MRI BRAIN TUMOR CLASSIFICATION USING HYBRID DATA AGUMENTATION AND A NOVEL EFFICIENT DEEP LEARNING APPROACH

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This is to certify that this project entitled **"MRI BRAIN TUMOR CLASSIFICATION USING HYBRID DATA AGUMENTATION AND A NOVEL EFFICIENT DEEP LEARNING APPROACH**" is the bonafied work carried out by **P.HARIKA J.VIGNESH P.SAIRAM A.RAMAKANTH** as a Major project for the partial fulfillment to award the degree **BACHELOR OF TECHNOLOGY** in **ELECTRONICS & COMMUNICATION ENGINEERING** during the academic year 2023-2024 under our guidance and Supervision.

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ABSTRACT

Image classification is the act of labeling groups of pixels or voxels of an image based on some rules. It finds applications in medical image analysis, and satellite image identification, along with others. learning eliminates some of data pre-processing that is typically involved with machine learning. These algorithms can ingest and process unstructured data, like text and images, and it automates feature extraction, removing some of the dependency on human experts.This project presents MRI classification through Deep Transfer learning(DTL) model . The proposed model employs a data set from the kaggle.In this we are using EfficientNET transfere learned image classification is employed we modified the EfficientNET Dataset for Brain Tumor. The performance proposed DTL model is evaluated in terms of accuracy,precision,Accuracy ,recall.The results shows that, the proposed DTL model achieves better accuracy as compared to conventional models

The multimodal MRI scans described in this article are used to categorize brain tumors based on their location and size. Brain cancers must be classified to assess the tumors and choose the most appropriate course of action for each class. Many different imaging methods are used to detect brain tumors. However, because MRI does not use ionizing radiation and generates better images, it is commonly used. Deep learning (DL), a branch of machine learning, has recently demonstrated impressive results, particularly in segmentation and classifiable tasks. In this study, a convolutional neural network-based DL model that includes EfficientNet and transfer learning is suggested to categorize several types of brain tumors utilizing publicly available datasets. The first divides cancers into three categories: glioma, meningioma, and pituitary tumor. Compared to conventional deep learning techniques, the suggested approach produces superior results. The Python platform can be used to complete the task.

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LIST OF ACRONYMS

ACRONYM	ABBREVIATION
DTL	**D**eep **T**ransfer **L**earning
CNN	**C**onvolution **N**erual **N**etwork
DL	**D**eep **L**earning
ML	**M**achine **L**earning
CL	**C**onvolution **L**ayer
SVM	**S**upport **V**ector **M**achine

CHAPTER 1
INTRODUCTION

1.1 OVERVIEW OF THE PROJECT

Thousands of people around the world have died from brain tumors, which are a lethal condition. Most brain tumours are caused by the brain's tissues growing abnormally. Because the human skull is rigid and compact, depending on where growth originates and where it is located, it can have an impact on how well the brain functions. The functionality of other body parts may also be affected if it spreads there. Depending on where the tumor is located, brain tumours are typically divided into primary and secondary classes [1]. 30% of all brain cancers are secondary, with 70% being primary tumors. Primary brain cancers are defined as tumors that originate in brain tissue, whereas secondary brain tumors start in another organ before moving to the brain by blood flow. A research by the NBTF found that in the USA, primary brain tumors claim the lives of about 13,000 people annually, out of an estimated 29,000 cases that have been diagnosed. Similar numbers show that each year in the UK, more than 42,000 people with primary brain tumors pass away.

Glioma has the highest rates of death and mobility of the different primary brain tumours [2]. High-grade (HG) and low-grade (LG) gliomas are two different types of gliomas that often develop from glial cells in the brain. The victim of HG glioma typically has a two-year survival rate. It is more intense and life-threatening. Meningioma tumours typically form in the membrane layer that serves as a cover for the spinal cord and the human brain. Meningioma tumours are often non-lethal and slow-growing. The pituitary gland, which is located at the base of the brain and is important in the synthesis of several vital hormones in the body, is where the pituitary tumour initially begins to form [12-13, 17-19]. Although a pituitary tumor is benign, significant side effects of hormone overproduction or hormonal shortages can result in permanent visual loss.

Consequently, there has been a great deal of interest in the research community for computer-aided brain tumour segmentation methods that use magnetic resonance imaging

(MRI) to identify and classify brain tumors. Therefore, tumour segmentation and identification strategies that are both automated and efficient are highly needed. The following factors make accurate tumour segmentation a difficult task even with recent advances in automated or semi-automated procedures.

First, there is a significant range in the size, shape, location, and appearance of tumours across patients. Second, because healthy surrounding tissue frequently occupies tumour sites, tumor boundaries may be irregular or hazy. Third, the accuracy of the final segmentation can be negatively impacted by the inclusion of an insufficient signal-to-noise ratio or picture distortion, which can be produced by a variety of variables, including differences in imaging equipment or MRI acquisition techniques. There are two categories of brain tumor detection techniques: deep learning (DL) and machine learning (ML) based techniques [21-22]. Among the principal components, analysis-based techniques are fuzzy random forests, fuzzy c-means, decision trees, fuzzy random forests, and support vector machines. These methods require manual features. When we talk about hand-made features, we imply that in order to initiate the learning process, the features must be extracted from the training photos. It may be necessary for an expert with in-depth knowledge to determine which characteristics are most crucial. As a result, when working with big data sets, the detection accuracy of ML-based algorithms is limited and prone to error because it depends on the quality and representation of the extracted features. Meanwhile, DL-based algorithms have shown excellent performance across a variety of sectors, including medical imaging [2]. The Convolutional neural networks (CNNs) are the most widely used or well-known deep learning (DL) model. Due to its weight-sharing mechanism, CNN can automatically learn dense features from the training data. Researchers are interested in DL-based brain tumour segmentation because of these benefits. Patch-based CNN, patch-based DCNN, multiscale patch-based CNN, fully convolution-based CNN (FCNN), and U-net brain tumour segmentation model are examples of related studies. Patch-based methods decrease the connection between picture content and labels by using a tiny subset of the image as input to the CNN and classifying each patch into a distinct class. On the contrary, pixel-wise probability distribution predictions are made by FCNN, a modified version of CNN, as

opposed to patch-wise probability distribution predictions. With this enhancement, FCNN can now provide predictions for the full image in a single pass on a full-sized image. The computational cost of existing DL-based approaches is increased due to the requirement for numerous convolutional layers (CLs) and kernels, even with the latest advancements. Consequently, there is still a need for an efficient technique that can reliably identify and segment tumours while using a less sophisticated network in terms of memory consumption and processing power.

Glioma has the greatest death and mobility rates of the different primary brain tumor forms . Low-grade (LG) and high-grade (HG) gliomas are two different types of gliomas that often develop from glial cells in the brain . The victim of HG glioma typically has a two-year survival rate . It is more intense and life-threatening. Meningioma tumors typically form in the membrane layer that serves as a cover for the human brain and spinal cord. Meningioma tumors are often non-lethal and slow-growing . The pituitary gland, which is situated at the base of the brain and is important in the synthesis of several vital hormones in the body, is where the pituitary tumor initially begins to form . Despite the fact that a pituitary tumor is benign, significant side effects from hormone overproduction or hormonal shortages can result in permanent visual loss.

Therefore, the use of computer-aided brain tumor segmentation algorithms using MRI to identify and segment brain tumors has received significant attention from the research community. Therefore, the need for automated and efficient tumor segmentation and detection techniques is great. Despite recent developments in automated or semi-automated tumor segmentation techniques, accurate tumor segmentation remains a challenging task for the following reasons . First, there is considerable variation in tumor location, shape, appearance, and size from patient to patient . Second, tumor boundaries may be discontinuous or blurred because tumor areas are often occupied by surrounding healthy tissue. Third, the addition of insufficient signal-to-noise ratio or image distortion often caused by various factors such as MRI acquisition protocols or variations in imaging equipment can further increase the difficulty and affects the accuracy of the final

segmentation .Brain tumor detection methods can be divided into two types, called machine learning (ML)-based methods and deep learning (DL)-based methods. ML-based techniques mainly include support vector machines , conditional random forests , decision trees , principal component analysis , and fuzzy c-means . These techniques require manual features. Handcrafted features here means that the features need to be extracted from the training images to start the learning process and perhaps an expert with in-depth knowledge is needed to identify the features most important.

Therefore, the detection accuracy of ML-based techniques depends on the quality and representation of extracted features, and is therefore limited and error-prone when dealing with large data sets. Meanwhile, DL-based algorithms have shown high performance in various industries, including medical imaging . The most popular or well-known DL model is the convolutional neural network (CNN), which can instinctively learn dense features directly from training data due to its weight-sharing nature . Based on these advantages, brain tumor segmentation based on DL has attracted the attention of researchers . Related works include patch-based CNN , multi-scale patch-based CNN , patch-based DCNN, fully convolution-based CNN (FCNN) and based on U-net brain tumor segmentation model. Patch-based approaches take a small portion of the image as input to the CNN and classify each patch into a different class, which reduces the correlation between image content and labels. On the other hand, FCNN is a modified form of CNN that predicts the pixel-wise probability distribution instead of making patch-wise probability distribution predictions . This improvement allows FCNN to take a full-sized image and perform predictions for the entire image in one pass. Despite recent advances, current DL-based techniques require multiple convolutional layers (CLs) and kernels, thereby increasing the computational cost. Therefore, an effective method for accurate tumor identification and segmentation with a less complex network in terms of memory usage and computational resources is still required.

MRI scans, though crucial for brain tumor diagnosis, rely on subjective analysis by radiologists. Deep learning offers a powerful alternative. Deep learning models, especially

convolutional neural networks, can learn intricate features from various MRI modalities (T1-weighted, etc.) to identify and classify tumors automatically. This not only improves efficiency but has the potential to surpass traditional methods in accuracy. Training these models requires large datasets, often addressed through data augmentation techniques. Once trained, the models can assist radiologists by segmenting the tumor and providing classification, leading to faster and potentially more accurate diagnoses. Future research is geared towards creating AI models that can explain their reasoning, building trust and paving the way for deeper integration into clinical practice.

MRI brain tumor classification using deep learning methods represents a cutting-edge approach in medical imaging and diagnosis. Magnetic Resonance Imaging (MRI) provides detailed images of the brain, enabling the detection and characterization of tumors. Deep learning techniques, particularly convolutional neural networks (CNNs), have shown remarkable promise in automating the process of tumor classification. By analyzing vast amounts of MRI data, these neural networks can learn to distinguish between different types of brain tumors with high accuracy. This approach not only expedites the diagnosis process but also enhances its accuracy, potentially leading to earlier detection and better treatment outcomes for patients. Moreover, deep learning methods have the potential to assist radiologists by providing additional insights and reducing the burden of manual interpretation. As research in this field progresses, the synergy between MRI imaging and deep learning continues to advance the capabilities of brain tumor classification, offering hope for more effective interventions and improved patient care.

Certainly! In MRI brain tumor classification using deep learning methods, the key lies in the utilization of convolutional neural networks (CNNs) to automatically extract relevant features from MRI images. CNNs are particularly well-suited for this task due to their ability to learn hierarchical representations of data, making them adept at recognizing patterns within complex images like those generated by MRI scans.

One significant advantage of deep learning-based classification is its potential for multi-class classification, allowing for the differentiation of various types of brain tumors, including gliomas, meningiomas, and metastases. This capability is crucial because different tumor types often require different treatment strategies and have varying prognoses.

Furthermore, the development of robust and interpretable deep learning models is essential for clinical adoption. Researchers are not only focusing on improving the accuracy of classification but also on understanding the features learned by these models to enhance their interpretability and reliability. This interpretability aspect is crucial for gaining trust from medical professionals and ensuring the safe and effective integration of deep learning algorithms into clinical practice.

Moreover, ongoing efforts aim to address challenges such as data scarcity and model generalization across different imaging protocols and scanner types. Data augmentation techniques and transfer learning approaches are being explored to mitigate these challenges and improve the robustness of deep learning models for brain tumor classification.

Additionally, the integration of clinical data, such as patient demographics, genetic information, and histopathological findings, with MRI images holds promise for enhancing the accuracy and personalized nature of tumor classification models. By leveraging a holistic approach that combines imaging data with clinical information, deep learning methods can provide more comprehensive insights into brain tumor characterization and prognosis.

Overall, MRI brain tumor classification using deep learning methods represents a dynamic and rapidly evolving field at the intersection of medical imaging and artificial intelligence. Continued research and collaboration between clinicians, researchers, and machine learning experts are essential for advancing the capabilities of these technologies and ultimately improving patient outcomes in the diagnosis and treatment of brain tumors.

CHAPTER 2
LITERATURE SURVEY

2.1 EXISTING METHODS

2.1.1 **Convolutional Neural Networks (CNNs):** CNNs have been widely used for MRI brain tumor classification. They can automatically learn spatial hierarchies offeature from MRI images and have been effective in tasks such as tumor detection, segmentation, and classification.

2.1.2 **Transfer Learning:** Transfer learning involves using pre-trained models on large datasets for feature extraction, which can then be fine-tuned for specific tasks such as brain tumor classification. Models like VGG, ResNet, and Inception have been used in transfer learning for MRI brain tumor classification.

2.1.3 **Support Vector Machines (SVMs):** SVMs have been used for brain tumor classification by extracting features from MRI images and training the SVM model on these features. They can be effective in binary classification tasks where the goal is to distinguish between tumor and non-tumor regions.

2.1.4 **Random Forests**: Random Forests are ensemble learning methods that have been applied to MRI brain tumor classification. They can handle a large number of features and have the capability to provide feature importance, which can be valuable for understanding the characteristics of different tumor types.

2.1.5 **Deep Learning Architectures:** Apart from CNNs, other deep learning architectures such as U-Net, DenseNet, and Residual Networks have been employed for tasks like brain tumor segmentation and classification. These architectures leverage the power of deep learning to handle complex patterns and variations in the MRI images.

2.1.6 **Ensemble Learning**: Ensemble learning methods, including bagging and boosting techniques, have been used to combine multiple classifiers to improve the overall classification performance. These methods can help improve the robustness and generalization of the model for MRI brain tumor classification.

2.1.7 **Radiomics Analysis**: Radiomics involves the extraction of a large number of quantitative features from medical images, including MRI scans. These features can be used to build predictive models for tumor classification, leveraging the information hidden in the imaging data that might not be apparent to the human eye.

2.1.8 **Traditional Machine Learning Algorithms:** Before the rise of deep learning, traditional machine learning algorithms such as support vector machines (SVMs), random forests, and k-nearest neighbors (KNN) were commonly used for brain tumor classification. These methods rely on handcrafted features extracted from MRI images, such as intensity histograms, texture features, and shape descriptors. While these approaches can achieve reasonable classification performance, they often require extensive feature engineering and may struggle to capture complex spatial patterns present in MRI data.

2.1.9 **Feature-based Methods:** Feature-based methods involve extracting a set of informative features from MRI images and using these features as input to a classification algorithm. Feature extraction techniques include wavelet transforms, histogram of oriented gradients (HOG), and local binary patterns (LBP). While feature-based methods can provide interpretable results and are less computationally intensive compared to deep learning approaches, their performance may be limited by the handcrafted nature of the features and their inability to capture high-level representations.

2.1.10 **Deep Learning:** Deep learning techniques, particularly convolutional neural networks (CNNs), have revolutionized MRI brain tumor classification by automatically learning hierarchical representations directly from the raw MRI data. CNNs can

analyze entire MRI volumes and learn spatial patterns and relationships between voxels, enabling more accurate and robust tumor classification. Deep learning architectures such as 3D CNNs, 2D CNNs with transfer learning, and recurrent neural networks (RNNs) have been applied to MRI brain tumor classification tasks with impressive results. These models have the advantage of scalability, allowing them to handle large datasets and learn complex features without manual intervention.

2.1.11 **Ensemble Methods**: Ensemble methods combine multiple classifiers to improve classification performance. Techniques such as bagging, boosting, and stacking have been applied to MRI brain tumor classification to enhance the robustness and generalization ability of classification models. By aggregating the predictions of multiple base classifiers, ensemble methods can reduce overfitting and achieve higher accuracy compared to individual classifiers.

2.1.12 **Hybrid Approaches:** Hybrid approaches combine traditional machine learning algorithms with deep learning techniques to leverage the strengths of both methodologies. For example, handcrafted features extracted using traditional methods can be combined with features learned by deep learning models to improve classification performance. Hybrid approaches offer flexibility and can be tailored to specific datasets and classification tasks.

Overall, the choice of method for MRI brain tumor classification depends on factors such as the complexity of the classification task, the size and quality of the available data, computational resources, and the interpretability requirements of the application. Advances in machine learning and medical imaging continue to drive innovation in brain tumor classification, with the ultimate goal of improving diagnosis and treatment outcomes for patients.

2.2 RELATED WORK

Recently, deep learning has shown considerable potential in the identification and categorisation of brain tumors. As a new deep learning model for brain tumor classification, the BTFSC-Net combines magnetic resonance imaging (MRI) and CT (CT) scans to derive supplementary characteristics. The BTFSC-Net, a very promising deep learning network, shows great potential for use in clinical settings to improve the accuracy and efficiency of brain tumor classification [3].

2.2.1 Deep-transfer learning shows great potential as a method for detecting brain tumours. Multiple deep transfer learning networks are evaluated on the BraTS-2017 dataset for performance. The authors proposed using these networks to create therapeutic tools for the timely identification of brain cancers [4].

2.2.2 Classifying brain images is a difficult undertaking due to the intricate and diverse characteristics of the images. This study introduces an innovative deep learning model for classifying brain images, which uses the architecture of a Feed Forward Neural Network (FF-ANN). The model employs a hybrid methodology that integrates diverse classifiers, together with feature selection and a substantial dataset, to improve its performance. The authors assert that their proposed model is a proficient and successful approach for classifying brain images [6].

2.2.3 Brain tumor classification poses a challenging problem, but, deep learning models have exhibited exceptional promise in this field. This study introduces a novel deep learning model based on convolutional neural networks (CNNs) that utilizes a more complex structure and improves its performance by employing data augmentation and transfer learning techniques. The authors claim that their proposed model is a proficient and successful approach for categorising brain tumors, with potential applications in the development of therapeutic systems for the timely identification and detection of brain cancers [7].

2.2.4 The researcher introduces two innovative methodologies: a convolutional neural network (CNN) model for the classification of glioma grades, and an adaptive strategy that utilises histogram information for tumour segmentation. The proposed classification methodology partitions the MRI data into two distinct categories utilizing a Convolutional Neural Network (CNN) model to extract features from the images: Gliomas identified as either high-grade (HGG) or low-grade (LGG). The proposed segmentation technique initially normalizes the MRI images and subsequently integrates the various modalities. Subsequently, it obtains histogram characteristics from the fused image and uses them to partition the tumor area. The authors' conclusion asserts the use of their proposed approaches for segmenting and classifying brain tumour grades. Furthermore, these methods have the potential to be used in the development of clinical systems aimed at detecting and diagnosis of brain tumors [8].

2.2.5 The author suggests a novel deep learning model that utilizes a more complex CNN architecture, enhances performance through data augmentation and transfer learning. Upon evaluation using the BraTS-2017 dataset, the proposed model demonstrated state-of-the-art performance in the identification and categorisation of brain tumors [9].

2.2.6 The author presents a novel computer-aided diagnosis model that employs ensemble learning approaches to effectively utilise magnetic resonance imaging (MRI) data and classify brain tumours. Researchers create a robust framework that enhances classification accuracy by integrating multiple supervised machine learning approaches such as SVMs, random forests, and gradient boosting. This method shows that ensemble learning can improve medical diagnostic imaging [11].

2.2.7 This study addressed the difficult challenge of brain tumour detection in MRI scans using a large brain tumour image collection. The author demonstrated that implementing transfer learning to fine-tune a state-of-the-art YOLOv7 model significantly improved its ability to detect pituitary brain tumours, meningiomas, and

gliomas. Continued study is required to identify tiny tumours in the brain due to their intricate nature, as well as the need for continuous improvements in detection techniques. The author aims to enhance the diagnostic capabilities of physicians and patients in the difficult fight against brain tumours by following this approach [24].

2.2.8 The author uses a distinctive Graph Convolutional Neural Network (GCNN) structure to provide a feasible approach for classifying the grades of gliomas and brain tumors. Consequently, the GCNN is applicable in scenarios where resources are few and real-time tasks are involved. Moreover, the concise and clear elucidation facilitates the comprehension and reproduction by other researchers [16].

2.3 MOTIVATION

2.3.1 **Early Detection and Diagnosis:** Early detection of brain tumors is crucial for timely intervention and improved patient outcomes. MRI brain tumor classification aids in the early identification of tumors, enabling healthcare professionals to initiate prompt and appropriate treatment strategies.

2.3.2 **Treatment Planning and Monitoring:** Accurate classification of brain tumors through MRI imaging assists in formulating personalized treatment plans. It helps in determining the most effective treatment approach, such as surgery, chemotherapy, or radiation therapy, tailored to the specific characteristics and type of the identified tumor.

2.3.3 **Enhanced Patient Care:** Effective MRI brain tumor classification contributes to enhanced patient care by providing healthcare professionals with comprehensive insights into the nature, size, and location of the tumor. This, in turn, facilitates better patient management and care coordination, leading to improved quality of life for individuals undergoing treatment.

2.3.4 **Research and Development:** Advancements in MRI brain tumor classification support ongoing research and development in the field of medical imaging and oncology. By exploring innovative methodologies and technologies, researchers can continuously improve the accuracy, efficiency, and reliability of tumor classification, thereby advancing the understanding and treatment of various types of brain tumors.

2.3.5 **Reducing Manual Workload:** MRI brain tumor classification methods have the potential to reduce the burden on radiologists and healthcare providers by automating time-consuming and labor-intensive tasks. By leveraging machine learning and deep learning algorithms, these methods can assist radiologists in interpreting MRI scans more efficiently, freeing up their time to focus on other aspects of patient care.

2.3.6 **Improving Accuracy and Reliability:** Traditional methods of brain tumor classification, while effective, may be prone to human error and variability. By harnessing the power of machine learning and deep learning techniques, MRI brain tumor classification methods aim to improve the accuracy and reliability of tumor classification, minimizing diagnostic errors and discrepancies.

2.3.7 **Advancements in Imaging Technology:** The increasing availability of high-quality MRI imaging data, coupled with advancements in computational resources and machine learning algorithms, has created new opportunities for innovation in brain tumor classification. Researchers are motivated to leverage these technological advancements to develop more sophisticated and accurate classification models that can exploit the rich information contained within MRI scans.

2.3.8 **Research and Clinical Translation:** MRI brain tumor classification research bridges the gap between academia and clinical practice, facilitating the translation of cutting-edge research findings into real-world applications. By collaborating with clinicians and healthcare institutions, researchers can validate and refine their classification methods, ultimately improving patient care and outcomes in clinical settings.

2.3.9 **Prognostic Assessment:** Accurate classification of brain tumors is essential for prognostic assessment, helping clinicians predict disease progression and patient outcomes. By characterizing tumors based on their histological and molecular features, MRI brain tumor classification methods can provide valuable insights into prognosis, guiding treatment decisions and patient counseling.

2.3.10 **Monitoring Treatment Response:** MRI brain tumor classification techniques play a crucial role in monitoring treatment response and assessing the effectiveness of therapies over time. By tracking changes in tumor characteristics and dynamics on follow-up MRI scans, clinicians can evaluate treatment efficacy, adjust therapeutic regimens, and make informed decisions regarding patient management.

2.3.11 **Facilitating Research and Innovation:** MRI brain tumor classification research serves as a catalyst for innovation and scientific discovery in the field of neuro-oncology. By developing novel computational methodologies and analytical techniques, researchers aim to uncover new biomarkers, elucidate disease mechanisms, and identify potential therapeutic targets for brain tumors. These advancements contribute to a deeper understanding of tumor biology and facilitate the development of innovative treatment strategies.

2.3.12 **Addressing Clinical Challenges:** Brain tumor classification presents several clinical challenges, including tumor heterogeneity, overlapping imaging features, and variability in tumor morphology. MRI brain tumor classification methods aim to address these challenges by leveraging advanced machine learning algorithms and multimodal imaging data fusion techniques. By integrating complementary information from various MRI sequences (such as T1-weighted, T2-weighted, and diffusion-weighted imaging), these methods enhance the discriminative power and robustness of tumor classification models.

2.3.13 **Improving Patient Care and Quality of Life:** Ultimately, the overarching goal of MRI brain tumor classification research is to improve patient care and enhance the

quality of life for individuals affected by brain tumors. By providing accurate and timely diagnosis, personalized treatment recommendations, and prognostic information, these methods empower patients and healthcare providers to make informed decisions and optimize patient outcomes. Moreover, by facilitating early detection and intervention, MRI brain tumor classification contributes to improved survival rates and enhanced quality of life for patients living with brain tumors.

2.3.14 **Addressing Healthcare Disparities**: MRI brain tumor classification research aims to address healthcare disparities by democratizing access to advanced diagnostic tools and personalized treatment options. By developing automated classification algorithms that are robust, scalable, and applicable across diverse patient populations and healthcare settings, researchers seek to bridge gaps in healthcare access and improve outcomes for underserved communities. Additionally, efforts to standardize imaging protocols and optimize algorithm performance in resource-constrained environments contribute to equitable healthcare delivery worldwide.

2.3.15 **Driving Technological Innovation:** MRI brain tumor classification research drives technological innovation in medical imaging and artificial intelligence. By pushing the boundaries of algorithmic performance, computational efficiency, and clinical utility, researchers spur the development of next-generation imaging technologies and intelligent diagnostic systems. This continuous cycle of innovation enhances the capabilities of MRI scanners, image reconstruction algorithms, and machine learning frameworks, paving the way for more accurate, reliable, and patient-centric approaches to brain tumor diagnosis and management.

2.3.16 **Empowering Patient Advocacy and Education:** MRI brain tumor classification research empowers patients and caregivers to advocate for their own healthcare needs and make informed decisions about treatment options. By increasing awareness of the role of imaging biomarkers in brain tumor diagnosis and prognosis, researchers enable patients to actively participate in discussions with their healthcare providers and contribute to shared decision-making processes. Moreover, efforts to disseminate

knowledge through patient education initiatives and advocacy organizations empower individuals affected by brain tumors to seek support, access resources, and engage in research efforts aimed at improving outcomes for future generations.

2.3.17 **Exploring Novel Biomarkers**: MRI brain tumor classification research endeavors to identify and validate novel imaging biomarkers that can serve as indicators of tumor aggressiveness, treatment response, and patient prognosis. By leveraging advanced image analysis techniques and machine learning algorithms, researchers aim to extract quantitative imaging features that correlate with underlying tumor biology and clinical outcomes. These biomarkers have the potential to augment traditional histopathological assessments and provide non-invasive insights into tumor behavior and patient management.

2.3.18 **Enhancing Interdisciplinary Collaboration:** MRI brain tumor classification research fosters interdisciplinary collaboration between radiologists, neurosurgeons, oncologists, computer scientists, and biomedical engineers. By bringing together expertise from diverse fields, researchers can leverage complementary knowledge and perspectives to develop innovative approaches for tumor classification, interpretation, and treatment planning. This collaborative effort promotes synergy and cross-fertilization of ideas, driving advancements in both clinical practice and academic research.

2.4 SCOPE OF THE WORK:

2.4.1 **Algorithm Development and Optimization:** The scope of work involves the development and optimization of advanced algorithms and models for MRI brain tumor classification. This includes the exploration of various machine learning and deep learning techniques, as well as the integration of cutting-edge methodologies to enhance the accuracy and efficiency of classification.

2.4.2 **Data Analysis and Interpretation:** Analyzing and interpreting complex MRI data is a critical aspect of the work scope. Researchers delve into the intricate details of MRI images, extracting meaningful patterns, features, and biomarkers that contribute to the accurate classification and characterization of brain tumors.

2.4.3 **Integration of Multimodal Imaging:** The scope extends to the integration of multimodal imaging techniques, such as functional MRI (fMRI), diffusion tensor imaging (DTI), and perfusion-weighted imaging (PWI), to provide a comprehensive and holistic understanding of brain tumor characteristics. Integrating these modalities enables a more comprehensive assessment and accurate classification of tumors based on their distinct imaging signatures.

2.4.4 **Clinical Application and Validation**: Implementing and validating the developed models and algorithms in a clinical setting forms a crucial part of the work scope. This involves rigorous testing, validation, and real-world application of the classification systems to ensure their reliability, accuracy, and compatibility with existing clinical protocols and practices.

2.4.5 **Collaboration and Interdisciplinary Research**: The scope extends to collaboration and interdisciplinary research efforts involving healthcare professionals, radiologists, data scientists, and biomedical engineers. Collaborative research initiatives foster the exchange of knowledge and expertise, leading to the development of comprehensive and effective solutions for MRI brain tumor classification.

2.4.6 **Data Collection and Preprocessing:**Gathering MRI datasets containing images of patients with brain tumors. This involves obtaining consent from patients and ensuring data privacy.Preprocessing MRI images to standardize formats, correct artifacts, and normalize intensities. Preprocessing may also involve skull stripping, registration, and bias field correction.

2.4.7 **Feature Extraction and Representation:**Extracting relevant features from MRI images that can effectively discriminate between different types of brain tumors and healthy tissue.Feature representation can include intensity-based features, texture features, shape features, and features derived from different MRI sequences (e.g., T1-weighted, T2-weighted, FLAIR).

2.4.8 **Model Development and Training**:Designing and implementing machine learning or deep learning models for tumor classification. This includes choosing appropriate architectures, optimization algorithms, and regularization techniques.Training the models using labeled MRI datasets. This involves splitting the data into training, validation, and test sets and tuning hyperparameters to optimize performance.

2.4.9 **Evaluation and Validation:**Evaluating the performance of the trained models using metrics such as accuracy, sensitivity, specificity, and area under the receiver operating characteristic curve (AUC-ROC).Cross-validation and external validation on independent datasets are essential to assess the generalization ability of the models.

2.4.10 **Clinical Integration and Interpretability**:Integrating the developed models into clinical workflows for assisting radiologists and clinicians in diagnosing brain tumors.Ensuring interpretability of the models by providing explanations for their predictions. Interpretability techniques such as saliency maps, attention mechanisms, and feature importance analysis help in understanding the model's decision-making process.

2.4.11 **Robustness and Generalization:**Investigating the robustness of the models to variations in MRI acquisition parameters, scanner types, and patient

demographics.Generalizing the models to different tumor types, grades, and anatomical locations to ensure their applicability across diverse clinical scenarios.

2.4.12 **Ethical and Regulatory Considerations**:Adhering to ethical guidelines and regulatory requirements for handling patient data, ensuring patient privacy, and obtaining necessary approvals for conducting research involving human subjects.Ensuring transparency and accountability in model development, deployment, and usage.

2.4.13 **Clinical Impact and Translation**:Assessing the clinical impact of the developed models in terms of diagnostic accuracy, efficiency, and patien outcomes.Collaborating with clinicians and stakeholders to facilitate the translation of research findings into clinical practice, potentially leading to improved patient care and management strategies.

2.5 PROBLEM STATEMENT:

2.5.1 To improve the generalizability of the network or To improve the performance of the network by using more than one dataset.

2.5.2 To address overfitting issues and small dataset, we can use hybrid data agumentation.

2.5.3 To remove the bias towards the selecting of the training data (70%+30%, 90%+10%,80%+20%).

2.5.4 To improve the overall performance we can use a novel CNN method.

CHAPTER 3

PROPOSED METHODOLOGY

3.1 DESCRIPTION

The proposed CNN model was trained and then put to the test on the Google Colab, a well-known cloud-based laptop with access to high-performance graphics processing units (GPUs).I've used **CNN** to perform Image Classification on the Brain Tumor dataset.

Since this dataset is small, if we train a neural network to it, it won't really give us a good result.

Therefore, this project going to use the concept of **Transfer Learning** to train the model to get really accurate results.

This section outlines the implementation of the proposed strategy and provides the following description.

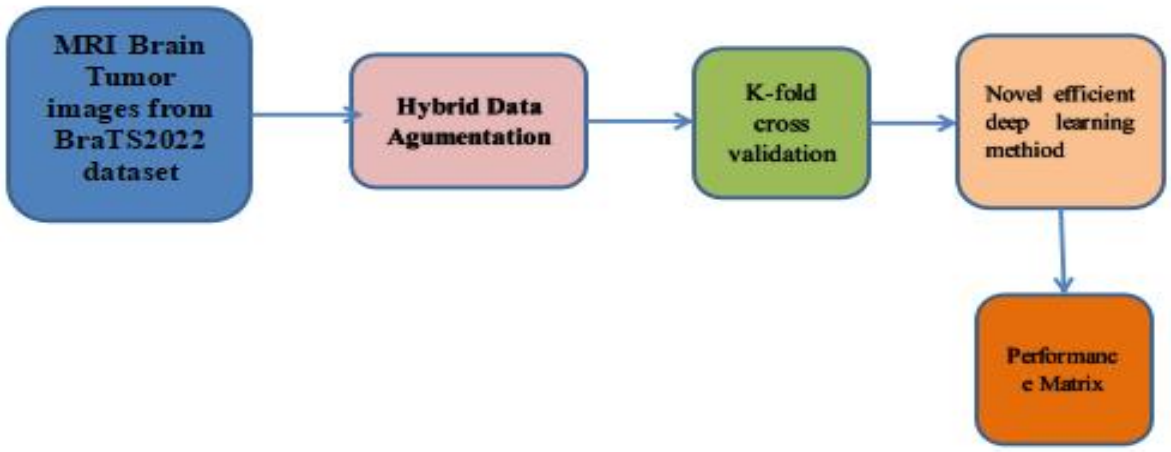

Fig.1. The general block diagram for the proposed method

3.2 Hybrid Data Agumentation

Hybrid data augmentation for MRI brain tumor classification involves employing a combination of techniques to enrich the training dataset used for training machine learning models. MRI images provide detailed information crucial for diagnosing brain tumors, but the availability of labeled data for training can be limited. To address this challenge, hybrid augmentation techniques are applied, including rotations, flips, scaling, translations, and adjustments to brightness or contrast. Moreover, domain-specific augmentation methods are utilized to simulate variations in tumor appearance and imaging conditions, ensuring that the model learns to recognize diverse tumor characteristics. Maintaining class balance is essential to prevent bias in model predictions, so augmentation strategies are carefully designed to preserve the relative proportions of different tumor types. By training on an augmented dataset, machine learning models can better generalize to unseen data and demonstrate improved performance in accurately classifying MRI brain tumor images.

Hybrid data augmentation for MRI brain tumor classification represents a sophisticated approach to bolstering the efficacy of machine learning models in interpreting MRI scans. MRI is a staple tool in diagnosing brain tumors, offering high-resolution images that reveal intricate details of brain anatomy. However, the success of machine learning models in this domain heavily relies on the availability and diversity of training data. Given the challenges associated with obtaining large, diverse datasets, especially concerning rare tumor types, data augmentation emerges as a pivotal technique. By combining various augmentation methods such as geometric transformations (e.g., rotations, flips, and scaling) and pixel-level manipulations (e.g., adjusting brightness, contrast, and introducing noise), a hybrid approach ensures the generation of a rich and varied training dataset. Importantly, domain-specific augmentation techniques are integrated to emulate realistic variations in tumor appearance and imaging conditions, thus enhancing the model's adaptability to real-world scenarios. Furthermore, strategies are employed to address class imbalance, crucial for ensuring the model's ability to accurately classify different tumor types. Through training on

augmented data, machine learning models are equipped with robustness and generalization capabilities, enabling them to effectively classify MRI brain tumor images with improved accuracy and reliability, ultimately contributing to enhanced clinical decision-making and patient care.

3.3 K-Fold Cross Validation

K-fold cross-validation is a widely employed technique for assessing the performance of machine learning models, particularly in scenarios with limited data, such as MRI brain tumor classification. In this method, the original dataset is partitioned into k subsets of approximately equal size. The model is then trained and evaluated k times, with each subset serving as the validation data once while the remaining k-1 subsets are used for training. This process allows for comprehensive evaluation, as each data point is used for validation exactly once. In the context of MRI brain tumor classification, k-fold cross-validation helps ensure that the model's performance metrics, such as accuracy, sensitivity, and specificity, are robust and not heavily influenced by the particular choice of training and testing data. Moreover, it provides insights into the model's ability to generalize to unseen data, which is crucial for its clinical utility. By iteratively training and evaluating the model on different subsets of the data, k-fold cross-validation enables researchers and clinicians to make informed decisions about model selection and parameter tuning, ultimately leading to more reliable and effective brain tumor classification systems.

K-fold cross-validation is a fundamental technique in machine learning for evaluating model performance, especially when dealing with limited datasets, as often encountered in MRI brain tumor classification. In this method, the dataset is divided into k subsets, or "folds," where each fold is used once as the validation set while the remaining k-1 folds are used for training. This process is repeated k times, with each fold serving as the validation set exactly once. The performance metrics, such as accuracy, precision, recall, and F1-score, are then averaged over the k iterations to obtain a more reliable estimate of the model's performance. K-fold cross-validation provides several benefits in MRI brain tumor

classification. Firstly, it helps in mitigating the risk of overfitting by assessing the model's performance on multiple validation sets. Secondly, it ensures that the evaluation is not biased by the specific partitioning of the data, thus providing a more robust estimation of the model's generalization ability. Additionally, k-fold cross-validation allows researchers to explore the variability in model performance across different subsets of the data, providing insights into the model's stability and reliability. Overall, k-fold cross-validation is a valuable tool in the development and evaluation of machine learning models for MRI brain tumor classification, enabling more accurate and reliable diagnoses in clinical settings.

3.4 Novel Efficient Deep Learning Method

Efficient deep learning methods are continuously advancing to mitigate challenges like model complexity and resource demands. Techniques such as sparse neural networks, which prune insignificant connections or entire neurons, contribute to reducing model size and inference time without sacrificing performance. Knowledge distillation transfers insights from larger models to smaller ones, minimizing memory usage and computational costs. Quantization decreases precision in weights and activations, diminishing memory footprints and computational expenses. Neural Architecture Search (NAS) automates the exploration of architecture design spaces, yielding models tailored to specific resource constraints. Transfer learning and few-shot learning leverage pre-trained models to swiftly adapt to new tasks with minimal data. Attention mechanisms focus on pertinent input elements, optimizing computational efficiency. Dynamic computation graphs and knowledge-based compression further refine model efficiency through adaptive graph construction and domain-specific constraints, respectively. These approaches collectively drive advancements in deep learning, promising models that are not only effective but also economical in terms of resources and computation.

Efficient deep learning methods encompass a spectrum of techniques aimed at optimizing model performance while minimizing computational resources. Sparse neural networks employ pruning strategies to trim redundant connections or neurons, reducing model size and inference time without compromising accuracy. Knowledge distillation

transfers insights from complex models to smaller counterparts, enabling streamlined inference on resource-constrained devices. Quantization reduces numerical precision, shrinking model footprints and facilitating faster computations on hardware platforms. Neural Architecture Search automates the quest for optimal model architectures, tailoring designs to specific constraints or tasks. Transfer learning and few-shot learning leverage pre-trained models to expedite learning on new tasks with limited data. These methods collectively represent a concerted effort to democratize deep learning, making it more accessible across diverse applications and platforms by striking a balance between performance and efficiency.

3.5 Dataset

Brain tumor images from the BraTS2022 database [23] have been used to assess the effectiveness of the proposed approach.

Brain tumor images can be classified into several disease categories, such as glioma tumors (91), meningioma tumors (96), healthy (53), and pituitary tumors (87) (refer to Fig. 3). The number of images is 327 in total. Fig. 2 depicts the sample images of the MRI brain tumor.

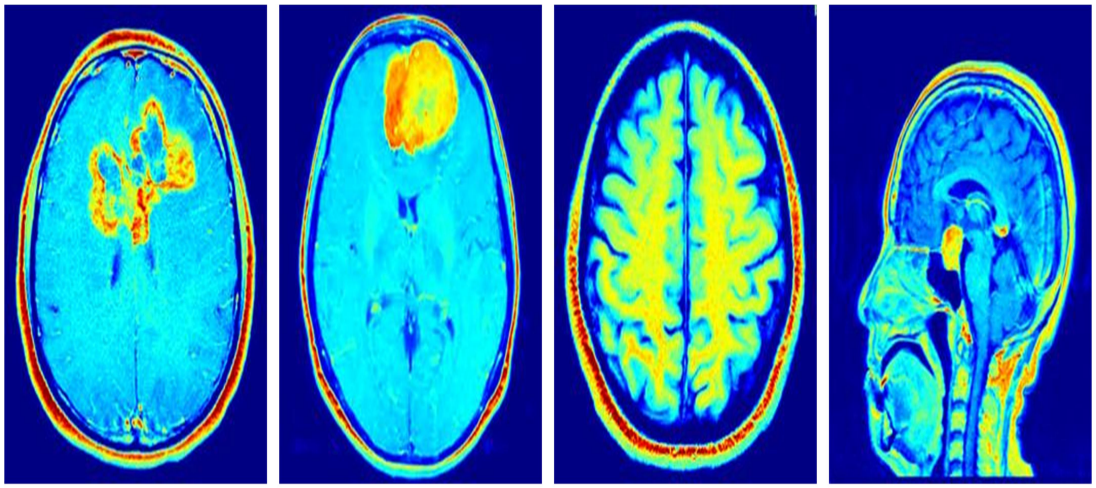

Fig.2. Sample MRI brain tumor images (a) Glioma tumor, (b) Meningioma tumor, (c) Healthy and (d) Pituitary tumor

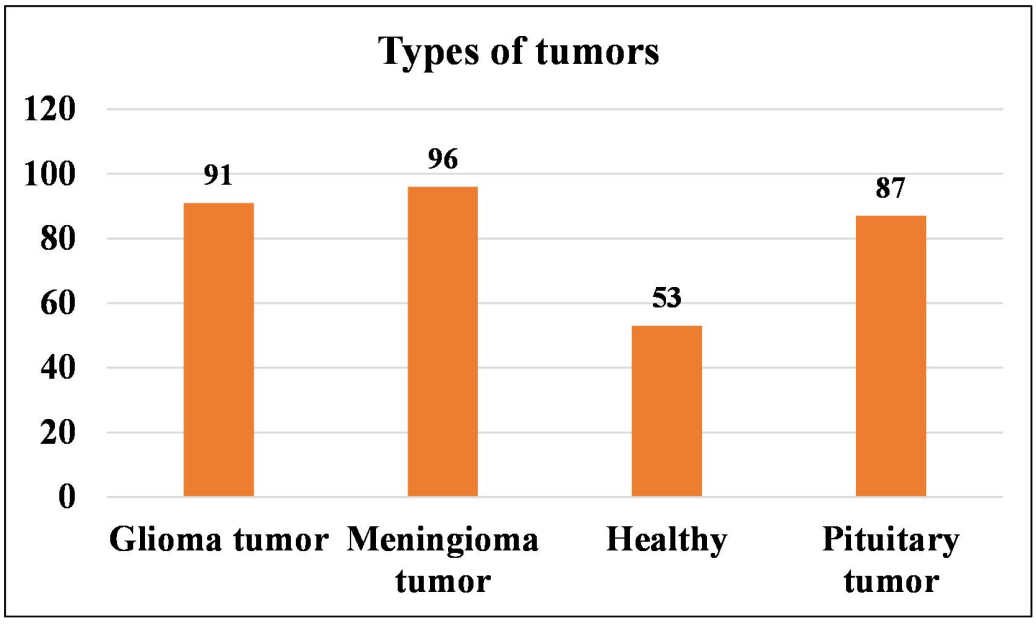

Fig. 3. Different types of MRI brain tumor image data

3.6 EfficientNet CNN model

The proposed CNN model is described as follows (refer to Fig.4):

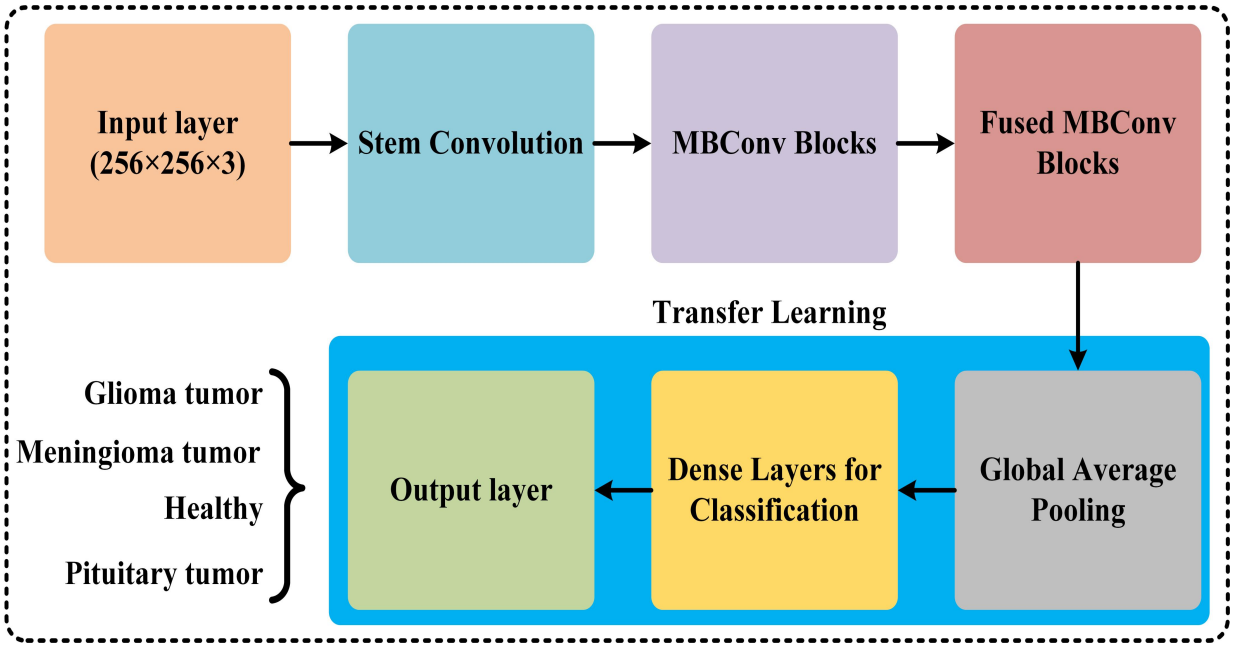

Fig. 4. Proposed block diagram of the EfficientNet with transfer learning

Input Layer:

Input layer with shape (256, 256, 3) representing the image size (256x256) with three color channels (RGB).

Stem Convolution:

Initial convolutional layer to process the input image. Applies convolutional operations to capture basic features.

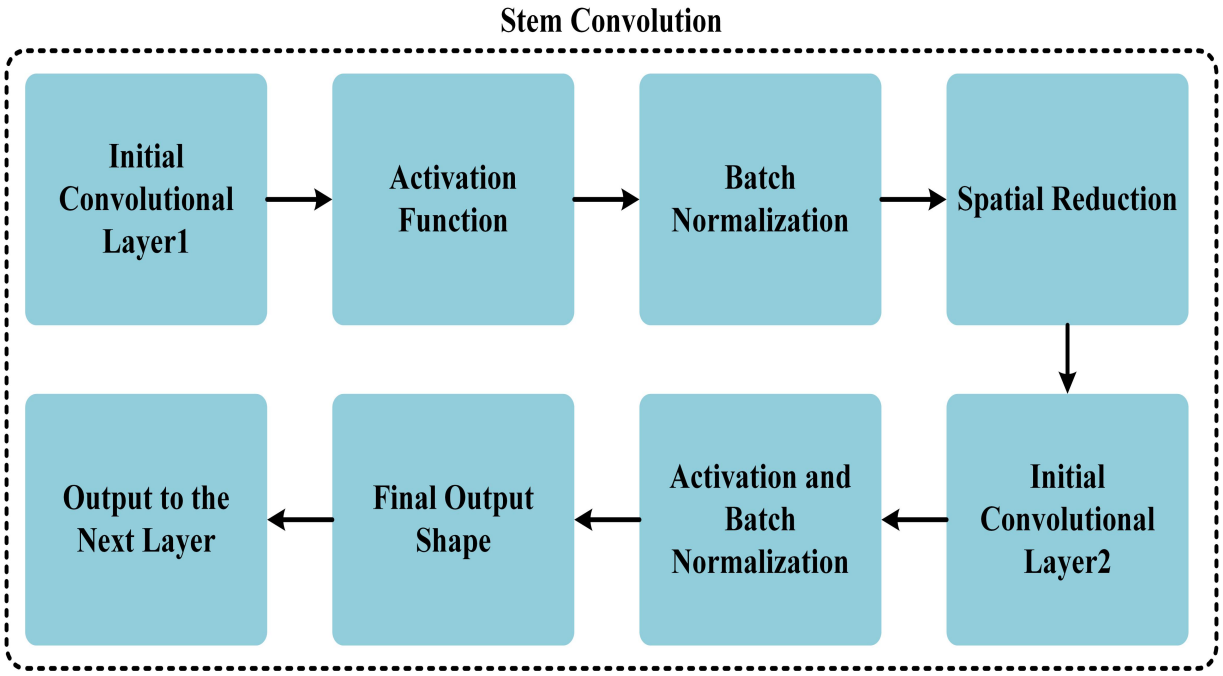

Fig. 5. Internal layers of the stem convolution

Fig.5 depicts the internal layers of the stem convolution, which consist of the following components: initial convolutional layer1, activation function, batch normalization, spatial reduction, initial convolutional layer2, activation function and batch normalization, final output form, and output to the next layer.

MBConv Blocks:

Multiple repetitions of MBConv blocks form the backbone of EfficientNet [25]. Each MBConv block consists of the following operations (refer to Fig. 6):

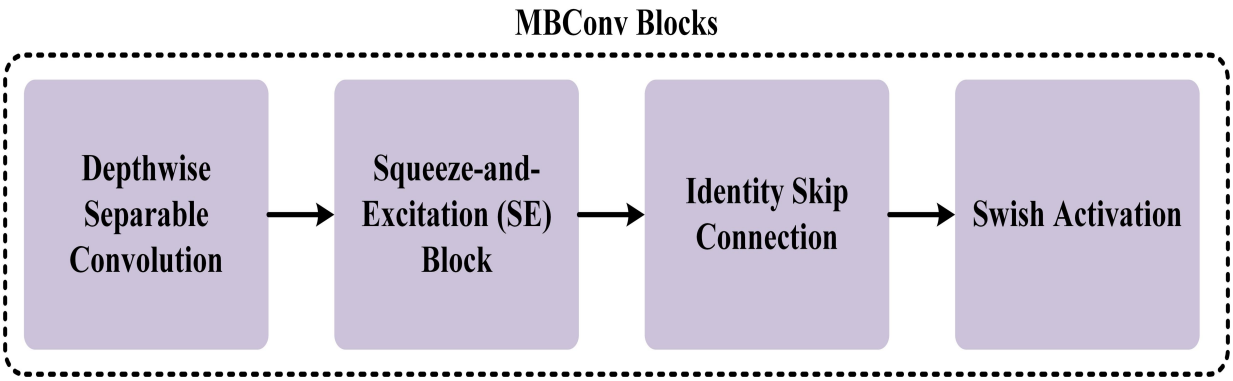

Fig. 6. Internal layers of the MBConv Blocks

- **Depthwise Separable Convolution**: Applies a spatial convolution followed by a point-wise convolution.
- **Squeeze-and-Excitation (SE) Block**: Enhances channel-wise information.
- **Identity Skip Connection**: Residual connection to help with the flow of gradients during training.
- **Swish Activation:** Non-linear activation function.

Feature Pyramid Network (Fused MBConv Blocks):

Combines features from multiple resolutions to create a feature pyramid. Enables the model to capture both low-level and high-level features.

3.7 Transfer Learning

The objective of deep transfer learning, a methodology in machine learning, is to leverage pre-trained neural network models to address a distinct problem or achieve a novel task. Transfer learning involves leveraging information acquired from one activity to another, particularly when the source work has ample labeled data and the target task has little labeled data. Transfer learning [14-15, 20] often begins using a pre-trained neural network model.

Image classification and object recognition are two instances where these models typically require extensive training on large datasets. In this approach, we use feature extraction transfer learning that includes global average pooling, dense layers for classification, and output layer.

Global Average Pooling (GAP):

Reduces the spatial dimensions to a single vector by taking the average across spatial dimensions and also captures global features.

Dense Layers for Classification:

One or more dense (fully connected) layers follow the GAP layer. Serves as the classifier for mapping features to specific classes. It may include dropout layers to reduce overfitting.

Output Layer:

Output layer with softmax activation for multiclass classification or sigmoid activation for binary classification produces final class probabilities.

Results and Discussions:

This section presents the results of the proposed method, using performance metrics such as precision, recall, sensitivity, F1-score, Macro-F1, Weighted-F1, Misclassification Rate, and accuracy [5, 10].

3.4 Performance metrics

Precision*:* The following is the definition of precision (equation 1)

$$Pr = \frac{TP}{TP + FP} \tag{1}$$

Recall or Sensitivity: The following is the definition of sensitivity (equation 2)

$$Se = \frac{TP}{TP + FN} \tag{2}$$

F1-score: The following is the definition of F1-score (equation 3)

$$F1 = \frac{2 * Precision * Recall}{Precision + Recall} \tag{3}$$

Macro-F1*:* The following is the definition of Macro-F1-score (equation 4)

$$Macro - F1 = average\ of\ F1\ Scores \tag{4}$$

Weighted-F1: The following is the definition of Weighted -F1-score (equation 5)

$$Weighted - F1 = weighted - averaged\ of\ F1\ Scores \tag{5}$$

Misclassification Rate*:* The following is the definition of misclassification rate (equation 6)

$$MR = \frac{Number\ of\ incorrect\ predictions}{total\ predictions} \tag{6}$$

Accuracy: The following is the definition of accuracy (equation 7)

$$Ac = \frac{TP + TN}{(TP + FN) + (FP + TN)} \tag{7}$$

Where TP stands for true positive, TN represents true negative, FP denotes false positive, and FN implies false negative.

3.5 Performance of the proposed method

The efficacy of the suggested approach has been evaluated using a confusion matrix, precision, recall or sensitivity, F1 score, Macro-F1, Weighted-F1, Misclassification Rate, and accuracy. The quantitative findings of the proposed methodology are displayed in Table I.

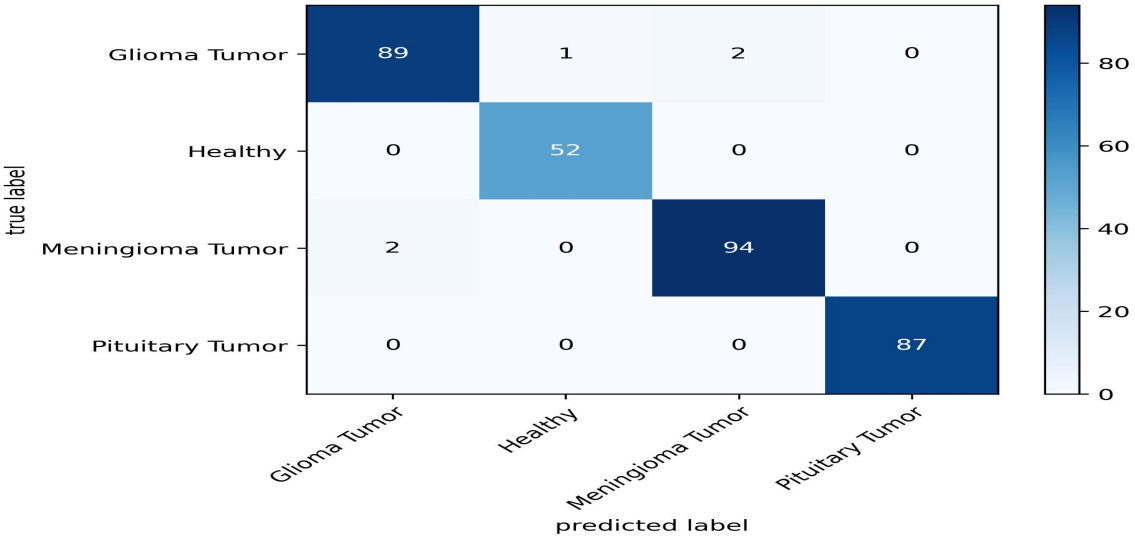

Fig. 7. Confusion matrix of the proposed method

TABLE I

QUANTITATIVE RESULTS OF THE PROPOSED METHOD

Class Name	**Number of images**	**Precision**	**Recall**	**F1 score**
Glioma Tumor	91	96.74%	97.80%	97.27%
Healthy	53	100%	98.11%	99.05%
Meningioma tumor	96	97.92%	97.90%	97.91%
Pituitary tumor	87	100%	100%	100%
Accuracy: 98.47%				
Misclassification Rate: 1.53%				
Macro-F1: 98.56%				
Weighted-F1: 98.47%				

Table I indicates that the proposed technique exhibits higher values of performance parameters. Fig. 7 presents the confusion matrix of the proposed approach, encompassing four distinct classes: There are a total of 91 images of glioma tumors, 53 images of healthy, 96 images of meningioma tumors, and 87 images of pituitary tumors. Fig.8 represents the levels of accuracy for both the training and validation sets, whereas

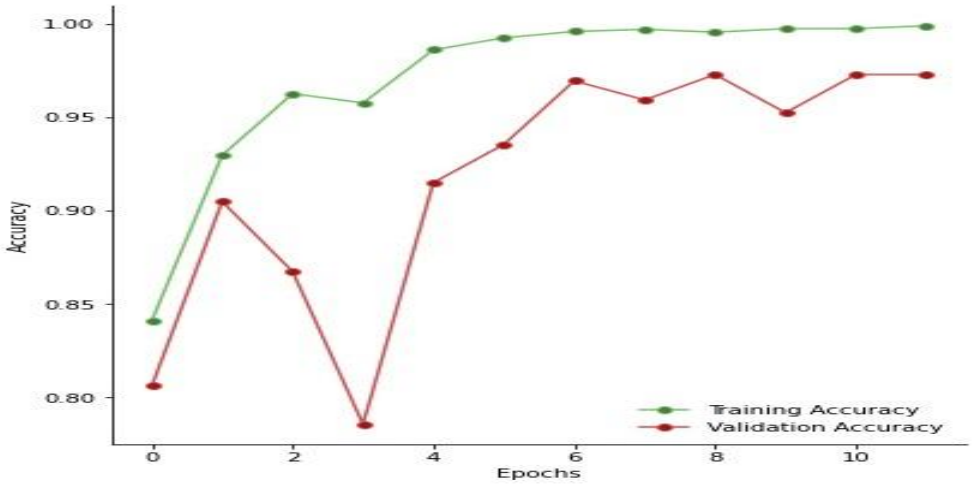

Fig.8. Training and validation accuracies of the proposed model

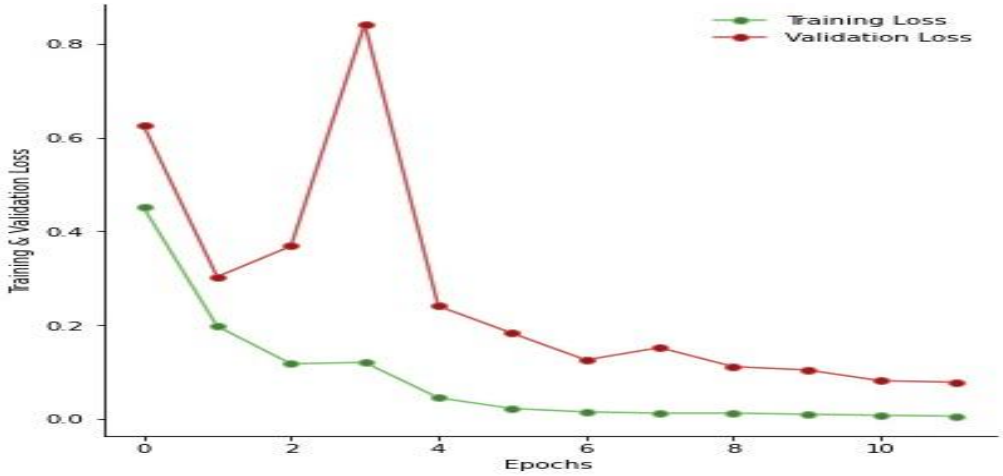

Fig.9. Training and validation losses of the proposed model

Comparison of the proposed and existing approaches

This section provides a comparative analysis of the proposed methodology and existing methodologies [3, 4, 8, 11] using precision, recall or sensitivity, F1- score, Macro-F1, Weighted-F1, Misclassification Rate, and accuracy as evaluation metrics.

TABLE II

COMPARISON BETWEEN THE PROPOSED METHOD AND EXISTING METHODS

Methods	**Reference Number**	**Precision**	**Recall**	**F1 score**	**Macro-F1**	**Weighted-F1**	**Misclassification Rate**	**Accuracy**
Proposed method	-	98.66%	98.45%	98.55%	98.56%	98.47%	1.53%	98.47%
Yang et al.	[11]	96.64%	95.89%	96.01%	96.19%	97.16%	3.13%	96.87%
Özkaya et al.	[8]	95.13%	94.68%	94.95%	95.92%	95.22%	5.45%	94.55%
Bayleyegn et al.	[3]	93.78%	92.88%	93.17%	94.69%	94.78%	6.65%	93.35%
Ahmad et al.	[4]	92.49%	91.94%	92.12%	93.72%	93.24%	7.85%	92.15%

Table II presents a comparison of the results obtained from the proposed method with the existing approaches [3, 4, 8, 11].

Table II illustrates the superior performance of the proposed CNN methodology compared to existing approaches, such as Yang et al. [11], Özkaya et al. [8], Bayleyegn et al. [3], and Ahmad et al. [4], in terms of precision (98.66%), recall or sensitivity (98.45%), F1-score (98.55%), Macro-F1 (98.56%), Weighted-F1 (98.47%), Misclassification Rate (1.53%), and accuracy (98.47%).

CHAPTER 4

4.CONCLUSION

4.1 CONCLUSION

In this project, we have been identified some drawbacks in the existing methods and to address those issues, objectives have been defined.

Based on objectives, we presented a novel efficient model for MRI brain tumor classification that is robust to variations in tumor size and location, can be trained and deployed on resource-constrained devices, and is interpretable and can explain its prediction.

4.2 FUTURE SCOPE

4.2.1 Multi-modal Fusion: Integrating information from multiple MRI modalities, such as T1-weighted, T2-weighted, and FLAIR images, can provide a more comprehensive view of tumor characteristics. Future research may focus on developing algorithms that effectively fuse information from these modalities to improve classification accuracy and robustness.

4.2.2 Attention Mechanisms: Applying attention mechanisms to MRI brain tumor classification can help the model focus on relevant regions of interest within the images. By dynamically weighting different parts of the image, attention mechanisms can enhance interpretability and accuracy, particularly in cases where tumors may be subtle or located in complex anatomical regions.

4.2.3 Continual Learning: MRI brain tumor classification models could benefit from continual learning approaches that enable them to adapt and improve over time as new data becomes available. Continual learning techniques mitigate the risk of model degradation due

to concept drift or changes in data distributions, ensuring that the model remains relevant and accurate in clinical practice.

4.2.4 Explainable AI: Developing models with built-in explainability mechanisms can enhance trust and interpretability in MRI brain tumor classification systems. Future research may focus on designing models that provide transparent insights into the decision-making process, helping clinicians understand why certain classifications are made and facilitating more informed treatment decisions.

4.2.5 Robustness to Heterogeneous Data: MRI datasets for brain tumor classification often exhibit heterogeneity in terms of image quality, acquisition protocols, and patient demographics. Future research could explore techniques for training models that are robust to such variations, ensuring consistent performance across diverse clinical settings and populations.

4.2.6 Integration with Clinical Data: Integrating MRI images with clinical data, such as patient demographics, genetic information, and treatment history, can provide a more holistic understanding of tumor behavior and prognosis. Future research may focus on developing hybrid models that leverage both imaging and clinical data to improve classification accuracy and patient stratification.

4.2.7 Deployment in Clinical Settings: Bridging the gap between research and clinical practice requires addressing practical challenges related to model deployment, such as regulatory approval, interoperability with existing healthcare systems, and integration into clinical workflows. Future efforts should focus on streamlining the translation of MRI brain tumor classification models from research laboratories to real-world clinical settings, ensuring their accessibility and usability by healthcare professionals.

4.2.8 Integration of Artificial Intelligence and Deep Learning: The future will witness the integration of more sophisticated artificial intelligence (AI) and deep learning techniques in MRI brain tumor classification. This will involve the development of advanced neural networks capable of learning complex patterns and subtle variations in MRI images, leading to enhanced accuracy and efficiency in tumor classification.

4.2.9 Multi-omics Data Integration: There is a growing focus on integrating multi-omics data, including genomics, proteomics, and metabolomics, with MRI imaging data for a more comprehensive understanding of the molecular characteristics and behavior of brain tumors. Integrating multi-omics data will enable a more precise and personalized approach to tumor classification and treatment, leading to improved patient outcomes.

4.2.10 Quantitative Imaging Biomarkers: The future will see the identification and validation of novel quantitative imaging biomarkers for MRI brain tumor classification. These biomarkers will play a crucial role in characterizing tumor heterogeneity, monitoring treatment response, and predicting patient prognosis, thereby facilitating more precise and personalized treatment strategies.

4.2.11 Functional and Metabolic Imaging Analysis: There will be a greater emphasis on the integration of functional and metabolic imaging techniques, such as functional MRI (fMRI) and positron emission tomography (PET), for a comprehensive assessment of brain tumor characteristics. Combining structural, functional, and metabolic information will provide a more holistic view of tumor biology, aiding in more accurate and reliable classification and treatment planning.

4.2.12 Real-time Image Analysis and Decision Support Systems: The future will witness the development of real-time image analysis and decision support systems for MRI brain tumor classification. These systems will enable prompt and accurate diagnosis, aiding healthcare professionals in making informed and timely treatment decisions, ultimately improving patient care and outcomes.

4.2.13 Enhanced Imaging Resolution and Sensitivity: Advancements in MRI technology will continue to improve imaging resolution and sensitivity, allowing for the visualization of finer details and subtle changes in brain tumor morphology and physiology. High-resolution imaging will enable more precise and reliable tumor classification, leading to improved diagnostic accuracy and treatment planning.

4.2.14 Clinical Translation and Personalized Medicine: The future will see a stronger emphasis on the clinical translation and implementation of advanced MRI brain tumor classification techniques into routine clinical practice. The integration of these techniques with personalized medicine approaches will lead to tailored and optimized treatment strategies, resulting in improved patient outcomes and quality of life.

4.2.15 The future scope of MRI brain tumor classification is dynamic and multifaceted, encompassing advancements in technology, data integration, and clinical applications. These advancements will play a pivotal role in transforming the landscape of brain tumor diagnosis, treatment, and patient care, ultimately leading to improved survival rates and enhanced quality of life for individuals affected by brain tumors.

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CHAPTER 5

SOURCE CODE

```
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
import seaborn as sns
import cv2
import tensorflow as tf
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tqdm import tqdm
import os
from sklearn.utils import shuffle
from sklearn.model_selection import train_test_split
from tensorflow.keras.applications import EfficientNetB0
from tensorflow.keras.callbacks import EarlyStopping, ReduceLROnPlateau, TensorBoard,
ModelCheckpoint
from sklearn.metrics import classification_report,confusion_matrix
import ipywidgets as widgets
import io
from PIL import Image
from IPython.display import display,clear_output
from warnings import filterwarnings
for dirname, _, filenames in os.walk('/kaggle/input'):
    for filename in filenames:
        print(os.path.join(dirname, filename))
```

```
colors_dark = ["#1F1F1F", "#313131", '#636363', '#AEAEAE', '#DADADA']
colors_blue = ["#331313", "#582626", '#9E1717', '#D35151', '#E9B4B4']
colors_green = ['#01411C','#4B6F44','#4F7942','#74C365','#D0F0C0']

sns.palplot(colors_dark)
sns.palplot(colors_green)
sns.palplot(colors_blue)

labels = ['glioma_tumor','no_tumor','meningioma_tumor','pituitary_tumor']

deX_train = []
y_train = []
X_train = []

image_size = 150
for i in labels:
    folderPath = os.path.join('../input/brain-tumor-classification-mri','Training',i)
    for j in tqdm(os.listdir(folderPath)):
        img = cv2.imread(os.path.join(folderPath,j))
        img = cv2.resize(img,(image_size, image_size))
        X_train.append(img)
        y_train.append(i)

for i in labels:
    folderPath = os.path.join('../input/brain-tumor-classification-mri','Testing',i)
    for j in tqdm(os.listdir(folderPath)):
        img = cv2.imread(os.path.join(folderPath,j))
```

```
        img = cv2.resize(img,(image_size,image_size))
        X_train.append(img)
        y_train.append(i)

X_train = np.array(X_train)
y_train = np.array(y_train)

k=0
fig, ax = plt.subplots(1,4,figsize=(20,20))
fig.text(s='Sample Image From Each Label',size=18,fontweight='bold',
             fontname='monospace',color=colors_dark[1],y=0.62,x=0.4,alpha=0.8)
for i in labels:
    j=0
    while True :
        if y_train[j]==i:
            ax[k].imshow(X_train[j])
            ax[k].set_title(y_train[j])
            ax[k].axis('off')
            k+=1
            break
        j+=1

X_train, y_train = shuffle(X_train,y_train, random_state=101)

X_train.shape

X_train,X_test,y_train,y_test = train_test_split(X_train,y_train,
test_size=0.1,random_state=101)

'''y_train_new = []
```

```
for i in y_train:
    y_train_new.append(labels.index(i))
y_train = y_train_new
y_train = tf.keras.utils.to_categorical(y_train)



y_test_new = []
for i in y_test:
    y_test_new.append(labels.index(i))
y_test = y_test_new
y_test = tf.keras.utils.to_categorical(y_test)'''

import numpy as np

# Assuming labels is a list of arrays
labels = [np.array([1., 0., 0., 0.], dtype=np.float32), ...]

y_train_new = []
for i in y_train:
    # Convert the NumPy array to a list for comparison
    i_list = i.tolist()
    y_train_new.append(labels.index(i_list))

y_train = y_train_new

effnet =
EfficientNetB0(weights='imagenet',include_top=False,input_shape=(image_size,image_size,
3))

model = effnet.output
```

```
model = tf.keras.layers.GlobalAveragePooling2D()(model)
model = tf.keras.layers.Dropout(rate=0.5)(model)
model = tf.keras.layers.Dense(4,activation='softmax')(model)
model = tf.keras.models.Model(inputs=effnet.input, outputs = model)

model.summary()

model.compile(loss='categorical_crossentropy',optimizer = 'Adam', metrics= ['accuracy'])

tensorboard = TensorBoard(log_dir = 'logs')
checkpoint =
ModelCheckpoint("effnet.h5",monitor="val_accuracy",save_best_only=True,mode="auto",v
erbose=1)
reduce_lr = ReduceLROnPlateau(monitor = 'val_accuracy', factor = 0.3, patience = 2,
min_delta = 0.001,
                        mode='auto',verbose=1)

history = model.fit(X_train,y_train,validation_split=0.1, epochs =12, verbose=1,
batch_size=32,
                callbacks=[tensorboard,checkpoint,reduce_lr])

epochs = [i for i in range(12)]
fig, ax = plt.subplots(1,2,figsize=(14,7))
train_acc = history.history['accuracy']
train_loss = history.history['loss']
val_acc = history.history['val_accuracy']
val_loss = history.history['val_loss']

fig.text(s='Epochs vs. Training and Validation Accuracy/Loss',size=18,fontweight='bold',
            fontname='monospace',color=colors_dark[1],y=1,x=0.28,alpha=0.8)
```

```
sns.despine()
ax[0].plot(epochs, train_acc,
marker='o',markerfacecolor=colors_green[2],color=colors_green[3],
        label = 'Training Accuracy')
ax[0].plot(epochs, val_acc, marker='o',markerfacecolor=colors_red[2],color=colors_red[3],
        label = 'Validation Accuracy')
ax[0].legend(frameon=False)
ax[0].set_xlabel('Epochs')
ax[0].set_ylabel('Accuracy')

sns.despine()
ax[1].plot(epochs, train_loss,
marker='o',markerfacecolor=colors_green[2],color=colors_green[3],
        label ='Training Loss')
ax[1].plot(epochs, val_loss, marker='o',markerfacecolor=colors_red[2],color=colors_red[3],
        label = 'Validation Loss')
ax[1].legend(frameon=False)
ax[1].set_xlabel('Epochs')
ax[1].set_ylabel('Training & Validation Loss')

fig.show()

pred = model.predict(X_test)
pred = np.argmax(pred,axis=1)
y_test_new = np.argmax(y_test,axis=1)

print(classification_report(y_test_new,pred))

fig,ax=plt.subplots(1,1,figsize=(14,7))
```

```
sns.heatmap(confusion_matrix(y_test_new,pred),ax=ax,xticklabels=labels,yticklabels=labels,
annot=True,
          cmap=colors_green[::-1],alpha=0.7,linewidths=2,linecolor=colors_dark[3])
fig.text(s='Heatmap of the Confusion Matrix',size=18,fontweight='bold',
           fontname='monospace',color=colors_dark[1],y=0.92,x=0.28,alpha=0.8)

plt.show()

def img_pred(upload):
    for name, file_info in uploader.value.items():
        img = Image.open(io.BytesIO(file_info['content']))
    opencvImage = cv2.cvtColor(np.array(img), cv2.COLOR_RGB2BGR)
    img = cv2.resize(opencvImage,(150,150))
    img = img.reshape(1,150,150,3)
    p = model.predict(img)
    p = np.argmax(p,axis=1)[0]

    if p==0:
        p='Glioma Tumor'
    elif p==1:
        print('The model predicts that there is no tumor')
    elif p==2:
        p='Meningioma Tumor'
    else:
        p='Pituitary Tumor'

    if p!=1:
        print(f'The Model predicts that it is a {p}')

uploader = widgets.FileUpload()
```

```
display(uploader)

button = widgets.Button(description='Predict')
out = widgets.Output()
def on_button_clicked(_):
    with out:
        clear_output()
        try:
            img_pred(uploader)

        except:
            print('No Image Uploaded/Invalid Image File')
button.on_click(on_button_clicked)
widgets.VBox([button,out])
```

PUBLICATION

Paper titled “A Novel DL Structure for Brain Tumor Identification Using MRI Images “ is accepted at IEEE confrence named International Conference on Computing, Power and Communication Technologies (IC2PCT), Greater Noida, India, 2024.

S. Kollem *et al*., "A Novel DL Structure for Brain Tumor Identification Using MRI Images," *2024 IEEE International Conference on Computing, Power and Communication Technologies (IC2PCT)*, Greater Noida, India, 2024, pp. 1475-1481, doi: 10.1109/IC2PCT60090.2024.10486662.