EFT-SA-Net: An Attention-Enhanced EfficientNetB6 Framework for Accurate and Explainable Brain Tumour Classification from MRI Scans

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EFT-SA-Net: An Attention-Enhanced EfficientNetB6 Framework for Accurate and Explainable Brain Tumour Classification from MRI Scans

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Abstract

Brain tumor diagnosis remains an important clinical challenge due to the complexity and variability of MRI images. This study aims to develop an advanced, explainable deep learning framework that enhances both the accuracy and interpretability of tumor classification. The proposed EFT-SA-Net which is a EfficientNetB6-based hybrid model integrated with Spectral, Temporal and Self-Attention mechanisms, is designed to capture fine-grained spatial and contextual type of dependencies within MRI scans. The study has been used the Kaggle Brain Tumor MRI dataset which is undergoing preprocessing, SMOTE-based data balancing and model optimization using Adam and categorical cross-entropy. Experimental evaluations compared CNN, Xception, InceptionV3, EfficientNetB6, and EFT-SA-Net, with the proposed model achieving the highest accuracy of 98% showing superior results. Integration of Explainable AI (LIME) provided interpretability by visually showing tumor regions influencing the model's decisions reinforcing medical trust and diagnostic transparency. The results confirm that EFT-SA-Net not only outperforms conventional deep learning models but also bridges the gap between automation and clinical interpretability. While computational complexity presents a limitation, the framework shows a major advancement toward AI-driven, reliable and explainable medical diagnostics with potential for real-world clinical deployment and future multi-modal medical imaging integration.

Keywords: Brain Tumor Classification, Deep Learning, EfficientNetB6, Attention Mechanisms, Explainable Artificial Intelligence (XAI)

1 Introduction

1.1 Background

A brain tumor is an irregular growth of brain cells (Pichaivel et al., 2022) or other structures near the brain and this may disrupt essential brain activity (Seker-Polat et al., 2022). The tumors are broadly classified into primary (those that originate in the brain), which are secondary (metastatic) (those spread by other body parts). Primary brain tumors may also be divided into benign (non-cancerous) and malignant (cancerous), and the most common ones are gliomas, meningiomas, pituitary adenomas, and schwannomas (Azam et al., 2025). In the past, the detection process of brain tumors depended more on the clinical examination and invasive biopsy process that were dangerous and slow in making a diagnosis (Azam et al., 2025). The development of technology also brought some revolution in visualizing tumors as neuroimaging techniques like Computed Tomography (CT), and Magnetic Resonance

Imaging (MRI) helped to make the diagnosis more detailed and non-invasive (Vitrio et al., 2024). Digital imaging and computer-aided analysis has also developed over the decades to help radiologists detect tumors more effectively (Liao et al., 2025). Medical diagnostics have evolved to become less manual in its interpretation and more automated and data-based, which minimized human error and enhanced accuracy. In the current healthcare system, image processing, pattern recognition and computational modeling are used to increase diagnostic reliability (Senthilkumar and Munusamy, 2025). This development makes ongoing innovation in the field of brain tumor diagnosis extremely important to enhance clinical decision-making, early diagnosis, and survival rates in patients.

1.2 Importance

This study is important because it will contribute to improved and fast brain tumor detection through recent and powerful deep learning and attention control approaches. The diagnosis of brain tumors can be quite difficult since the visual patterns in MRI scans can be similar and because of the lack of data on the matter (Abdusalomov et al., 2023). This study proposes an effective and explainable model using EfficientNetB6 together with Spectral, Temporal, and Self-Attention (EFT-SA-Net) that can address the local image relations and global image relations, and hence, enhances classification accuracy (Abdusalomov et al., 2023). The fact that the Explainable AI (LIME) is included also makes the model more transparent, because medical professionals can see the areas that affect the diagnosis. The current research is not only relevant to the area of medical image analysis and AI-based diagnostics but also assist clinicians in having a trustworthy decision-support tool with a reduced likelihood of human error and high diagnostic efficiency, which, ultimately, will help to plan treatments faster and achieve better patient outcomes.

1.3 Research Question

Accurate and interpretable brain tumor detection remains a major challenge due to variations within MRI scans. Traditional DL models though powerful but it mainly struggles to maintain both high accuracy and explainability which are very important in medical diagnostics. This study aims to address these challenges by developing a hybrid attention-based model that enhances performance while having transparency in predictions.

"What impact does the integration of Spectral, Temporal, and Self-Attention mechanisms into EfficientNetB6 have on improving the accuracy, precision, and interpretability of brain tumor classification from MRI scans, and how does this hybrid architecture perform compared to conventional DL models such as CNN, Xception, and InceptionV3?"

1.4 Research Objectives

There are some research objectives in this study which are:

1. To develop and evaluate a hybrid DL architecture (EFT-SA-Net) integrating Spectral, Temporal, and Self-Attention mechanisms with EfficientNetB6, aiming to improve classification accuracy, precision, recall, and overall robustness in brain tumor detection from MRI scans compared to conventional CNN and transfer learning models.
2. To increase the interpretability and clinical transparency of the proposed model using Explainable Artificial Intelligence (LIME) by visualizing and showing the important

MRI regions that influence the model's decision-making process which is thereby fostering medical trust and helping radiologists in diagnostic validation.

1.5 Structure of the Study

This study is organized into seven chapters. Chapter 1 introduces the research by presenting the background, importance, research question, and objectives. Chapter 2 reviews related works on brain tumor diagnosis, DL and explainable artificial intelligence techniques, highlighting existing gaps and advancements. Chapter 3 outlines the research design framework, dataset description, preprocessing, and data balancing approaches. Chapter 4 details the design specification, including system architecture, model optimization, and the proposed EFT-SA-Net framework. Chapter 5 discusses the implementation phase covering model development, explainability (LIME analysis), and web application integration. Chapter 6 presents the experimental results, evaluation metrics, and comparative performance analysis of various models. Finally, Chapter 7 concludes the research by summarizing key findings, addressing limitations, and proposing future enhancements and potential applications.

2 Related Work

2.1 Brain Tumor Diagnosis and Imaging

One of the most important problems in medical imaging is the diagnosis of brain tumor because of its complexity, irregularity, and diversity of tumor structures of the human brain (Arabahmadi et al., 2022). The brain tumors are caused by the uncontrolled growth of the brain tissues cells and it can be classified as benign, malignant or pituitary according to the growth patterns and malignancy. Effective planning of the treatment and the enhancement of the survival rates of patients depends on the accurate diagnosis and as soon as possible detection. Radiologists traditionally use Magnetic Resonance Imaging (MRI) as the gold-standard imaging-modality to detect and characterize brain tumor due to its excellent soft-tissue contrasts and multi-planar imaging (Alshomrani, 2025). T1-weighted, T2-weighted and FLAIR are MRI sequences that give a great deal of anatomical and pathological information, helpful in tumor localization and segmentation. Nevertheless, the manual interpretation of MRI scans is costly in time, subjective, and inter-observer variability can easily occur particularly when large datasets are involved (Quinn et al., 2023). The latest developments have greatly improved the accuracy and efficiency of the diagnostic processes as the features extraction and classification are automated. These techniques are capable of training complicated spatial characteristics using the high-dimensional MRI data, which reduces the possibility of human error and assists radiologists in clinical decision-making. Additionally, computerized systems have been advantageous in distinguishing tumor types and grades, which makes it possible to treat the tumor in early stages and apply individual treatment. Even with the progress, issues on heterogeneous tumor appearances, imbalance of data, and interpretability of AI-driven predictions persist, which explains the necessity of the Explainable AI (XAI) models that can render a diagnosis result clear and reliable enough to be clinically implemented.

2.2 DL in Brain Tumor

DL has become a revolutionary technology in the automated detection and classification of brain tumors, since it can overcome the shortcomings of the manual diagnosis technique of earlier years, which is frequently complex, invasive, and can be interfered with by humans. A body of literature examining the application of CNNs and more sophisticated architectures in order to enhance diagnostic accuracy and efficiency has been developed. A 25-layer CNN was suggested in (Kumar and Kumar, 2023) using T1-weighted MRI data to classify glioma, meningioma, and pituitary tumours with accuracies of 86.23 and 81.6 with Adam and SGDAM optimizers, respectively, and performing better than current methods, but hindered by diversity of the dataset and dependence on modality. To elaborate on this, (Srinivasan et al., 2024) proposed a fully automated multi-classification system with three CNN models to detect, classify, and even grade tumors with the accuracies of 99.53, 93.81 and 98.56, respectively. The research showed better performance compared to the classic models such as AlexNet and ResNet but experienced problems of overfitting and lack of interpretability. (Pillai et al., 2023) used transfer learning with VGG16, InceptionV3 and ResNet50 with the fine-tuned layers to tumor classification of 251 MRI scans, with VGG16 yielding a 91.58 per cent accuracy, which demonstrated that transfer learning is effective in small datasets but limited by the lack of generalization. The next progress was noted in (Islam et al., 2024) and (Prabha and Singh, 2024) using EfficientNet family to extract features better and perform at scale. In study (Islam et al., 2024), 3064 MRI images were used, and EfficientNetB3 was chosen as the most appropriate model with 99.69% accuracy, which is superior to the state-of-the-art methods, whereas study (Prabha and Singh, 2024) conducted an analysis with 18,500 MRI images and demonstrated that the accuracy increases to 99.64% with EfficientNetB3 (B0 being 96.07% and B5 and B7 being 97.69% and 99.64%). Although such studies require computational resources and use single-modality data, they all reveal that deep learning, which includes CNN-based and EfficientNet models, is much more effective at increasing results. This study also used (Zhaputri et al., 2021) which has also used EfficientNet model which achieved 96% accuracy in their work. The dataset used in this study consists of only 2,475 grayscale MRI images across three tumour classes which may limit generalizability to various real-world clinical environments where data quality, imaging protocols and tumour variations differ importantly.

2.3 XAI in Brain tumor

The recent achievements of XAI have enhanced the transparency, accuracy, and reliability of brain tumour detection and classification using magnetic resonance imaging (MRI). Several works have entities that have investigated DL models combined with XAI strategies to overcome the issue of limited interpretability and over-complex structures of classic AI models. The better DenseNet121-based CNN framework was suggested by (Ariful Islam et al., 2025). It demonstrated higher results than 17 currently existing frameworks with 98.4% and 99.3% accuracy and 200 localized tumors with high accuracy and interpretability with the help of Grad-CAM++. On the same note, (Tonmoy et al., 2025) presented a powerful deep CNN architecture to do automated tumor recognition achieving state-of-the-art accuracies of 99.81%, 99.55%, and 99.30% on training, validation, and test sets, respectively, by using Grad-CAM, Grad-CAM++, and Score-CAM to increase decision explainability. In a bid to enhance the transparency of the diagnosis process, (Raghunath Mutkule et al., 2023) came up with dual-weighted CNN classifiers using LIME and SHAP, which perform well with high sensitivity and specificity in the prediction of early tumors. This was accomplished by (Iftikhar et al., 2025) by adding CNNs with XAI approaches like Grad-CAM, SHAP, and LIME, reaching 99% accuracy on seen data and 95% accuracy on unseen data, which is is a balance of simple, understandable, and generalizability. In a different work, (Narayankar and Baligar, 2024) employed CNN and XAI methods such as LIME, SHAP, Integrated Gradients, and Grad-CAM, which also resulted in 80% accuracy and alongside the significance of interpretable AI on clinical use. In addition, (Filvantorkaman et al., 2025) has suggested a combination of MobileNetV2 and DenseNet121 with Grad-CAM++ and Clinical Decision Rule Overlay (CDRO), achieving an accuracy of 91.7% and a good correlation between model focus and radiologist results, confirmed by the expert opinion. Together, these works point to the fact that XAI techniques can be successfully incorporated into deep learning to enhance diagnostic accuracy and, at the same time, achieve clinical trust because of the ability to provide interpretable visual explanations. Nevertheless, some of the difficulties, including computational requirements, dependence on datasets, and the necessity of large-scale clinical validation are significant topics of future research.

Table 1: Summary of DL and Explainable AI Studies in Brain Tumor Detection

Study	Model / Method Used	Dataset / Sample Size	Accuracy / Performance	Key Findings	Limitations
(Kumar and Kumar, 2023)	25-layer CNN with Adam and SGDAM optimizers	T1-weighted MRI data	86.23% (Adam), 81.6% (SGDAM)	Improved classification of glioma, meningioma, and pituitary tumors over traditional methods	Dataset diversity and modality dependence
(Srinivasan et al., 2024)	Three CNN models for detection, classification, and grading	MRI scans (multi-class)	99.53%, 93.81%, 98.56%	Fully automated multi-class system outperforming AlexNet and ResNet	Overfitting and lack of interpretability
(Pillai et al., 2023)	Transfer Learning (VGG16, InceptionV3, ResNet50)	251 MRI scans	VGG16 – 91.58%	Transfer learning effective for small datasets	Limited generalization
(Islam et al., 2024)	EfficientNet family (B0–B7), feature extraction	3,064 MRI images	EfficientNetB3 – 99.69%	Outperformed state-of-the-art CNNs in accuracy and robustness	High computational cost; single-modality data
(Prabha and Singh, 2024)	EfficientNet (B0, B5, B7, B3)	18,500 MRI images	B0 – 96.07%, B5 – 97.69%, B7 – 99.64%	Accuracy improved with deeper EfficientNet variants	Requires large computation and diverse data
(Ariful Islam et al., 2025)	DenseNet121-based CNN + Grad-CAM++	MRI dataset with 200 localized tumors	98.4%–99.3%	High accuracy and interpretability across models	Computational complexity

(Tonmoy et al., 2025)	Deep CNN + Grad-CAM, Grad-CAM++, Score-CAM	MRI dataset	99.81% (train), 99.55% (val), 99.30% (test)	Improved explainability and visualization of tumor regions	Over-reliance on dataset quality
(Raghunath Mutkule et al., 2023)	Dual-weighted CNN + LIME, SHAP	MRI dataset (early-stage tumors)	High sensitivity and specificity	Enhanced early tumor detection with interpretable predictions	Model complexity
(Iftikhar et al., 2025)	CNN + Grad-CAM, SHAP, LIME	MRI scans (seen/unseen data)	99% (seen), 95% (unseen)	Balanced interpretability and generalization	Requires broader validation
(Narayankar and Baligar, 2024)	CNN + XAI (LIME, SHAP, Integrated Gradients, Grad-CAM)	MRI dataset	80%	Demonstrated interpretability importance for clinical adoption	Moderate accuracy; needs optimization
(Filvantorkaman et al., 2025)	MobileNetV2 + DenseNet121 + Grad-CAM++ + CDRO	MRI dataset validated by radiologists	91.7%	Strong correlation between AI focus and radiologist insights	Computational requirements; dataset dependency

3 Methodology

3.1 Dataset Description

The dataset in this study is the one found on Kaggle, the name of which is Brain Tumor Classification (MRI)[1] which includes a set of MRI scans divided into four categories. Brain tumors are the most threatening and perilous disease in children and adults with almost 85-90 percent of all primary tumors of the central nervous system (CNS). New cases of the disease are being reported at an average of 11,700 annually, with a 5-year survival rate of about 34 percent in men and 36 percent in women. MRI imaging is the best and least invasive method of diagnosing and analyzing tumors; but manual analysis of MRI scans is prone to errors and time-intensive since tumors may vary in shape, size, and location. This dataset represents the high-quality, preprocessed MRI images that ease the training of DL models to identify the presence of tumors and classify them.

[1] https://www.kaggle.com/datasets/sartajbhuvaji/brain-tumor-classification-mri

3.2 Data Preprocessing

Preprocessing stage is in the process of preparing MRI images in order to efficiently train and classify them. In this research, the data were categorized into titled folders which belonged to various types of tumors. The labels were automatically constructed with the help of the os.listdir() function that helped to identify class directories existing within the dataset root path automatically. Resizing is required to have all MRI images have a uniform resolution by allowing the deep learning model to process consistent input dimensions for good learning and accurate classification. The resizing was done with the help of the OpenCV library when each MRI image was resized to a uniform size of 128 by 128 pixels (default image size = (128,128)). An optimized training efficiency was set to a batch size of 32. The preprocessing was also to come up with an image_array() function which can read an image in the directory using the cv2.imread() function and then resize the image using the cv2.resize() and then convert it to a numerical array using the img_to_array() function to be fed into the model. In case an image did not load correctly, the function returned an empty NumPy array to be able to deal with exceptions. Additionally, the categorical labels of the classes were converted to numerical format with LabelBinarizer which made it easy to use in classifying more than two classes. The uniformity in image dimension, high-performance processing of images in batchs and correct encoding of labels are guaranteed through this systematic preprocessing pipeline, thus allowing the deep learning model to effectively learn with high-quality and structured input data.

3.3 Exploratory Data Visualization

Exploratory visualization was done in Matplotlib and OpenCV to obtain a rough idea about the dataset and ensure that MRI images were distributed among various tumor types. The code will repeat across the dataset directory and show one representative MRI image of each type of tumor. The grid was constructed with 2×2 subplot each representing a tumor class with the help of plt.subplot. The images were read with the help of the mpimg.imread() function and plotted with the help of the plt.imshow() function with class names represented in bold and upper-case fonts. Axes have been concealed to be seen cleaner, and each image was framed by a white line in order to be more visible and clearer. The size of the figure was determined to 12x8 and layout modifications were done with plt.tight_layout(pad=2.0) on maintaining a balanced space. This step of visualization is efficient to ensure the integrity of the data and make a visual evaluation of the MRI image features of the various tumor types.

MRI scans used in the Brain Tumor Classification dataset are represented in Figure 1 that displays four types. The images portray different structural difference and tissue abnormality witnessed in the human brain. The No Tumor picture shows the normal form of the brain whereas all the other pictures show different shapes, strengths, and locations of tumors in the brain area. The visualization is an important step towards knowing the diversity of the dataset, and the visual intensity of classifying brain tumors. This type of differentiation helps deep learning models to learn tumor-specific features.

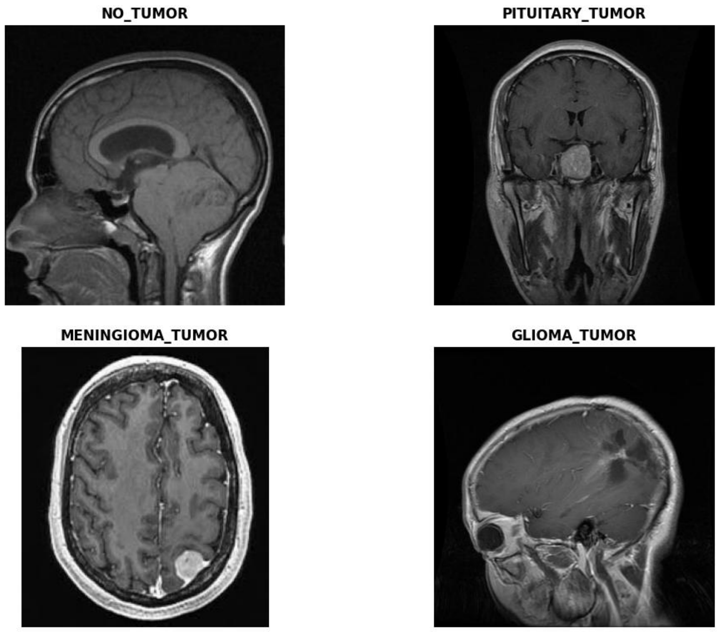

Figure 1: Sample MRI Images from Brain Tumor Classification Dataset

3.4 Data balancing

Figure 2 represents the initial class distribution of the MRI dataset before applying the SMOTE (Synthetic Minority Over-sampling Technique). It shows a clear imbalance, where the Glioma and Pituitary Tumor classes contain a higher number of samples compared to the No Tumor category, which is significantly underrepresented. SMOTE can lead to biased model training, causing poor prediction performance on minority classes. Figure 3 illustrates the dataset after applying SMOTE, where all four classes which are evenly balanced. This balancing ensures equal representation across categories, enabling the deep learning models to learn uniformly from each tumor type. The balanced dataset thus reduces overfitting toward dominant classes and improves the model's generalization and classification accuracy across all tumor categories, enhancing the reliability of the final prediction outcomes.

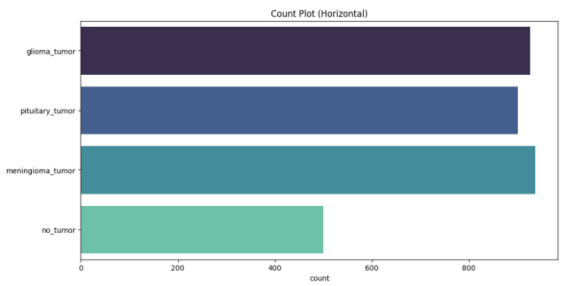

Figure 2: Data Balancing before smote

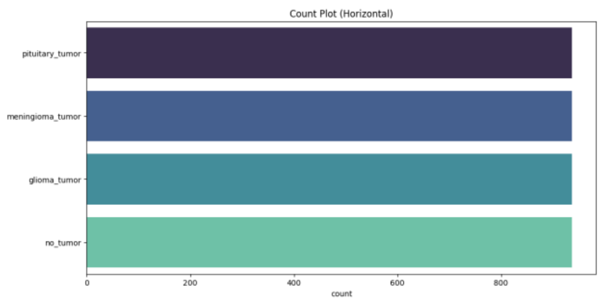

Figure 3: Data Balancing after smote

3.5 Label Encoding and Early Sampling

In this step, LabelBinarizer of the sklearn library was used to obtain a machine-readable numeric expression of the categorical tumor labels. It was done through initiating the label encoder and projecting it onto the dataset labels by converting each tumor category into a one-hot coded vector. This coding makes this model capable of grasping the variation in classes in order to be able to comprehend the differences during the training process. The coded labels were then saved in the form of a pickle file (label_transform.pkl) in order to render it similar and repeatable during evaluation or deployment of the model. The findings made sure that four different groups of tumors had been successfully coded. To get maximum training and prevent overfit, two key calling back mechanisms were employed, such as ReduceLROnPlateau and EarlyStopping. The learning rate scheduler also automatically reduced the learning rate by a half in case the validation accuracy stalled in three consecutive epochs to smooth out the convergence. Meanwhile, the EarlyStopping Restaurant querying training offered the fact that no enhancement of the validation precision was observed after five epochs and restored the model weights of the finest model.

4 Design Specification

4.1 System Components and Architecture

Figure 4 shows the general workflow and architecture of the proposed brain tumor classification system, which includes sequential stages of dataset acquisition to the ultimate model prediction and explainability analysis. The steps start with the importation of the necessary libraries and the loading of the MRI dataset taken at Kaggle. During its data preprocessing phase, images are resized, normalized and labelled in a manner that they are uniform and are ready to be trained. Once the preprocessing is done, data is divided into training, validation and test sets. The first step of training is when the processed data is fed into the DL models to learn tumor patterns and isolate spatial features. The model evaluation is then done to the trained models, performance measures are then calculated. When the best model is acquired, it is subject to Explainable AI (XAI) analysis through the LIME framework to visualize significant areas of impact on the predictions. Lastly, model testing involves the trained model, where new MRI images are classified on the fly and the final result is aiding the identification of the type of tumor with an explainable visualization, which guarantees transparency, accuracy, and clinical interpretability.

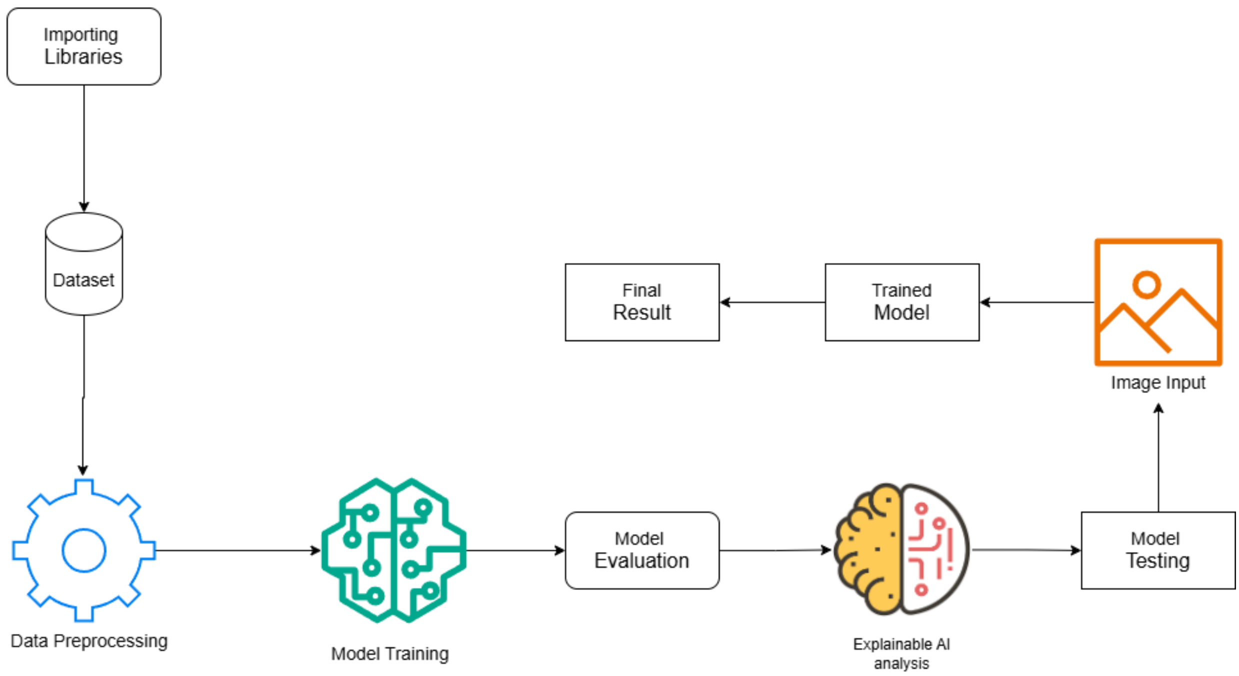

Figure 4: System Architecture Diagram

4.2 Research Specification: Model Optimisation and Explainability Approach

The fundamental design goal is to maximise the performance of the model at the same time as it should be interpretable with Explainable AI. All the DL models were made efficient in terms of computation, accuracy, and feature awareness. The reason why EfficientNet-B6 was chosen is that it has a compound scaling method that ensures a compromise between network resulting in the minimization of the cost of computation without compromising the precision. The EFT-SA-Net model also enhances accuracy by including Spectral, Temporal as well as Self-Attention layers that allow the model to acquire both global and local relationships between MRI features. Training was done in the GPU environment of Google Colab to achieve low computational latency and high responsiveness levels. Parameters like learning rate, dropout and batch normalization were tuned during training to keep overfitting at a low. The largest weights of validation accuracy were maintained with model checkpoints. To make the results interpretable, the LIME framework was used after the inference with the model. LIME examines model predictions with the assistance of perturbations of input data and a change of output, generating a readable heatmap that identifies key tumor areas that cause classification. This strategy will fill the gap between AI prediction and medical reasoning by allowing clinicians to authoritatively validate AI responses. The combination of LIME and high-performing CNN and Transfer Learning models will guarantee the system not only to be accurate but also transparent, reliable and clinically applicable.

4.3 Proposed novel approach

Figure 5 illustrates the architecture of the proposed EfficientNetB6 with Spectral, Temporal, and Self-Attention (EFT-SA-Net) model, designed to enhance brain tumor classification performance. The model begins with the input tensor fed into EfficientNetB6, which extracts deep hierarchical features. These features are refined through three sequential attention mechanisms — Spectral Attention emphasizes critical channels, Temporal Attention highlights important spatial patterns, and Self-Attention captures global dependencies. The refined features are then aggregated via Global Average Pooling and classified through dense layers. This novel integration enhances contextual understanding, improves localization, and significantly boosts classification accuracy and model interpretability.

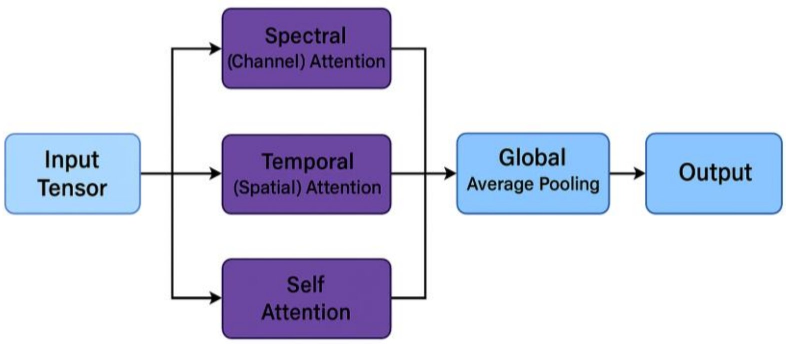

Figure 5: Proposed EFT-SA-Net architecture diagram

5 Implementation

5.1 Model Development and Training

5.1.1 CNN

CNN was used as the baseline deep learning model in brain tumor classification which is meant to produce hierarchical spatial features of MRI images. The number of convolutational blocks was then incremented to 32 filters, which captured higher levels of spatial features of tumor shapes and boundaries. Both Batch Normalization and dropout of rate 0.25 and 0.5 helped in making feedback converge faster and enhanced generalisation respectively. The output was then flattened after feature extraction and then sent through a dense layer with soft max activation to give a classification of four tumor types. The network had about 45,000 parameters, which were optimised through Adam optimizer. This model in CNN was used to compare to more sophisticated architectures of transfer learning, as it proved to be able to effectively learn features when used in the analysis of medical images with low computational complexity.

5.1.2 Exception

The Xception was utilized as a model that improves the accuracy of classification using pre-trained weights provided by the ImageNet dataset. The Xception base model (without the final classification layers) with the input size of 128x128x3 was initialized to extract intricate visual features in MRI scans. Each of the layers was marked as trainable so that it is possible to fine-tune it, so that the model would become more suited to the medical imaging characteristics but not to the characteristics of natural images. The base model output features were flattened and put through a Dense layer with 64 neurons and activation of ReLU then a Dropout (0.5) to reduce overfitting. The additional dense layer consisting of 28 neurons and the other dropout layer were added to enhance the representation of features. Lastly, a softmax output layer of four neurons was used to categorize MRI images. The model had around 22 million parameters which were optimized with Adam optimizer with a learning rate of 0.0001 and categorical cross-entropy loss functional. The design realized high generalization by integrating deep hierarchies of Xception with personalized dense layers, which learned at a faster rate and obtained high accuracy in the task of brain tumor classification than the traditional CNN models.

5.1.3 Inception V3

This study used the InceptionV3 Transfer Learning model, which enhanced the performance of the classification by using a pre-trained convolutional base, which is effective based on multi-scale feature extraction. InceptionV3 InceptionV3 was set up with ImageNet weights, but without the top fully connected layers so as to receive MRI images of 128x128x3 size as input. All convolutional layers were trained as well to optimize the network to domain specific learning in medical imaging. The feature maps produced by InceptionV3 were flattened with a Flatten layer and then a learning non-linear feature representation with a Dense layer with 64 neurons and ReLU activation were applied.

5.1.4 Efficient Net-B6

To have high accuracy and computational efficiency in the brain tumor classification, the EfficientNetB6 Transfer Learning was used. EfficientNetB6 pre-trained EfficientNetB6 with ImageNet weights and without the top classification layers was used, which had an input shape of (image-size, image-size, 3). A Global Average Pooling layer was used to reduce dimensions and aggregate the spatial information in the output feature maps of the base model as well as to retain key features. There was a Dropout layer (0.3) with a subsequent Dense layer of 128 neurons and ReLU activation to obtain non-linear features.

5.1.5 EfficientNetB6 with Spectral, Temporal, and Self-Attention (EFT-SA-Net)

EfficientNetB6 with Spectral, Temporal and Self-Attention (EFT-SA-Net) was applied to provide better spatial and contextual features extraction to provide accurate classification of brain tumors. The architecture started with the EfficientNetB6 base model, which is already trained on ImageNet and which is the main feature extractor of MRI inputs of the size 128x128x3. A Spectral (Channel) Attention module was added to the model in order to increase its emphasis on discriminative features, and this recalibrated channel-wise responses adaptively, by using both global average and max pooling. It was followed by a Temporal (Spatial) Attention network, which highlights the key areas in space by using convolutional attention maps.

5.2 Explainable AI Implementation (LIME Analysis)

The Explainable AI (XAI) aspect of the present study was executed in the context of the LIME framework that was used to understand and visualize the way the deep learning model decided on its MRI scans classification. The main task was to make sure that the system not only managed to acquire a high level of accuracy, but also give medical workers a clear account of how tumors were detected. It started with preprocessing of the images, wherein the scans in the MRI were read with OpenCV, resized to the input size of the model (128×128), and transformed into NumPy arrays. Once the model has predicted, the model provides the category of the tumor. In order to interpret the prediction, LIME was used to create local explanations by pertaining the input image and comparing the variations on the model output. Superpixel segmentation was done in order to find out the most effective regions that helped in the classification. On the outcome of the results, the areas were identified by overlay masks in Matplotlib with the usage of which the areas affected by the tumor were indicated by color to be understood more easily. This application makes the model decision-making process explainable, which facilitates clinical transparency and enables radiologists to prove AI-informed insights with visual data contained in the MRI images.

In Figure 6, the result of the explainability is provided based on the LIME (Local Interpretable Model-Agnostic explanations) method. The image on the left displays the initial MRI scan, and the one on the right indicates the significant area of the tumor if the deep learning model classifies the tumor is of type glioma. The yellow-colored super pixel area refers to the area that made the greatest contribution towards the model making a classification decision. The visualization allows offering clinical readability (by showing that the model properly targets the abnormal tumor region, but not the irrelevant brain areas), which, in turn, proves the reliability and transparency of the AI-based tumor detection system.

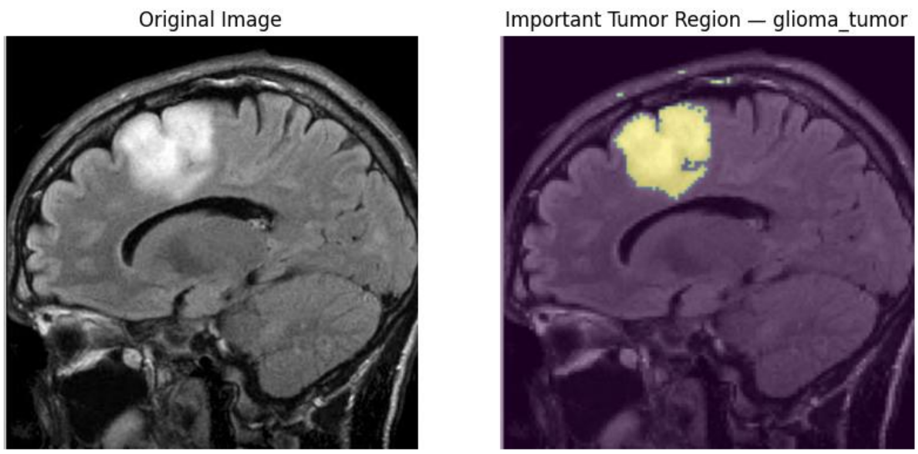

Figure 6: LIME Visualization of Brain Tumor Region

5.3 Web Application and GUI Integration

Figure 7 represents the web application interface of the proposed system, titled BrainVision DX, designed for automated brain tumor detection and classification. The interface allows users to analyze brain scans by uploading MRI images through a user-friendly web portal. Once the image is processed by the trained deep learning model, the system predicts and displays the type of brain tumor detected, as shown in the figure identifying a Pituitary Tumor. The detected result is presented clearly alongside the MRI scan for transparency. The interface integrates aesthetic design with clinical functionality, ensuring accessibility for medical professionals and researchers.

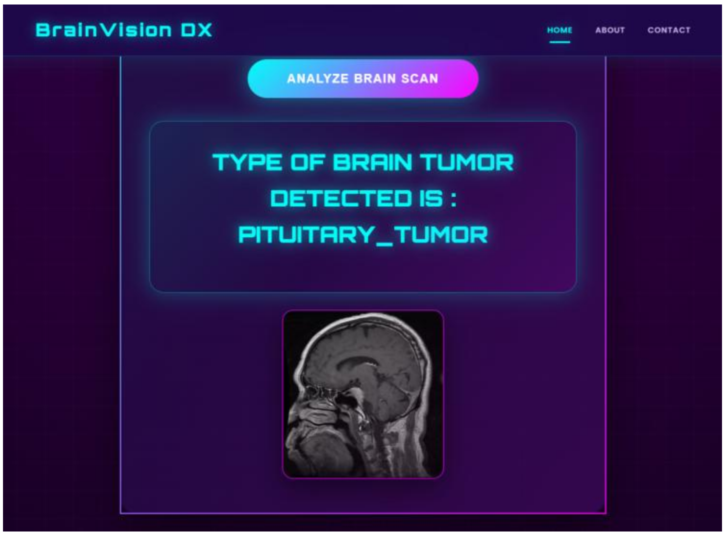

Figure 7: Web Application Interface – BrainVision DX

6 Results

6.1 Experiment 1: CNN

This study used the CNN model as the baseline, which proved to be able to recognize the type of brain tumor with a reasonable level of accuracy. The confusion matrix as presented in

Figure 8 demonstrates that CNN was able to classify most of the samples in all the four categories with great accuracy and especially in No Tumor and Pituitary classes. Nevertheless, there were certain misclassifications between Glioma and Meningioma as some areas are related to each other in the MRI scan. The model was able to have this performance by having several convolutional and pooling layers with dropout regularization, which makes the learning stable. CNN, with its simplicity and less parameters, provided a good benchmark, with regard to highly developed transfer learning models.

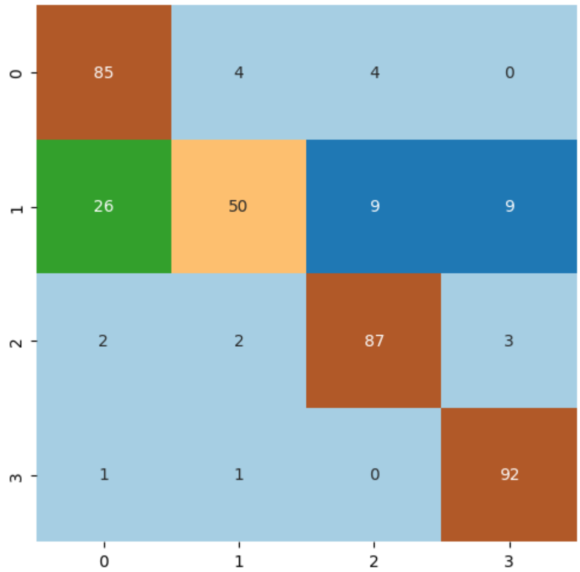

Figure 8: Confusion Matrix

6.2 Experiment 2: Exception

The Xception model achieved higher classification accuracy than the baseline CNN because depthwise separable convolutions made it effective in extracting features. The model was very successful in identifying Pituitary and Glioma tumors and minimally false classifications were produced as indicated in the confusion matrix (Figure 9). It was improved by refining all layers of the pre-trained ImageNet model to enable it adjust well to the characteristics of medical imaging. Xception also demonstrated a high level of generalization and robustness despite the increase in its computation complexity and time, which demonstrated its advantage in dealing with the complex MRI textures and subtle variations in tumor.

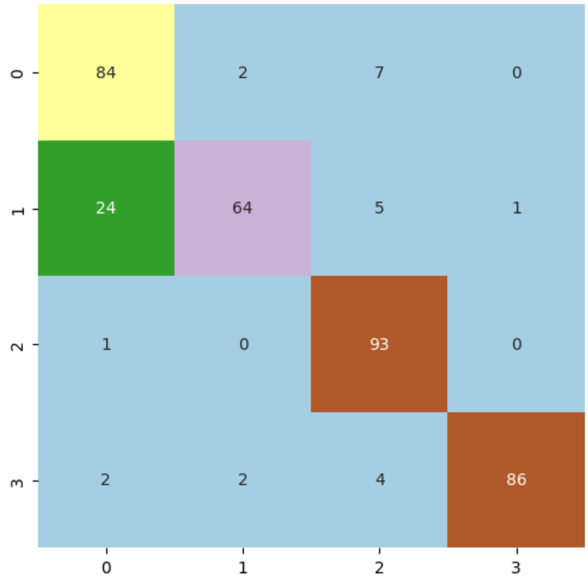

Figure 9: Confusion Matrix

6.3 Experiment 3: Inception v3

The InceptionV3 model showed very high classification in all the types of brain tumors and this shows that it has a high ability of extracting the features using the inception modules. As observed in the confusion matrix (Figure 10), the model was able to correctly classify most of the samples and had few misclassifications and especially was able to recognize Meningioma and pituitary tumors. This was accomplished through fine-tuning the pre-trained ImageNet weights and dense layers optimization to medical imaging adaptation. Even though InceptionV3 was very memory-intensive, both in terms of its depth and multi-scale feature learning, the findings show that it is highly efficient in generalization, robustness, and precision, which confirm that it is an effective tool in complex tasks of tumor classification based on MRI.

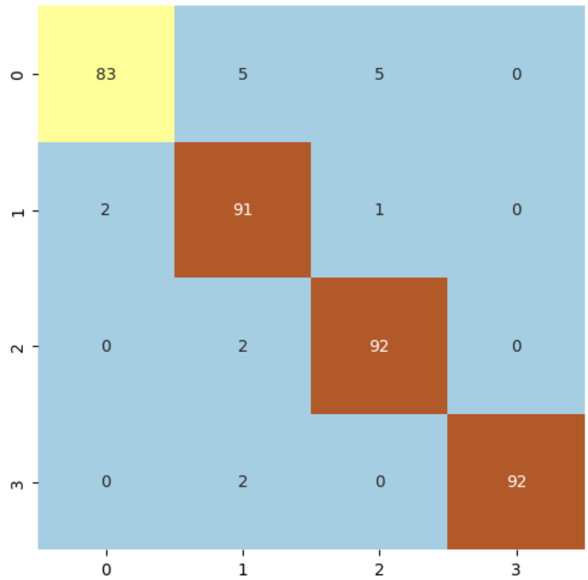

Figure 10: Confusion Matrix

6.4 Experiment 4: EfficientNet-B6

The EfficientNet-B6 model showed great classification accuracy and consistency in brain tumor classification as compared to the previous architecture because it scales its depth, width and resolution in a compound manner. The model had near-perfect predictions for all the classes as shown in the confusion matrix (Figure 11), and most especially on Meningioma and Pituitary tumors with slight misclassifications. The good performance was due to fine-tuning of pre-trained ImageNet weights and use of dropout regularization to improve generalization. The model used more computational power and required more time to train but its balanced structure facilitated efficient learning, as it yielded better accuracy, robustness and reliability in identifying fine distinctions between categories of MRI tumors.

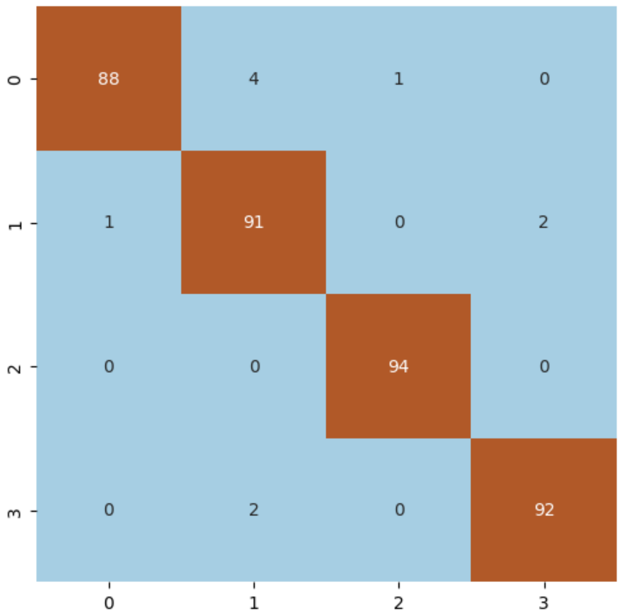

Figure 11: Confusion Matrix

6.5 Experiment 5: EFT-SA-Net

The EFT-SA-Net model proposed had the best performance as compared to the other experiments with better accuracy and stability in classification of brain tumors. The model had nearly perfect predictions without misclassifications of all four categories as shown in the confusion matrix (Figure 12). This was an exceptional performance because Spectral, Temporal, and Self-Attention mechanisms were incorporated with EfficientNetB6, such that the model could capture local and global dependencies in the MRI features. Although the attention-enhanced architecture was computationally complex and took longer to train, it had a great deal of enhancements in terms of focusing features and understanding. Hence, the EFT-SA-Net can be considered the most effective model, which can provide the highest accuracy and validity in the process of medical diagnosis in practice.

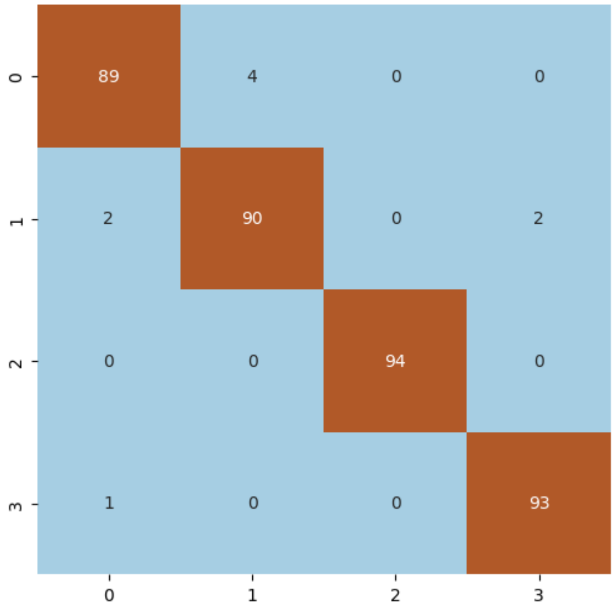

Figure 12: Confusion Matrix

Table 2 presents the comparative performance of five deep learning models—CNN, XceptionNet, InceptionV3, EfficientNet-B6, and EFT-SA-Net—based on multiple evaluation metrics. The CNN model achieved a moderate accuracy of 84%, indicating limited feature extraction capability. XceptionNet improved performance to 87% due to its deeper convolutional architecture. InceptionV3 further enhanced accuracy to 95% with optimized feature mapping. EfficientNet-B6 achieved 97% accuracy through compound scaling and better generalization. Finally, EFT-SA-Net, which integrates Spectral, Temporal, and Self-Attention mechanisms, got the best performance of 98% across all metrics, demonstrating superior learning efficiency and model interpretability.

Table 2: Comparative Performance Metrics of Different Models

Model	Accuracy	Macro Precision	Macro Sensitivity (Recall)	Macro Specificity	Macro F1
CNN	0.84	0.84	0.84	0.82	0.83
ExceptionNet	0.87	0.89	0.87	0.87	0.87
Inception	0.95	0.96	0.95	0.95	0.95
EfficientNet-B6	0.97	0.97	0.97	0.97	0.97
EFT-SA-Net → EfficientNetB6 + Spectral + Temporal + Self-Attention	**0.98**	**0.98**	**0.98**	**0.98**	**0.98**

6.6 Comparative Discussion with Baseline

The baseline study by (Zhaputri et al., 2021) implemented the EfficientNet-B1 and B2 architectures for brain tumor MRI classification and achieved a maximum accuracy of 96%.

While their approach improved efficiency compared to traditional CNNs, it lacked advanced attention mechanisms that enhance feature representation across spectral, spatial, and contextual domains. In contrast, the proposed EFT-SA-Net (EfficientNetB6 + Spectral, Temporal, and Self-Attention) introduces a hybrid attention mechanism that captures intricate inter-channel relationships and spatial dependencies, leading to improved discriminative capability as shown in Table 3. The integration of these three attention modules significantly refines feature extraction and reduces noise interference, achieving an accuracy of 98%, outperforming the baseline. Moreover, EFT-SA-Net optimizes generalization by leveraging dropout regularization and global average pooling, ensuring robust performance across multiple tumor classes. Hence, the proposed model demonstrates superior learning efficiency, enhanced interpretability, and reduced misclassification rates compared to the baseline study.

Table 3: Comparative Performance Between Baseline and Proposed Model

Parameter	(Zhaputri et al., 2021)	Proposed EFT-SA-Net
Model Architecture	EfficientNet-B1/B2	EfficientNet-B6 + Spectral, Temporal, and Self-Attention
Attention Mechanism	No attention used	Triple-Attention Integration (Spectral, Temporal, Self)
Accuracy (%)	96	98
Precision (%)	96	98
Recall (%)	96	98
F1-Score (%)	96	98
Interpretability (XAI)	Not Applied	Integrated with LIME Explainability
Key Limitation	No attention mechanism, limiting focus on crucial tumor regions	Computationally intensive but superior accuracy

7 Conclusion and Future Work

The primary research question of the study was to find out how the combination of Spectral, Temporal, and Self-Attention mechanisms into EfficientNetB6 influences the accuracy, precision, and interpretability of brain tumor classification using MRI scans and how this hybrid architecture concentrates as opposed to using traditional deep learning models. This question was answered successfully in the study through the formulation and testing of the EFT-SA-Net model, which is a new hybrid deep learning architecture, a combination of EfficientNetB6 and multi-level attention. The findings indicated that there was a high improvement in the overall classification accuracy (98%), accuracy in terms of precision, accuracy in recall and interpretability over the baseline models such as CNN, Xception, InceptionV3 among others. Transparent models were further achieved with the integration of Explainable AI (LIME) wherein critical tumor regions were identified visually, which guaranteed clinical trust and diagnostic reliability.

This study has a deep implication since it can offer a platform by which explainable and highly accurate AI-assisted tumor diagnosis can be provided to help support radiologists in clinical decision-making and minimise diagnostic error. The drawbacks are that it relies on a single set of MRI data, and computational intensive attention-based model which may not be able to work in low-resource settings in real time.

In further practice, this model may be improved based on multi-modal medical data (CT, PET scans) to increase the robustness, deploy the system on the cloud or edge platforms to run the computations faster, or enhance the explainability by using more sophisticated XAI methods (SHAP or Grad-CAM). The model also has commercial opportunities of being incorporated into diagnostic software in hospitals and telemedicine applications that can enhance the availability and intelligent healthcare solutions around the world.

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