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Original Article

Collective Intelligence: Harnessing Multiple Models to Enhance Brain Tumor Detection and Classification Utilizing Deep Learning Techniques

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Abstract

Brain tumors arise from abnormal cell growth near or within the brain due to genetic changes. They pose a significant health risk, particularly in children, ranking as the second most common childhood cancer in the United States. Existing detection methods, though necessary, are invasive, time-consuming, and prone to errors. Therefore, there is a pressing need for a more efficient and reliable approach to improve diagnostic accuracy and speed. This study explores collective intelligence by employing multiple deep learning models using transfer learning techniques for brain tumor detection and classification. It combines InceptionV3, DenseNet201, and ResNet50 to create an ensemble that enhances performance. Based on 1,311 high-resolution brain MRI scans covering four types of brain tumors, the research applies data preprocessing and augmentation to improve dataset quality and diversity. The ensemble method addresses the limitations of single models, increasing the reliability and robustness of detection and classification. The ensemble model achieved superior performance, with an accuracy of 95.6%, an F1-score of 94.4%, and a precision of 94.9%, underscoring the effectiveness of ensemble learning in enhancing brain tumor diagnostic capabilities.

Categories: Ensemble Learning, Deep Learning, AI applications

Keywords: collective intelligence, transfer learning, inceptionv3, resnet50, densenet201

Introduction

Brain tumors develop when cells in or near the brain undergo changes in their DNA, which contains instructions that control cell behavior [1]. These changes cause cells to grow rapidly and survive longer than normal, leading to an accumulation of abnormal brain cells. In 2023, approximately 5,230 people were diagnosed with brain and other central nervous system diseases. In the United States, brain tumors are particularly prevalent among children aged 0-19. It is the second most common childhood cancer after leukemia, accounting for about 26% of cases in children under 15 years and 21% of cases in adolescents aged 15-19 [2]. Different types of central nervous system tumors were examined in this cohort, and varying survival rates were observed. In general, the 5-year relative survival rate for children aged 0-14 years with central nervous system tumors, excluding benign brain tumors, is about 74%, while it is approximately 75% for adolescents aged 15-19 years. Survival rates vary depending on factors such as tumor type, stage, patient age, overall health, and the effectiveness of the treatment plan [3]. In both medical and general contexts, the term "brain tumor" is widely recognized and frequently used, referring to an abnormal growth of cells in the brain. According to Rathore et al. [4], the brain is an invaluable as well as sophisticated organ responsible for many vital functions, including temperature regulation, hunger control, motor skills, sensory perception, emotions, cognition, memory, and vision. According to the World Health Organization, more than 120 types of brain tumors have been identified and classified into four grades based on their level of aggressiveness. According to Tsukamoto and Miki [5], the three types of brain tumors most commonly studied today are pituitary tumors, meningiomas, and lymphomas. Brain tumors have the potential to induce seizures and headaches, according to Healthline Media [6]; thus, an accurate and timely diagnosis is imperative. Complications from tumors may also lead to physical impairments. To properly control or lessen these difficulties, patients may require protracted and frequently difficult rehabilitation. Furthermore, brain function can be significantly affected depending on the size, location, and type of the tumor [7]. In traditional diagnostic approaches, physicians or radiologists face significant challenges and often spend considerable time identifying tumors, particularly in complex cases. Proficiency is necessary to recognize the tumor and distinguish it from surrounding tissues. Filters can be applied to the image to enhance clarity if needed. Lastly, the physician or radiologist can determine whether it is a tumor, its type, and its stage. This diagnostic approach is known to have many drawbacks, including its long duration, invasiveness, and proneness to sampling errors. As a result, a trustworthy and practical strategy is required to address the brain tumor detection issue. Ultimately, this approach will shorten the time needed for an appropriate diagnosis by enhancing the diagnostic proficiency of doctors and radiologists [8]. The detection and classification of abnormal tissues using traditional methods can take a long time, which is the reason behind the use of computer-aided diagnostics. This helps automate tumor detection at an early stage without the need for human participation. As digital systems have been introduced in the medical field, activities like brain tumor detection have been digitized [9]. To improve accuracy and performance in detection, machine learning and deep learning models, along with appropriate datasets, have been used. There have been many research studies on modern methods conducted using a single machine learning model and a dataset; some used a hybrid model on a specified dataset, and many more variations exist. In almost all the studies carried out, the researchers achieved a high percentage in performance analysis; however, although the model was able to detect the tumor, it mostly had issues with precision on smaller, low-quality images. Some of the models employed include pre-trained VGGNet16 and ResNet50, GlobalNet, multi-task learning, and FusionNet.

In this study, we propose a collective intelligence-based deep ensemble framework in which three complementary deep architectures are employed, namely InceptionV3, DenseNet201, and ResNet50, as base learners under a transfer learning setting. Their heterogeneous structural properties facilitate representational diversity, which is key to good ensemble construction. A weighted prediction fusion mechanism is proposed to integrate model predictions in a collective intelligence scheme, which is expected to improve classification results and reduce the weaknesses of individual models.

The major contributions of this work are as follows:

• To develop and evaluate an ensemble of deep learning models, namely InceptionV3, DenseNet201, and ResNet50, as base learners through transfer learning, and to explore ensemble techniques, specifically a weighted average, to effectively combine the predictions of the individual models within the ensemble, resulting in more reliable and robust outcomes.

• To compare the impact of collective intelligence on key performance metrics in comparison with individual models and existing models from other research works.

• To develop a simple web application for the proposed model to classify brain tumors from a given MRI image.

Materials And Methods

Dataset collection

A dataset of 1,311 tumor images with high-resolution MRI scans was employed in our study. This dataset, obtained from the Kaggle website [10], encompasses thousands of images across various categories. It classifies tumors into glioma, meningioma, pituitary, and cases where no tumor is present. Figure *1* presents some images from these categories. The dataset comprises 300 images of pituitary tumors, 306 of meningioma, 300 of glioma, and 405 images of no tumor before augmentation, as shown in Table *1*. This dataset is an essential resource for developing and evaluating machine learning models as well as deep learning models, particularly convolutional neural networks (CNNs), of automated identification and classification of tumors in the brain. Figure *2* depicts the bar plot distribution of the dataset for all classes in both the training and testing subsets. Also, Figure *3* represents the percentage of each tumor category in the dataset.

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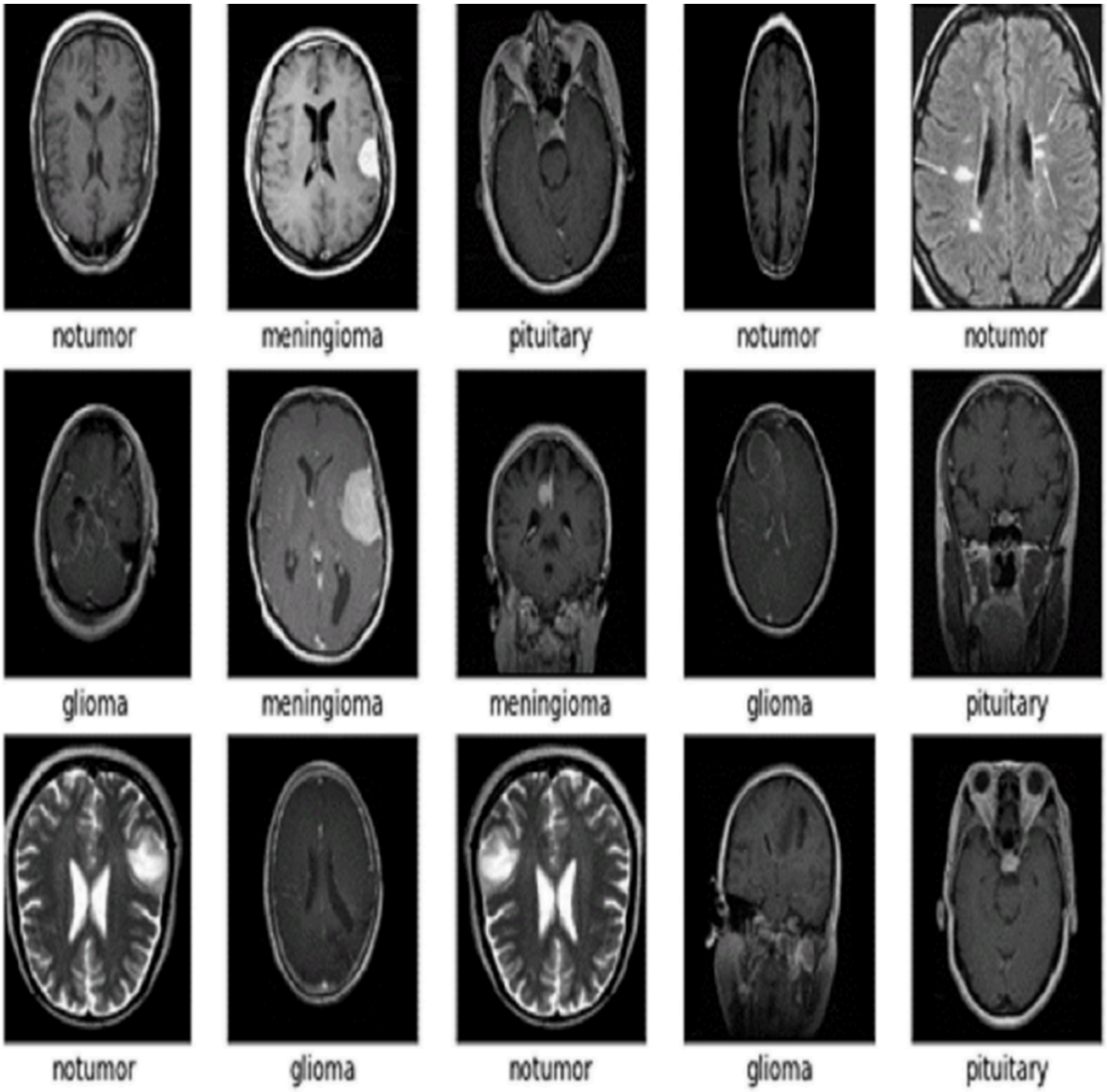

FIGURE 1: Sample images of the tumor dataset

Phases	Glioma	Meningioma	Pituitary	No tumor	Total
Training	240	244	240	324	1,048
Testing	60	62	60	81	263
Total	300	306	300	405	1,311

TABLE 1: Dataset distribution

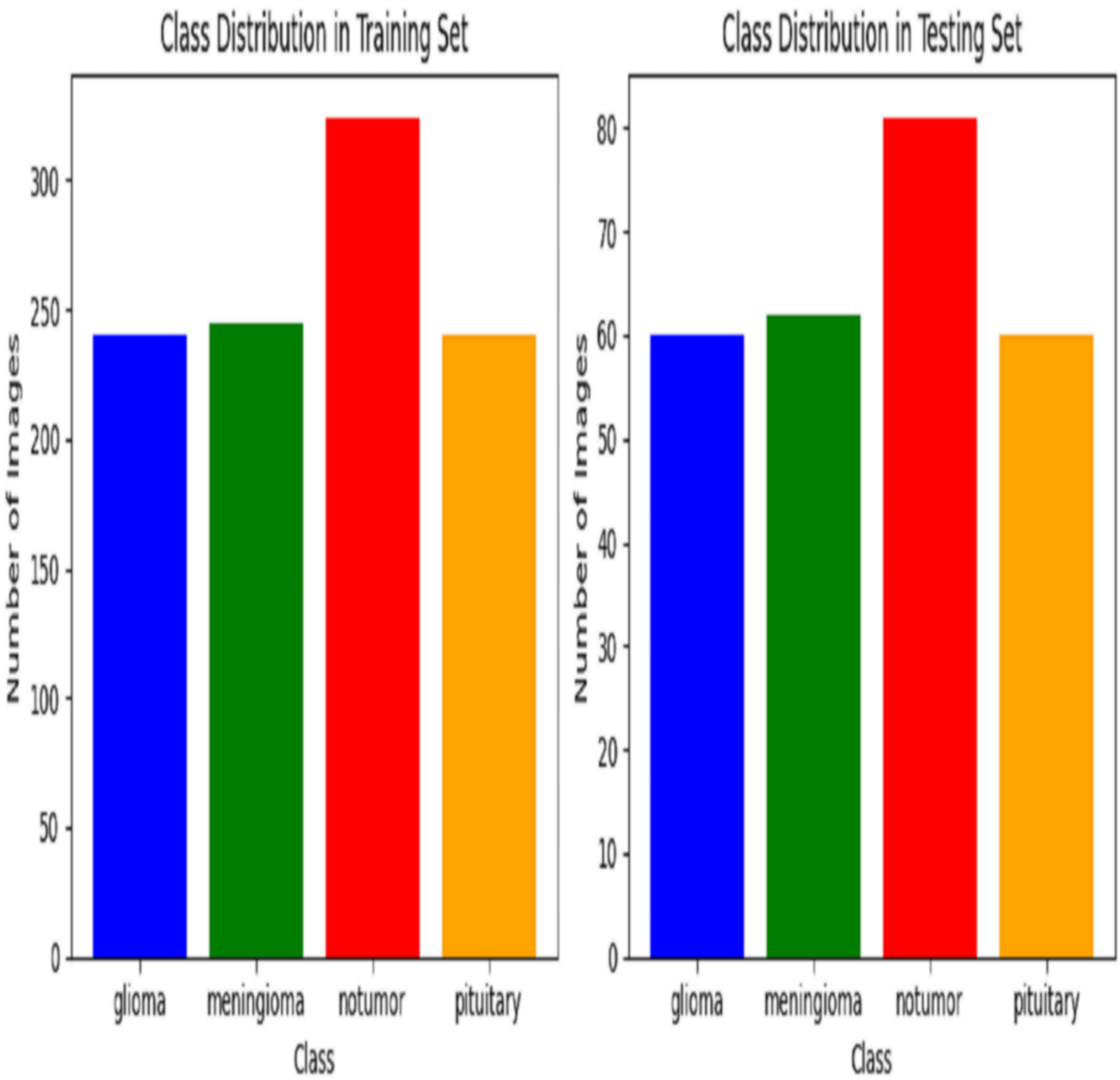

FIGURE 2: Dataset distribution bar plot: training and testing

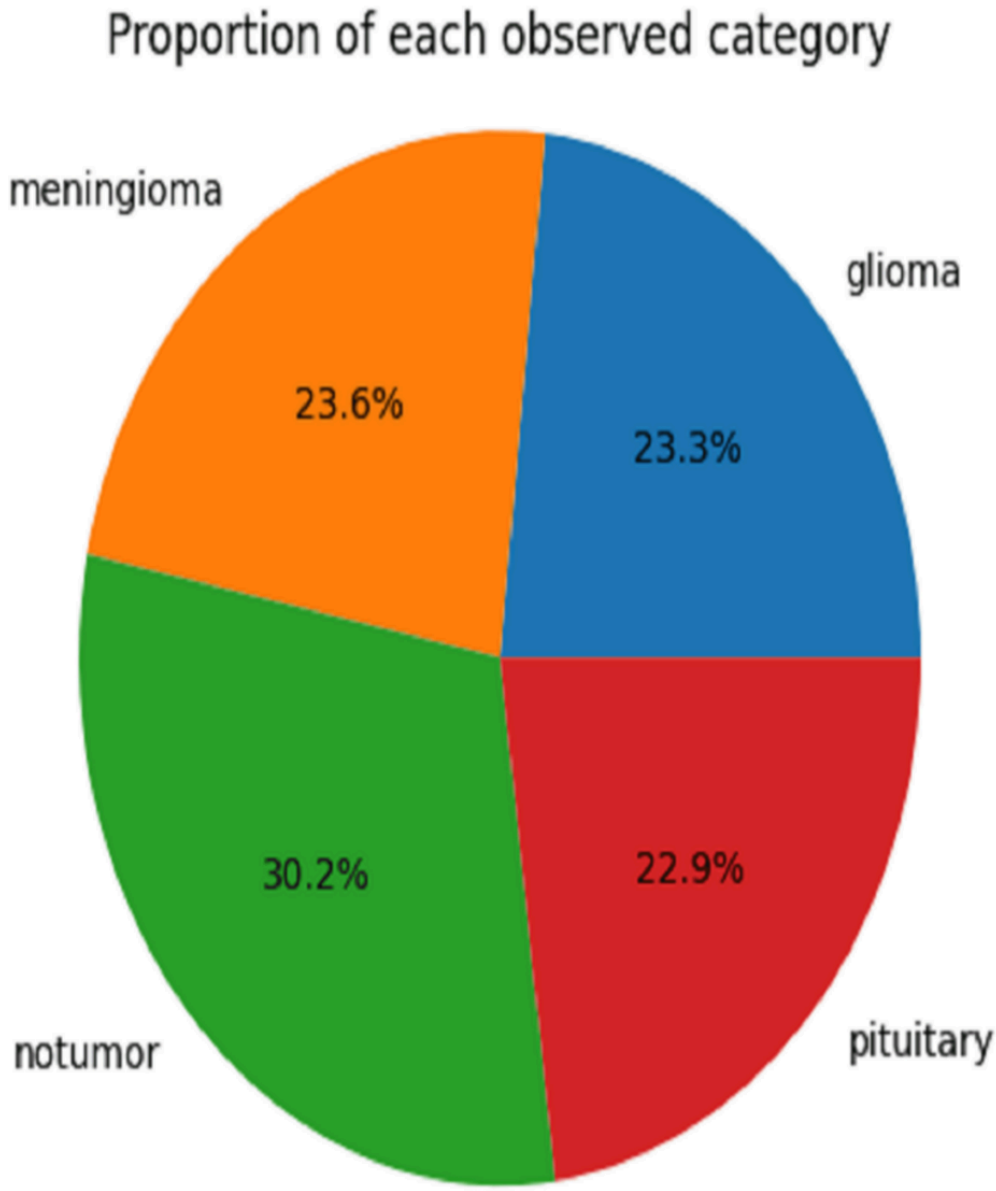

FIGURE 3: The chart for proportion of the tumor category in the dataset

Data exploration, cleaning, and data augmentation

Data Exploration and Data Cleaning

The downloaded dataset must undergo processing before it is ready for use. Preprocessing techniques are essential for data normalization and eliminating redundancy within the dataset. This preprocessing stage involves data conversion, specifically converting the data format .Mat to .jpg, to prepare it for the next stage. The dataset was thoroughly examined for inconsistencies and missing values. Upon exploration, it was discovered that some parts of the dataset contain inconsistent data. One folder, representing one of the four classes, had a higher number of images than the others, which could contribute to lower accuracy. The number of images was adjusted to achieve close equivalency across the classes.

Data Augmentation

Data augmentation is an important method in machine learning, as it improves the generalization capability of training images by dynamically increasing their variations, allowing the model to encounter more diverse examples and make better predictions [11]. In this study, numerous augmentations were applied to the images to represent various orientations of tumors in medical imaging. The specific techniques used depend on the implementation within augmentation tools, such as TensorFlow and Keras' Image Data Generator. These tools apply transformations to the original images, creating multiple variations for each image based on the specified augmentation parameters and settings. The operations performed are presented in Table *2*.

Technique	Applied
Flip mode	Nearest
Rotation	200
Width-shift	0.2
Height-shift-range	0.2
Shear-range	0.2
Zoom-range	0.2
Horizontal-flip	True

TABLE 2: Specified augmentation parameters and setting

Image Resizing

The image is read from a specified file path using cv2.imread(img_path), loading it into a variable named 'image 'as a NumPy array in the BGR (Blue, Green, Red) color space, the default format for OpenCV. Subsequently, the code cv2.cvtColor(image, cv2.COLOR_BGR2RGB) was used for the conversion of the image color from BGR which stands for (Blue Green, and Red) to RGB which also stands for (Red, Green, and Blue). This conversion is vital as many other libraries and tools, like matplotlib and deep learning models, anticipate the images in this converted format (RGB) format. Converting the image to RGB ensures compatibility and prevents color misinterpretation in subsequent processing steps. The images were then resized to a specified dimension using cv2.resize(image, image_size). The cv2.resize (image, image_size) function takes the image and a tuple representing the desired width, height, and 'image_size' as arguments. Resizing is crucial in many applications, particularly in machine learning, where models often require input images to have uniform dimensions. This uniformity simplifies computations and enhances model performance. While resizing, the aspect ratio may or may not be preserved, depending on the values provided in image_size. In our work, the default size of the images used in the input was resized to (224, 224, 3), where the first digits represent the width of the images, the second represents the height and the last represents the number of channels, and this is because the images vary in size.

Data Modelling

There were a total of 1,311 images in the dataset, which were then split into training and testing subsets. Eighty percent of the images (1,048) were used for training, while the remaining 20% (263 images) were used for testing.

Deep learning algorithms

DenseNet201 Model

DenseNet201 is among the types of CNN architecture, known as (Densely Connected Convolutional Networks). It is used in the classification of images. This model has each layer connected to all others in the architecture, promoting feature reuse and ensuring efficient gradient flow. Each layer comprises Batch Normalization (BN), ReLU activation, and a Convolutional layer (Conv). The network also includes 1×1 convolutions as bottleneck layers to reduce the number of input feature maps before applying 3×3 convolutions, enhancing computational efficiency. The transition layers Batch Norm, 1×1 convolution, and 2×2 Average Pooling, were used to decrease the dimension of feature maps. The network's growth rate decides on number of feature maps for every layer added, controlling the complexity of the model. The DenseNet201 architecture begins with initial layers including a 7×7 Convolution with 64 filters, followed by 3×3 Max Pooling. This is followed by four dense blocks, each comprising multiple layers, with transition layers in between. The Global Average Pooling layer was connected to an end of the network for classification [12]. In our proposed fine-tuned DenseNet201 model, the fully connected layer was modified. The initial weights for DenseNet201 were kept constant during training, focusing solely on training the top layer. Additionally, four layers were added. The fine-tuned DenseNet201 model is displayed in Figure *4*.

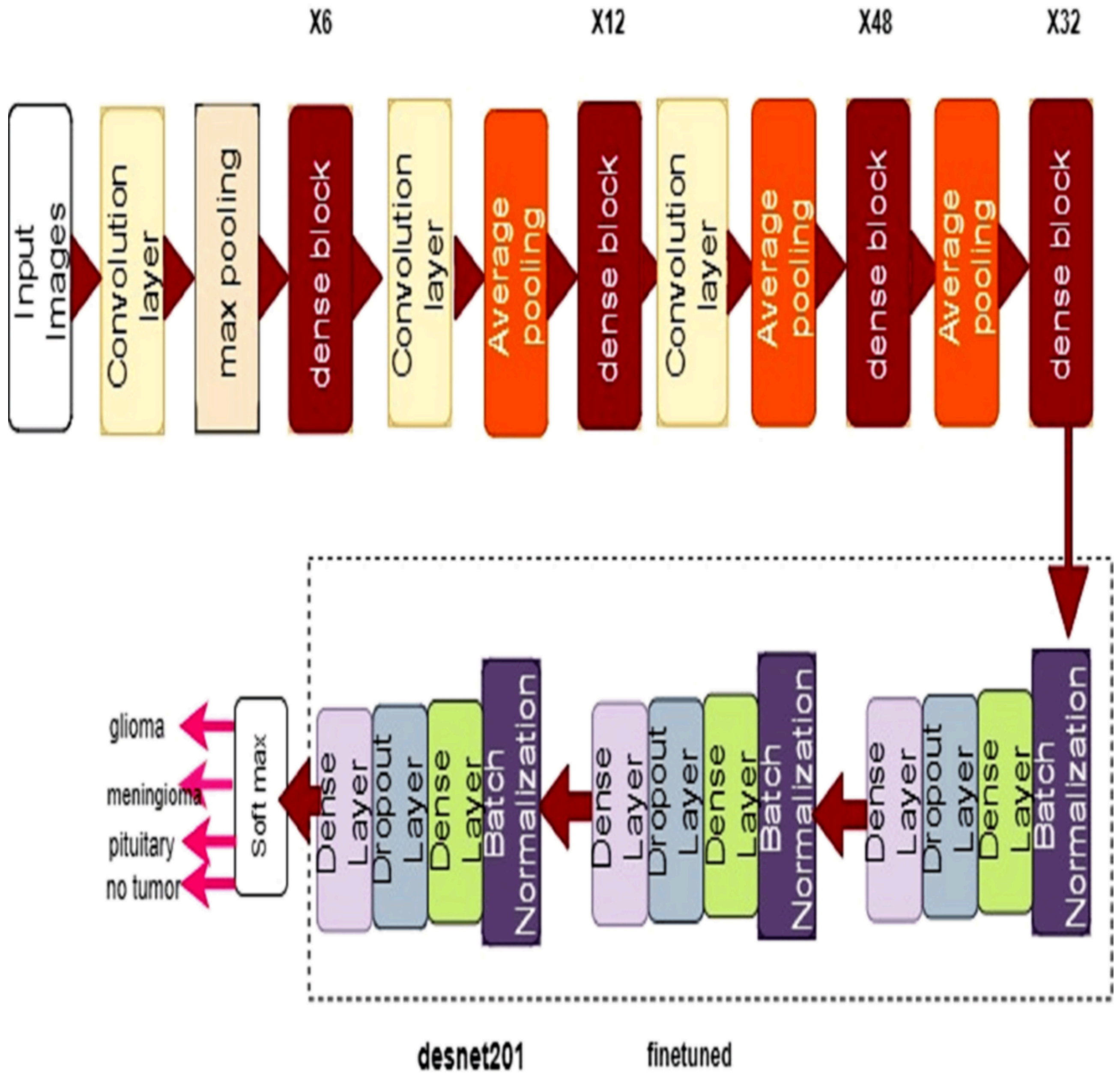

FIGURE 4: Proposed DenseNet201

InceptionV3 Model

InceptionV3 CNN architecture is crafted for image classification and diverse computer vision applications. The model of inceptionV3 integrates modules that apply plentiful CNN filters of varied sizes simultaneously to take various scales. To enhance computational efficiency, InceptionV3 uses factorized convolutions, which replace larger convolutions with smaller, sequential ones. During training, auxiliary classifiers provide additional gradient signals to mitigate the vanishing gradient problem. The architecture also employs stride convolutions instead of pooling for efficient grid size reduction, extensive batch normalization for improved training stability, and label smoothing to prevent overconfidence. InceptionV3 comprises initial convolutional and pooling layers, multiple blocks of Inception modules, and a final classification layer. Trained on large datasets like ImageNet, it achieves exceptional accuracy, and this makes it appropriate and fitted for classifying images, transfer learning and also detecting objects. The initial weights for InceptionV3 were kept constant during training, focusing solely on training the top layer [13]. Additionally, four layers were added. The proposed model for fine-tuned InceptionV3 is displayed in Figure 5.

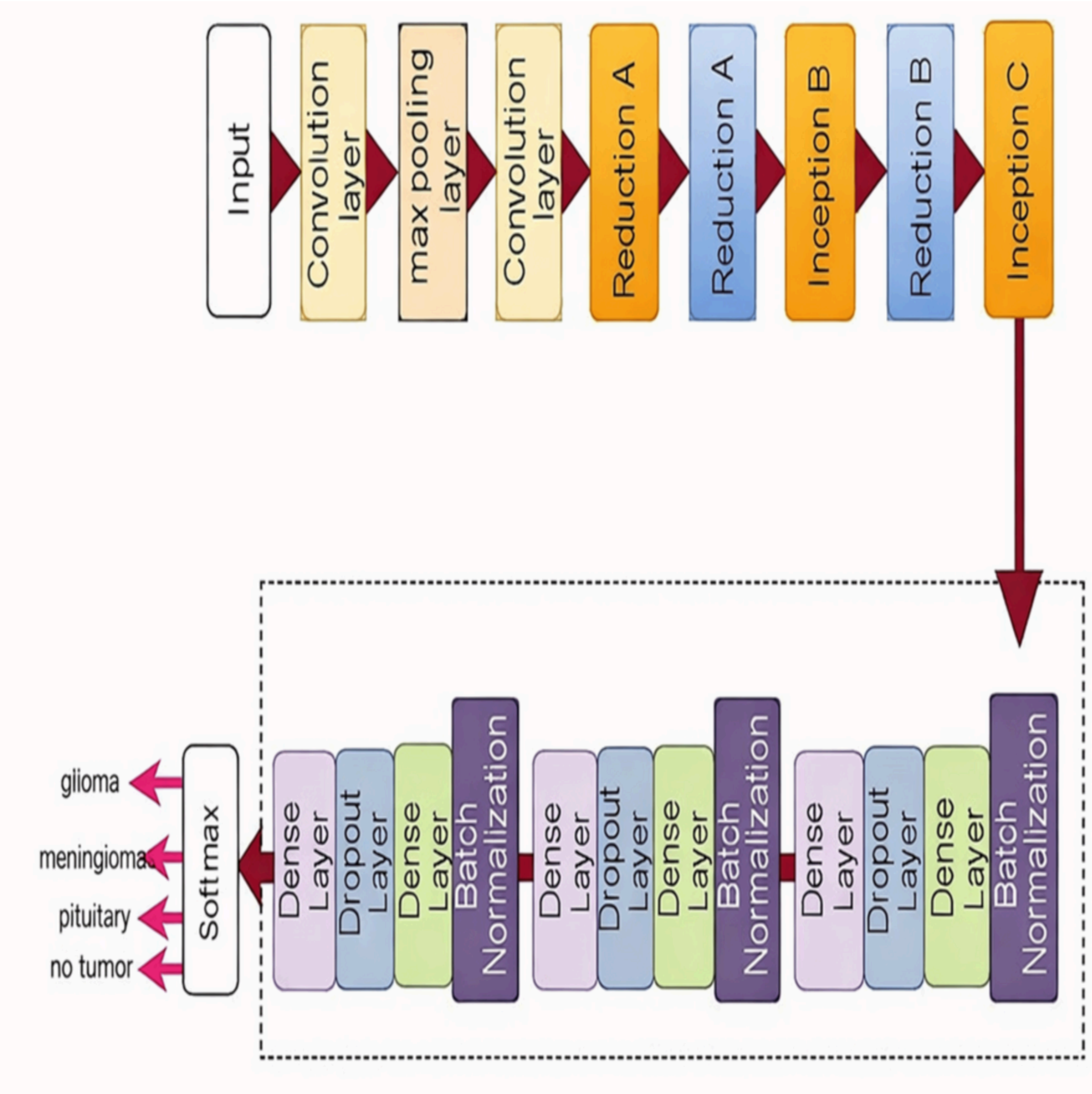

FIGURE 5: Fine-tuned InceptionV3

ResNet-50 Model

This is a CNN model introduced in 2015. It solves the problem that occurs when the loss function becomes very small in backpropagation, which results in the difficulty of the model to learn well. It employs skip connections as an extra connection which enables the model to discover identity functions and minor adjustments by bypassing one or more layers and minor adjustments by bypassing one or more layers. The ResNet-50 architecture begins with an initial 7×7 convolutional layer with 64 filters, followed by multiple stages of residual blocks with a bottleneck design using [1×1, 3×3, 1×1] convolutional layers. The model finishes with a layer called global average pooling and then a fully connected layer that contains 1,000 units [14]. ResNet-50 is well-regarded for its ease of optimization, high accuracy, and strong generalization capabilities, making it widely used for classification of images, segmentation of images as well as detection of objects. The suggested model for fine-tuned ResNet-50 is shown in Figure *6*.

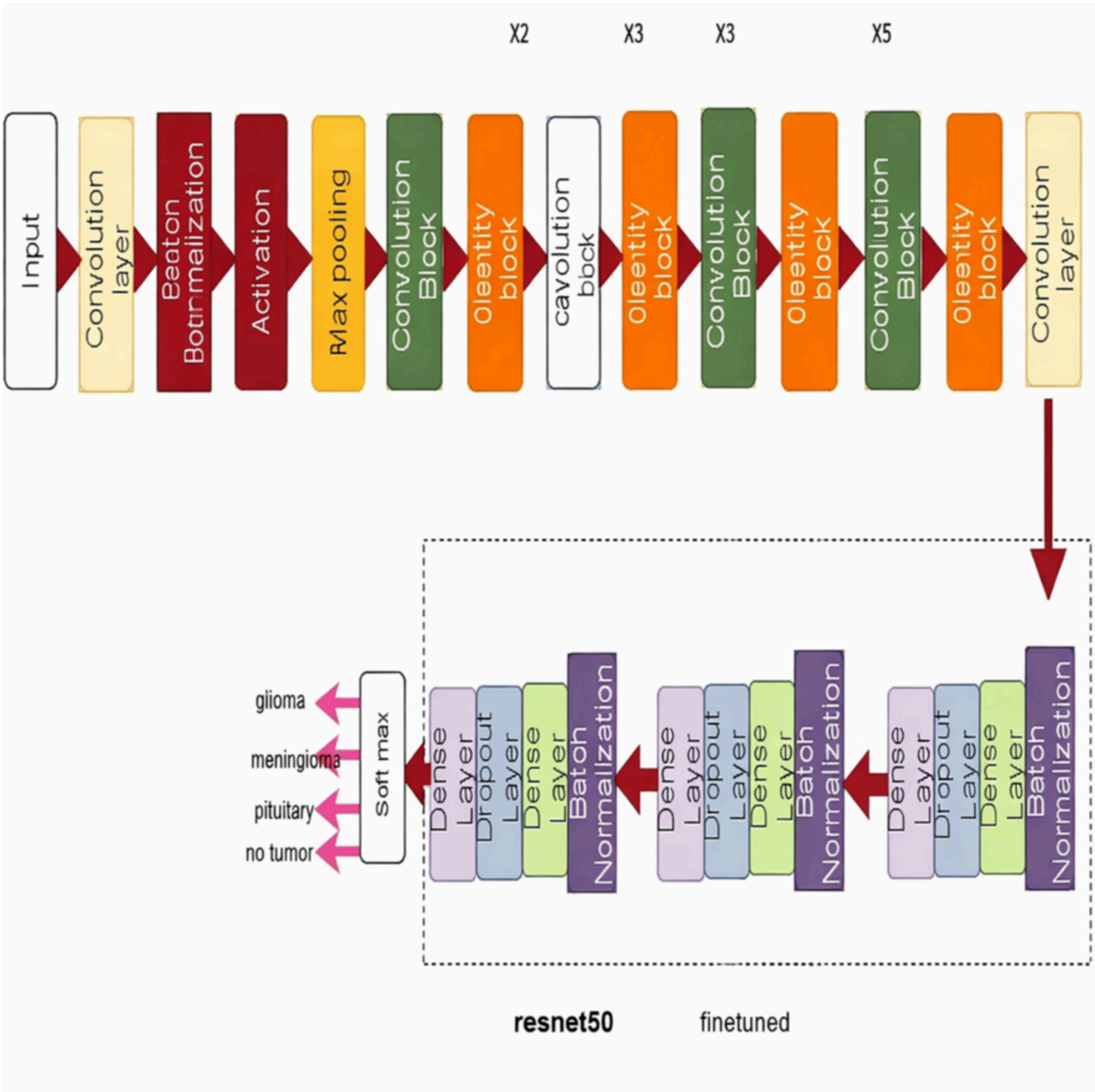

FIGURE 6: Proposed fine-tuned ResNet 50 architecture for brain tumor detection

Proposed ensemble model

The term ensemble refers to a machine learning technique that allows the combination of multiple models to create an improved predictive model. Various ensemble methods are discussed in the literature, but this study employs the weighted average method, commonly used in classification tasks. In this method, several models generate predictions for each data point, and their predictions are combined using weighted averaging. In our research, we implemented a weighted average ensemble model that integrates three pre-trained deep learning models: ResNet50, InceptionV3, and DenseNet201, illustrated in Figure *3*. To adapt these models to our specific objectives, we appended four additional layers to the final layers of each pre-trained architecture. These additional layers consist of a batch normalization layer, dropout, and dense. Also, concerning the final layer, we utilized the SoftMax activation function, which is suitable for categorizing brain MRI tumor images into four distinct classes. The Adam optimizer was employed in the dense layer, with careful adjustment of training parameters such as epochs, batch size, and learning rates. Through comprehensive analysis, we identified a set of parameters that consistently yield superior overall individual performance to generate the final prediction. The proposed model for an ensemble using a weighted average is displayed in Figure *7*.

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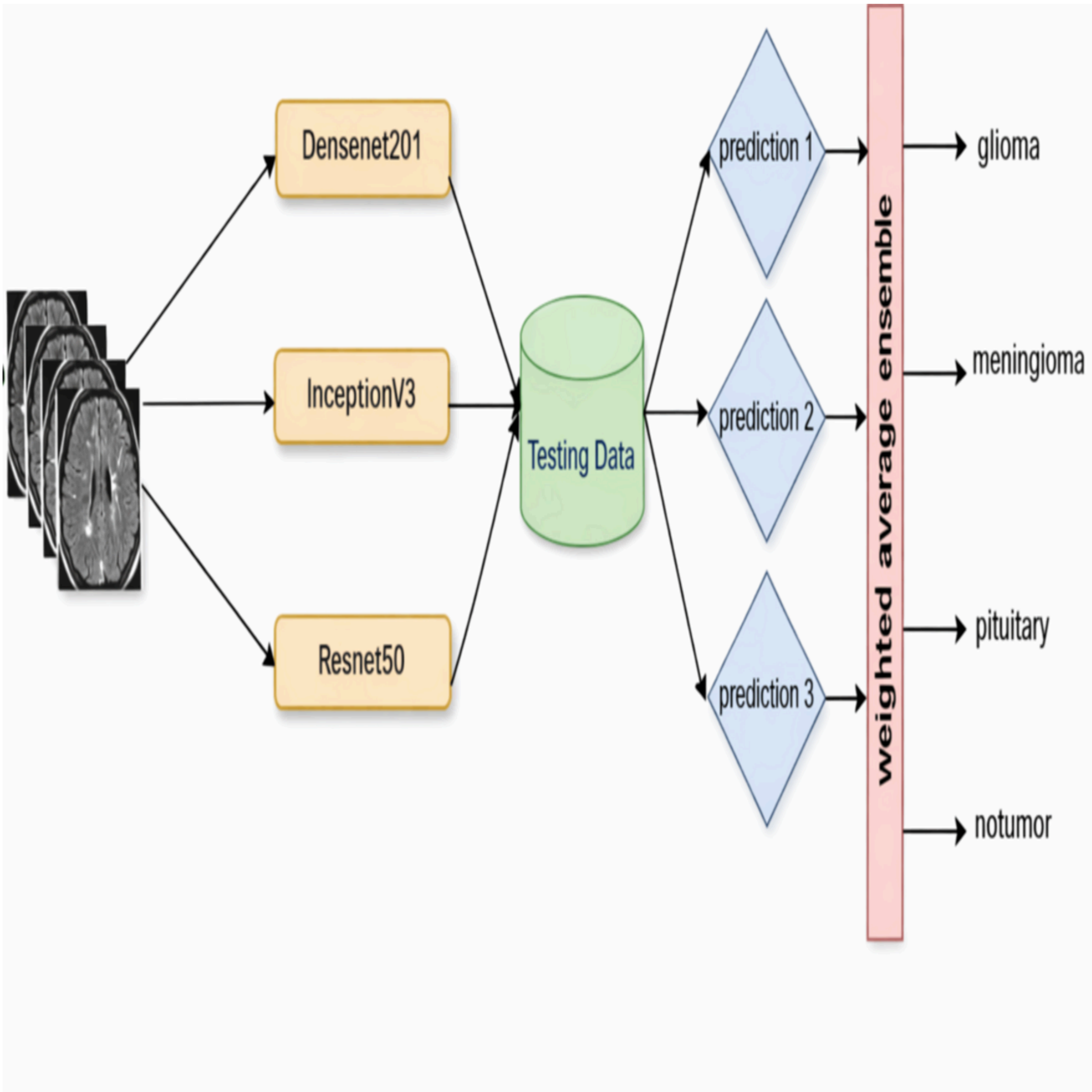

FIGURE 7: Proposed ensemble model using weighted average

Results And Discussion

Experimental environment

This section describes the experiments and outcomes conducted on the free cloud environment Google Colab, which supports Python code execution in a Jupyter notebook interface. Featuring GPU and TPU support, Google Colab is an optimal platform for performing machine learning and data analysis. It also facilitates easy collaboration through notebook sharing. The experiments employed libraries such as Scikit-learn, NumPy, TensorFlow, and Matplotlib.

Model architecture and fine-tuning strategy

In our study, we fine-tuned models by leveraging the pre-trained architecture of the three models used and only replacing fully connected layers. Three new fully connected layers were added, and Dropout and Batch Normalization were applied to these layers. Additionally, a fully connected layer with SoftMax activation function was included.

An ensemble model was also proposed by combining the predictions of the individual base models (ResNet50, InceptionV3, and DenseNet201) using weighted averages with weights of [0.3, 0.4, and 0.3]. The ensemble weights were selected empirically based on validation performance during experimentation. InceptionV3 demonstrated slightly more stable validation behavior during training, and therefore was assigned a marginally higher contribution in the weighted fusion process. The main goal of the proposed model is to enhance the classification of tumor types into three classes, with a fourth class representing cases where no tumor is present.

Training configuration

During model training, we used the Adam optimizer to accelerate training and improve the accuracy of our results. Despite significant memory constraints, the Adam optimizer demonstrated effective performance. We employed a starting learning rate of 0.000001 while utilizing dynamic learning in training the proposed model, and applied ReduceLROnPlateau with the following parameters: factor = 0.3 and patience = 2, to control and adapt the learning rate based on validation loss. To reduce the risk of overfitting, dropout layers, batch normalization, and data augmentation techniques were applied during training. Furthermore, to ensure reliability and obtain the best model, checkpointing techniques were used to monitor validation accuracy, saving the optimal model with the highest accuracy after each epoch. A batch size of 32 and 50 epochs were used for our multi-class classification, and the sparse categorical cross-entropy loss function was employed.

Model evaluation metrics

For evaluation, we measured accuracy, precision, recall, and F1-score using true positive (TP), true negative (TN), false positive (FP), and false negative (FN) values. The primary goal of our model was to detect and analyze brain tumors, classifying the data into glioma tumors, meningioma tumors, pituitary tumors, and no tumors.

1. **Accuracy**: This parameter represents the ratio of correctly classified instances, including both tumor and no-tumor classes, to the total number of instances. While useful, accuracy alone can be misleading, especially in cases of imbalanced datasets.

2. **Precision**: Precision represents the ratio of true positive results to the total number of positive predictions. High precision indicates a low false positive rate in the model.

3. **Recall (Sensitivity)**: Recall evaluates the proportion of true positives detected among all actual positives. High recall ensures that most actual tumors are correctly identified.

4. **F1-Score**: The F1-Score represents arithmetic mean reciprocal, which is called harmonic by name. This parameter is used to stabilize the classes considering the two opposite classes (false positives and false negatives).

5. **Confusion Matrix:** This offers a comprehensive analysis of the four different classes in the confusion matrix. To assess our model's performance, we built a 4 × 4 confusion matrix and calculated the values. This helps to identify images affected by the diseases as well as detecting them.

6. **Specificity:** Specificity measures the ratio of true negatives correctly identified. It indicates the model's ability to detect the absence of disease in images and accurately identify no-tumor cases.

Results and performance analysis

Performance metrics obtained from disease classification are presented in a table. The training dynamics and detailed performance of the individual models are visualized in Figure *8*, which includes (a) training and validation loss curves of the proposed fine-tuned InceptionV3 model, (b) training and validation accuracy curves of InceptionV3, (c) confusion matrix of InceptionV3, (d) training and validation accuracy curves of ResNet50, (e) training and validation loss curves of

ResNet50, (f) confusion matrix of ResNet50, (g) training and validation accuracy curves of DenseNet201, (h) training and validation loss curves of DenseNet201, and (i) confusion matrix of DenseNet201. The ensemble model outperformed the individual models, achieving the best performance with an accuracy of 95.6%. For glioma tumors, which originate from glial cells, it attained a precision of 95%, recall of 97%, and an F1-score of 87%. The no-tumor category achieved a precision of 98%. The pituitary tumor class also performed well, with an F1-score of 96% and a recall of 97%. Meanwhile, DenseNet201, InceptionV3, and ResNet50 also demonstrated robust performance across classes, with accuracies of 88.55%, 89.31%, and 87.79%, respectively. The performance metric scores for the proposed fine-tuned InceptionV3, fine-tuned DenseNet201, and ResNet50 are shown in Table *3*.

	Classes	Precision	Recall	F1-score
InceptionV3 model	Glioma	92	88	90
	Meningioma	80	80	80
	No tumor	100	96	98
	Pituitary	79	88	84
ResNet50 model	Glioma	88	88	88
	Meningioma	78	70	74
	No tumor	100	98	99
	Pituitary	77	88	82
DenseNet201 model	Glioma	75	96	84
	Meningioma	88	66	75
	No tumor	98	94	96
	Pituitary	90	100	95

TABLE 3: The performance metric score for the proposed fine-tuned InceptionV3, fine-tuned DenseNet201, and ResNet50

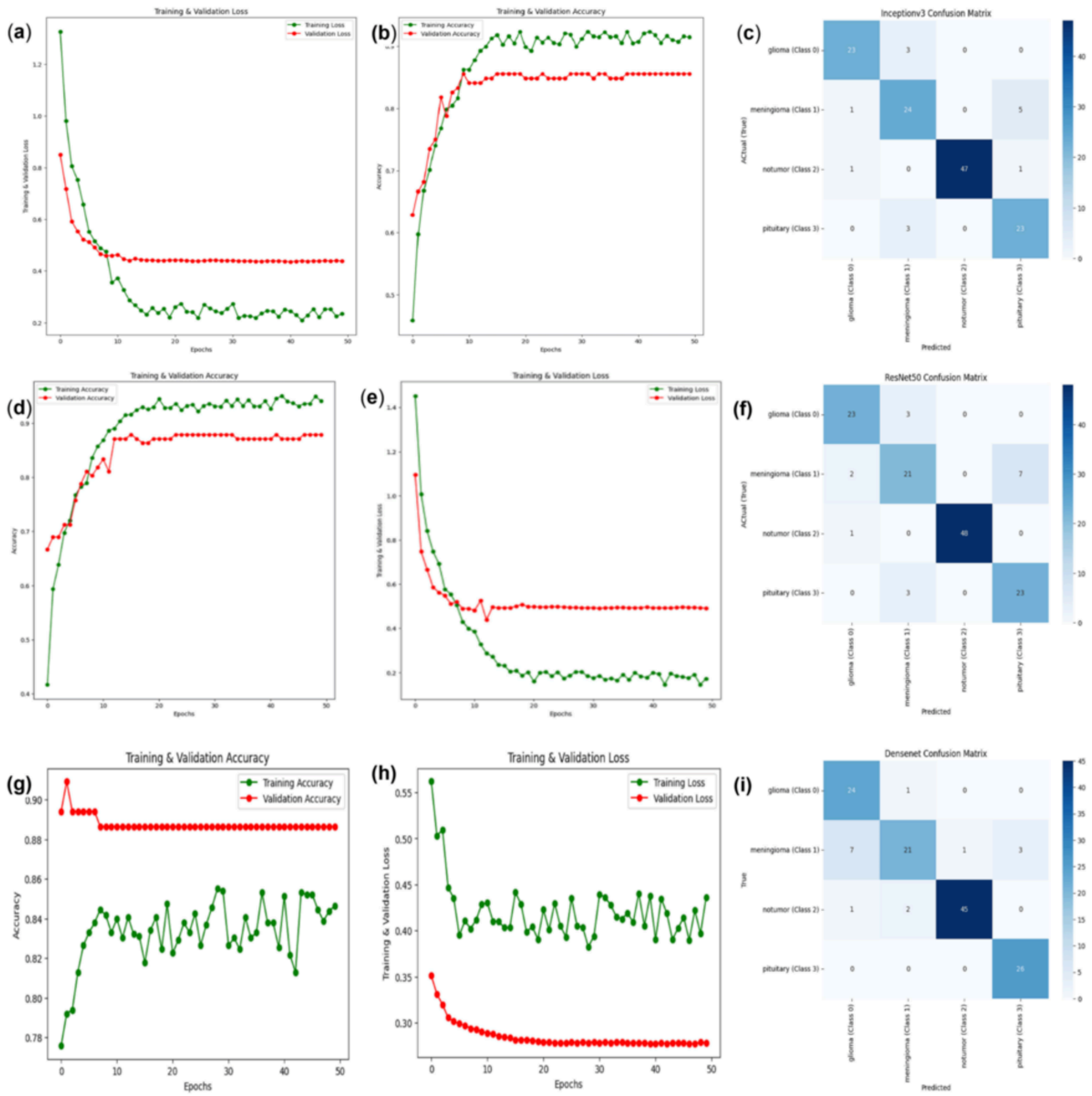

FIGURE 8: (a) Training and validation loss curves of the proposed fine-tuned InceptionV3 model, (b) training and validation accuracy curves of InceptionV3, (c) confusion matrix of InceptionV3, (d) training and validation accuracy curves of ResNet50, (e) training and validation loss curves of ResNet50, (f) confusion matrix of ResNet50, (g) training and validation accuracy curves of DenseNet201, (h) training and validation loss curves of DenseNet201, and (i) confusion matrix of DenseNet201

The performance metrics for each class, based on the proposed ensemble model using weighted averages, are shown in Table *4*.

	Algorithms			
	Classes	Precision	Recall	F1-score
Proposed ensemble model	Glioma	96.00	93.00	94.00
	Meningioma	94.00	90.00	92.00
	No tumor	95.00	97.00	96.00
	Pituitary	95.00	95.00	95.00

TABLE 4: The performance metrics for the weighted average

Table *5* presents the accuracy comparison between the proposed model and the individual models.

Models	Accuracy (%)	F1-score (%)	Precision (%)
Desnet201	88.55	88.24	89.33
Inception-V3	89.31	89.45	89.73
ResNet50	87.79	87.75	87.99
Proposed Ensemble Model	95.60	94.40	94.90

TABLE 5: Comparison of accuracy between individual models and the proposed ensemble model

Figure *9* presents a pictorial representation of the accuracy comparison between the proposed model and the individual models.

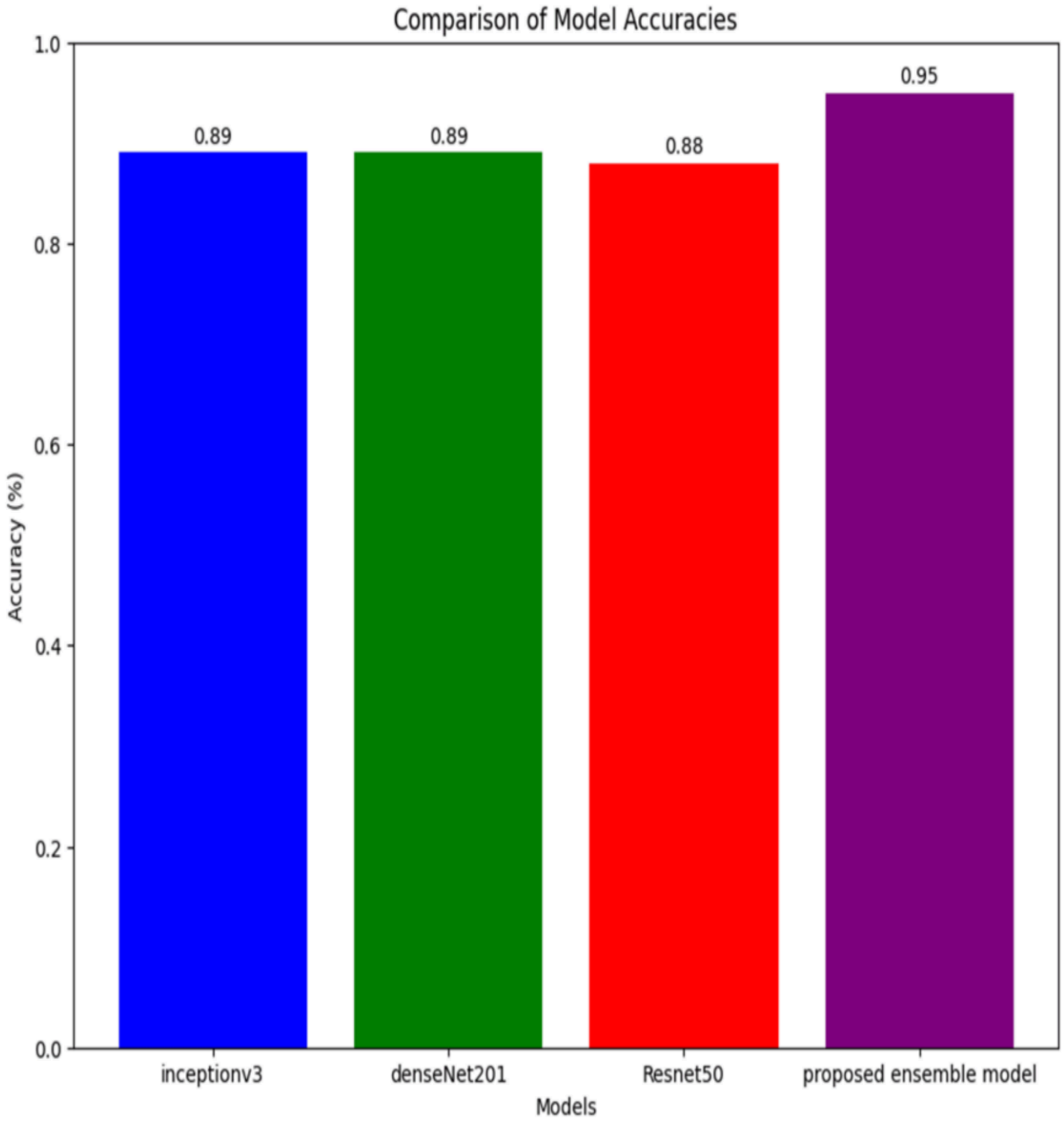

FIGURE 9: Comparison of accuracy between individual models and the proposed ensemble model

Comparison of accuracy between existing individual models and the proposed model is shown in Table *6*.

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Papers	Methodology	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)
[15]	Finetuned Inception-v3	94.34	Not stated	Not stated	Not stated
[16]	Finetuned CNN	94.82	94.2	93.7	93.9
[17]	CNN+VGG	94	XX	XX	85
[18]	Transfer learning	93.3	XX	91.19	XX
This paper	Ensemble through transfer learning	95.60	94.90	94.10	94.60

TABLE 6: Comparison of performance metrics between existing models and the proposed ensemble model

CNN, Convolutional Neural Network; VGG, Visual Geometry Group

Web application implementation

Moreover, after building the model, a web application was developed to test the classification and detection of images with or without tumors. Figure *10* shows a snapshot of the brain tumor application.

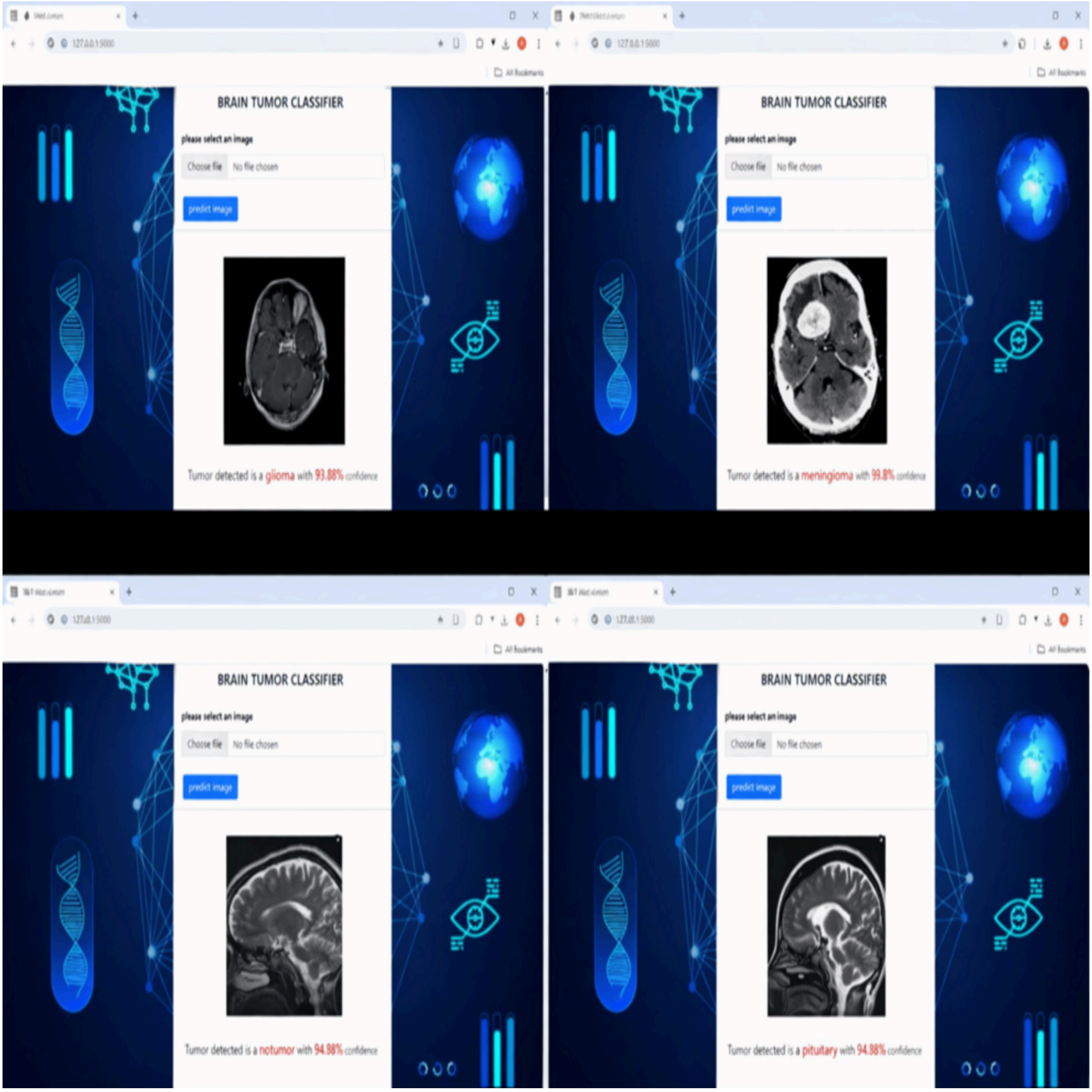

FIGURE 10: Snapshot of a web application showing prediction for the tumor type implemented using the proposed model

Conclusions

Conclusively, this research utilized Google Colab to conduct machine learning experiments focused on classifying brain tumors. It involved fine-tuning pre-trained models by incorporating custom layers, dropout, and batch normalization, culminating in an ensemble model that combined weighted averages. This approach notably enhanced the accuracy of classifying glioma, meningioma, pituitary tumors, and non-tumor cases. Accuracy, precision, specificity, and recall were used to evaluate the model. The ensemble model achieved an overall accuracy of 95.6%, demonstrating improved performance compared with the individual deep learning models. The study highlighted the advantages of ensemble learning and advanced optimization techniques, such as the Adam optimizer and dynamic learning rates, which

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contributed to its superior performance. Checkpointing mechanisms were implemented to ensure reliability by preserving the best-performing configurations. Overall, the research successfully showcased the capability of ensemble models in detecting and categorizing brain tumors, achieving substantial improvements over individual model approaches.

The research encountered several constraints, including reliance on a single dataset of 1,311 MRI images, limited computational power, and challenges with feature interpretability. These factors negatively impacted model accuracy, particularly for smaller or low-resolution images. In addition, the use of deep learning as a black-box approach made it difficult to understand the processes underlying classification decisions. Future research should focus on enhancing the model's generalization by collecting more representative data, applying more sophisticated data augmentation techniques, and incorporating additional data types. Optimization strategies are needed to reduce the computational burden, enabling deployment in resource-limited environments. Exploring explainable AI approaches and conducting clinical trials will help increase trust and adoption of the models. Finally, employing hybrid approaches and performing error diagnostics will be beneficial for improving precision and addressing existing challenges.

Additional Information

Author Contributions

All authors have reviewed the final version to be published and agreed to be accountable for all aspects of the work.

Concept and design: Abdulaziz N. Kani, Sani M. Isah, Swati Sah

Acquisition, analysis, or interpretation of data: Abdulaziz N. Kani, Sani M. Isah, Swati Sah

Drafting of the manuscript: Abdulaziz N. Kani, Sani M. Isah

Critical review of the manuscript for important intellectual content: Abdulaziz N. Kani, Sani M. Isah, Swati Sah

Supervision: Swati Sah

Disclosures

Human subjects: All authors have confirmed that this study did not involve human participants or tissue. **Animal subjects:** All authors have confirmed that this study did not involve animal subjects or tissue. **Conflicts of interest:** In compliance with the ICMJE uniform disclosure form, all authors declare the following: **Payment/services info:** All authors have declared that no financial support was received from any organization for the submitted work. **Financial relationships:** All authors have declared that they have no financial relationships at present or within the previous three years with any organizations that might have an interest in the submitted work. **Other relationships:** All authors have declared that there are no other relationships or activities that could appear to have influenced the submitted work.

Data Availability Statements

The data supporting this study are openly available in Kaggle at https://www.kaggle.com/datasets/shreyag1103/brainmri-scans-for-brain-tumor-classification.

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