In-depth Analysis of Deep Learning Architectures for Brain Tumor Classification in MRI Scans

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A thesis submitted to the Department of Computer Science and Engineering
in partial fulfillment of the requirements for the degree of

B.Sc. in Computer Science
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Declaration

It is hereby declared that

1. The thesis submitted is our own original work while completing degree at Brac University.
2. The thesis does not contain material previously published or written by a third party, except where this is appropriately cited through full and accurate referencing.
3. The thesis does not contain material which has been accepted, or submitted, for any other degree or diploma at a university or other institution.
4. We have acknowledged all main sources of help

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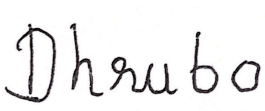

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Abstract

One of the deadliest and most difficult tumors to cure is a brain tumor. Patients diagnosed with brain tumors tend to have a comparatively shorter lifespan. This tumor can affect any individual of any age. To mitigate the damages of brain tumors, early prognosis, and diagnosis are mandatory for a comparatively longer lifespan. Our primary goal is to develop a functional convolutional neural network (CNN) model that can reliably identify brain tumor cells in a patient's magnetic resonance imaging (MRI). Unfortunately, this is a hard task as there are not many resources available as around 2 to 3 cases occur each year in 100,000 individuals in Bangladesh. For this purpose, a dataset was collected and augmented into a larger dataset by splitting, rotating, changing orientation, etc. Three categories were added to the dataset: training, validation, and testing where 70% of the data was for training, 15% for validation, and 15% for testing. Finally, we trained our dataset for 50 epochs to get the accuracy rate and then tested the same data sets with other pre-trained models like MobileNetV2, DenseNet121, and ResNet50. In this course of training our custom CNN model, we gained the highest accuracy rate, which is 97.07% in training, 95.99% in validation, and 96.51% for testing.

Ethics Statement

Writing the thesis is a crucial step strictly in compliance with the university's rules and regulations, as well as ethical principles for doing research. Original data has been incorporated into our thesis. In our document, all additional sources of information have been mentioned. We double-checked our citations and references. Each of the paper's co-authors accepts responsibility for any violations of the thesis rule. There were several questionnaire-free tools, articles, and YouTube videos that helped us address problems. In addition, we would like to take this opportunity to thank everyone who has assisted us along the journey. We would also like to state that the following thesis has never been submitted to any other university or institute to obtain a degree, in whole or in part. Our thesis was completed with guidance from the BRAC University code of ethics and without the use of unethical tactics.

Acknowledgement

Foremost, we give thanks to Almighty Allah for allowing us to finish our thesis without any major interruption.

Without the expertise of Dewan Ziaul Karim sir, our esteemed thesis supervisor, we would not have been able to complete this work. We would like to express our sincere gratitude for his patience, motivation, enthusiasm, and immense knowledge.

Moreover, a debt of gratitude is owed to Avijit Biswas sir, our co-supervisor, for his invaluable assistance and suggestions till the last moment.

Finally, without our parents' unwavering support, it may not be conceivable. We are currently on the verge of graduating for which we are thankful to their kind support and prayer.

Table of Content

List of Figures

List of Tables

Chapter 1

Introduction

A brain tumor is one of the deadliest and most challenging illnesses to identify in the modern world. It happens in several brain regions, some of which develop quite fast and have an impact on the patient's conduct. These tumors are classified as malignant varieties, and there is typically no full recovery from them. Although there is no known treatment for this illness, an early diagnosis can extend the patient's life as much as possible. Our primary goal is to create a model that uses magnetic resonance imaging (MRI) to identify and classify brain tumors at an extremely early stage, allowing medical professionals and patients to take the appropriate precautions to lessen the damage.

1.1 Background Information

The use of image-processing techniques has revolutionized the diagnosis and treatment of many diseases in the realm of medical research and technology, and brain tumors are no exception [16]. Brain tumors are a complicated and frequently fatal medical illness that necessitates early and precise identification for successful treatments. It has become clear that using image processing techniques to anticipate brain tumors is a viable way to increase the precision and effectiveness of diagnosis, allowing for prompt medical interventions that can considerably benefit patient outcomes[22][21].

This thesis report explores the field of brain tumor prediction by image processing for a thorough study of the most recent state-of-the-art approaches, difficulties, and developments in this important area. The investigation of the complex interactions between medical imaging modalities, image processing techniques, and the precise prediction and categorization of brain tumors is the main goal of this study[11]. This project aims to contribute to the improvement of brain tumor diagnosis through computational tools and machine learning algorithms, ultimately resulting in better patient care and prognosis[29].

It is recorded that, in the USA alone, over 13000 cases arrive every year with early to severe forms of glioblastoma, meningioma, pituitary, and other forms of brain tumors[23]. Statistics show that the rate of these cases is increasing every year as shown in fig:1.1 and there are not many effective ways to find these cases in the very early stage.

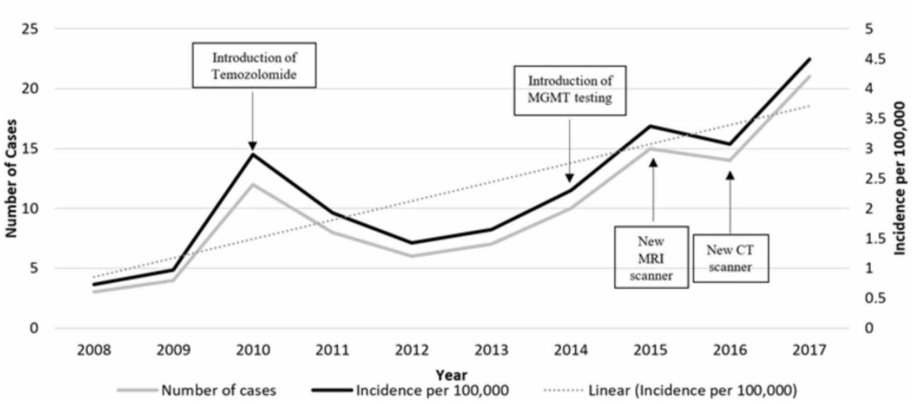


Figure 1.1: Rising incidents of Brain Tumor

Unfortunately, there is not a large number of information about the incidence of brain tumors in Bangladesh. However, Dr. Arman Reza Chowdhury, in his report 'Deadly Brain Tumors', estimates that the incidence of brain tumors in Bangladesh is generally around 2-3 per 100,000 people. A small percentage of patients (about 1%) survive for at least 10 years following diagnosis, even though the typical life expectancy is 1 to 18 months. Only 0.71% of GBM patients survive for more than 10 years, with the median relative survival being 15 months[29].

While it may affect anyone at any age, individuals between the ages of 45 and 70 are the ones who experience it most commonly. It is fast-growing and lacks a genetic foundation. Its prevalence is uncertain as to why curing brain tumors is impossible. Tragically, most people with such tumors only live an average of 12 to 18 months after their diagnosis. Although the focus of treatments is on eliminating or shrinking the tumor to improve symptoms, they are ineffective for long-term survival[29].

In recent years, advancements in medical imaging technology and the huge amount of datasets found online and offline have paved the way for the proper use of deep learning techniques in medical image analysis[12]. Artificial intelligence's deep learning subset has shown impressive results in several fields, such as pattern recognition and computer vision. Its capacity to automatically extract intricate information from unprocessed data makes it a useful instrument for illness identification and forecasting.

Like other forms of brain tumors, glioblastoma, meningioma, etc. are complicated conditions with several underlying causes. Although the precise causes of brain tumors are not entirely known, several variables have been linked to their occurrences[4]. These elements consist of:

- **Genetic mutations:** Brain tumor development is significantly influenced by genetic changes. it has been associated with certain gene mutations, such as those in the TP53 and PTEN genes.

- **Environmental variables:** Although the data is sparse, exposure to specific environmental conditions may raise the chance of developing brain tumors. Ionizing radiation, certain substances, and electromagnetic fields are a few examples of these influences. However,

if there is a direct causal relationship between these characteristics and brain tumors, more investigation is required.

- **Family history:** While most cases of brain tumors occur sporadically without any family history, a small percentage of cases may have a genetic predisposition. In some rare cases, there is a familial clustering of brain tumors, suggesting a genetic component.

The thesis aims to investigate how deep learning algorithms may be used to predict brain tumors using medical imaging data, to improve the accuracy of the findings. Specifically, We will focus on MRI (magnetic resonance imaging) scans, which are often employed in the diagnosis and surveillance of brain tumors and offer organized, comprehensive information about the brain[1]. Our goal is to create a strong prediction model that can precisely identify regions of interest and forecast the existence of brain tumors by utilizing the most recent deep-learning methods.

The findings of these observations suggest that image processing can be used to improve the precision of MRI scans for detecting brain tumors[24]. This could lead to earlier diagnosis and treatment of the tumor, which could improve survival rates for patients with this disease. Here are some of the benefits of using image processing to predict brain tumors:

- Early detection: Image processing can assist in the early detection of brain tumors, which can result in better treatment results.

- Improved accuracy: Image processing can increase the precision of MRI scans, hence lowering the incidence of false-positive and false-negative results.

- Reduced costs: Image processing can help to reduce the costs of diagnosis and treatment by making it easier to identify glioblastomas, meningiomas, and other brain tumors and by reducing the need for more expensive tests.

The proposed research will be conducted in several steps. Firstly, a large dataset will be acquired made up of MRI scan results from people who have been diagnosed with glioblastoma, meningioma, or other forms of brain tumors along with a control group of healthy individuals. These images will be preprocessed to enhance contrast, remove noise, change orientation, and standardize the data. The dataset will then be expanded to include more data for accurate calculations after that. Subsequently, we will employ Convolutional Neural Networks (CNN) to extract meaningful features from the MRI scans. These features will be used to train and fine-tune the predictive model which will increase the accuracy ratio.

Validation of the predictive model will be conducted using a separate set of MRI scans, ensuring an unbiased assessment of its execution. Among the metrics for evaluation are sensitivity, specificity, accuracy, and area under the receiver operating characteristic curve (AUC-ROC)[4].

Additionally, the performance will be compared of the developed model with existing conventional methods such as MobileNetV2, DenseNet121, etc. to demonstrate its superiority in efficiency accuracy and.

The successful implementation of a reliable brain tumor prediction model using image analysis can transform effective diagnosis and treatment of this devastating disease[2]. Early detection can facilitate prompt intervention and personalized treatment plans, leading to the point of improved patient outcomes and enhanced survival rates. Moreover, The findings of this study may aid in the creation of automated instruments that support radiologists in making clinical decisions, ultimately benefiting both patients and healthcare professionals.

By acknowledging these objectives, This dissertation will add to the expanding corpus of knowledge on brain tumor prediction using image processing[8]. The results will show the method's potential to increase early detection and diagnostic accuracy and efficiency, which might eventually improve treatment results and patient prognosis.

1.2 Problem Statement

The health of people can be seriously jeopardized by brain tumors, and prompt and precise identification is essential to successful treatment strategies and patient outcomes. Because magnetic resonance imaging (MRI) has a high spatial resolution and can record complex anatomical features, it has become an effective diagnostic tool for the identification and assessment of brain tumors.

However, manual interpretation of MRI scans to classify brain tumors is a time-consuming and subjective process, and diagnostic accuracy often varies between radiologists. In recent years, deep learning has achieved remarkable results in various medical image analysis tasks, such as brain tumor detection and classification[4]. In automating the categorization of brain tumors in MRI images, convolutional neural networks (CNNs) and other cutting-edge deep learning architectures have demonstrated encouraging results. However, there are not many thorough reviews of the performance, robustness, and generalizability of several deep-learning architectures for brain tumor classification in the literature that is currently available.

One of the biggest challenges in classifying brain tumors using deep learning is the inherent complexity and heterogeneity of tumors. Brain tumors can have a variety of morphological features. Therefore, it is important to explore and identify the most effective deep learning architectures that can capture subtle changes in image data[30]. Additionally, the lack of labeled datasets containing a variety of tumor types and sizes poses challenges to the development and evaluation of robust and generalizable deep-learning models for brain tumor classification. Furthermore, the Interpretability and transparency of deep learning models in the medical field have raised considerable concerns.

Understanding the decision-making processes of these models is important for gaining the trust of medical professionals and for the responsible use of automated systems in clinical practice. To bridge the gap between the black-box nature of deep learning models and clinical decision-making

processes, it is essential to explore interpretability and explainability techniques in the context of brain tumor classification.

This research aims to address the following key questions:

- What is the comparative performance of different deep learning architectures, including CNNs and potentially new architectures, in terms of brain tumor classification in MRI scans?
- How do these deep learning models perform on the dataset with different characteristics? What are the tumor types, sizes, and image processing protocols?
- What techniques may be used to improve the deep learning models' generalizability and robustness for classifying brain tumors?
- How can interpretability and explainability be integrated into deep learning models to increase transparency and foster trust among healthcare professionals?

1.3 Motivation

One of the deadliest and most serious illnesses is brain tumors. Most importantly, it not only causes physical side effects such as constant headaches, seizures, and persistent fatigue but also shortens the patient's lifespan. A very important reason for conducting this research is that the number of patients has increased in the last 10 years since 2010. The number of cases of brain tumors in various categories was only 4,366[13] in the past decade but in 2020 the number increased to 9,500, and no cure is guaranteed. Surgery, radiation therapy, and chemotherapy are some of the main treatments to alleviate the consequences. The best treatment for this disease lies in early detection of the tumor, but in our country, there are only a few methods to detect and diagnose this tumor, and most of them are retrospective. Creating a customized convolutional neural network (CNN) model is the primary objective of our research, which can predict early-stage brain tumors with accuracy and efficiency, giving doctors more time to diagnose and treat this disease, and prolonging patients' lives. For this purpose, we acquired a dataset, augmented it with information, trained it with your custom CNN model and other pre-trained models, and compared the results to determine the accuracy percentage of your own custom CNN model. This will help in achieving the desired results in our models' accuracy resulting in a large contribution in the medical area.

1.4 Research Problem

Glioblastoma (GBM) and Meningioma are both brain tumors while a Pituitary tumor develops in the pituitary gland of the human body. Glioblastoma is a malignant brain tumor which results in it being one of the most formidable diseases in the world. Meningioma is one of the most common types of primary brain tumor which originates in the meninges membrane between the skull and the brain. While most Meningioma is benign, in some rare cases it can be malignant[15]. Pituitary tumors as mentioned earlier develop in the pituitary gland and are mostly non-cancerous as pituitary

cancer is very rare. Still, both Pituitary and Meningioma tumors can cause serious problems either because of their size or because they make extra hormones that our body doesn't need[6].

Our research mainly focuses on detecting Glioblastoma, Meningioma, and Pituitary tumors and also detecting and acknowledging if there is no tumor at all. Although there have been research papers earlier on Glioblastoma, Meningioma, and Pituitary tumors individually, there have not been many research papers on all three tumors collectively and comperatively[25]. Also, the resources available are not as vast as any other common research topic.

The inefficiency of the treatment and biomarker development process is a major problem. Improving the development process can result in increased effectiveness, which will help treatments and biomarkers move closer to clinical testing[14][18]. This enhancement may be made by fostering an atmosphere where mistakes are viewed as learning opportunities and by enhancing the assessment of the likelihood of success at each stage of the growth curve.

Another research problem lies in the limited predictive ability of preclinical models for brain tumor therapeutic development[21]. It is essential to strengthen theories based on fundamental research unique to these tumors. Furthermore, creating preclinical models that are proven to be capable of predicting clinical success and putting in place a formal approach to assess their efficacy might offer a strong case for converting theories into clinical trials[13].

The identification and validation of predictive biomarkers are critical for early-phase clinical trials in these tumors. Research is needed to identify biomarkers that accurately predict therapeutic response and efficacy. Furthermore, establishing a causal link between preclinical effects and specific pharmacodynamic effects measurable in early-phase clinical trials is essential.

Selecting appropriate endpoints for early-phase clinical trials poses another chall- enge[5] Given the limitations of using historical control data, endpoints that directly attribute drug effects, such as pharmacodynamic endpoints or imaging-based responses, should be considered. Developing and validating such endpoints will enable the evaluation of therapies targeting specific molecular aberrations in small subpopulations of patients.

Improving the design of late-stage and pivotal trials is vital[26]. Exploring alternative designs, such as platform trials under master protocols, can efficiently compare overall survival outcomes and evaluate multiple therapeutic and biomarker questions simultaneously[6]. Such designs can enhance efficiency and decision-making in the middle phase of development, where the transition from early signs of efficacy to late-stage randomized trials occurs.

Efforts should also focus on evaluating and validating response biomarkers. Establishing a systematic framework to assess the relationship between early endpoints (e.g., pharmacodynamic or imaging responses) and overall survival outcomes can enhance the efficiency and reliability of therapeutic development in these tumors[31].

In conclusion, rethinking the research and clinical trials enterprise in GBM, Meningioma, Pituitary tumors, as well as brain without tumor is necessary for improved patient outcomes. Addressing the research problems highlighted here, such as enhancing the development process, improving

preclinical models, identifying predictive biomarkers, selecting appropriate endpoints, and refining trial designs, can pave the way for more effective therapies and biomarkers in these conditions.

1.5 Reseacrh Objective

The primary goal of this research is to develop a precise and effective imaging-based system for brain tumor existence and progression prediction. The major objective is to investigate the possibility of enhancing brain tumor early detection and prognosis by merging medical imaging data, particularly magnetic resonance imaging (MRI) scans, with cutting-edge imaging techniques.

To achieve this objective, the following specific goals will be pursued:

- Dataset Acquisition and Preprocessing
- Feature Extraction and Selection
- Classification Model Development
- Comparison with Other Pre-trained Models
- Model Evaluation and Validation
- Integration with Clinical Practice
- Comparative Analysis

By achieving these research goals, this study will provide an innovative and reliable approach for predicting this progressive brain tumor using imaging technology, thus potentially leading to the early detection of brain tumors. It is intended to contribute to the research field. The results of this study may support health professionals in early detection, personalized evaluation of patients, and treatment planning with Glioblastoma, Meningioma, and Pituitary tumors ultimately improving patient outcomes and quality of life.

Chapter 2

Literature Review

Previous studies on brain cancers have mostly demonstrated the effectiveness of image-processing models in accurately identifying brain malignancies using magnetic resonance imaging (MRI). However, the combined topics of glioblastoma, meningioma, and pituitary tumors have not been the subject of many studies. Additionally, the accuracy rates of the earlier studies were not very great. In this section, we will discuss prior studies on this subject, their shortcomings and limitations, and the strategies we want to employ in our model to get around these issues.

2.1 Brain Tumor Classifications

Glioblastoma, meningioma, and pituitary are the aggressive and malignant type of brain tumors that originates from brain cells within the central nervous system. Its hallmark characteristics include rapid growth, aggressiveness, and a high degree of resistance to treatment. Brain tumor poses significant challenges in clinical care and is associated with a grim prognosis (Davis ME, 2016)[1] To improve treatment planning and enhance patient outcomes, early and accurate identification of brain tumor tumors is imperative[3]. Utilizing cutting-edge methods—especially those based on deep learning—for the identification and diagnosis of brain tumors from medical imaging data has gained traction in recent years.

However, the landscape of brain tumor research extends beyond glioblastoma alone[19]. In the pursuit of comprehensive and effective solutions, it is crucial to consider multiple tumor types and include a broader spectrum of cases in the analysis. Therefore, in this research, we aim to expand the scope by encompassing three distinct categories, creating a classification task with four classes:

Glioblastoma: Glial cells give birth to glioblastoma. It is the most dangerous primary brain tumor in adults (fig2.1). Treatment is difficult due to the condition's quick development, invasiveness, and capacity to generate new blood vessels. The prognosis is still serious through therapy, emphasizing the critical need for cutting-edge treatment approaches.

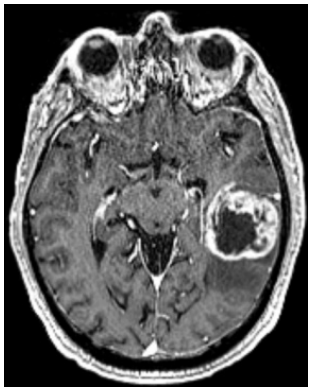


Figure 2.1: Glioblastoma Multiforme

Meningioma: Meningioma is a typical benign brain tumor that arises from the meninges[28]. It is the coverings that protect the brain and spinal cord. It is a frequent condition. Even though they are often slow-growing and curable with surgery and radiation, some cases might cause challenges (fig:2.2). If we use additional research, we can improve better treatment methods and outcomes.

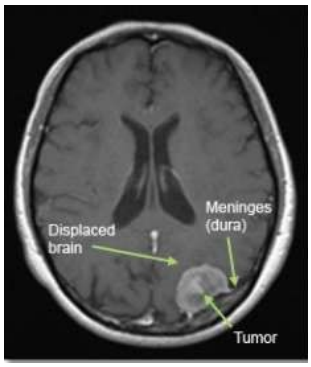


Figure 2.2: Meningioma

Pituitary: A pituitary tumor originates in the pituitary gland, disrupting hormone regulation. While often benign,(fig:2.3) it can impact hormone levels and affect various bodily functions[7]. This treatment involves surgery, medications, or radiation therapy, emphasizing the need for precise therapeutic approaches and ongoing research to optimize patient care.

No tumor: In addition, in our three categories of tumors we added a class for situations where there is no brain tumor. To avoid unneeded treatments and interventions, accurate classification between tumor and non-tumor situations is essential. Using this expanded strategy, we can investigate a wider variety of brain tumor scenarios and obtain insights into how well deep learning models can categorize various tumor kinds and separate them from non-tumor cases. To improve patient care and results in the field of neurooncology, we hope to contribute to the development of stronger, more precise methods for early brain tumor detection and diagnosis.

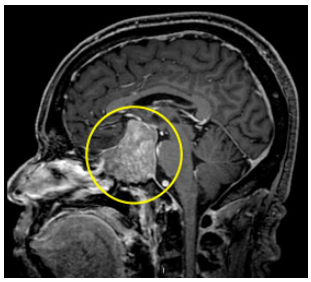


Figure 2.3: Pituitary Tumor

2.2 Advances in Medical Imaging

Brain tumor early identification and diagnosis have been greatly aided by medical imaging. In the past, methods like computed tomography (CT) scans and X-ray imaging has proved crucial in identifying abnormalities in the brain[28]. These techniques, however, frequently lack the accuracy needed for precise tumor characterization. Unbalanced datasets, a lack of adequate methodologies, improper categorization, and a decreased accuracy rate all contribute to the underestimation of these methodologies[21].

2.3 Brain tumor detection using CNN Model

For identifying brain tumors, a Convolutional Neural Network (CNN) model has been used. Glioblastoma, Meningioma, Pituitary Tumor, and No Tumor are the four unique classifications that the CNN model is intended to separate images into. A summary of the CNN model's application in this situation may be found in the parts below:

Data Preparation: The dataset consists of medical images representing the four classes of brain tumors and non-tumor cases. Data augmentation techniques, including shearing, rotation, shifting, zooming, and horizontal flipping, were applied to augment the dataset. This augmentation enhances the model's capacity to deal with variances in real-world medical pictures and to generalize more effectively[12].

Model Architectures: MobileNetV2, pre-trained on ImageNet, served as the base model. To improve the brain tumor classification model, more layers were added, such as Dropout, Batch Normalisation, Global Average Pooling, and Dense layers. The model's accuracy in identifying brain tumors was assessed after training.

Custom CNN Model: A custom CNN architecture was designed from scratch to handle the classification task. To maximize performance, the model incorporates dropout, max-pooling, fully connected layer, batch normalization, and convolutional layers[7]. Training and evaluation were performed to assess the model's ability to identify and classify brain tumors accurately.

Pre-trained Models: DenseNet121, ResNet50, and InceptionNetV2 are pre-trained on Ima-

geNet, and was used as another base model. Similar to MobileNetV2, additional layers were added for fine-tuning and improving the model's suitability for brain tumor classification. Training and evaluation of the model were conducted to achieve precise calculations and results.

Evaluation and Results: These three CNN models (MobileNetV2, Custom CNN, and DenseNet121) were trained and evaluated on the dataset. The test accuracy was used as a metric to assess the models' performance in classifying brain tumors[6]. The models were evaluated not only on their ability to classify brain tumors but also on their capacity to differentiate between different tumor types and non-tumor cases.

2.4 Architecture for Brain Tumor Detection CNN Model

We have designed This Brain Tumor Detection CNN Model to classify medical images into four categories: Glioblastoma, Meningioma, Pituitary Tumor, and No Tumor. A Convolutional Neural Network (CNN) architecture is used in the construction of the model. It is particularly well-suited for image classification tasks. Model Components

Input Layer: The input layer receives grayscale or RGB images of size 224x224 pixels, depending on the specific dataset and preprocessing used.

Convolutional Layers: A series of convolutional layers are employed to extract relevant features from the input images. These layers use learnable filters to perform convolutions across the input data, capturing spatial information. These layers are responsible for detecting edges, textures, and patterns in the images[7]. The number of filters typically increases as we go deeper into the network.

Activation Functions: Each convolutional layer is followed by an activation function, such as ReLU (Rectified Linear Unit), which adds non-linearity and improves the network's capacity to recognise intricate patterns.

Pooling Layers: To downsample the spatial dimensions of the feature maps, max-pooling layers come after some of the convolutional layers[12]. Reducing computing complexity and concentrating on the most pertinent data are two benefits of max-pooling.

Fully Connected Layers: After feature extraction, the model contains one or more fully connected (dense) layers. Through these layers, all neurons of the previous layer are connected to the current layer. Predictions based on previously extracted features are processed by fully connected layers. The number of output classes (four in this example) matches the number of neurons in the last dense layer.

Batch Normalization: To normalize the activations of the preceding layer and increase the training stability and convergence speed, batch normalization layers are added.

Dropout: Layers of dropout are added to avoid overfitting. During training, they sporadically kill certain neurons to make sure the model does not become overly dependent on any one neuron.

Output Layer: There are as many neurons in the output layer as there are classes—in this example, four. Class probabilities are obtained by using a softmax activation function.

Training and Evaluation: Through the use of labeled data, the model is trained to map input photos to the appropriate classes. An optimizer (like Adam) is used to optimize a loss function (usually categorical cross-entropy) during training. Backpropagation is used to guide training, and gradients are computed to minimize loss. A different test dataset is used to gauge the model's performance, and measures like accuracy are used to gauge how well it can classify data.

2.5 Related Works

This section provides a critical analysis of earlier relevant studies on the subject of brain tumors, concentrating on brain tumor detection and diagnosis. We review the various methods used and highlight the most significant outcomes. Brain tumor detection and diagnosis present unique challenges due to the complex nature of the disease, the heterogeneity of tumor characteristics, and the limitations of available imaging modalities.

Researchers have looked into radionics-based methods, deep learning, and machine learning for the detection and diagnosis of brain tumors[30]. To increase the precision and effectiveness of tumor classification and grading, these strategies make use of the analysis of MRI images and other clinical data.

Brain tumor research has made extensive use of deep-learning techniques. A Deep Convolutional Neural Network (CNN) approach for brain tumor segmentation is presented in BrainLes (2015)[24]. The method uses tiny convolutional kernels, Dropout, and Leaky Rectifier Linear Units (LReLU) to prevent overfitting. The study's goal is to identify High-Grade and Low-Grade brain tumors independently, and it has shown promise in doing so using the BraTS dataset[15].

The proposed method employs CNN architectures with small kernels, data augmentation, and LReLU activation. The processing pipeline involves pre-processing, CNN classification, and post-processing stages, including morphological filtering and volumetric constraints. The evaluation primarily assesses the performance of key tumor regions, demonstrating competitive results.

Furthermore, while predicting grades from the entire brain and the cancer region of interest, respectively, Pereira et al. (2018)[9] used CNN to properly estimate the grade of brain tumors based only on imaging data. of 89.5% and 92.98%, respectively. A straightforward CNN architecture was used by Abiwinanda et al. (2019) to identify three common forms of brain tumors: pituitary, meningioma, and glioma, with a validation accuracy of 84.19%. To distinguish between various glioma grades and categorize brain tumors into meningioma, glioma, and pituitary, Hossam et al. (2019) suggested a CNN architecture. A radionics-based approach was proposed by Narmada M.

Balasooriya (2017) to evaluate glioblastoma. The study produced promising results in accurately estimating the grade of glioblastoma, which is important information for customized treatment regimens.

Additionally, the researchers used transfer learning with a pre-trained CNN model to build a brain tumor classification model. For example, Inar and Yildirim (2020) modified a pre-trained ResNet-50 CNN model to identify brain tumors using MRI scans with 97. 2% accuracy. Kawalde et al(2017)[18] classified brain MRI images into three categories: healthy low-grade brain tumors and high-grade brain tumors, overall classification using a modified version of the AlexNet CNN model The accuracy was 91.16%. Taro et al.(2019) achieved 100% detection accuracy in brain tumor identification using a small dataset and a pre-trained ResNet-34 CNN model. In 2020, Rehman et al. Mehrotra et al. identified brain tumors with up to 98.69% classification accuracy using pre-trained CNN models such as AlexNet, GoogleNet, and 'balasooriya2017sophisticated'.(2020)[17] used a range of popular CNN models to classify brain tumor pictures as benign or malignant, with a pre-trained AlexNet model achieving the highest accuracy of 99.04%. Deepak and Ameer (2019) employed a pre-trained GoogleNet CNN model to differentiate between different types of brain tumors, achieving a mean classification accuracy of 98%. Yang et al. (2018) assessed the effectiveness of transfer learning and fine-tuning using pre-trained GoogleNet and AlexNet models, achieving classification accuracy of 86.6% and 87.4% for low-grade glioma and high-grade glioma, respectively.

Moreover, Ronneberger (2015) described U-Net, a radionics-based technique for brain tumor grading in their study[24]. U-Net is a deep learning architecture created especially for tasks involving the segmentation of biomedical pictures, such as the segmentation of tumors in MRI scans. Ronneberger's [23] technique, which makes use of U-Net, successfully extracts quantitative features from the MRI images and combines them with clinical information for precise brain tumor grade prediction. The use of U-Net in their strategy demonstrated how deep learning approaches can raise the precision and accuracy of tumor analysis based on radionics. This study advances the use of tailored treatment options and has the potential to improve brain tumor management techniques[23].

A strategy for brain tumor grading based on radionics was introduced by Kamnitsas et al.[16] in their 2016 article[10]. Their approach intended to precisely predict the grade of brain tumor by extracting quantitative information from MRI images and combining clinical data. The study's conclusions showed encouraging outcomes, demonstrating the potential of this strategy to support decisions about individualized treatment. With the help of radiomics and clinical data, it was possible to grade brain tumors more accurately, opening the door to better prognostication and treatment options. In addition to making a substantial contribution to the field of brain tumor classification, Kamnitsas[16] and colleagues' study also demonstrated the value of fusing clinical and imaging data to improve patient care.

From the above discussion, it is observed that most of the Researchers working on brain tumors focus on understanding their genetic and molecular mechanisms, as well as improving tumor detection through advanced imaging techniques[6]. By incorporating tailored techniques like machine learning, data mining, and pattern recognition, researchers can enhance their studies. Machine

learning algorithms enable the analysis of large-scale datasets for accurate diagnosis and prognosis. Data mining extracts valuable insights from diverse data sources, revealing factors influencing brain tumors. Pattern recognition aids in precise tumor analysis for better visualization and treatment planning. By utilizing these techniques, researchers aim to discover new therapeutic targets, personalize treatments, and advance early detection methods, ultimately improving patient outcomes in brain tumor research.

An effective brain tumor classification system based on convolutional neural networks (CNNs) is presented in this research. The study uses three widely used transfer learning-based pre-trained CNN models: VGG19, InceptionV3, and MobileNetV2. Its accuracy is 92%, MobileNetV2 stands out and demonstrates its potential for early tumor detection. The comparative examination of these models highlights how transfer learning techniques might improve classification accuracy for the detection of brain tumors in medical images (Tazin et al., 2021). This development is essential for early and accurate diagnosis since it allows for quick medical intervention and may even improve patient outcomes shortly[2].

The varied composition of tumor cells makes diagnosing a brain tumor a challenging undertaking. Magnetic resonance imaging (MRI)-based computer-aided diagnosis tools have evolved to help radiologists. This work proposes a novel technique that uses multi-level feature extraction and concatenation to enhance early brain tumor diagnosis. To extract and concatenate characteristics for the detection and classification of brain tumors, two pre-trained deep learning models—Inception-v3 and DenseNet201—are used[10].

This novel study makes use of a publicly available dataset that includes three different types of brain tumors. The use of concatenation-based techniques with DenseNet201 and Inception-v3 demonstrates impressive testing accuracies of 99.51% and 99.34%, respectively.

These results highlight the trained models' outstanding performance and demonstrate their superiority over other current approaches to brain tumor classification. The solid outcomes substantially progress our knowledge of tumor categorization and demonstrate the value of concatenation-based methods for improving precision and dependability in this vital area of medicine. (Noreen et al., 2014)[20].

This study integrates the Enhanced Watershed Segmentation (EWS) algorithm with a modified ResNet50 architecture to propose a novel method for brain tumor diagnosis. Accurate diagnostic techniques are essential to combat the increased frequency of brain cancers. This study focuses on deep feature extraction for successful brain tumor diagnosis, in contrast to standard machine learning approaches that stress classification effectiveness. The suggested approach modifies the ResNet50 architecture and combines it with the EWS algorithm to provide maximum computing effectiveness while capturing high-dimensional deep data. using the EWS-based and modified ResNet50 models, respectively, Sharma et al. (Sharma et al., 24 Feb 2022) achieved an excellent classification accuracy of 92% and 90% utilizing the resulting composite feature set, formed from several deep features of the ResNet50 model.

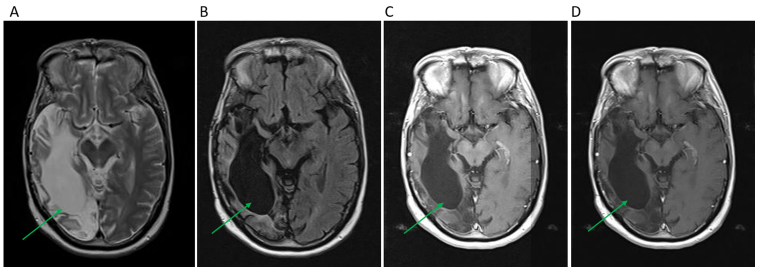


Figure 2.4: Different stages of downsizing brain tumors

Chapter 3

Methodology and Work Plan

We shall discuss our research's methodical workflow in this part. We'll talk about the methodical examination of the techniques we used in our research and the procedures we followed to get the results we wanted.

3.1 Work Plan

We have implemented Convolutional neural networks (CNNs) in the proposed brain tumor detection model to find anomalies in brain MRI images. A system that can recognize and examine MRI brain scans to detect whether or not they contain brain tumors. Our approach can quickly and effectively extract important information from the images, enabling precise detection and diagnosis. Our goal is to reach the highest accuracy level possible without any problems. Our model was developed using a dataset with a lot of input to process. We trained our model using multiclass classification such that it can accurately determine whether a tumor is there as well as whether it is a glioblastoma tumor. By facilitating early medical action in glioblastoma instances and increasing patient outcomes, this strategy increases the accuracy of tumor identification. The model design, depicted in Figure 3.1, provides a high-level overview of the architecture we have developed. The process is described progressively in the phases listed below:

- Dataset Collection
- Pre-Processing of Data
- Custom CNN model
- Pre-Trained Convolutional Neural Network models
- Evaluate the CNN model's accomplishment

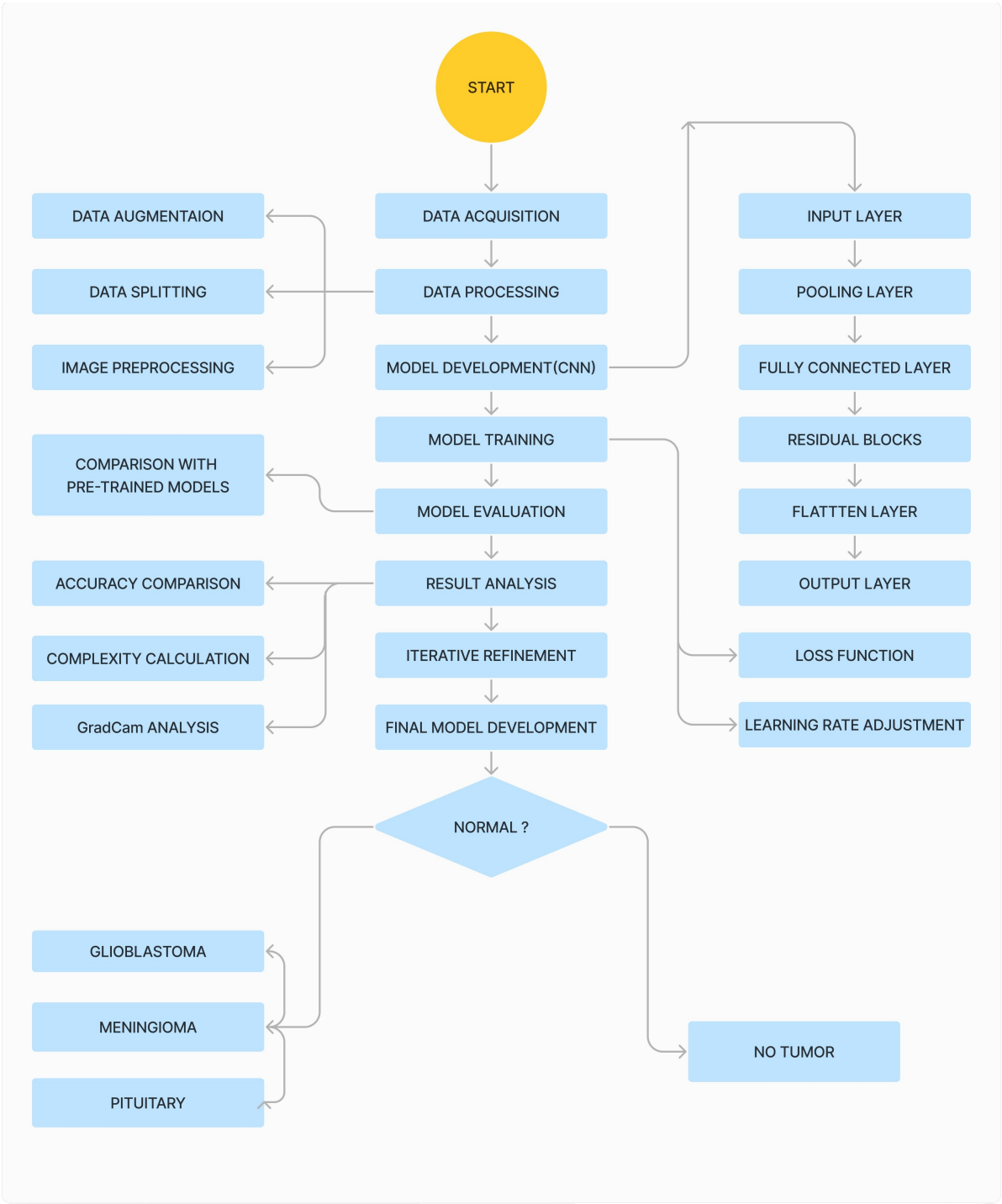
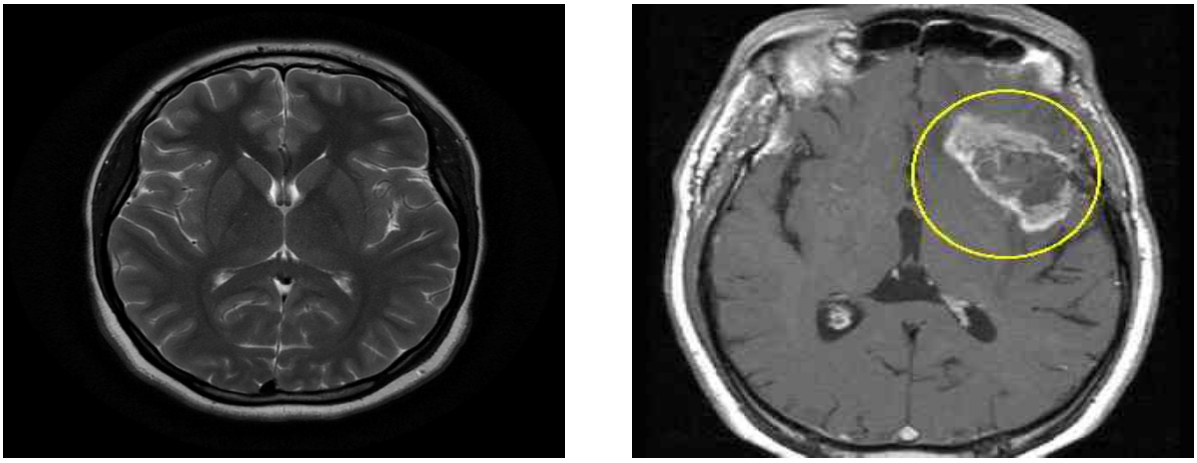


Figure 3.1: The Flow Chart of the Proposed CNN Model

CNN model consists few steps those are:

- Data augmentation techniques are used during the preprocessing of brain MRI images for improving dataset quality and model generalization.
- The dataset is split into training, testing, and validation sets to train, test, and validate the efficacy of the model.
- Convolutional, pooling, flattening, dense, and dropout layers are used to build a CNN model that extracts features from the MRI images.
- The model we have used is compiled with an optimizer, evaluation metric and loss function so that we can describe the learning process and performance measurement.
- The model is trained on the training data for a predefined amount of epochs to learn how to differentiate between photos with and without tumors.
- Determining the predictability and accuracy ratio of the model, its effectiveness has been evaluated using the validation data.
- The model's evolution and potential overfitting are explained by the display of training and validation accuracy.
- comparing our own pre-trained model's accuracy against that of other pre-trained models utilizing the same dataset



(a) Healthy Brain MRI (b) Tumor Affected Brain MRI

Figure 3.2: Detection of non-affected and affected results between Two MRIs

One kind of deep learning model is the convolutional neural network (CNN). which are structured for analyzing visual data like images. The model uses convolution layers to find patterns in

the images and learn how different parts of the image are related to each other. The extracted features are then processed to reduce their size and highlight the most important information. More convolutional and pooling layers create a more complex understanding of the image. Flattening and fully connected layers learn to identify patterns, and the output layer makes predictions. CNN models are trained using images with labels to learn how to identify patterns. They can then be used to predict labels for new images(fig:3.2). So that's why the CNN model is good at finding tumors in medical images.

3.2 Data Description

This study uses the information collected from TCIA(the cancer imaging archive). It offers recent cases of different types of brain tumors like glioblastoma, pituitary, and meningioma tumors from different patients. This dataset was furthermore split to clear noise and other inconveniences. This dataset initially had more than a hundred images in each class[4]. Furthermore, this dataset was augmented to a larger dataset containing almost a thousand images in each class for more accuracy. the dataset is divided into 4 basic classes.

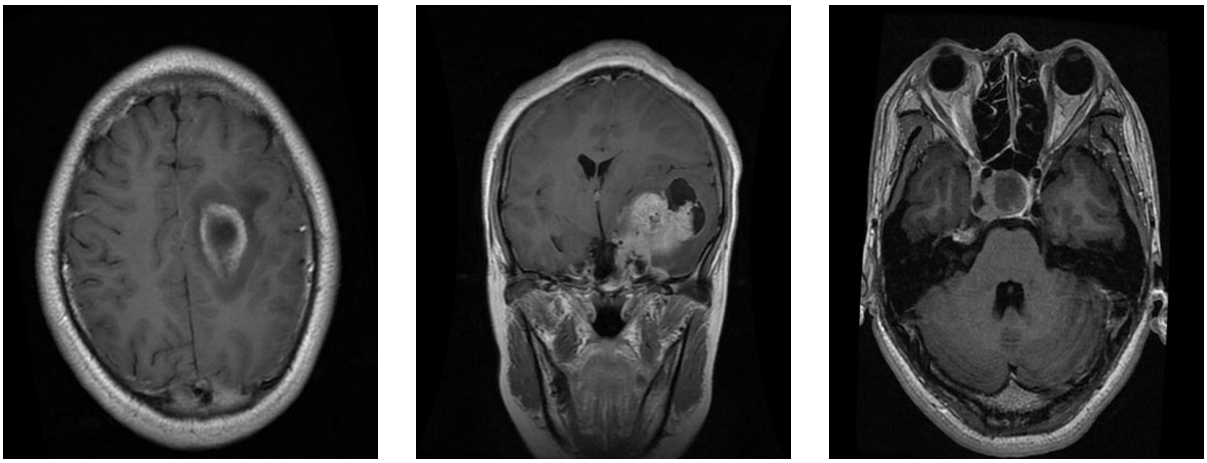
- Glioblastoma
- Meningioma
- Pituitery
- No Tumor

Each of these classes contains almost 1000 images to run the model properly with a maximum accuracy rate. The data set then was split into 3 parts where 70% of the data would be used for training, 15% for validation, and 15% for testing. The validation was used to simulate a real-life event for calculation and to reduce the problem of data leaking. So that an equal number of photos from each class could be utilized for training, validation, and testing, the data was arranged in an orderly fashion.

3.2.1 Data Pre-processing

Initially, we carefully selected a dataset that was designed to be used in brain tumor classification. Four unique classes were included in our dataset: glioma tumor, meningioma tumor, no tumor, and pituitary tumor. These classifications each corresponded to a particular kind of brain tumor or its nonexistence. The dataset's diversity was intended to provide readers with a thorough grasp of the many tumor kinds.

Selection and Augmentation of the Dataset: The dataset, though diverse, exhibited an imbalance in the number of images across different classes. Some examples from the Dataset are shown in figure:3.3. To rectify this and ensure uniformity, we implemented a data augmentation process.



(a) Glioblastoma (b) Meningioma (c) pituitary

Figure 3.3: Some Samples from the Dataset

The augmentation was carried out using the Augmentor library, a Python package designed for image augmentation. The process involved the following steps:

- **Installation and Import of Augmentor:** We began by installing Augmentor using the command`pip install Augmentor` and importing necessary libraries.
- **Downloading and Unzipping the Dataset:** The dataset was obtained from a Dropbox link and subsequently unzipped for usage.
- **Augmentation Process:** We established separate folders for each class within the dataset. Our augmentation strategy involved rotating the images, allowing a maximum left rotation of 5 degrees and a maximum right rotation of 10 degrees. The goal was to generate a total of 1000 images for each class, thereby equalizing the representation of each tumor type in the dataset.
- **Execution of Augmentation:** For each class, the Augmentor pipeline was initialized, and the specified number of augmented images was generated, ensuring a balanced and comprehensive dataset.

3.2.2 Data Splitting

Following the process of augmentation, our primary objective was to partition the dataset into subgroups for training, validation, and testing. This was executed through the following steps:

- **Defining Split Ratios:** We adopted a split ratio of 70% for training, 15% for validation, and 15% for testing. This distribution was chosen to ensure a significant portion of data for model training while maintaining adequate data for validation and testing purposes.

- **Randomized Data Splitting:**The splitting process involved shuffling the files within each class and then allocating them according to the predefined ratios. This randomization ensured that the model would be exposed to a diverse range of data during training.
- **Organize data for input:**The files were organized into respective directories for training, validation, and testing, maintaining the structure necessary for efficient model training and evaluation.

3.2.3 Image Preprocessing

The final step in our data pre-processing phase was image preprocessing. Normalizing the input data for the neural network required this procedure. We employed the following approach:

- **Image Data Generator:** For image preprocessing, we utilized the ImageDataGenerator from Keras. This tool allowed us to apply real-time data augmentation techniques and prepare the dataset for input into the neural network.
- **Training and Validation categorization:** The images we pre-processed earlier will be categorized into training and validation, whether the ratio will be maintained of 7:3
- **Image Resizing and Batch Processing:** All images were resized to a uniform dimension of 224x224 pixels. We also defined batch sizes for the training and validation processes, with a larger batch size for training and a batch size of one for validation and testing.
- **Categorical Classification and Shuffling:** The class mode was set to 'categorical', facilitating multi-class classification. Additionally, the training dataset was shuffled to ensure randomness in model training.

We made sure that our dataset was well-balanced, varied, and suitable for training and evaluating machine learning models for brain tumor classification by the use of our thorough data pre-processing technique.

Chapter 4

Model Architecture and Design

4.1 Model Overview

In this part, we will discuss data preparation and model selection strategy. Firstly, we collected and prepared data and divided the dataset into a 7:3 ratio. There we used 70% for training and 15% for validating the model. We have chosen different training models: MobileNetV2, DenseNet121, ResNet50, InceptionResNetV2, and a custom CNN model. Our goal is to compare and evaluate these models based on their accuracy and predictions.

4.2 CNN Model

This model is an image categorization deep learning system. CNN model is specifically designed to identify brain tumors. It takes on convolutional blocks with batch normalization and ReLU activation to extract features. It combines shortcut connections for effective learning, followed by pooling layers for dimension reduction. Also, the model concludes with dense layers and a softmax activation for precise classification into four categories. It balances detailed feature extraction with computational efficiency.

The CNN model is a powerful deep-learning architecture designed to automatically learn and extract hierarchical representations from brain tumor images for accurate classification. Convolutional, pooling, and fully linked layers are influenced to successfully capture angular hierarchies and abstract characteristics from the input pictures.

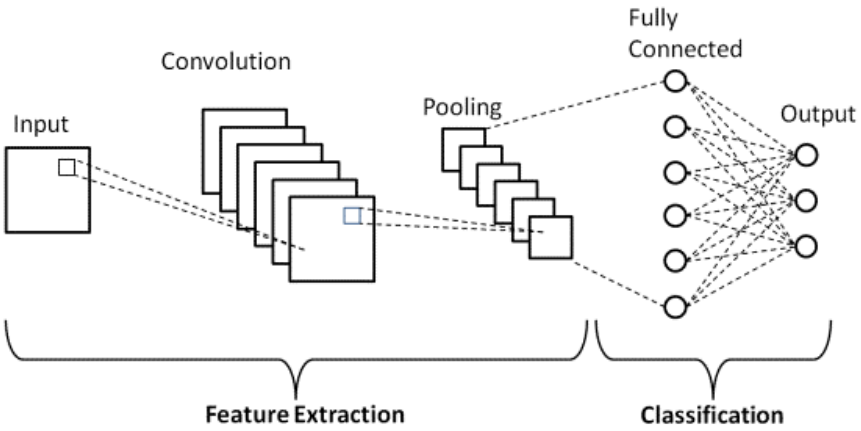


Figure 4.1: CNN Model Architecture

4.2.1 Architecture Overview

Input Layer

It accepts images with dimensions 224x224 pixels and represents MRI scans of brain tumors.

Convolutional Blocks

Multiple convolutional layers are employed to identify low-level characteristics, including textures and edges. introduces non-linearity by using rectified linear unit (ReLU) activation functions. Applies batch normalization to stabilize and accelerate training.

Pooling Layers

It employs max-pooling layers to downsample spatial dimensions and reduce computational complexity. Facilitates the maintenance of essential features while discarding less relevant information.

Flattening Layer

To provide a one-dimensional vector as input for further fully connected layers, it converts the output from the convolutional and pooling layers.

Fully Connected Layers

It incorporates densely connected layers to capture global patterns and relationships in the data. Leverages ReLU activation functions and dropout layers to enhance model generalization and prevent overfitting.

Output Layer

Using a softmax activation function, it produces class probabilities for the multi-class classification of Glioma tumor, Meningioma tumor, Pituitary tumor, and no tumor. The model predicts that the class with the highest probability will be the final classification.

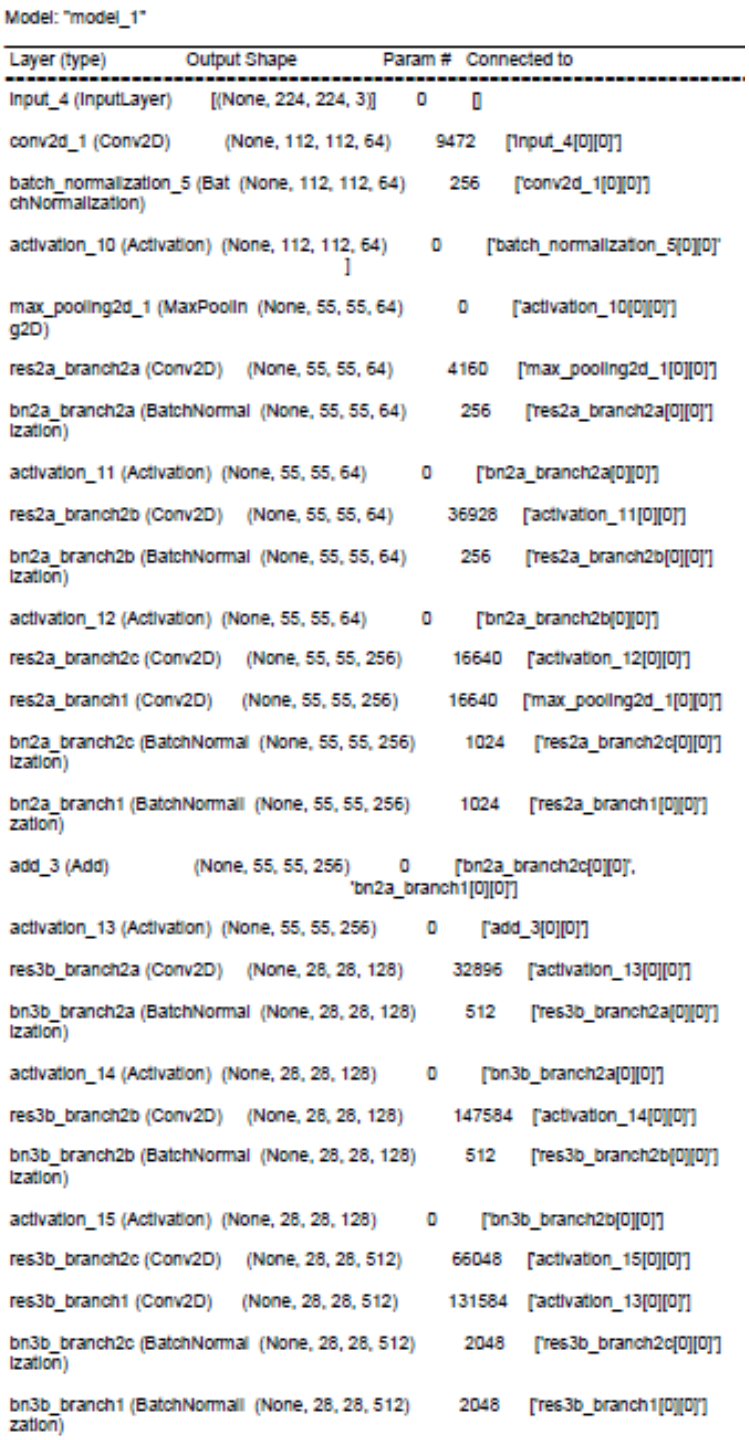
4.2.2 Training Process

Optimization Algorithm

To efficiently update the model weights during training, we used Adam optimizer.
Loss Function:
The loss function is the categorical cross-entropy, which quantifies how different the true and predicted class distributions are from one another.
Learning Rate Adjustment:
The learning rate is strongly adjusted during training to optimize convergence.

CNN Model Summary

The CNN model is designed to effectively discern intricate patterns within brain tumor images and enable accurate classification into distinct tumor classes as shown in fig:4.2 and fig:4.3. The architecture is trained on augmented and preprocessed data that provides a robust and reliable tool for automated brain tumor classification in medical imaging applications.



```
Model: "model_1"
_________________________________________________________________
Layer (type)                 Output Shape              Param #   Connected to
=================================================================
input_4 (InputLayer)         [(None, 224, 224, 3)]     0         []

conv2d_1 (Conv2D)            (None, 112, 112, 64)      9472      ['input_4[0][0]']

batch_normalization_5 (Bat  (None, 112, 112, 64)      256       ['conv2d_1[0][0]']
chNormalization)

activation_10 (Activation)  (None, 112, 112, 64)      0         ['batch_normalization_5[0][0]'
                                                                ]

max_pooling2d_1 (MaxPoolin  (None, 55, 55, 64)        0         ['activation_10[0][0]']
g2D)

res2a_branch2a (Conv2D)     (None, 55, 55, 64)        4160      ['max_pooling2d_1[0][0]']

bn2a_branch2a (BatchNormal  (None, 55, 55, 64)        256       ['res2a_branch2a[0][0]']
lzation)

activation_11 (Activation)  (None, 55, 55, 64)        0         ['bn2a_branch2a[0][0]']

res2a_branch2b (Conv2D)     (None, 55, 55, 64)        36928     ['activation_11[0][0]']

bn2a_branch2b (BatchNormal  (None, 55, 55, 64)        256       ['res2a_branch2b[0][0]']
lzation)

activation_12 (Activation)  (None, 55, 55, 64)        0         ['bn2a_branch2b[0][0]']

res2a_branch2c (Conv2D)     (None, 55, 55, 256)       16640     ['activation_12[0][0]']

res2a_branch1 (Conv2D)      (None, 55, 55, 256)       16640     ['max_pooling2d_1[0][0]']

bn2a_branch2c (BatchNormal  (None, 55, 55, 256)       1024      ['res2a_branch2c[0][0]']
lzation)

bn2a_branch1 (BatchNormali  (None, 55, 55, 256)       1024      ['res2a_branch1[0][0]']
zation)

add_3 (Add)                 (None, 55, 55, 256)       0         ['bn2a_branch2c[0][0]',
                                                                'bn2a_branch1[0][0]']

activation_13 (Activation)  (None, 55, 55, 256)       0         ['add_3[0][0]']

res3b_branch2a (Conv2D)     (None, 28, 28, 128)       32896     ['activation_13[0][0]']

bn3b_branch2a (BatchNormal  (None, 28, 28, 128)       512       ['res3b_branch2a[0][0]']
lzation)

activation_14 (Activation)  (None, 28, 28, 128)       0         ['bn3b_branch2a[0][0]']

res3b_branch2b (Conv2D)     (None, 28, 28, 128)       147584    ['activation_14[0][0]']

bn3b_branch2b (BatchNormal  (None, 28, 28, 128)       512       ['res3b_branch2b[0][0]']
lzation)

activation_15 (Activation)  (None, 28, 28, 128)       0         ['bn3b_branch2b[0][0]']

res3b_branch2c (Conv2D)     (None, 28, 28, 512)       66048     ['activation_15[0][0]']

res3b_branch1 (Conv2D)      (None, 28, 28, 512)       131584    ['activation_13[0][0]']

bn3b_branch2c (BatchNormal  (None, 28, 28, 512)       2048      ['res3b_branch2c[0][0]']
lzation)

bn3b_branch1 (BatchNormali  (None, 28, 28, 512)       2048      ['res3b_branch1[0][0]']
zation)
```

Figure 4.2: CNN Model Summary

```
add_4 (Add)                 (None, 28, 28, 512)       0         ['bn3b_branch2c[0][0]',
                                                                 'bn3b_branch1[0][0]']

activation_16 (Activation)  (None, 28, 28, 512)       0         ['add_4[0][0]']

res4c_branch2a (Conv2D)     (None, 14, 14, 256)       131328    ['activation_16[0][0]']

bn4c_branch2a (BatchNormal  (None, 14, 14, 256)       1024      ['res4c_branch2a[0][0]']
lzation)

activation_17 (Activation)  (None, 14, 14, 256)       0         ['bn4c_branch2a[0][0]']

res4c_branch2b (Conv2D)     (None, 14, 14, 256)       590080    ['activation_17[0][0]']

bn4c_branch2b (BatchNormal  (None, 14, 14, 256)       1024      ['res4c_branch2b[0][0]']
lzation)

activation_18 (Activation)  (None, 14, 14, 256)       0         ['bn4c_branch2b[0][0]']

res4c_branch2c (Conv2D)     (None, 14, 14, 1024)      263168    ['activation_18[0][0]']

res4c_branch1 (Conv2D)      (None, 14, 14, 1024)      525312    ['activation_16[0][0]']

bn4c_branch2c (BatchNormal  (None, 14, 14, 1024)      4096      ['res4c_branch2c[0][0]']
lzation)

bn4c_branch1 (BatchNormall  (None, 14, 14, 1024)      4096      ['res4c_branch1[0][0]']
zation)

add_5 (Add)                 (None, 14, 14, 1024)      0         ['bn4c_branch2c[0][0]',
                                                                 'bn4c_branch1[0][0]']

activation_19 (Activation)  (None, 14, 14, 1024)      0         ['add_5[0][0]']

flatten_1 (Flatten)         (None, 200704)            0         ['activation_19[0][0]']

dense_7 (Dense)             (None, 1024)              2055219   ['flatten_1[0][0]']
                                                      20

batch_normalization_6 (Bat  (None, 1024)              4096      ['dense_7[0][0]']
chNormalization)

dropout_4 (Dropout)         (None, 1024)              0         ['batch_normalization_6[0][0]'
                                                                 ]

dense_8 (Dense)             (None, 512)               524800    ['dropout_4[0][0]']

batch_normalization_7 (Bat  (None, 512)               2048      ['dense_8[0][0]']
chNormalization)

dropout_5 (Dropout)         (None, 512)               0         ['batch_normalization_7[0][0]'
                                                                 ]

dense_9 (Dense)             (None, 4)                 2052      ['dropout_5[0][0]']

==================================================================================================
Total params: 208044932 (793.63 MB)
Trainable params: 208032772 (793.58 MB)
Non-trainable params: 12160 (47.50 KB)
__________________________________________________________________________________________________
None
```

Figure 4.3: CNN Model Summary (cont.)

4.3 MobileNetV2 Model

The MobileNetV2 mode is distinguished for its computational efficiency. We adapted this model for the classification of brain tumors in our study. It was originally developed for mobile applications. This model stands out due to its lightweight architecture and rapid processing capabilities. It is initialized with pre-trained ImageNet weights and leverages a vast array of features learned from a comprehensive image dataset.

In this model, the base layers of the model are set as non-trainable to preserve the sophisticated feature extraction capabilities already developed. This ensures that the model retains its ability to recognize a vast diversity of patterns and textures, which is crucial for analyzing complex medical images like brain MRIs. Several additional layers are appended to tailor the model for brain tumor classification. This includes a global average pooling layer to condense feature maps, enhancing the model's focus on relevant patterns. Dense layers with ReLU activation are incorporated to interpret these features effectively. A dropout layer is also included to prevent overfitting and ensure that the model remains generalizable to new data. The architecture culminates in a softmax-activated output layer, designed for multi-class classification, providing probabilities for each tumor type.

The model achieves a balance of efficiency and accuracy by combining the pre-learned features of MobileNetV2 with these custom layers. It has become a powerful tool for medical image analysis(fig:4.4). Also, it is capable of delivering precise classifications swiftly, making it ideal for both high-performance and resource-constrained environments.

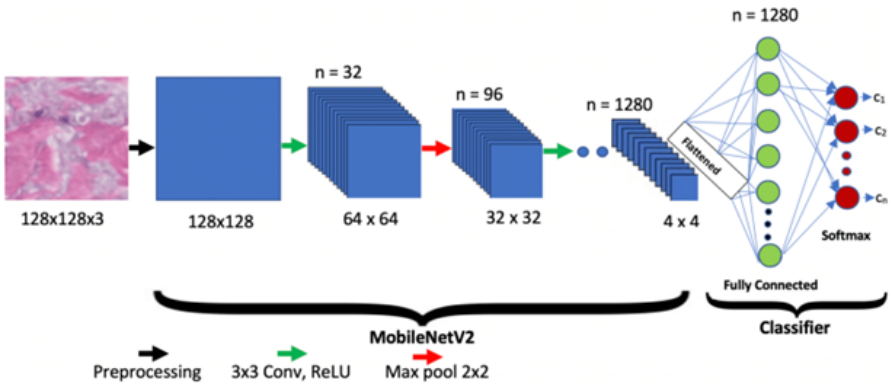


Figure 4.4: MobileNteV2 Model

4.4 DenseNet121 Model

The DenseNet121 model is a well-established architecture in the field of deep learning. The model is utilized for brain tumor classification in our study. It is known for its densely connected convolutional network. DenseNet121 is particularly effective in image recognition tasks due to its unique structure that promotes feature reuse. It can be both efficient and powerful for complex image analysis. The model DenseNet121l is preloaded with weights from ImageNet. A large dataset of diverse images provides a substantial foundation of learned image features. This pre-trained model serves as a reliable foundation. Particularly when it comes to jobs like medical picture analysis, where precise feature identification is essential.

The construction of DenseNet121 is characterized by its dense blocks and transition layers. In a thick block, all layers that come before it provide inputs to each layer. Also, fostering feature propagation and reducing the vanishing gradient problem. This aspect makes the network particularly adept at preserving and utilizing information throughout the network. This model works extremely well at brain tumor classification to suit the specific requirements of the task. A thick layer with softmax activation and a global average pooling layer follow at the end. Specific multi-class categorization is supported. Additionally, it offers probabilities for several tumors, including pituitary, glioma, and meningioma.

In general, the DenseNet121 model has interconnected layers and efficient feature utilization. It offers a strong framework for the accurate classification of brain tumors(fig:4.5) and makes it a valuable tool for medical imaging.

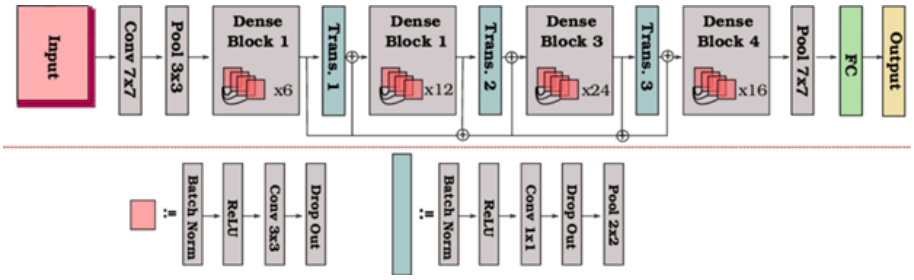


Figure 4.5: DenseNet121 Model

4.5 ResNet50 Model

The ResNet50 model is a well-known deep-learning architecture that is skillfully used for brain tumor classification. ResNet50 stands out for having a deep residual learning architecture. This allows it to solve the vanishing gradient issue that arises frequently while training deep networks, which makes it ideal for complex image processing applications such as medical imaging. The skip connections or shortcuts in ResNet50's make the architecture unique, they let data move between levels without getting declined. This feature makes sure that even with its enormous 50-layer depth, the network learns efficiently. Weights from ImageNet are preloaded into the model, offering a wide variety of pre-learned picture features that are crucial for initial feature recognition in intricate medical images(fig:4.6). We fine-tune the pre-trained layers of ResNet50 to precisely identify patterns and abnormalities suggestive of brain tumors in our adaption for brain tumor classification. The model's final layers are a fully linked dense layer with softmax activation and a globally average pooling layer. Because of this structure, the model can produce exact probability distributions for a variety of tumor types, which makes classification more accurate. ResNet50 is a powerful tool for medical image analysis because of its deep but effective design and improved feature circulation. It is a helpful tool in the detection and research of brain cancers because of its capacity to accurately classify and learn from deep layers.

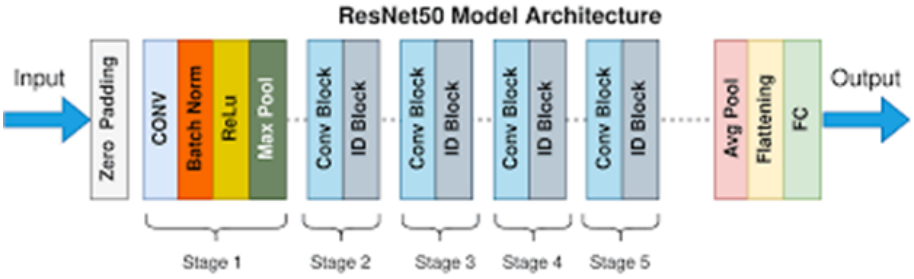


Figure 4.6: Resnet50 Model

4.6 InceptionResNetV2 Model

The InceptionResNetV2 model is renowned in deep learning. It is leveraged for brain tumor classification. This model has two most powerful models one is Inception and another is ResNet. This hybrid model is known for its high accuracy and efficiency. Also, this model is particularly useful in complex image recognition tasks like medical imaging.

Inception modules are extracted at multiple scales and they capture a wide range of information from the input images. This processing allows the model to identify the patterns and anomalies crucial for detecting the brain tumor.

The model InceptionResNetV2 benefits from a vast array of pre-learned features. It is very much advantageous for medical image analysis. The layers of InceptionResNetV2 are specialized in the nuances of MRI brain scans. It also concludes with pooling layers and a softmax-activated dense layer that ensures multi-class tumor classification.

Overall, the model has a unique combination of depth, complexity, and feature diversity that makes it exceptionally capable in medical imaging applications for brain tumor diagnosis and research.

4.7 Custom CNN Model

Our custom CNN model is designed for image classification tasks. It has multiple convolutional layers and residual blocks that incorporate batch normalization and dropout for improved training and generalization. The model takes as input images which have 224 x 224 pixels and 3 RGB color channels. The convolutional layers capture low-level features while the residual blocks facilitate the learning of complex hierarchical representations. It uses categorical cross-entropy loss and the Adam optimizer which are trained. The architecture of the model employs residual connections and it allows learning residual functions and easing the optimization process. After convolutional and dense layers, batch normalization is applied and dropout layers are used to prevent overfitting. The final layer utilizes softmax activation to output probabilities for each of the 4 classes in the classification task. The model demonstrates a high capacity to learn intricate patterns in the input data with a total of 208,044,932 parameters. The use of convolutional and residual blocks, along with normalization and regularization techniques, contributes to the model's effectiveness in image classification.

4.7.1 Input Layer

Images with three color channels (RGB) and a pixel size of 224 x 224 are sent into the input layer. It serves as the entry point for the neural network, accepting the raw image data for further processing.

4.7.2 Convolutional Layer

To extract low-level information from the input pictures, the first convolutional layer (Conv2D 1) uses 64 filters with kernel sizes of (7, 7) and strides of (2, 2). ReLU activation and batch normalization are used to assist in normalizing activations and add non-linearity.

4.7.3 Max Pooling Layer

The max pooling layer (MaxPooling2D 1) follows the convolutional layer, reducing spatial dimensions (55x55x64) through a pooling window of (3, 3) and strides of (2, 2). Three residual blocks (2a, 3b, 4c) are employed, each containing three convolutional layers with batch normalization and ReLU activation. These blocks utilize shortcut connections to allow the model to learn residual functions, aiding in the optimization process.

4.7.4 Flatten Layer

The output of the last residual block is transformed into a one-dimensional vector by the flattening layer (Flatten_1), readying it for input into the fully linked layers.

Fully Connected (Dense) Layers

Dense Layer 1(Dense_7)

- 1024 neurons with ReLU activation.
- Followed by batch normalization and dropout (50%).

Dense Layer 2(Dense_8)

- 512 neurons with ReLU activation.
- Followed by batch normalization and dropout (50%).

Output Layer(Dense_9)

- Consists of 4 neurons corresponding to the output classes for image classification.
- Utilizes softmax activation to produce class probabilities.

Model Parameters

The model has a total of 208,044,932 parameters, with 208,032,772 being trainable and 12,160 non-trainable. These parameters collectively define the weights and biases in the neural network, letting it pick up on the provided picture categorization challenge and make predictions .

Training and Optimization

Categorical cross-entropy loss, a well-liked solution for multi-class classification issues, is used to train the model. During training, the Adam optimizer is employed for effective optimization. The model's architecture combines convolutional and residual blocks with normalization and dropout to enhance its ability to learn intricate patterns and generalize well with fresh input.

To summarize, the convolutional layers, residual blocks, and fully connected layers of the customized CNN model are designed specifically for image classification. For effective learning and generalization, it processes 224x224 RGB images using batch normalization, dropout, and residual connections. Softmax activation is used in the last layer to handle class probabilities. The model's design, which combines convolutional and residual blocks with normalization and dropout, allows for efficient pattern learning and generalization. It was trained using categorical cross-entropy loss and the Adam optimizer.

Chapter 5

Result Analysis and Comparison

5.1 Result Analysis

In our study of brain tumor classification, we have implemented various advanced Convolutional Neural Network (CNN) models, each of them working uniquely to the task. The models we have used are MobileNetV2, Custom CNN, DenseNet121, ResNet50, and InceptionResNetV2. Each model was strictly trained and validated over 50 epochs using a specialized dataset.

The MobileNetV2 model is one of the most widely used models which is known for its efficiency. 96.07% training accuracy and 91.31% validation accuracy were attained by the model. Its test accuracy was especially high at 93.01%, with a test loss of 0.2186. This performance emphasizes MobileNetV2's suitability for handling complex image data while maintaining computational efficiency.

The Custom CNN model, customized specifically for this study, the model illustrated exceptional performance, surpassing others in accuracy. Our model achieved a training accuracy of 97.07% and a validation accuracy of 95.99%. We have got a 96.51% test accuracy for our model which was quite impressive, and the test loss was 0.1405. The success of this model can be attributed to its convolutional blocks, which were specifically created to capture the complex characteristics of brain tumors.

DenseNet121, the model known for its dense connectivity pattern, also performed impressively, the model achieved a training accuracy of 93.46% and a validation accuracy of 91.65%. The test accuracy was recorded at 91.01%, with a test loss of 0.2557. DenseNet121's performance highlights its capability in feature conservation and utilization.

ResNet50, displayed a distinct performance range as it has a deep residual learning framework. The model's results showed 74.70% training accuracy, 76.62% validation accuracy, and 80.69% test accuracy with a test loss of 0.5506. Although these numbers are lower than those of other models, the model illustrates the difficulties in maximizing deeper networks, such as ResNet50, for certain tasks, such as the classification of medical images.

Lastly, the **InceptionResNetV2** model, which is a fusion of Inception and ResNet architectures,

achieved a training accuracy of 92.39%, a validation accuracy of 90.15%, and a test accuracy of 91.85%, with a test loss of 0.2324. This model's performance shows the effectiveness of combining features from different architectures.

To sum up, Our work provides a comprehensive comparison and analysis of different CNN architectures to classify brain tumors. The results demonstrate that while each model has its advantages, the Custom CNN model which was created especially for this task shows the greatest promise in terms of effectiveness and accuracy. The development of computerized diagnostic equipment for medical imaging might be greatly advanced by the findings of this study.

5.2 Performance Analysis

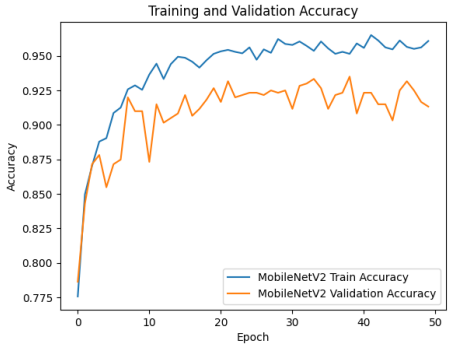


Figure 5.1: MobileNetV2 Accuracy Graph

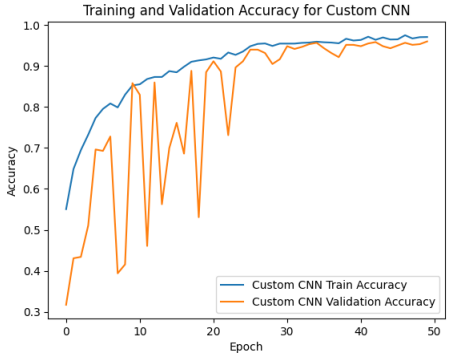


Figure 5.2: Custom CNN accuracy graph

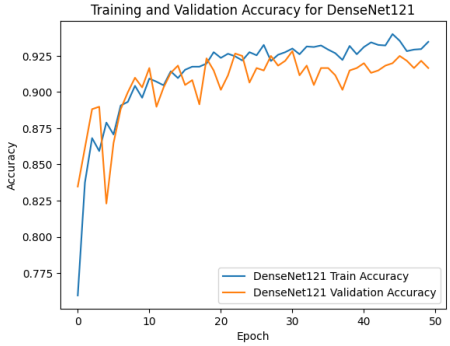


Figure 5.3: DenseNet121 accuracy graph

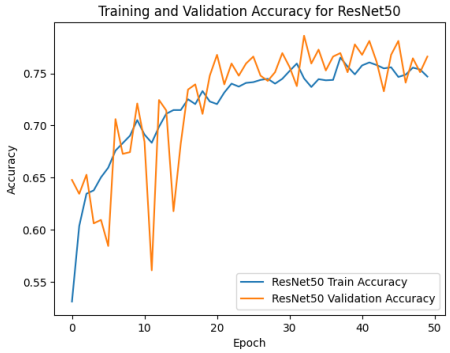


Figure 5.4: ResNet50 accuracy graph

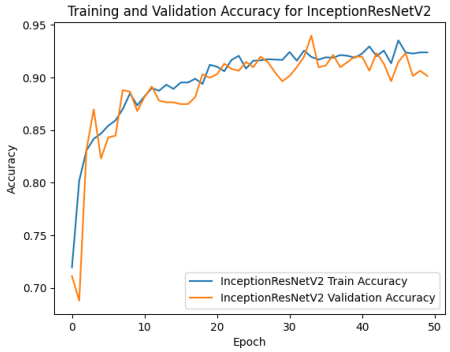


Figure 5.5: InceptionResNetV2 accuracy graph

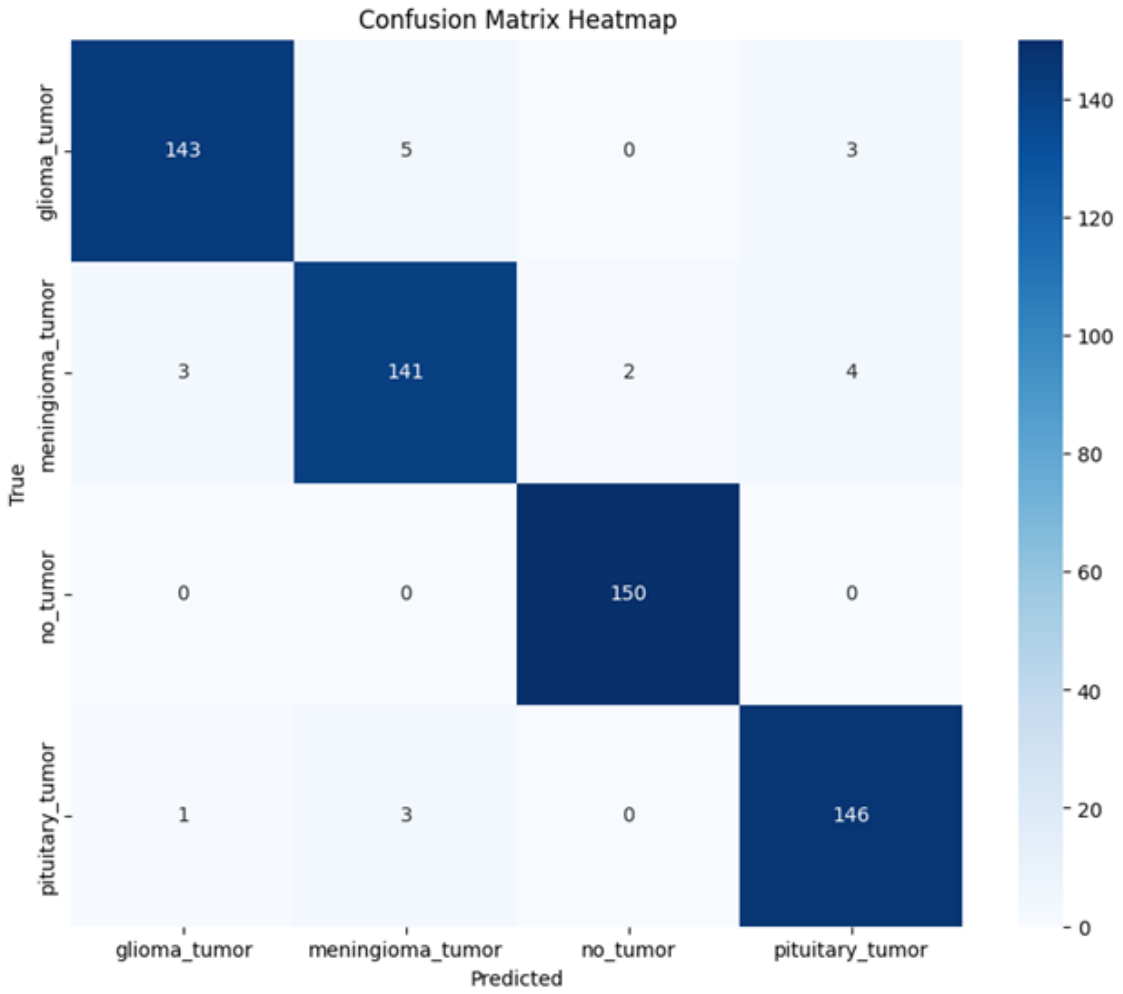


Figure 5.6: Confusion Matrix for Custom CNN Model

Class	Precision	Recall	f1-score	Support
Glioma_tumor	0.97%	0.95%	0.96%	151%
Meningioma_tumor	0.95%	0.94%	0.94%	150%
No_tumor	0.99%	1.00%	0.99%	150%
Pituitary_tumor	0.95%	0.97%	0.96%	150%
Accuracy			0.97%	601%
Macro avg	0.94%	0.97%	0.96%	601%
Weighted avg	0.97%	0.97%	0.96%	601%

Table 5.1: Classification Report Based on Custom CNN Model

The confusion matrix and classification report offer valuable insights into the efficacy of our Custom CNN model's brain tumor categorization. Pituitary tumor, meningioma tumor, glioma tumor, and no tumor are the four categories in which the model has exceptional recall, f1-scores, and precision.

In the classification report, we can see, that the glioma tumors show impressive precision and recall, with a 97% precision rate and a 95% recall, leading to an f1-score of 96%. This indicates the model's strong ability to accurately identify glioma tumors with few false positives. Meningioma tumors also exhibit high precision 95% and recall 94%, achieving an f1-score of 94%. The model is slightly less precise in differentiating meningioma tumors, which suggests a potential area for improvement.

Specifically, the model was working exceptionally to identify no tumor cases, with a perfect recall of 100% and a precision of 99%, resulting in an f1-score of 99%. This plays a vital role, as accurately ruling out tumors is as critical as detecting them.

Pituitary tumors are also well-classified with a precision of 95% and a recall of 97%, the f1-score of 96%. This shows the model's effective learning in recognizing this tumor type.

The confusion matrix shows that the model mostly makes accurate classifications with slight confusion between tumor types. Such as, it correctly identified 143 out of 151 glioma tumors, with minimal confusion between glioma, meningioma, and pituitary tumors. However, the overall accuracy of 97% displays the model's robustness and reliability as a diagnostic tool in medical imaging. Its high performance across all categories, particularly in correctly identifying cases with no tumors, emphasizes its potential in clinical applications for brain tumor detection.

5.3 Result Comparison

In this section a comparison of models and their performance will be discussed from our research, a comparison study of different deep learning models for brain tumor classification shows that the Custom CNN model demonstrates exceptional performance compared to other tested models, including MobileNetV2, DenseNet121, ResNet50, and InceptionResNetV2.

Custom CNN Model: In our research, the Custom CNN Model demonstrated an exceptional accuracy rate, a training accuracy of 97.07%, and a validation accuracy of 95.99%. The test accuracy got impressively 96.51% accuracy, with a low test loss of 0.1405. This demonstrates its remarkable capacity to correctly classify images of brain tumors, maybe it has become possible because of its layers of fine-tuning specialized just for this purpose.

MobileNetV2 this model is known for its efficiency, MobileNetV2 illustrated a training accuracy of 96.07% and validation accuracy of 95.99%. The test accuracy was a bit lower at 93.01%, with a test loss of 0.2186. Although MobileNetV2 displayed good performance, it falls short of the Custom CNN model in terms of its overall accuracy and precision.

DenseNet121 For this model the training accuracy achieved is 93.46% and the validation accuracy is 91.65%, the test accuracy for this model is 91.01% and the test loss for DenseNet121 was 0.2557, this indicates that it performed slightly less effectively classifying brain tumors compared to the Custom CNN model.

ResNet50 ResNet50 achieved a training accuracy of 74.70% and a validation accuracy of 76.62%, making it the model with the lowest accuracy among the models. This model has a greater test loss of 0.5506 and an accuracy of 80.69%. This implies that the model's depth may not have been completely optimized for the particular job of classifying brain tumors.

InceptionResNetV2 The model attained a training accuracy of 92.39% and a validation accuracy of 90.15%, combining the Inception and ResNet architectures. With a test loss of 0.2324, the model's test accuracy was reported as 91.85%. Although the model performed well, it was still not as good as the Custom CNN model.

Model	Training Accuracy	Validation Accuracy
Custom CNN Model	97.07%	95.99 %
MobileNetV2	96.07%	91.31%
DenseNet121	91.65%	91.65%
ResNet50	74.70%	76.62%
InceptionResNetV2	92.39%	90.15%

Table 5.2: Accuracy and Validation Percentage of the models

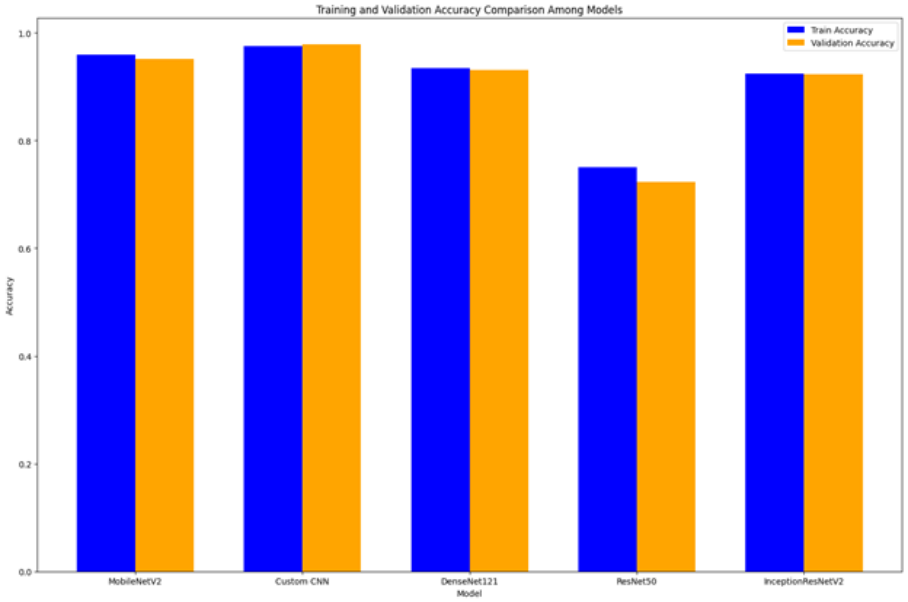


Figure 5.7: Graphical Representation of different models

In summary, our Custom CNN model outperforms other models in accuracy and loss metrics as shown in (fig:**??**) and (fig:5.7)The model design and optimization for this particular task likely contribute to its exceptional performance and make it a highly suitable choice for medical image analysis in this context.

5.4 Visualization of Model analysis using GradCAM :

In our research, we have implemented GradCAM (Gradient-weighted Class Activation Mapping) to enhance the analysis of our Custom CNN model, especially in the context of brain tumor classification from MRI scans(from fig:5.8 to fig:5.11). GradCAM is known for its powerful tool to visualize and illustrate the areas where the image mostly influences the model's prediction. This approach demonstrates the inside workings of the CNN model and enlightens on how particular image features contribute to the model's settlement process.

While utilizing GradCAM we have used the 'conv2d' layer of the Custom CNN model, by this the gradients of the predicted class were calculated against this layer's output feature map. This calculation creates a heatmap that highlights the critical parts of the image. Then the heatmap was superimposed onto the original MRI image, this allows us to visually correspond the model's focus areas with the actual features of the brain scan.

The method of this visualization ensures that it is crucial in validating the accuracy of the model. GradCAM increases the transparency of CNN's decision-making process and boosts the accuracy of its diagnostic predictions after correctly illustrating the model's focus region. This approach is particularly significant for medical imaging when diagnostic accuracy is not as vital as comprehending the underlying concept of a model's prediction. Consequently, the use of GradCAM significantly enhanced the reliability and interpretability of our Custom CNN model in the classification of brain tumors.

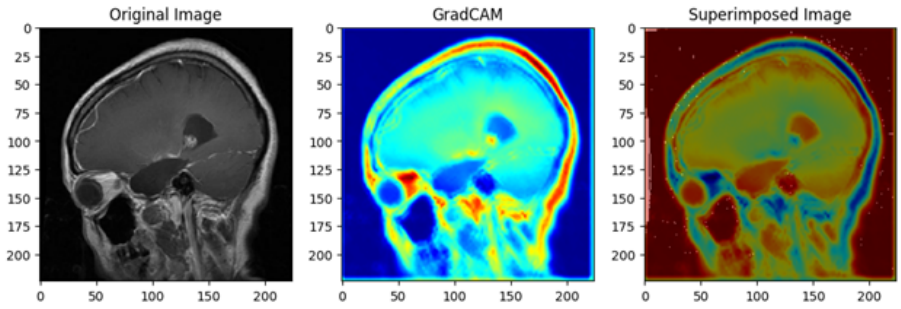


Figure 5.8: Gradcam visualization of the Glioma Tumor prediction

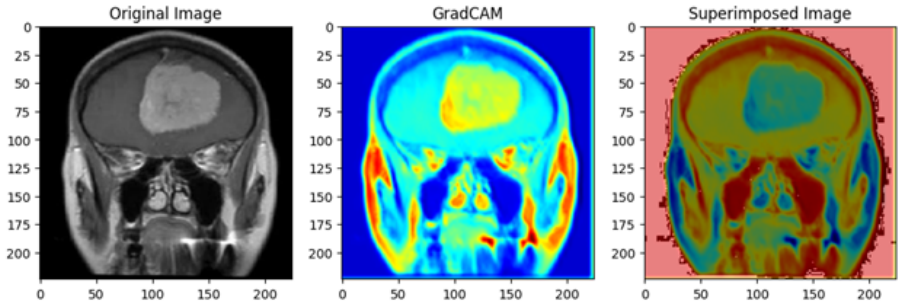


Figure 5.9: Gradcam visualization of the Meningioma Tumor prediction

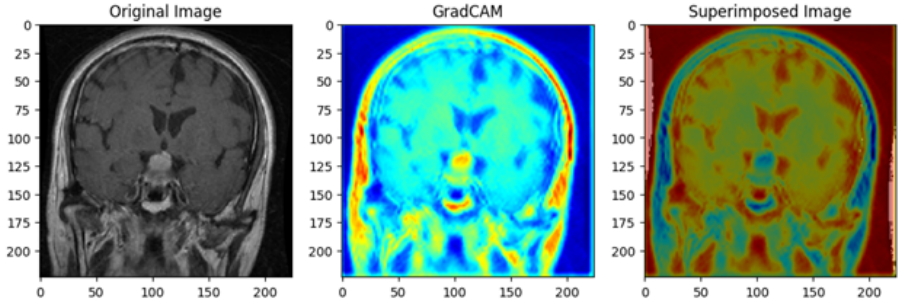


Figure 5.10: Gradcam visualization of the Pituitary Tumor prediction

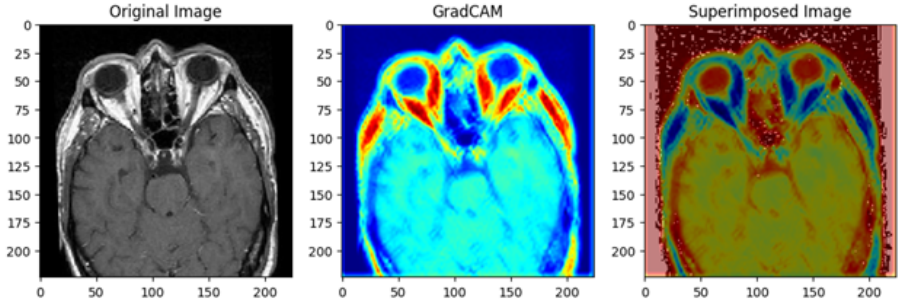


Figure 5.11: Gradcam visualization of the no Tumor prediction

Chapter 6

Conclusion and Future Works

6.1 Conclusion

In summary, the primary focus of this work was the development and evaluation of an imaging-based method for the prediction of different forms of brain tumors. Our work also makes use of machine learning algorithms and advanced image processing techniques to try to increase the success rate and accuracy of brain tumor prediction using medical imaging data, mostly from Magnetic Resonance Imaging (MRI)[27].

Research goals were successfully achieved through a systematic approach. A comprehensive dataset of MRI scans from patients diagnosed with brain tumors was acquired and preprocessed to improve data quality and standardization. To determine the most significant characteristics for brain tumor prediction, pertinent features were extracted from the preprocessed pictures, and feature selection techniques were used. Using the characteristics that were retrieved, a deep learning model was created to categorize cases of brain tumors. Additionally, a thorough and descriptive dataset was utilized to train the model, enabling comparisons of its accuracy and efficiency with other models that have already been trained. Model performance was rigorously evaluated using appropriate metrics and cross-validation techniques were used to ensure generalizability. Developed imaging methodologies are being explored for integration into clinical practice, highlighting their potential to help healthcare professionals make informed decisions, plan treatments, and monitor the progression of brain tumors. This methodology could contribute to improved outcomes, individualized treatment strategies, and improved survival for patients with this aggressive brain tumor by providing more accurate and early predictive capabilities[4].

Comparative analysis demonstrated the superiority of the imaging-based approach over existing methods for brain tumor prediction, such as conventional radiological interpretation and molecular biomarkers. The developed methodology showed higher accuracy, efficiency, and interpretability, demonstrating its potential as a valuable tool in brain tumor research and clinical practice[7].

In summary, by utilizing image processing techniques, this thesis has significantly advanced the science of brain tumor prediction. With its ability to properly forecast various forms of brain tumors, the established technique has shown promise and holds great potential for influencing clinical decision-making, treatment planning, and patient outcomes.

6.2 Future Works

For our research, further research and collaboration are encouraged to refine and expand upon the findings of this study, ultimately leading to improved diagnostic capabilities and better management of brain tumor patients.

Further improvements to existing architectures are required to improve classification accuracy. Transfer learning techniques have been explored on various medical image datasets to improve model generalization.

Multimodal information integration, including the inclusion of additional imaging modalities and clinical data, is being explored for comprehensive tumor characterization.

Furthermore, the practical use and validation of the developed model in clinical practice, taking into account factors such as interpretability and ethical considerations, will be an important aspect of future research.

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