APPLICATION OF DEEP LEARNING IN BRAIN TUMOR DETECTION AND CLASSIFICATION

1. INTRODUCTION

The brain is known as the world's most complex structure (Dolan, 2007), with over 86 billion nerve cells (Azevedo et al., 2009). Each of these cells, on average, forms connections with thousands of other neurons, culminating in an astounding 100 trillion connections (Caruso, 2023). A brain tumour is an abnormal growth of cells either in the brain or adjacent areas such as nerves, the pituitary and pineal glands, and the surrounding membranes (NHS, 2023). These tumours can originate in the brain, termed primary brain tumours, or spread from other parts of the body, known as metastatic or secondary brain tumours. There are various types of primary brain tumours; some are noncancerous (benign) and might grow slowly on the brain tissue. Conversely, malignant brain tumours or brain cancers grow rapidly, damaging the surrounding tissue. Tumour size can vary, with some detected early due to immediate symptoms and others growing significantly before discovery, especially if located in a less active brain region (Mayo Clinic, 2023).

Every year, approximately 250,000 people globally are diagnosed with primary brain tumours, which represent fewer than 2% of all cancer types (Wikipedia, 2023). In the United Kingdom, new cases of brain tumours each year (2016 - 2018) are 12,288 on average, and 5,456 deaths were recorded every year from 2017 to 2019 (Cancer Research UK, 2023). Diagnosing a brain tumour usually begins with Magnetic Resonance Imaging (MRI). Once MRI shows that there is a tumour in the brain, the most common way to determine the type of malignancy is to look at the result from a sample of tissue called biopsy – an invasive measure (Hoffman, 2023), this can be challenging and time-consuming considering the shortage of neurosurgeons and abnormalities in the sizes and locations of the brain cancer.

Deep learning (DL) model is an aspect of Artificial Intelligence that can recognize complex patterns in pictures, text, sounds, and other data to produce accurate insights and predictions (Amazon Web Services, 2023). Recently, Deep Learning (DL) techniques have gained traction in creating automated systems that can swiftly and accurately diagnose or segment brain cancers. DL harnesses the power of pre-trained and Convolutional Neural Networks (CNN) to classify medical images, particularly those related to brain cancer (ZainEldin et al., 2022). Computational Intelligence and Deep Learning models can help in the detection and classification of brain tumours in the early stages without invasive measures.

The main research questions of this project are:

a. How do various CNN architectures, from simpler 2D models to more advanced ones compare in terms of accuracy and efficiency in brain tumour detection and classification?

b. How do hyperparameter tuning and data augmentation techniques impact the performance of CNN models in detecting and classifying brain tumours?

c. How does the integration of transfer learning with pre-trained models like Inception V3 and EfficientNet B0 influence the model's precision and computational efficiency in brain tumour diagnosis?

By answering these research questions, this project will contribute to the broader body of research that seeks to leverage AI for better healthcare outcomes, ultimately aiding in the quick and accurate diagnosis of life-threatening conditions like brain tumours.

1.1 AIM

This project aims to improve the accuracy and efficiency of brain tumour detection and classification using various Deep Learning models and architectures.

1.2 OBJECTIVES

a. Compare the optimized baseline model's performance with that of pre-trained models such to evaluate the advantages and shortcomings of each.

b. Assess the performance of each model in terms of the percentage of accuracy, the number and impact of hyperparameters employed, reduction of validation loss, and other relevant metrics, ensuring a comprehensive understanding of each model's strengths and areas for improvement.

c. Visualise the learning patterns and progress of each model during its training and validation phase.

2. LITERATURE REVIEW: BACKGROUND AND RELATED WORKS

In recent times, there have been a plethora of studies which take advantage of deep learning convolutional neural networks (CNNs), aided by pre-trained models, for brain tumour detection through MRI imaging. Srinivas et al. (2022) conducted a thorough evaluation of three CNNs - VGG-16, Inception-V3, and ResNet50 - to distinguish between benign and malignant brain tumours. Notably, VGG-16 emerged as the best model in both the training

and validation stages. While the Inception-V3 model showed unstable validation accuracies, ResNet50 had misclassification issues, particularly in detecting false negatives. The study emphasized the potential of transfer learning with these architectures but was limited to just these three models, even though it did hint at the potential of expanding to others like VGG-19 and MobileNet.This project will take a similar approach but with variations. This will start with analysing with a different dataset of 4 classes - glioma, meningioma, pituitary and no tumour, then a simpler 2D CNN as a baseline, with further enhancing it with hyperparameter tuning and data augmentation. While the aforementioned research hinted at other architectures, this project will be diving deeper by additionally exploring models like EfficientNet B2.

Solanki et al. (2021) utilized both traditional machine learning approaches and deep learning with Convolutional Neural Networks (CNNs). Their experimental setup tested various configurations of CNNs, ranging from 5 to 7 layers, and among traditional classifiers, the SVM was highlighted for its efficacy. This study achieved an impressive 97.86% accuracy using a 5-layer CNN with a learning rate of 0.001 over 10 epochs on an 80:20 data split. Although their findings are insightful, the emphasis on accuracy without broader considerations may pose generalization concerns for real-world applications. While this existing research has showcased powerful methodologies, this project aims for clarity and simplicity, starting with a 2D CNN model as a foundational baseline. This approach ensures a clearer grasp and sets initial accuracy benchmarks. Additionally, hyperparameter adjustments and data augmentations was undertaken, targeting optimized model outcomes. Furthermore, the use of transfer learning not only resonates with current industry practices but also improves a model performance.

ZainEldin et al. (2022) focused on detecting and classifying brain cancers using an optimized Convolutional Neural Network (CNN) model called BCM-CNN. This model was particularly notable for its utilization of the BRaTS 2021 Task 1 Dataset, a repository of clinically acquired multi-parametric MRI images of gliomas, and for its remarkable accuracy of 99.99%. This was achieved by leveraging a unique optimization technique involving the adaptive dynamic sine-cosine fitness grey wolf optimizer (ADSCFGWO) algorithm. Additionally, the study introduced a 3D U-net segmentation model for finer tumour detection, showcasing a validation accuracy of up to 99.33%. Despite its innovative approach and impressive accuracy rates, the BCM-CNN model bears computational limitations due to its inherent complexity. The mentioned research and this study are only connected with a shared aim – to detect and classify brain cancer as this project employs an alternative methodology. The distinction between the two works lies in the choice of models, the optimization techniques, and the explicit exploration of pretrained models with transfer learning.

Furthermore, Hamid et al. (2022) researched on automating the diagnosis of brain tumours using 253 pre-processed MRI images belonging to two classes. Machine learning techniques struggled due to the variability in tumour sizes, shapes, and regions. Deep learning, particularly when used in combination with specific classifiers, proved superior in their

findings. Hybrid models, incorporating architectures such as CNN, GoogleNet/VolumeNet/AlexNet, and NADE, were touted as potential avenues to overcome these challenges. This study used 3264 pre-processed MRI images belonging to four classes to predict and classify brain tumours. While Hamid et al. (2022) highlighted the potential of deep learning hybrids, our methodology extends this by beginning with a simple baseline model and incrementally integrating hyperparameter tuning and more advanced models.

Santos and Santos (2022) applied an Artificial Neural Network (ANN) for brain tumor detection, classifying images into 'No Tumor' and 'Tumor'. A training accuracy of 91.72% and a validation accuracy of 89.24% was achieved. Their results, combined with a precision and recall of approximately 89.2%, showcase the potential of deep learning in this domain. Although the goal is to detect brain tumor, this study employs a more extensive approach to detect as well as classify the type of tumor. The data is categorized into 'glioma_tumor', 'meningioma_tumor', 'no_tumor', and 'pituitary_tumor'. Different models will be used for adequate comparison in achieving optimal performance.

3. METHODOLOGY

3.1 Data Acquisition and Preprocessing:

This research journey began with a well-organized dataset, categorized into distinct training and testing directories. The data were loaded ensured they were had a consistent dimension of, which is 150x150 pixels. Once loaded, the images were systematically stored in specific arrays, X_train for images and y_train for corresponding labels. Leveraging the Min-Max Scaler, I normalized all image pixel intensities, ensuring they fell within the 0 to 1 range, promoting faster convergence during model training (Han, Kamber and Pei, 2012b). To further prep the data, we converted human-readable string labels into numerical labels through label encoding, followed by a one-hot encoding transformation. Importantly, all images were also converted to numpy arrays to ensure compatibility with our deep learning frameworks as well as efficient computational capacity (GeeksforGeeks, 2020).

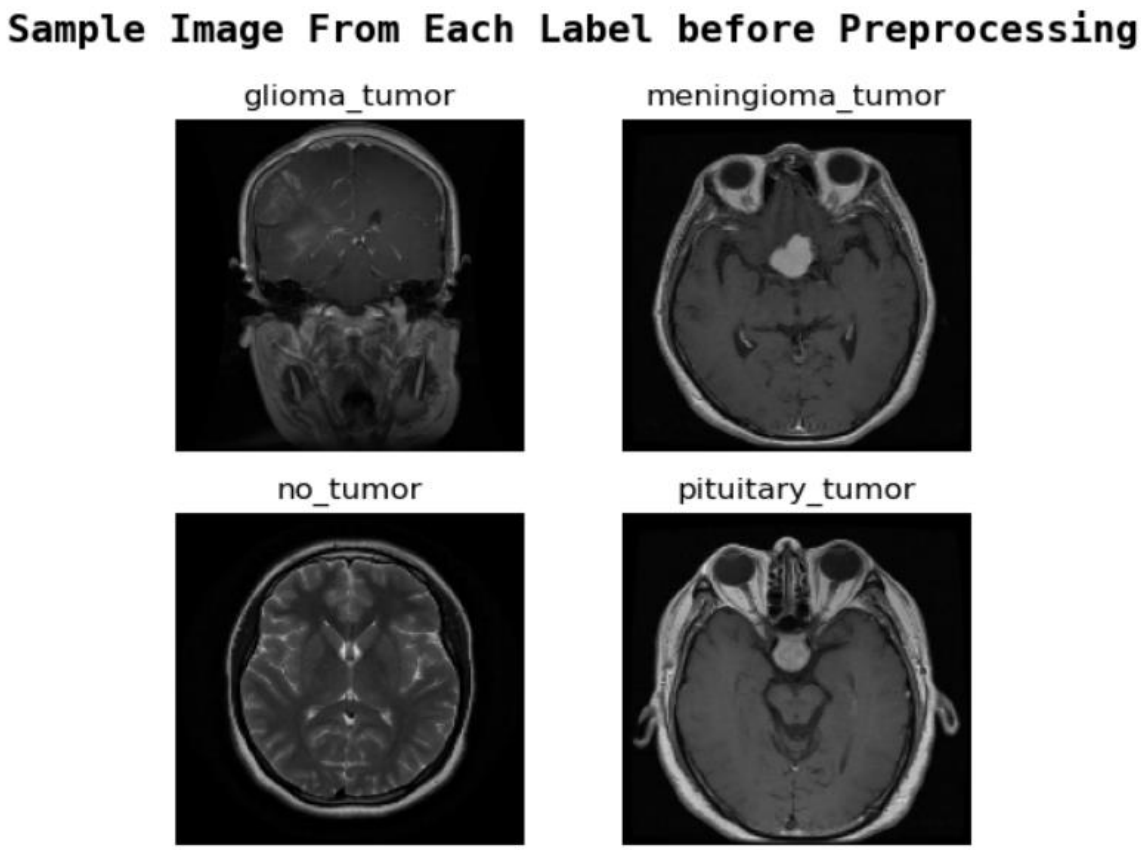

Figure 2: Sample Image From Of Classes After Augmentation And Preprocessing

3.2 Baseline 2D Convolutional Neural Network:

The data modeling was initiated with a baseline 2D CNN architecture. This model comprises three convolutional layers, each being succeeded by a max-pooling layer. Post-convolution operations, the data stream passes through dense layers, culminating in a softmax activation tailored for our multi-class classification task. The model's architecture was solidified by leveraging the Adam optimizer, characterized by a predefined learning rate of 0.01. The categorical_crossentropy was set as the loss function, given the multi-class nature of the problem.

3.3 Enhanced Model Refinements:

Acknowledging the potential limitations of the initial dataset's size, the dataset was enriched in the training phase with data augmentation techniques after the baseline model, to compare the performance. This expansion encompassed strategies such as rotations, shifts, zooms, and flips. With the augmented data in place, I proceeded to explore the model by hyperparameter tuning. For example, the first model not only expanded the baseline but also integrated L2 regularization, dropout, and batch normalization, serving as countermeasures against overfitting. The second model iteration took complexity a notch higher by introducing an

additional convolutional layer and a dense layer, aiming to harness deeper patterns within our dataset etc.

SAMPLE IMAGE FROM OF CLASSES AFTER AUGMENTATION AND PREPROCESSING

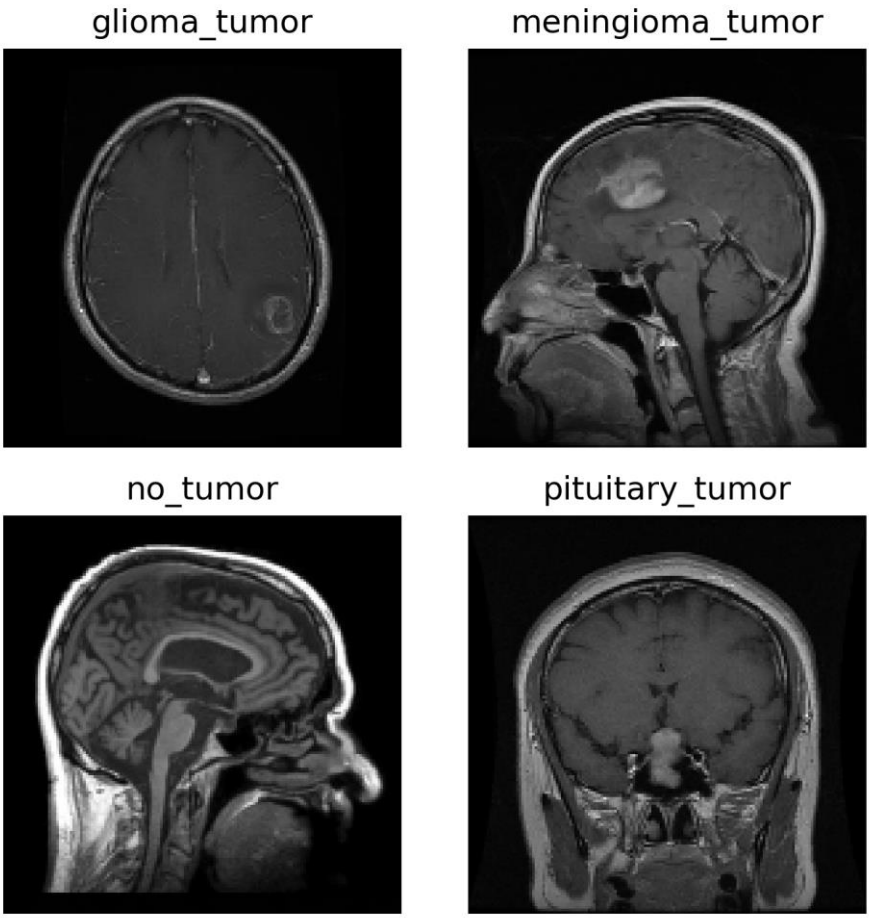

Figure 2: Sample Image From Of Classes After Augmentation And Preprocessing

3.4 Transfer Learning Integration:

In our pursuit of excellence, we embraced the power of transfer learning by integrating pre-trained architectures, namely VGG16 and ResNet50, InceptionV3, VGG19 and EfficientNetB2. All were originally trained on the vast ImageNet dataset. These models underwent fine-tuning to align with the specific classification task. Recognizing the nuances of transfer learning, we adopted a reduced learning rate to prevent drastic weight updates. Concurrently, batch normalization was integrated to ensure consistent and faster training, capitalizing on the generic features learned from ImageNet and the specific patterns present in our dataset.

3.5 Model Evaluation and Preservation:

Upon concluding our iterative training phases, the models were evaluated. The metrics of interest includes accuracy and loss, both of which were observed for training and validation datasets. To delve deeper into model performance, confusion matrix was employed, offering granular insights into the model's performance across different tumour types.

4. CHOICE OF OPTIMIZER AND MODELS

The **Adam optimizer** is frequently employed in image detection and classification as it adeptly blends features of Momentum (SGD) and RMSProp, offering adaptive learning rates for each parameter, and its robust design caters to non-stationary objectives, minimal memory overhead, and reduced hyperparameter sensitivity, thereby ensuring efficient and empirically successful results in deep learning contexts (Chandrashekar and N, 2021), (Jason Brownlee, 2017).

VGG16 & VGG19: Renowned for their simplicity and depth, VGG architectures are proficient at capturing hierarchical patterns in images, making them apt for intricate tasks like brain tumor detection (Mascarenhas and Agarwal, 2021).

ResNet50: With its residual connections, ResNet50 tackles the vanishing gradient issue, enabling the training of deeper networks, and thus, capturing complex features pertinent to brain tumors (Mascarenhas and Agarwal, 2021).

InceptionV3: Its multi-scale convolutional approach permits the model to capture spatial hierarchies at different scales, beneficial for detecting varied tumour shapes and sizes (Irla, 2019).

EfficientNetB2: Designed through compound scaling (scaling depth, width, and resolution), EfficientNetB0 offers a balance between computational efficiency and accuracy, making it suitable for comprehensive tumour characterization while ensuring optimal resource utilization (Computer Vision Project, n.d.).

4.0 EXPERIMENT

The research involved analyzing a dataset sourced from Kaggle, consisting of 3,264 brain MRI images. These images, sized at 150x150 pixels with three color channels, were categorized into four different brain tumor classes: glioma, meningioma, no tumor, and pituitary. Before delving into model architecture, the dataset underwent preprocessing as elaborated in the research methodology.

For the experimental framework, a total of eight different Convolutional Neural Network (CNN) models were constructed. The first was a 2D baseline model, a rudimentary CNN configuration with three convolutional layers, supplemented with max-pooling and fully connected layers. It employed a learning rate of 0.01, optimized by Adam. Following this, seven tuned models were established, each varying in hyperparameters like dropout rate, learning rate, batch size, convolutional layers, and epoch count. Most of these models incorporated elements like dropout regularization of 0.5, batch normalization, and different configurations of convolutional blocks.

An essential step in the experiment was model compilation, where the Adam optimizer, with its varying learning rates, was employed consistently across models due to its optimal performance. Categorical cross-entropy acted as the loss function, with accuracy being the primary evaluation metric. These models were then trained on 80% of the dataset, with the remaining 20% reserved for testing. Techniques like early stopping, with a patience ranging between 5 to 10 epochs, were applied to avert overfitting.

To ensure optimal performance, hyperparameter tuning was conducted on factors like learning rate and dropout rate for the baseline model, using cross-validation. A variety of optimizers were tested along with epochs. The addition of batch normalization and L2 regularization didn't necessarily augment model performance but did aid in mitigating overfitting.

Further enhancing the experimental breadth, transfer learning was executed utilizing pre-established models like ResNet50, VGG19, InceptionV3, and EfficientNetB2. These models were fine-tuned on the dataset, with custom dense layers affixed atop the pre-trained structures. Simultaneously, data augmentation techniques were employed.

To gauge the efficacy of the models, accuracy was the chosen primary metric. For a comprehensive performance overview, confusion matrices were formulated for each model and subsequently visualized as heatmaps. In addition, classification reports detailing precision, recall, F1-score, and support were produced. The initially constructed models (from the Baseline to Tuned Model 7) set the performance benchmark, which was then challenged by the

models fortified through transfer learning using renowned architectures like ResNet50 and VGG19.

5.0 RESULT

All the trained model and their performance.

MODELS	TRAIN ACCURACY	TRAIN LOSS	VALIDATION ACCURACY	VALIDATION LOSS	ACCURACY
SIMPLE 2D CNN BASELINE MODEL	0.71	0.63	0.72	0.73	0.72
AUGMENTED AND CNN MODEL1	0.76	0.85	0.68	1.37	0.68
AUGMENTED AND CNN MODEL2	0.82	0.8	0.64	1.75	0.64
AUGMENTED AND CNN MODEL3	0.68	0.75	0.74	0.64	0.74
AUGMENTED AND CNN MODEL4	0.87	0.36	0.89	0.33	0.89
AUGMENTED AND CNN MODEL5	0.87	0.33	0.88	0.34	0.88
AUGMENTED AND CNN MODEL6	0.92	0.21	0.92	0.21	0.92
AUGMENTED AND CNN MODEL7	0.86	0.36	0.89	0.3	0.89
TRANSFER LEARNING					
EFFICIENTNET B2	0.99	0.02	0.95	0.12	0.95
VGG16	0.8	0.52	0.85	0.42	0.85
VGG19	0.81	0.43	0.91	0.23	0.91
RESNET50	0.67	0.79	0.72	0.73	0.73
INCEPTION V3	0.81	0.49	0.84	0.47	0.82
VGG16 OPTIMISED	0.86	0.36	0.89	0.31	0.89

Figure 3. Table of model performances

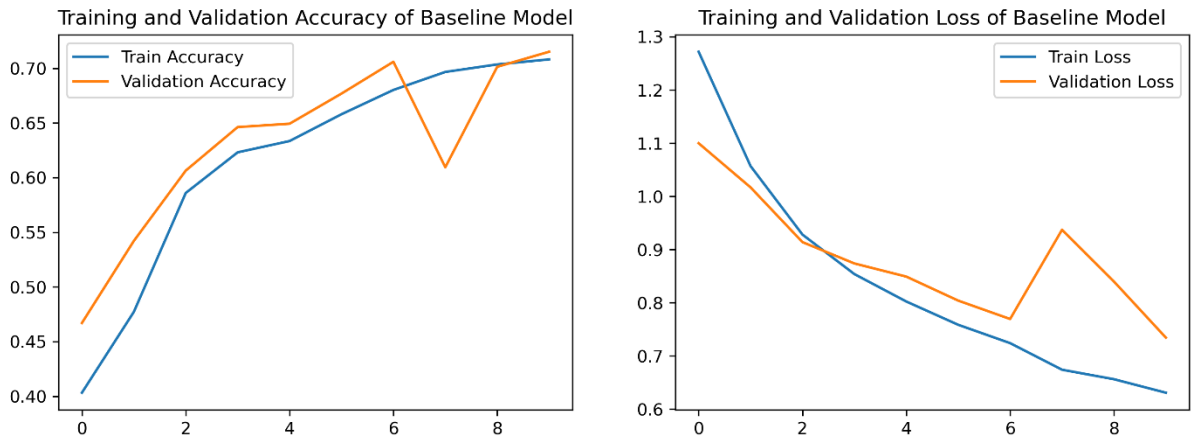

Figure 4. Baseline model Training and validation loss and accuracy

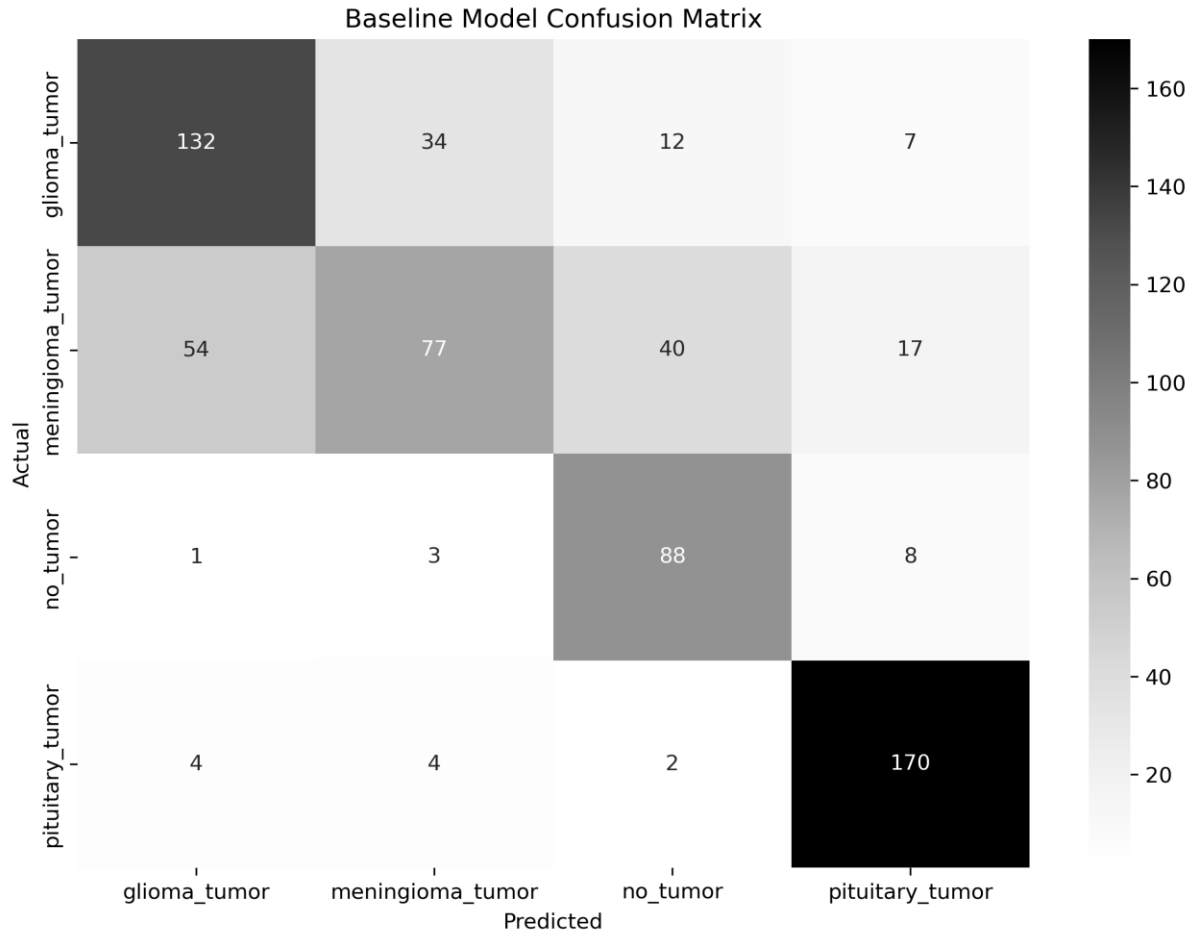

Figure 5. Baseline model Confusion Matrix

	precision	recall	f1-score	support
glioma_tumor	0.69	0.71	0.70	185
meningioma_tumor	0.65	0.41	0.50	188
no_tumor	0.62	0.88	0.73	100
pituitary_tumor	0.84	0.94	0.89	180
accuracy			0.72	653
macro avg	0.70	0.74	0.71	653
weighted avg	0.71	0.72	0.70	653

Figure 6. Baseline model Classification Report

The baseline model reported an overall accuracy of 72% on a test set of 653 samples. Specific performance for each tumor type is: glioma at 70% F1-score, meningioma at 50%, no tumor at 73%, and pituitary at 89%. The weighted average F1-score across all classes is 70%. The model overfitted at some point.

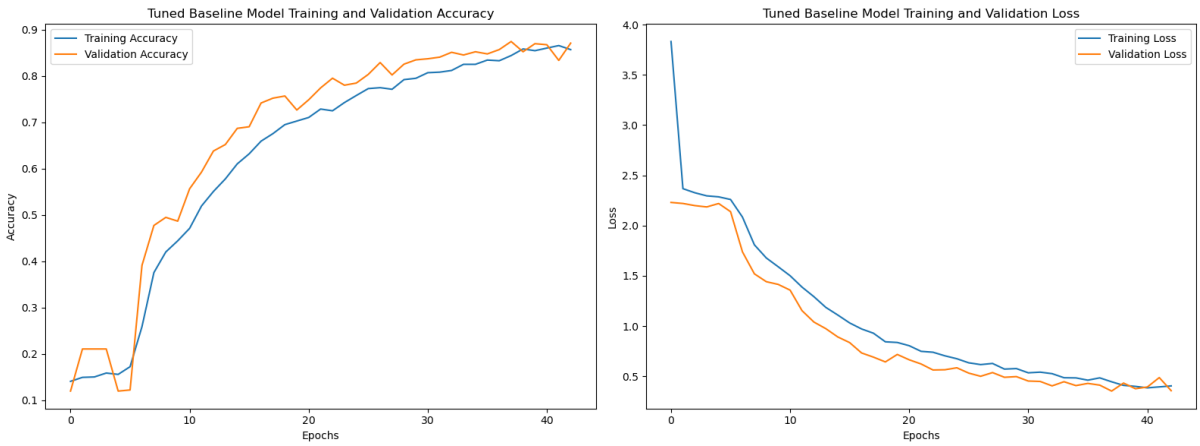

Figure 7. Tuned model 1Training and validation loss and accuracy

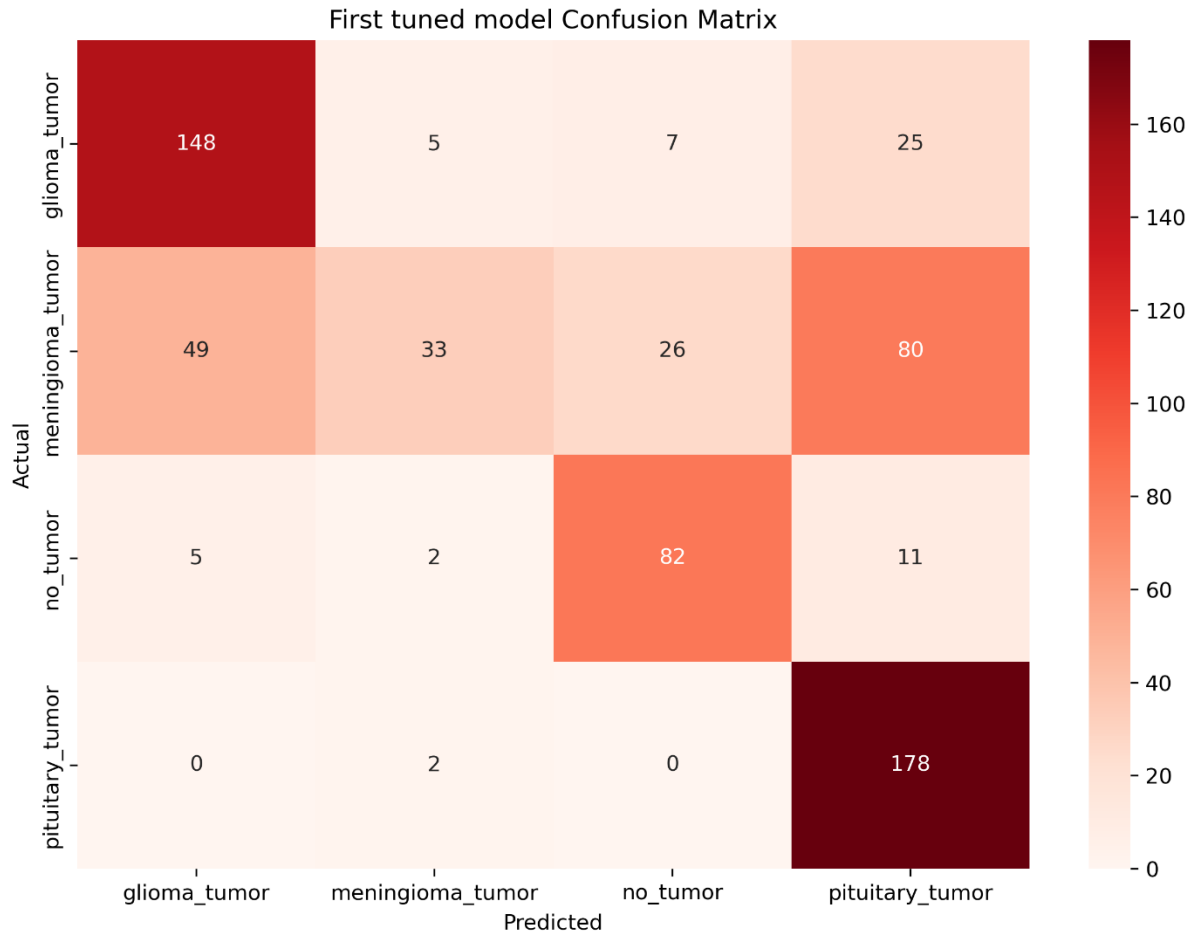

Figure 8. Tuned model Confusion Matrix

	precision	recall	f1-score	support
glioma_tumor	0.73	0.80	0.76	185
meningioma_tumor	0.79	0.18	0.29	188
no_tumor	0.71	0.82	0.76	100
pituitary_tumor	0.61	0.99	0.75	180
accuracy			0.68	653
macro avg	0.71	0.70	0.64	653
weighted avg	0.71	0.68	0.62	653

Figure 8. Tuned model1 Classification Report

The tuned model1 achieved an overall accuracy of 68% on a test set of 653 samples. When observing the F1-scores for each tumor type: glioma stands at 76%, meningioma at 29%, no tumor at 76%, and pituitary at 75%. The weighted average F1-score across all classes is 62%.

TUNED MODEL 6 (Best Tuned Model)

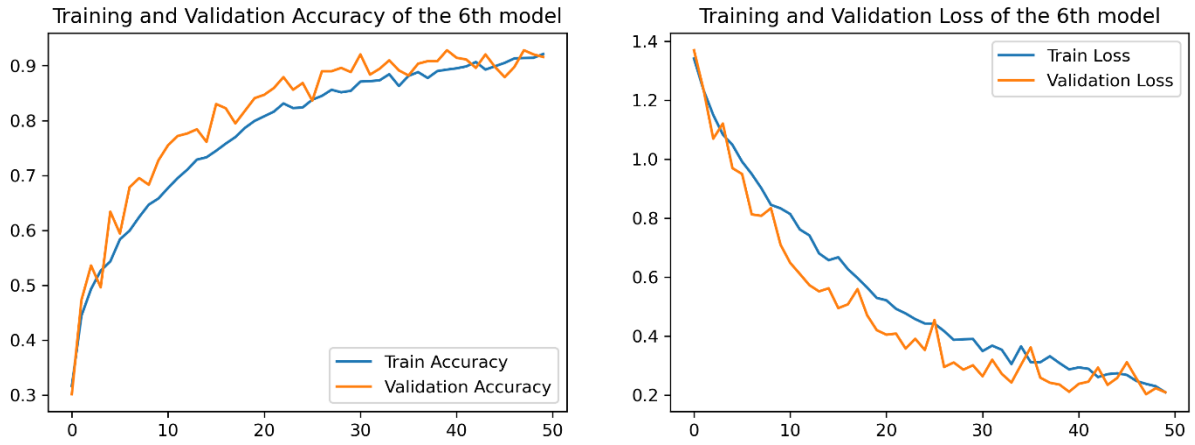

Figure 9. Tuned model 6 Training and validation accuracy and loss

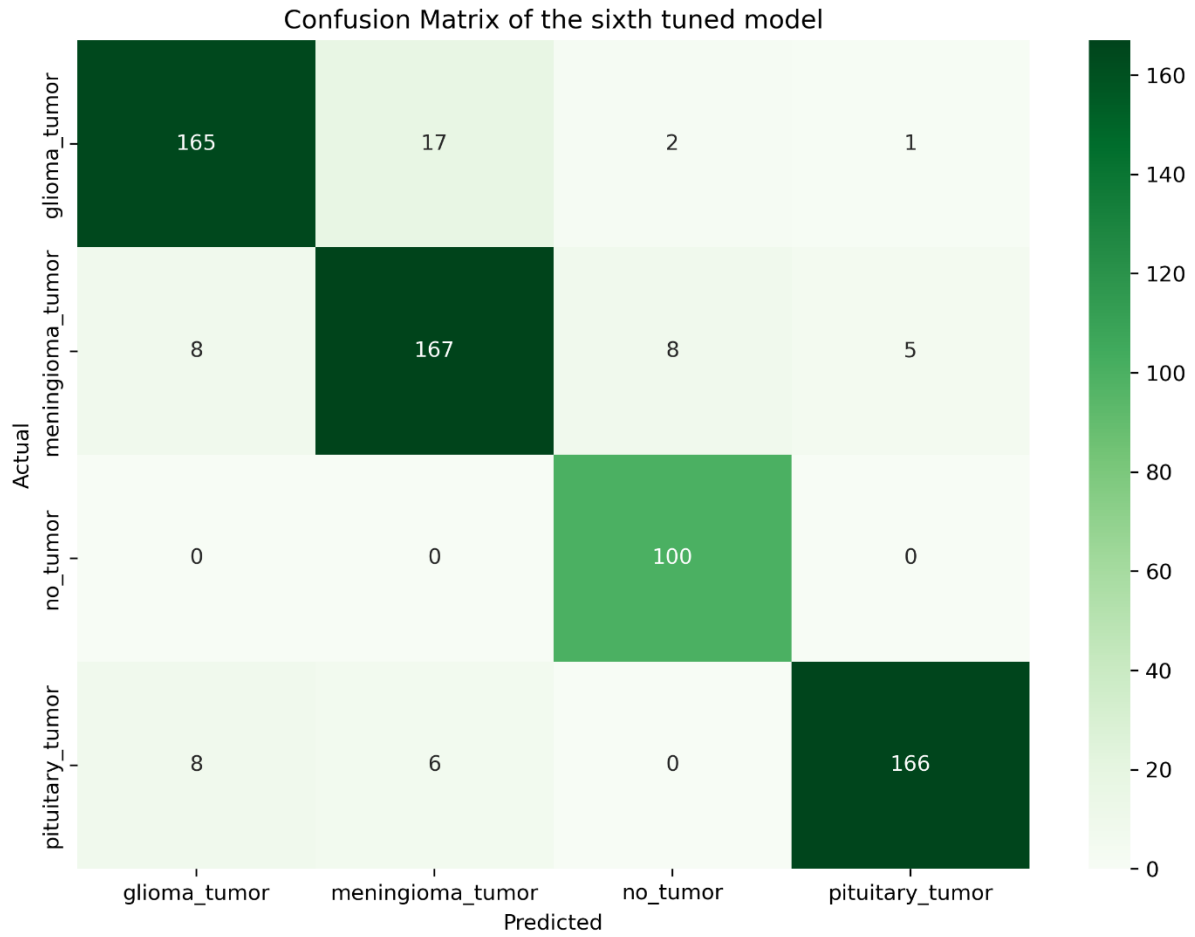

Figure 9. Tuned model6 confusion matrix

	precision	recall	f1-score	support
glioma_tumor	0.91	0.89	0.90	185
meningioma_tumor	0.88	0.89	0.88	188
no_tumor	0.91	1.00	0.95	100
pituitary_tumor	0.97	0.92	0.94	180
accuracy			0.92	653
macro avg	0.92	0.93	0.92	653
weighted avg	0.92	0.92	0.92	653

Figure 10. Tuned model6 Classification Report

In the sixth iteration of the tuned model, there is a commendable enhancement in performance across all tumor classes on a test set of 653 samples. The results for each tumor class are as follows:

Glioma tumor: The model achieved a precision of 91% and a recall of 89%, resulting in an F1-score of 90%.

Meningioma tumor: The precision and recall stood at 88%, culminating in an F1-score of 88%

-**No tumor:** With a precision of 91% and an impressive recall of 100%, the model yielded an F1-score of 95%

Pituitary tumor: Achieving a precision of 97% and a recall of 92%, the F1-score is a robust 94%.

Overall, the model boasts an accuracy of 92%. When considering averages across all classes, both macro and weighted averages for precision, recall, and F1-score are consistent at 92%, indicating a harmonized high performance across all categories. Notably, this model exhibits no signs of overfitting, making it exceptionally well-tuned and reliable.

VGG19 (BEST PERFORMING TRANSFER LEARNING MODEL)

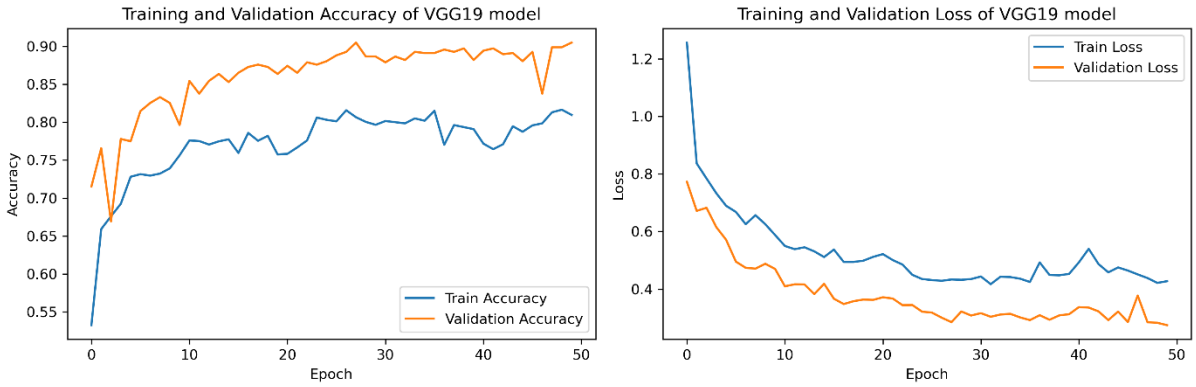

Figure 11. VGG19 training and validation loss and accuracy

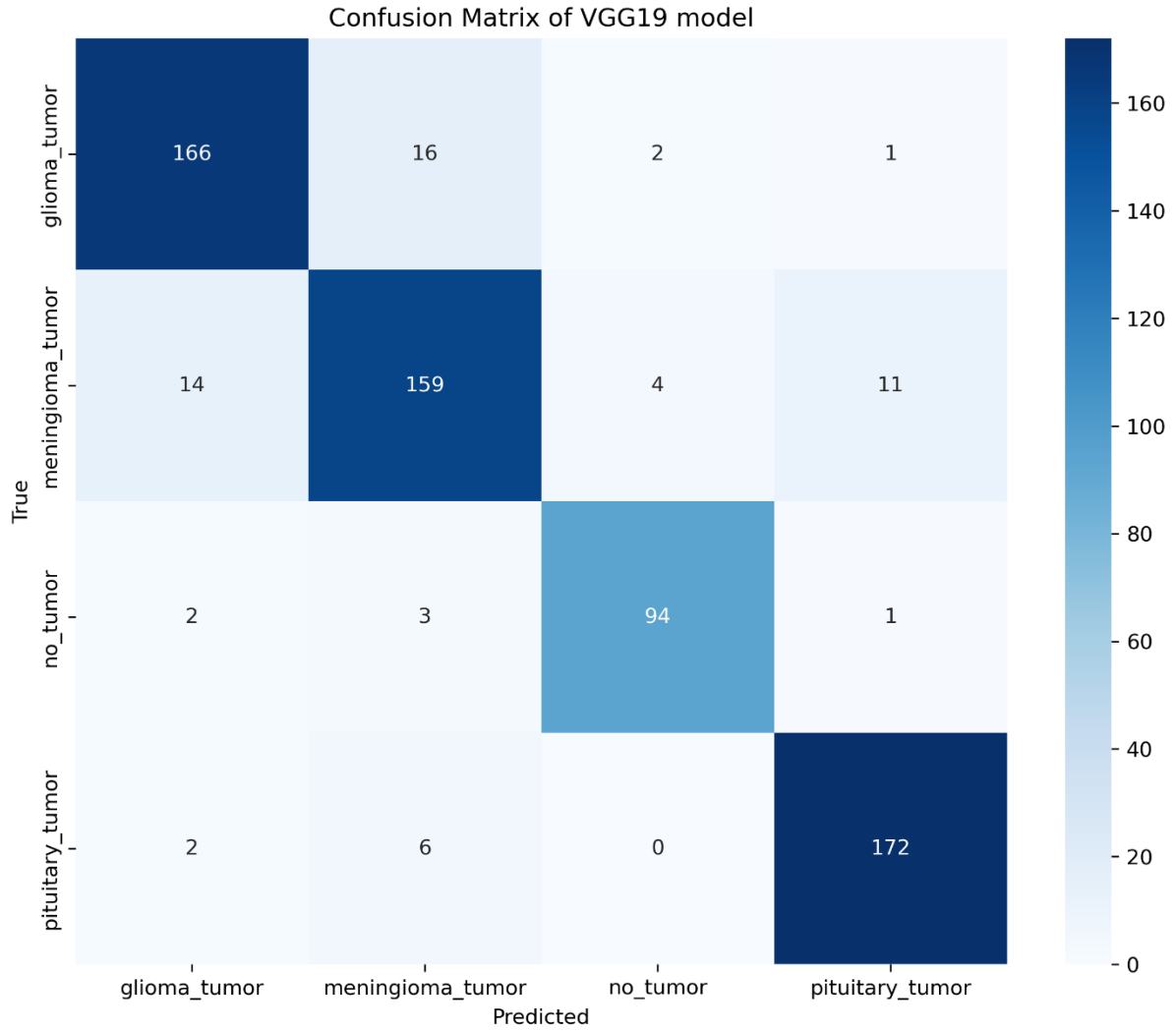

Figure 12. VGG19 Confusion Matrix

	precision	recall	f1-score	support
glioma_tumor	0.90	0.90	0.90	185
meningioma_tumor	0.86	0.85	0.85	188
no_tumor	0.94	0.94	0.94	100
pituitary_tumor	0.93	0.96	0.94	180
accuracy			0.91	653
macro avg	0.91	0.91	0.91	653
weighted avg	0.90	0.91	0.90	653

Figure 13. VGG19 Classification Report

Utilizing transfer learning with the VGG19 model on a test set of 653 samples yielded notable results:

Glioma tumor: F1-score of 90%.

Meningioma tumor: F1-score of 85%.

No tumor: F1-score of 94%.

Pituitary tumor: F1-score of 94%.

Overall, the model achieved an accuracy of 91%. The balanced macro and weighted averages for precision, recall, and F1-score were all around 90-91%. This indicates a consistent high performance across tumor types with the VGG19 model.

TUNED MODEL 4

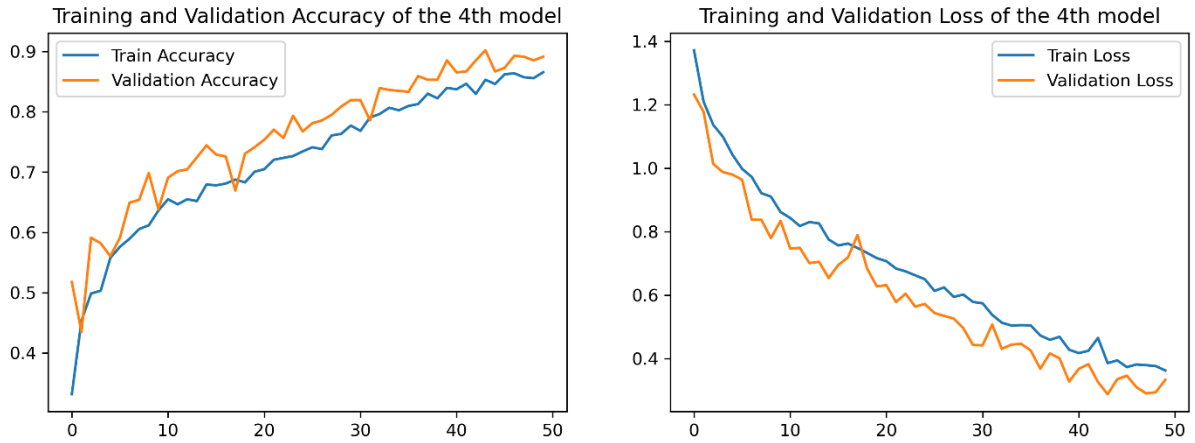

Figure 14. Tuned Model 4 training and validation loss and accuracy

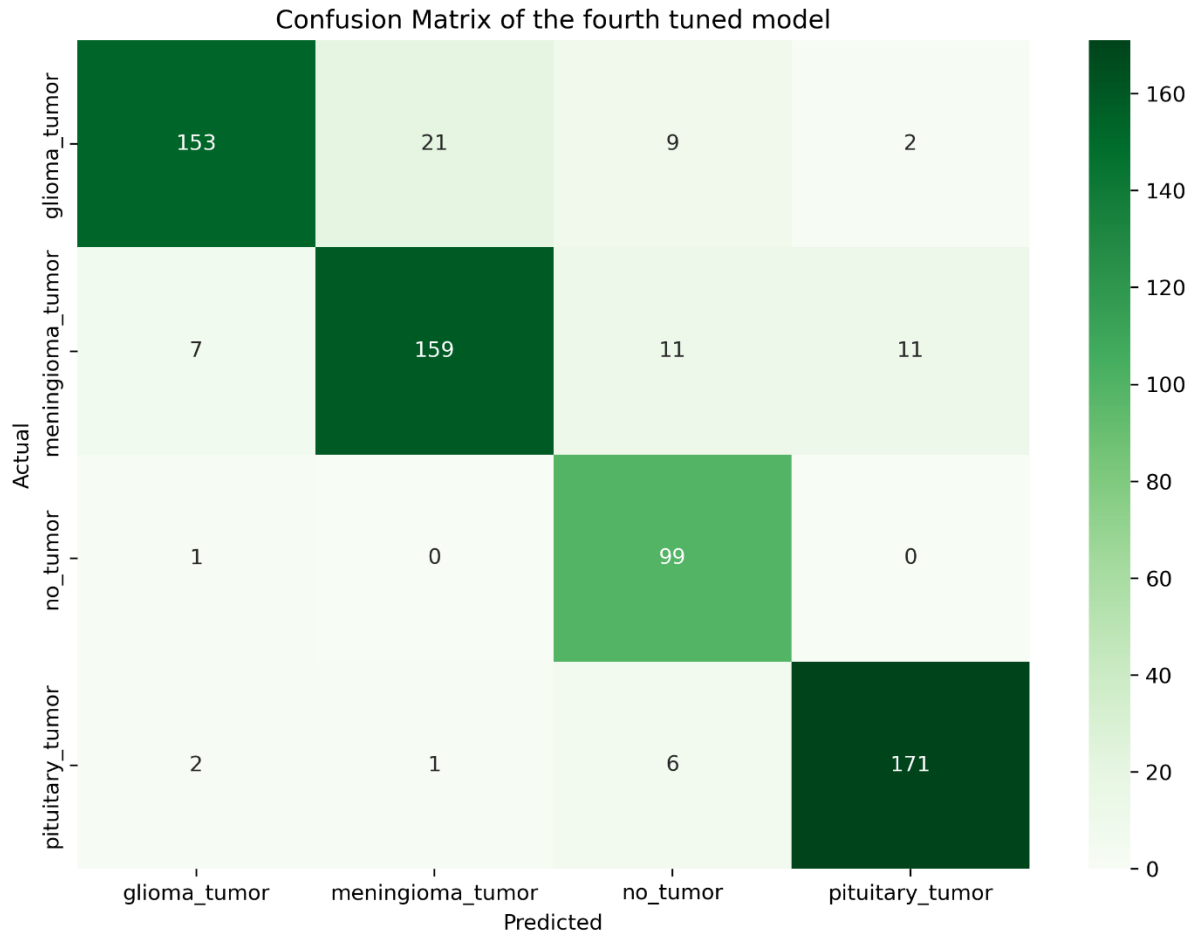

Figure 15. Tuned Model 4 Confusion Matrix

	precision	recall	f1-score	support
glioma_tumor	0.94	0.83	0.88	185
meningioma_tumor	0.88	0.85	0.86	188
no_tumor	0.79	0.99	0.88	100
pituitary_tumor	0.93	0.95	0.94	180
accuracy			0.89	653
macro avg	0.88	0.90	0.89	653
weighted avg	0.90	0.89	0.89	653

Figure 15. Tuned Model 4 Classification Report

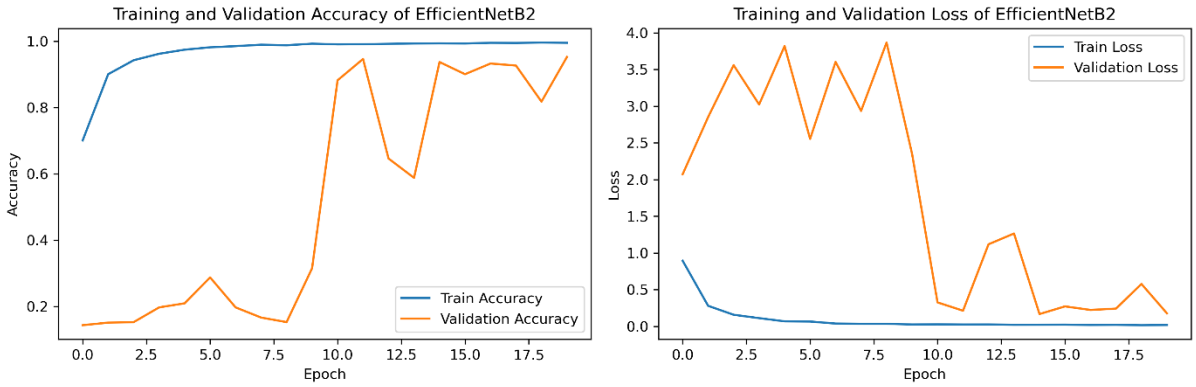

Figure 16. EfficientNet B2 Train and Val loss and accuracy

EfficientNet B2 despite high accuracy overfitted badly

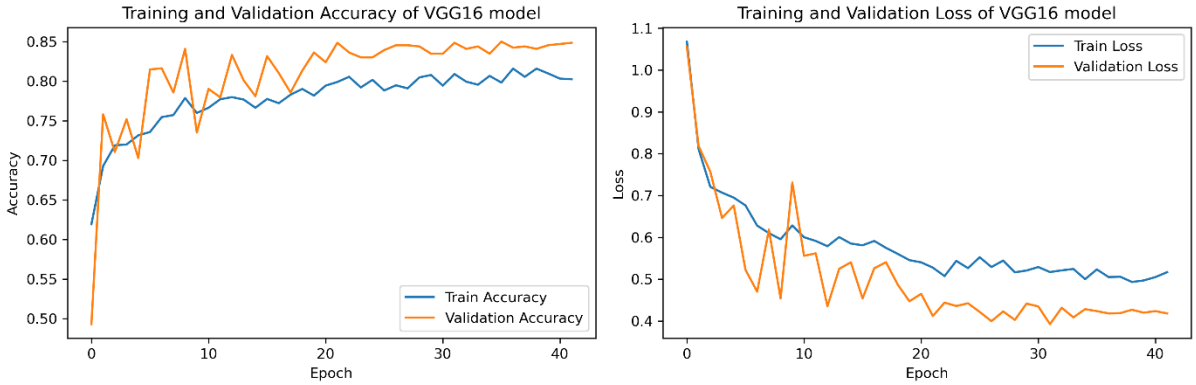

Figure 17. VGG16 Train and Val loss and accuracy

VGG16 did not generalize well.

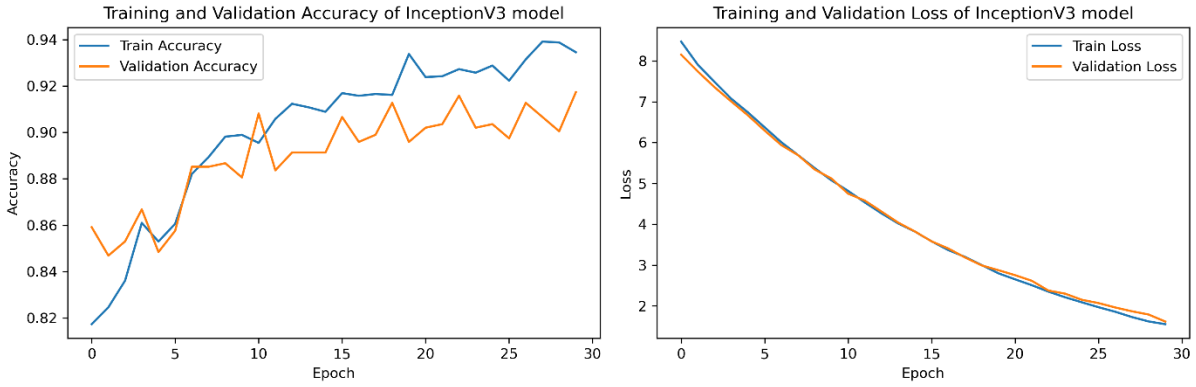

Figure 18. InceptionV3 Train and Val loss and accuracy

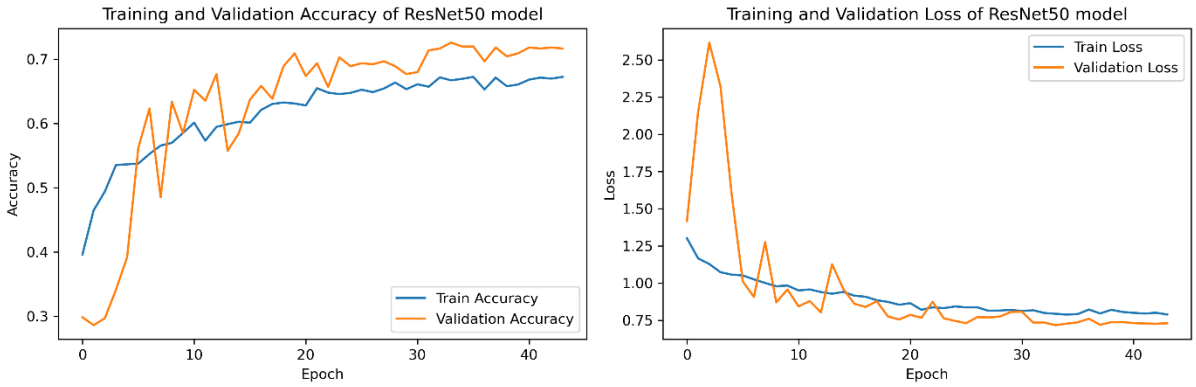

Figure 19. ResNet 50 Train and Val loss and accuracy

6.0 CONCLUSION

In this research, the VGG19-based transfer learning model and the well-optimized Tuned Model 6, which utilized data augmentation, reduced regularization, and five convolutional layers, stood out in their performance. Both models showcased the potential of sophisticated deep learning techniques for brain tumour categorization from MRI images. Looking ahead, delving into diverse data augmentation methods, incorporating additional imaging modalities, expanding the dataset, employing model ensembling, and improving model interpretability could further enhance diagnostic precision and trustworthiness.

In addressing the research questions:

a. Advanced CNN architectures, specifically the VGG19-based transfer learning model and Tuned Model 6, demonstrated a marked improvement in accuracy over simpler 2D models for brain tumour detection.

b. Techniques such as hyperparameter tuning and data augmentation played pivotal roles in optimizing model performance, making them indispensable in the model development process.

c. The use of transfer learning, especially with pre-trained models like VGG19, not only enhanced the model's precision but also provided a boost in computational efficiency, proving invaluable for timely medical diagnostics.

With these findings, this study adds valuable insights to the domain of medical imaging, especially in the early detection and classification of brain tumours using deep learning techniques.

REFERENCES

1. Amazon Web Services (2023) *What is deep learning*. Amazon Web Services. Available online: https://aws.amazon.com/what-is/deep-learning/ [Accessed 6/9/2023].

2. Azevedo, F.A.C., Carvalho, L.R.B., Grinberg, L.T., Farfel, J.M., Ferretti, R.E.L., Leite, R.E.P., Filho, W.J., Lent, R. & Herculano-Houzel, S. (2009) Equal numbers of neuronal and nonneuronal cells make the human brain an isometrically scaled-up primate brain. *The Journal of Comparative Neurology*, 513(5), 532–541.

3. Cancer Research UK (2023) *Brain, other cns and intracranial tumours statistics*. Cancer Research UK. Available online: https://www.cancerresearchuk.org/health-professional/cancer-statistics/statistics-by-cancer-type/brain-other-cns-and-intracranial-tumours#:~:text=Brain%2C%20other%20CNS%20and%20intracranial%20tumours%20is%20the%2010th%20most,year%20(2017%2D2019). [Accessed 6/9/2023].

4. Caruso, C. (2023) *A new field of neuroscience aims to map connections in the brain*. A New Field of Neuroscience Aims to Map Connections in the Brain | Harvard Medical School. Available online: https://hms.harvard.edu/news/new-field-neuroscience-aims-map-connections-brain [Accessed 6/9/2023].

5. Chandrashekar, L. and N, D.M. (2021) Selecting an optimizer to detect the field of view for CT and MRI brain images. 1–25.

6. Computer Vision Project (n.d.) EfficientNet-B2 | Efficient Convolutional Neural Network for Image Classification. computervisionproject.com. Available online: https://computervisionproject.com/classification/efficientnetb2.html [Accessed 6/9/2023].

7. Dolan, B. (2007) Soul searching: A brief history of the mind/body debate in the neurosciences. *Neurosurgical Focus*, 23(1), 1–7.

8. GeeksforGeeks (2020) How to Convert images to NumPy array? GeeksforGeeks. Available online: https://www.geeksforgeeks.org/how-to-convert-images-to-numpy-array/ [Accessed 6/9/2023].

9. Hamid, K., Iqbal, M. waseem, Fuzail, M., Muhammad, H., Muhammad, B., Nazir, Z. and Ghafoor, Z. (2022) Detection of brain tumor from brain MRI images with the help of machine learning & deep learning.

10. Han, J., Kamber, M. and Pei, J. (2012b) 3 - data preprocessing. In: J. Han, M. Kamber and J. Pei, eds., Third Edition. [online] Morgan Kaufmann, 83–124. Available online: https://www.sciencedirect.com/science/article/pii/B9780123814791000034.

11. Hoffman, M. (2023) *Biopsy: types, what to expect, and uses*. WebMD. Available online: https://www.webmd.com/cancer/what-is-a-biopsy [Accessed 6/9/2023].

12. Irla, T. (2019) Transfer Learning using Inception-v3 for Image Classification. Analytics Vidhya. Available online: https://medium.com/analytics-vidhya/transfer-learning-using-inception-v3-for-image-classification-86700411251b [Accessed 6 Sep. 2023].

13. Jason Brownlee (2017) Gentle Introduction to the Adam Optimization Algorithm for Deep Learning. Machine Learning Mastery. Available online: https://machinelearningmastery.com/adam-optimization-algorithm-for-deep-learning/ [Accessed 6/9/2023].

14. Mascarenhas, S. and Agarwal, M. (2021) A comparison between VGG16, VGG19 and ResNet50 architecture frameworks for image classification. 96–99.

15. Mayo Clinic (2023) *Brain tumor*. Mayo Clinic. Available online: https://www.mayoclinic.org/diseases-conditions/brain-tumor/symptoms-causes/syc-20350084 [Accessed 6/9/2023].

16. NHS (2023) *Brain tumours*. NHS choices. Available online: https://www.nhs.uk/conditions/brain-tumours/ [Accessed 6/9/2023].

17. Sadad, T., Rehman, A., Munir, A., Saba, T., Tariq, U., Ayesha, N. & Abbasi, R. (2021) Brain tumor detection and multi-classification using Advanced Deep Learning Techniques. Microscopy Research and Technique, 84(6), 1296–1308.

18. Santos, D. and Santos, E. (2022) Brain tumor detection using deep learning.

19. Solanki, S., Singh, U., Singh Chouhan, S. and Jain, S. (2021) International Journal of INTELLIGENT SYSTEMS AND APPLICATIONS IN ENGINEERING Original Research Paper Brain Tumour Detection and Classification by using Deep Learning Classifier. International Journal of Intelligent Systems and Applications in Engineering IJISAE, 2023(2s), 279–292.

20. Srinivas, C., K. S., N.P., Zakariah, M., Alothaibi, Y.A., Shaukat, K., Partibane, B. & Awal, H. (2022) Deep Transfer Learning Approaches in performance analysis of brain tumor classification using MRI images. *Journal of Healthcare Engineering*, 2022, 1–17.

21. Wikipedia (2023) *Brain tumor*. Wikipedia. Available online: https://en.wikipedia.org/wiki/Brain_tumor [Accessed 8/9/2023].

22. ZainEldin, H., Gamel, S.A., El-Kenawy, E.-S.M., Alharbi, A.H., Khafaga, D.S., Ibrahim, A. & Talaat, F.M. (2022) Brain tumor detection and classification using deep learning and sine-cosine fitness grey wolf optimization. *Bioengineering*, 10(1), 18.