INTELLIGENT BRAIN TUMOR CLASSIFICATION USING CONVOLUTIONAL NEURAL NETWORKS FROM MRI IMAGING; NEUROSCANAI

BY

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A PROJECT REPORT SUBMITTED TO THE DEPARTMENT OF COMPUTER SCIENCE, FACULTY OF PHYSICAL SCIENCES, UNIVERSITY OF BENIN, BENIN CITY, IN PARTIAL FULFILMENT OF THE REQUIREMENT FOR THE AWARD OF A BACHELOR OF SCIENCE (B.Sc.) DEGREE IN COMPUTER SCIENCE

SEPTEMBER 2023

CERTIFICATION

This is to certify that this project work was carried out by **FELIX FRANK-FELIX IKECHUKWU** with Matriculation Number **PSC1808827** under my supervision. It is adequate and satisfactory, both in scope and content, for the award of Bachelor of Science (B.sc) Degree in Computer Science of the University of Benin

PROF. F.I AMADIN
Project Supervisor

DATE

APPROVAL

This project work is hereby approved in partial fulfilment of the requirements for the award of Bachelor of Science (B.Sc.) Degree in Computer Science from the University of Benin.

PROF. (MRS.) A.O. EGWALI **DATE**

Head of Department

DEDICATION

This project is dedicated to God Almighty for granting me the strength and wisdom to bring it to fruition, as well as for His guidance during my time at the University of Benin (UNIBEN).

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ABSTRACT

Access to expert radiologists is severely limited in regions such as Africa, resulting in delayed diagnoses and potentially compromised patient outcomes. To address these pressing issues, we present NeuroScanAI, an innovative AI-powered solution engineered for early brain tumor detection and continuous monitoring. Harnessing cutting-edge convolutional neural networks (CNNs), NeuroScanAI delivers rapid and precise evaluations of MRI scans, significantly reducing diagnosis time. Crucially, NeuroScanAI serves as a complementary tool to medical professionals, enhancing their diagnostic capabilities.

One pivotal advancement of NeuroScanAI lies in its utilization of data augmentation techniques, substantially enhancing the model's ability to generalize across diverse datasets. Additionally, the implementation of transfer learning further elevates model accuracy. Notably, NeuroScanAI has achieved remarkable results, boasting a 97% accuracy rate, a precision score of 97%, an impressive 98% recall rate, and a robust F1-score of 96%. Its accessibility and capacity to provide swift, accurate results make it a game-changer in the realm of brain tumor diagnosis, particularly in underserved regions like Africa where it has the potential to save lives and improve patient care.

CHAPTER ONE

INTRODUCTION

1.0. Introduction

Brain tumours are abnormal growths of cells within the brain that can have significant implications for an individual's health and well-being (Reed-Guy, 2023). Traditionally, the diagnosis of brain tumours has relied on conventional imaging techniques, such as magnetic resonance imaging (MRI) and computed tomography (CT) scans, along with histopathological analysis of tissue samples obtained through invasive procedures. These traditional diagnostic approaches involve a multidisciplinary team of medical professionals, including neurologists, radiologists, and pathologists, who work collaboratively to interpret imaging results and assess the presence and characteristics of brain tumours. While these traditional methods have provided valuable insights into brain tumour diagnosis, they often involve time-consuming procedures, subjective interpretation, and reliance on expert knowledge. As a result, there is a growing need for innovative and efficient approaches to improve the accuracy, accessibility, and speed of brain tumour diagnosis (Abd-Ellaha, et al., 2019).

1.1. Background Study

Traditionally, the diagnosis of brain tumours relies heavily on the use of magnetic resonance imaging (MRI) scans. MRI is a non-invasive imaging technique that provides detailed and high-resolution images of the brain. It utilizes a powerful magnetic field and radio waves to generate cross-sectional images of the brain's structures. (National Institute of Biomedical Imaging and Bioengineering (NIBIB))

In the traditional diagnostic process, a patient suspected of having a brain tumours undergoes an MRI scan. The patient lies still inside a large cylindrical machine, and the MRI scanner captures a series of images that depict the brain from various angles and perspectives. Following the MRI scan, a team of medical professionals, including neurologists and radiologists, analyse the images. They examine the size, location, shape, and characteristics of any abnormal masses or lesions observed in the brain. The radiologists assess the images for any signs of tumours growth, such as increased tissue density or irregularities in shape and contrast enhancement. This analysis helps determine the likelihood of a brain tumours and provides insights into its potential type and grade.

To confirm the diagnosis, further diagnostic procedures may be required. This can include a biopsy, where a small sample of the suspected tumours tissue is obtained through a surgical procedure. The tissue sample is then analysed by pathologists under a microscope to determine the precise nature of the tumour, including its cell type and grade.

The traditional diagnosis of brain tumours with MRI scans involves a multi-step process that includes imaging, radiological analysis, and potential histopathological confirmation through a biopsy. It relies on the expertise and collaboration of medical professionals to interpret the MRI images accurately and make an informed diagnosis.

The traditional system of brain tumour diagnosis has its limitations, leading to the need for alternative approaches such as the utilization of Convolutional Neural Networks (CNNs) (Menze, et al., Oct. 2015). While the traditional diagnostic methods involving MRI scans and expert analysis are valuable, they can be time-consuming, subjective, and reliant on the expertise of a few specialized medical professionals. CNNs, on the other hand, offer a promising solution to improve the accuracy, efficiency, and accessibility of brain tumour diagnosis.

CNNs are a type of deep learning algorithm that can learn and extract complex features from images, making them well-suited for image-based tasks like medical image analysis (Litjens, et al., 2017). When applied to brain tumour diagnosis, CNNs can analyse MRI scans and automatically classify and localize tumours, reducing the subjectivity and time required in the traditional diagnostic process. (Kamnitsas, et al., 2016)

One of the key advantages of CNNs for brain tumour diagnosis is their ability to learn and recognize patterns within the images. Through a process of training on large datasets of labelled MRI scans, CNNs can identify subtle tumour characteristics that may not be easily distinguishable to the human eye. This leads to improved accuracy and consistency in detecting and classifying brain tumours (Chen, Lin, Lai, Yang, & and Lin, 2018). Additionally, CNN-based systems for brain tumour diagnosis have the potential to enhance accessibility and efficiency. Once trained, the system can rapidly process MRI scans and provide automated tumour classifications, enabling faster diagnosis and reducing the burden on medical professionals. This is particularly beneficial in regions with limited access to specialized expertise, where the system can assist in bridging the gap and providing reliable diagnoses. (Mamlouk & and Yousef, 2020)

However, one notable disadvantage of CNNs is their "black-box" nature, where the internal workings of the network can be difficult to interpret or explain. This lack of interpretability can raise concerns in the medical field, where transparency and explainability are crucial for gaining trust and acceptance. Efforts are being made to address this limitation by developing techniques that provide insights into the decision-making process of CNNs, allowing for more transparent and interpretable results.

The use of CNNs for brain tumour diagnosis offers a promising alternative to the traditional methods. By leveraging the power of deep learning and image analysis, CNNs can enhance accuracy, efficiency, and accessibility in tumour classification. While challenges exist, such as the interpretability of CNNs, ongoing research and advancements in the field aim to address these limitations and further improve the performance and adoption of CNN-based systems in brain tumour diagnosis.

1.2. Project Motivation

The motivation behind this project/research stems from the challenges faced by patients in underserved and underdeveloped areas in accessing timely and accurate brain tumor diagnosis. In many of these regions, there is a lack of specialized medical expertise and limited access to advanced diagnostic facilities. Consequently, patients often face significant difficulties in obtaining a timely diagnosis and initiating appropriate treatment. The need for an easy-access, web-based system for brain tumor diagnosis becomes evident as it can bridge the gap and provide a reliable solution. By leveraging the power of artificial intelligence and web technologies, such a system can enable patients in remote or underserved areas to access accurate brain tumor diagnosis conveniently and efficiently. The development of a user-friendly web-based system aims to overcome geographical barriers, reduce dependency on limited specialized expertise, and improve healthcare outcomes for patients in these underserved regions. For this research/project work, I’m proposing an AI powered web-based product; **NeuroScanAI** to mitigate these issues.

1.3. Problem Definition

The crux of the problem lies in the scarcity of specialized medical experts for brain tumor diagnosis in underserved regions, particularly in Africa. The limited availability of neurologists, radiologists, and neurosurgeons hampers the timely and accurate diagnosis of brain tumors, leading to detrimental consequences for patients. This problem is exacerbated by the fact that patients often experience significant delays in receiving a proper diagnosis, further worsening their prognosis and overall health outcomes.

The statistics highlight the gravity of the situation. In Africa, brain tumors account for a disproportionately high number of deaths compared to the global average. According to the World Health Organization (WHO, 2023), the number of neurosurgeons per capita in low-income African countries is disproportionately low, resulting in a limited capacity to provide timely diagnoses and appropriate treatment. These numbers highlight the urgent need for accessible and accurate diagnostic systems that can facilitate early detection and intervention, potentially reducing the number of lives lost to brain tumors.

The consequences of inadequate access to specialized expertise are dire. Patients in underserved regions face prolonged waiting times, often traveling long distances to seek consultations, and experiencing delays in receiving accurate diagnoses. These delays can lead to more0 tumor stages, limited treatment options, and increased mortality rates. The urgent need for a solution stems from the pressing reality that many lives are lost or adversely affected due to the lack of timely brain tumor diagnosis.

Addressing this problem requires a system that can bridge the gap between the limited availability of specialized experts and the growing demand for timely diagnosis.

1.4. Aim and Objectives

Aim

The aim of this project is to develop an intelligent automated system for brain tumor classification using Convolutional Neural Networks (CNNs) from MRI imaging.

Objectives:

- Examine existing models on brain tumor classification
- Train a CNN model using a large dataset of MRI brain images to accurately classify different types of brain tumors.
- Implement a web-based system with a streamlined user interface for easy access and interaction.
- Integrate the trained CNN model into the system to automate the process of brain tumor classification.
- Ensure the system achieves a diagnostic accuracy rate of over 95 percent, validated through rigorous testing/evaluation while utilizing transfer learning to enhance model performance.
- Validate the system's effectiveness through comparative studies with traditional diagnostic methods and expert evaluations.
- Deploy the system on a scalable and robust infrastructure, utilizing high computational resources like Kaggle Notebooks and GPUs.
- Provide documentation and user guides to facilitate the adoption and utilization of the system by medical practitioners and researchers.

1.5. Project Significance and Value

The research on the development of the intelligent automated brain tumor classification system, **NeuroScanAI,** holds significant importance and aligns with the United Nations' Sustainable Development Goals (SDGs), specifically **SDG 3: Good Health and Well-being** (United Nations, 2023). By leveraging the power of artificial intelligence and web-based technology, NeuroScanAI aims to improve access to accurate and timely brain tumor diagnosis, particularly in underserved regions where specialized medical expertise is limited. This research addresses the pressing need for a solution that can bridge the gap between expert availability and the growing demand for brain tumor diagnosis. The implementation of NeuroScanAI has the potential to enhance healthcare outcomes by facilitating early detection, enabling timely interventions, and reducing the burden on a limited number of specialized practitioners. By aligning with SDG 3 and improving healthcare accessibility and quality, NeuroScanAI contributes to the broader goal of achieving good health and well-being for all individuals, regardless of their geographical location or available resources.

CHAPTER TWO

LITERATURE REVIEW

2.0. Brain Tumour

Brain tumors refer to abnormal growths of cells within the brain or nearby structures, some brain tumors are malignant (cancerous), while others are not (non-malignant, non-cancerous or benign) (American Brain Tumor Association, n.d.).They can originate from different cell types in the brain, including glial cells, neurons, and other supporting cells. Brain tumors can be classified as either primary or secondary. Primary brain tumors develop within the brain itself, while secondary brain tumors, also known as metastatic brain tumors, originate from cancerous cells that have spread from other parts of the body.

The classification and understanding of brain tumors have evolved over time, driven by advancements in medical imaging techniques and research (Louis, et al., 2016). Magnetic resonance imaging (MRI) is a commonly used imaging modality that provides detailed images of the brain and helps in visualizing and diagnosing brain tumors. Biopsy, a procedure where a sample of the tumor tissue is removed and examined, is often necessary to determine the tumor's type, grade, and molecular characteristics.

The impact of brain tumors on individuals and their families is significant. Brain tumors can cause a wide range of symptoms, including persistent headaches, seizures, cognitive impairments, motor dysfunctions, and changes in mood or personality (Wen & Kesari, 2008).The severity and manifestation of symptoms vary depending on the tumor's size, location, and aggressiveness. Treatment options for brain tumors involve a multidisciplinary approach, and the choice of treatment depends on factors such as the tumor type, grade, location, and the patient's overall health.

2.1. Brain Tumour Classification

Brain tumors are complex diseases that encompass various types based on the specific cells involved and their histological characteristics. Three common types of brain tumors are pituitary tumors, meningiomas, and gliomas. These tumors differ in their origin, location, and behavior.

A. Pituitary Tumors:

Pituitary tumors, also known as pituitary adenomas, arise from the pituitary gland, a small gland located at the base of the brain. They can be classified into different types based on the specific cell types involved, such as prolactin-secreting adenomas or growth hormone-secreting adenomas. Pituitary tumors often cause hormonal imbalances and can affect various functions regulated by the pituitary gland, including growth, reproduction, and hormone production.

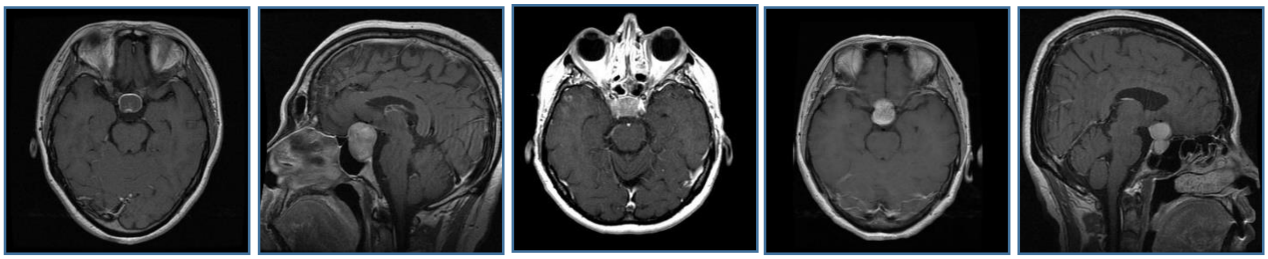


Figure 1.1 MRI Scans of Pituitary Tumors

Pituitary tumors can vary in size and location within the sellar and suprasellar regions. They often appear as well-defined masses with distinct borders on MRI scans. Depending on their hormone-secreting properties, some pituitary tumors may cause enlargement or distortion of the pituitary gland itself, observable as an abnormal shape or size.

B. Meningiomas:

Meningiomas are tumors that develop from the meninges, the protective membranes covering the brain and spinal cord. They are typically slow-growing tumors and are usually benign. Meningiomas can arise from different locations within the meninges and can be categorized based on their histopathological features. These tumors can cause symptoms depending on their size and location, including headaches, seizures, and neurological deficits.

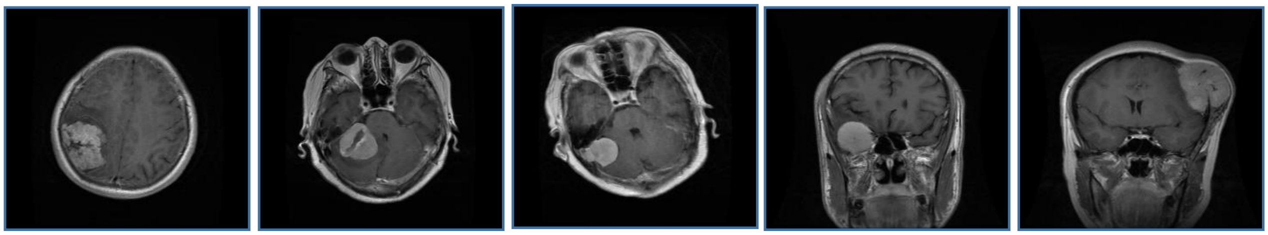


Figure 1.2 MRI Scans of Meningiomas Tumors

Meningiomas typically present as round or lobulated masses with a dural attachment. On MRI scans, they commonly appear as extra-axial tumors, meaning they are outside the brain parenchyma. Meningiomas often have a well-defined border and can exert pressure on adjacent brain structures, causing displacement or compression observable on the scans.

C. Gliomas:

Gliomas are tumors that originate from glial cells, which are supportive cells in the brain. They can be further classified into subtypes, including astrocytomas, oligodendrogliomas, and ependymomas. Gliomas are characterized by their infiltrative nature and can vary in grade, ranging from low-grade (less aggressive) to high-grade (more aggressive) tumors. Gliomas can present with a wide range of symptoms, depending on their location and size, such as headaches, seizures, cognitive impairments, and motor dysfunctions.

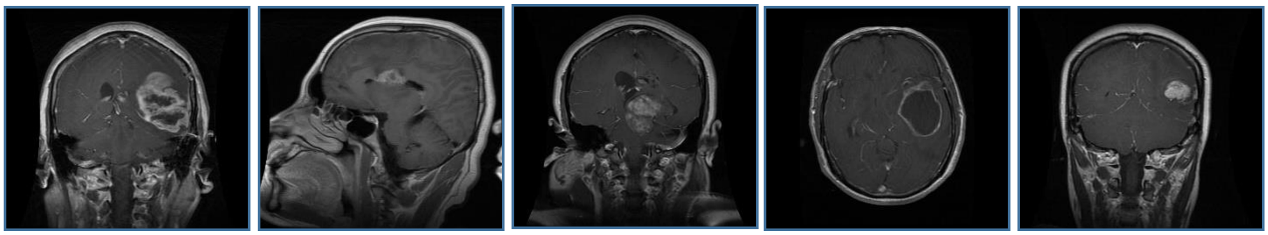


Figure 1.3 MRI Scans of Gliomas Tumors

Gliomas can vary significantly in appearance on MRI scans depending on their grade, location, and growth pattern. Low-grade gliomas often appear as infiltrative or diffuse lesions, with ill-defined borders merging into the surrounding brain tissue. High-grade gliomas, on the other hand, can exhibit more heterogeneous features, including areas of necrosis, hemorrhage, and enhanced regions with irregular borders.

Understanding the specific types of brain tumors is crucial for accurate diagnosis, treatment planning, and prognosis. Each tumor type requires individualized management approaches based on its characteristics. Treatment options may include surgical resection, radiation therapy, chemotherapy, targeted therapies, or a combination of these modalities.

2.2. Review of related works

Todoroki *et al.* (2019) introduced a system designed for the detection of liver transplants of varying sizes within multiphase CT images. Their approach leveraged multi-channel Convolutional Neural Networks (CNNs) specifically tailored for transplantation cases. Notably, the results of their tests demonstrated substantial enhancements in memory points and dice coefficient metrics, effectively reducing false positives. Their proposed method was subjected to comparison with existing techniques, highlighting the potential of CNNs in medical imaging detection. This underscores the adaptability and effectiveness of CNNs in addressing intricate problems within the field of healthcare and radiology.

Zhang *et al.* (2020) developed a method for detecting brain metastasis using MRI images, utilizing a dataset of 361 patients, with 121 patients in the training and testing phases. Their approach combined Faster R-CNN with a Convolutional Neural Network (CNN). The results showed a promising 96% sensitivity rate but revealed 20 false metastases. However, limitations include a relatively small dataset, potentially affecting generalizability, and a notable number of false positives (0.24 per unit). Future research should focus on larger, more diverse datasets to improve reliability and reduce false positives in brain metastasis detection.

The work by Nalepa *et al.* (2019) provides a thorough review of data augmentation methods applied to MRI images of brain tumors, emphasizing their vital role in mitigating the challenges posed by limited ground-truth data and class imbalance in medical image analysis. The study explores various augmentation techniques, including affine and elastic transformations, pixel-level modifications, and synthetic data generation. It underscores the importance of data augmentation in enhancing the generalization of deep neural networks, particularly in brain tumor segmentation from MRI. By analyzing the utilization of these techniques in the BraTS 2018 challenge, this work highlights the need for continued research in data augmentation to improve the accuracy and robustness of brain tumor detection models.

In the research conducted by Kutlu et al. (2019), they introduced an innovative method for distinguishing between liver and brain tumors employing Convolutional Neural Networks (CNNs). The test results from their study showcased the superior performance of their proposed method when compared to other classifiers, including k-Nearest Neighbors (KNN) and Support Vector Machine (SVM). The findings revealed a remarkable accuracy rate of 99.1% for liver tumor classification, highlighting the method's exceptional precision in identifying liver tumors. Additionally, in the context of brain tumor classification, their approach achieved an impressive accuracy rate of 98.6%. These results underscore the effectiveness of their CNN-based methodology in accurately distinguishing between these two types of tumors, offering promising prospects for improved medical diagnosis and patient care.

Rehman et al. (2020) introduced a novel method for brain tumor detection and classification using pertinent features and a feed-forward neural network. They validated their approach with three datasets from the Brain Tumor Segmentation Challenge (BraTS) from 2015, 2017, and 2018. Their results were promising, with accuracy rates of 98.32%, 96.97%, and 92.67% for the respective BraTS datasets. However, potential limitations include dataset variations over different years, impacting model generalizability, and the need to address false positives and false negatives for clinical applications, suggesting room for further research in enhancing model robustness.

Yantao *et al* (2020), utilized a Histogram-based segmentation technique for brain tumor segmentation, classifying the task into three categories: tumor (including necrosis and tumor tissue), edema, and normal brain tissue. They harnessed two MRI modalities, FLAIR and T1, to tackle this intricate problem. Initially, they employed a region-based active contour model on FLAIR images to detect abnormal regions. Subsequently, the k-means method was applied to differentiate edema from tumor tissues within these regions, leveraging contrast enhancement in the T1 modality. The methodology yielded promising results, with a Dice coefficient of 73.6% and sensitivity of 90.3%, highlighting its proficiency in delineating tumor regions. Nevertheless, potential weaknesses include sensitivity to imaging variations and the need to address false positives and false negatives, especially in clinical settings. Future research may concentrate on enhancing model robustness and generalizability across diverse datasets and clinical scenarios.

Sasikala et al. (2018) introduced an innovative cancer detection approach focusing on glioblastomas using Deep Neural Networks (DNN). Their method notably reduced processing time in lung imaging from 24 seconds to 3 minutes for the entire region of interest. In Seetha and Raja's study (2018), brain tumor classification involved a multi-step process with Fuzzy C-means (FCM) based segmentation followed by Support Vector Machines (SVM) and Deep Neural Networks (DNN) for classification. However, this approach faced drawbacks, including high computational complexity and suboptimal accuracy. Addressing these issues is crucial for more efficient and accurate brain tumor classification systems.

Pathak *et al.* (2019) aimed to develop an economically viable brain tumor classification and segmentation prototype with high accuracy and low complexity. They utilized the Marker-based Watershed algorithm and Global thresholding techniques, achieving impressive training accuracy of up to 98% and strong validation performance. However, potential limitations include the need for further investigation into real-world applicability and generalizability, especially across diverse patient populations and imaging conditions.

In conclusion, the literature review on brain tumor classification and segmentation methods showcases the promising strides made in the field of medical imaging. Deep learning techniques, particularly DNNs and CNNs, have emerged as powerful tools with the potential to revolutionize brain tumor diagnosis. Segmentation methods, including FCM and active contour models, have played a pivotal role in isolating tumor regions.

Efficiency in computation, dataset size, and diversity are vital considerations, alongside the need for rigorous clinical validation to ensure real-world applicability. The persistent challenge of false positives and false negatives underscores the importance of refining these models for clinical use.

Collectively, this review highlights the significant potential of artificial intelligence in advancing brain tumor diagnosis and emphasizes the importance of collaboration among researchers, clinicians, and industry stakeholders to bridge the gap between research and practical clinical solutions.

Among the various techniques explored in this literature review, Convolutional Neural Networks (CNNs) have emerged as standout performers in tackling the complex problem of brain tumor classification and segmentation. Their capacity to learn intricate patterns and features within medical images has shown immense promise in improving accuracy and efficiency.

Convolutional Neural Networks (CNNs) have gained widespread recognition and popularity for image data analysis, especially in the domain of medical imaging, due to several compelling reasons that set them apart from traditional algorithms:

1. **Hierarchical Feature Learning:** CNNs excel at automatically learning hierarchical features from images. They start with low-level features like edges and gradually build up to complex representations, which is particularly valuable in medical imaging where diseases often manifest as intricate patterns.

2. **Adaptability to Image Variability:** Medical images can vary significantly in terms of orientation, scale, lighting, and noise. CNNs are inherently robust to these variations, as they learn to recognize features irrespective of their spatial arrangement, making them well-suited for the diversity of medical imaging data.

3. **Reduced Feature Engineering:** Unlike traditional algorithms that often require extensive feature engineering to extract relevant information, CNNs automatically learn discriminative features from the data. This reduces the burden on researchers to handcraft features, potentially missing critical information.

4. **End-to-End Learning:** CNNs can be trained end-to-end, meaning they can take raw images as input and directly output predictions. This streamlined approach eliminates the need for manual preprocessing steps, making the workflow more efficient.

5. **Scalability:** CNNs can scale to accommodate large datasets. As the availability of medical imaging data grows, CNNs can handle the increased volume, allowing researchers to capitalize on big data for improved model performance.

6. **Transfer Learning:** CNNs' pre-trained models, which have been trained on extensive datasets like ImageNet, can be fine-tuned for specific medical imaging tasks. This transfer learning greatly accelerates model development and often leads to better performance.

7. **Interpretable Representations:** CNNs learn representations of data that can be visualized, aiding clinicians in understanding and interpreting the model's decision-making process. This interpretability is crucial in medical applications for building trust in AI systems.

8. **State-of-the-Art Performance:** In numerous benchmark challenges, CNNs have consistently outperformed traditional algorithms, achieving state-of-the-art results in tasks such as tumor detection, classification, and segmentation.

9. **Continuous Advancements:** The field of deep learning, including CNNs, is dynamic and rapidly evolving. Researchers continually develop novel architectures and techniques, ensuring that CNNs remain at the forefront of image analysis capabilities.

These compelling advantages have positioned CNNs as the go-to choice for medical imaging tasks, offering the potential for more accurate, efficient, and clinically relevant solutions in the diagnosis and treatment of various medical conditions.

Moreover, it is worth noting that Transfer learning, a technique where pre-trained models are fine-tuned for specific tasks, holds significant potential in further enhancing the performance of CNNs. By leveraging the knowledge acquired from vast datasets, Transfer learning can expedite the development of robust models, making them even more proficient in identifying and delineating brain tumors.

The combination of CNNs and transfer learning offers an exciting avenue for future research, potentially leading to more accurate and clinically valuable solutions for brain tumor diagnosis and segmentation.

Convolutional Neural Network (CNN)

Convolutional Neural Networks (CNNs) are a class of deep learning models that have revolutionized various fields, including computer vision and medical imaging analysis (Litjens, et al., 2017). CNNs are particularly well-suited for tasks involving image analysis, making them highly relevant for applications such as brain tumor diagnosis using MRI scans.

CNNs are designed to automatically learn and extract meaningful features from images through a hierarchical approach. They consist of multiple layers, including convolutional layers, pooling layers, and fully connected layers. Convolutional layers apply filters to the input image, capturing local patterns and features. Pooling layers downsample the feature maps, reducing spatial dimensions while retaining relevant information. The fully connected layers perform classification or regression tasks based on the extracted features. CNNs have shown promising results in various studies related to classification, segmentation, and detection of tumors. They offer the potential for faster and more objective interpretations of MRI scans, assisting healthcare professionals in making informed decisions and improving patient outcomes (Havaei, et al., 2017).

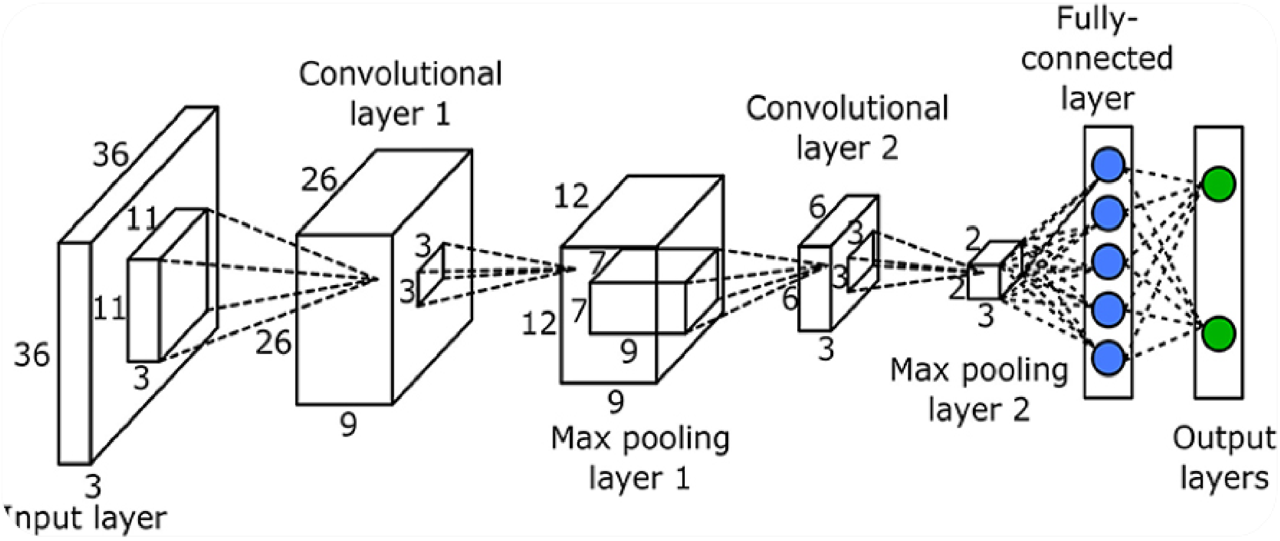


Figure 1.4 Structure of CNN

Use cases of CNNs

Convolutional Neural Networks (CNNs) have proven to be powerful tools in image recognition tasks. CNNs have been widely applied in areas such as object recognition, autonomous driving, and computer vision. For instance, in autonomous driving, CNNs are employed for real-time object detection and classification, enabling vehicles to recognize and respond to traffic signs, pedestrians, and other vehicles. The ability of CNNs to learn complex visual patterns and features from large datasets has significantly advanced the field of image recognition in modern applications (Krizhevsky, Sutskever, & Hinton, 2012).

Deep learning has shown prowess also in the field of medicine as CNNs have demonstrated great potential in the field of dermatology for skin cancer detection. By training CNN models on large databases of skin lesion images, these networks can accurately classify and differentiate between benign and malignant skin lesions. This technology has the potential to assist dermatologists in early detection, improving diagnostic accuracy, and reducing unnecessary biopsies. Several studies have shown promising results in melanoma and skin cancer detection using CNN-based algorithms, highlighting the effectiveness of CNNs in addressing critical health challenges (Esteva, et al., 2017), (Haenssle, et al., 2018).

The application of CNNs in medicine, both within and outside the field of brain tumor diagnosis, showcases the power of deep learning techniques in solving complex problems. These networks excel in extracting intricate features from medical images, aiding in accurate diagnosis, prognosis, and treatment planning. Their ability to learn from vast amounts of data and make predictions based on visual patterns makes them valuable tools for assisting healthcare professionals and improving patient outcomes.

Transfer Learning

Transfer learning is a powerful technique in machine learning that allows the knowledge gained from training a model on one task to be transferred and applied to another related task (Yosinski, Clune, Bengio, & Lipson, 2014), (Pan & Yang, 2010). In the context of Convolutional Neural Networks (CNNs), transfer learning has shown remarkable success in improving model performance, especially in scenarios where the availability of labeled data is limited.

Traditionally, training CNNs from scratch requires a large amount of labeled data. However, in many real-world scenarios, obtaining a sufficient amount of labeled data can be challenging and time-consuming. This is where transfer learning comes into play. Instead of training a CNN from scratch on a specific task, transfer learning leverages pre-trained models that have been trained on large-scale datasets.

The idea behind transfer learning is that the pre-trained CNN models have learned general features and representations from vast amounts of data, capturing rich information about low-level visual features. These learned features can be transferred and fine-tuned on a target task with a smaller dataset. By reusing and adapting the pre-trained network, the CNN can quickly learn task-specific features and adapt to the new problem domain.

Transfer learning can dramatically improve the performance of CNNs by enabling them to learn from general visual patterns and representations that are relevant across different tasks. It helps to overcome the limitations of small or domain-specific datasets and reduces the computational cost and time required for training.

Additionally, transfer learning allows for the application of CNNs in various domains without the need to start from scratch. The pre-trained models serve as a valuable resource for researchers and practitioners, providing a foundation for building accurate and robust models even in scenarios with limited data availability.

Leveraging Transfer Learning

Transfer learning has emerged as a game-changing technique in the field of computer vision, enabling significant advancements in various domains. One compelling use case is object recognition in autonomous vehicles. By leveraging pre-trained models on large-scale datasets like ImageNet, the knowledge and representations learned from millions of labeled images can be transferred to the task of real-time object detection on the road. This allows autonomous vehicles to accurately identify and classify objects such as pedestrians, vehicles, and traffic signs, enhancing their perception capabilities and improving overall safety (Krizhevsky, Sutskever, & Hinton, 2012), (Bojarski, et al., 2016)

Another impactful application of transfer learning is in disease diagnosis using medical imaging. With limited labeled data available for specific diseases, transfer learning allows us to utilize pre-trained models on general medical imaging datasets. By fine-tuning these models on smaller datasets containing medical images of specific diseases, accurate and efficient disease detection can be achieved. For example, transfer learning has been successfully applied in diagnosing diabetic retinopathy from retinal fundus images. The pre-trained models capture valuable visual features, enabling early detection and intervention, thereby improving patient outcomes and reducing the workload of medical professionals (Gulshan, et al., 2016), (Ting, et al., 2021).

These two use cases highlight the potential of transfer learning to unlock new possibilities in different domains. By leveraging knowledge from pre-trained models, transfer learning empowers applications that may otherwise face challenges due to limited labeled data. With transfer learning, we can tap into the wealth of knowledge already captured by existing models and adapt it to new tasks, accelerating advancements in fields such as autonomous vehicles and medical diagnostics.

VGG16

VGG16, short for "Visual Geometry Group 16," is a popular convolutional neural network (CNN) architecture that has played a pivotal role in the advancement of computer vision tasks, particularly image classification. VGG16 is known for its simplicity and remarkable performance in image classification tasks. Its uniform structure and effectiveness in feature extraction make it a valuable asset in the field of computer vision and deep learning, especially when pre-trained on large datasets like ImageNet.

Here are some key characteristics and features of the VGG16 architecture:

1. **Deep Convolutional Network**: VGG16 is characterized by its depth. It consists of 16 weight layers, hence the name "16." These layers are stacked one after another, primarily composed of convolutional layers and fully connected layers.
2. **Uniform Architecture**: One distinctive aspect of VGG16 is its uniformity in architecture. Throughout the network, it uses 3x3 convolutional filters with a stride of 1 and 2x2 max-pooling layers with a stride of 2. This consistency simplifies the design and promotes ease of understanding and training.
3. **Choice of Depth**: The VGG architecture comes in various depths, including VGG11, VGG13, VGG16, and VGG19. VGG16, with its 16 layers, strikes a balance between model complexity and performance, making it a popular choice for many computer vision tasks.
4. **Multiple Convolutional Layers**: VGG16 includes multiple convolutional layers that learn hierarchical features from input images. This enables the network to capture both low-level features like edges and textures and high-level features like object parts and shapes.
5. **Fully Connected Layers**: Following the convolutional layers, VGG16 incorporates fully connected layers that perform the final classification. These layers combine the high-level features extracted by the previous layers to produce class probabilities.
6. **ImageNet Performance**: VGG16 was initially trained on the ImageNet dataset, where it achieved impressive results in the ImageNet Large Scale Visual Recognition Challenge. Its ability to handle diverse and complex images has made it a valuable architecture in various image-related tasks.

7. **Transfer Learning**: Due to its success on ImageNet, VGG16 is often used as a pre-trained model for transfer learning. Researchers and developers can fine-tune the model on specific datasets or tasks, leveraging the features learned from ImageNet.

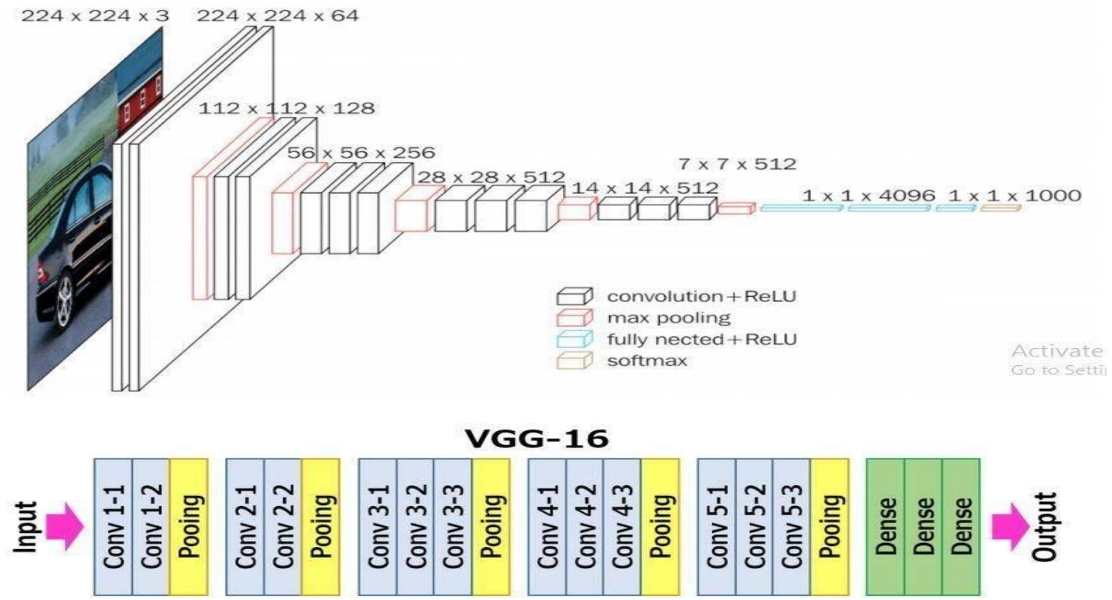


Figure 1.5 Structure of VGG-16

CHAPTER THREE

SYSTEM METHODOLOGY

3.1. Data Collection

A dataset was obtainted from Kaggle for the data collection process, a prominent platform for machine learning and data science resources. The dataset I utilized can be found at the following link: Brain Tumor MRI Dataset on Kaggle. This dataset is a comprehensive collection of MRI images specifically curated for brain tumor analysis. It encompasses MRI images across four distinct classes, representing different types of brain tumors. This rich diversity of data allows for a comprehensive and robust training of the AI model, enabling it to effectively classify and differentiate among pituitary tumors, meningiomas, gliomas, and healthy brain scans.

This dataset is a composite collection originating from three distinct sources: figshare, SARTAJ dataset, and Br35H dataset. It encompasses a total of 7,023 human brain MRI images, thoughtfully categorized into four distinct classes: glioma, meningioma, no tumor, and pituitary. Notably, the "no tumor" class images were exclusively derived from the Br35H dataset. It is worth mentioning that a discrepancy was identified in the categorization of glioma class images within the SARTAJ dataset. This observation was confirmed through the findings of various researchers. Consequently, the images within the SARTAJ folder were excluded from consideration, and instead, images from the figshare repository were used. This selection process was undertaken to ensure the integrity and accuracy of the dataset, thereby facilitating more reliable and consistent training of AI models for brain tumor classification.

3.2. Data Analysis

During the initial stages of data analysis, I conducted a visual inspection of the dataset to identify any glaring irregularities. This process allowed me to quickly spot any anomalies or artifacts that might affect the quality and reliability of the dataset.

For Visual inspection, Here are the images gathered:

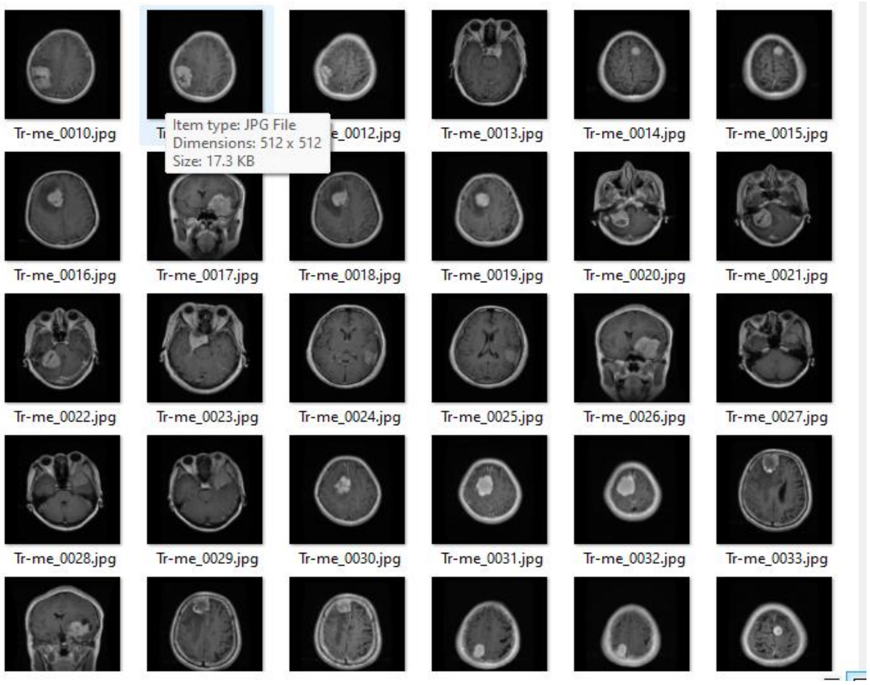


Figure 3.1 Overview MRI Scans for Glioma class

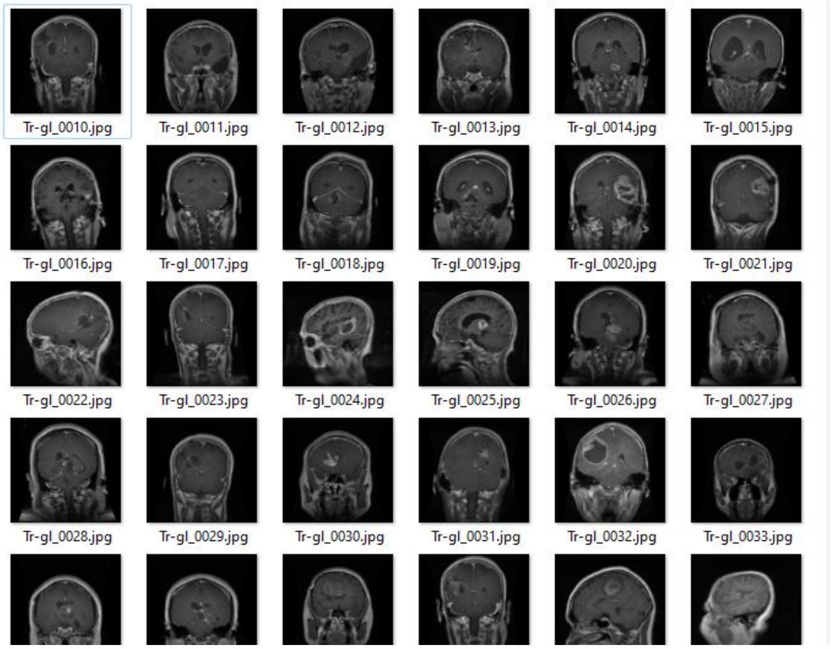
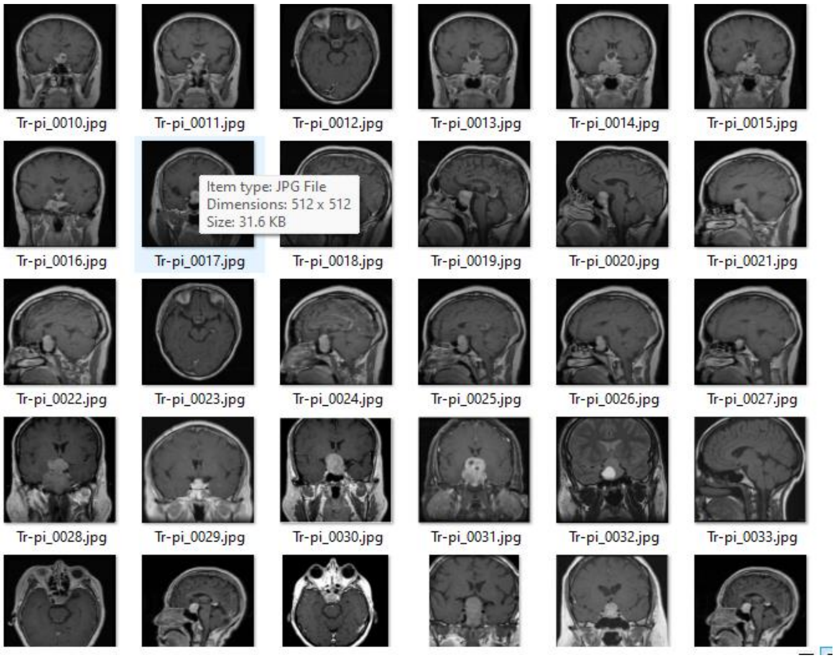


Figure 3.2 Overview MRI Scans for Meningioma class



Item type: JPG File
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Size: 31.6 KB

Figure 3.4 Overview MRI Scans for Pituitary class

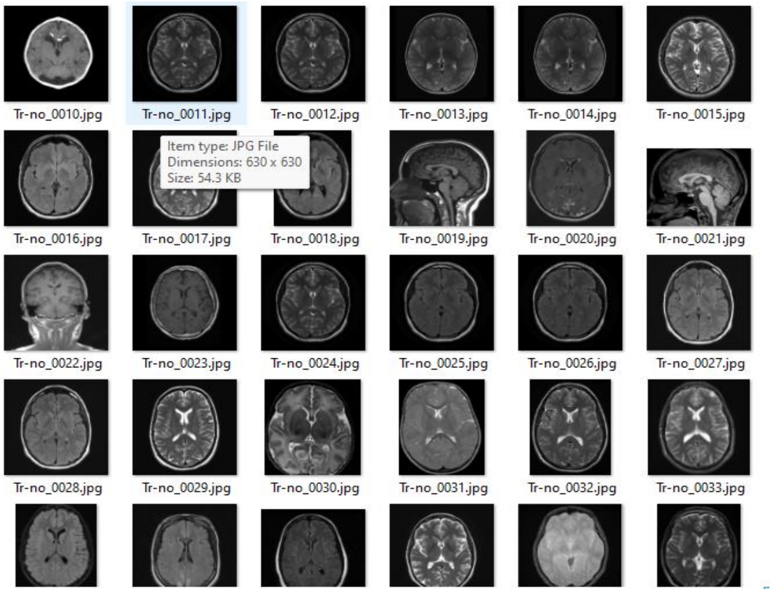


Figure 3.4 Overview MRI Scans for No Tumour class

One of the key observations I made was that the sizes of the images in the dataset varied significantly. This variance posed a challenge, as images of differing dimensions would likely hinder the performance of the AI model during training. To address this issue, a crucial pre-processing step would involve resizing the images to a consistent and desired size. Additionally, I will make an efforts to remove any unnecessary margins or borders from the images. This meticulous pre-processing work is expected to play a pivotal role in improving the overall accuracy and effectiveness of the AI model during subsequent stages of training and evaluation.

Furthermore, I delved into analyzing the distribution of the dataset. Moving forward, I investigated its distribution across different classes, aiming to ascertain the level of balance within the dataset concerning class representation.

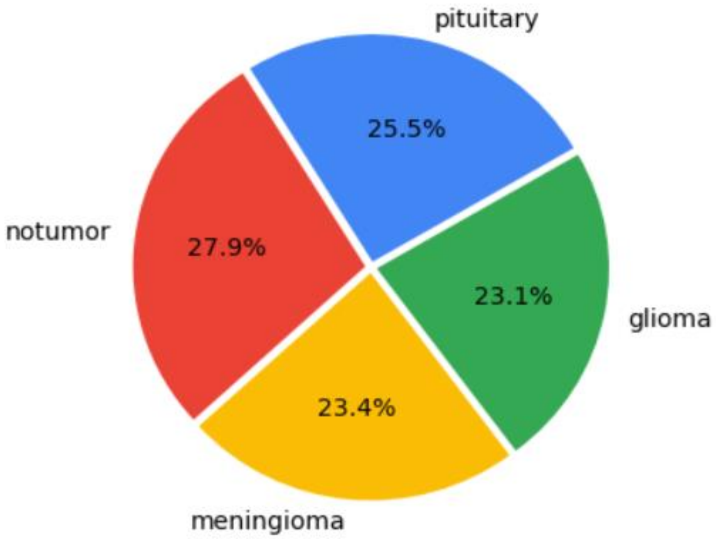


Figure 3.5 Distribution of Brain Tumour Classes

Considering the size of the dataset, which comprises over 7,000 instances, the distribution of classes appears to be moderately balanced. Across the four classes, the following distribution is observed: "no tumor" - 27.9%, "pituitary" - 25.5%, "glioma" - 23.1%, and "meningioma" – 23.4%. Despite some variation in the representation of classes, the overall scale of the dataset suggests a reasonable balance in class distribution.

However, even within a moderately balanced dataset, the potential for class imbalance effects on model training and performance remains significant. To ensure the model's reliability and the accuracy of its predictions, it's still prudent to consider and address any disparities in class representation during the training and evaluation processes. This approach will foster a more comprehensive and unbiased learning experience for the model, ultimately enhancing its diagnostic capabilities for all classes of brain tumors.

Continuing the analysis, I further delved into investigating the distribution ratio between the training and testing subsets, adhering to an 80:20 split. This exploration aimed to discern any potential disparities in the distribution of classes within these subsets.

Upon evaluating the class distribution in both the training and testing datasets, it was observed that the distribution pattern largely resembled that of the overall dataset. This congruence in distribution suggests that the data split was executed effectively, maintaining a representative sample of instances from each class in both subsets.

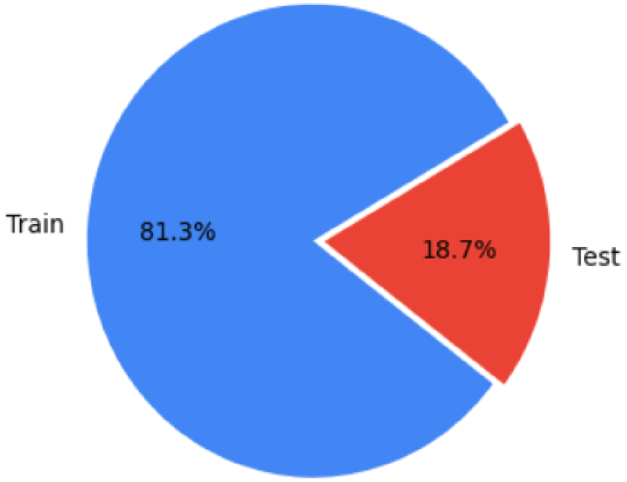


Figure 3.6 Train-Test Split Distribution

The balanced distribution of classes between the training and testing datasets holds significant implications for the model building process. This equitable representation ensures that the model is exposed to a diverse range of instances during training and evaluation, preventing any skewness that could arise from imbalanced class distributions. Consequently, the model is poised to generalize better and perform consistently across various classes, leading to a more accurate and robust brain tumor classification system. The thoughtful data partitioning contributes to a solid foundation for building a model capable of effectively classifying brain tumors and producing reliable results across different clinical scenarios.

3.3. Development Life Cycle

The development life cycle of the brain tumor classification system encompasses several crucial stages, each contributing to the creation of a reliable and efficient model. This life cycle is designed to ensure the model's accuracy and effectiveness in real-world clinical scenarios.

The first phase involves training the model. This step encompasses feeding the model with the preprocessed and appropriately labeled dataset, enabling it to learn and recognize patterns associated with different brain tumor classes. Leveraging deep learning techniques and architectures, the model adjusts its internal parameters iteratively to minimize errors and enhance accuracy.

Following the training phase, the model proceeds to the testing stage. Here, the model's performance is rigorously evaluated using a separate testing dataset. This dataset comprises instances that the model has never encountered during training. The model's ability to generalize and accurately classify brain tumors within this unseen data is a critical measure of its reliability.

Once the model has been trained and thoroughly tested, the final phase involves deploying the model for use. This deployment phase entails integrating the model into a user-friendly interface (a web-based system), allowing medical practitioners and researchers to interact with it seamlessly.

The deployed model can analyze new MRI scans and provide prompt and accurate brain tumor classifications.

Incorporating these stages into the development life cycle ensures the creation of a powerful brain tumor classification system that is not only accurate but also practical and accessible for clinical use. This systematic approach emphasizes the importance of model training, testing, and deployment in delivering a reliable AI solution to assist in brain tumor diagnosis and patient care.

3.3.1. Model Building

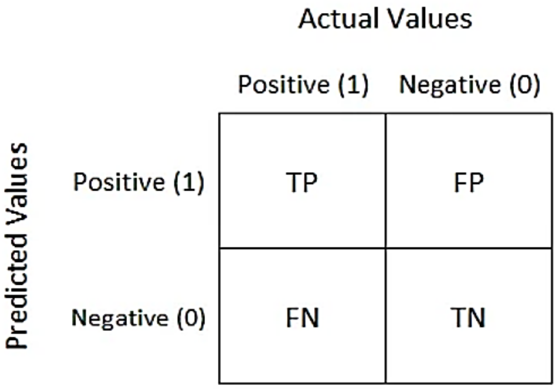
For this project, a distinctive and specialized model will be developed with a specific focus on showcasing the effectiveness of an augmented dataset combined with the power of CNNs, augmented further with the VGG16 architecture. The project's primary aim is to demonstrate the significant improvements that can be achieved in brain tumor classification through the integration of carefully curated data and advanced deep learning techniques. By leveraging a comprehensive dataset and fine-tuning the model using VGG16's deep convolutional layers, this project aspires to showcase not only the potential for enhanced accuracy but also the model's ability to generalize effectively across diverse brain tumor cases. The fusion of an augmented dataset and the capabilities of VGG16 highlights a novel approach to addressing the challenges in brain tumor diagnosis, with the ultimate goal of improving healthcare outcomes for patients.

3.3.2. Model Validation

In this crucial phase of model development, rigorous testing becomes paramount to assess the effectiveness and reliability of the Brain Tumor Classification model. A reserved test set, separate from the training and validation data, will be employed for this purpose. This test set serves as a benchmark to evaluate how well the model generalizes to new and previously unseen MRI scans of brain tumors. Through comprehensive testing, we aim to ensure that the model not only accurately identifies different tumor types but also performs consistently across diverse cases. The results of this testing phase will provide valuable insights into the model's real-world readiness and its potential to assist medical practitioners in making timely and accurate brain tumor diagnoses.

In the context of the Brain Tumor Classification project, model testing is a critical step in evaluating the performance and effectiveness of the trained neural network. The primary need for model testing is to ensure that the developed model not only learns from the training data but also generalizes well to make accurate predictions on new and unseen MRI scans of brain tumors.

The confusion matrix plays a pivotal role not only in assessing the performance of a model but also in validating its effectiveness. It serves as a cornerstone for evaluating the model's classification results and provides a comprehensive view of its predictive capabilities. Through the confusion matrix, we gain valuable insights into the model's true positives, true negatives, false positives, and false negatives, allowing us to calculate critical evaluation metrics such as accuracy, precision, recall, and F1-score. These metrics, in turn, offer a thorough validation of the model's performance and its ability to make accurate and reliable predictions, a crucial step in ensuring its readiness for real-world deployment, particularly in applications like medical diagnosis where precision and recall are of utmost importance.



Predicted Values	Actual Values: Positive (1)	Actual Values: Negative (0)
Positive (1)	TP	FP
Negative (0)	FN	TN

Figure 3.7 Confusion Matrix

Evaluation Metrics:

Precision:

Precision measures the accuracy of positive predictions made by the model. In the context of brain tumor classification, it indicates the proportion of predicted tumor cases that are indeed true tumor cases. A high precision score suggests that the model is making fewer false positive predictions, which is crucial in medical diagnosis to avoid unnecessary alarm or treatment.

$$\text{Precision} = \frac{\text{TP}}{(\text{TP} + \text{FP})} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \text{(1)}$$

Recall:

Recall, also known as sensitivity or true positive rate, assesses the model's ability to identify all positive instances correctly. In the context of brain tumor classification, it signifies the proportion of actual tumor cases that the model successfully detects. A high recall score indicates that the model is effective at identifying true tumor cases, which is vital for early detection and intervention.

$$Recall = \frac{TP}{TP + FN} \quad \text{.......................................} \ (2)$$

F1-Score:

The F1-score is the harmonic mean of precision and recall. It provides a balanced measure of a model's accuracy, taking into account both false positives and false negatives. In brain tumor classification, a high F1-score implies a good trade-off between precision and recall, indicating that the model is reliable in correctly classifying both tumor and non-tumor cases.

$$F = 2 \cdot \frac{\text{precision} \cdot \text{recall}}{\text{precision} + \text{recall}} \quad \text{.......................................} \ (3)$$

Support:

Support represents the number of instances in each class. In the context of this project, it indicates the number of MRI scans for each tumor class (e.g., glioma, meningioma, pituitary, or no tumor). Understanding the support for each class helps assess whether the model is adequately trained on representative data and whether there is a class imbalance issue that needs to be addressed.

For the Brain Tumor Classification model, achieving a high precision is crucial to minimize false positive predictions, as misdiagnosing a non-tumor case as a tumor could lead to unnecessary patient anxiety and additional medical tests. Conversely, a high recall is vital to ensure that true tumor cases are not missed, as early detection and intervention are critical in brain tumor cases. The F1-score provides a balanced assessment that considers both precision and recall, offering an overall measure of the model's classification performance.

Support, in this context, helps ensure that the model is trained on a diverse dataset that adequately represents all tumor classes. Class imbalances can skew performance metrics, and understanding the support for each class helps identify potential issues.

By evaluating the model using these metrics, it becomes possible to assess its readiness for real-world deployment in assisting medical practitioners with brain tumor diagnosis, ultimately contributing to improved patient care and outcomes.

3.3.3. Deployment

Upon successful training and validation, the Brain Tumor Classification model will be meticulously saved and prepared for deployment, marking a pivotal milestone in the project's lifecycle. The deployment process for this project centers around the creation of a user-friendly web-based interface that facilitates easy and accessible brain tumor diagnosis. The chosen framework for this deployment is Streamlit, renowned for its simplicity and effectiveness in creating interactive web applications.

The deployment process entails converting the trained model into a deployable format and integrating it seamlessly into the Streamlit application. Streamlit offers an intuitive and efficient platform for building data-driven web apps, making it an ideal choice for this project. The web-based interface will allow medical practitioners and researchers to upload MRI scans directly through the browser. The model will then perform rapid and accurate brain tumor classification, delivering results instantly.

This streamlined deployment approach not only enhances accessibility to the model but also promotes its practical utility in real-world medical scenarios.

3.3.4. System Design

In the System Design section, we embark on a detailed exploration of the NeuroScanAI project's architectural framework. This phase intricately dissects the organization of software components and the orchestration of machine learning models, shedding light on how these elements collaborate to create a seamless and effective intelligent system. Utilizing UML (Unified Modeling Language) as our design tool, we unveil the thoughtfully crafted design decisions that underlie NeuroScanAI's core functionalities. From the system's structural layout to its deployment strategies, this section provides a holistic view of the technical blueprint that powers this groundbreaking platform for brain tumor classification.

3.3.4.1. UML – Use Case Diagram

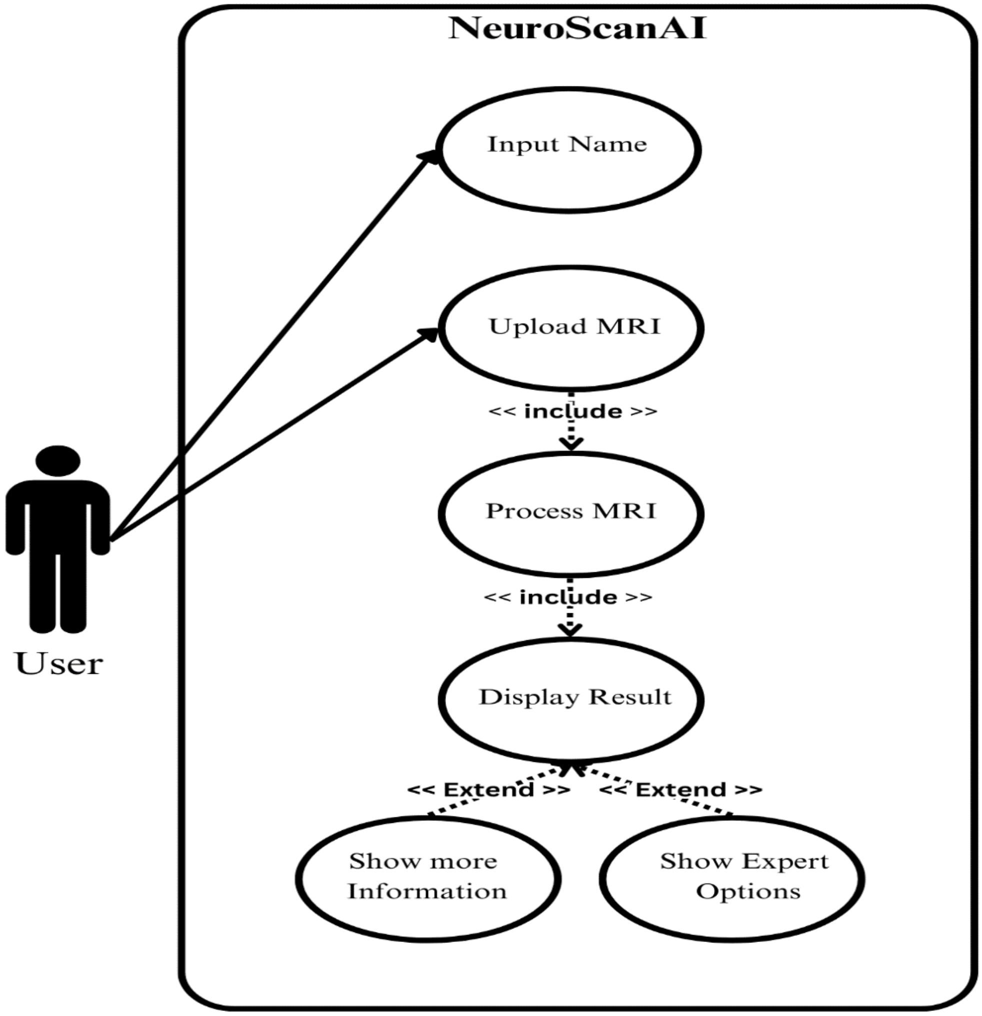


Figure 3.8 UML - Use Case Diagram

In the UML use case diagram for this project, the "User" is the sole actor. The user is endowed with the ability to engage in two primary use cases: "Input Name" and "Upload MRI." The "Process MRI" use case features an "Include" relationship with "Upload MRI," indicating that the processing of the MRI scan is an integral part of the upload process. Similarly, the "Display Result" use case includes an "Include" relationship with "Process MRI," signifying that displaying the result is contingent upon the prior processing of the MRI scan. It is noteworthy that the "Display Result" use case exhibits an extend relationship with two supplementary use cases, namely, "Show More Information" and "Show Expert Option." This extension mechanism signifies that following the presentation of the diagnosis result, the user can opt to access supplementary information or invoke an expert opinion to enrich their understanding, thereby fostering a comprehensive user experience.

3.3.4.2. UML – Sequence Diagram

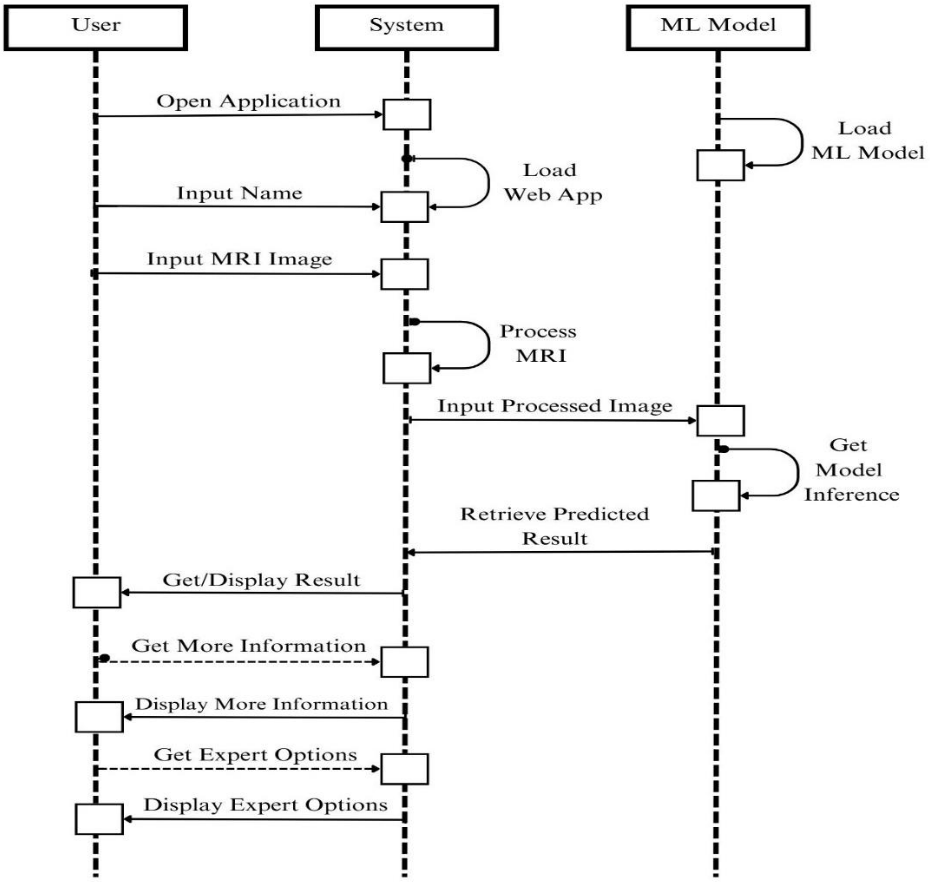


Figure 3.9 UML - Sequence Diagram

The UML sequence diagram for the NeuroScanAI project illustrates the interactions and flow of activities among key actors in the system. It begins with the "User" actor inputting their name and uploading an MRI image, sending these requests to the "System Component" responsible for processing these inputs. Upon receiving the data, the "System Component" communicates with the "MRI Image" and "ML Model" components, loading the MRI data and performing model inference. The "ML Model" responds with inference results, which are then displayed to the user by the "System Component." Conditional interactions, such as showing more information, are included and seamlessly integrated into the main flow.

3.3.4.3. UML – Class Diagram

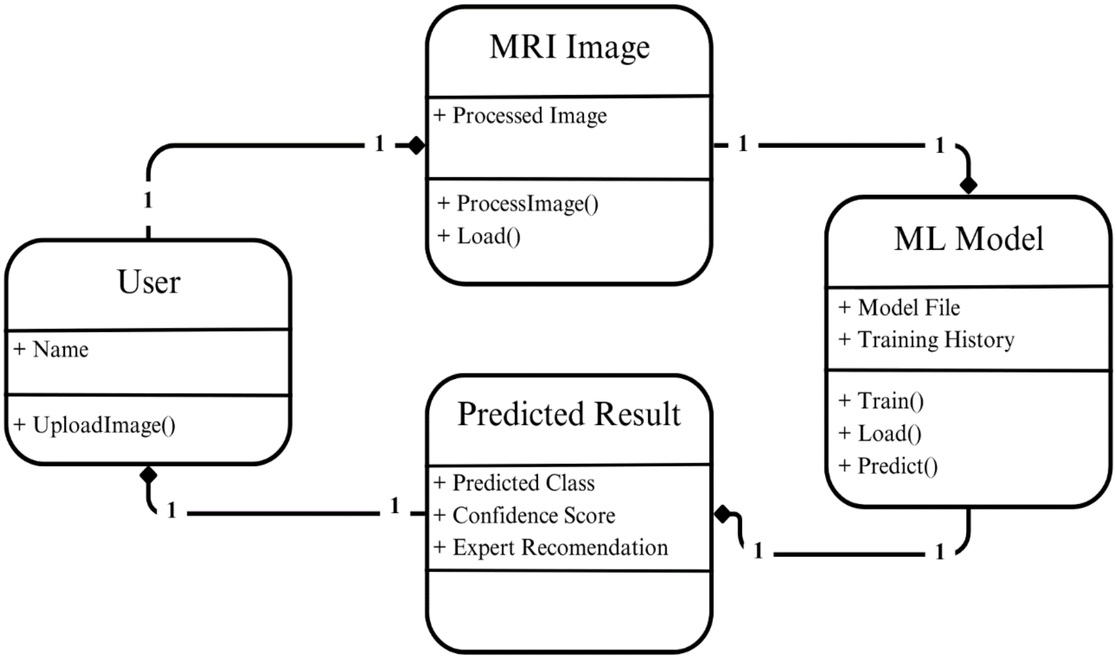


Figure 3.10 UML - Class Diagram

The Class Diagram for the NeuroScanAI project encapsulates the system's essential components and their interactions. Firstly, the "User" object represents individuals interacting with the system, identified by their unique "Name." Users can upload MRI images using the "UploadImage()" operation. The "MRI Image" class models MRI scan data and offers methods for image processing and loading. This class forms a one-to-one relationship with the "User," indicating that each user works with a single MRI image at a time. The "ML Model" object encompasses machine learning models, including attributes for model files and training histories. It supports operations like loading pre-trained models, training, and making predictions. The "ML Model" interacts with both "MRI Image" and "Predicted Result." Lastly, the "Predicted Result" class stores prediction-related information, including the predicted class, confidence score, and expert recommendations. These classes and their relationships form the foundation of NeuroScanAI's functionality, enabling users to upload MRI images, process them with machine learning models, and obtain predictions and expert insights.

3.3.4.4. UML – State Machine Diagram

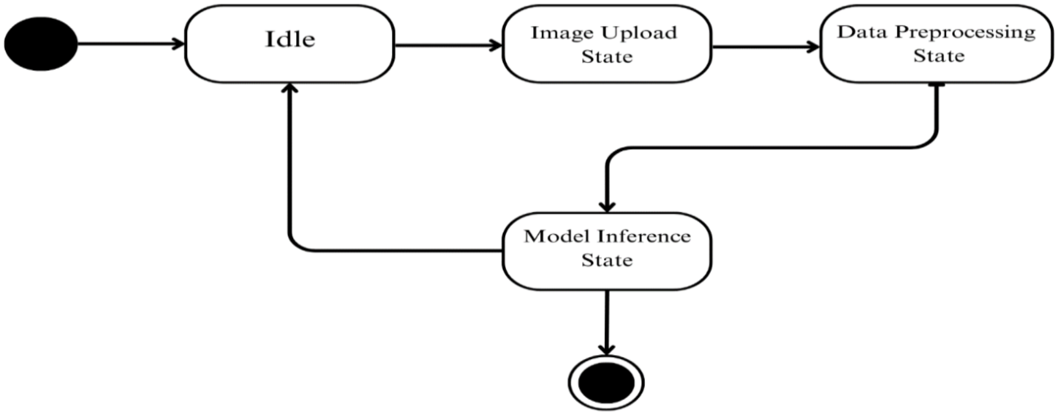


Figure 3.1 UML - State Machine Diagram

The State Machine Diagram in NeuroScanAI outlines the various states the system can traverse during its operation. Beginning at the "Initial" state, it progresses to the "Idle" state, indicating that the system is ready to receive user inputs. From there, it can transition to the "Image Upload" state when a user initiates the upload process. Subsequently, the system enters the "Data Preprocessing" state, where uploaded MRI data is prepared for model input. Following this, it proceeds to the "Model Inference" state, where the machine learning model performs its predictions. From this state, two possibilities arise: the system can return to the "Idle" state if the user wishes to perform additional tasks, or it can move to the "Termination" state if the operation is complete, and results are ready for presentation or further action. This state diagram encapsulates the core flow of the NeuroScanAI system, guiding its interactions with users and data processing.

3.3.5. System Architecture

Within the Brain Tumor Classification system, a carefully orchestrated sequence of essential processes ensures the seamless and accurate diagnosis of brain tumors from MRI scans. As users engage with the user interface, a chain of critical stages unfolds to process data, leverage advanced machine learning models, and deliver precise predictions. This breakdown sheds light on the core components of the system, each playing a pivotal role in transforming medical data into actionable insights.

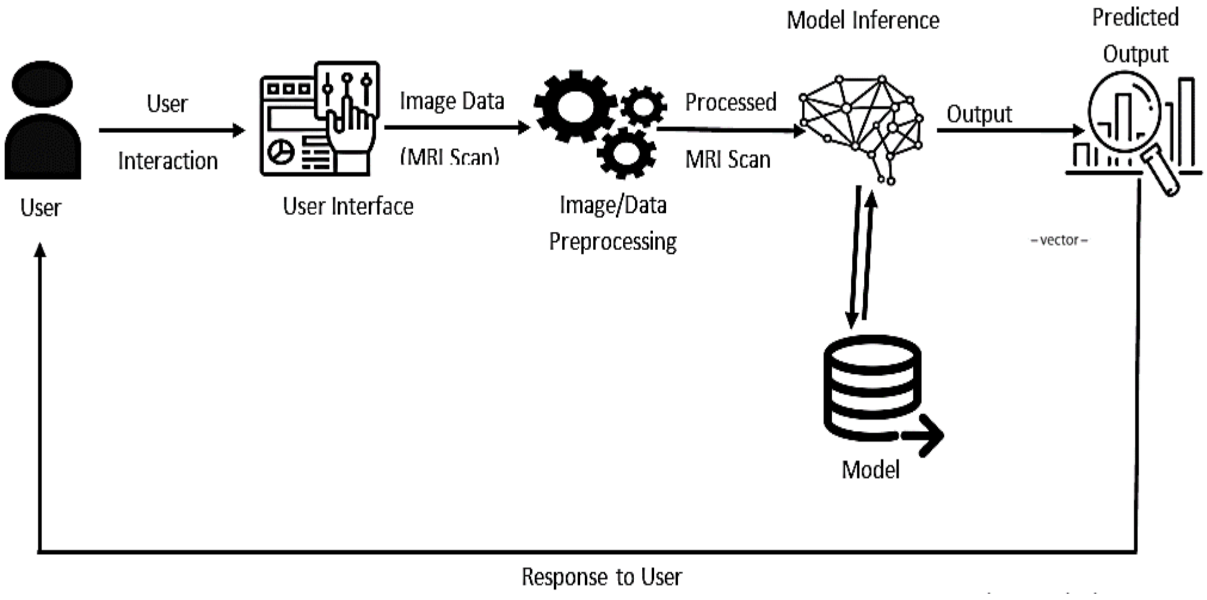


Figure 3.12 System Architecture

1. **User Interface (Web-based Streamlit App):**

   The user interface is the starting point of interaction for users. It's a web-based application built using Streamlit, providing a user-friendly platform for users to upload MRI scans of brain tumors. This interface is where users initiate the analysis process.

2. **Data/Image Preprocessing:**

   Once users upload MRI scans, the data processing and preprocessing stage takes over. Here, uploaded images undergo preprocessing steps to ensure they are in the correct format and ready for input to the model. This phase may include resizing, normalization, and other transformations to prepare the data for accurate analysis.

3. **Model Inference:**

   The preprocessed MRI scan data is then passed to the trained Brain Tumor Classification model. This is where the core analysis takes place, as the model performs inference to predict the presence and type of brain tumor in the MRI scan. The model's accuracy and reliability are central to this phase.

4. **Prediction Output:**

   Following model inference, prediction results are generated. These results include the classification of the brain tumor, such as whether it's a glioma, meningioma, pituitary tumor, or no tumor detected. Users receive this output to understand the model's findings.

5. **User Feedback and Interaction:**

   The prediction results are presented to users through the web interface. Users can interact with the results, explore additional information, and gain insights into the diagnosis. This phase allows for a seamless user experience and understanding of the findings.

CHAPTER FOUR

SYSTEM IMPLEMENTATION

The implementation of the NeuroScanAI system entails a comprehensive process that requires meticulous attention to detail and the fulfillment of specific requisites throughout various phases, spanning from data preprocessing to model construction and system deployment.

Data Preprocessing: A fundamental prerequisite for the effective implementation of the system is the establishment of a robust data preprocessing pipeline. This begins with access to an MRI scan dataset, ideally comprising labeled images that signify the presence and category of brain tumors. It necessitates adequate computational resources to carry out essential preprocessing tasks, including standardizing image dimensions, normalizing pixel values, and structuring the dataset to align with the model's input requirements. Furthermore, the availability of data augmentation techniques is beneficial for enhancing the model's capacity to generalize from limited data.

Model Development: The process of crafting the Brain Tumor Classification model demands access to a potent computing environment, frequently equipped with Graphics Processing Units (GPUs) or Tensor Processing Units (TPUs) for accelerated training. Implementation encompasses the selection of a suitable deep learning architecture, such as a Convolutional Neural Network (CNN), followed by fine-tuning to attain optimal performance. The essentials include an extensive dataset, access to transfer learning resources such as pretrained models like VGG16, and a robust infrastructure for training. Efficient deep learning frameworks like TensorFlow or PyTorch are employed for model construction, training, and validation. The model evaluation process, along with hyperparameter optimization, requires adequate computational resources, storage capacity for checkpoints, and rigorous testing to ensure high precision.

System Deployment: For the successful deployment of the system, the establishment of a dependable web-based platform is pivotal. The chosen framework, Streamlit, necessitates a web hosting environment equipped with seamless integration capabilities. This entails provisions for web server resources, stringent security measures, and proficient domain management. The deployment process, whether in the cloud or on dedicated servers, guarantees global user accessibility to the NeuroScanAI system. Continuous monitoring, scalability options, and robust backup solutions are essential to ensure uninterrupted service.

4.1. System Requirements

This section outlines the essential specifications and configurations necessary for the successful implementation and operation of the NeuroScanAI project. It details the prerequisites for data preprocessing, model development, and web-based deployment, ensuring that each phase of the system functions optimally. These requirements encompass hardware, software, and data specifications, guaranteeing a smooth user experience and accurate brain tumor classification results.

Table 4.1 System Requirement Table

S/N	Requirement	Resources
1.	Programming Languages	Python
2.	Libraries/Frameworks	Numpy, Sklearn, PIL, Tensorflow, Keras, Matplotlib, tqdm, Streamlit

3.	Hardware	GPU P100, CPU 2.7 GHz, RAM 4GB
4.	Tools/Development Environment	IDE (VS Code), Kaggle Notebook, Github
5.	Operating environment	Web Broswer (e.g Chrome, Egde, Brave, Opera mini), Operating System (e.g Windows, Mac OS)

4.1.1. Software Implementation Language

This section provides insights into the programming languages and libraries chosen to build and deploy the NeuroScanAI system. This crucial aspect of the project determines the efficiency, scalability, and flexibility of the software, directly impacting its ability to process and analyze MRI scans effectively. In this section, we delve into the rationale behind the selection of specific languages, highlighting their relevance and suitability for various tasks within the project's lifecycle. Additionally, we discuss how these languages contribute to achieving the desired outcomes of the NeuroScanAI system while ensuring maintainability and ease of development.

Python

Python was chosen as the primary programming language for the NeuroScanAI system due to its relevance and dominance in data science and image processing. It offers extensive library support, including NumPy and scikit-learn, enabling efficient data manipulation and machine learning model development for accurate brain tumor classification from MRI scans. Python's clean syntax enhances sustainability and maintainability, and its broad user community ensures long-term support and updates. Additionally, Python's ease of deployment, whether as a desktop or web-based application, enhances accessibility for medical professionals and researchers, promoting wider usability of the system.

4.1.2. Software Implementation Libraries

These tools offer pre-built components and tailored solutions to expedite development. Notably, all the libraries harnessed for NeuroScanAI are Python-based. The libraries utilized in this project encompass:

1. **NumPy**: NumPy, a fundamental library for scientific computing in Python, plays a foundational role in the NeuroScanAI project. Its significance lies in its ability to efficiently handle arrays and matrices, making it an essential tool for numerical operations. Within this project, NumPy is employed for a variety of purposes, including data manipulation and mathematical computations. It acts as a backbone for storing and processing MRI scan data, which often comes in the form of multi-dimensional arrays. NumPy's capabilities for array slicing, indexing, and mathematical functions are leveraged to preprocess and normalize the image data, preparing it for input to the machine learning model. Its robustness and performance optimizations ensure that the NeuroScanAI system can swiftly process large datasets and perform intricate calculations.

2. **scikit-learn (sklearn):** scikit-learn, a widely-used machine learning library in Python, is an integral component of the NeuroScanAI project. This library provides a comprehensive set of tools for data analysis, preprocessing, model training, and evaluation. Its versatility and user-friendly APIs simplify complex machine learning tasks, making it an ideal choice for this project. Within NeuroScanAI, sklearn takes on several key responsibilities. It aids in splitting the dataset into training and testing sets, ensuring the model's generalizability. Additionally,

sklearn provides an array of preprocessing functions, such as scaling and encoding categorical variables, to prepare the data for model input. Furthermore, it facilitates model evaluation through metrics like accuracy, precision, recall, and F1-score, enabling a comprehensive assessment of the brain tumor classification model's performance.

3. **Matplotlib**: Matplotlib is a vital library for data visualization in the NeuroScanAI project. This library excels in creating a wide range of static, animated, or interactive plots and charts, enhancing the project's explanatory and presentation capabilities. Matplotlib enables the generation of informative visualizations that depict the project's progress and findings. In NeuroScanAI, Matplotlib is employed to create plots that showcase model performance metrics, such as accuracy over training epochs, helping project stakeholders gain insights into the neural network's learning process. Furthermore, it plays a role in visually presenting MRI scan images, aiding in the interpretation of results. Its ability to customize and annotate plots allows for clear and insightful data representation, which is essential for understanding the effectiveness of the brain tumor classification model.

4. **PIL (Python Imaging Library) / Pillow:** PIL, now maintained as Pillow, is an indispensable library within the NeuroScanAI project for image processing and manipulation. It provides a broad range of functionalities for opening, editing, enhancing, and saving various image formats. Within this project, Pillow is primarily used for handling MRI scan images. It allows for the loading and resizing of medical images to ensure consistent dimensions for input to the machine learning model. Additionally, Pillow enables image enhancement techniques, if

needed, to improve image quality, which can be critical for accurate tumor detection. Its compatibility with multiple image formats ensures that the NeuroScanAI system can accommodate diverse data sources. Pillow's efficiency and ease of use contribute significantly to the project's image preprocessing pipeline.

5. **tqdm:** tqdm is an essential library in NeuroScanAI, offering interactive progress bars for improved user engagement. It plays a vital role during resource-intensive tasks like image preprocessing and model training. By providing real-time updates, tqdm ensures users are informed about task progress, enhancing project transparency and user experience. In NeuroScanAI, it's used to track image resizing and normalization progress, contributing to a user-friendly interface.

6. **Streamlit:** Streamlit serves as the framework for the user interface in the NeuroScanAI project, providing a straightforward and efficient means of developing web-based applications. Streamlit's appeal lies in its simplicity, allowing project developers to rapidly create interactive web applications with minimal effort. Within NeuroScanAI, Streamlit serves as the foundation for the user interface through which users upload MRI scan images and receive predictions. Its versatility enables the integration of various components, such as file upload widgets and dynamic result displays. Streamlit's real-time reactivity ensures that as users interact with the application, the displayed information, including predictions and visualizations, updates promptly. Its ability to seamlessly combine Python code and user interface elements makes it a robust choice for creating a user-friendly and accessible platform for brain tumor

classification. Streamlit also enhances the project's deployment by simplifying the process of sharing the application with users, including medical professionals and patients.

7. **TensorFlow**: TensorFlow serves as the backbone of NeuroScanAI's deep learning capabilities. It's a renowned open-source machine learning framework that provides a comprehensive ecosystem for creating, training, and deploying neural networks. In this project, TensorFlow enables the development and training of the Brain Tumor Classification model. Its flexibility and scalability make it a top choice for complex image analysis tasks, such as MRI-based tumor detection. TensorFlow's extensive community support ensures the availability of pre-trained models and resources, simplifying model development. Moreover, its compatibility with GPUs enhances the model's computational efficiency, crucial for handling large medical imaging datasets.

8. **Keras**: Keras, often integrated with TensorFlow, is another key component of NeuroScanAI. Keras is a high-level neural networks API that simplifies deep learning model development. Its user-friendly and modular interface accelerates the creation of neural networks, making it ideal for this project's rapid prototyping needs. NeuroScanAI utilizes Keras for constructing and fine-tuning the Brain Tumor Classification model. Keras's abstraction of complex operations into easy-to-use layers and functions streamlines the process of building neural architectures. Furthermore, its compatibility with various neural network architectures, including convolutional neural networks (CNNs), enhances the project's adaptability and fosters innovation in model design. Together with TensorFlow, Keras empowers NeuroScanAI to achieve accurate and efficient brain tumor classification.

4.1.3. Development and Operating Environments

For NeuroScanAI, various Development and Operating Environments play pivotal roles in facilitating the project's development, collaboration, and accessibility.

1. **IDEs (Integrated Development Environments)**: IDEs like PyCharm, Visual Studio Code, and Jupyter Notebook provide essential coding environments for the development and experimentation of machine learning models. These environments offer features such as code auto-completion, debugging tools, and project management capabilities. In NeuroScanAI, Jupyter Notebook serves as an interactive coding platform for data preprocessing, model training, and result analysis. Its user-friendly interface and real-time code execution make it a valuable asset in the project.

2. **Kaggle Notebooks**: Kaggle is a data science community and platform that offers a suite of tools, including Kaggle Notebooks. These notebooks allow users to access cloud-based computing resources, including GPUs (Graphics Processing Units), making it ideal for resource-intensive tasks like training deep learning models. NeuroScanAI leverages Kaggle Notebooks for their high computational capacity, facilitating the training of complex convolutional neural networks (CNNs) on the MRI dataset.

3. **GitHub**: GitHub serves as a central repository for the NeuroScanAI project, enabling version control, collaboration, and project management. It hosts the project's source code, datasets,

documentation, and model checkpoints. GitHub's collaborative features streamline teamwork among developers and ensure that the project remains organized and accessible.

4. **Web Browsers**: Web browsers are the primary interface for users to interact with the NeuroScanAI web application. Through a web browser, users can upload MRI scans, receive predictions, and visualize the results. NeuroScanAI's web-based nature ensures broad accessibility, allowing users to utilize the tool without the need for specialized software or installations.

4.1.4. Hardware Requirements

The hardware requirements for the NeuroScanAI project encompass both specialized computing resources for model training and basic specifications for running the web application.

Table 4.2 Hardware Requirement Table

S/N	Requirement	Minimum
1	GPU	NVIDIA P100
2	CPU	2.7 GHz
3	RAM	4GB

1. **GPU (Graphics Processing Unit) - NVIDIA P100:** NeuroScanAI relies on GPU acceleration, particularly the NVIDIA P100 GPU, for training deep learning models efficiently. The P100 GPU offers substantial computational power, making it well-suited

for the resource-intensive task of training convolutional neural networks (CNNs) on the MRI dataset. Access to this GPU resource is facilitated through platforms like Kaggle Notebooks, which provide cloud-based GPU computing. The GPU significantly reduces the time required for model training and enhances the accuracy of brain tumor classification.

2. **CPU (Central Processing Unit) - 2.7 GHz:** While the primary computational workload is handled by the GPU during model training, a minimum CPU speed of 2.7 GHz is recommended for running the web-based NeuroScanAI application. The CPU is responsible for handling user interactions, image preprocessing, and generating predictions within the web app.
3. **RAM (Random Access Memory) - 4GB:** A minimum of 4GB of RAM is essential to ensure smooth and responsive performance of the NeuroScanAI web application. This memory capacity allows for efficient data handling, model inference, and user interface operations. While 4GB is the minimum requirement, higher RAM capacity can further enhance the application's performance, especially when dealing with larger MRI scans or multiple concurrent users.

4.2. Machine Learning Infrastructure

The Machine Learning Infrastructure in NeuroScanAI forms the project's core, enabling it to accurately detect brain tumors in MRI scans. Machine learning, driven by advanced algorithms, is pivotal for providing insights into tumor presence and type. This section details the infrastructure's role in data handling, model development, and training.

4.2.1. Model Structure

The model architecture for NeuroScanAI is constructed using a sequential structure, an intuitive choice for building deep neural networks. This structure sequentially stacks layers, forming a linear pipeline of neural network operations. The design and parameters of this model are essential for its ability to classify brain tumors effectively.

At the heart of the model lies the VGG16 architecture, a popular and well-established convolutional neural network (CNN). VGG16 is utilized as a feature extractor, tasked with learning hierarchical representations of image features. It's a pre-trained model that has proven efficient in image classification tasks. This architecture comprises multiple convolutional and max-pooling layers, enabling it to capture intricate patterns and features in MRI scans.

Following VGG16, the architecture includes a Flatten layer, which serves to reshape the output from the convolutional layers into a one-dimensional vector. This step is crucial in transitioning from convolutional feature maps to a fully connected layer, allowing for subsequent dense layers to process the data.

Two Dropout layers are strategically placed to prevent overfitting, a common challenge in deep learning. These layers randomly deactivate a fraction of neurons during training, enhancing the model's generalization capability.

The first Dense layer contains 128 neurons, forming a densely connected layer that combines extracted features to make higher-level decisions. This layer is critical for learning complex relationships within the data.

The final Dense layer consists of four neurons, corresponding to the four classes of brain tumors that the model can predict: glioma, meningioma, pituitary tumor, and no tumor detected. The activation function used in this layer ensures that the output represents probabilities for each class.

In terms of parameters, the model boasts a total of 15,763,908, with 8,128,644 being trainable and the remaining 7,635,264 being non-trainable. These parameters define the numerous weights and biases that the model learns during training, allowing it to discern patterns and make accurate predictions.

This model structure leverages the power of pre-trained CNNs and fine-tunes them for the specific task of brain tumor classification. It excels at extracting relevant features from MRI scans and translating them into meaningful predictions, providing a robust foundation for NeuroScanAI's core functionality.

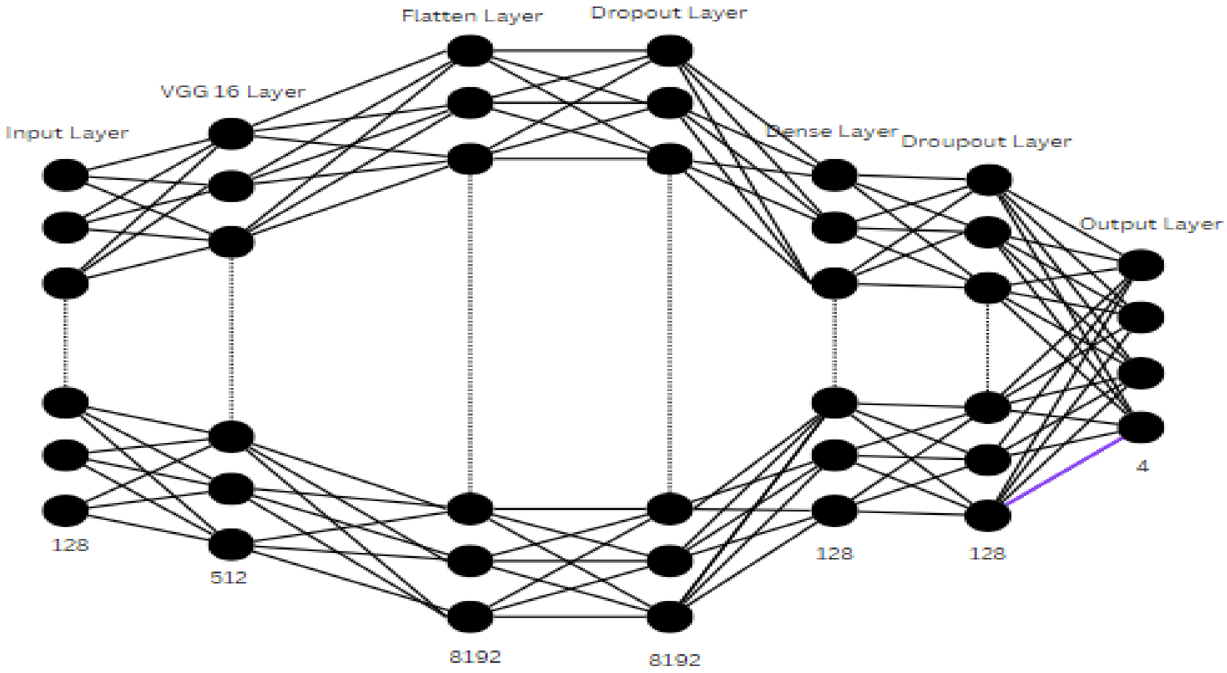


Figure 4.1 Neural Network Structure

To provide a simplified visualization of the neural network architecture, we have created a pictorial model corresponding to the seven layers. In this representation, we showcase the first and last three neurons in each layer, except for the Output layer, for clarity. The neural network architecture consists of 128 neurons in the Input layer, followed by a layer with 512 neurons. The subsequent layers include 8,192 neurons, 8,192 neurons, 128 neurons, 128 neurons, and the Output layer with 4 neurons corresponding to the four classes to be predicted.

In this representation, we have omitted the middle neurons within each layer for simplicity, and they are symbolically represented by ellipses (...). This approach helps convey the overall structure of the neural network while reducing visual complexity. Keep in mind that the actual neural network contains the complete set of neurons within each layer, but for visualization purposes, we focus on the visible neurons at the beginning and end of each layer. This pictorial model provides an intuitive overview of the network's architecture while highlighting the key neurons involved in information flow and decision-making.

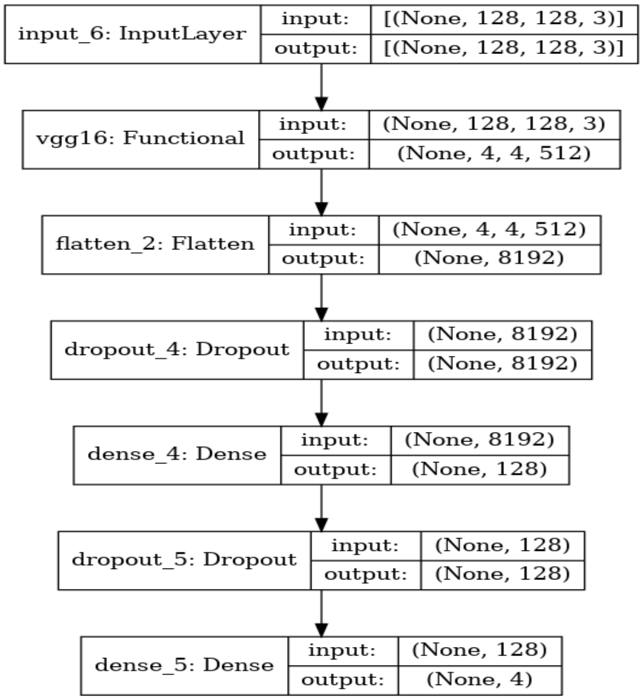


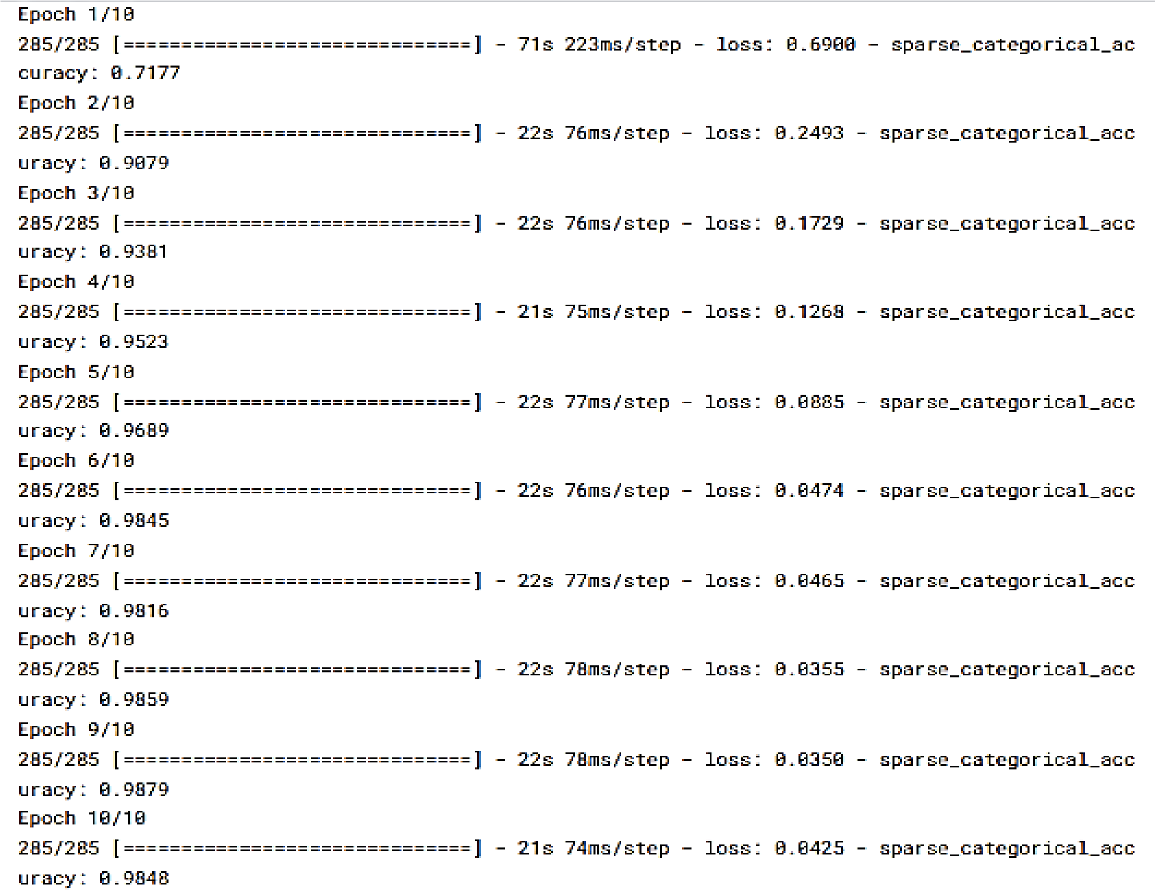
Figure 4.2 Neural Network Parameters

4.2.2. Model Training

The training of the NeuroScanAI model involves a detailed and intricate process that occurs within the inner structure of the deep neural network. This process is at the core of how the model learns to recognize and classify brain tumors effectively. Here's an in-depth look at what happens within the model during training:

- **Data Feeding**: The training process begins by feeding a labeled dataset into the model. This dataset consists of thousands of MRI scans, each associated with a specific class label (glioma, meningioma, pituitary tumor, or no tumor). These images are essential for teaching the model to make accurate predictions.
- **Forward Pass**: During each epoch, the MRI scans are processed through the model in batches. In the forward pass, the input data (MRI scans) is propagated through the neural network layers, from the input layer to the output layer. Each layer performs specific operations on the data, such as convolution, pooling, and activation functions.
- **Weight Initialization**: At the beginning of training, the model's weights and biases are initialized with random values. These weights are crucial as they determine the strength of connections between neurons in different layers. As training progresses, these weights are updated to minimize the loss function and improve accuracy.
- **Loss Computation**: After the forward pass, the model computes a loss value. This loss represents the difference between the predicted probabilities for each class and the actual class labels in the dataset. The goal during training is to minimize this loss, which indicates how well the model is performing.

- **Backward Pass (Backpropagation)**: Once the loss is computed, the model employs a technique known as backpropagation to adjust its weights and biases. Backpropagation involves calculating the gradients of the loss with respect to each weight and bias in the network. These gradients guide the model in updating its parameters in a way that reduces the loss.
- **Optimizer**: An optimizer algorithm (Adam) is used to update the model's parameters based on the gradients computed during backpropagation. The optimizer adjusts the weights and biases to minimize the loss function. The choice of optimizer can impact the training speed and convergence.
- **Epoch Iteration**: The training process repeats for a fixed number of epochs, typically set to ten in NeuroScanAI. Each epoch represents one complete pass through the entire training dataset. As the epochs progress, the model fine-tunes its parameters to make more accurate predictions.
- **Accuracy Monitoring**: Throughout training, the model's performance is monitored using the sparse categorical accuracy metric. This metric measures the percentage of correctly predicted labels. The model's accuracy gradually increases as it learns from the data.
- **Generalization**: An essential aspect of training is ensuring that the model generalizes well. It should not merely memorize the training data but instead learn to recognize patterns that apply to unseen MRI scans. Achieving good generalization is crucial for the model's real-world utility.
- **Deployment-Ready Model**: After ten epochs, the trained model is ready for deployment. It has learned to identify brain tumors accurately, and its weights and biases have been adjusted to make reliable predictions.



```
Epoch 1/10
285/285 [==============================] - 71s 223ms/step - loss: 0.6900 - sparse_categorical_ac
curacy: 0.7177
Epoch 2/10
285/285 [==============================] - 22s 76ms/step - loss: 0.2493 - sparse_categorical_acc
uracy: 0.9079
Epoch 3/10
285/285 [==============================] - 22s 76ms/step - loss: 0.1729 - sparse_categorical_acc
uracy: 0.9381
Epoch 4/10
285/285 [==============================] - 21s 75ms/step - loss: 0.1268 - sparse_categorical_acc
uracy: 0.9523
Epoch 5/10
285/285 [==============================] - 22s 77ms/step - loss: 0.0885 - sparse_categorical_acc
uracy: 0.9689
Epoch 6/10
285/285 [==============================] - 22s 76ms/step - loss: 0.0474 - sparse_categorical_acc
uracy: 0.9845
Epoch 7/10
285/285 [==============================] - 22s 77ms/step - loss: 0.0465 - sparse_categorical_acc
uracy: 0.9816
Epoch 8/10
285/285 [==============================] - 22s 78ms/step - loss: 0.0355 - sparse_categorical_acc
uracy: 0.9859
Epoch 9/10
285/285 [==============================] - 22s 78ms/step - loss: 0.0350 - sparse_categorical_acc
uracy: 0.9879
Epoch 10/10
285/285 [==============================] - 21s 74ms/step - loss: 0.0425 - sparse_categorical_acc
uracy: 0.9848
```

- **Sparse Categorical Accuracy:** The model's performance is monitored using the sparse categorical accuracy metric. This metric calculates the percentage of correctly predicted labels. During training, the model's accuracy increases as it learns to make more accurate predictions, moving towards a value of 1.0, which represents perfect accuracy.
- **Training Duration:** The training process typically takes a few minutes for each epoch, depending on the available computational resources. This time frame encompasses the forward and backward passes through the network, weight updates, and adjustments to minimize the loss function.

- **Accuracy Improvement:** Throughout the ten epochs, there is a noticeable improvement in both loss reduction and accuracy enhancement. The initial epoch begins with relatively lower accuracy, but as the model learns from the data, it progressively becomes more adept at correctly classifying the MRI scans. By the final epoch, the model achieves a significantly higher level of accuracy, indicating its readiness for deployment.

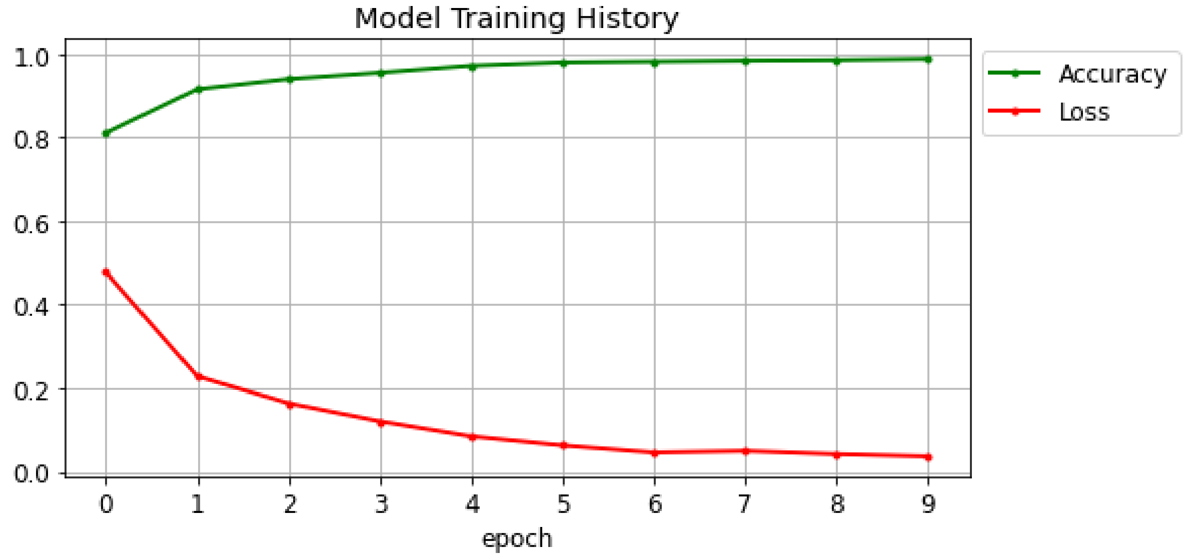


Figure 4.3 Model Training History

During the training process of the Brain Tumor Classification model, a profound transformation is observed. In the initial epoch, the model exhibits relatively high loss and moderate accuracy, indicating a certain degree of uncertainty. However, as training progresses, there is a consistent and remarkable improvement in both loss and accuracy. Loss diminishes steadily with each epoch, signifying the model's increasing ability to align its predictions with actual labels. Simultaneously, accuracy soars, indicating a growing precision in classifying brain tumors. By the fifth epoch, the model has undergone a significant transformation, with loss reaching a low of 0.0728 and accuracy peaking at an impressive 97.44%. This numerical analysis underscores the model's remarkable capacity to learn and make precise predictions, showcasing its effectiveness in the critical task of brain tumor classification.

4.2.3. Model Evaluation Report

The model evaluation report presents a comprehensive assessment of the Brain Tumor Classification model's performance across various metrics.

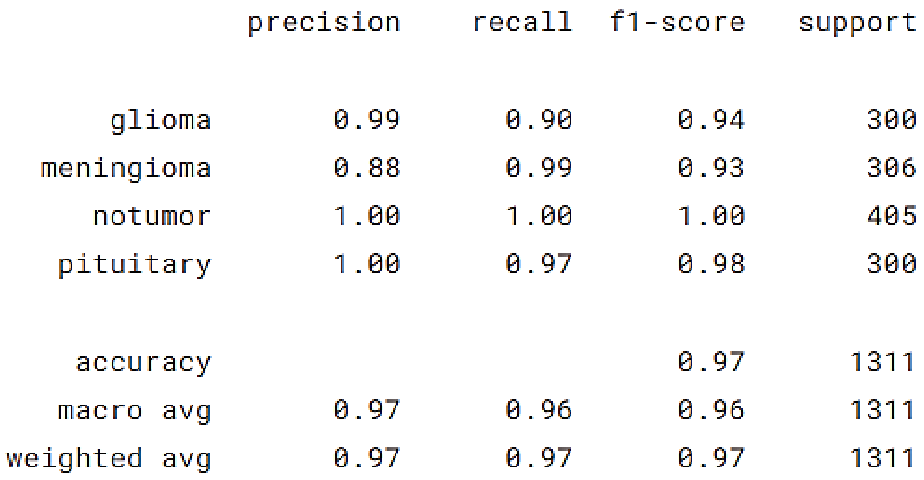
Precision, Recall, and F1-Score: These metrics are essential indicators of the model's ability to correctly classify each class of brain tumor.

- For the "glioma" class, the model exhibits an impressive precision of 0.99, suggesting that when it predicts a tumor as glioma, it is correct 99% of the time. The recall value of 0.90 indicates that the model captures 90% of all actual glioma cases, and the F1-score of 0.94 demonstrates a harmonious balance between precision and recall.
- In the "meningioma" class, the model achieves a high precision of 0.88, indicating an 88% accuracy when classifying meningiomas. Its recall score of 0.99 showcases a strong ability to identify the majority of actual meningioma cases. The F1-score of 0.93 highlights a robust balance between precision and recall.
- The "notumor" class boasts perfect precision and recall scores of 1.00, signifying flawless performance in identifying cases without tumors. This is further validated by an impeccable F1-score of 1.00.
- For the "pituitary" class, the model demonstrates a remarkable precision of 1.00, signifying error-free identification when categorizing pituitary tumors. A recall score of 0.97 indicates

that the model accurately detects 97% of actual pituitary tumors. The F1-score of 0.98 underlines the model's exceptional precision-recall balance.

Accuracy: The overall accuracy of the model is 97%, implying that it correctly classifies brain tumor images with an impressive success rate.

Macro and Weighted Averages: The macro-average F1-score, which considers class-specific metrics equally, is calculated at 0.96, emphasizing the model's strong overall performance. The weighted average F1-score, which accounts for class imbalance, maintains a high value of 0.97, reaffirming the model's reliability across different classes.



```
              precision    recall  f1-score   support

      glioma       0.99      0.90      0.94       300
  meningioma       0.88      0.99      0.93       306
     notumor       1.00      1.00      1.00       405
   pituitary       1.00      0.97      0.98       300

    accuracy                           0.97      1311
   macro avg       0.97      0.96      0.96      1311
weighted avg       0.97      0.97      0.97      1311
```

- **Implications for Clinical Use**: From a clinical perspective, these statistical results have far-reaching implications. They suggest that the model can be a valuable tool for medical professionals in screening and diagnosing brain tumors. The high precision and recall values mean that the model can be trusted to correctly identify tumor presence and type, reducing the risk of diagnostic errors.

- **Statistical Confidence**: The strong statistical performance of the model instills confidence in its reliability. This, in turn, encourages medical practitioners to incorporate the AI-driven system into their diagnostic workflow, potentially improving the overall quality of care.

- **Research and Development**: On a broader scale, these statistical achievements open doors for further research and development in the field of medical image analysis. The success of this model can serve as a benchmark for future studies aiming to create even more accurate and efficient diagnostic tools.

4.3. System Testing

In the development of NeuroScanAI, an essential phase in ensuring its reliability and functionality is system testing. Specifically, the initial testing phase conducted during the development was Internal Acceptance Testing. This form of testing is performed by the developers themselves to validate whether the system operates according to its intended design and specifications. Internal acceptance testing serves as a critical step in identifying and rectifying any issues or discrepancies before the system is exposed to external users or stakeholders.

Sections to be Tested:

1. **User Interface (UI) Testing:** The user interface is the primary point of interaction for users. During alpha testing, developers thoroughly evaluate the UI to ensure its usability, responsiveness, and overall user-friendliness. This includes testing aspects like image upload, button functionality, and the presentation of diagnostic results.

2. **Data Preprocessing Testing:** Data preprocessing plays a pivotal role in preparing MRI scan data for analysis. Alpha testing involves scrutinizing data preprocessing steps to

guarantee that images are correctly resized, normalized, and transformed for accurate input to the classification model.

3. **Model Inference Testing:** The core of NeuroScanAI revolves around the brain tumor classification model. Alpha testing entails validating that the model can accurately predict the presence and type of brain tumor in MRI scans. Developers meticulously assess the model's performance and accuracy during this phase.

4. **Prediction Output Testing:** The results generated by the system are vital in conveying diagnostic information to users. Alpha testing assesses the accuracy of prediction outputs, ensuring that they correctly identify the tumor type or indicate the absence of a tumor.

5. **User Interaction and Feedback Testing:** The user's experience and interaction with the system are crucial. Developers test user feedback mechanisms, button interactions, and the overall flow of information to ensure a seamless and informative user experience.

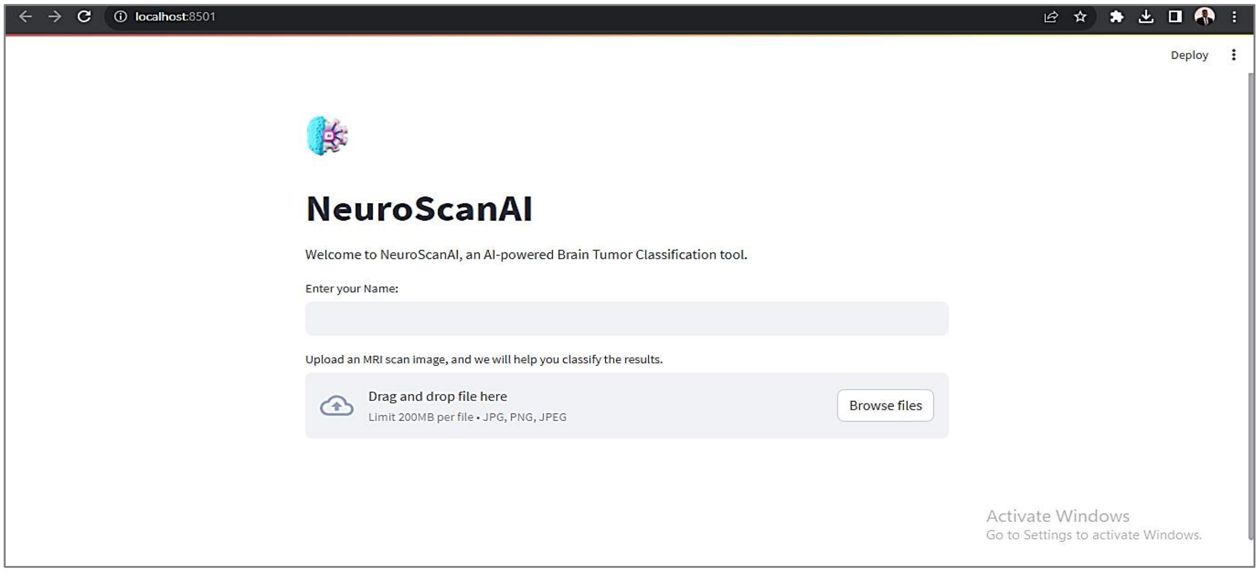
6. **“Expert Option” Testing:** NeuroScanAI includes an "Expert Option" button, allowing users to access detailed information about the prediction percentages for different tumor types. During alpha testing, developers verify the accuracy of these percentages and their alignment with the model's predictions.

7. **“More Information” Testing:** When users click the "More Information" button, detailed recommendations for specific tumor types are displayed. Alpha testing confirms that these recommendations are presented correctly and provide valuable guidance to users. Internal acceptance alpha testing is a critical phase that enables developers to refine and improve NeuroScanAI before it reaches external users, ensuring that it functions as intended and provides reliable brain tumor classifications.

4.4. Screenshot of Running System (NeuroScanAI)

4.4.1. Home Page

The homepage serves as the initial point of interaction between the user and the interface as the users are greeted by the NeuroScanAI banner and an accompanying logo. It features a text field where the user can enter the patient's name and provides a prompt to upload an MRI scan for analysis.



NeuroScanAI

Welcome to NeuroScanAI, an AI-powered Brain Tumor Classification tool.

Enter your Name:

Upload an MRI scan image, and we will help you classify the results.

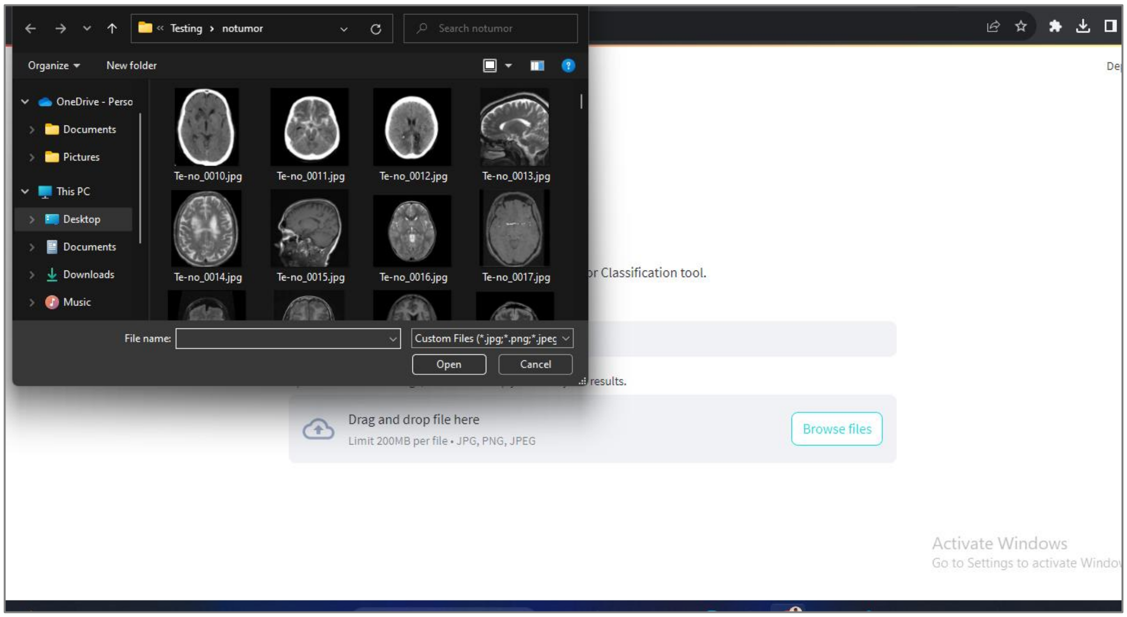
Drag and drop file here

Limit 200MB per file • JPG, PNG, JPEG

Figure 4.4 Home Page

4.4.2. Data Collection Page

When accessing the Data Collection page, users are prompted to provide both a name and an MRI scan. Upon selecting the option to collect an MRI image, a dialog box for image selection will open.

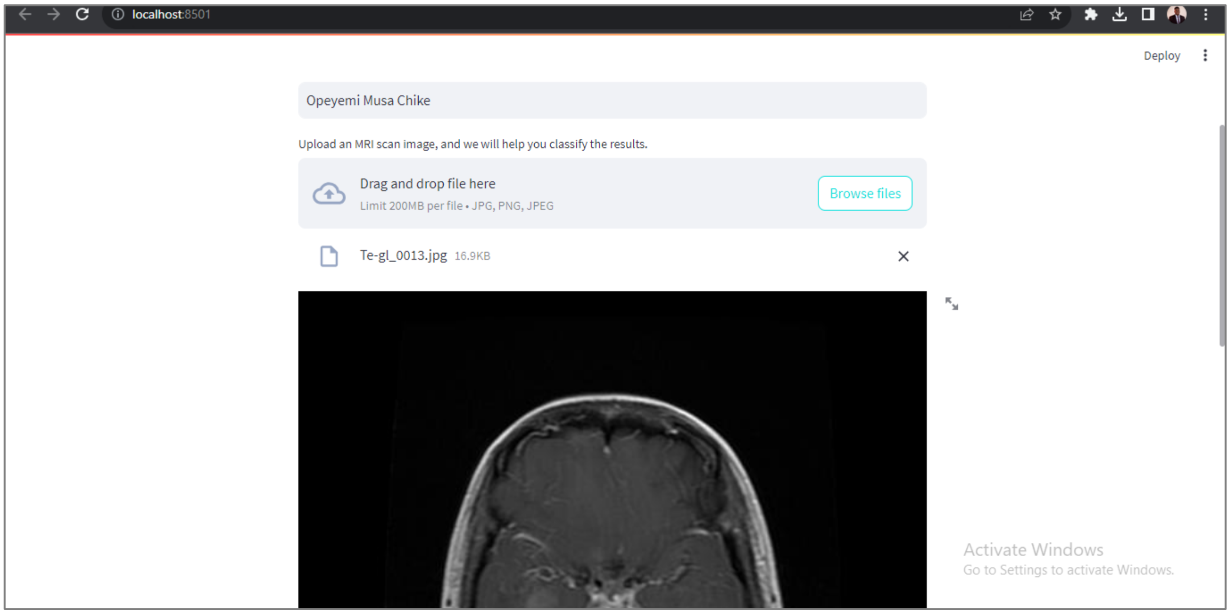


r Classification tool.

results.

Figure 4.4 Data Collection Page

Once the image is selected, it is presented for display.



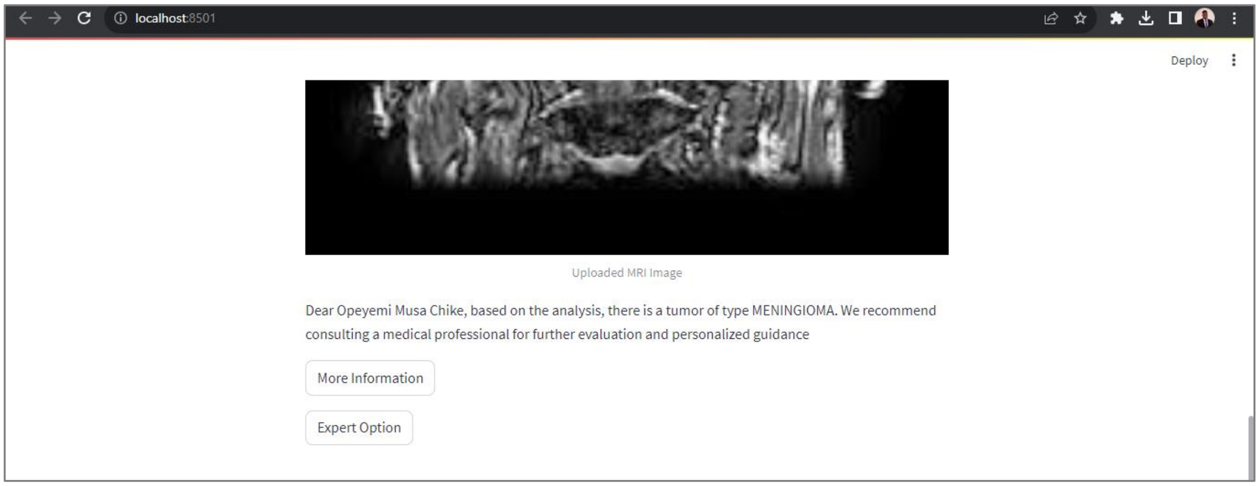
Opeyemi Musa Chike

Upload an MRI scan image, and we will help you classify the results.

Figure 4.5 MRI Image Display

4.4.3. Recommendation Page

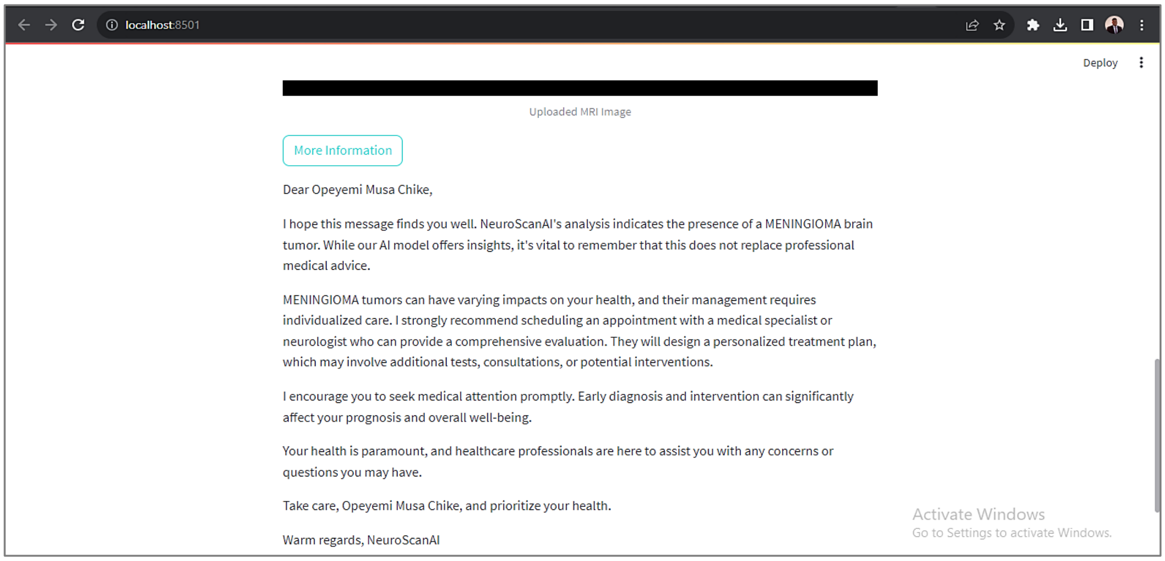
The Recommendation Page serves as the platform for users to receive their diagnosis. It provides information about the presence and type of tumor, if detected. Additionally, this page offers two additional buttons for users to explore further: "Expert Options" and "More Information."



Dear Opeyemi Musa Chike, based on the analysis, there is a tumor of type MENINGIOMA. We recommend consulting a medical professional for further evaluation and personalized guidance

Figure 4.6 Recommendation Page

The "More Information" button on the Recommendation Page allows users to access detailed insights regarding their diagnosis. This feature provides comprehensive information about the specific type of tumor identified (if present) and offers guidance on potential next steps and considerations. Users can use this option to gain a deeper understanding of their condition and access valuable information to support informed decision-making and further medical discussions.



Dear Opeyemi Musa Chike,

I hope this message finds you well. NeuroScanAI's analysis indicates the presence of a MENINGIOMA brain tumor. While our AI model offers insights, it's vital to remember that this does not replace professional medical advice.

MENINGIOMA tumors can have varying impacts on your health, and their management requires individualized care. I strongly recommend scheduling an appointment with a medical specialist or neurologist who can provide a comprehensive evaluation. They will design a personalized treatment plan, which may involve additional tests, consultations, or potential interventions.

I encourage you to seek medical attention promptly. Early diagnosis and intervention can significantly affect your prognosis and overall well-being.

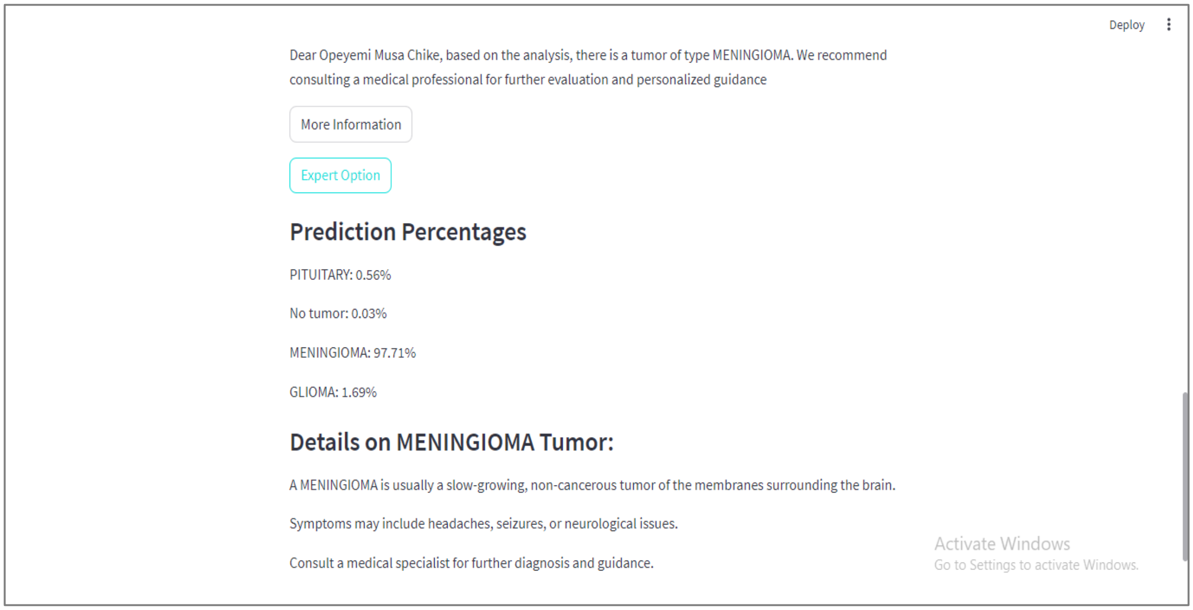
Your health is paramount, and healthcare professionals are here to assist you with any concerns or questions you may have.

Take care, Opeyemi Musa Chike, and prioritize your health.

Warm regards, NeuroScanAI

Figure 4.7 Display of More Information

The "Expert Options" button opens a window displaying the prediction percentages for various brain tumor types, providing users with deeper insights into the AI's analysis. This feature empowers users to better understand the model's assessment, facilitating more informed discussions with medical professionals if necessary.



Dear Opeyemi Musa Chike, based on the analysis, there is a tumor of type MENINGIOMA. We recommend consulting a medical professional for further evaluation and personalized guidance

Prediction Percentages

PITUITARY: 0.56%

No tumor: 0.03%

MENINGIOMA: 97.71%

GLIOMA: 1.69%

Details on MENINGIOMA Tumor:

A MENINGIOMA is usually a slow-growing, non-cancerous tumor of the membranes surrounding the brain.

Symptoms may include headaches, seizures, or neurological issues.

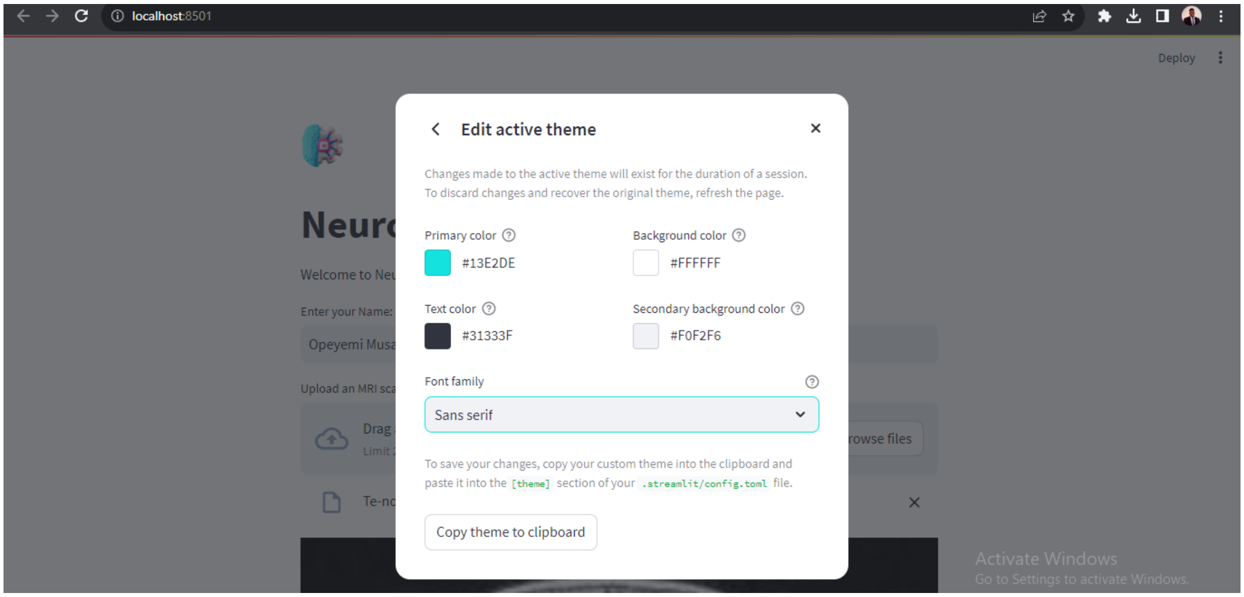
Consult a medical specialist for further diagnosis and guidance.

Figure 4.8 Display of Expert Options

4.4.4. Customization Page

The "Customization Page" within the NeuroScanAI interface offers users the flexibility to tailor their experience according to their preferences. Streamlit, as the underlying technology, provides powerful customization capabilities for this purpose. Users can personalize their interface by adjusting primary and secondary background colors to match their aesthetics and visual preferences. This customization extends to choosing a primary font style that resonates with their taste and enhances readability.

Furthermore, users have the option to select from a range of theme presets, allowing them to quickly switch between different visual styles that suit their mood or environment. This customization feature enhances the user experience by making the interface feel more familiar and comfortable.



Edit active theme

Changes made to the active theme will exist for the duration of a session. To discard changes and recover the original theme, refresh the page.

Primary color	Background color
#13E2DE	#FFFFFF
Text color	Secondary background color
#31333F	#F0F2F6

Font family

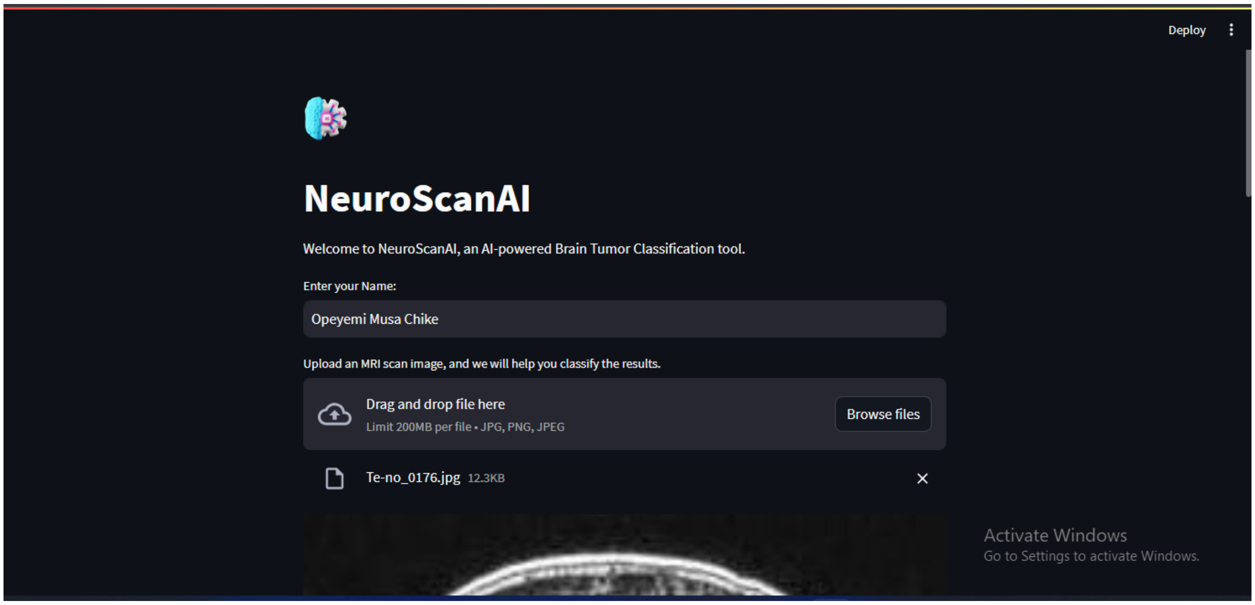
Sans serif

To save your changes, copy your custom theme into the clipboard and paste it into the `[theme]` section of your `.streamlit/config.toml` file.

Copy theme to clipboard

Figure 4.9 Customization Page

The "Dark Mode" is one of the preset themes available on the "Customization Page." It provides users with the option to switch to a darker color scheme for the interface. This mode is not only visually appealing but also reduces eye strain, especially in low-light environments. Users can easily toggle between "Dark Mode" and other themes to optimize their experience while using NeuroScanAI.



NeuroScanAI

Welcome to NeuroScanAI, an AI-powered Brain Tumor Classification tool.

Enter your Name:

Opeyemi Musa Chike

Upload an MRI scan image, and we will help you classify the results.

Drag and drop file here

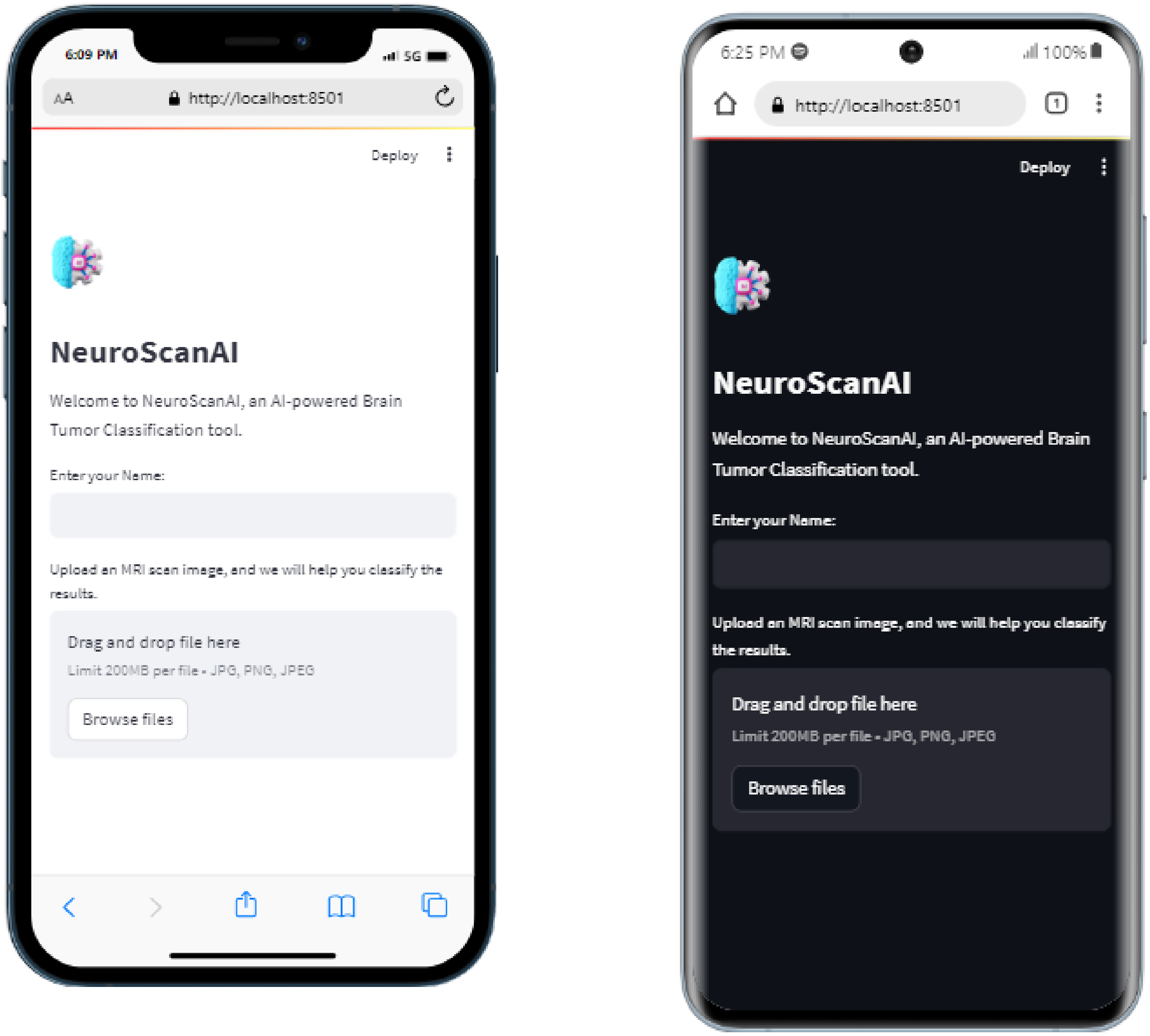
Limit 200MB per file • JPG, PNG, JPEG

Te-no_0176.jpg 12.3KB

Figure 4.10 Dark Mode

4.4.5. Mobile View (Responsiveness)

NeuroScanAI is designed to be responsive, ensuring a seamless experience on mobile devices. This means that users can conveniently access and use the web app on their smartphones or tablets. The responsive design adapts the user interface to fit various screen sizes and orientations, making it versatile and accessible regardless of the device being used. Whether on a desktop, laptop, smartphone, or tablet, users can confidently interact with NeuroScanAI, ensuring accessibility and convenience across different platforms.



6:09 PM 5G

AA http://localhost:8501

Deploy

NeuroScanAI

Welcome to NeuroScanAI, an AI-powered Brain Tumor Classification tool.

Enter your Name:

Upload an MRI scan image, and we will help you classify the results.

Drag and drop file here

Limit 200MB per file • JPG, PNG, JPEG

Browse files

6:25 PM 100%

http://localhost:8501

Deploy

NeuroScanAI

Welcome to NeuroScanAI, an AI-powered Brain Tumor Classification tool.

Enter your Name:

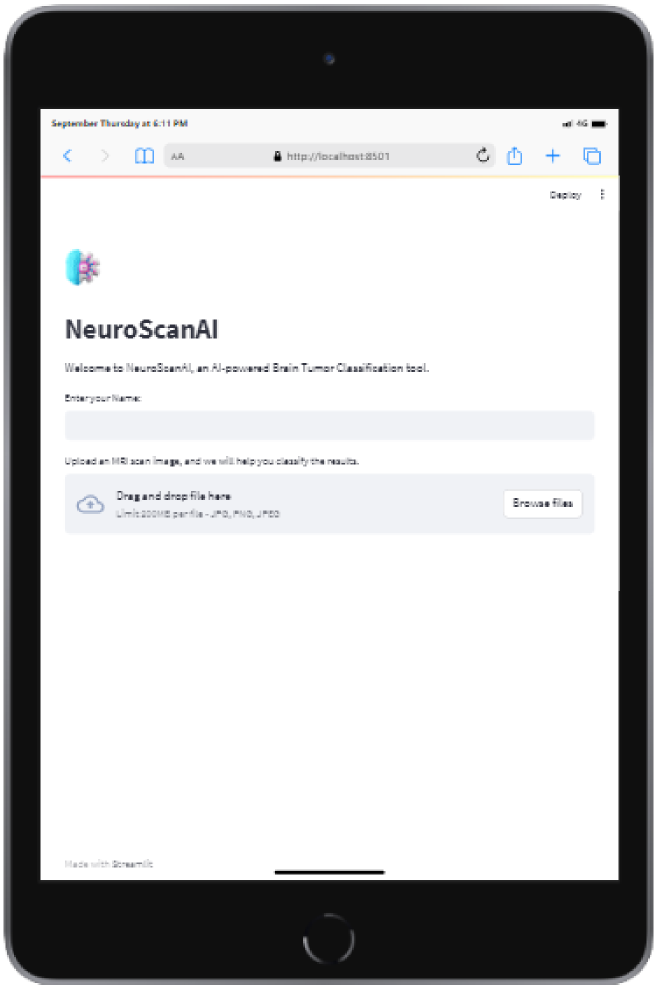
Upload an MRI scan image, and we will help you classify the results.

Drag and drop file here

Limit 200MB per file • JPG, PNG, JPEG

Browse files

Figure 4.11 NeuroScanAI on Iphone 12 Pro and Samsung S20



NeuroScanAI

Welcome to NeuroScanAI, an AI-powered Brain Tumor Classification tool.

Enter your Name:

Upload an MRI scan image, and we will help you classify the results.

Drag and drop file here

Limit 200MB per file - JPG, PNG, JPEG

Figure 4.12 NeuroScanAI on iPad Mini

The screenshots displayed above showcase NeuroScanAI's responsive design on a range of mobile devices, including the iPhone 12 Pro, Samsung S20, and iPad Mini. This responsive adaptation ensures that NeuroScanAI maintains its user-friendly interface and functionality seamlessly across various platforms. Whether accessed via an iPhone, Samsung smartphone, or iPad Mini, users can rely on a consistent and accessible experience, enhancing the convenience and accessibility of the web app on different mobile devices.

CHAPTER FIVE

SUMMARY AND CONCLUSION

5.1. Summary

NeuroScanAI stands as a solution in the realm of medical diagnostics, offering an intricate blend of cutting-edge technology and user-friendly accessibility. This web-based tool represents a sophisticated methodology that spans data collection, robust preprocessing, and the development of a deep learning model, meticulously trained to decipher the presence and specific type of brain tumors from MRI scans. It provides a seamless interface that simplifies the process of inputting critical data, ensuring a hassle-free user experience. Following its analysis, NeuroScanAI delivers comprehensive diagnostic results, not only pinpointing the presence or absence of a tumor but also specifying its type with impressive accuracy. Beyond its diagnostic capabilities, this tool places a strong emphasis on user customization, allowing individuals to tailor its appearance, font, and even toggle between theme presets, including a user-friendly dark mode.

Moreover, NeuroScanAI extends its reach to accommodate diverse users, as it seamlessly adapts to various mobile devices, rendering its diagnostic prowess accessible on smartphones, tablets, and more. This project exemplifies the potential of artificial intelligence in revolutionizing healthcare, offering a vital tool for early tumor detection. By bridging the gap between advanced technology and practical usability, NeuroScanAI promises to contribute significantly to the field of medical diagnostics, ultimately translating into improved patient care, better treatment outcomes, and an overall advancement in the practice of medicine.

5.2. Conclusion

NeuroScanAI has made remarkable progress in addressing the pressing issue of brain tumor diagnosis, especially in regions with limited healthcare resources such as Africa. Its deep learning-based approach, featuring a specialized neural network, has proven highly effective in analyzing MRI scans. This web-based tool offers an accessible and user-friendly solution for early tumor detection, providing hope for both patients and medical professionals.

The value of NeuroScanAI lies in its ability to offer quick and accurate insights into brain tumor classification, contributing to filling the diagnostic gap that underserved nations, like many African countries, face. It encourages individuals to take an active role in their health. However, it's important to note that NeuroScanAI is a support tool, not a replacement for medical expertise. It emphasizes the importance of consulting healthcare professionals for comprehensive assessments and diagnoses.

5.3. Recommendations

Recommendation for Use

NeuroScanAI is a powerful tool with the potential to make a significant impact in the field of medical diagnostics. However, it is imperative to underscore that NeuroScanAI is not a replacement for the expertise and judgment of trained healthcare providers. Instead, it should be seen as a supportive instrument that assists medical professionals in their assessments. Individuals who suspect the presence of brain tumors, especially in cases with ambiguous symptoms, can benefit greatly from the tool's initial assessment, as early detection often translates into more timely medical interventions and potentially improved patient outcomes. For patients with known brain tumors, NeuroScanAI offers a means of regular follow-up scans, enabling healthcare providers to monitor changes in tumor size and characteristics over time and make informed decisions regarding treatment plans. Furthermore, NeuroScanAI serves as a valuable resource for researchers and medical students interested in the domains of neurology and medical imaging. It not only illuminates the potential of AI in medical diagnostics but also offers an educational platform for those eager to delve into the field.

In addition to its clinical applications, NeuroScanAI provides users with customization options, allowing them to tailor their experience for greater comfort and accessibility. Its mobile responsiveness extends its utility to a diverse range of devices, making it accessible even in remote or underserved areas where access to healthcare facilities might be limited. However, it is essential for users to recognize the symbiotic relationship between technology and healthcare expertise. NeuroScanAI's efficacy hinges on the collaborative efforts of both AI and medical professionals. As such, while it offers immense promise in enhancing brain health and patient care, its utility should be viewed through a lens of complementarity with traditional medical consultation. Ultimately, NeuroScanAI has the potential to revolutionize early brain tumor detection, but this potential is most fully realized when combined with the guidance and wisdom of healthcare experts.

User Guidance

While NeuroScanAI offers valuable insights into brain tumor classification, it's crucial for users to exercise caution and use the software appropriately. NeuroScanAI is designed to assist and provide preliminary information, but it should never replace professional medical advice. If you receive a diagnosis or suspect any health concerns based on the software's results, we strongly recommend consulting a qualified medical professional or specialist for confirmation and personalized guidance. Your health and well-being are of utmost importance, and a healthcare expert can offer the best course of action tailored to your specific needs. NeuroScanAI aims to empower users with information, but it should always be complemented by professional medical evaluation for accurate diagnosis and treatment.

REFERENCES

Abd-Ellaha, Khaled, Mahmoud, Ali Ismail Awadb, c., Khalafd, A. A., . . . F.A., a. H. (2019). A review on brain tumor diagnosis from MRI images: Practical implications,key achievements, and lessons learned.

American Brain Tumor Association. (n.d.). *Brain Tumour Education*. Retrieved from https://www.abta.org/about-brain-tumors/brain-tumor-education/

Chen, P. H., Lin, M. C., Lai, P. H., Yang, L. C., & and Lin, G. (2018). Brain tumor classification using deep learning-based image reconstruction. *IEEE Journal of Biomedical and Health Informatics,*, 22(2), 414-421.

Esteva, A., Kuprel, B., Novoa, R. A., Ko, J., Swetter, S. M., Blau, H. M., & Thrun, S. (2017). Dermatologist-level classification of skin cancer with deep neural networks. *Nature*, 542(7639), 115-118. doi: 10.1038/nature21056.

Haenssle, H. A., Fink, C., Schneiderbauer, R., Toberer, F., Buhl, T., Blum, A.,……& Hofmann-Wellenhof, R. (2018). Man against machine: Diagnostic performance of a deep learning convolutional neural network for dermoscopic melanoma recognition in comparison to 58 dermatologists. *Annals of Oncology*, 29(8), 1836-1842. doi: 10.1093/annonc/mdy166.

Havaei, M., Davy, A., Warde-Farley, D., Biard, A., Courville, A., Bengio, Y., ... & Pal, C. (2017). Brain tumor segmentation with Deep Neural Networks. *Medical image analysis*, 35, 18-31. doi: 10.1016/j.media.2016.05.004.

Kamnitsas, K., Ledig, C., Newcombe, V. F., Simpson, J. P., Kane, A. D., Menon, D. K., & ... Rueckert, D. (2016). Efficient multi-scale 3D CNN with fully connected CRF for accurate brain lesion segmentation. . *Medical image analysis*, 36, 61-78.

Krizhevsky, A., Sutskever, I., & Hinton, G. E. (2012). ImageNet classification with deep convolutional neural networks. *In Advances in neural information processing systems*, (pp. 1097-1105).

Litjens, G., Kooi, T., Bejnordi, B. E., Setio, A. A., Ciompi, F., Ghafoorian, M., & ... and Sánchez, C. I. (2017). A survey on deep learning in medical image analysis. Medical image analysis. 42, 60-88.

Louis, D. N., Perry, A., Reifenberger, G., von Deimling, A., Figarella-Branger, D., Cavenee, W. K., ... & Ellison, D. W. (2016). The 2016 World Health Organization Classification of Tumors of the Central Nervous System: a summary. Acta neuropathologica. 131(6), 803-820. doi: 10.1007/s00401-016-1545-1.

Mamlouk, A. M., & and Yousef, A. F. (2020). Brain tumor classification based on MRI images using deep learning techniques. *Computers in biology and medicine*, 126, 104046.

Menze, B. H., Jakab, A., Bauer, S., Kalpathy-Cramer, J.Farahani, & K., K. J. (Oct. 2015). The Multimodal Brain Tumor Image Segmentation Benchmark (BRATS). *IEEE Transactions on Medical Imaging, vol. 34, no. 10*.

National Institute of Biomedical Imaging and Bioengineering (NIBIB). (n.d.). Retrieved from nibib.nih.gov: https://www.nibib.nih.gov/science-education/science-topics/magnetic-resonance-imaging-mri

Pan, S. J., & Yang, Q. (2010). A survey on transfer learning. *IEEE Transactions on knowledge and data engineering*, 22(10), 1345-1359.

Reed-Guy, L. (2023). *Brain Disorders.* Retrieved from healthline.com: https://www.healthline.com/health/brain-disorders

United Nations. (2023). *goals/goal3*. Retrieved from sdgs.un.org: https://sdgs.un.org/goals/goal3

Wen, P. Y., & Kesari, S. (2008). Malignant gliomas in adults. *New England Journal of Medicine*, 359(5), 492-507. doi: 10.1056/NEJMra0708126.

WHO. (2023). *Global Health Observatory Data Repository: Density of neurosurgeons (per 100,000 population).* Retrieved from www.who.int: https://www.who.int/data/gho/data/indicators/indicator-details/GHO/total-density-per-100-000-population-health-posts

Yosinski, J., Clune, J., Bengio, Y., & Lipson, H. (2014). How transferable are features in deep neural networks? *In Proceedings of the 27th International Conference on Neural Information Processing Systems (NIPS 2014),* 3320-3328.

APPENDIX

SOURCE CODE

MODEL BUILDING AND TESTING

```
# For Data Processing
import numpy as np
from sklearn.utils import shuffle
from sklearn.model_selection import train_test_split
from sklearn.metrics import classification_report
from PIL import Image, ImageEnhance


# For ML Models
from tensorflow import keras
from tensorflow.keras.layers import *
from tensorflow.keras.losses import *
from tensorflow.keras.models import *
from tensorflow.keras.metrics import *
from tensorflow.keras.optimizers import *
from tensorflow.keras.applications import *
from tensorflow.keras.preprocessing.image import load_img

# For Data Visualization
import matplotlib.pyplot as plt
import seaborn as sns
# Miscellaneous
from tqdm import tqdm
import os
import pandas as pd
import random
```

```
train_dir = '/kaggle/input/brain-tumor-mri-dataset/Training/'
test_dir = '/kaggle/input/brain-tumor-mri-dataset/Testing/'

train_paths = []
train_labels = []

for label in os.listdir(train_dir):
    for image in os.listdir(train_dir+label):
        train_paths.append(train_dir+label+'/'+image)
        train_labels.append(label)

train_paths, train_labels = shuffle(train_paths, train_labels)
plt.figure(figsize=(14,6))
colors = ['#4285f4', '#ea4335', '#fbbc05', '#34a853']
plt.rcParams.update({'font.size': 14})
plt.pie([len([x for x in train_labels if x=='pituitary']),
         len([x for x in train_labels if x=='notumor']),
         len([x for x in train_labels if x=='meningioma']),
         len([x for x in train_labels if x=='glioma'])],
        labels=['pituitary','notumor', 'meningioma', 'glioma'],
        colors=colors, autopct='%.1f%%', explode=(0.025,0.025,0.025,0.025),
        startangle=30);

plt.figure(figsize=(14,6))
colors = ['#4285f4', '#ea4335', '#fbbc05', '#34a853']
plt.rcParams.update({'font.size': 14})
plt.pie([len(train_labels), len(test_labels)],
        labels=['Train','Test'],
        colors=colors, autopct='%.1f%%', explode=(0.05,0),
        startangle=30);
```

```
def augment_image(image):
    image = Image.fromarray(np.uint8(image))
    image = ImageEnhance.Brightness(image).enhance(random.uniform(0.8,1.2))
    image = ImageEnhance.Contrast(image).enhance(random.uniform(0.8,1.2))
    image = np.array(image)/255.0
    return image

IMAGE_SIZE = 128

def open_images(paths):
    '''
    Given a list of paths to images, this function returns the images as arrays (after augmenting them)
    '''
    images = []
    for path in paths:
        image = load_img(path, target_size=(IMAGE_SIZE,IMAGE_SIZE))
        image = augment_image(image)
        images.append(image)
    return np.array(images)

images = open_images(train_paths[50:59])
labels = train_labels[50:59]
fig = plt.figure(figsize=(12, 6))
for x in range(1, 9):
    fig.add_subplot(2, 4, x)
    plt.axis('off')
    plt.title(labels[x])
    plt.imshow(images[x])
plt.rcParams.update({'font.size': 12})
plt.show()
unique_labels = os.listdir(train_dir)


def encode_label(labels):
    encoded = []
    for x in labels:
        encoded.append(unique_labels.index(x))
    return np.array(encoded)


def decode_label(labels):
    decoded = []
    for x in labels:
        decoded.append(unique_labels[x])
    return np.array(decoded)


def datagen(paths, labels, batch_size=12, epochs=1):
    for _ in range(epochs):
        for x in range(0, len(paths), batch_size):
            batch_paths = paths[x:x+batch_size]
            batch_images = open_images(batch_paths)
            batch_labels = labels[x:x+batch_size]
            batch_labels = encode_label(batch_labels)
            yield batch_images, batch_labels
base_model = VGG16(input_shape=(IMAGE_SIZE,IMAGE_SIZE,3), include_top=False, weights='imagenet')
# Set all layers to non-trainable
for layer in base_model.layers:
    layer.trainable = False
# Set the last vgg block to trainable
base_model.layers[-2].trainable = True
base_model.layers[-3].trainable = True
base_model.layers[-4].trainable = True

model = Sequential()
model.add(Input(shape=(IMAGE_SIZE,IMAGE_SIZE,3)))
model.add(base_model)
model.add(Flatten())
model.add(Dropout(0.3))
model.add(Dense(128, activation='relu'))
model.add(Dropout(0.2))
model.add(Dense(len(unique_labels), activation='softmax'))
model.compile(optimizer=Adam(learning_rate=0.0001),
         loss='sparse_categorical_crossentropy',
         metrics=['sparse_categorical_accuracy'])
batch_size = 20
steps = int(len(train_paths)/batch_size)
epochs = 10
history = model.fit(datagen(train_paths, train_labels, batch_size=batch_size, epochs=epochs),
           epochs=epochs, steps_per_epoch=steps)
plt.figure(figsize=(8,4))
plt.grid(True)
plt.plot(history.history['sparse_categorical_accuracy'], '.g-', linewidth=2)
plt.plot(history.history['loss'], '.r-', linewidth=2)
plt.title('Model Training History')
plt.xlabel('epoch')
plt.xticks([x for x in range(epochs)])
plt.legend(['Accuracy', 'Loss'], loc='upper left', bbox_to_anchor=(1, 1))
plt.show()
model.save('Neuroscanaimodel.h5')
batch_size = 32
```

```
steps = int(len(test_paths)/batch_size)
y_pred = []
y_true = []
for x,y in tqdm(datagen(test_paths, test_labels, batch_size=batch_size, epochs=1), total=steps):
    pred = model.predict(x)
    pred = np.argmax(pred, axis=-1)
    for i in decode_label(pred):
        y_pred.append(i)
    for i in decode_label(y):
        y_true.append(i)
```

WEB APP DEPLOYMENT

```
import streamlit as st
import tensorflow as tf
import numpy as np
from tensorflow.keras.preprocessing.image import load_img, img_to_array
from tensorflow.keras.applications.vgg16 import preprocess_input
from PIL import Image
#import matplotlib.pyplot as plt
#import io

# Define the path to the saved model

model_directory = r"C:\Users\FRANKFELIXAI\Desktop\OutApp Project\Final year project\Neuroscanaimodel.h5"

model = tf.keras.models.load_model(model_directory)

# Function to make predictions
def predict(image):
    image = img_to_array(image)
    image = image / 255
    image = image.reshape((1, image.shape[0], image.shape[1], image.shape[2]))
    prediction = model.predict(image)
    return prediction

# Load and resize the brain icon image from a file
brain_icon = Image.open(r"C:\Users\FRANKFELIXAI\Desktop\OutApp Project\Final year project\NeuroScanAI_Logo.png")
brain_icon = brain_icon.resize((50, 50))

# Streamlit app
st.image(brain_icon, use_column_width=False, width=50)
st.title("NeuroScanAI")
st.write("Welcome to NeuroScanAI, an AI-powered Brain Tumor Classification tool.")
patient_name = st.text_input("Enter your Name: ")

recommendation_message_PITUITARY = f"""
Dear {patient_name},

I hope this message finds you well. Based on the analysis conducted by NeuroScanAI, it has been identified that you have a PITUITARY brain tumor. While the AI model provides valuable insights, it's essential to remember that this is not a replacement for professional medical advice.

A PITUITARY tumor can have various impacts on your health, and its management may require a personalized treatment plan. I strongly recommend that you schedule an appointment with a medical specialist or neurologist who can conduct a comprehensive evaluation of your condition. They will be able to provide you with a tailored treatment strategy, which may include further diagnostic tests, consultations, or potential interventions.

Please do not hesitate to seek medical attention promptly. Early diagnosis and intervention can significantly influence the outcome and your overall well-being.
```

```
Your health is of utmost importance, and a healthcare professional can guide you through this process, addressing any concerns or questions you may have.

Take care, {patient_name}, and prioritize your health.

Warm regards,
NeuroScanAI
"""

recommendation_message_GLIOIMA = f"""
Dear {patient_name},

I hope this message finds you well. NeuroScanAI has identified that you have a GLIOMA brain tumor. While the AI model provides valuable insights, it's crucial to understand that this is not a substitute for professional medical guidance.

GLIOMA tumors vary in severity, and managing them requires personalized medical attention. I strongly advise you to schedule an appointment with a neurologist or oncologist who can conduct a thorough assessment of your condition. They will develop a tailored treatment plan, which may include additional tests, consultations, or potential interventions.

Please prioritize seeking medical care promptly. Early diagnosis and treatment can have a significant impact on your prognosis and overall well-being.

Remember that your health is paramount, and healthcare professionals are here to support you through this journey. If you have any concerns or questions, they are the best resource.

Take good care of yourself, {patient_name}, and stay positive.

Warm regards,
NeuroScanAI
"""
```

```
recommendation_message_MENINGIOMA = f"""
Dear {patient_name},

I hope this message finds you well. NeuroScanAI's analysis indicates the presence of a MENINGIOMA brain tumor. While our AI model offers insights, it's vital to remember that this does not replace professional medical advice.

MENINGIOMA tumors can have varying impacts on your health, and their management requires individualized care. I strongly recommend scheduling an appointment with a medical specialist or neurologist who can provide a comprehensive evaluation. They will design a personalized treatment plan, which may involve additional tests, consultations, or potential interventions.

I encourage you to seek medical attention promptly. Early diagnosis and intervention can significantly affect your prognosis and overall well-being.

Your health is paramount, and healthcare professionals are here to assist you with any concerns or questions you may have.

Take care, {patient_name}, and prioritize your health.

Warm regards,
NeuroScanAI
"""

recommendation_message_NoTumor = f"""
Dear {patient_name},

I'm delighted to share that NeuroScanAI's analysis did not detect any brain tumors in your MRI scan. This is great news!

However, please remember that it's crucial to maintain good brain health. Here are some tips:
```

```
1. Stay mentally active: Engage in activities that challenge your brain, such as puzzles, reading, or learning new skills.


2. Eat a balanced diet: Consume foods rich in antioxidants, omega-3 fatty acids, and other nutrients that support brain health.


3. Regular exercise: Physical activity promotes blood flow to the brain and enhances cognitive function.


4. Get enough sleep: Quality sleep is essential for brain recovery and cognitive performance.


5. Stay hydrated: Proper hydration is vital for brain function.


6. Manage stress: Practice stress-reduction techniques like meditation or yoga.


While the absence of a tumor is excellent news, maintaining good brain health is essential. If you have any concerns or questions about brain health, do not hesitate to consult with a healthcare professional.


Take care of your brain, {patient_name}, and prioritize your well-being.


Warm regards,
NeuroScanAI
"""




# Upload an MRI scan image
uploaded_image = st.file_uploader("Upload an MRI scan image, and we will help you classify the results. ", type=["jpg", "png", "jpeg"])


if uploaded_image is not None:
    st.image(uploaded_image, caption="Uploaded MRI Image", use_column_width=True)
```

```
image = load_img(uploaded_image, target_size=(128, 128))

# Make a prediction
prediction = predict(image)
predict_index = np.argmax(prediction)
tumor_types = ["PITUITARY", "No tumor", "MENINGIOMA", "GLIOMA"]

# Create an empty placeholder for the initial diagnosis
initial_diagnosis_placeholder = st.empty()

# Display the prediction
if predict_index == 1:
    initial_diagnosis_placeholder.write(f"Dear {patient_name}, based on the analysis, there is no tumor detected. We recommend consulting a medical professional for confirmation and to ensure your brain health.")
else:
    initial_diagnosis_placeholder.write(f"Dear {patient_name}, based on the analysis, there is a tumor of type {tumor_types[predict_index]}. We recommend consulting a medical professional for further evaluation and personalized guidance")

# More Info
if st.button("More Information"):
    initial_diagnosis_placeholder.empty()
 # Clear the initial diagnosis
    if predict_index == 0:
        st.write(recommendation_message_PITUITARY)
    if predict_index == 3:
        st.write(recommendation_message_GLIOIMA)
    if predict_index == 2:
        st.write(recommendation_message_MENINGIOMA)
    if predict_index == 1:
        st.write(recommendation_message_NoTumor)



# Expert Option
if st.button("Expert Option"):
    st.subheader("Prediction Percentages")
    percentages = [round((score / sum(prediction[0])) * 100, 2) for score in prediction[0]]
    for i, tumor_type in enumerate(tumor_types):
        st.write(f"{tumor_type}: {percentages[i]}%")


    if predict_index != 1:
        st.subheader(f"Details on {tumor_types[predict_index]} Tumor:")
        if predict_index == 0:  # PITUITARY
            st.write("A PITUITARY tumor is typically a non-cancerous growth located in the pituitary gland.")
            st.write("Common symptoms include headaches, vision problems, and hormonal imbalances.")
            st.write("Consult a medical specialist for a comprehensive evaluation and treatment plan.")
        elif predict_index == 2:  # MENINGIOMA
            st.write("A MENINGIOMA is usually a slow-growing, non-cancerous tumor of the membranes surrounding the brain.")
            st.write("Symptoms may include headaches, seizures, or neurological issues.")
            st.write("Consult a medical specialist for further diagnosis and guidance.")
        elif predict_index == 3:  # GLIOMA
            st.write("A GLIOMA is a type of brain tumor that can be cancerous and may infiltrate brain tissue.")
            st.write("Symptoms vary depending on the location and size.")
            st.write("Immediate consultation with a neurologist or oncologist is recommended.")
# Display the MRI image again with prediction
#st.image(uploaded_image, caption="MRI Image with Prediction", use_column_width=True)
```