lengthy process that requires the expertise of radiologists. Brain tumors are classified into types such as glioma, meningioma, pituitary tumors, and no tumor. With increasing patient numbers and data volumes, traditional diagnostic methods have become both costly and inefficient.

Objectives: Consequently, researchers have developed algorithms aimed at detecting and classifying brain tumors with an emphasis on accuracy and efficiency. Deep learning techniques are now commonly used to create automated systems capable of accurately diagnosing or segmenting brain tumors, particularly in classifying brain cancer.

Methods: This approach often incorporates transfer learning models in medical imaging. In this study, a modified Xception model is proposed, incorporating additional parameters to enhance the model's efficiency.

Results: This modified Xception model was tested on the Sartaj brain-tumor-MRI dataset, achieving an accuracy of 99.02%, sensitivity of 99.0%, and specificity of 99.1%, with an F1 score of 99.1%. These performance metrics confirm that the proposed model is highly effective for diagnosing brain tumors.

Conclusions: Comparative analysis with other models indicates that this framework offers reliable and timely detection of various brain tumors. The results validate the proposed model as a valuable decision-making tool for experts in brain tumor diagnosis.

Keywords: Machine learning; Deep learning; Xception model; Brain tumor; MRI.

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INTRODUCTION

A brain tumor is one of the most aggressive diseases affecting both children and adults. Brain tumors make up 85 to 90 percent of all primary Central Nervous System (CNS) tumors, with approximately 11,700 new cases diagnosed each year. The 5-year survival rate for individuals with cancerous brain or CNS tumors is roughly 34 percent for men and 36 percent for women. Brain tumors can be categorized into types such as Benign Tumor, Malignant Tumor, and Pituitary Tumor. Effective treatment planning and precise diagnostic methods are essential to improving patient survival rates. Magnetic Resonance Imaging (MRI) is the most reliable technique for detecting brain tumors, generating a vast amount of image data that radiologists review [1]. However, manual analysis can be prone to errors due to the complexities and variations in brain tumors. Automated classification techniques using Machine Learning (ML) and Artificial Intelligence (AI) have shown higher accuracy rates compared to manual methods. Therefore, implementing a system for brain tumor detection and classification using Deep Learning algorithms, such as Convolutional Neural Networks CNN, Artificial Neural Networks ANN, and Transfer Learning TL, could greatly support healthcare professionals globally. Brain tumors are complex, with variations in size and location that make understanding their nature challenging. This complexity requires expert analysis, often by a neurosurgeon. In developing countries, limited access to skilled specialists and a lack of knowledge about tumors can delay MRI report generation. An automated cloud-based system could address these issues efficiently. To detect and classify brain tumors using CNN and TL as deep learning tools, with capabilities for tumor segmentation to help identify tumor position accurately. The process of analyzing medical images and reporting findings heavily relies on accurate computer-based diagnostic systems. Manual analysis of medical images is not only time-consuming but also prone to errors. Furthermore, artificial intelligence AI plays a crucial role in the diagnosis and detection of brain tumors. Radiologists and neuropathologists face challenges in diagnosing brain tumors early, especially those caused by abnormal growth of brain cells. Identifying brain tumors through magnetic resonance imaging MRI is a complex, manual process that is susceptible to mistakes. These tumors are characterized by the abnormal growth of nerve cells, leading to the formation of a mass. Brain and central nervous system tumors can vary greatly in rarity, prevalence, and malignancy, ranging from extremely rare to common and from benign to malignant. The Nervous System oversees a wide range of essential bodily functions, including the organization, analysis, decision-making, integration of information, and issuing commands to the body. Research suggests that AI has significantly boosted the confidence of neuropathologists in diagnosing brain tumors, leading to more informed treatment decisions for patients. Recent advancements in deep learning have enabled AI to achieve remarkable feats in areas such as speech recognition, object detection, pattern recognition, and decision-making. Consequently, AI is revolutionizing medical imaging by enhancing diagnostic accuracy, speed, and patient care. This progress is made possible through the integration of AI techniques, particularly deep learning algorithms, which have improved the accuracy of image segmentation, classification, and detection of medical images from MRI, CT, and ultrasound [2-4]. This has led to significant advancements in the diagnosis of diseases such as cancer and liver diseases, as demonstrated by studies such as [5]. AI is divided into two main categories: machine learning (ML) and deep learning (DL). These categories involve several steps, including data preprocessing, feature extraction, feature selection, feature reduction, and classification. Most of the applications of AI in medical imaging focus on deep learning, especially Convolutional Neural Networks (CNN), known for their ability to extract detailed features from medical images. These algorithms are typically trained on large datasets, and the use of the Digital Imaging and Communications in Medicine (DICOM) standard facilitates the storage and transfer of these medical images, enabling the learning of complex patterns and anomalies within the images [6-8]. The advantages of artificial intelligence (AI) in the field of medical imaging extend beyond just high accuracy, encompassing improved efficiency in managing workflows. AI systems are capable of handling standard tasks autonomously, such as capturing images and initial analysis, allowing healthcare professionals to concentrate more on complex decision-making processes. Additionally, AI's ability to process vast amounts of data quickly is crucial for prompt interventions, especially in critical medical scenarios, like the COVID-19 pandemic, where rapid diagnosis significantly affects patient outcomes. The integration of AI also facilitates personalized medicine by identifying complex imaging biomarkers that can guide treatment decisions tailored to individual patients [9, 10]. AI is increasingly being utilized in diagnostics and treatment across various medical specialties, including oncology, cardiology, and ophthalmology. For instance, AI algorithms have been applied to analyze MRI scans for the detection of cervical cancer, and in ophthalmology, AI technologies can identify subtle changes in retinal images that indicate early disease [11]. Beyond that, AI in radiomics is revolutionizing the analysis of medical images for predictive modeling and treatment planning. Recent research in this area has been highlighted by [8, 9]. The use of AI in medical imaging is poised to transform the landscape of healthcare, offering enhanced diagnostic accuracy, more efficient workflows, and new avenues for personalized treatment approaches. However, challenges remain, including issues related to data privacy, algorithm transparency, and regulatory compliance. Researchers heavily rely on machine learning (ML) algorithms such as Naive Bayes, k-NN, decision trees, and support vector machines, among others, in their work. For example, deep learning algorithms like GoogleNet, ResNets, VGGNets, and trained convolutional neural networks (CNNs), have shown promise in aiding the diagnosis of brain tumors. Despite these advancements, the lack of extensive medical datasets due to privacy concerns continues to hinder progress. Furthermore, current methods often suffer from low recall and precision, leading to delays in image classification, which in turn can delay the start of treatment [12]. This paper discusses the use of an enhanced Xception model that has been shown to improve the accuracy of diagnosing brain tumors and reduce the time required for the diagnosis process. The paper reviews previous studies that have utilized various machine learning algorithms for brain tumor analysis. It provides a detailed overview of our research, including the proposed architecture and methodology. The paper also covers the process of training the model. Additionally, it explores the findings from our evaluation, focusing on the functioning of the deep learning models and the performance metrics used. The paper concludes with a final assessment of the research conducted.

RELATED WORKS

This section explores the methods for analyzing brain tumors and interpreting medical images through the lenses of machine learning and deep learning. Over the last two decades, the healthcare sector has increasingly shown interest in medical image analysis, especially in the areas of patient examination and diagnosis [13]. [14] described a deep learning neural network designed to extract features from magnetic resonance images, which were then used to train machine learning models such as Multilayer Perceptrons (MLPs), Support Vector Machines (SVMs), and Naive Bayes. The proposed method achieved a 96% accuracy rate using SVMs. [15] utilized the VGG19 CNN architecture and K-means clustering for the segmentation and classification of brain cancers in MRI images. Their approach involved normalizing intensities and preprocessing the MRI data into slices, achieving an overall precision of 94%. Research has suggested the use of machine learning techniques to classify and study the structure of the brain. [16] conducted a detailed comparison between traditional machine learning and deep learning approaches in diagnosing brain MRI scans, highlighting their unique strengths and weaknesses. Furthermore, the authors introduced a new semi-automatic technique for segmenting brain tumor images. [17] proposed an ensemble of deep CNN features and machine learning classifiers for the exploration of brain tumor categorization, testing it on datasets of varying sizes. Among the classifiers evaluated, an SVM with a radial basis function kernel was found to perform the best. Another significant contribution [18] performed an extensive study using various deep learning and machine learning techniques, including SVMs, k-nearest neighbors, MLPs, Naive Bayes, and random forest algorithms, for the segmentation and detection of brain tumors. Notably, SVMs demonstrated the highest accuracy rate at 92.4%. Additionally, the research team developed a unique CNN architecture with five layers for the detection of brain tumors in MRI images, achieving an impressive 97.2% accuracy. Similarly, [19] applied deep learning and machine learning techniques, including SVMs, k-nearest neighbors, MLPs, Naive Bayes, and random forest algorithms, for the analysis of brain tumor categorization, testing it on datasets of various sizes. The method using DenseNet achieved an accuracy of 92%, while specialized three-dimensional CNN models reached an accuracy of 85%. [20] using a deep CNN model that has already been trained. They evaluated their approach using the T1-weighted Magnetic Resonance Imaging Contrast-Enhanced (CE-MRI) benchmark dataset. Compared to previous methods that rely on heavily preprocessed data and manually developed characteristics, their approach is more flexible. The average accuracy after five cross-validations was 94.082%. Alongside traditional machine learning methods. [21] developed a machine learning network-based automated system for the classification of brain tumors, distinguishing between high-grade gliomas and low-grade gliomas. The researchers used a gradient boosting model to achieve accuracies of 90% and 95% in classifying brain tumors in the central nervous system, including the brain. Zar Nawab et al introduced a transfer learning block-wise method based on fine-tuning. For these contributions the research presents an optimal method that enhances the performance of machine learning in disease diagnosis, particularly brain tumors diagnosis and early detection, by using effective techniques for selecting hyperparameter values, and combines a new CNN architecture with transfer learning techniques, offering a promising method for diseases diagnosis tasks.

METHODS

DATA COLLECTION

To confirm the validity of our findings, the study employed an openly available dataset of MRI scan images from the Kaggle website, www.kaggle.com [22]. MRI scan images, which are regarded as the gold standard for diagnosing brain cancers, are included in this collection. Every image in the collection had its vertical and horizontal vertices rescaled to 299 pixels. 394 MRI images were utilized for testing, while 2870MRI images were used for training in our analysis. According to Table 1, the dataset is divided into four subsets based on the number of images in each of the following categories: glioma, pituitary, meningioma, and no tumor.

Table 1 Brain tumor dataset

Brain Tumor Types	No. of Samples Training	No. of Samples Testing
Glioma	826	100
Meningioma	822	115
Pituitary	827	74
No Tumor	395	105
Total	2870	394

These subsets are categorized in sagittal, coronal, and axial views. It is important to keep in mind that, in comparison to natural photos, medical images are more complex and require a greater level of expertise for accurate interpretation and analysis. The brain tumor dataset was labeled under the guidance of a medical practitioner to guarantee accuracy and consistency. Figure 1 showing different examples of the dataset

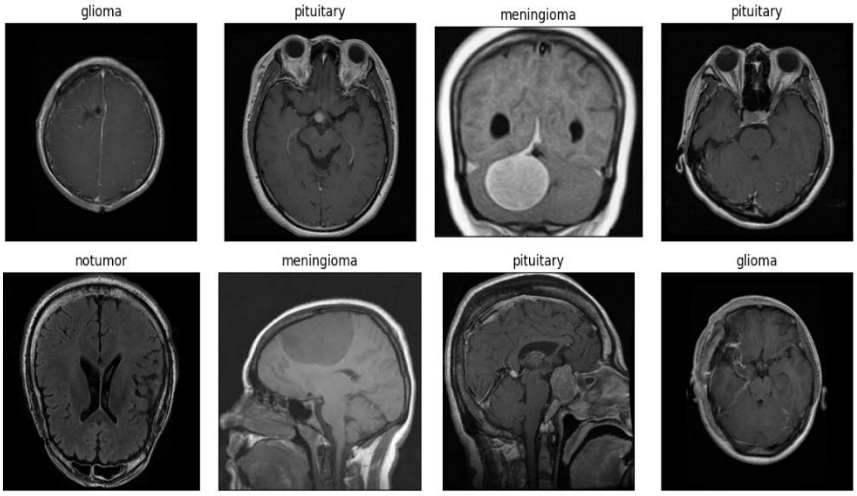

Fig. 1 Sample of MRI brain tumor image

For illustrating the data set characteristics Principal Component Analysis (PCA) was been performed as a graphical representation of the dataset as shown in Figure 2.

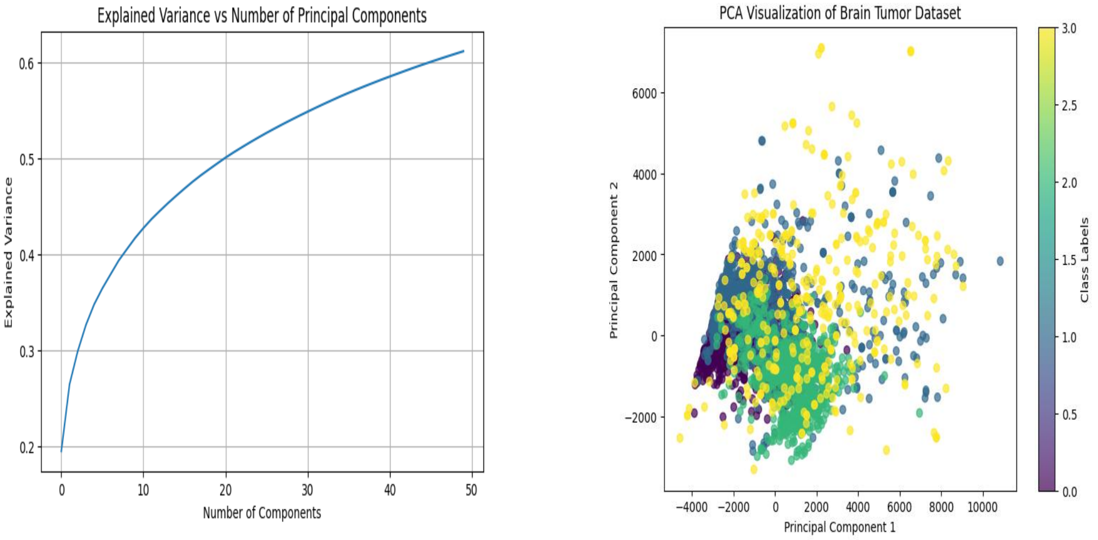

Fig. 2 Principal component analysis representation of the dataset.

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DATA PREPROCESSING

Two preprocessing steps data augmentation and input picture normalization are specified by the training data generator module. Only normalization is used for the validation and test data generators, guaranteeing consistent assessments that are in line with the original dataset. Rotation, flipping, zooming, shifting, shearing, and altering image brightness are some of the changes that are included in data augmentation as in Figure 3. In order to ensure uniformity and facilitate model convergence during training, normalization rescaled pixel values to the [0, 1] range. This is because features (pixels) of a same scale make it easier to optimize the cost function. Additionally, test and validation photos are standardized to preserve consistency.

Here are the mathematical equations for various image transformations:

1. Rotation: To rotate an image by an angle θ, the transformation matrix is:

$$\begin{bmatrix} x' \\ y' \end{bmatrix} = \begin{bmatrix} \cos(\theta) & -\sin(\theta) \\ \sin(\theta) & \cos(\theta) \end{bmatrix} \begin{bmatrix} x \\ y \end{bmatrix}$$

   Where (x, y) are the original coordinates and (x', y') are the new coordinates after rotation with angle θ.

2. Flipping (Horizontal or Vertical):
   - Horizontal flip: Flip the x-coordinate. $x' = -x$
   - Vertical flip: Flip the y-coordinate. $y' = -y$

3. Zooming (Scaling): Zooming is performed by scaling the coordinates by a factor ss (zoom factor).

$$\begin{bmatrix} x' \\ y' \end{bmatrix} = \begin{bmatrix} \delta . x \\ \delta . y \end{bmatrix}$$

   Where (x, y) are the original coordinates and (x', y') are the new coordinates after scaling with δ

4. Shifting (Translation): Shifting involves moving the image by a certain amount along the x and y axes. The equation is:

$$\begin{bmatrix} x' \\ y' \end{bmatrix} = \begin{bmatrix} x + \Delta x \\ y + \Delta y \end{bmatrix}$$

   Where Δx and Δy are the amounts of shift in the x and y directions respectively.

5. Shearing: Shearing involves shifting the image along one axis, depending on the other axis. The shearing transformations are:
   - Horizontal shearing: $x' = x + \alpha . y \; , \; y' = y$
   - Vertical shearing: $x' = x \; , \; y' = y + \beta . x$

   Where α and $\beta$are shear factors for horizontal and vertical shearing, respectively.

6. Altered Brightness: Brightness adjustment is done by adding a constant cc to the pixel values:

$$\mathrm{I}'(\mathrm{x}, \mathrm{y}) = \mathrm{I}(\mathrm{x}, \mathrm{y}) + \mathrm{c}$$

   Where $\mathrm{I}(\mathrm{x}, \mathrm{y})$ is the original intensity at position (x, y), and $\mathrm{I}'(\mathrm{x}, \mathrm{y})$ is the new intensity. If c is positive, the image becomes brighter; if cc is negative, it becomes darker.

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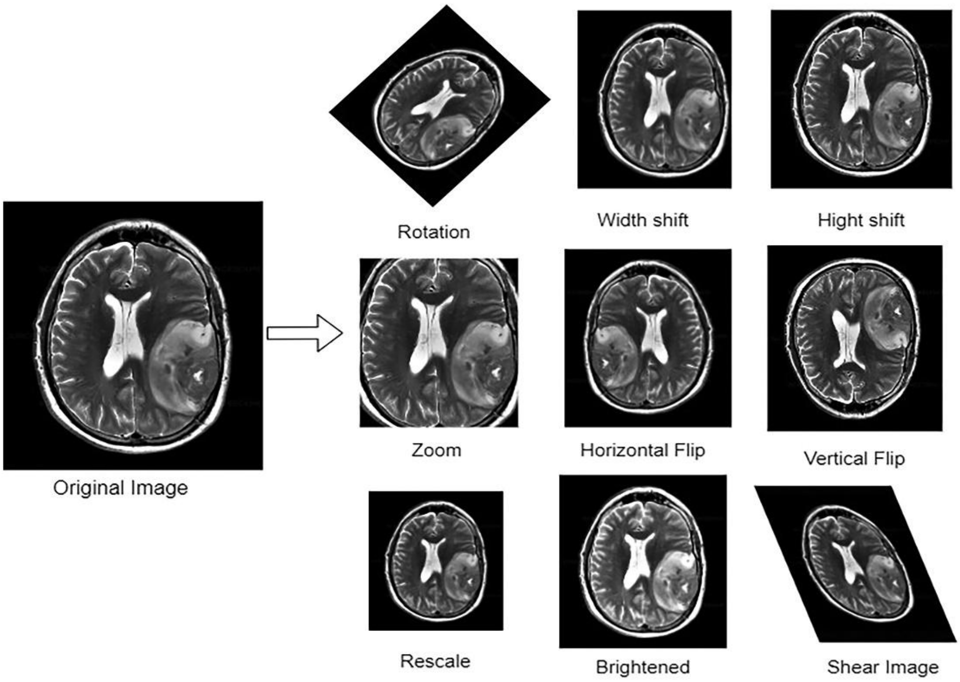

Fig. 3 Sample of augmented MRI brain tumor image

PROPOSED MODEL

The Xception model is a powerful convolutional neural network (CNN) structure that uses depthwise separable convolutions to maintain excellent accuracy in image classification applications while also greatly enhancing computational performance. Together with ImageNet, this architecture's linear stack of depthwise separable convolution layers results in better overall performance on large datasets, surpassing the Inception V3 model [23] while also considering a more environmentally friendly use of parameters than traditional convolutional layers. Higher feature extraction and type competency are made possible by the residual connections in the architecture's layout, which help to mitigate the vanishing gradient issue and school deeper networks [24]. The Xception model has demonstrated its superiority across a range of packages in the field of medical imaging. For instance, it has been demonstrated that a modified version of the Xception model significantly improves mammography analysis in the identification of breast cancer, with higher sensitivity and accuracy than traditional methods [25, 26]. This analysis demonstrated the model's capacity to use self-attention and transfer learning mechanisms, which can be essential for enhancing diagnostic precision in intricate scientific images. Furthermore, COVID-19 has been accurately analyzed from chest X-ray pictures using the Xception framework. For example, the CoroNet version, which is entirely based on the Xception architecture, was specifically created to help radiologists quickly identify COVID-19 infections and has shown excellent accuracy and performance [27]. Further demonstrating the efficacy of the Xception architecture on this crucial region, the COVID-AleXception version, which combines functionalities from both AlexNet and Xception, achieved an exceptional type correctness of 98.68% [28]. Along with the automated detection of nasal hollow spaces, the Xception version has been used in many additional scientific imaging situations. It has demonstrated a typical accuracy of 79.2% across multiple kinds of lesions [29]. This adaptability highlights the version's resilience and adaptability to unique medical imaging tasks, hence solidifying its position as a preeminent architecture in the realm of deep learning for scientific diagnoses. The unique structure of the Xception model, which maximizes performance while lowering computational costs, makes it stand out. Its medical imaging program has produced enormous improvements in diagnosis accuracy across a wide range of diseases, particularly in the detection of COVID-19 and breast cancers, demonstrating its capacity to enhance scientific decision-making and patient outcomes. The Xception Model is used. By substituting depthwise separable convolutions for the conventional Inception modules, this deep convolutional neural network design enhances the Inception model. Numerous image classification tasks have demonstrated the better performance of this very efficient design. Because the Xception model can capture finegrained characteristics and patterns, it is especially well-suited for medical picture analysis. The suggested model's work flow was shown in Fig 4.

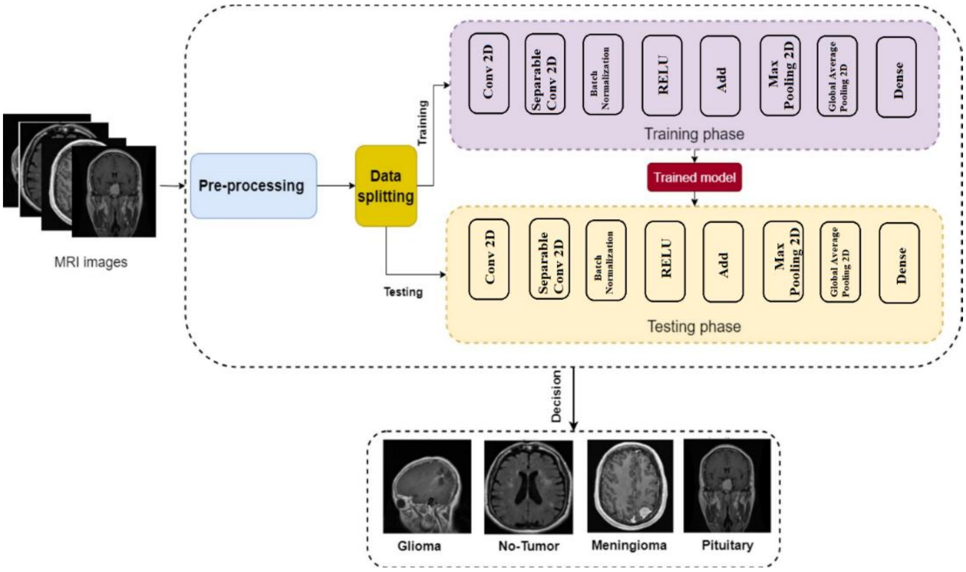

Fig. 4 Work flow of the proposed Xception model

MODEL ARCHITECTURE AND TRAINING

This paper used MRI scans of brain cancers from the brain tumor MRI dataset. Rotation, scaling, translation, and flipping are some of the data augmentation techniques used to enhance the dataset and boost the performance of the suggested model. By increasing the diversity of the training data, these augmentations aid in avoiding overfitting. Transfer learning-based models are a useful way to take advantage of pre-trained models because medical imaging datasets are small. A reliable feature extractor is the Xception model, which was pre-trained on the brain tumor MRI dataset. By substituting layers specifically designed for our particular objective of brain tumor identification for the final classification layers, we improve the model. Input Layer accepts MRI pictures that have been scaled to 299 * 299 pixels in order to meet Xception's input size requirements. uses the Xception model that has already been trained, but without the top layers. To preserve the pre-trained features, the basic model's weights are first frozen. learns intricate patterns unique to brain tumors by utilizing one or more dense layers with ReLU activation mechanisms. To avoid overfitting, dropout regularization is used. Output Layer consists of a dense layer with an activation function called softmax for multi-class classification. At first, the base model layers are frozen and only the recently added fully connected layers are trained. The top layers of the suggested model are unfrozen once initial convergence is achieved, and all model layers are adjusted with a reduced learning rate. For loss of multi-class classification, it makes advantage of categorical cross-entropy loss. Because of its effectiveness and adaptable learning rate characteristics, the Adam optimizer is utilized. The F1 score, sensitivity, specificity, and accuracy are used to assess the model's performance.

The proposed Xception model architecture can be described in three stages: Entry Flow, Middle Flow, and Exit Flow.

a) Entry Flow

1. Initial Convolution and Max Pooling: $Z_1 = Maxpooling\ (\sigma(X * W_1 + b_1))$

   where:

   - X is the input image,
   - W1 and b1 are the convolution weights and bias,
   - σ is ReLU activation function.

2. Depthwise Separable Convolutions:

- Depthwise: $Y = \sigma(X * K_d)$
- Pointwise: $Z_2 = \sigma(Y * W_p + b_p)$

b) Middle Flow

The middle flow consists of N repeated blocks of depthwise separable convolutions. Each block:

1. Depthwise Convolution: $Y_{d,n} = \sigma(X_{d,n} * K_{d,n})$
2. Pointwise Convolution: $Z_{p,n} = \sigma(Y_{d,n} * W_{p,n} + b_{p,n})$

c) Exit Flow

1. Final Depthwise Separable Convolution: $Y_{exit} = \sigma(X_{middle} * K_{exit})$
2. Global Average Pooling: $z_{gap} = \frac{1}{H.W}\sum_{i=1}^{H}\sum_{j=1}^{W} Y_{exit}(i,j)$
3. Fully Connected Layer: $y = Softmax(W_f \cdot z_{gap} + b_f)$

RESULTS AND DISCUSSION

The main objective of this work was to enhance the performance of brain tumor detection model's in order to enable accurate patient diagnosis. The datasets were initially divided into two groups, with 70% set aside for training and 15% for testing, and 15% were used for validation. Python programming and the Keras library were used to create the model, with TensorFlow serving as the backend. Manual methods for finding optimal hyperparameter values are considered traditional, time-consuming, and primitive. For these reasons, automated methods have been used as Bayesian Optimization, where it uses probabilistic models (usually Gaussian Processes) and acquisition functions (like Expected Improvement or Upper Confidence Bound) to systematically explore the hyperparameter space and optimize the objective function efficiently. A batch size of 128, a maximum of 20 epochs, and a learning rate value of 0.001 were the optimum hyperparameter values. On test data, the model's accuracy was 99.02%. The accuracy and loss of the training and validation data is displayed by the number of epochs in Figure 5. With batch size 128, the confusion matrix between true and predicted labels is shown in Figure 6 using the suggested Xception model. With high precision, recall, and F1 scores for every category, these confusion matrices demonstrate the model's excellent performance across all classes. The relationship between the expected and true labels demonstrates how the suggested model enhanced the diagnostic procedure. With no indications of overfitting, the training and validation accuracy lines show a superb training procedure.

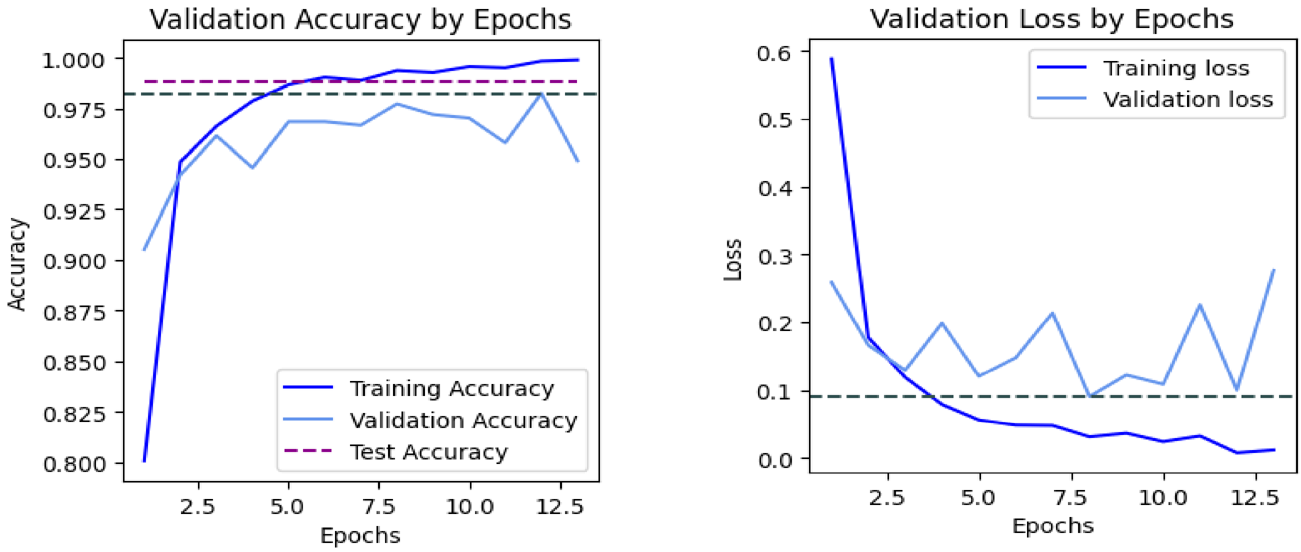

Fig. 5 Validation accuracy and loss

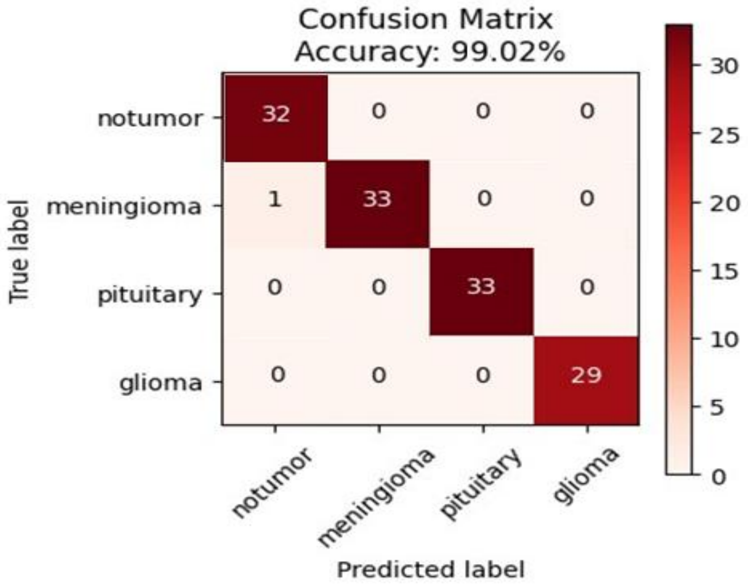

Fig. 6 Confusion matrix for test data with batch size 128

The model was tested using the testing data once it was constructed. The findings of the testing data set with batch size 128 are shown in Table (2).

Table 2 Results of test data with 128 batch size

	Precision	Recall	F1-Score	Support
Glioma	0.99	0.99	0.99	29
Meningioma	0.99	0.98	0.98	34
Pituitary	0.99	0.99	0.99	33
No Tumor	0.99	0.99	0.99	32
accuracy			99.02	128
macro avg	0.99	0.99	0.99	128
weighted avg	0.99	0.99	0.99	128

The suggested model employing the enhanced Xception model is the best contribution in brain tumor diagnosis, according to the performance metrics for the Glioma, Meningioma, Pituitary, and No Tumor classes of brain tumors. These results show that the model can function accurately.

In this section, we contrasted the proposed model with five other models. According to Table (3), the various CNN designs are InceptionV3, ResNet50, InceptionResNetV2, EfficientNet, and VGG16. Although the settings for the convolutional and fully connected (FC) layers remained the same, the number of layers varied throughout CNN architectures. As seen the accuracy rates of the proposed model are thought to be superior to those of the other deep learning models.

Table 3 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	99.0	99.0	99.0	99.1	99.0	99.1

According to the data, all models aside from InceptionResNetV2, which at first shown some overfitting showed extremely little error gaps during the training phases. On the other hand, losses were steadily decreased over time by the other models. The suggested model is the best in diagnosing brain tumors, according to comparisons with other studies' evaluation metrics.

When compared to existing models, particularly those also utilizing deep learning frameworks for brain tumor categorization, the proposed model exhibits competitive or superior performance. Table (4) and Figure 7 compares the accuracy of the proposed model with that of other studies, showcasing its competitive or superior performance.

TABLE 4 Examination of the proposed model in context.

References	Technique	Accuracy
Rahman and Islam, 2023 [30]	CNN	97.33%
Bingol and Alatas, 2021 [31]	Utilization Of Deep Learning Architectures (Alexnet, Googlenet, Resnet50) For Brain Tumor Image Detection	85.71%
Pillai et al., 2023 [32]	Deep Learning Models	91.58%
Shahajad et al., 2021 [33]	GLC (Gray Level Co-Occurrence Matrix)	92%
Gaur et al., 2022 [34]	Integration of Gaussian Noise Into CNN	94.64%.
Alshammari, 2022 [35]	Utilization Of Vgg-16 With Integration Of CNN	93.74%
Kumar et al., 2023 [36]	CNN Based Model	96.2%
Nishat et al., 2021 [37]	Support Vector Classifier	95.71%
Vankdothu and Hameed, 2022 [38]	RCNN	95.17%
Sathya R et al., 2024 [39]	Deep Learning Model Architecture (Xception CNN)	98.039%
Proposed Model	Modified Xception Model	99.02%

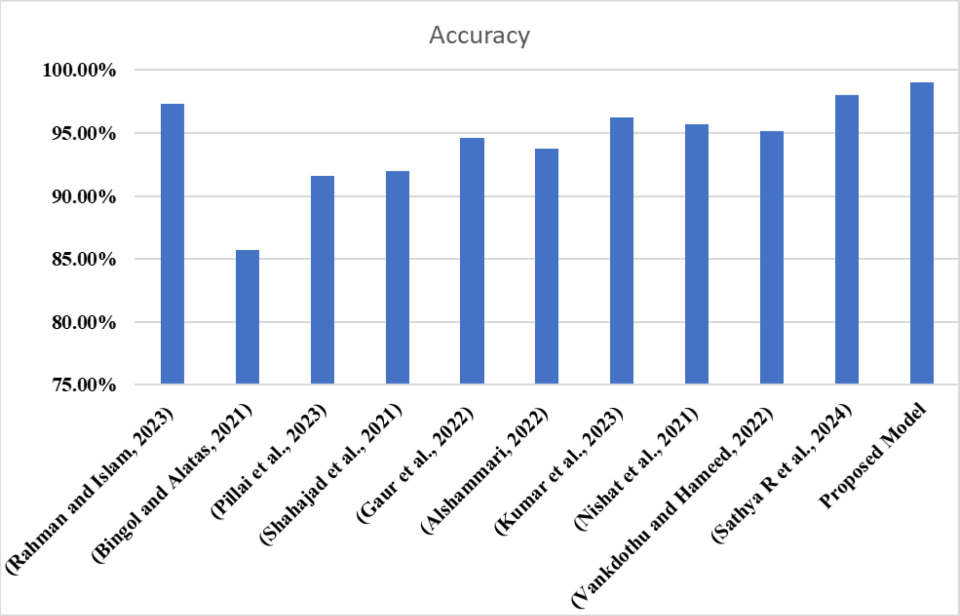

Fig. 7 Examination of the proposed model in context

CONCLUSIONS AND FUTURE WORK

To improve the early diagnosis of brain cancers, the study combined an open-source collection of MRI scan images with a deep learning model. A potent method for diagnosing brain tumors is to use the enhanced Xception model in conjunction with transfer learning and data augmentation approaches. The proposed model accuracy for the testing data was 99.02%. The model has a great performance in diagnosing diseases and other medical applications is a result of its robustness, which was pre-trained on a sizable dataset such as the brain tumor MRI dataset, and its capacity to capture intricate information. With improved f1-scores, accuracy, precision, and recall, the proposed model outperformed earlier efforts in brain tumor diagnosis. It is a useful tool for early diagnosis and monitoring because of its effectiveness and dependability, which are reinforced by its shorter training period. Future research will concentrate on diagnosing additional illnesses as Alzheimer's disease, enhancing the model, verifying the method on bigger and more varied datasets, and investigating interpretability tools further.

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