Brain Tumor Detection Through Image Segmentation Using Deep Learning Approach

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List of Abbreviations and Acronyms

PET Positron Emission Tomography

CNN Convolutional Neural Network

MRI Magnetic Resonance Imaging

BraTS Brain Tumor Segmentation

GPU Graphics Processing Unit

IoU Intersection over Union

C-Unet Customized Unet

CT Computed Tomography

ReLU Rectified Linear Unit

Declaration

We do hereby declare that the research works presented in this thesis entitled, "Brain Tumor Classification Through Image Segmentation Using Deep Learning Approach" are the results of our own works. We further declare that the thesis has been compiled and written by us and no part of this thesis has been submitted elsewhere for the requirements of any degree, award or diploma, or any other purposes except for publications. The materials that are obtained from other sources are duly acknowledged in this thesis.

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Approval

We do hereby declare that the research works presented in this thesis entitled, "Brain Tumor Classification Through Image Segmentation Using Deep Learning Approach", is the outcome of the original work carried out by Nazmunnahar Amie, Al Mahabub Nur, Hossain Bin Walid ,Sadia Islam, and Faria Rahman Nourin under my supervision. I further declare that no part of this thesis has been submitted elsewhere for the requirements of any degree, award diploma, or any other purposes except for publications. I further certify that the dissertation meets the requirements and standards for the degree of Bachelor of Science in Computer Science and Engineering.

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Dedication

"Dedicated to the pursuit of knowledge and to the countless individuals who have illuminated our path with their guidance, encouragement, and unwavering belief in the power of research."

Acknowledgement

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Abstract

Brain tumors are a fatal condition that might result in a very limited life span. Misdiagnosis can lead to the improper medical action and lower a patient's probability of surviving. We address these difficulties by doing extensive experiments with the proposed framework that uses a hybrid Unet CNN architecture to classify MRI slices of healthy brain and brain tumors such as meningioma, glioma, and pituitary. In this study, we suggest a hybrid deep-learning technique for classifying brain tumors. We used a publicly available brain tumor dataset from Kaggle that included MRI images of brains with no tumors and three different types of tumors: pituitary, meningioma, and glioma. On the dataset, preprocessing was done. Our base model was the pre tained Unet, and we then added CNN layers both in downsampling and upsampling portion to it. We trained the additional layers that we added while using transfer learning to freeze the base model layers. A range of textures, shapes, and features associated with medical imaging are recognizable to the pre-trained Unet model. Moreover, we added extra CNN layers that discovered more complex and distinctive task-related brain tumor pattern features. Our model provided 95.78% test accuracy.

Chapter 1

1 Introduction

1.1 Introduction

Brain diseases are mainly caused by the abnormal growth of brain cells that may damage the brain structure and eventually lead to malignant brain cancer [1]. These tumors can either develop in the brain itself (primary brain tumors) or spread to the brain from other regions of the body (metastatic brain tumors). They can be benign (noncancerous), malignant (cancerous), or both (secondary brain tumors or metastatic tumors). All ages can develop brain tumors, but older adults are more likely to do so. The signs and symptoms of a brain tumor depend on the brain tumor's size and location [2]. Headaches, seizures, vision changes, limb weakness or numbness, and alterations in speech or cognitive function are among the common symptoms. Certain brain tumors, nonetheless, could not even show any symptoms. Although the precise cause of brain tumors is not yet completely understood, numerous risk factors have been found. Ionizing radiation exposure, a family history of brain tumors, and particular genetic disorders are some of these risk factors. To treat brain tumors, a combination of surgery, radiation therapy, and chemotherapy is frequently used. The particular treatment strategy is determined by the type and location of the tumor, the patient's overall health, and personal preferences. Brain tumors continue to present a serious medical challenge despite improvements in identification and treatment, with a high mortality rate for some tumor types. Thus, there is a need for ongoing study into the causes and treatment of brain tumors. To increase the accuracy and efficiency of diagnosis, we implemented a deep learning approach in this study for the identification and categorization of brain tumors. We want to contribute to the development of more efficient tools for the early diagnosis and treatment of brain cancers by extending a publicly available dataset with data augmentation techniques.

1.2   Problem Statement

A brain tumor develops when one or more brain tissues turn malignant and begin to grow abnormally. It is a malignant disease with a high fatality rate. Moreover, it interferes with the regular operation of the brain and other tissues. Early brain tumor detection and classification is highly challenging for medical professionals. Noise and other environmental disturbances are more likely to affect MRI pictures. As a result, identifying the tumor and its causes becomes challenging for doctors. A brain tumor is the development of aberrant brain cells, some of which may progress to cancer. So, in this research, to help doctors accurately and promptly detect brain tumors to save patients' lives, we developed a system that would detect and classify brain tumors on MRI.

1.3   Problem Background

Tumors affecting the brain and its surrounding tissues can lead to diverse symptoms and impact the normal functioning of the brain. Three common types of brain tumors are meningioma, glioma, and pituitary tumors. Meningiomas are usually slow-growing and non-cancerous. Gliomas are a type of tumor that arises from the glial cells, which are a type of cell that provides physical and chemical support to neurons and maintains their environment. Gliomas can vary widely in terms of aggressiveness, ranging from slow-growing and benign to highly malignant. Pituitary tumors originate in the pituitary gland, a small gland at the base of the brain that regulates hormone production. These tumors can be benign, and the majority are non-cancerous. For successful treatment and better patient outcomes, brain tumors must be identified early and properly classified. Brain tumors are typically diagnosed and categorized using a variety of imaging techniques, including computed tomography (CT), positron emission tomography (PET), and magnetic resonance imaging (MRI). We require an automated method to substitute the manual systems. Traditional methods involve labeling methods to detect diseased areas in the brain, and present techniques cannot identify inner peripheral pixels, posing a challenge in

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their compatibility with brain tumor detection and classification protocols. Owing to the area highlighted by the contrast agent and its clarity, we prefer MRI over Computed Tomography (CT). As a result, MRI modalities are used in numerous methods to detect brain cancer. [3] Machine learning and deep learning algorithms have drawn increasing attention in recent years as a potential tool for brain tumor diagnosis and classification. These algorithms can examine a lot of imaging data and aid medical professionals in making more precise diagnoses and treatment choices.

1.4 Research Objectives

The following research objectives can be achieved from this research:

- Segmented the image properly

- Detect the affected tumor cell from segmented image within efficient way

- To construct a hybrid UNet network to accurately detect brain tumors from MRI images

1.5 Motivation

The need for more precise and effective brain tumor treatment and diagnosis is what spurred the development of a deep learning-based method for brain tumor classification. The manual segmentation of MRI images by radiologists, a traditional technique for identifying and classifying brain tumors, can be time-consuming and prone to inaccuracy. Also, the radiologist's experience can have an impact on these approaches' accuracy. By constantly evaluating a large amount of medical imaging data, deep learning algorithms have the potential to increase the precision and rapidity of brain tumor identification and classification. These algorithms can recognize small details that might not be visible to the human eye by learning from patterns in the data. They can also be taught to recognize different kinds of brain tumors and the difference between benign and malignant tumors. Deep learning algorithms can assist doctors in choosing the best treatment strategy and improve patient outcomes by increasing the precision of brain tumor identification and classification.

For instance, they can help locate and determine the size of a tumor, which can help with surgery scheduling and lower the risk of complications. They can also aid in tracking a tumor's development and gauging a treatment's efficacy over time.

1.6 Flow of Research

The study is being conducted in stages. First, We examined the research subjects and then studied the fundamental principles of brain tumors. Following that, the drawbacks of the existing system are studied and encouraged to design a deep learning-based architecture. Following that, the dataset had been finalized. Figure 1.1 displays the stages of the research activity.
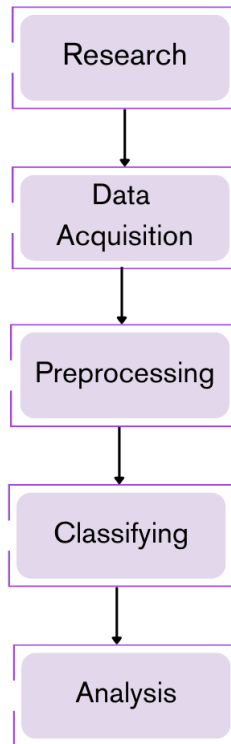

Figure 1.1: Flow Diagram of the Thesis Work

1.7 Significance of the Research

To effectively identify tumors in the vast field of radiology, greater medical science knowledge, and comprehension are required. Therefore, the need for a tumor classifi-

cation program overcomes the shortage of skilled radiologists. The proposed study's initial goal is to deal with the existing issues of brain tumor classification. Its main goal is to help doctors detect and classify brain cancers quickly and early. Doctors can assist in treating patients by using our proposed approach since it makes predictions with a better degree of accuracy. The radiologist is aided in decision-making by these predictions. Typically, medical diagnosis can be performed using the proposed approach. Additionally, it could also be utilized for academic research.

1.8   Research Contribution

The overall contribution of the research work is as follows.

- Determining the present barriers to analyzing brain tumor detection issues with segmentation based model

- Utilizing a hybrid UNet Architecture, to identify brain tumor with segmentation

- Conducting comparative analysis in terms of accuracy between our proposed model and some existing models

1.9   Thesis Organization

The rest of the paper is organized as follows: Chapter 2, known as the "Literature Review", lays the groundwork by thoroughly examining existing research, and preparing the path for the upcoming chapters. Next, Chapter 3, "Proposed Model", takes center stage, explaining our research approach in detail. It covers aspects like feasibility analysis, dataset specifics, algorithm details, design considerations, implementation, and an important simulation phase. Then, Chapter 4, "Implementation and Testing," shifts from theory to practice, diving into the dataset, data flow, thorough evaluation, results interpretation, and comprehensive discussions. Chapter 5, named "Standards, Constraints, and Milestones," looks at broader aspects like standards, societal impacts, ethics, challenges, and constraints, and offers a visual

timeline with a Gantt chart for tracking progress. Lastly, Chapter 6 serves as the "Conclusion", summarizing our research findings.

1.10 Summary

The article discusses brain diseases caused by abnormal growth of brain cells, leading to brain tumors. Symptoms of a brain tumor depend on its size and location, with common symptoms being headaches, seizures, vision changes, limb weakness or numbness, and alterations in speech or cognitive function. Although the causes of brain tumors are not fully understood, some risk factors have been identified, such as exposure to ionizing radiation, family history of brain tumors, and particular genetic disorders. To aid in the early diagnosis and treatment of brain tumors, a deep learning approach is proposed to categorize brain tumors using MRI data. Deep learning algorithms can analyze a large amount of medical imaging data, which can increase the precision and speed of brain tumor detection. By recognizing small details that may not be visible to the human eye, deep learning algorithms can assist doctors in choosing the best treatment strategy and improve patient outcomes. The proposed approach will use a publicly available dataset for brain tumor classification and process MRI scans using various preprocessing techniques.

Chapter 2

2 Literature Review

2.1 Introduction

A literature review is a summary of the earlier written works on a subject. The phrase can be used to describe an entire academic paper or a specific piece of academic work, like a book or an article. Researchers have come up with a variety of techniques and solutions for locating brain tumors using MRI images in recent years. From traditional machine learning algorithms to deep learning models, these techniques range. Here, we discuss related research on the detection and classification of brain tumors using various machine-learning methods and deep-learning models.

2.2 Literature Review

Ayadi et al. [4] introduces a novel deep CNN model for MRI brain tumor classification. The model incorporates various layers and utilizes a Softmax classifier. Three public datasets are employed for experimental validation: Figshare (3064 images), Radiopaedia (121 original MRI images with 4 grades), and a third dataset tested under two scenarios (before and after augmentation). The Figshare dataset was used to classify Meningioma, Glioma, and Pituitary tumor. They achieved an overall accuracy of 94.74% for this dataset. The second dataset was tested based on two scenarios: before and after augmentation. The original dataset attained an overall accuracy of 90.35%. The augmented dataset achieved 93.71% overall accuracy.

Rehman et al. [5] employed a novel deep learning-based approach for brain tumor detection and classification. They used a 3D Convolutional Neural Network with a pre-trained VGG19. BraTS 2018 dataset which has 476 images including 285 training cases and 191 testing cases was used in their research. This dataset

contains 3D brain MRI images. Their model gained an accuracy of 92.67% for the BraTS 2018 dataset. The limitation of their work is that their model's accuracy was not that good and also they used a small number of images in their work.

Mahmud et al. [6] proposed a deep analysis of brain tumor detection from MR Images using deep learning networks. The dataset they used, which was obtained from Kaggle, contained 3264 brain MRI images. The dataset included meningioma (937 images), no tumor (500 images), pituitary tumor (900 images), and glioma tumor (926 images). 80% of the dataset was utilized for training, 10% for testing, and 10% for validation. They normalized the images during the preprocessing stage and used augmentation techniques like width and height shifting, zooming, and rotation. They used CNN architecture in their study and evaluated its performance with other models such as ResNet-50, VGG16, and Inception V3. They have achieved the maximum accuracy of 93.3%. The only drawback of their study was limited training and testing images.

Shraddha et al. [7] proposed a convolutional neural network-based brain tumor detection. The dataset they used, which was obtained from Google, contained 200 images only. They used an augmentation technique to expand the tiny data set into a larger one. In their dataset, a single image had been transformed into seven images by rotating and analyzing it from various angles. After augmentation, 2065 images were used to train the model. 80% of the dataset was utilized for training, 20% for testing. They used CNN architecture in their study. They have achieved an accuracy of 87.42%. The drawback of their study was limited MRI images and low accuracy.

Deepak et al. [8] combined convolutional neural networks (CNN) and support vector machines (SVM) to create a robust system for categorizing brain tumors in MRI scans, achieving an impressive 95.82% classification accuracy. However, a limitation highlighted in the paper is the availability of small medical image databases,

which can restrict the system's real-world application due to the diverse range of brain images encountered in clinical settings. While the system's accuracy is commendable, expanding medical image datasets is crucial to enhance its practicality and reliability in clinical use.

Waghmare et al. [9] explore the application of deep learning techniques, specifically convolutional neural networks (CNNs), for brain tumor classification. They utilize the pre-trained VGG-16 model and fine-tune select layers to enhance accuracy, with a focus on adjustments within the fully connected layers. The research work yields an impressive outcome, achieving a substantial 95.71% accuracy in detecting brain tumors when evaluated using an online dataset. However, it's essential to note that the paper requires further elaboration and refinement in several areas. A comprehensive comparative analysis with other deep learning models or traditional machine learning algorithms for brain tumor classification is lacking. Moreover, the paper does not provide substantial insight into the size and diversity of the dataset used for the training and testing phases of the deep learning model.

Natak et al. [10] classified brain tumors using dense Efficient-Net. 3260 distinct types of brain MRI pictures were included in the dataset they used, which was collected from Kaggle. The dataset contained meningioma, glioma, and pituitary brain MRI pictures, respectively. Due to noise and inadequate lighting, the photographs of brain tumors were of poor quality. Their proposed technique uses the min-max normalization method. They have used data augmentation techniques like rotation, width shift, height shift, and zoom. For improved training, the original data was enhanced 21 times. This increased the amount of training data, which helped their model learn more quickly. Also, they were able to cut down on overfitting as the volume of the data increased as a result of data augmentation. For the classification of brain tumors into three classes—meningioma, glioma, and pituitary—they employed EfficientNet-B0, which has 237 layers. They got an accuracy of 98.78% for their testing dataset. Their model took quite a long time to compute.

Noreen et al. [11] proposed a deep learning model for the diagnosis of brain Tumor. They utilized the openly accessible brain tumor dataset Figshare. 3064 MR images from 233 patients make up this brain dataset. This dataset contains three different forms of tumors, including meningiomas, gliomas, and pituitary tumors. They used two pre-trained models: Inceptionv3 and DensNet201. For feature extraction and feature concatenation in Inceptionv3, the C, D, and E inception blocks have been employed. The softmax classifier received these concatenated features. For feature extraction and feature concatenation for DensNet201, the Denseblock, which has twelve (12) convolutional layer blocks, forty-eight (48), and thirty-two (32) convolutional layer blocks, has been employed. The softmax classifier received these concatenated features. Using Inception-v3 and DensNet201 on test samples, their suggested method achieved 99.34% and 99.51% testing accuracy, respectively.

Arshia et al. [12] proposed a deep learning-based framework for brain tumor classification using transfer learning. They used the Figshare dataset in their study. 3064 brain MRI slices from 233 people made up the dataset. 15% of the dataset was utilized for validation, 15% for testing, and 70% for training. They refined and improved the input data throughout the preprocessing stage. Several versions of images were produced utilizing conventional data augmentation techniques (rotations and flipping) to enhance the dataset samples, which aid in lowering over-fitting during the training of CNNs. For feature extraction, they made use of three pre-trained architectures from CNN, including AlexNet, GoogLeNet, and VGGNet. The two transfer learning scenarios, i.e., fine-tune and freeze utilizing each architecture, individually, are used to extract the discriminative visual features. AlexNet, GoogLeNet, and VGGNet obtained an accuracy of 97.39%, 98.04%, and 98.69% using fine-tuning. AlexNet, GoogLeNet, and VGGNet each achieved an accuracy of 95.77%, 95.44%, and 89.79% for the freeze approach. With the help of the optimized VGG16 network, they have achieved the maximum accuracy of 98.69% among the optimized AlexNet and GoogleNet networks. While using the transfer learning

freezing technique, AlexNet outperformed GoogLeNet and VGG16 with an accuracy of 95.77%. The only limitation of their study was it took a long time.

A. Hasan et al. [13] proposed a hybrid deep tumor network for brain tumor classification and detection. For their work, they used Kaggle's Br35H dataset. 1500 brain MRI scans with tumors and 1500 scans without tumors are included in this dataset. Each image had the skull stripped, and if it showed a tumor, it was labeled yes; otherwise, it was labeled no. CNN serves as the foundational component of their hybrid DeepTumorNet model, which also includes GoogleNet. There are a total of 22 layers in the fundamental Google Net model. They removed the final five levels of GoogleNet, and 14 layers—each one deeper than the previous in the CNN model were added in their place. When the modifications were made, the total number of layers rose from 22 to 33. Their proposed model achieved an accuracy of 99.51%. The limitation of their study was that the dataset they used was insufficient.

Irmak [14] proposed a fully optimized framework using a deep convolutional neural network for the multi-classification of brain tumor MRI images. He used four different publicly available datasets. He used three CNN architectures for three classification tasks. There are 13 layers in the CNN utilized for Classification-1. The Classification-2 CNN has 25 layers. There are 16 layers in the CNN utilized for Classification 3. Brain tumor detection is referred to here as "Classification-1," brain tumor classification is "Classification-2," and tumor grading is "Classification-3." Brain tumor detection was successful, with a 99.33% accuracy rate. Brain MR imaging classification had an accuracy of 92.66%. Glioma brain tumors were accurately classified into grades II, III, and IV with a 98.14% accuracy rate. Brain tumor classification was low for his proposed model.

Hamza et al. [15] proposed an optimal and efficient deep learning model for brain tumor MRI classification and analysis. For their study, they used the Figshare

dataset. The collection contained 1426 photos from the Glioma class, 708 images from the Meningioma class, and 930 images from the Pituitary class. Their proposed methodology's pre-processing stage includes the skull stripping processes. The Xception model with 71 layers was applied to feature extraction. Finally, the classification of BT into distinct classes was done using the ALSTM model. Their suggested model achieved 99.06% accuracy, 98.34% precision, 98.61% recall, and 99.30% specificity. Their suggested model achieved 99.06% accuracy, 98.34% precision, 98.61% recall, and 99.30% specificity.

Maqsood et al. [16] used deep neural networks and multiclass SVM for brain tumor detection. Two datasets, figshare and Brain Tumor Segmentation (BraTS) 2018 were used to test their suggested strategy for diagnosing brain tumors. A modified MobileNetV2 deep CNN model is used to extract the features. Then, brain tumor classification is performed using the M-SVM classifier. The proposed method achieved an accuracy of 97.47% for the BraTS 2018 dataset and 98.92% for the Figshare dataset. The study had two drawbacks: the feature selection procedure required some time, and it could only be used with 2D MRI scans.

Ahmed et al. [17] predicted the overall survival of glioblastoma patients using ensembles of convolutional neural networks from MRI. A subset of glioblastoma cases from the BraTS 2019 training dataset was used in their investigation; there were 163 cases for training and 46 cases for testing. The dataset had 3D MRI pictures. A 3D convolutional neural network was utilized for feature extraction and classifier training. Their suggested method produced a result with a very poor accuracy of 57.1%.

Musallam et al. [18] proposed a new convolutional neural network architecture for the detection of brain tumors in magnetic resonance imaging images. For the purpose of classifying brain tumors, the quality of MRI images was improved using preprocessing methods. In order to extract the exact brain object, 100 pixels were

cropped from either side of the image in the initial step of the image preprocessing procedure to remove distracting elements like blank regions. In their research, they proposed a novel deep-learning model that can address typical problems with related models. The convolutional component and the classifier component make up this new model. When tested on a dataset of 3394 MRI pictures, the suggested architecture demonstrated exceptional competitive accuracy of 98.22% overall, with 99% in recognizing glioma, 99.13% in detecting meningioma, 97.3% in detecting pituitary, and 97.14% in detecting normal images.

Alanazi et al. [19] proposed a brain tumor/mass classification framework using magnetic resonance imaging and developed a transfer, deep-learning model. Three distinct online datasets of brain MRI images were used in the study. A publicly available dataset from Kaggle that had 3000 brain MRI scans of tumor and non-tumor classes was the first dataset, designated dataset-I in the paper. The second dataset, designated dataset-II in the paper, was likewise obtained from Kaggle and includes, respectively, 826, 822, 395, and 827 brain MRI pictures of tumors, including pituitary tumors, meningiomas, gliomas, and no tumors. The paper's third dataset, dataset-III, contained 3064 brain MRI scans which included 1426 glioma tumors, 708 meningioma tumors, and 930 pituitary tumors. To test how well standalone CNN models performed on brain MRI images, several layers were developed from scratch. While using dataset I to classify brain MRI pictures into tumor and non-tumor classes, the 22-layer CNN performed most accurately. In order to classify tumors into sub-classes (glioma tumor, meningioma tumor, and pituitary tumor) for various tumor images from dataset II, the pre-trained was used using the transfer-learning approach. Their model attained a high level of accuracy, 95.75% for images taken with the same MRI machine.

Gómez-Guzm et al. [20] classified brain tumors on MRI by using CNN. The evaluation of seven deep convolutional neural network (CNN) models for brain tumor classification using neuroimaging was the main focus of their research. Generic

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CNN, ResNet50, InceptionV3, InceptionResNetV2, Xception, MobileNetV2, and EfficientNetB0 are the CNN models that were examined in their study. They made use of a set of MRI scans that were made available to the public. It contained 7023 grayscale MRI images of four different types of brain tumors: gliomas, meningiomas, no-tumors, and pituitary. 9139 photos were produced after the images underwent preprocessing techniques like resizing and augmentation. Using both the pre-trained CNN models and the generic CNN model, training, and validation approaches were used. According to their test results, the pre-trained model InceptionV3 had the best accuracy for classifying brain tumors, coming in at 97.12%.

2.3   Problem Analysis

The papers we have reviewed so far on brain tumor detection and classification using various machine-learning methods and deep-learning models have found that almost all are incomplete or have some kind of limitations. There were a number of papers with poor accuracy, overfitting problems, insufficient datasets, and time complexity problems. So there are opportunities to improve brain tumor detection and classification tasks.

2.4   Summary

We have reviewed quite a number of papers. We identified that most of the previous research works are incomplete or have opportunities to improve. Methodological improvements can be made from those papers. The limitations of those papers, such as low accuracy, overfitting issues, insufficient datasets, long computation times, etc., can be improved. Our goal is to overcome these limitations and perform brain tumor classification tasks with better accuracy.

Chapter 3

3 Proposed Model

3.1 Introduction

A brain tumor is the growth of cells within or close to the brain. Brain tumors can happen inside the brain or close to it. Brain tumors can be either malignant (cancerous) or benign (not cancerous), and they can affect both children and adults. Brain tumors can affect our brain function whether or not they are malignant if they enlarge to the point where they press against nearby tissues. A brain tumor puts one's life in danger and impacts the body's normal functions. So, detecting a brain tumor in its early stages is essential for an accurate diagnosis and effective treatment planning. Many brain tumors, particularly malignant ones, develop and spread quickly. Early detection can help detect these cancers when they are smaller and at a lower stage, increasing the probability of successful treatment. Early detection and treatment can improve the patient's quality of life by preventing or delaying the progression of symptoms such as pain, cognitive impairment, and physical restrictions. To detect and categorize brain tumors, we utilized a deep learning approach. This chapter highlights the proposed model, Feasibility study including technical feasibility, operational feasibility, economic feasibility and scheduling feasibility, requirement analysis, research methodology, Feature selection, Algorithm and Design, Implementation, and Simulation. It also explains how we obtained the data we used for the research.

3.2 Feasibility Analysis

Brain tumors have a significant impact on people's quality of life and health. A feasibility analysis is a systematic and complete evaluation of the practicality, viability, and possible success of a proposed project. It is often carried out during the early stages of a project to determine whether it is worthwhile to pursue. This

section will now discuss whether the system is feasible for development or not. This research includes the availability of the resources, cost analysis, potential organizational benefits, and system maintenance after development. This analysis' four levels of feasibility—technical, economic, operational, and scheduling—were assessed.

3.2.1 Technical Feasibility

The technical feasibility of the project hinges upon the accessibility and compatibility of essential hardware and software components. The development process is poised to unfold on the Kaggle Kernel platform, capitalizing on its robust GPU resources to facilitate the efficient training of the hybrid model. The decision to employ Kaggle Kernel is underpinned by its widespread accessibility and the cost-effective use of utilization of cloud-based GPU resources. The choice of Kaggle Kernel as the development platform is a well-considered decision aimed at optimizing technical feasibility. By aligning with the platform's accessibility, GPU capabilities, and cost-effectiveness, the project positions itself to navigate the intricacies of developing a hybrid model for brain tumor classification with efficiency and innovation.

3.2.2 Economic feasibility

The economic feasibility of this project stands as a robust pillar, driven by judicious resource utilization and strategic decisions. Also, the required software components for our project are completely free, so we don't have to purchase any software. The central factor contributing to the favorable economic outlook is the judicious use of free GPU resources offered by Kaggle Kernel. This resource allocation ensures that no direct monetary costs will be incurred during the developmental phase of the project, presenting a significant advantage in terms of cost-effectiveness.

The absence of direct monetary costs in the developmental phase underscores the project's commitment to economic efficiency. This is particularly noteworthy in the context of research initiatives, where budget constraints often pose substantial challenges. The ability to leverage free GPU resources not only streamlines the

development process but also democratizes access to cutting-edge technologies, fostering an environment of inclusively within the research community.

Furthermore, the economic feasibility extends beyond the absence of direct costs to encompass the optimization of human resources. While time investment is a critical component, the primary resource utilized in the project, it remains a non-monetary investment predominantly constituted by the expertise and efforts of the project team. The tools employed, such as Python, TensorFlow, and Keras, contribute to this economic efficiency by being open-source and free, eliminating additional software licensing expenses.

In essence, the economic feasibility of the project is fortified by a combination of prudent resource utilization and strategic tool choices. The judicious use of free GPU resources on Kaggle Kernel not only minimizes direct monetary costs but also reflects a commitment to fostering an economically efficient and collaborative ecosystem within the field of machine learning research.

3.2.3 Operational feasibility

One of the distinctive strengths contributing to operational feasibility is the minimal training requirement for medical professionals. The intuitive design and user-friendly interface mean that practitioners will be able to readily incorporate the brain tumor classification model into their diagnostic routines. The aim is to empower medical practitioners with a tool that not only enhances the accuracy of brain tumor diagnosis but does so without necessitating extensive retraining. This accessibility is paramount, especially in medical settings where time is of the essence. By requiring minimal training, the model positions itself as a valuable addition to the toolkit of healthcare professionals, allowing them to efficiently harness the benefits of automated brain tumor classification without disrupting their established workflows.

3.2.4   Scheduling feasibility

In the event of deviations or unexpected challenges, the project team is equipped to make prompt adjustments to the schedule. This adaptability is crucial in the dynamic landscape of research and development, where unforeseen circumstances can arise. The proactive adjustment mechanism is designed not only to mitigate risks but also to ensure that the project remains on track, meeting deadlines and delivering outcomes in accordance with the pre-defined timeline.

Recognizing the potential for unforeseen challenges is a key aspect of schedule feasibility. Issues such as data quality concerns or unexpected complexities in model training may arise during the course of the project. However, these challenges are not viewed as impediments but as opportunities for learning and refinement. The project team is prepared to address such challenges through a collaborative approach, drawing upon the diverse expertise within the team to find innovative solutions and maintain the project's momentum.

In essence, the schedule feasibility of this project is not just a static plan but a dynamic and adaptive framework. It acknowledges the potential for challenges, embraces a culture of continuous improvement, and establishes robust communication channels to navigate uncertainties effectively. Through this comprehensive approach, the project is positioned to meet its milestones and deliver outcomes in a timely manner, ensuring its resilience in the face of the unpredictable nature of research and development.

3.3   Requirement Analysis

The choice of dataset was a fundamental requirement for the project. The selected Kaggle dataset comprises two distinct classes:tumor, and no tumor. This diversity in classes is essential for training a robust brain tumor detection model capable of accurately identifying tumor & non-tumor cases.

The use of Kaggle Kernel as the primary coding environment was a requirement to harness its free GPU resources, facilitating efficient model training. This choice was driven by the need for cost-effective and accessible computational power during the development phase. Python, TensorFlow, and Keras were selected as the primary programming languages and frameworks for implementation. This requirement aimed to capitalize on the rich ecosystem of deep learning tools and libraries, ensuring compatibility and ease of implementation

3.4 The Research Methodology

In this section, Figure 3.2 provides an illustration of the procedures followed to perform this research. The approach is divided into a few key stages. The first dataset we used for our research was brainTumor by PALAK PATEL, which is a publicly accessible dataset from Kaggle. Following that, we preprocessed our dataset. Our dataset was divided into three categories: training, testing, and validation. We attempted to detect brain tumors through segmentation. After that, we assessed performance using several types of metrics such as accuracy, Dice Coefficient (F1 score), and Intersection Over Union (IoU).
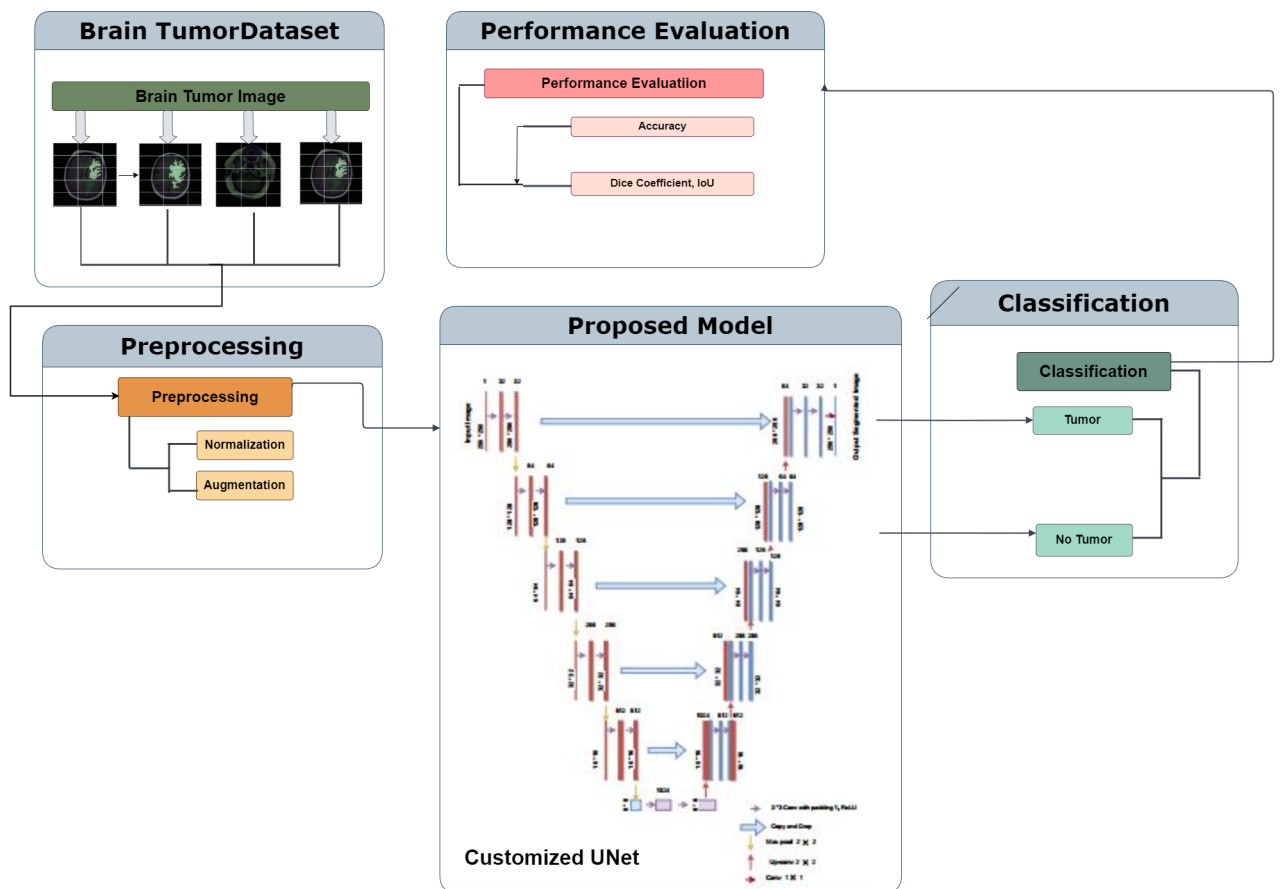
Figure 3.2: Research Methodology of the Proposed Model

3.4.1 Hybrid Unet Network

In our study, we used Unet, a pre-trained model, as our base model. It is trained on the ImageNet dataset. The pre-trained Unet model has knowledge of various textures, shapes, and features that are relevant to medical images. Further, we added additional CNN layers both in downsampling and upsampling portion that learned more complex and task-specific patterns related to brain tumor features that might not be present in the original ImageNet dataset. Finally, we added a flattened layer followed by dense layers.

3.4.2 UNet

The UNet is a well-liked convolutional neural network (CNN) architecture for deep learning that is mostly utilized for computer vision applications like object and image classification. This is a pre-trained model. The model has been trained on a large set of data before being made accessible for specific tasks. UNet has 23 layers of neural networks, comprising 22 convolutional layers and 1 fully connected layers. We used UNet as our base model.

3.4.3 Convolutional Layer

The convolution layer is the fundamental building component of CNNs. It is used in deep learning to perform image and pattern recognition tasks. The purpose of this layer is to extract features from the input data, which is typically images. These characteristics can be as simple as edges or as complicated as shapes, textures, or patterns. In order to find patterns or features in the input data, convolutional layers use filters (also known as kernels) that move over the data. The convolutional layer multiplies the filter and part of the input data element by element and then generates a sum of these products. As their output, convolutional layers generate feature maps, which describe the existence of particular features or patterns in the input data. These feature maps can be used for additional analysis and decision-making in subsequent levels of the network. Their effectiveness in processing visual input

makes them an essential component in recent deep-learning networks for image-related tasks.

3.4.4 MaxPooling Layer

Convolutional neural networks (CNNs) frequently employ a Max Pooling layer for processing and reduction of feature maps. It is essential for reducing the spatial dimensions of the feature maps because doing so helps to reduce the computational workload in the network. The Max Pooling layer's primary objective is to minimize the feature maps that the preceding convolutional layers generated. By reduction, significant characteristics are preserved but less information is included in the feature maps. The Max Pooling layer only keeps the maximum value while discarding the remainder. This maximum value indicates the most significant feature in that feature map region. The spatial dimensions of the feature map are decreased by retaining only the maximum values and discarding the rest. Because it simplifies the input, lowers the computational effort, and preserves crucial information for classification or other tasks, max pooling is a crucial part of CNNs.

3.5 Proposed hybrid UNet-CNN model

To build our hybrid model, we used the pre-trained UNet as the base model, which has an input shape of 256 x 256 x 3. We then added additional layers. We added convolutional layer both in downsampling and upsampling portion total 128 filters and a kernel size of 3X3. Here, we also use padding 1. ReLU is used as an activation function in this layer. Then we added a max pooling layer with a 2X2 kernel to minimize the spatial dimensions of the feature maps. The output of the convolutional layer was then sent to a max-pooling layer. The max-pooling method chose the most elements or pixels from the feature map area that the filter had covered. This outcome was then fed into another convolutional layer with 128 filters and a kernel size of 2X2. The output was then sent to the next max-pooling layer with a 2X2 kernel size. Then, to turn the output into a 1D vector, we applied a flattened layer. The RELU activation function was then applied to a dense layer of 128 neurons.
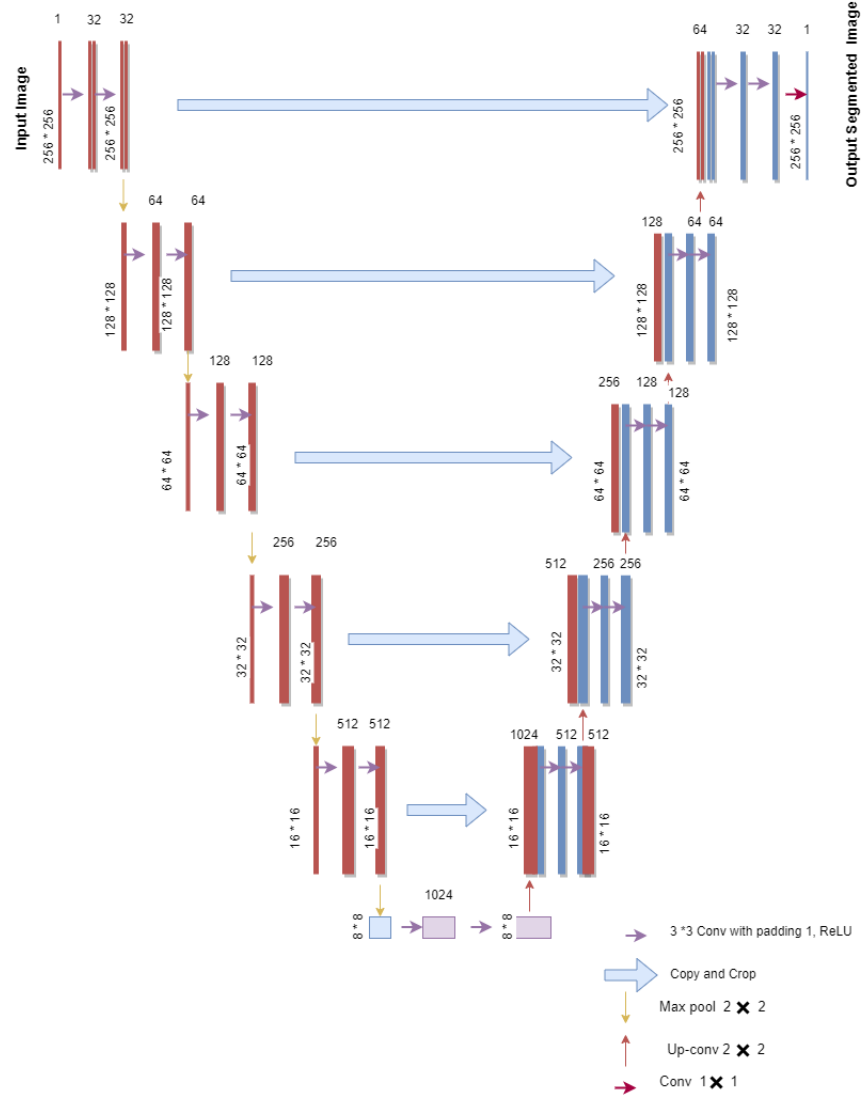
Figure 3.3: Proposed Hybrid UNet-CNN Model

Again, we used a dense layer of 64 neurons with the RELU activation function. Another dense layer with 32 neurons with the same activation function was added. Because our output is divided into four classes, we ended up with four neurons in the final dense layer. Finally, in the last output layer, a Sigmoid activation function was applied. Figure 3.3 shows the architecture of the proposed model.

3.6 Data Set

3.6.1 Dataset Collection

In this research, we utilized a publicly available 3D Brain Tumor MRI (Magnetic Resonance Imaging) dataset from Kaggle. The dataset contains 3929 MRI images of four different types of brain tumors, of which 2828 images were used for training (containing 1555 tumors, 1273 no tumors). There were 393 images for testing (216 tumors, and 177 no tumors) and 708 images for validation (389 tumors, and 319 no tumors).

Class Name	Count		
	Training	Testing	Validation
Tumor	1555	216	389
No Tumor	1273	177	319
	=2828	=393	=708

Table 1: Dataset Classes Table

3.6.2 Dataset Preprocessing

The pre-processing stage is crucial since it involves transforming the data to make them useful for training. We resized the MRI images to have a height of 256 pixels and a width of 256 pixels and we also performed normalization and data augmentation. The two stages of data preprocessing are data normalization and data augmentation. The following provides descriptions of these two methods.

Data Normalization:

Data normalization is the process of converting the data into a standard scale to make sure that various features or variables have comparable ranges. Image normalization is a crucial preprocessing technique. In order to transform the features such that they are on a comparable scale, we normalized the images. This improves the model's functionality and training stability. Neural networks often converge faster when input data is within a certain range. Normalizing pixel values to a specific range can facilitate quicker convergence during training. By ensuring that pixel val-

ues are consistent across different images, the model is better able to learn features that are applicable to a variety of inputs.

$$P' = \frac{P - P_{\min}}{P_{\max} - P_{\min}} \tag{1}$$

Since we will be using an image dataset we have to normalize the pixel values. To do so we used the formula in equation (1). In the equation, P' denotes the normalized pixel value and P denotes the original pixel value. $P_{\max}$ denotes the maximum pixel value, and $P_{\min}$ denotes the minimum pixel value. For grayscale images, pixel values are typically in the range [0, 255], where 0 represents black and 255 represents white.

Data Augmentation:

Data augmentation is the process of creating new training instances from existing data using various transformation techniques such as rotating, flipping, zooming, translation, and cropping. Image data augmentation is the act of making new, altered versions of existing pictures to increase the diversity of an image collection. Data augmentation is an efficient method for reducing overfitting and increasing model generalization. We used data augmentation to expand our dataset by zooming, rotating, and flipping. We augmented each training image three times. We set the zoom range to 0.2. This parameter controls the range of random zooming that can be applied to the input images during training. For the rotation technique, we set the rotation range to 0.05. This parameter specifies the range of random rotations that can be applied to the input images during training. For the rotation range set to 5 degrees, each image can be randomly rotated by an angle between -5 and +5 degrees. We also used horizontal flipping which involves randomly flipping images horizontally (left to right) to create new training samples from the existing dataset.

3.7 Design, Implementation, and Simulation

3.7.1 Design

The brain tumor classification system was designed with a modular architecture to effectively integrate the UNet model and additional convolutional neural network(CNN) layers both in downsampling and upsampling portion. The architecture comprises distinct modules for data preprocessing, feature extraction, and classification. The decision to incorporate the UNet model stems from its proven efficacy in image classification tasks, providing a strong foundation for our hybrid model. Additional CNN layers were strategically introduced to capture more intricate features relevant to brain tumor characteristics. Prior to model training, a meticulous data preprocessing pipeline was established. This included the normalization of pixel values, resizing of images to a standardized format, and augmentation techniques to address data scarcity. Given the sensitivity of medical imaging data, special attention was devoted to preserving critical features during preprocessing to avoid any loss of diagnostically relevant information.

3.7.2 Implementation

The implementation phase was conducted in the Python programming language, utilizing TensorFlow and Keras frameworks for deep learning. The development environment was Kaggle Kernel, chosen for its provision of free GPU resources. The cloud-based nature of Kaggle significantly expedited model development, allowing for rapid prototyping and iteration. The UNet model was configured as the base architecture, with additional convolutional and dense layers appended to facilitate deeper feature extraction.

3.7.3 Simulation

The training process involved iterative refinement of the model through multiple epochs. Convergence behavior was carefully monitored, and training/validation loss curves were analyzed to ensure optimal model performance. The use of GPU re-

sources on Kaggle kernel significantly expedited the training phase, allowing for a more comprehensive exploration of the model's parameter space.

Performance evaluation was conducted using standard metrics, including accuracy, Intersection over Union (IoU), and Dice Coefficient(F1-score). The model exhibited promising results in classifying brain tumors into meningioma, glioma, pituitary, and non-tumor classes. The evaluation also considered confusion matrices to provide insights into specific areas of model strength and potential improvement. A comparative analysis was also carried out to compare our model's performance with existing works.

3.8   Summary

In this chapter, we attempted to integrate all feasibility analyses, including technical, operational, economic, and scheduling feasibility, as well as the prerequisites that this research requires. This chapter explained how the proposed technique works, how data was acquired and preprocessed, and model selection, design, and implementation. This chapter describes our research strategy. The development of the application will be helped by this chapter.

Chapter 4

4   Implementation and Testing

4.1   Introduction

This section goes into great detail about how our brain tumor classification model was implemented, and tested, and the results were analyzed. The architecture of our model, which is supported by a hybrid UNet network, is examined in detail. This section provides a thorough examination of the results. We examine the model's accuracy, precision, recall, and other important criteria.

4.2   Dataset

In this undertaking, we used a publicly available 3D Magnetic Resonance Imaging (MRI) dataset known as "brainTumor" from Kaggle, a popular platform for data science competitions. The dataset, a valuable resource in medical imaging, comprises a total of 3929 MRI images capturing various manifestations of brain tumors. All the images were color 3D. For training our model, we used 2828 images, encompassing a diverse array of brain tumor types. This training subset includes 1555 tumors, and 1273 images representing cases with no tumors. We augmented the training images three times using augmentation techniques known as zooming, rotating, and horizontal flip. These images provide the foundational knowledge necessary for our model to learn and generalize patterns associated with different tumor categories. We used 393 images for testing our model. This test set is further categorized into 216 tumors, and 177 images without tumors. Finally, 708 additional images, comprising 389 tumors, and 319 images without tumors, were set aside for validation. With this dataset, in the next sub-sections, we explain how our proposed model works, and what we found out. Some images from our dataset are given below:
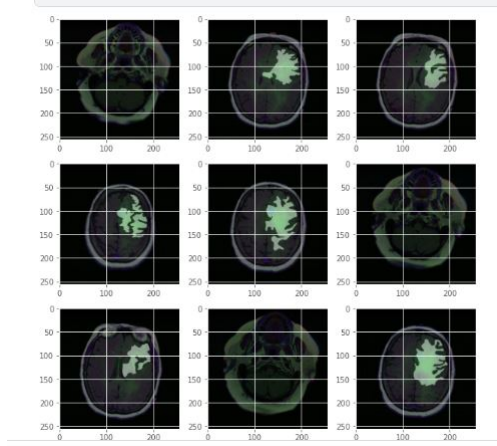
Figure 4.4: Samples of Training Dataset
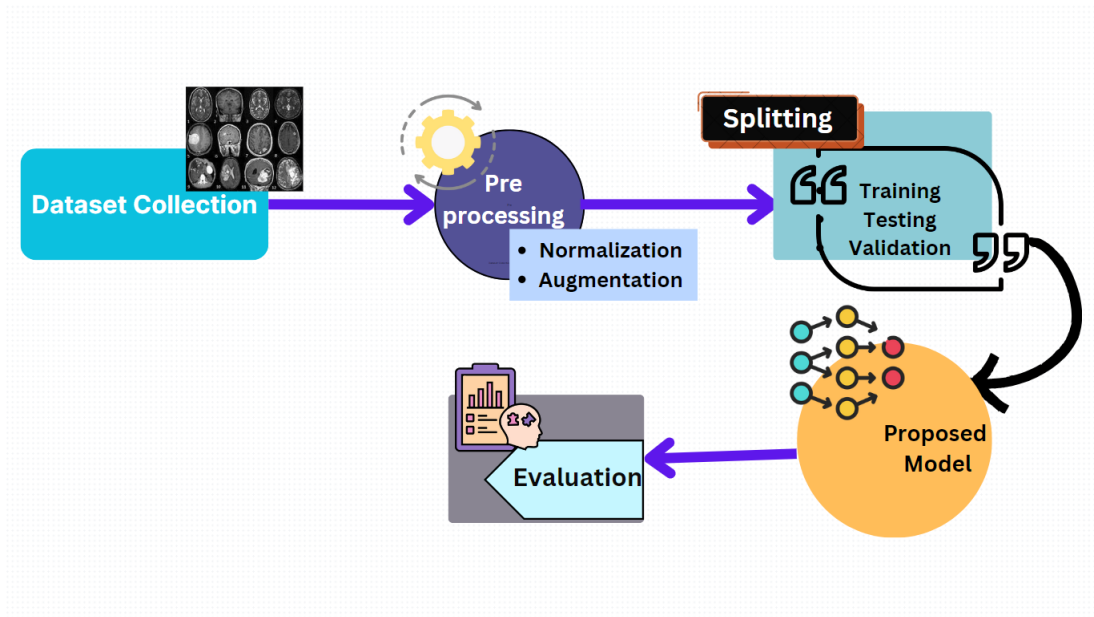
Figure 4.5: Data Flow Diagram

4.3 Data flow diagram

The dataflow diagram in Figure 4.5 depicts the key stages of this research. The initial step is to acquire data. We then preprocessed our dataset. The dataset was then separated into three categories: training, testing, and validation. Then we select our proposed model. We attempted to categorize brain tumors into four types. After that, we evaluated performance using a variety of metrics.

4.4 Evaluation

In assessing the performance of our brain tumor classification model, the use of evaluation metrics is crucial to gain a comprehensive understanding of its effectiveness. Evaluation metrics serve as benchmarks that help us measure and quantify how well our model is performing. They provide valuable insights into its strengths and potential areas of improvement. To assess our model, we used some evaluation metrics: accuracy, Intersection over Union (IoU), and f1-score(Dice coefficient).

Accuracy Accuracy is defined as the ratio of correctly predicted instances to the total number of instances in the dataset. It provides a general overview of how well a model is performing across all classes or categories.

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \tag{2}$$

A high accuracy, close to 100%, suggests that the model is making accurate predictions for the majority of instances in the dataset. It implies that the model is effective in generalizing patterns and capturing the underlying structure of the data. Conversely, a low accuracy indicates that the model is struggling to make correct predictions. This might be due to issues such as insufficient training data or the complexity of the problem. Accuracy may not be an ideal metric in cases where there is a significant imbalance in the number of instances across different classes. But for cases where the number of instances is balanced across different classes, accuracy can be an ideal metric.

Precision Precision is formally defined as the ratio of true positives to the sum of true positives and false positives. It is calculated using the following formula:

$$Precision = \frac{\text{TP}}{\text{TP} + \text{FP}} \tag{3}$$

Precision is a crucial evaluation metric that provides insights into the accuracy of positive predictions made by a model. It specifically measures the proportion of true positive predictions (correctly predicted positive instances) among all instances predicted as positive. Precision is particularly relevant in situations where minimizing false positives is essential.

A high precision value indicates that the model is accurate in its positive predictions. It suggests that when the model says something belongs to a certain class, it is very likely to be correct. High precision enhances the trustworthiness of the model's positive predictions.

Conversely, a low precision value implies that the model is making a significant number of false positive predictions. In other words, when the model predicts something as positive, it might not be accurate very often.

In applications where the consequences of false positives are effective, precision becomes a key factor in decision-making. In datasets where the classes are imbalanced, meaning one class significantly outnumbers the other, precision becomes more informative than accuracy. This is because accuracy can be misleading in imbalanced datasets, but precision specifically focuses on the accuracy of positive predictions.

Recall Recall is formally defined as the ratio of true positives to the sum of true positives and false negatives. It is calculated using the following formula:

$$Recall = \frac{\text{TP}}{\text{TP} + \text{FN}} \tag{4}$$

Recall, also known as sensitivity or true positive rate, is a vital evaluation metric in machine learning and classification tasks. It specifically measures the model's ability to correctly capture or recall all the positive instances in a dataset. Recall is particularly important in situations where missing positive instances (false negatives) is a critical concern.

A high recall value indicates that the model is effective in capturing the majority of positive instances. It suggests that the model is sensitive to detecting positive cases and minimizing the chances of missing actual positive instances. Conversely, a low recall value implies that the model is missing a significant number of positive instances. This might be a concern in scenarios where false negatives have substantial consequences, such as in medical diagnoses where failing to identify a disease can lead to delayed treatment.

In datasets where the classes are imbalanced, meaning one class significantly outnumbers the other, recall becomes a more informative metric than accuracy. This is because accuracy can be misleading in imbalanced datasets, but recall specifically focuses on the ability to capture positive instances.

F1-score: The F1 score is the harmonic mean of precision and recall. It is calculated using the following formula:

$$F1 Score = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \tag{5}$$

The F1 score is a widely used metric in machine learning and classification tasks that combines precision and recall into a single value. It is particularly useful in situations where there is an imbalance between the classes or when both false positives and false negatives are important considerations.

The F1 score ranges from 0 to 1, where 1 indicates perfect precision and recall, and 0 indicates poor performance. A high F1 score suggests a balance between precision and recall. It means that the model is good at making accurate positive predictions (high precision) and capturing most of the positive instances (high recall). The F1 score helps navigate the trade-off between precision and recall. It is particularly valuable when there is a need to balance the importance of minimizing false positives and false negatives.

Dice Coefficient: The precision and recall of a prediction are used to determine

the dice coefficient. Subsequently, the overlap between the ground truth and the expected segmentation is scored. Additionally, it penalizes false positives, a typical problem in datasets with extreme class imbalances, such as medical image segmentation. The harmonic mean of recall and precision is the dice coefficient, or F1 score. Put differently, the calculation involves dividing the total number of pixels in both images by the product of 2*intersection. The equation can be expressed as follows.

$$\text{Dice Coefficient} = \frac{2TP}{2TP + FP + FN} \tag{6}$$

Or it can also be rewrite as following way.

$$\text{Dice Coefficient} = \frac{2 * Area\ of\ overlap}{Total\ area} \tag{7}$$

Intersection over Union (IoU): The area where the anticipated segmentation and the ground truth meet over union is known as the intersection over union (IoU). The equation can be expressed as follows.

$$\text{IoU} = \frac{TP}{TP + FP + FN} \tag{8}$$

Or it can also be rewrite as following way.

$$\text{IoU} = \frac{Area\ of\ overlap}{Total\ area} \tag{9}$$

4.5   Result Evaluation

We conducted training using 50 epochs and a batch size of 32. On the 47th epoch, the training accuracy was 95.80% and validation accuracy was 95.78%.

4.5.1   Performance Evaluation-Metric

Table 2 shows the proposed model performance after training and testing in terms of Accuracy, Dice Coefficient or F1-score, and IoU.

Phases	Accuracy	DiceCoefficient	IoU
Training	95.80%	0.88	0.80
Validation	95.78%	0.90	0.80
Test	95.75%	0.90	0.80

Table 2: Performance Evaluation table

4.5.2   Training accuracy vs. validation accuracy curve

The training accuracy vs. validation accuracy curve is a graphical representation of the performance of a machine learning model during training and validation. It shows how the accuracy of the model evolves over different epochs or iterations of the training process. The x-axis represents the number of epochs, while the y-axis represents the accuracy of the model. The curve consists of two lines: one for training accuracy and another for validation accuracy. The training accuracy line displays the model's performance on the training data over time. The model hasn't learned anything at this point; therefore, the training accuracy is initially low. The training accuracy continuously improves as the model continues to learn and modify its parameters based on the training data. It's crucial to remember that the training accuracy by itself does not give a full picture of the model's performance. If the model doesn't generalize effectively to new, unknown input and just memorizes the training data, it may be misleading. The model's performance on a different validation dataset is shown by the validation accuracy line. The model's performance on data that it hasn't encountered during training is assessed using the validation dataset. The model's initial validation accuracy rises as it discovers broad patterns

in the training data. The validation accuracy could eventually plateau or possibly begin to decline, though. This suggests that the model is overfitting, which means it has become overly specialized to the training data and is having trouble generalizing to new data. In machine learning, overfitting is a typical issue that the validation accuracy curve aids in spotting.

Figure. 4.6 shows that the training accuracy steadily increases with each epoch, indicating that the model is learning from the training data and improving its performance. The validation accuracy also shows improvement but might exhibit fluctuations. It generally follows the trend of the training accuracy, but it's slightly lower. It's important to monitor the training and validation curves for signs of overfitting. If the training accuracy is significantly higher than the validation accuracy, the model may be overfitting to the training data. the model seems to generalize well, as both training and validation accuracy are increasing and converging.
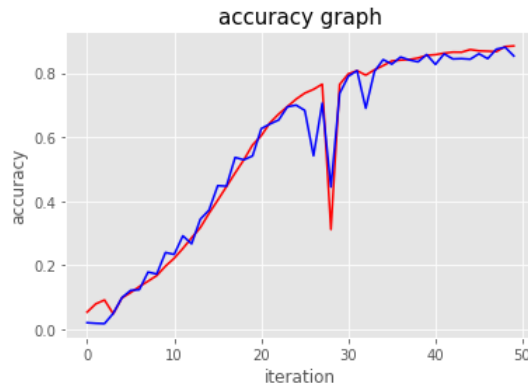
Figure 4.6: Training Accuracy vs. Validation Accuracy Curve

4.6 Results and discussion

Comparisons between our suggested model and a few of the previously published research by other writers are shown in Table 3. We can see that the most reliable model is ours. Poor accuracy was one of the shortcomings of the existing models. Comparatively, our model outperformed comparable models.

In Table 4, we show the accuracy of some pre-trained models that were tested on the same dataset we are working on. We compared the accuracy of our model with InceptionV3, ResNet50, and VGG16. We can see from Table 4 that our model has

Authors	Model	Accuracy
Proposed Model	**Hybrid UNet-CNN**	**95.78%**
Ahmed et al. [17]	Ensembles of convolutional neural networks	57.1%
Ayadi et al. [4]	CNN	93.71%
Rehman et al. [5]	CNN, VGG19	92.67%
Mahmud et al. [6]	CNN	93.3%
Shraddha et al. [7]	CNN	87.42%
Irmak [14]	25 layered CNN	92.66%

Table 3: Comparison of our proposed model with some existing models

Models	Accuracy
InceptionV3	91.21%
ResNet50	62.79%
VGG16	94.30%
Proposed model	**95.78%**

Table 4: Comparison of our proposed model with some existing pre-trained models

the highest accuracy among the pre-trained models.

Our model has achieved impressive accuracy, demonstrating superior performance in Dice-coefficient, and IoU. Upon comparing our model's accuracy with various models from different authors and existing pre-trained models, it stands out as the top performer, attaining the highest accuracy. Consequently, we can confidently assert that our model excels in the detection of brain tumors.

4.7   Summary

In this section, a comprehensive evaluation of the proposed model's performance was conducted, employing a range of metrics to assess its effectiveness in classification tasks. The metrics utilized included accuracy, IoU, and the Dice-coefficient or F1 score, providing a well-rounded understanding of the model's predictive capabilities.

Furthermore, the section featured a comparison between the proposed model and existing models within the same domain. The results of this comparative analysis highlighted the superior accuracy achieved by the proposed model, affirming its competitive edge in classification tasks. Additionally, the model was benchmarked

against pre-trained models, revealing that it outperformed these established benchmarks, achieving the highest accuracy.

To complement these quantitative assessments, visual representations in the form of training versus validation accuracy curves were incorporated. These curves illustrated the model's learning dynamics over epochs, providing valuable insights into its training process and its ability to generalize to new, unseen data.

High accuracy, coupled with superior performance in precision, recall, and the F1 score, underscores the robustness of the proposed model in addressing classification challenges within the specified domain. These findings position the model as a promising and competitive solution within the broader landscape of machine learning applications.

Chapter 5

5 Standards, Constraints and Milestones

5.1 Introduction

In the introduction section of this chapter, we begin a study of the focal concepts of establishing standards, recognizing constraints, and defining milestones within the complex territory of brain tumor classification research. These fundamental pillars not only contribute to the orientation of our research but also serve as guiding lights, illuminating the way toward enhanced diagnostic precision and the subsequent improvement of patient outcomes.

5.2 Standards

Industry Standards: The expansive domain of healthcare and medical research is naturally connected with a comprehensive framework of industry standards and best practices. In the context of brain tumor detection, strict adherence to these standards is not only encouraged but essential. These standards surround the entire spectrum of protocols for data acquisition, patient confidentiality, and the evaluation of diagnostic models. By adhering to these well-established standards, researchers ensure the integrity, reliability, and ethical foundation of their work. This includes rigorous processes for data collection, stringent privacy protections, and meticulous evaluation criteria, all of which converge to form the bedrock of trustworthy research and results.

Methodological Standards: At the heart of our research lies the development of a sophisticated deep-learning model engineered to unravel the complexities of brain tumor classification. These attempts are anchored by methodological standards and guidelines that serve as the compass for our research voyage. The adoption of these standards is not merely a matter of procedural compliance; it is the key to unlocking

the doors to accuracy, robustness, and generalizability. Methodological standards surround every aspect of model development, including the intricate refinement of architecture, data preprocessing, and validation techniques. By adhering to these methodological standards, we ensure that our models are constructed on the bedrock of scientific severity, and assured to stand up to scrutiny.

5.3   Impacts on society

Healthcare Transformations: The significance of our research echoes far beyond the laboratory or clinic walls; it extends its embrace to the entirety of the healthcare ecosystem. The advancements in brain tumor detection that our research could potentially promise could unleash a wave of transformative changes within healthcare practices. A heightened accuracy in diagnosis equates to the gift of time—time for early intervention, time for targeted treatment, and time for improved patient care. By reducing diagnostic uncertainty and enabling swifter, more precise treatment decisions, our research not only stands to elevate healthcare standards but also to curtail costs. The ripple effect is felt in resource optimization, where the judicious allocation of healthcare resources becomes a feasible reality.

Societal Implications: Yet, the societal implications extend far beyond the responsibilities of healthcare. The societal burden of brain tumors is profound, impacting not just the individuals directly affected but their families, communities, and the broader fabric of society. By providing a more precise and efficient means of detection, our research has the potential to ease this burden significantly. It serves as a beacon of hope, offering a promise of improved overall quality of life for those touched by brain tumors. In this sense, our research transcends the realm of academia and healthcare, becoming a catalyst for a positive shift in society's well-being.

5.4 Ethics

Data Ethics: In our pursuit of scientific excellence, we find ourselves navigating the delicate territory of data ethics. It is an ethical obligation of supreme significance to ensure that every piece of patient data utilized in our research is handled with the utmost care, respect, and diligence. Patient privacy, the cornerstone of medical ethics, takes priority. The principles of informed consent and data security are carefully observed, with every bit of data treated as sacred and confidential. It is our persistent commitment to the responsible and ethical use of patient data that anchors our research within the realm of trustworthiness and credibility.

AI Ethics: The introduction of artificial intelligence into the realm of healthcare amplifies the ethical considerations that steer our work. The principles of AI ethics—transparency, fairness, and interpretability—are woven into the very fabric of our research. Each decision made by our AI models is transparent, enabling healthcare professionals to comprehend and contextualize the outcomes. Fairness is not an afterthought but a foundational principle, ensuring that our models do not maintain biases or discrimination. Interpretability is our guiding star, providing clarity and confidence in the diagnostic decisions made by our AI-driven model. Upholding these ethical standards in the realm of AI applications is both a moral imperative and a practical necessity.

5.5 Challenges

Data Challenges: As we begin the journey of brain tumor detection research, we are certainly confronted with a multitude of data-related challenges. Data quality becomes a focal point of our efforts. The quality of the data we collect and employ directly influences the reliability and efficacy of our models. Additionally, the diversity and representations of the data play crucial roles in ensuring that our models can generalize their findings to a wide spectrum of cases. The challenges associated with data are not merely obstacles; they are opportunities for innovation, promoting

the creation of sophisticated data curation and preprocessing pipelines to extract valuable insights from complex datasets.

Model Complexity: The utilization of deep learning models within the context of brain tumor detection presents us with a double-edged sword. While these models exhibit remarkable power and versatility, their complexity can pose significant challenges. Interpretability becomes a central theme in our research, as healthcare professionals and patients require a clear understanding of the reasoning behind diagnostic outcomes. The balance between model sophistication and interpretability is a constant challenge, necessitating the development of novel techniques and methodologies to make our models more accessible and comprehensible.

5.6 Constraints

Data Constraints: The very essence of our research, the data, often imposes constraints. These constraints are frequently dictated by the availability of high-quality and relevant datasets. The limitations existing in data availability can significantly affect the scope and generalizability of our research findings. Addressing these constraints necessitates careful data selection, careful data preprocessing, and a steady commitment to extracting valuable insights even within the confines of available data.

Computational Constraints: As we go through the complexities of deep learning, we must navigate the maze of computational constraints. These constraints surround limitations in hardware resources, software capabilities, and computational time. The nature of deep learning models necessitates careful consideration of the computational infrastructure at our disposal. These constraints shape not only the feasibility but also the efficiency of our research. It compels us to make strategic choices in model architectures and experimentation scales, ensuring that our research remains within the realm of the practically attainable.

5.7   Timeline and Gantt Chart

Research Goals and Milestones: In our search to advance the field of brain tumor classification, we recognize the prime importance of establishing well-defined research goals and milestones. These objectives serve as signals, guiding our research efforts and progress. Research goals can encompass diverse dimensions, from achieving specific model accuracy thresholds to the expansion of dataset sizes or the completion of phases of our research. These milestones are not just markers of progress; they are the building blocks upon which our research success is constructed.

Gantt Chart Representation: To visualize and carefully manage our project's progression, we employ the time-honored Gantt chart. This visual representation offers a panoramic view of our research timeline, describing the sequence of tasks, milestones achieved, and anticipated future milestones. It serves as our compass, enabling us to stay on course and allocate resources judiciously, ensuring that our research advances in an organized and systematic manner.

The illustration in Figure 5.13 on the following page demonstrates our timeline for this thesis:

	Dec	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct
Identify research area	▓										
Establishing the approach, methodology, and framework	▓	▓									
Write research proposal		▓									
Literature Review		▓	▓	▓							
Data Collection				▓							
Data Analysis				▓							
Train and Evaluate Model					▓						
Result Analysis						▓					
Research summary and closure							▓				
Write thesis draft								▓	▓		
Review and Revisions										▓	
Finalization											▓

Figure 5.7: Gantt Chart

5.8   Summary

In this concluding segment of the chapter, we pause to reflect upon the extensive journey through the complex territory of standards, constraints, and milestones. These themes are not just components of our research; they are the guiding principles that steer our work. They underline the imperative of ethical conduct, the adherence to industry standards, the insightful resolution of challenges, and the subtle understanding of constraints. All these elements join within the broader context of societal impact, an influential reminder of the transformative potential that lies within the realm of brain tumor detection. This section not only summarizes the key takeaways but also serves as a seamless bridge, linking this chapter with the subsequent chapters in our thesis and reaffirming our commitment to severity, ethics, and innovation in the pursuit of scientific excellence.

Chapter 6

6 Conclusion

6.1 Introduction

Our research efforts have produced a strong hybrid model that has been developed and evaluated in an effort to advance the field of brain tumor detection. To tackle the difficult challenge for recognizing non-tumor instances, this combination of UNet and additional convolutional neural network (CNN) layers has been carefully built. As we conclude this exploration, we reflect on the accomplishments made and the methodologies employed. The following sections delve into the key outcomes and the potential avenues for future research, marking the culmination of our efforts to contribute to the broader landscape of medical image analysis.

6.2 Conclusion

In order to train our hybrid model, we required a significant number of instances. Employing preprocessing techniques such as normalization and augmentation played a pivotal role in preparing the images for training. Augmentation strategies, including zoom, rotation, and horizontal flip, not only increased the dataset size but also enriched the diversity of the training samples, contributing to the robustness of our model. The suggested model's accuracy was 95.78%. Because we used transfer learning on our hybrid model, the training period went by quickly as the base model's layers were frozen. The pre-trained UNet model has knowledge of various textures, shapes, and features that are relevant to medical images. Further, we added additional CNN layers that learned more complex and task-specific patterns related to brain tumor features that might not be present in the original ImageNet dataset. So we got a high accuracy of 95.78% from our hybrid model.

6.3 Future Works and Direction

The advancements gained in this brain tumor detection effort provide opportunities for further study and development. Although the current model shows commendable accuracy, there are a number of areas that can be investigated and improved. Our present model only works with limited datasets from 3D medical imaging. A promising area for future research is extending its capacity to easily handle large amount of 3D datasets. This change would enable a more thorough investigation and maybe improve the accuracy of diagnosis. In the future, we want to train our model with a larger dataset that includes more classes of various brain tumors. Beyond the present two classes—tumor, and no tumor—the addition of new tumor types has the potential to improve the model's ability to distinguish between a wider range of clinical diseases. However, the inclusion of a bigger dataset demands careful consideration of data quality, class balance, and the management of computational resources for effective processing.

We intend to investigate new deep learning models in the future and include them in our methodology to produce even better outcomes. The goal is to harness the advancements in deep learning to achieve even better results in terms of accuracy and efficiency.

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