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A New Convolutional Neural Network Using Xception Architecture for Automatic Detection of Brain Tumors in Magnetic Resonance Imaging Images

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Abstract: Brain diseases are mainly caused by abnormal growth of brain cells that may damage the brain structure, and eventually will lead to malignant brain cancer and other discussed models in this paper is conducted. The classification of brain tumors from medical imaging is pivotal for accurate medical diagnosis but remains challenging due to the intricate morphologies of tumors and the precision required. Existing methodologies, including manual MRI evaluations and computer-assisted systems, primarily utilize conventional machine learning and pre-trained deep learning models. These systems often suer from overfitting due to modest medical imaging datasets and exhibit limited generalizability on unseen data, alongside substantial computational demands that hinder real-time application. To enhance diagnostic accuracy and reliability, this research introduces an advanced model utilizing the Xception architecture, enriched with additional

batch normalization and dropout layers to mitigate overfitting. This model is further refined by leveraging large-scale data through transfer learning and employing a customized dense layer setup tailored to efectively distinguish between meningioma, glioma, and pituitary tumor categories. This hybrid method not only capitalizes on the strengths of pre- trained network features but also adapts specific training to a targeted dataset, thereby improving the generalization capacity of the model across different imaging conditions. Demonstrating an important improvement in diagnostic performance, the proposed model achieves a classification accuracy of 98.039% on the test dataset, with precision and recall rates above 96% for all categories.

These results underscore the possibility of the MRI Images model as a reliable diagnostic toolin clinical settings, significantly surpassing existing diagnostic protocols for braintumors.

Keywords: brain tumor classification, medical imaging, deep learning, convolutional neural networks (CNN), Xception architecture, transfer learning

I. INTRODUCTION

Aberrant cell development inside the brain or central spinal canal is called a brain tumor. Depending on their growth rate and location, brain tumors can disrupt normal brain function and are potentially life-threatening. Brain tumors are typically categorized into primary tumors, which begin in the brain, and secondary or metastatic tumors, which spread from other regions of the body Tumors that Originating from the meninges, which are the

protective membranous layers enveloping the brain and spinal cord, are called meningiomas. Typically benign, meningiomas are generally amenable to surgical interventions, with a favorable prognosis following complete resection. However, their location and size can cause significant neurological impairments if they impinge on critical areas of the brain or spinal structures.

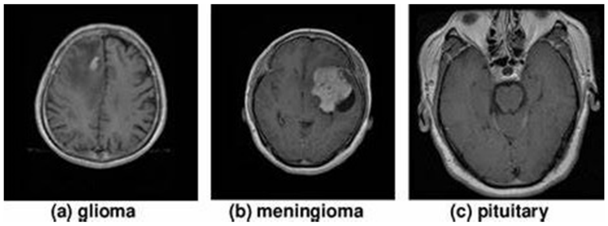

(a) glioma (b) meningioma (c) pituitary

FIG NO 1: Types of tumors

Gliomas, which originate from the glial cells that support nerve cells in the brain, represent a more heterogeneous group characterized by varying degrees of malignancy. The origin of these tumors cells determines the category in which they fall, such as astrocytoma's or oligodendrogliomas. High-grade gliomas (grades III and IV), such as glioblastoma multiforme, are noted for their aggressive nature and poor prognosis, often infiltrating surrounding brain tissue to an extent that makes complete surgical removal challenge.

Pituitary tumors arise from the pituitary gland, a critical hormone-regulating organ seated at the base of the brain. While these tumors are predominantly benign, they can significantly affect bodily functions due to hormonal imbalances they induce, manifesting symptoms such as vision disturbances, infertility, and other endocrine disorders. The treatment protocol may involve surgery, medication, or radiation therapy, depending on the tumor's size, growth rate, and hormonal activity.

These modalities allow for detailed visualization of tumor size, location, and potential infiltration into adjacent tissues, thereby guiding therapeutic strategies. For instance, employing machine learning models in image processing can improve both the accuracy and speed of tumor classification,

aiding radiologists in making well-informed diagnostic and treatment decisions. The motivation behind this study's requirement to improve the precision and effectiveness of brain tumor diagnosis using methods for medical imaging such as MRI. Traditional methods in medical imaging, whose interpretations can vary significantly complex nature of brain imaging. Furthermore, existing automated methods often struggle with issues like overfitting, generalization, and computational inefficiency, making them less effective in clinical settings. The advent of deep learning offers a promising avenue to overcome these challenges, given its prowess in pattern recognition and feature extraction in complex datasets. However, the deployment of such models in a medical context requires careful adaptation and validation to meet the stringent accuracy and reliability standards necessary for clinical diagnosis .

A. The Objectives of the Research

1) Develop a robust model that can precisely classify brain tumors into meningioma, glioma, or pituitary tumor.
2) Implement advanced techniques such as batch normalization and dropout help reduce overfitting and enhance the MRI Images generalization capacity of the model to new, unseen data.
3) Provide a framework for further adaptation and use of deep learning models in the medical imaging field, promoting more accurate and rapid diagnosis processes. The further organization of the paper is
4) An analytical detailed comparison of Glioma, Meningioma and Pituitary detection is conducted between the proposed architecture and well-known approaches including (VGG16 and VGG19) and the recent approaches likeCNN-SVM.

II. RELATED WORK

A variety of studies have explored different aspects of applying deep learning models to enhance the diagnosis and classification of brain tumors. These studies have generally focused on enhancing the precision, efficiency, generalizability predictive models. Despite these advancements, several challenges remain. Traditional methods for brain tumor analysis primarily involved manual inspection of medical images by experienced radiologists. These techniques depended on visual assessments using MRI scans, and other imaging modalities to identify irregularities suggestive of tumors. The accuracy of these diagnoses heavily relied on the individual expertise and experience of the

medical professionals, leading to variability in diagnostic accuracy and potential for human error. Additionally, these methods were time-consuming and often required corroborative tests to confirm diagnoses. With the advent of digital imaging and increased computational

power, early machine learning techniques began to be integrated into the analysis of brain tumors. Earlier machine learning models tried to automate the process of extracting features from photos and determining important attributes that would indicate the existence of a tumor. However, these methods still struggled with handling the high dimensionality of medical images and often required extensive preprocessing of data to be effective. They provided a foundation for automated analysis but were limited by the quality and amount of the data available, which could introduce biases.

Convolutional Neural Networks (CNNs) became particularly influential because of their capacity to automatically and effectively learn features from raw imaging data. Unlike traditional machine learning techniques, CNNs could handle complex image data. directly, learning hierarchical features that improved classification and segmentation tasks (9). Initial deep learning models, such as AlexNet and later more complex architectures like GoogLeNet and VGG, demonstrated substantial improvements in accuracy and efficiency, reducing reliance on manual feature engineering and significantly improving generalization across diverse datasets.

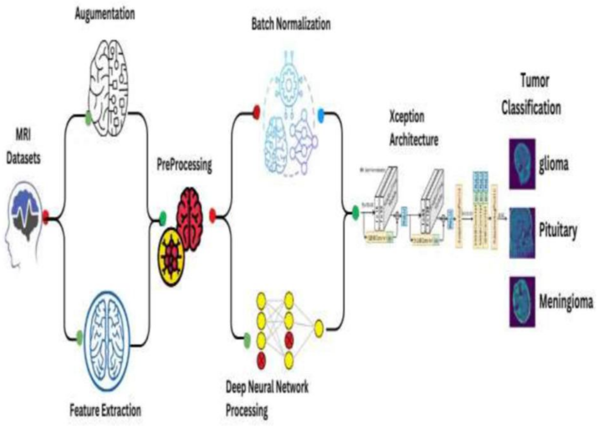


FIG NO 2: Architectural visualization of the proposed model

III. THE METHODOLOGIES

This comprehensive approach integrates data preprocessing, augmentation, and the deployment of a convolutional neural network (CNN) leveraging the Xception architecture, followed by statistical analysis. Figure 4 depicts Schematic of the enhanced Xception CNN architecture tailored for brain tumor classification.

IV. DATASET DESCRIPTION

The MRI images utilized in this study are derived from a ublicly accessible dataset created and shared by Jun Chenge. The dataset used in this study consists of MRI images, which are categorized into three main types: meningioma, glioma, and pituitary tumors. The images are originally grouped into espective folders by class, facilitating straightforward extraction and manipulation. The dataset is substantial enough to train a deep learning model, with each category containing hundreds of images, thereby enabling diverse tumor features. The variability within each category includes different stages and sizes of tumors, further enriching the dataset's complexity and providing a robust challenge for the deep learning model to tackle, ensuring it learns to identify subtle and critical differences among the tumor types. The MRI Images dataset comprises T1-weighted contrast-enhanced images from 299 patients. These images were initially presented " in.mat" format and were converted to ".png" format for this study. The selection criteria for the images included in the dataset were primarily based on the clarity and diagnostic relevance of the MRI scans, ensuring that each image distinctly represented the tumor characteristics necessary for effective training of the deep learning model. Images that did not meet these quality standards were excluded to maintain the integrity and reliability of the dataset.

V. REMOVING THE CONFUSING OBJECTS

Confusing objects such as texts and black areas on the right and left corners have been removed by cropping 299x299 pixels from each side of the image to get the exact brain.

FIG NO 3: MRI scan images across tumor types in training dataset.

A. Data Preprocessing

The preprocessing steps, including Data augmentation, image resizing and normalization, made a substantial contribution to the model's performance by guaranteeing dataset homogeneity and improving the model's capacity to generalize over a range of MRI images. Data preprocessing for MRI images is crucial for ensuring homogeneity and optimization for deep learning. Each image undergoes normalization, scaling pixel values from 0 to 1 to enhance the model's numerical stability and speed up convergence during training. Additionally, to accommodate the Xception architecture in this study, all images are resized to a uniform dimension of 229 × 229 pixels, eliminating size variability that could impact learning efficiency. Furthermore, data augmentation techniques such as random horizontal flipping and rotations are applied to the training dataset. These techniques mimic potential variations in clinical image capture, enhancing the model's generalizability and diagnostic accuracy in realworld settings. Data augmentation simulates a variety of plausible scenarios that could occur during image capture. This process is particularly beneficial in medical imaging, where different patient positions or imaging angles can vary significantly. For instance, a brain tumor might appear in different locations and orientations depending on how the scan was conducted. augmentation techniques such as scaling, translation, and shear can mimic variations due to different scanner settings or patient movements. These transformations make the model more robust, enabling it to maintain high performance regardless of these variabilities in new, unseen images. Equation 1 represents the flipping transformation on an image. Equation 2 represents the rotation of an image by an angle, using the rotation matrix. transformations applied during data augmentation to enhance model robustness.

$$I\ \text{flipped}\ (x,y)=I(W-x,y)$$

$$I\ \text{rotated}\ (0)=R\ (0).I$$

VI. IMAGE RESIZING

This uniformity is crucial as it standardizes the input size for the neural network, ensuring that the network architecture does not have to cope with variability in image size which could lead to inefficiencies in learning and performance. Resizing is typically performed before any augmentation or further processing of the original medical images. Incorporating dropout and batch normalization into the neural network architecture significantly enhances training and overall performance. Dropout, a regularization method, randomly ignores subsets of neurons during training, preventing the model from relying excessively on specific neurons or groups, thereby mitigating overfitting and encouraging the network to develop more robust features. atch normalization tackles internal covariate shift by normalizing network activations, which stabilizes the training process and allows for higher learning rates, speeding up training and reducing overfitting. These techniques are vital in our network configuration, with dropout simulating the training of multiple networks by approximating different neuron subsets, enhancing generalization. Meanwhile, batch normalization facilitates more independent learning across layers, aids in maintaining effective gradient flow during backpropagation, and helps avoid the vanishing or exploding gradients often problematic in deep networks, ensuring more stable and efficient learning.

VII. DEEP LEARNING TECHNIQUES

The top layers of this deep learning model are removed to accommodate the integration of custom layers specifically designed for brain tumor classification. Following the feature extraction capabilities of Xception model, architecture is enhanced with a batch normalization layer that stabilizes the learning process, essential for adapting the model to the specific challenges of medical imaging. Subsequently, a dense layer comprising 256 neurons is incorporated. This layer utilizes both L2 and L1 regularization techniques to mitigate the risk of the model's overfitting, a crucial factor to take into inherent complexity and the finite nature of the dataset available for brain tumor studies. The strategic choice of the Xception model and the meticulous configuration of the subsequent layers exemplify a deliberate approach to leverage advanced machine learning techniques for enhanced diagnostic accuracy in medical imaging. Transfer learning is pivotal in this research, utilizing a pretrained Xception model originally developed on a diverse dataset of natural images to enhance brain MRI image analysis, specifically for tumor classification. By beginning with weights that have learned generic features, the model is fine-tuned with brain MRI images, allowing it to adapt these universal features to the specialized task of identifying tumors, thereby enhancing its generalizability across domains. This adaptability is particularly vital in medical settings, where the model must perform consistently across images from various MRI technologies that differ in calibration, imaging techniques, and might produce variations in image contrast, resolution, or anatomical positioning. Transfer learning obviates the need for extensive datasets typically required for training models from scratch—a significant advantage in medical imaging where obtaining large, annotated datasets can be challenging. By leveraging a model pre-trained on heterogeneous data, transfer learning not only helps prevent overfitting but also ensures that the model doesn't merely memorize specific training data but genuinely learns to discern underlying patterns indicative of tumors across different imaging conditions, thereby bolstering diagnostic accuracy and robustness (22). CNNs are particularly effective at capturing spatial hierarchies in data. Equation 9 adds an L2 penalty to the cost function to prevent overfitting by penalizing large weights. Equation 10 adds an L1 penalty to encourage sparsity in the neural network parameters. Equation 11 represents General form of the loss function including regularization term R. Equation 12 explains the sigmoid activation function, used to map values to a (0, 1) range, typically in the output layer of binary classifiers. Equation 13 represents the output of a neural network layer.

$$J_{reg}\left(\theta\right) = J\left(\theta\right) + \lambda|\theta|^2$$

$$J_{reg}\left(\theta\right) = J\left(\theta\right) + \lambda|\theta|_1$$

$$J\left(\theta\right) = L\left(\theta\right) + \lambda R\left(\theta\right)$$

$$\sigma\left(x\right) = \frac{1}{1+e^{-x}}$$

$$y = f\left(Wx|+b\right)$$

Algorithm 1 encapsulate a thorough approach to classifying brain tumors using advanced deep learning techniques, tailored to specific requirements and challenges of medical image analysis. The final layer of the deep learning model is configured as a softmax layer, which plays a critical role in the multi-class classification of the MRI images into three distinct categories of brain tumors meningioma, glioma, and pituitary tumor. This layer is essential for transforming the logits—outputs of the last neural network layer before the softmax—into probabilities by mapping the unbounded scores into a (0, 1) range that sums to one, effectively providing a probabilistic interpretation of the model's predictions.

A. *Confusion Matrix*

A Confusion Matrix is another performance evaluation tool in machine learning for classification problems. It gives a summary of prediction results on a classification problem by showing how many predictions your model got right and wrong, broken down by each class.

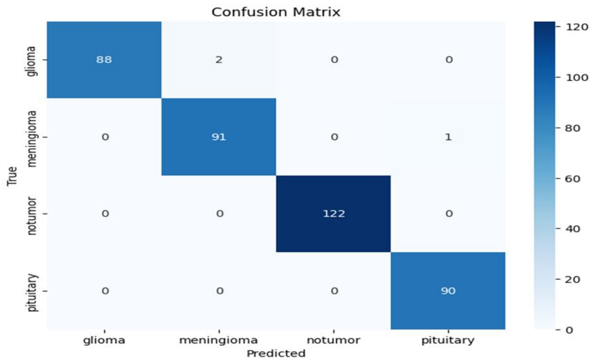


FIG NO 4: Confusion matrix

B. *Accuracy, Precision, Recall And Loss Plot*

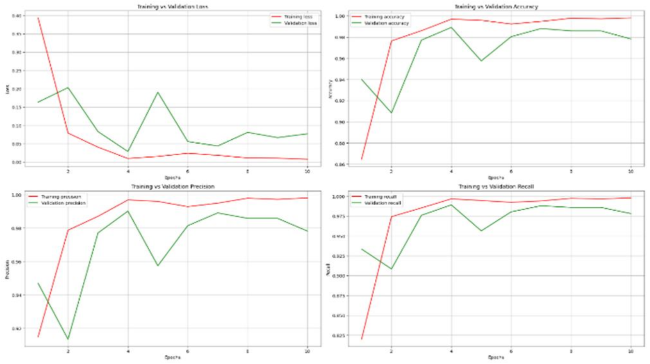
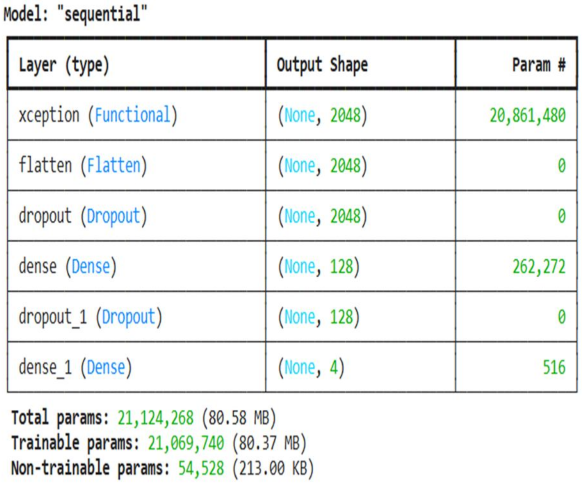


Fig no 5: Training and validation accuracy.

C. Model



```
Model: "sequential"
┌──────────────────────────┬──────────────────────┬──────────────┐
│ Layer (type)             │ Output Shape         │      Param # │
├──────────────────────────┼──────────────────────┼──────────────┤
│ xception (Functional)    │ (None, 2048)         │   20,861,480 │
├──────────────────────────┼──────────────────────┼──────────────┤
│ flatten (Flatten)        │ (None, 2048)         │            0 │
├──────────────────────────┼──────────────────────┼──────────────┤
│ dropout (Dropout)        │ (None, 2048)         │            0 │
├──────────────────────────┼──────────────────────┼──────────────┤
│ dense (Dense)            │ (None, 128)          │      262,272 │
├──────────────────────────┼──────────────────────┼──────────────┤
│ dropout_1 (Dropout)      │ (None, 128)          │            0 │
├──────────────────────────┼──────────────────────┼──────────────┤
│ dense_1 (Dense)          │ (None, 4)            │          516 │
└──────────────────────────┴──────────────────────┴──────────────┘
 Total params: 21,124,268 (80.58 MB)
 Trainable params: 21,069,740 (80.37 MB)
 Non-trainable params: 54,528 (213.00 KB)
```

Table no 1: Model Sequntial

Xception base model (pre-trained on ImageNet) is used without top layers, followed by a Flatten layer. Then, a Dense layer with 128 units and ReLU activation is applied, followed by a dropout layer (rate 0.25). Finally, a Dense output layer with 4 units and softmax activation is used for classification.

VIII. RESULTS

This study employed a sophisticated deep learning methodology, utilizing a convolutional neural network (CNN) specifically designed around the Xception architecture, to effectively classify brain tumors from a set of medical imaging data. Data augmentation methods included horizontal flipping of images, which is critical in diversifying the training dataset and enhancing model robustness (27). Additionally, normalization of pixel values was performed to ensure uniformity in the input data, which is essential for achieving consistent performance across various imaging conditions. These strategies were crucial in simulating a real-world environment for medical imaging diagnostics, thus providing a comprehensive test of the model's capabilities in accurately identifying and categorizing different brain tumor types based on their radiographic images. The deep learning model based on Xception architecture wastasked with classifying brain tumor types from medical imaging. The dataset consisted of three categories: glioma, meningioma, and pituitary tumors. Below are the detailed results from the MRI Images classification report and the analysis of the confusion matrix, ROC curves, and AUC values. Figure 7 depicts the decrease in training and validation loss over epochs, highlighting model learning efficiency. Figure 8 indicating model performance improvements. Table 4 provides a detailed epoch-by-epoch review of the model's loss and accuracy trends. The model demonstrates impressive overall accuracy of 98% in classifying brain tumors, showcasing its effectiveness across various tumor types. Specifically, for Glioma, it achieves a precision of 0.98 and a recall of 0.99, indicating high accuracy in identifying Glioma cases and a balanced F1-score of 0.98. Meningioma classification shows a precision and recall of 0.96, suggesting strong accuracy in predicting and identifying Meningioma cases, with an F1-score of 0.96. For Pituitary Tumor, the model achieves a precision of 1.00 and a recall of 0.99, demonstrating near-perfect accuracy in identifying this tumor type, with an F1-score of 0.99. The matrix shows a commendable correct classification rate for all tumor types, with minor confusion primarily between glioma and meningioma, which could indicate similar imaging characteristics that challenge the model. Only a few instances of misclassification occur, demonstrating the model's accuracy in practical scenarios. This level of precision is crucial for clinical applications, where correct tumor classification can significantly influence treatment decisions. Figure 10 shows the Visualization of model predictions vs. true labels, pinpointing accuracy and misclassifications. This analysis will extend beyond listing true positives, false positives, true negatives, and false negatives for each tumor type, by also examining misclassifications, such as the model's tendency to confuse glioma with meningioma more than with pituitary tumors, potentially due to similarities in tumor appearance or MRI signal characteristics. Attention will be given to the sensitivity and specificity for each tumor category to provide a nuanced view of the model's performance, supported by visual aids like heatmaps or color-coded matrices to improve readability and comprehension. This detailed breakdown will not only address the reviewer's request but also clarify areas where the model excels and identify where it might benefit from further tuning or additional training data to enhance its diagnostic capabilities.

ROC curves and their corresponding AUC values are critical in evaluating the discriminatory power of the model across different classes. An AUC of 0.99 for glioma and 1.00 for pituitary tumors signifies excellent model performance. The slightly lower AUC of 0.97 for meningioma, while still high, points to a bit more challenge in distinguishing these cases accurately. These metrics affirm the model's robustness in handling binary classification tasks, making it a reliable tool which is vital for targeted therapy and patient management in a medical setting. Figure 11 depicts ROC curves for each tumor type with AUC metrics, assessing the diagnostic ability of the model.

IX. OUTPUT

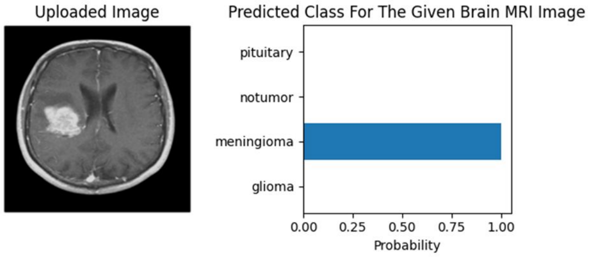


Fig no 5: Output

dataset: https://www.kaggle.com/datasets/masoudnickparvar/brain-tumor-mri-dataset.

X. FUTURE WORK

The successful application of this model in diagnosing brain tumors suggests its potential for broader use in medical imaging diagnostics. Future research could extend this deep learning framework to classify other tumor types, such as those in the lungs, liver, or breast, using CT scans or mammography. By leveraging the Xception architecture's robust feature extraction capabilities through transfer learning, and employing similar preprocessing, augmentation, and optimization techniques, the model could be adapted for a wide range of imaging tasks. It could also be expanded to detect non-cancerous conditions like cardiovascular diseases, neurological disorders, and musculoskeletal issues. Further, integrating multimodal data, such as genetic profiles, histopathological data, and patient demographics with MRI data, could enhance the model's utility, providing deeper insights into disease states and supporting more personalized medical treatments. As medical imaging technology advances with higher resolution scans and new techniques, the model must be updated and refined for ongoing effectiveness. Future research could focus on real-time diagnostic capabilities to provide immediate feedback during procedures, supporting timely and accurate clinical decisions. Essential to this is continuous learning, allowing the model to adapt to evolving medical knowledge and practices through periodic retraining with the latest MRI data and patient demographics. Integrating the model into clinical workflows facilitates automatic learning from diagnostic outcomes, creating a feedback loop that improves pattern recognition and predictions. Employing transfer learning enables rapid adaptation, ensuring the model evolves with medical advancements and remains relevant and accurate in clinical settings. To maintain the long-term relevance of the model in medical diagnostics, a framework for ongoing training and adaptability is crucial. It should include periodic retraining with new MRI datasets of emerging or rare tumor types using transfer learning, preserving performance on known tumors while updating knowledge. The model must also adapt to changes in treatment protocols, such as chemotherapy or radiotherapy, which impact tumor appearance on MRIs. Integrating a continuous data collection and monitoring system into clinical workflows will enable the model to learn from real-world outcomes and detect new patterns. This feedback loop will improve the model's ability to generalize, keeping it responsive to advances in imaging technologies, patient demographics, and treatment approaches, thereby ensuring its clinical effectiveness and relevance. This study on brain tumor classification using MRI images could significantly benefit from integration with other diagnostic tools like genetic testing and patient history to enhance accuracy. Genetic profiling can reveal tumor-specific mutations, helping to distinguish between tumors that are morphologically similar but genetically distinct. Adding patient history, such as age, gender, and medical background, to the model can refine diagnoses by correlating these factors with imaging data, improving predictive capabilities. This holistic approach combines imaging, genetic, and clinical data for personalized treatment recommendations. A critical future development for the model is incorporating explainability tools to increase transparency in decision-making, essential in clinical settings where trust is paramount. Techniques like Grad-CAM or LIME could visualize influential MRI image areas in the model's decisions, allowing clinicians to verify the model's focus on significant tumor regions. This transparency not only builds trust but also aids in refining the model by highlighting its focus areas and limitations.

Such explainability is crucial for regulatory approval and adoption in clinical workflows, Frontiers in Medicine 13 frontiersin. ensuring the model meets the interpretability standards required for medical decision-making. The study should evaluate the model's performance internationally to ensure its generalizability across varied geographic regions and healthcare settings. Collaborating with global medical institutions will provide access to diverse imaging data, crucial for validating the model across different populations and healthcare systems. This global approach aids in creating datasets that are representative worldwide and helps adapt the model for use in regions with varying MRI technologies, thus broadening the model's applicability and enhancing its reliability as a diagnostic tool. Integrating advancements in hardware like modern GPUs and emerging technologies such as NVIDIA's Tensor Cores and Google's TPUs could significantly boost the model's performance and efficiency. These technologies provide enhanced processing power, enable parallel computing, and optimize matrix operations essential for deep learning tasks. Leveraging these hardware solutions can reduce training times, facilitate the exploration of more complex architectures, and efficiently manage larger datasets, leading to improved accuracy, quicker deployment, and enhanced scalability for extensive medical imaging tasks in clinical settings.

XI. CONCLUSION

This study developed and validated a deep learning model using the Xception architecture to classify brain tumors from MRI images, demonstrating high accuracy, precision, recall, and AUC scores. The comprehensive methodology encompassed data preprocessing, the application of an advanced convolutional neural network, and rigorous evaluation using diverse metrics, proving the model's ability to differentiate various types of brain tumors effectively. Looking forward, enhancing the model through the integration of larger and more diverse datasets could improve robustness and accuracy, particularly for complex or rare tumor types. Future work could also explore additional transfer learning strategies and fine-tuning approaches to enhance performance. Collaboration with medical professionals for clinical validation could confirm model's utility in real-world settings, ensuring compliance with clinical standards. Moreover, incorporating multimodal data, such as genetic information and patient demographics, could offer a more comprehensive diagnostic tool, suggesting that deep learning could significantly enhance diagnostic processes in healthcare, providing tools that support radiologists and contribute to more personalized and precise medical treatments.

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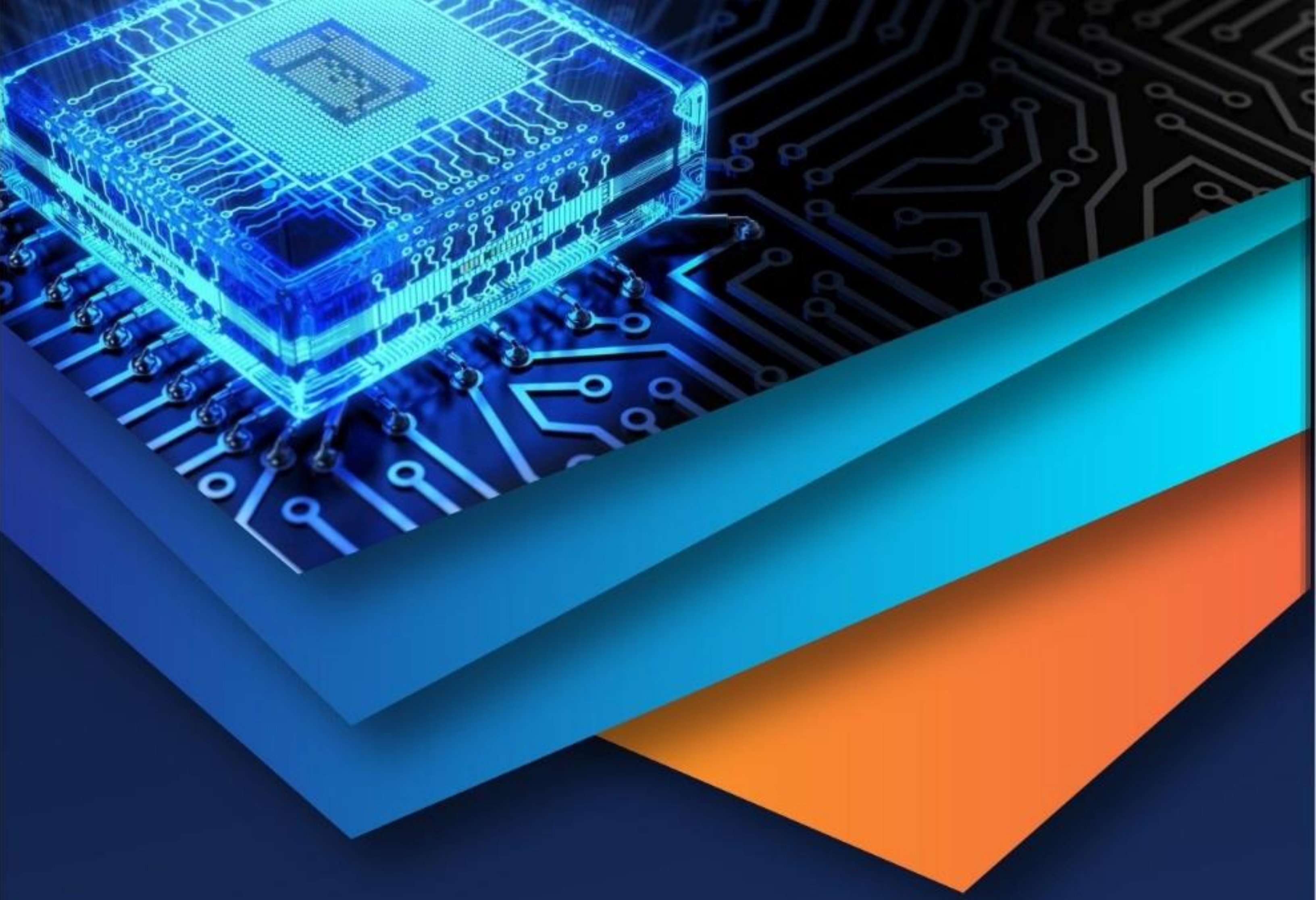

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