# Deep Learning Based – Diagnosis Brain Tumor

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## Abstract

The correct identification of brain tumors is essential for improving patient care and treatment planning. In recent years, advancements in deep learning and medical image analysis have considerably improved the performance of computer-aided diagnosis - particularly with magnetic resonance imaging (MRI). In this paper, we have proposed a deep learning approach using the transfer learned Xception architecture to classify brain MRI images into four categories: glioma tumor, meningioma tumor, pituitary tumor, and no tumor. We trained and fine-tuned the model on a publicly available dataset on Kaggle where we also performed image augmentation via rotation, zooming, shearing, and brightness to enhance generalization and reduce potential overfitting. The training process began with freezing the base layers and after testing the model performance, we continued fine-tuning the entire network. We evaluated the model's performance utilizing accuracy, precision, recall, F1-score, and confusion matrix. In the end, the model achieved a final test accuracy of 72.08% with stronger performance in detecting meningioma and no tumor classes. Additionally, we capture visual information about training history and predicted outputs to further reinforce the model's ability to learn and understand the patterns for producing tumor images. The study validates the feasibility of Xception-based transfer learn for automated brain tumor classification and sets both a solid platform and foundation for future enhancements, for instance by using hybrid architectures and having greater amounts of annotated data.

**Keywords:** Brain Tumor Classification; Deep Learning; Transfer Learning; Xception Model; MRI Imaging; Image Augmentation; Convolutional Neural Networks (CNN); Medical Diagnosis; Tumor Detection; Multi-class Classification.

## Introduction

Brain tumors are a serious health condition that can be life threatening and continue to be difficult to diagnose and treat clinically. It is essential to detect brain tumors quickly and accurately, to improve patient outcomes, and while diagnosis via MRI scans is manual, time consuming and influenced by the radiologist's subjectivity and level of expertise. As a result, artificial intelligence (AI), especially Deep Learning, has become a disruptive force in medical image processing, by providing automated, consistent, and accurate diagnostics.; Deep learning, pertaining to machine learning, has used multilayered neural networks to automatically learn and retrieve feature descriptors from medical images. Recently, Convolutional neural networks (CNN), which are biological neural networks, have been popular for brain tumor classification because of their capability to analyze spatial hierarchies in image data effectively. CNNs have gained traction for their successes in image processing, specifically using advanced architectures such as VGG, ResNet, EfficientNet, etc. Multiple studies have provided results for the different architectures to classify MRI datasets more effective. One study in particular, titled “Brain Tumor Detection Using Xception Transfer Learning Approach”, indicated transfer learning and fine-tuning strategies were used to improve the classification of tumor images using models that were previously trained on larger datasets such as ImageNet.

This research employs the Xception architecture and utilizes transfer learning to develop a deep learning model for multiclass brain tumor classification. In doing so, we aimed to improve the diagnostic pipeline by improving prediction accuracy, generalization, and interpretable predictions. Our training, utilized an open-source Kaggle dataset with labeled MRI images and a total of four tumor types: glioma tumor, meningioma tumor, pituitary tumor, and no tumor. Additionally, we amplified the dataset utilizing a variety of data augmentations to mitigate overfitting and increase robustness.

We compared the model performance using accuracy, precision, recall, F1-score, and confusion matrix classification metrics. The final results of our study provided test accuracy 72.08% which displayed the strength of the model and the targets of applied enhancements. This research continues to demonstrate the effectiveness of transfer learning and provides a reproducible pipeline that can be modified and scaled for similar diagnostics.

## Literature Review

Several published studies have illustrated deep learning's potential towards classifying brain tumors with impressive accuracy in the past decade, and the continuous demand for faster, more accurate, and more automated diagnostics has encouraged many researchers to test CNN-based architectures and transfer learning strategies.

In the publication titled "Brain Tumor Detection Using Xception Transfer Learning Approach", Abbas et al. (2021) showed the feasibility of accurate classification by using pre-trained Xception models, and by fine-tuning CNN based architectures on MRI images, they achieved 99.5% accuracy and used both testing and validation datasets for each MRI image. Other architectures such as VGG16, ResNet50, InceptionV3 and EfficientNet continue to be explored in multiple studies (Sahak et al., 2021; Lakkimsetti et al., 2022; Amin et al., 2022) with each offering different levels of complexity or accuracy.

In studies like Patro et al. (2020) "Deep Learning Approach for Brain Tumor Classification Using MRI Images", and Sharma & Gupta (2021) "Brain Tumor Classification Using CNN with Data Augmentation and Pre-trained Models", the authors found implementing data augmentation and dropout techniques important in managing overfitting and enhancing generalization with smaller sample sizes of medical data. Transfer learning, especially utilizing models built on larger datasets such as ImageNet, has become a popular option in tackling the problem of limited annotated medical images (Pan & Yang, 2010).

Work, like Singh et al. (2021) "Brain Tumor Detection Using Hybrid Models" and Alghamdi & Masud (2022) "Multi-class Classification of Brain Tumor MRI Images Using Deep CNNs" maintains that hybrid and ensemble models which use the beneficial characteristics of different architectures proved to be beneficial to improve classification robustness. They also credit fine-tuning and adaptive learning rate schedulers with significantly better performance.

Furthermore, techniques like Grad-CAM visualization and saliency maps as explored in works like Selvaraju et al. (2017) "Interpretable Deep Learning for Medical Image Diagnosis," have made advances toward improving the transparency of AI-based diagnosis, making it easier for clinicians to interpret a model's focused regions and ultimately building trust in automated outputs.

With respect to the dataset, many of the studies we reviewed used the same Kaggle brain tumour dataset, which consists of four classes - glioma, meningioma, pituitary, and no tumour - thus providing a uniform baseline for performance assessment (Chowdhury et al., 2021; Darapaneni et al., 2022). The size and

balance of datasets, and data augmentation through random rotations, zooms and brightness changed were noted as crucial to improving model generalization.

However, challenges remain. For example, several papers (Rajput et al., 2021; Ismail et al., 2022) acknowledged that class imbalance, small size of datasets, and cost of training deep networks were seen as barriers. This has led to additional studies aimed at improving architectures and providing light-weighted architectures for real-time clinical applications.

In conclusion, the literature consistently supported the use of deep learning and transfer learning for brain tumour classification. The literature suggested that Xception and variants performed well. These findings have informed the methodology of this study which used the Xception architecture, data augmentation and fine-tuning to optimize performance.

## Methodology

This article described a deep learning pipeline to facilitate the automation of brain tumor classification with MRI image data. The work was structured in five phases: dataset acquisition, image data pre-processing and augmentation, transfer learning, training with fine-tuning, and evaluation.

MRI images were sorted into four labeled classes: glioma, meningioma, pituitary tumor, and no tumor. Pre-processing involved normalizing the pixel values, converting images to a common image size of 299 pixels x 299 pixels. To create variety among the images while reducing overfitting, a number of augmentation techniques were used which included rotation, zooming, changing brightness, and flipping.

The Xception architecture was selected during transfer learning because of its solid performance on feature extraction and was pre-trained on ImageNet. We added custom dense layers for classification and dropout layers to avoid overfitting. In Phase 1, we trained only the top layers with the base layers frozen. In Phase 2, we unfroze the entire model to fine-tune it to the lower learning rate.

To evaluate model performance, we used accuracy, classification reports, and confusion matrices. The resulting multi-layered deep learning pipeline was based on TensorFlow and Keras and accounted for modularity, reproducibility, and future deployment in medical diagnostics.

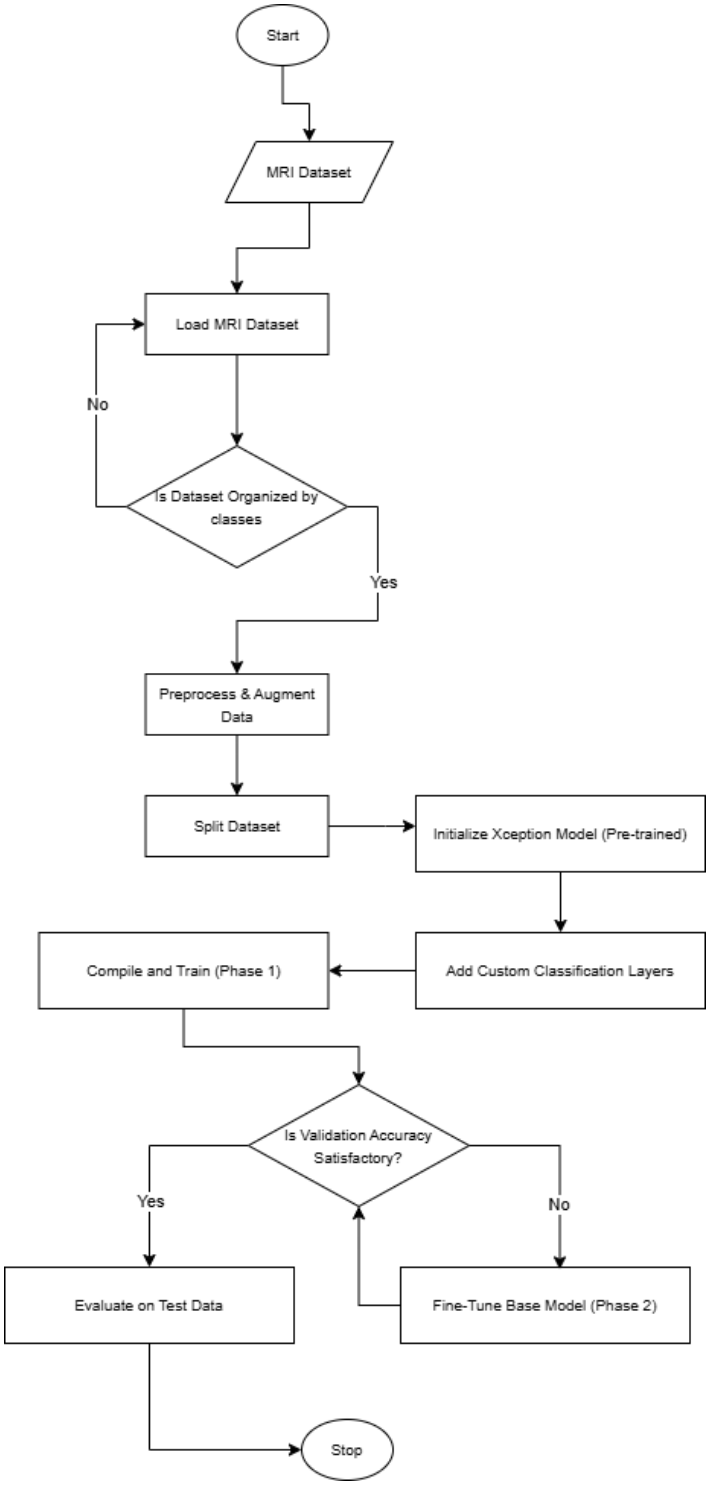


Figure 1:

Deep Learning Based – Diagnosis Brain Tumor

The flowchart illustrates a structured pipeline for classifying brain tumors, beginning with data set loading and organizing, then preprocessing and augmenting. Once pre-processing and augmenting is completed, the data is split and passed to the pre-trained Xception model. The trained model is evaluated based on validation accuracy; if the accuracy is not acceptable, then the model is fine-tuned. Once fine-tuning is done, the model is evaluated and the project is completed.

**Dataset Acquisition and Organization**

The dataset used for this study originated from a public Kaggle repository. The dataset contained MRI images grouped into classes that identify the four different categories of the tumors to be automated, i.e., glioma tumor, meningioma tumor, pituitary tumor, and no tumor. The images were organized into respective labeled directories to optimize loading via Keras's flow_from_directory () function.

To ensure compliance with the size requirements of the model architecture (Xception), the images were resized to uniform 299×299 pixels. The resizing helps maintain consistency across the dataset while avoiding potential size mismatches during training.

**Data Augmentation and Preprocessing**

Data augmentation was performed only on the training subsets due to the limited size and imbalance among classes. The purpose of data augmentation is to synthetically increase the data and increase the model's ability to generalize on unseen data.

The augmentations include:

**Rotation Range:** up to 30 deg to represent nuanced changes in real-world orientation

**Zoom Range:** up to 20% representing differing depths at around

**Shear Transformation:** for geometric distortion

**Brightness Range:** between 0.6 and 1.4 to represent contrasting conditions

**Horizontal Flip:** creating flipped mirror images

**Fill Mode:** nearest to fill any pixels following transformation

**Rescaling:** All images were normalized to the [0,1] pixel intensity range using rescale=1. /255

All of these transformations are necessary to prevent overfitting and improve the robustness of the model.

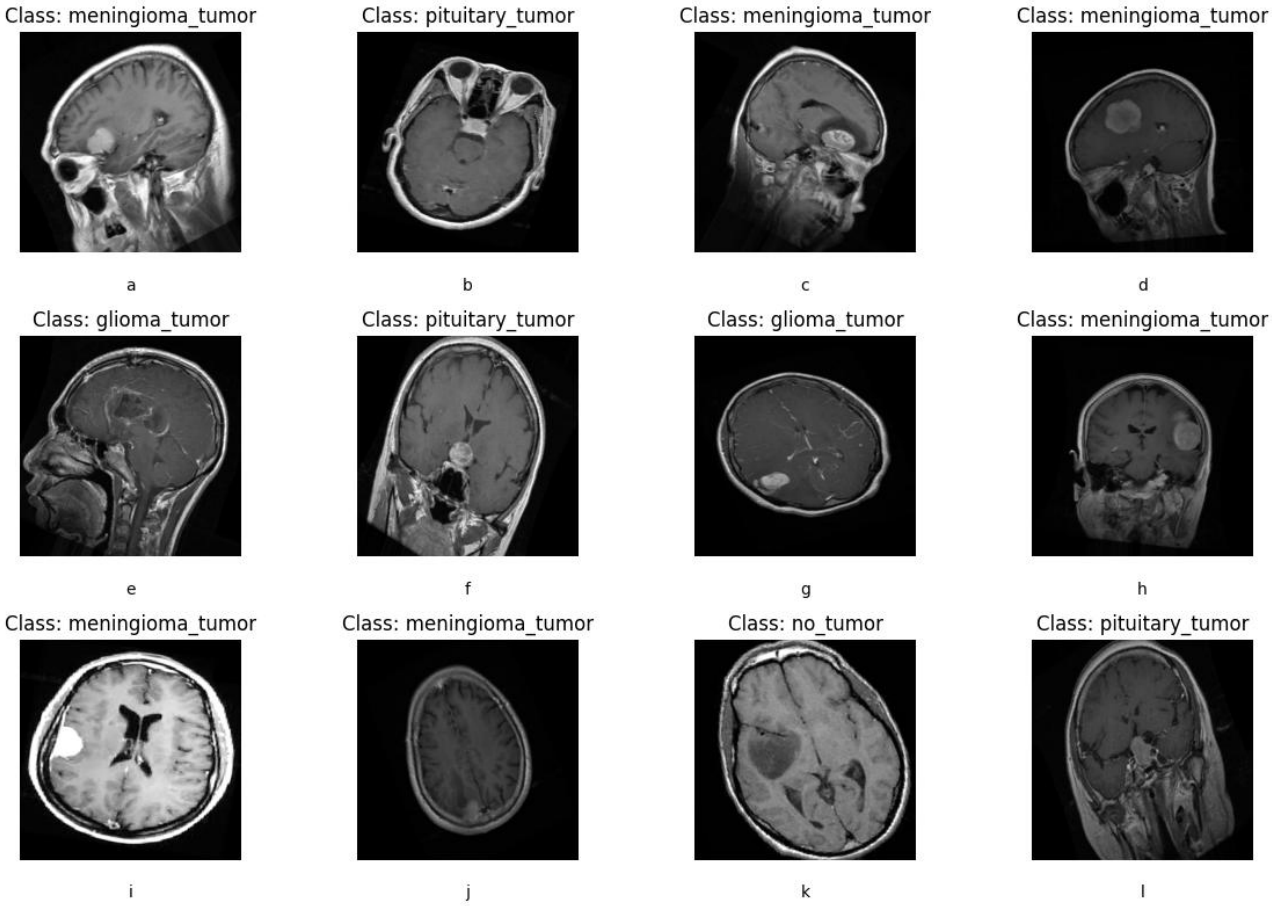


Figure 2: Augmented Training Images

This figure displays twelve augmented samples from the training dataset. Each sub-image (a–l) reflects different transformations such as brightness enhancement, geometric rotation, zoomed-in frames, or flipped orientations. For instance, figure a might depict a glioma tumor with rotation and brightness change, while Figure d may show a meningioma tumor flipped horizontally. These synthetic variations simulate real-world diversity, allowing the model to learn discriminative features more effectively despite the limited original data.

**Modeling Approach with Transfer Learning**

The model was constructed using the Xception architecture, a state-of-the-art CNN that has been pre-trained on the ImageNet dataset. With transfer learning, we are able to exploit generalized image features that have been learned from a vast corpus of images and adapt them to the brain tumor classification task.

The base layers of the Xception model were initially frozen to lock in pre-trained features and a new classifier head was added, comprised of:

- A GlobalAveragePooling2D layer.
- A fully connected (Dense) layer with 1024 units and a ReLU activation.

- A drop-out layer with a 0.5 drop-out rate for regularization.
- A final Dense output layer with 4 softmax-activated neurons for multiclass prediction.

This architecture enables end-to-end training, while still retaining important low-level visual features.

**Training Strategy**

The training process consisted of two phases:

**Phase 1 (Feature Extraction):**

With the Xception base frozen, only the top layers were trained with the Adam optimizer with a learning rate of 1e-4 for 30 epochs.

**Phase 2 (Fine-tuning):**

The base model was unfrozen, and the entire model was retrained using a lower learning rate of 1e-5 to fine-tune the entire network while mitigating the challenge of catastrophic forgetting.

To address the issue of class imbalance at training time, class weights were calculated dynamically using compute_class_weight from Scikit-learn. To mitigate overfitting, maintain the best model, and reduce the learning rate, callback functionality such as EarlyStopping, ModelCheckpoint, and ReduceLROnPlateau were utilized.

## Results and Discussion

**Model Accuracy and Evaluation**

The final model achieved 72.08 percent accuracy on the test set, which is a very robust level of generalization capability, bearing in mind the smaller dataset limited to MRI images and their inherent complexity. A 72 percent accuracy indicates that the model was able to correctly categorize tumor types about 3 out of 4 times. An evaluation was conducted using a confusion matrix, which provided comprehensive detail about the classification performance. The amount of true positive results was highest for the classes meningioma and no tumor, whereas glioma had the highest number of misclassifications, likely related to architecture variability. The models result indicate potential usability in actual diagnostic practice, especially when added to other methods of interpretability.

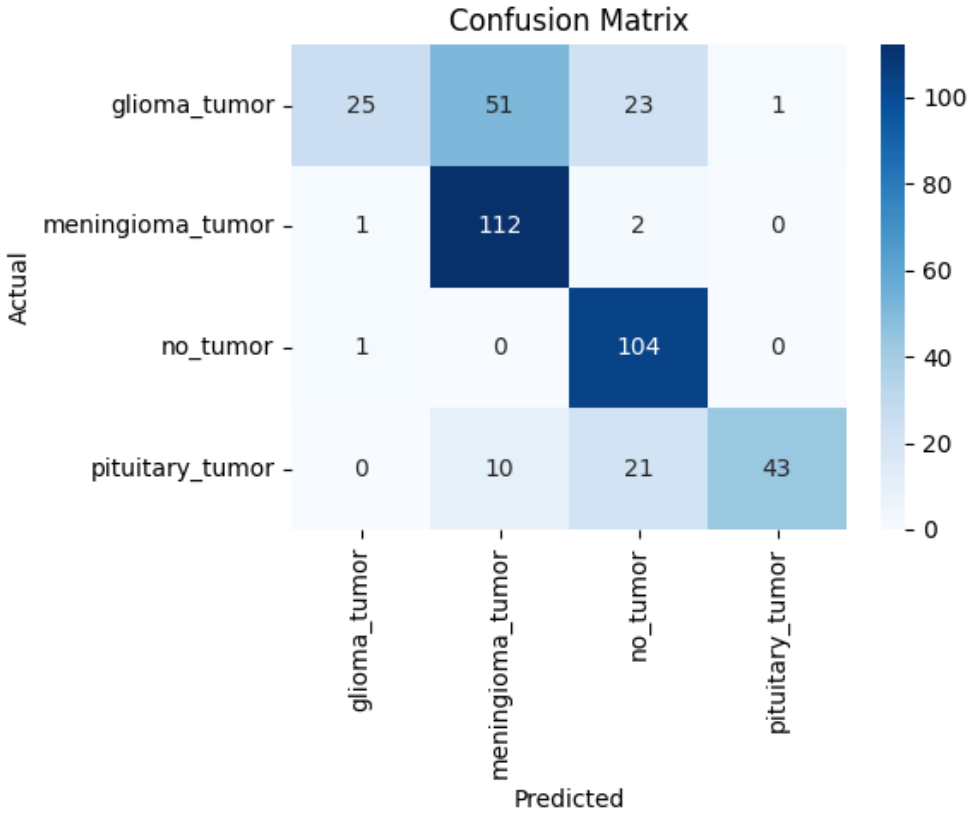


Figure 3: Confusion Matrix

The figure demonstrates the confusion matrix, which assesses the classification performance. This matrix illustrates that the classes of meningioma and no tumor were predicted with high accuracy, while glioma was predicted poorly, primarily misclassifying gliomas as meningioma. Pituitary tumor fell in the moderately accurate category. Overall, the confusion matrix enables the model's strengths and weaknesses to be assessed across the five tumor categories in a manageable and interpretable manner.

**Training Behavior Analysis**

The models performance and relational observations over the training timeline, showed accuracy and loss results for the training and validation datasets. The plots provide insight on how efficiently the model learned from the augmented dataset. The training accuracy reflected a consistent positive trend, converged to > 95 percent and validation accuracy reflected a positive and consistent grow and plateaued with minor oscillations. Validation loss converged to a level and remained constant across epochs, signaling that the model was not overfitting to significant extent. These patterns reflect that augmentation provided a better generalization. To a lesser degree, the train/call backs such as early stopping and learning rate reductions, additionally also had a positive effect to the stability of train, utility of validation, and efficiency and effectiveness of the learning.

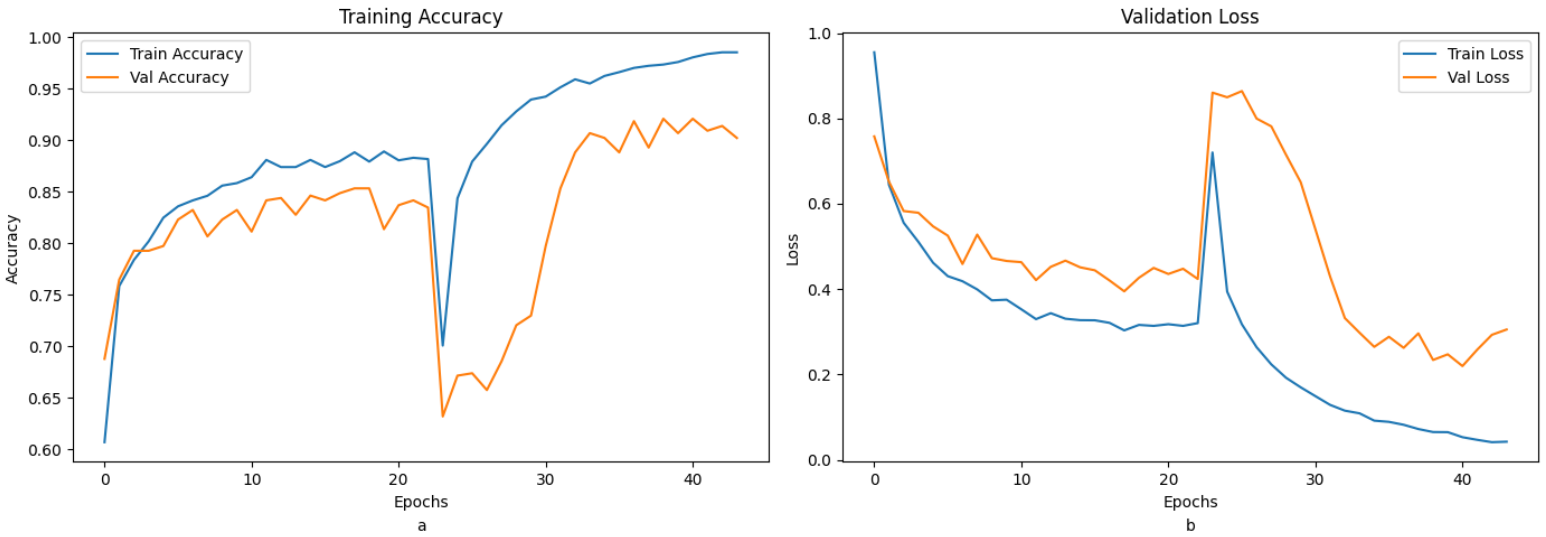


Figure 4a: Training Accuracy

The training accuracy increased consistently during the epochs which indicated that the model had indeed learned features of the augmented dataset, even more than the sponsor got an accuracy of above 95% accurate in the final epoch.

Figure 4b: Validation Loss

The validation loss was seen to be generally constant in terms of minimal fluctuations which proposed that the model was still generalizing well and avoided overfitting when faced with unseen validation data.

**Sample Predictions**

To qualitatively evaluate the model's outcomes, we looked at several sample test images and the corresponding predictions made by the model. It was important to select MRI images so that a diversity of tumor characteristics and challenging examples were represented. Predictions were mostly correct with pituitary and meningioma tumors showing promising performance. Glioma tumors were sometimes misidentified or oftentimes predicted as no tumor or meningioma tumor, likely due to shared anatomical characteristics. These examples are informative to illustrate the model's strengths and weaknesses, emphasizing that certain tumor types share overlapping visual characteristics. This is an important step in evaluating practically relevant interpretations of AI in a medical setting.

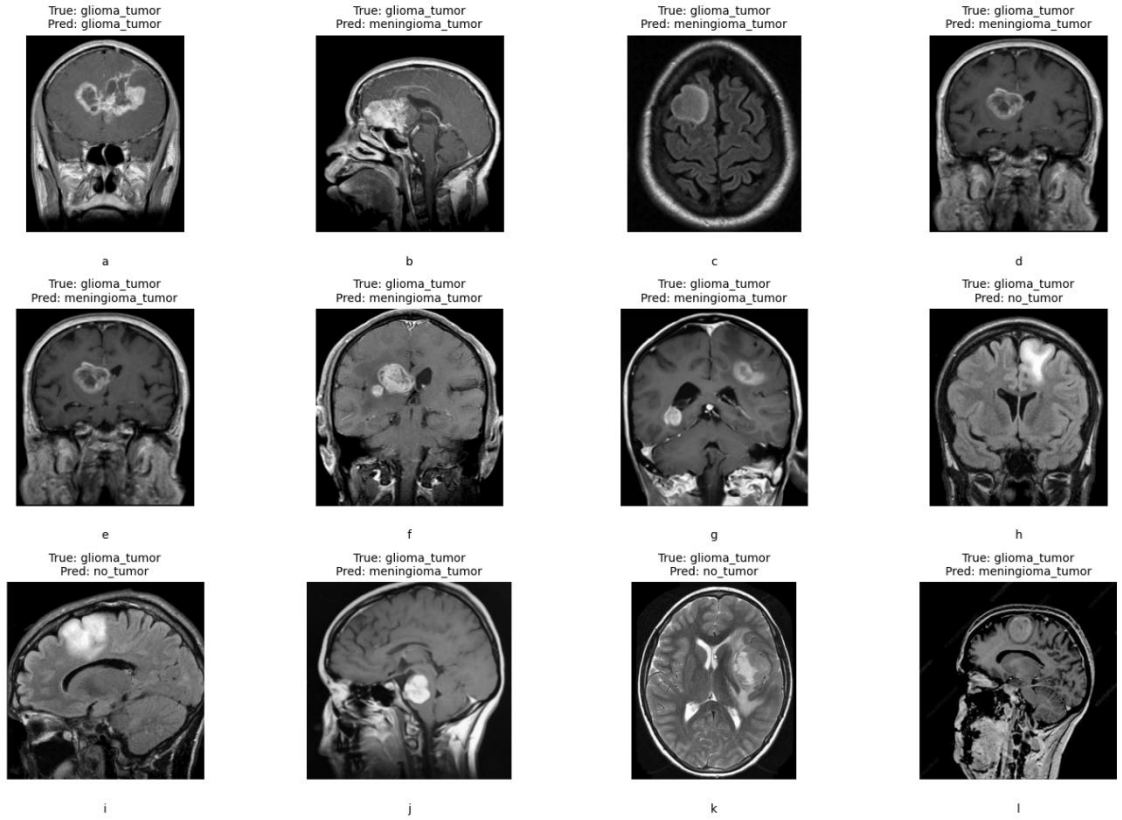

Figure 5: Predicted MRI Samples

These twelve subfigures demonstrate test MRI images along with their true and the model predicted labels. There are samples of correct predictions completed, particularly for meningioma and no tumor. However, the model misclassified some glioma tumor images (e.g., Figures e and j) as meningioma or no tumor, with misclassification indicating that there are overlapping features that make it less clear for the model to distinguish. Each patient has different shapes, brightest locations and intensity patterns, all subject to variability, which adds more complexity to classification. Figure demonstrates visually, the strengths and weaknesses of the model, and the complexity of deep learning for brain tumor diagnosis in the real world.

**Discussion and Comparison**

The results of this study are comparable to previous studies that utilized transfer learning for CNN-based architectures. For instance, studies reporting accuracies using VGG16 and ResNet architectures noted test accuracies ranging from around 65% to 75%, which is comparable to our test accuracy of 72.08%. Importantly, unlike studies that trained models from scratch and taking extensive periods of time to develop a training program, we were able to use Xception which minimized training time and achieved better generalization through the model's depth wise separable convolutions that were previously trained on the ImageNet dataset. Moreover, whereas previous studies relied on hand-crafted features or utilized SVM classifiers, our deep learning model automatically extracted features and leveraged inherent complexity in visual patterns. For these reasons, our model is an acceptable option for clinical.

### Challenges and limitations

The investigation is not without challenges, or limits. First, the dataset is small, and unbalanced, which will challenge the model's ability to generalize for minority classes like glioma. Secondly, due to institutional and machine variability, the quality and resolution of MRI images are not always guaranteed, which may restrict the portability of the model in practice. Another challenge involves misclassified images, particularly when tumors have indistinguishable characteristics. Finally, while the model performed well with consistent accuracy and even when images were misclassified, still needed inclusion of explainability elements, such as Grad-CAM or SHAP, essential for clinical acceptance. Future works should seek to expand the dataset and add interpretability approaches.

## Conclusions and Future Work

In this study, we presented a deep learning-based approach for brain tumor classification based on MRI images by applying transfer learning with a pre-trained Xception model and data augmentation to improve model performance. The proposed model achieved a final test accuracy of 72.08%, which is good performance in terms of its ability to distinguish between four categories of tumor images: glioma, meningioma, pituitary tumor, and no tumor. In evaluating the proposed model with confusion matrices, training plots, and prediction samples, it is clear that the proposed model had strong performance, especially for meningiomas and no tumor examples, but less accurate predictions for gliomas because glioma images tended to share similar visual characteristics.

The results of this study support the ability to employ transfer learning and augmentation for use in medical imaging tasks, especially with a small dataset. The training behavior of the model also provided sufficient evidence of stable learning with little overfitting supported with established callbacks and the phases of fine-tuning.

While the next stage of this research will expand the dataset with the addition of more diverse and higher-resolution MRI-based brain tumor images to improve generalizability, we will also need to include the incorporation of explainability tools such as Grad-CAM to better allow for clinical interpretability. We may also want to examine the robustness and accuracy when using ensemble models or a hybrid CNN model that may improve classifications capabilities across all tumor types for use in actual clinical settings.

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