UNDERGRADUATE FINAL YEAR PROJECT REPORT

Department of Software Engineering

NED University of Engineering and Technology

Advancing Radiogenomics: AI Enabled Glioblastoma Subtype Prediction

Group Number: <u>20</u>   **Batch: 2020 – 2024**

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Project Advisor

Author's Declaration

We thus proclaim that we are this project's only authors. It is the exact version of the project that our advisor(s) approved, including with any adjustments that were required. We further authorise NED University of Engineering and Technology to duplicate this project in hard copy or electronic format and disseminate it.

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Statement of Contributions

Each member of our team has made significant contributions to our project, bringing their unique expertise and dedication to the table, ensuring its success through meticulous planning, execution, and collaboration.

Tanazzah Rehman's exceptional management skills were the cornerstone of our project's smooth coordination and progress across all stages. Utilizing Jira for agile project management, she ensured that tasks were clearly defined, assigned, and tracked, allowing the team to stay aligned with the project schedule and deadlines. Her expertise in 3D GAN architecture was pivotal; she applied advanced techniques for feature scaling and optimization, followed by transfer learning to enhance the model's performance. Her strategic approach not only streamlined our 3D object preprocessing but also significantly improved the efficiency and accuracy of our AI training and model optimization processes.

Muskan Fatima played a crucial role in the pre-processing of 2D data. She adeptly converted DICOM to PNG format, ensuring the data was in a usable state for further processing. Muskan also applied cropping, resizing, and conversion to NIfTI format, enabling the creation of 3D models. She fine-tuned several algorithms to optimize data processing and performance, and her meticulous documentation of these processes ensured clarity and efficiency in our workflows. Through GitHub, she maintained a well-organized repository, facilitating seamless collaboration and version control among the team members.

Mir Arshan Ali's efforts were pivotal in bridging the gap between our backend models and the user interface. He took charge of training the initial models and seamlessly integrating them with our UI, ensuring a cohesive and functional user experience. Arshan designed the front-end using Bootstrap, HTML, and CSS, creating a responsive and visually appealing interface. He also managed the 3D rendering of models on the web, providing users with an interactive and immersive experience. His comprehensive documentation, stored and maintained on GitHub, serves as a valuable resource for future reference, ensuring that our project's knowledge base is well-preserved and easily accessible.

Executive Summary

This report was written to call the attention of relevant stakeholders to the dire necessity of enhancing the diagnostic accuracy and treatment outcomes of glioblastoma, a highly fatal malignant brain tumor. The present-day diagnostic technique includes tissue biopsies for genetic investigation that can pose a huge burden to the patient besides offering scant therapeutic possibilities. In order to address these challenges, the current research study, ''Advancing Radiogenomics: AI enabled Glioblastoma Subtype Prediction'', uses radiogenomics and AI to identify glioblastoma genetic subtypes based on non-invasive imaging biomarkers (MRI).

The past researches restores the imperfection of the existing diagnostic system and reveals the possibilities that lie in AI and radiogenomics to change the approach to glioblastoma. Implementing the use of 3-Dimensional AI algorithms, the project seeks to increase diagnostic accuracy, intensity of ideal treatment, and reduce the likelihood of invasive process hence better patients outcomes the necessary invasive procedures.

It also entails data collection and preparation; Their approach is to obtain a range of MRI datasets, and the ensuing data is preprocessed for assessment. In the context of images derived from MRI scans, there is transformation from two-dimensional to three-dimensional models that provides a means for model training via 3DCNN and Conv3D machine learning algorithms. Given model performance measures include accuracy, sensitivity and specificity and the views emphasized include interpretability with clinician's validation.

Key discoveries show how deep learning techniques effectively infer glioblastoma genetic subtypes from MRI images with high coordinates of accuracy and specificity. The models prove to be efficacious and versatile for different patient profiles while establishing future uses of the app in clinical setting. Explainable models augment the reliability and accessibility of a model among doctors by offering an understanding of predictions.

Acknowledgments

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List of Abbreviations

1. **AI:** Artificial Intelligence
2. **GB/GBM:** Glioblastoma
3. **3D:** Three Dimensional
4. **CNN:** Convolutional Neural Network
5. **SDG:** Sustainable Development Goals
6. **MRI:** Magnetic Resonance Imaging
7. **CT:** Computed Tomography
8. **BM:** Brain Malignancy
9. **FLAIR:** Fluid Attenuated Inversion Recovery
10. **T1W:** T1-weighted
11. **T2W:** T2-weighted
12. **T1WCE:** T1-weighted with contrast enhancement
13. **DICOM:** Digital Imaging and Communications in Medicine
14. **PNG:** Portable Network Graphics
15. **NIfTI:** Neuroimaging Informatics Technology Initiative
16. **L2:** L2 Regularization
17. **17. Resnet:** Residual Network
18. **HTML:** Hyper Text Markup Language
19. **WebGL:** Web Graphics Library
20. **WSGI:** Web Server Gateway Interface

United Nations Sustainable Development Goals

The roadmap to a brighter and more sustainable future for everybody is found in the Sustainable Development Goals (SDGs). They tackle the world's problems, such as injustice, poverty, inequality, and environmental degradation as well as peace and justice. The list of SDGs is 17 in total, as follows. Verify the relevant SDGs for the project.

☐   No Poverty

☐   Zero Hunger

■   Good Health and Well being

■   Quality Education

☐   Gender Equality

☐   Clean Water and Sanitation

☐   Affordable and Clean Energy

☐   Decent Work and Economic Growth

■   Industry, Innovation and Infrastructure

☐   Reduced Inequalities

☐   Sustainable Cities and Communities

☐   Responsible Consumption and Production

☐   Climate Action

☐   Life Below Water

☐   Life on Land

☐   Peace and Justice and Strong Institutions

■   Partnerships to Achieve the Goals

Similarity Index Report

Following students have compiled the final year report on the topic given below for partial fulfillment of the requirement for Bachelor's degree in Software Engineering.

Project Title: **Advancing Radiogenomics: AI Enabled Glioblastoma Subtype Prediction**

S. No.	Student Name		Seat Number
1.	Tanazzah Rehman		SE-20083
2.	Muskan Fatima		SE-20090
3.	Mir Arshan Ali		SE-20063

This is to certify that Plagiarism test was conducted on complete report, and overall similarity index was found to be less than 10%, with maximum 3% from single source, as required.

Signature and Date

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Sana Fatima

G20_glioblastoma_final_formatted.pdf

Chapter 1

Introduction

1.1 Background Information

Glioblastoma is among the most aggressive and challenging brain tumors to treat, with a poor prognosis and limited treatment options. Current diagnostic methods often involve invasive surgeries for genetic analysis, which not only pose risks to patients but also limit the accessibility of timely and accurate diagnoses. The exact cause of GBM is unknown, but some risk factors include genetic disorders particularly change in MGMT (MethylGuanine MethylTransfarese), previous radiation therapy, exposure to certain chemicals, and viral infections. GBM can occur at any age, but it is more common in older adults and males. GBM symptoms depend on the location and size of the tumor, but they may include persistent headaches, nausea, vomiting, blurred vision, seizures, memory loss, personality changes, and weakness. There are diagnostic procedures for entertaining the case of GBM, which include imaging techniques such as MRI or CT scan and biopsy that focuses on the tumor tissues. It is usually aggressive, not responsive to treatment and has an unfavorable prognosis because of infiltrative growth and frequent post-treatment relapses and metastases [1]. Surgery, radiation therapy, chemotherapy, and tumor treating fields therapy are the treatments that are commonly favored for the treatment of the disease. In this sense, based on the data provided by the World Health Organization, the incidence of GBM around the world is 3%. The new cases of COVID-19 per day in the United States were 214,255 in January 2021, and the case fatality rate was 21 per 100,000 population in 2020, while the global mortality rate was 2. 81 per 100,000 population. In the United States, GBM constitutes roughly 47% of all malignancies, and almost 90% of all primary brain tumors. An estimated 24,810 new cases diagnosed and is the 7th most common primary malignant brain tumor with approximately 18,990 deaths predicted for 2023. The estimated survival time is 15 to 18 months median and the five-year survival is approximately 10% [2]. GBM form roughly 9% of all brain tumour s and 38% of all gliomas the Pakistan having 781 new reported in 2019. The median survival time of the patients is 3 days. 5 to 5. It may take 5 years for

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the cancer to kill the patient, and the five-year survival rate is about 19%. 4% [3]. The observation for the treatment and result of GBM in Pakistan is considered based on factors, which include accessibility to health care facility as well as available resources and socioeconomic characteristics. Genomic classification is an important tool in the characterization of these tumours, not only for the design of therapeutic options but also for understanding survival prognosis. But in genetic analysis, traditional methodologies are slow, expensive and often accompanied by complications involving tissue biopsy. There is therefore a requirement for techniques that can diagnose glioblastoma without any invasiveness and it effective treatments.

1.2. Significance and Motivation

This involves the context of the project where through the work reported here, the objectives of diagnosing glioblastoma and developing an effective treatment plan may be achieved. With the use of radiogenomics and machine learning features, we would like to reveal the MRI patterns that are associated with glioblastoma genetic subtypes. This approach will not only eventually lead to lightening the burden placed on patients but will also provide more accurate and subsequent treatment plans and as such add to the survival rates of patients. In addition, by fostering the development of AI tools and guidelines related to the field of health, it aids in the pursuit to utilize technology to address complex medical issues

1.2.1. Medical Diagnosis and Treatment Enhancement:

The general purpose of the project is to make this process extremely precise and accurate by enhancing the methods currently used to diagnose brain tumor. Utilizing this system, accurate discernment of tumor kind will enable the physicians to book surgeries, radiation therapy, and monitor the efficacy of the therapies planned. This would prove helpful in the management of patient care, and perhaps reduce the risks of invasive procedures.

1.2.2. Clinical Application:

The use of the built AI system in the clinical project is also part of the scope of work. For radiologists and oncologists, it can be integrated into existing medical imaging software available in the market today or stand alone on its own. These findings could potentially

help to advance the use of diagnostic tests by increasing the efficiency of the process and making significant information about the features of the cancer attributes available to physicians.

1.2.3. Research Contribution:

In addition to the clinical impact of the project, there are two major areas of research that the project will greatly benefit: the advancement of medical imaging and the development of artificial intelligence. It may result in the creation of new algorithms; novel mechanisms of processing images; and effective AI models that can be used to tackle other problems in the field of medical imaging apart from brain tumors.

1.2.4. Data Collaboration:

Besides the therapeutic intent, the ministry has the opportunity to significantly advance the area of medical imaging and artificial intelligence.

1.2.5. Global Healthcare Impact:

Since the technology produced can be used at any given location in the world to increase the chances of diagnosing and/or treating brain tumours, this project's future may therefore possibly go fully global. Perhaps, by providing the top diagnostic technologies to parts of the world that have low access to specialized medical personnel, it can help in minimizing healthcare disparities.

1.3. Aims and Objectives

The specific goal of this study is to create and assess the effectiveness of AI approaches to predict glioblastoma's genetic subtypes from MRI images. Specific objectives include:

- AI Algorithm Implementation:

Develop and optimize deep learning models for diagnoses of genetic subclass of Glioblastomas based on MRI scans.

- Performance Enhancement:

Implement new and re-developed machine learning and deep learning algorithms so as

to refine the accuracy and feasibility of the given predictive model.

- Algorithm Evaluation:

Conduct thorough assessments and benchmarking of AI models to track their performance over time, focusing on accuracy, precision, and robustness.

- Methodological Advancements:

Explore and develop novel methodologies and approaches in radiogenomics to advance the accuracy and precision of genetic subtype predictions.

- Model Iteration:

Implement iterative model development, making regular updates to adapt to emerging technologies and research findings.

- Data Enhancement:

Investigate techniques to improve the quality and quantity of data used for training and testing, potentially including data augmentation and fusion.

Investigating the potential impact of AI-based glioblastoma diagnosis on treatment planning and patient outcomes.

1.4. Methodology

1.4.1. Data Collection and Preparation:

- Gather a comprehensive dataset of MRI scans from glioblastoma patients, ensuring it includes a diverse range of cases with various types and sizes of tumors. Ensure the dataset includes information about MGMT promoter methylation status, genetic subtypes, and clinical outcomes.
- Preprocess the collected data to standardize image quality, resolution, and format for consistent analysis.
- Dataset can be gathered through Kaggle and other online sources

1.4.2. 3D Object Formation:
- Forming 3D Objects from set of 2D images
- Applying preprocessing techniques on 3D objects

1.4.3. Model Selection:
- Choose appropriate machine learning models and features for classification (3DCNN, Conv3D, MaxPool3D) for image analysis.
- Explore and compare different algorithms, considering their pros and cons.

1.4.4. Model Training:
- Split the dataset into training, validation, and test sets.
- Train the chosen models on the training data while optimizing hyperparameters.
- tilize techniques like data augmentation to increase model robustness.

1.4.5. Evaluation:
- Assess the model's performance using appropriate evaluation metrics (e.g., accuracy, sensitivity, specificity, AUC). It should detect tumors within the 3D reconstructions generated from MRI scans.
- Perform cross-validation to ensure the model's generalizability.

1.4.6. Interpretability:
- Implement techniques for explaining model predictions, such as saliency maps or feature importance analysis, to understand what the model is learning.

1.4.7. Clinical Validation:
- Collaborate with medical experts to validate the model's predictions against real clinical outcomes.
- Ensure the model's utility in real-world scenarios.

1.4.8. Performance Optimization:
- Fine-tune and optimize the AI model and algorithms to improve the speed and efficiency of tumor detection.

- Collect feedback from clinicians and patients to refine the model.
- Keep the model up to date with evolving medical knowledge and technologies.
- Address potential challenges such as noise reduction, artifact correction, and handling variations in scan quality.
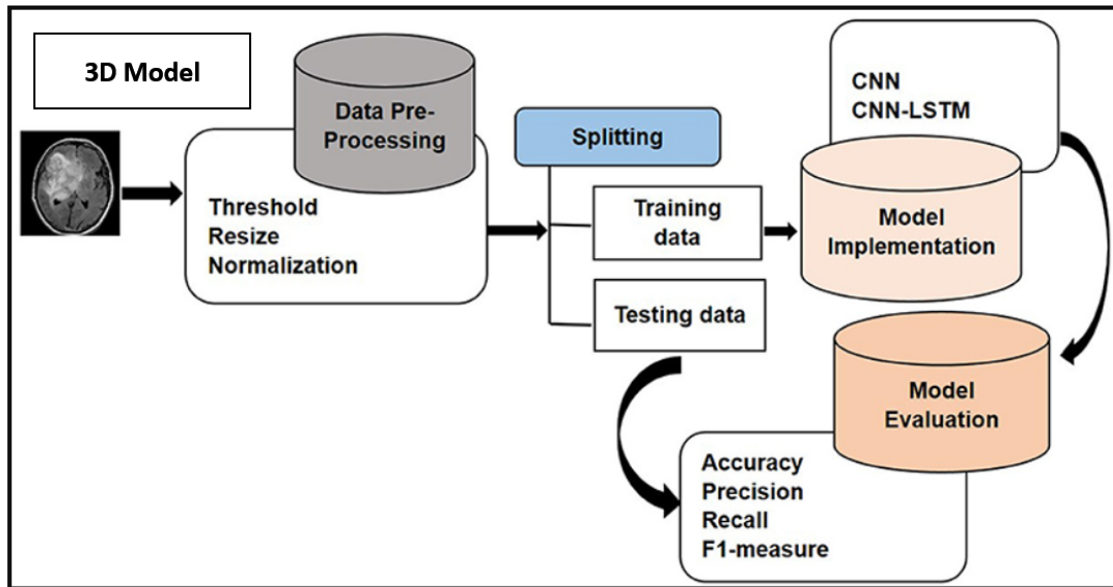
Figure 1 High Level Flow Chart of Project

1.5. Beneficiaries

1.5.1. Medical Staff

It is an advantage for radiologists, neurosurgeons, and oncologists to have better diagnostic tool as it will take less time as well as will be accurate. Expectant solutions to be helpful in treatment planning, performing surgical operations with less invasive procedures, and evaluating the progress.

1.5.2. Technical Companies

This can be of great interest to companies that research and build medical imaging and AI software products. It makes business sense because they could acquire or integrate our AI technology into their products, improving them.

1.5.3. International Organizations

Global healthcare entities like WHO that strive to narrowing the gap may find our project promising since it has a potential to aid in achieving their goals.

1.5.4. Patients

Global healthcare entities like WHO that strive to narrowing the gap may find our project promising since it has a potential to aid in achieving their goals.

1.6. Project Schedule

The process of the project went through certain phases and steps: the very first step was the Project Initiation that began on October 1, 2023; the last phases were the Research and Reporting that was completed by July 10, 2024. Over the course of the first stage the team worked out such preliminary essential factors as project scope and goals, as well as methodology for the following stages. Data Collection followed from October 26, 2023 to November 15, 2023 and in this phase, available data sources were determined as well as a glioblastoma MRI dataset was carefully collected and evaluated for its quality. Data Preprocessing was performed next in the period that ranged between November 15, 2023 to December 20, 2024 Clean up, conversion, and the derivation of new features were all performed as well as creative steps such as the development 3D objects and data augmentation. The AI Model Development phase was followed by Algorithm Development and Performance Optimization phases, which were implemented in a sequential manner in which design and development processes were comprehensively and systematically structured to address the specific objectives of fine-tuning algorithms, fine-tuning models, and optimizing performance at scale. Lastly, there is the research and reporting phase, which will entail the actual analysis of data gathered, documentation, preparation of reports and presentations to stakeholders, and Done, marking the end of a highly systematic and coordinated effort.
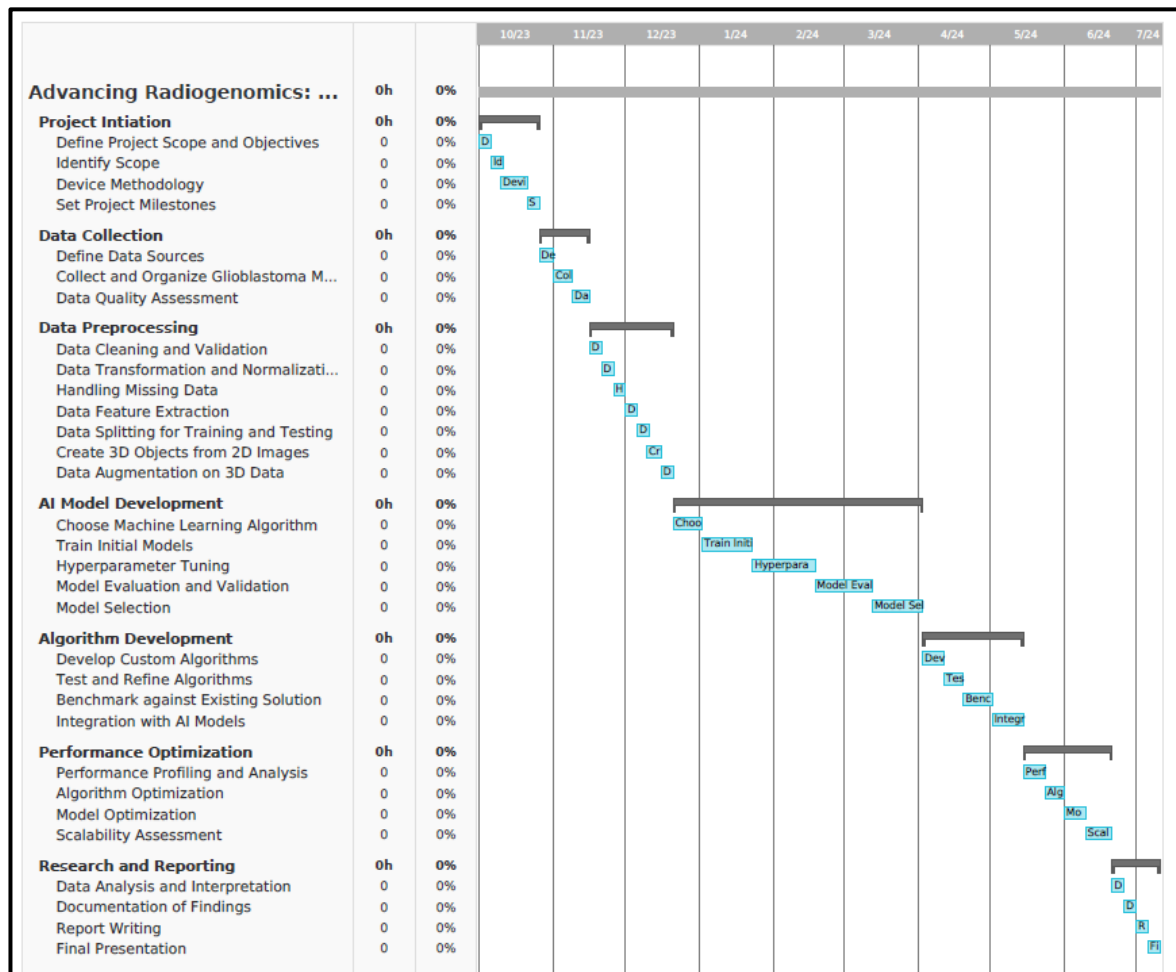
Figure 2: Gantt Chart

1.7. Report Outline

The report will provide a comprehensive overview of the project, including detailed descriptions of the related work, tools and techniques, methodology, conclusions, and recommendations for future research. Additionally, it will discuss the potential impact of the developed AI algorithms on glioblastoma diagnosis and treatment, as well as opportunities for further exploration in the field of radiogenomics and AI in healthcare.

Chapter 2
Literature Review

2.1. Introduction

Glioblastoma (GB) is a high-grade astrocytoma with a close proximity to the brainstem and an aggressive phenotype, thus posing diagnostic and therapeutic conundrums. Among these issues, Artificial Intelligence (AI) assumes the position in the realm of discussion to completely transform diagnostic imaging of healthcare. The educational promotion of artificial intelligence as a part of the medical profession represents a distinct avenue toward the processing of data and quantitative analysis within medical practice, especially in the radiological field. While there are promising studies that utilize AI algorithms in the healthcare field, the practical implementation of AI remains problematic due to the inability to integrate it into the existing work environment of most hospitals. Despite this, it can be identified that AI has the ability to act as a helpful and indispensable tool for clinicians, improving both customization and productivity [4]. Thus, advancement of AI techniques signifies their increased relevance to the medical imaging field and demonstrates their applicability toward solving the challenges of GB diagnosis and treatment.

2.2. Advances in Glioblastoma Imaging using AI

The role of AI in the context of brain tumor diagnosis can be to complement or perhaps even fully replace more invasive biopsy techniques with the help of both radiomic and non-radiomic signatures. Thus, the mature technology of deep learning belongs nowadays among the most frequently evaluated and applied artificial intelligence techniques within the medical diagnostics. For instance, Pasquini et al. [5] tried to build a subjective DL method that can be applicable for glioblastoma (GB) prediction of IDH mutation status as well as to distinguish between IDH-mutant and IDH-wildtype GB. Of these two general GB subtypes, it is important to distinguish between them because the GB subtypes have different proportions (90% of IDH-wildtype and 10% of IDH-mutant) and different survival rates of the patients (15 months for patients with IDH-wildtype, 31 months for patients with IDH-

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mutant) thus impacting on the decision making for the patients. Therefore, the need for noninvasive diagnostic approaches replaces the conventional biopsy approaches has led to the emergence of an even greater interest of AI usage in neuroradiology. With 83% maximum accuracy in differentiating the IDH status, the DL method is strengthened as a ground-breaking tool in the clinical application of radiomics. Considering these developments, precise determination of tumor type becomes imperative for subsequent patient treatment [6].

There are divergent views regarding the surgical management of GB based on the findings obtained from imaging; while some would prefer biopsy only in cases that are clinically indicted, the other group would recommend aggressive surgery involving the resection of all contrast enhancing lesion seen in MRI scans of these patients. In a study by Marcus et. al[7] in 2020, an Artificial Neural Network (ANN) was introduced to predict prognosis after an operation by adding some specifics of the anatomical parameters of the formation of tumors and the risks of neurological deficits. ANN, a type of machine learning which is found more suitable for small dataset inventories, was found exhibit better predictive capability than standard systems.

However, GB's infiltrative character and multiforme distribution across the brain raises obstacles in tumor demarcation, lesion resection, and radiation therapy, compounded by intratumoral heterogeneity, which may not be fully resolved by conventional MRI techniques. Although integration of AI with multiparametric imaging to predict tumor cell infiltration has been brought up, there is a need for indicating its practical value [8]. While such a strategy has been suggested for enhancing the extent of tumor resection, as well as for individual optimization of radiotherapy, further work needs to be done in order to determine whether or not its utility is real and whether it can be implemented efficiently in terms of financial and availability concerns.

Moreover, such a tumour being highly invasive and infiltrative, GB increases the risk of early recurrence after conventional treatment. Using the prediction model of early relapse by preoperative radiomics MRI assessments for GB patients, Wang et. Al. [9] indicated that this model can help stratify treatment planning of patients with GB characteristics. Moreover, Shim et al. [10] designed two neural networks models for the prediction of local and distant

recurrence after maximal surgical resection on GB patients. While the current study has its limitation due to the retrospective design and the limited number of cases, the approach that this study illustrates may set the stage for prospective multicenter future investigations and improvements.

2.3. AI in Differential Diagnostics of Glioblastoma

The current gold standard in identifying cerebral lesions usually requires pathological examination at which there are some drawbacks[11]. Nevertheless, the current research drop in AI has produced different radiomics, ML, and DL models that can non-invasively assess brain tumor characteristics using MRI features. Overall, these models may be deemed as having a potential in diagnosis enhancement and differentiation of various types of cerebral lesions. Glioblastoma (GB) and medical brain metastases (BM) are the two most prevalent brain malignancies, which need different approaches. The initial treatment of GB is mainly surgical with the goal of maximal tumor resection, followed by radiation therapy and temozolomide while treatment of BM mainly consists of stereotactic radiosurgery [12]. Specifically, the small sample size and similarities in radiological appearances of GB and BM make differentiation between the two-entity using routine brain MRI examination in clinical practice difficult [13]. While there are more developed MRI markers which can enhance this differentiation, none of the markers offers the necessary level of accuracy to guide clinical decisions based on MRI scans. The analyses of high-dimensional MRI sequences of brain tumors by ML techniques have demonstrated its capability to extract meaningful radiomics characteristics and classifiers that distinguish between the benign and malignant brain lesions easily, which can help the clinicians in diagnosis [14]. Figure 3 indicates that many papers have been published in the last few years with an effort towards employing AI for the differential diagnosis of GB and BM. Thus, other lesions known as BM also pose diagnostic worries in imaging differential diagnosis of GB. Despite the means employed by MRI in differentiating GB from PCNSL occasionally both of these pathologies may appear to be quite similar. The significance of using artificial intelligence, specifically, the use of machine learning in interpreting medical images, continues to escalate because this application can save patients from needless invasive procedures while freeing up the time of practitioners. McAvoy and colleagues [15] further created CNN to allow the brain to learn to identify relevant image features necessary for good classification, reaching 91–92% accuracy on GB and PCNSL in CE-T1W images. By incorporating these models into the

diagnostic process in conjunction with radiologists, highly diverse clinical diagnosis capacities are achieved, which play a vital role in patient management. Table 1 provides papers that are appeared in the construction of Figure 3 and the result of each of the seven AI models to be compared.
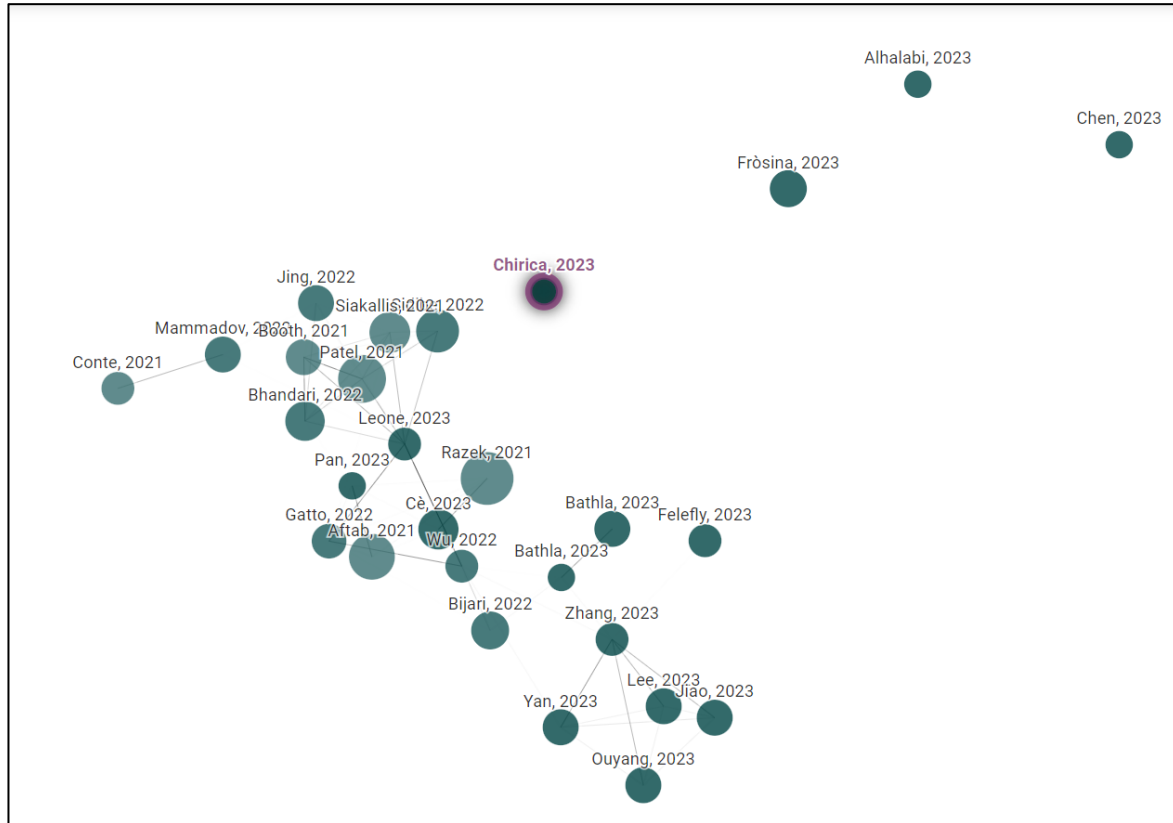
Figure 3: Connected Papers for AI based Glioblastoma detection

Table 1: Related Papers of AI Based Glioblastoma Detection

Study	Purpose	No. of Patients	Training Cohort / Validation Cohort	MRI Sequences	Features Extracted	Results
[16]	The use of deep CNN in conjunction with radiomics features acquired from MR-based oxygen metabolism (oxygen metabolic radiomics) to distinguish between GB and BM.	133	99/34	FLAIR, CE-T1w, DWI, GE-DSC perfusion	74	Compared to radiologists' evaluations, one-dimensional CNN surpassed human reading and showed superior diagnostic performance when it used radiomics features taken from the brain metabolic rate of oxygen as inputs.

[17]	The classification of GB and BM using appropriate radiomics models in accordance with MRI sequences.	91	50/41	T1WI, T2WI, CE-T1w, FLAIR	107	Gliobastoma and BM can be reliably classified using machine-learning based on radiomics.
[18]	Using DTCWT on regular MRI to distinguish GB from BM using a radiomics-based machine learning technique.	51	27/24	DWI, ADC, FLAIR, T1WI	264	By using DTCWT, it has been shown that it is technically possible to extract features from a picture and reduce its dimensions with excellent results, which makes it possible to distinguish between GB and BM.
[19]	Application of machine-learning methods based on radiomics to distinguish between GB and BM	120	60/60	T1WI, T2WI, FLAIR, DWI, ADC, CE-T1w	1070	In the majority of the top-performing models for every sequence combination, the diagnostic performance was between AUC 0.936 and 0.953.
[20]	GB and BM may be distinguished using a deep-learning based model.	527	445/82	T1WI, T2WI, CE-T1w, FLAIR	265	The potential for machine learning algorithms to perform as well as or better than human readers in terms of diagnosis could assist overcome prejudice and human error in the interpretation of medical images.

2.4. 3-Dimensional AI for Glioblastoma Detection

Three dimensional artificial intelligence (AI) is emerging as a top edge application in medical imaging and diagnostics, especially in the context of glioblastoma tumor identification due to the availability of better 3D medical data analysis and interpretation. Current approaches under this field are diverse, encompassing a broad range of methods and techniques such as the 3D convolutional neural networks (3DCNN) that is ideal for dealing with volumetric data like the MRI images. In contrast, traditional 2D CNN takes only the 2D image slices as input for analysis, while 3DCNN can directly model the spatial relations and structure of the whole volume; therefore, 3DCNN is suitable for the tasks that demand three-dimensional contextual understanding, such as tumor detection and segmentation.

Albeit numerous, one such research work provides an extensive bibliometric analysis of detection techniques of brain tumors that involves anatomy of brain tumors, enhancement techniques of the tumor region, and deep learning technique for the classification of brain tumor. In addition, the focus more detailed research explores the creation and assessment of

deep learning structures that are magnetic resonance imaging (MRI) based that include UNet and Deeplabv3, signifying the structures' capacity to provide a finer technique for rendering distinguishable between glioblastoma tumors and the normal brain tissue with technique precision and computational speed[21]. Some of these techniques include the use of generative adversarial networks (GANs) in 3D frameworks such as Pix2Pix and Vox2Vox, and these methods can be used to generate synthetic images and segmentations of glioblastoma tumours [22]. It is quite clear that this technique not only help in the augmentation of data but also give insight in to the specific tumour nature and how it grows.

Apart from computational approaches, innovative studies provide insight into discovering new directions with an emphasis on the bioprinting technology with the help of printing the whole functional active glioblastoma tumors. Researchers using bio-inks made of glioblastoma cells, ECM, and hydrogel have been in a position to create realistic organosheets that well depict real-life tumors in terms of structural and functional characteristics [23]. Such bio printed models have a potential to create a scaffold for investigating tumor microenvironments, invasion biology and therapeutic response that is amenable to translation into clinical practice.

Together, these papers do not only highlight the great promise of 3D AI in glioblastoma management, but also bring new knowledge and ideas into improving diagnostic and prognostic accuracy, as well as personalized treatment strategies. The combination of 3D AI techniques can significantly enhance the advancement of the existing research in this area and bring a new approach to clinical practice, enhancing healthcare and offering better outcomes for patients.

A comprehensive literature review was conducted using Scopus to gather research publications on glioblastoma, brain tumors, and the application of artificial intelligence (AI) in these areas. The search queries included various keywords to ensure a thorough investigation: "glioblastoma," "glioblastoma multiforme," "GBM," "artificial intelligence," "AI," "computer detection," "machine learning," "deep learning," "brain tumor," "brain tumour," "neuro-oncology," "3D," "three-dimensional," and "3-dimensional." By combining these terms in different configurations, the search aimed to capture a wide range of studies

related to AI's role in detecting and analyzing glioblastomas and other brain tumors, specifically focusing on three-dimensional approaches. Our first query was (TITLE-ABS-KEY("glioblastoma" OR "glioblastoma multiforme" OR "GBM")) as shown in figure 4. There have been over seven thousand papers in 2023 and more than 50 thousand papers in last 20 years. The domain was narrowed to AI in healthcare for brain tumors by searching the query (TITLE-ABS-KEY("artificial intelligence" OR "AI" OR "computer detection" OR "machine learning" OR "deep learning") AND TITLE-ABS-KEY("brain tumor" OR "brain tumour" OR "neuro-oncology"))

Which showed a graph as in figure 5 that tells around 1700 papers have been published on this topic in 2023 and around 5000 papers in last 20 years. When talking about 3-dimensional AI particularly in Glioblastoma our search query, (TITLE-ABS-KEY ("3D" OR "three-dimensional" OR "3-dimensional") AND TITLE-ABS-KEY ("artificial intelligence" OR "AI" OR "computer detection" OR "machine learning" OR "deep learning") AND TITLE-ABS-KEY ("brain tumor" OR "brain tumour" OR "glioblastoma" OR "GBM")) highlighted that out of 8000 papers on brain tumor and 1700 papers on AI in brain tumour, only 250 papers were published in 2023 about 3D AI for glioblastoma. The search results provided a detailed overview of global research activity, which was visualized in Figure 4, illustrating the distribution of publications by country or territory where 32 papers were written by Pakistan in 3D AI for Glioblastoma tumor. This methodology ensured a robust and comprehensive review of current advancements and research trends in the application of AI to neuro-oncology.
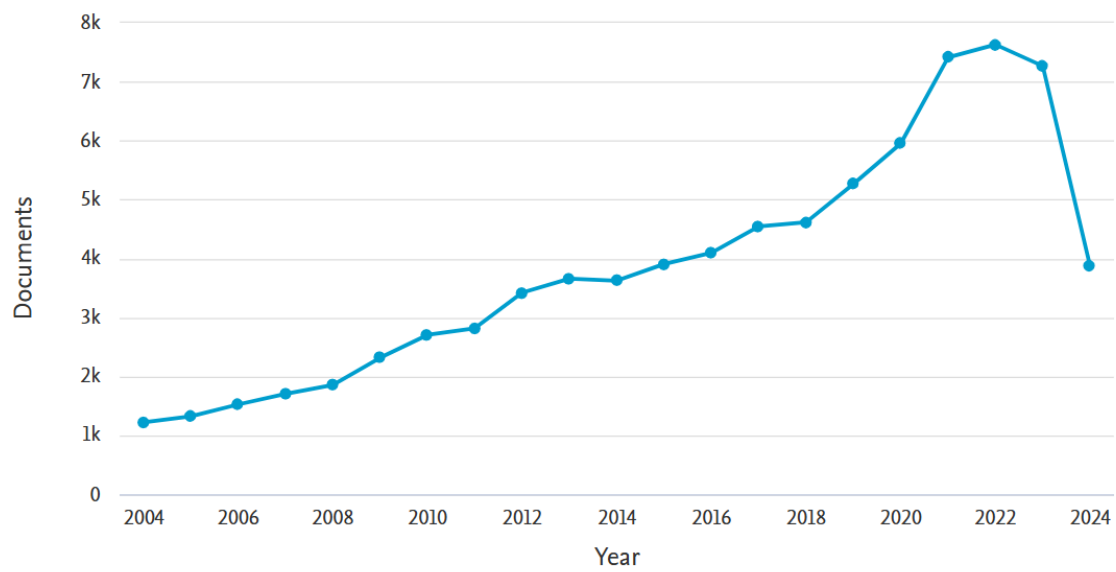
Figure 4: Documents about brain tumor published in last 20 years
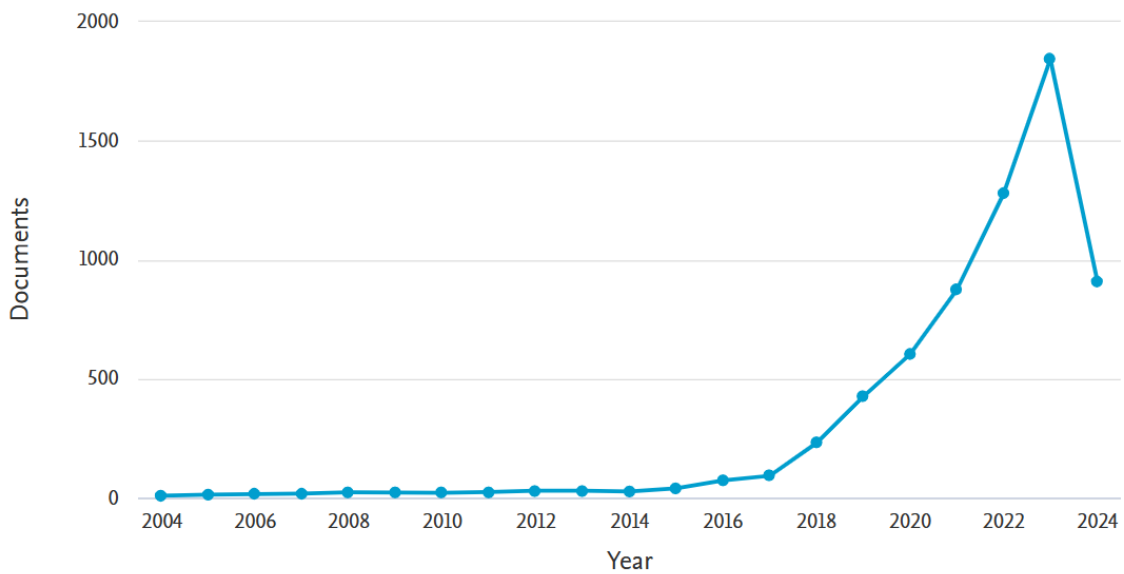
Figure 5: Documents about AI in brain tumor published in last 20 years
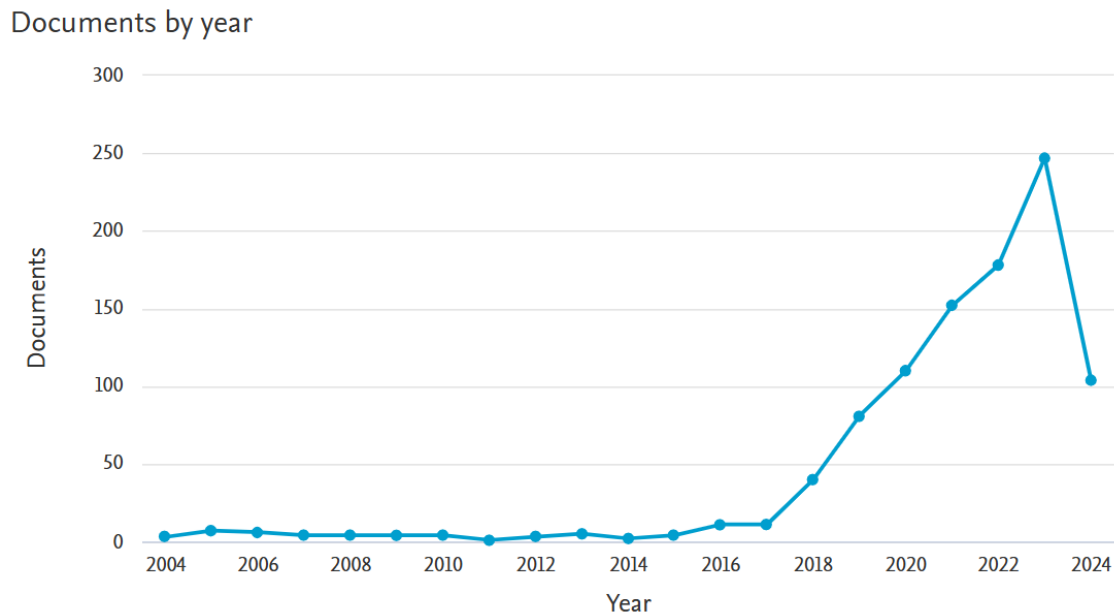
Figure 6: Documents about 3D AI for Glioblastoma published in last 20 years
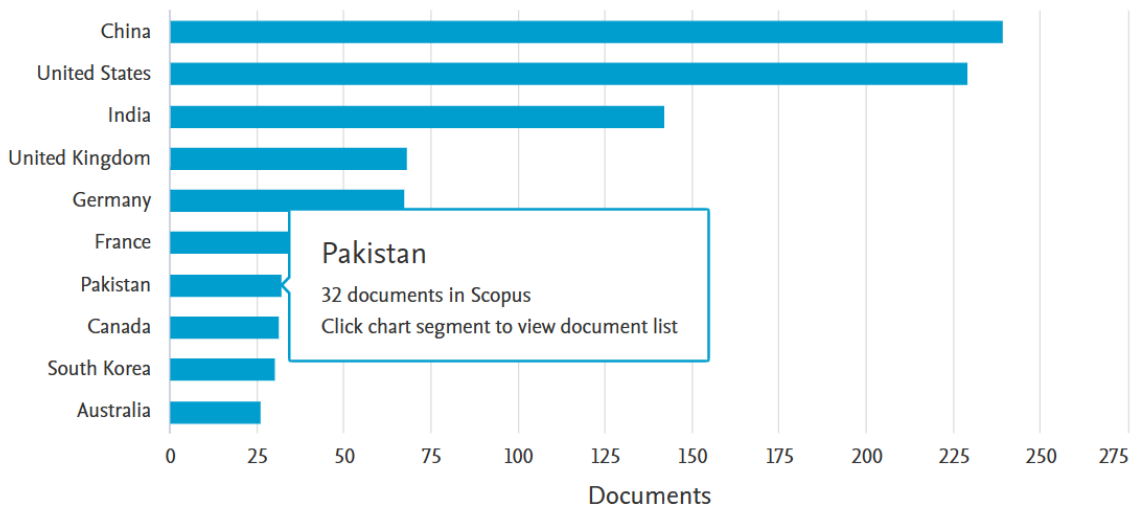
Figure 7: Research Publication on Glioblastoma by Country or Territory in last 20 years

2.5. Summary

A selection of current articles discussing the advances of artificial intelligence (AI) in medical imaging specifically on glioblastoma (GB) show that more developments in this field aims to tackle major issues regarding accurate diagnosis and assessment of tumor characteristics for treatment planning. Raw data from conventional and/or advanced MRI

have shown good results in assessment of essential molecular characteristics of GB, including accurate identification of the IDH mutation using powerful DL algorithms. ML algorithms, focused primarily on CNNs, provide accurate and discriminating separation between GB and BM, proving valuable in helping clinicians determine treatment strategies without resorting to invasive procedures. Furthermore, novel 3D Artificial Intelligence approaches are introduced as 3D convolutional neural networks and generative adversarial networks to apply latest advances in formal tumor detection and segmentation based on MRI in combination with advanced bioprinting strategies aimed at generating tumor models. All these combined innovations can be thought of as a sea change in neuro-oncology with potentials of better focusing diagnosis and treatment plans for the patient.

Chapter 3
Tools and Techniques

3.1. Introduction

There is a set of apt tools and techniques that need to be adopted accurately and efficiently for the glioblastoma detection based on artificial intelligence. In this chapter, emphasis is laid on various tools and different technology that are normally used within this field starting from programming languages to project management system like the Jira or the Python language. Of the tools discussed each plays a major part in varying degrees of the glioblastoma detection process; data preprocessing, model building and deployment, as well as making collaboration with other professionals easier. The following tool discusses the fundamental aspects as well as the benefits of employing these tools so that the researchers and developers can improve the efficiency of their functional structures and increase the pace of research for improving the glioblastoma detection methods.

3.2. Python:

Python is a general-purpose language renowned for use in the development of AI and machine learning because of its software libraries. Forest plots can be made using R and other statistical tools that can analyze the data and produce the desired plots of the forest. Due to that, it is suitable for several applications, particularly as a scientific tool and in production code.

3.3. Jira:

Jira is an online tool employed in AI-aided glioblastoma treatment projects to monitor the tasks assigned in the project and manage any issues arising within a team. Organizational functions encompass how to arrange work processes, distribute tasks, and then monitor the process, making sure that the project is still on track and each participant is aware of the project's status.
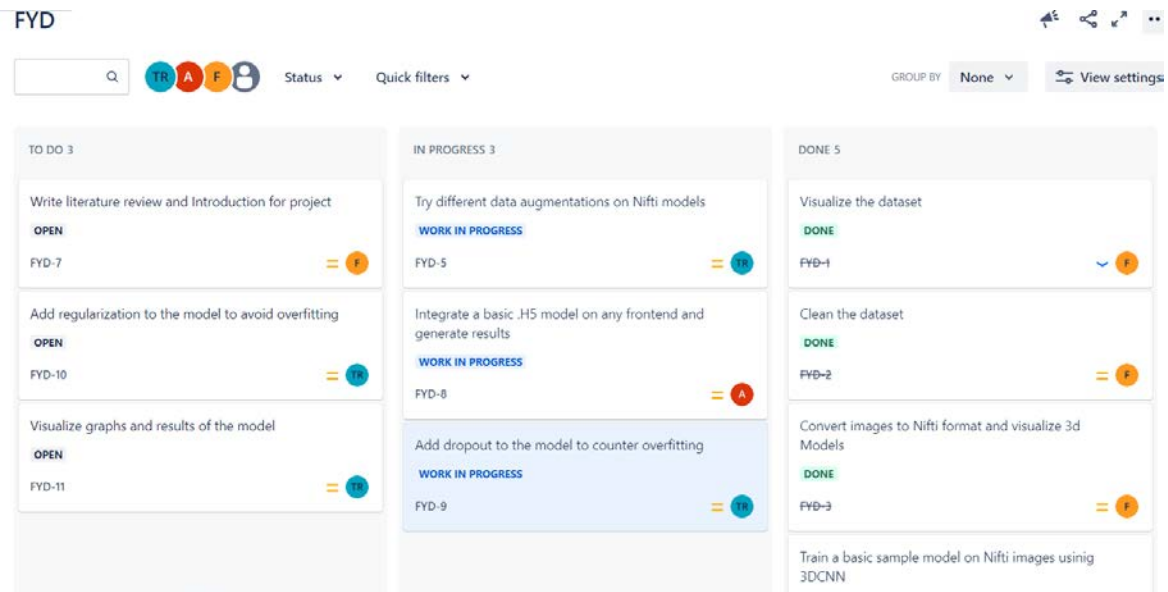
Figure 8: Jira setup for the team

3.4. GitHub:

GitHub is a popular service for managing versions and collaboration on code within teams carrying out various software projects, including those associated with glioblastoma and its identification using artificial intelligence. It let the researchers and developers to create the space where the code is stored to share with other members of the team, analyze the changes, manage the code reviews and more. GitHub also helps support an open source culture where people can easily share and work together on ideas and information with other researchers internationally.
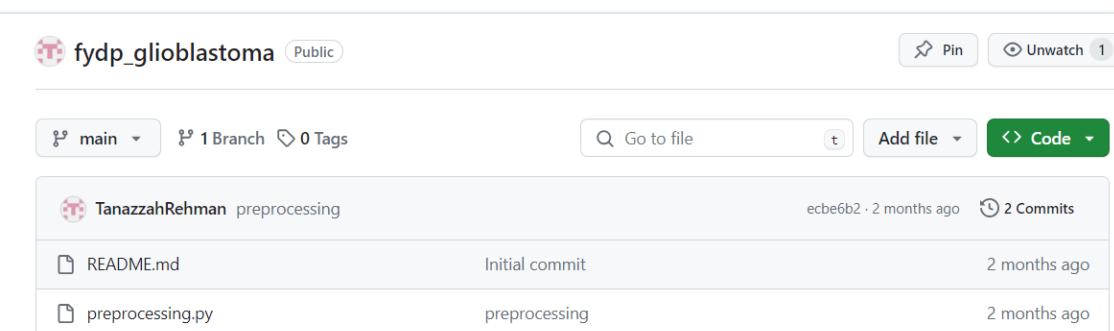
Figure 9: GitHub setup for the team

3.5. Google Colab:

Google Colab offers a custom cloud environment for the execution of Python programmes, which is particularly useful in machine learning applications and AI. This service provides users with free access to GPU and TPU hence making it suitable to train deep learning models with big data sets often used to detect glioblastoma. Google Colab also seamlessly works with almost all Google products such as Google Drive making it easier to store data and work with other teams.

3.6. Kaggle:

Kaggle is a website featuring competitions, datasets, and notebooks for data scientists. It deals with the proceedings of various domains and includes health and medical imaging so it when it comes to glioblastoma detection, it may be of great use. Project's participants can use datasets, discuss and also share codes; using the Kaggle community to promote the advancement of research in the field.

3.7. Jupyter Notebook:

Jupyter Notebook is an interactive computing environment that allows researchers to create and share documents containing live code, equations, visualizations, and narrative text. It is widely used in glioblastoma detection research for exploratory data analysis, model development, and documentation of results. Jupyter Notebooks support multiple programming languages, including Python, making them versatile tools for collaborative research.

3.8. MLflow:

Jupyter notebook allows the creation of texts containing the actual code, math formulas, graphics, along with the interactive discussion by running code in the text in real time. It has been incorporated in glioblastoma detection study to conduct exploratory analysis, build supervised models, and write reports. Jupyter Notebooks are programmable environments that accept a variety of code languages, all of which encompass Python.

3.9. Torch:

Torch is an open-source environment that is used for the machine learning novel deep learning research and development. Tensor computations are one of its primary

specialties and this framework is very well-optimized for both CPU and GPU. Torch is also used often for implementing of neural network because it possesses a dynamic computation graph which makes modeling and debugging easier. Concisely, in the area of 3D AI, Torch has some benefits such as torch has exceptional performances when it is dealing with the nested structures of data and it works well with high-dimensional data set. For this reason, it is optimal in the use case scenarios that require spatial relations and volumetric information including three-dimensional picture recognition, computational medical imaging and identification of three-dimensional objects. Moreover, the library comprises PyTorch3D, a tool that strengthens the library's capacity in handling 3D data and models in its diverse ecosystem.

3.10. Tensorflow:

TensorFlow which has been created by a team at the Google Brain is actually a robust open-source platform for machine learning. It is highly scalable which means that it can be used in research institutions and production facilities. As for TensorFlow, it includes many tools, libraries, and references for building and running machine learning solutions. This feature of its dataflow graph enables it to execute seamlessly on all forms of computational platforms, whether the CPUs, GPUs, or TPUs. A wide range of tasks can be solved using TensorFlow and these include image and speech recognition, natural language processing, and reinforcement learning. Furthermore, the TensorFlow provides the strong placement policies so, fully fledge models can be place as per needs, whether it is cloud, mobile, edge and so on now TensorFlow is used in number of fields and industry.

3.11. Flask:

Flask is a micro web framework for Python which empowers fast and practical web application creation. Unlike some other similar frameworks, Flask is not very complex; instead, it includes only the fundamental tools one would need for a Web application and does not persistently dictate which tools to use for other, additional features. Due to this simplicity, Flask is best suited for middle scale projects and for any developer who wants more control in development of a website. Thus, Flask is a very simple framework but at the same time it is very powerful and has all necessary functions for building really complex applications, including routing, request handling and templating. It is the

most used for building APIs web services and for integrating machine learning models into web applications because it is easy to use.

3.12. MONAI:

Monitoring is another type of solution in healthcare imaging applications: MONAI is an open-source that focuses only on healthcare solutions. It has tools for constructing, training, and implementing deep learning models on areas of interest within the medical field. MONAI is implemented on the PyTorch foundation, which allows MONAI to incorporate the speed and feature modification of PyTorch as well as specialized medical imaging features, including data augmentation and data preprocessing and post-processing pipelines. Partially, MONAI helps to solve the problem by providing ready-to-use AI models, repeatable experiments, and detailed documentation for medical experts. This way, MONAI deals with the inherent issues of medical imaging such as the ability to handle vast amounts of features and dimensions and stability and performance of the model in a practical healthcare environment.

Any of these frameworks provides some unique features for the field of deep learning and can cover a great number of general tasks in the field of machine learning as well as more specific ones, such as 3D AI and medical imaging.

3.13. Summary

The tools and techniques discussed in this chapter are a source of a rather detailed ecosystem for the completion of AI-based glioblastoma detection projects. Python is used for building machine learning training while Jira is utilized for managing projects in conjunction with the team. Another useful platform is GitHub that allows code versioning and sharing, the other is Google Colab that lets run the code in a convenient cloud environment and use GPU. Kaggle provides data and competitions to encourage further development while Jupyter Notebook provides interactive environments for the development and documentation. Furthermore, it saves a lot of time during experimentation as well as models deployment all the ML processes. Combined, these tools assist researchers and developers to overcome the hurdles of detecting glioblastoma by enhancing their efficiency in the process thus being able to make progress towards the development of solutions for diagnosis and treatment of the condition.

Chapter 4
Methodology

4.1. Introduction

Glioblastoma is one of the most severe types of the brain cancer since this type of tumor tends to grow fast, and its survival rate is pretty low. In the current society, identifying glioblastoma in its early stages, or at least before the symptoms become intrusive, is fundamental to its successful treatment and the subsequent better outlooks for the clients. To date, medical imaging and artificial intelligence are new frontiers in medicine, especially in the field of glioblastoma, as the use of AI in diagnosis and analysis of the disease is on the rise.

As a pilot study for this project, we intend to develop a 3D version of Convolutional Neural Networks (3D CNN) that will be used to work on medical imaging data of Glioblastoma. In the context of our study, we shall focus on enriching the features derived from MRI images residing in DICOM format since such images have widespread utility in diagnosing brain tumors among patients. Preprocessing includes converting the scanned image from DICOM format to png format, using filters to optimize the image and applying the unity format to obtain the 3D NIfTI which is fed into the 3D CNN model.

Moreover, they utilize rotation and hyperparameters to make the model more reliable and accurate for time series data. With the integration of these state-of-the-art AI techniques with medical imaging data, we envision the creation of a usable application to detect and diagnose glioblastoma in the early stages, which can be instrumental in guiding the clinicians and help in making correct treatment decisions that would positively influence patient outcomes.
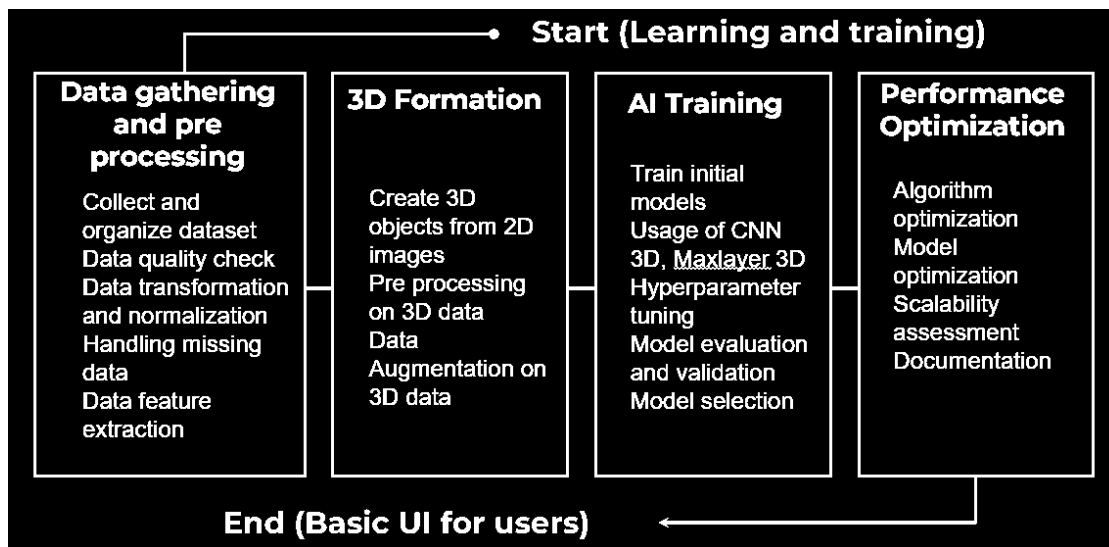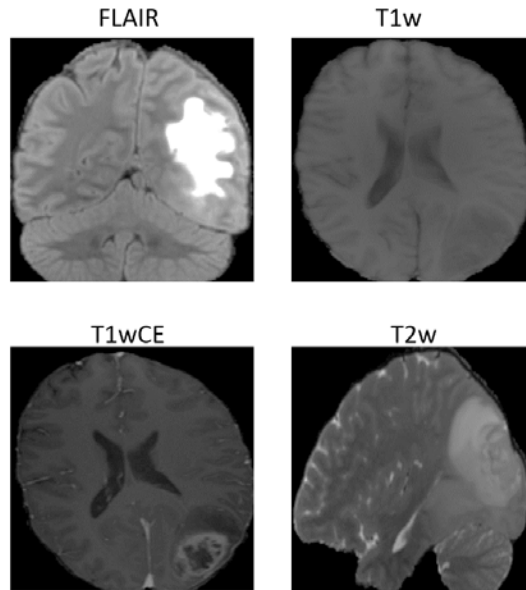
Figure 10 : Methodology for the project

4.2. Data Acquisition

The type of dataset used in this study involved MRI images of patients, and this data was sourced from Kaggle. In a dataset, 580 patients data are included to train the model and the rest of 87 patients data are used to test the model. Each patient's MRI data includes four types of scans: MRI imaging includes Fluid Attenuated Inversion Recovery (FLAIR), T1-weighted imaging (T1W), T2-weighted imaging (T2W) and T1-weighted imaging with contrast (T1WCE). These scans are in the DICOM format, which stands for Digital Imaging and Communications in Medicine – the format most commonly used to store digital medical images. The range of scans differs for each type where the number of scans typically ranges between twenty and two hundred of each type for each patient. It covers the Kings' College's diverse MRI set of images which provide richer data set to enhance numeric analytics and model training of different medical imaging applications. First, it is evident that MRI scans are diverse depending on the modality During the data collection process, the images obtained in this dataset are oriented at the axial level of the brain. This is due to the fact that the anatomical region of interest is maintained from one task to another, making it possible to devise measures that are coherent and pertinent when it comes to tasks in brain imaging and pathology diagnosis. In addition, the dataset contains marks specifying whether each detected individual has tumour or not. This annotation is very useful and provides a

requisite data set for learning and testing the machine learning models that are useful in tumor detection and classification. Thus, by further expanding it by the axial orientation and tumor labels, it can turn into a valuable resource for neuroimaging and medical image analysis research and development.

Figure 11: Types of MRI Scans

```
data/
└── train/
    ├── 0000/
    │   ├──FLAIR/
    │   │     ├── 000.dcm
    │   │     ├── 001.dcm
    │   │     .
    │   │     .
    │   │     .
    │   │     └──200.dcm
    │   ├── T1W/
    │   ├── T1WCE/
    │   └── T2W/
    .
    .
    .
    └── 0580/

└── test/
    ├── 0001/
    │   ├──FLAIR/
    │   │     ├── 000.dcm
    │   │     ├── 001.dcm
    │   │     .
    │   │     .
    │   │     .
    │   │     └──200.dcm
    │   ├── T1W/
    │   ├── T1WCE/
    │   └── T2W/
    .
    .
    .
    └── 0087/
├──trainlabels.csv
└──sample_labels.
```
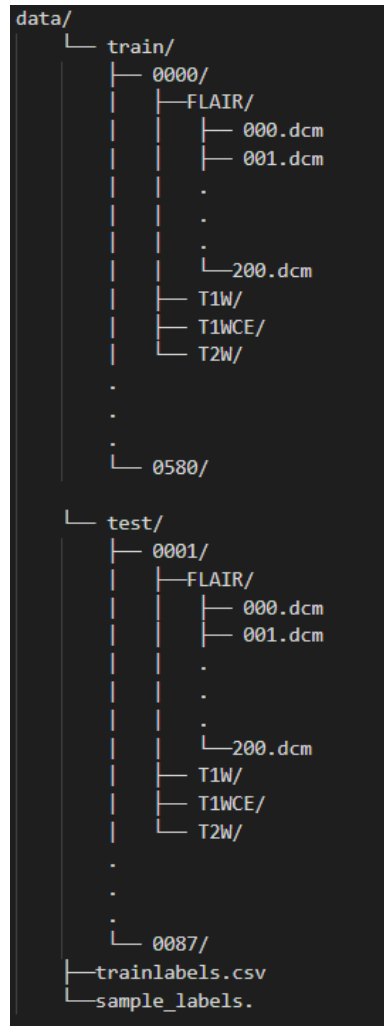
Figure 12: Folder hierarchy of the dataset

4.3. Data Preprocessing

MRI scans require data preprocessing before they can be used as input for Cognitive Networks in training a Convolutional Neural Network (CNN) model.

4.3.1. Conversion from DICOM to PNG

A recent image standard which is widely used in healthcare industry is the digital image and communication in medical association abbreviated as DICOM. Firstly, the images are preprocessed by loading DICOM format and by destructing pixel data corresponding to the intensity values. These intensity values are discretionary and are brought into the range [0, 255] for consistency in the different scans for three scans. Mathematically, the

normalization process can be expressed as: Mathematically, the normalization process can be expressed as:

$$\mathrm{X norm} = X_{max} - X_{min} X - X_{min} \times 255$$

where X equals to image intensity values of pixels, Xmin tells lower limit of intensity and X max is the upper limit of intensity and Xnorm equates to pixel intensity values after normalization.

Subsequently, these normalized pixel values are again preprocessed to convert pixel data in PNG format, and it saves in the output directory specified earlier. This conversion enhances compatibility with a range of image processing libraries and makes further process amenable. PNG format is the most used format because it has the benefited of being used in different platforms and applications. PNG files for an object are also more easily processed than DICOM images, which may contain additional information. The analysis and validation of a proposed PNG image can be done easily due to the availability of a common image viewing tool which can display the proposed PNG image.

4.3.2. Removal of Black Images

It is also common practice for the medical image datasets to have black images, either completely black or almost black with very few pixels of sizeable information. These images did not provide any value to the analysis process and can be discarded from the dataset.

The process of erasing black images involves the identification of images where the pixel array of that image is fully constituted of zeroes, in which case it would have to be erased. Deleting black pictures improves the quality of data set by detaching non-significant or entityless pictures thus improving on results yielded by a given analysis. This enables simplification of the pictures during the subsequent processing because there is no need for process the black images. The cleaning process make sure that the data is consistent and therefore contains no noise or artifacts, making it easier to analyze and yielding more accurate results..
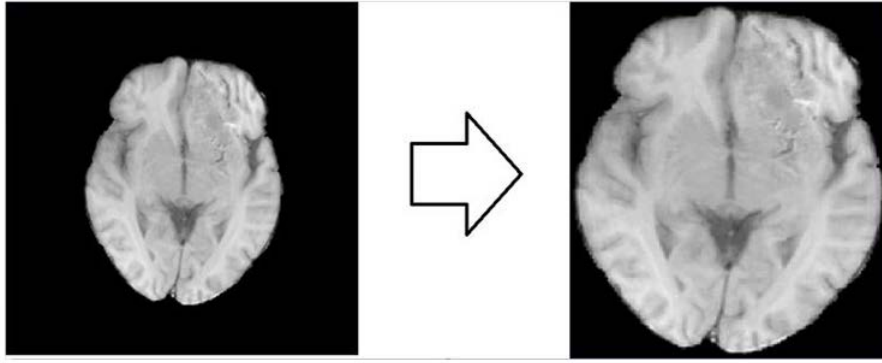
Figure 4 : Cropping of Images

4.3.3. Cropping and Resizing of Images

Crop and resize are two crucial features in the process of preparing images as they define the area of interest in specific sizes. Cropping helps to eliminate excess frames or there might be distortions on them, resizing is needed to make images of the same size which is crucial for deep learning algorithms. Cropping in commonly done by finding the display coordinate region encompassing the minimum and maximum values for the x, y, width, and height of the non-zero pixel and extracting that region from the image. The resizing operation modifies the size of the cropped image through resampling that use various techniques viz; lanczos resampling. Resizing and cropping bring the size of the medical images to a more preferable size for performing others analysis and tasks as well as models. ROI typically refers to cropping in which important parts such as specific body parts or regions of interest are targeted for analysis so that the overall efficiency and accuracy of the subsequent algorithms are enhanced. Downsampling is also beneficial because it makes the input size standardized, which in turn can lead to significant cost savings in terms of computation and memory because deep leaning frameworks often operate in a fixed-size environment. the cropped images are rescaled with Lanczos interpolation to a size of $64 \times 64 \times 64$, allowing to have a unified size for all images of the dataset. Mathematically, the resizing process can be expressed as: Mathematically, the resizing process can be expressed as:

New_image = resize(Cropped_image,(64,64),method=Lanczos)

4.3.4. Conversion from PNG to NIfTI

NIfTI (Neuroimaging Informatics Technology Initiative) is sort of popular format used for storage of neuroimaging data. Converting study PNG images into NIfTI format make them into one integrated file series for organizing the data or analysis. The conversion process includes organi zing the PNG images along the right axis to generate a 3D volume image of the desired organ. This volume is then saved in the NIfTI format using libraries for this purpose if available for the programming language of the script.

NIfTI format, for instance, combines multiple PNG images into one file that will facilitate the storage, transfer, and management of data. NIfTI format has been well adopted by the neuroimaging software tools there by increasing compatibility with previous software's and current workflow. NIfTI format facilitates quantitative examination of images for volume analysis, which is instrumental to three-dimensional imaging, segmentation, and registration purposes in medical applications.

4.3.5. Visualization of NIfTI Data

Visualizing NIfTI data is important for visual analysis of the data in terms of spatial location and density of anatomical structures or pathological conditions. Thus, it plays a great role in qualitative analysis, interpretation of results and validation of results analysis. Concerning specific diagnostic procedures, visualization helps the clinician or researcher make qualitative qualitative judgments on the appearance of the structure or lesion. Another advantage of 3D rendering is the ability to provide additional visual clues regarding the results of the analysis, which allows for more informed decisions when in the clinical environment. Through visual validation, it becomes easier to crosscheck the automated analysis results as well as detect any aspects that may have been missed or that should be corrected.
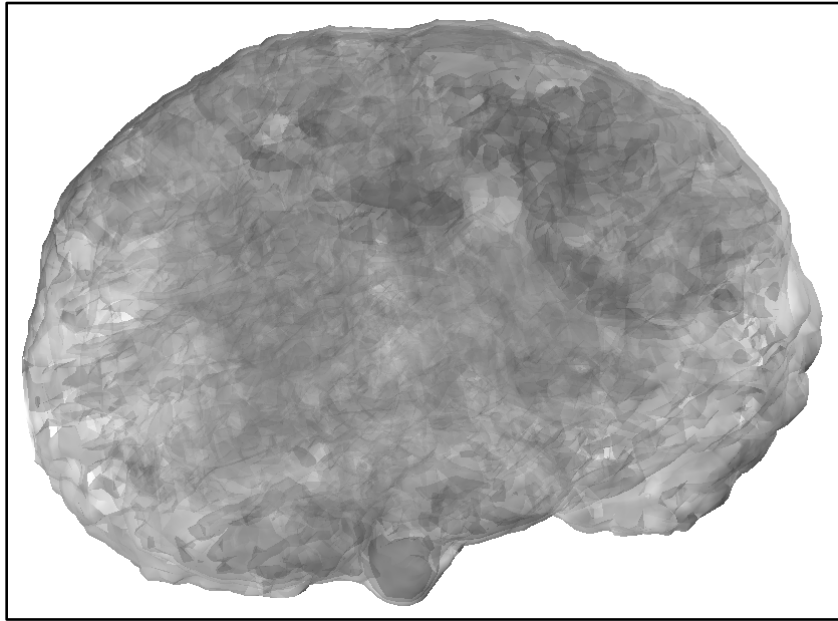
Figure 5: 3D Visualization of NifTi Model

In the first process of carrying out the training of the AI model, the first process that is undertaken involves the process of reading through NIfTI files that contain the MRI scans. This is carried out using the nibabel library which has a module that enables the loading of NIfTI image and extraction of the raw data from the same. The slight change in each voxel volume is made up of intensities showing properties of tissues in a brain. In mathematics, an MRI can be described as a single 3D image matrix that has dimensions W × H × D wherein the W is specific to the number of elements in the x direction, H refers to the amount of elements in the y direction, and D refers to the number of slices or the number of channels in the z direction. After data acquisition, the voxel intensities in the MRI scans will be scaled of their values between 0 and 1. This step helps obtain standard values for intensity within the scans which can be useful in avoiding distortion of patterns during modeling. Later on, size of the obtained MRI scans is then normalized to a basic size (64×64×64) through employing the methods of interpolation. Scaling helps in equal distribution of spatial exploitation aid bringing about uniformity in the data set. In summary, during the data preprocessing stage, readers are used to read the images and the normalization and resizing processes help to correct the contrast and size of MRI scans so that they can be later processed efficiently.

4.4. Data Augmentation:

Data augmentation is deemed as a significant method that aims at improving the quantity and variety of the training data to advance the ability of generalization of the CNN model. As discussed on MRI scans, they apply various augmentation methods, and rotation is among them. Rotation entails applying a random rotation value to the MRI volumes rather than scanning the head through different angles, with the possible values being a few degrees apart from each other. This random rotation adds a level of variety for the orientation of the MRI scans incorporated into the model, which offers it a wider set of views. Data augmentation is implemented through TensorFlow operations which were combined into a custom rotation function. This was done by increasing the data set with the rotated MRI scans of the same brains helping to enhance the performance of the model through handling rotated image data well making it easier to determine the presence of a brain tumor.
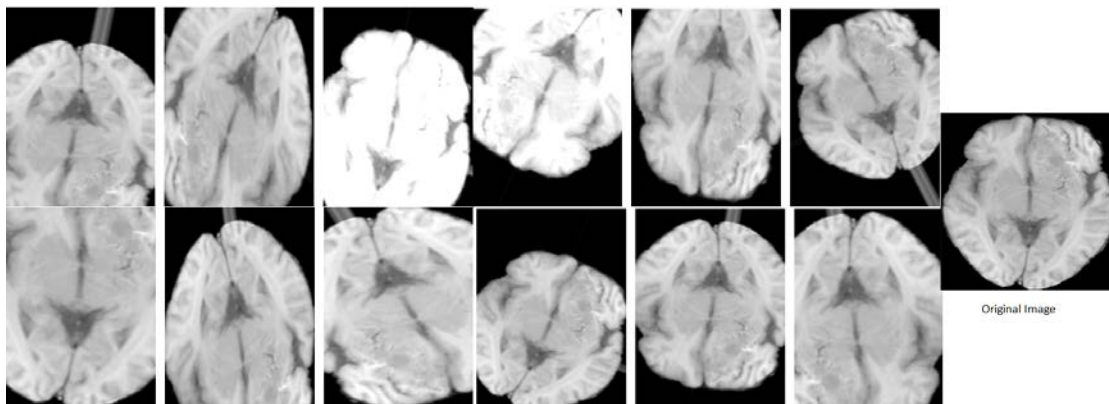
Figure 6: Data Augmentation

4.5. Data Visualization:

Through the process of analyzing the visual representation of MRI scans, it is possible to develop an understanding of the temporal and spatial characteristics that MRI images possess. One of the significant forms of portraying the visual analyses used in this code is presenting montages of different slices from the MRI volume. Montage plotting helps array several slices together to form one image, and thus provides a quick way for observing structures inside MRI scans and several features of it. Developed using the Matplotlib software package, montage plots offer a relative assessment of how data

augmentation impacts the MRI's slice angles for users while examining various orientations of the slices across the dataset. By making use of the developed visualization tools, the quality of the preprocessing steps, and the effect of the augmentation on the data, are well explained, and the users can gain some insights regarding the nature of the MRI scan data.
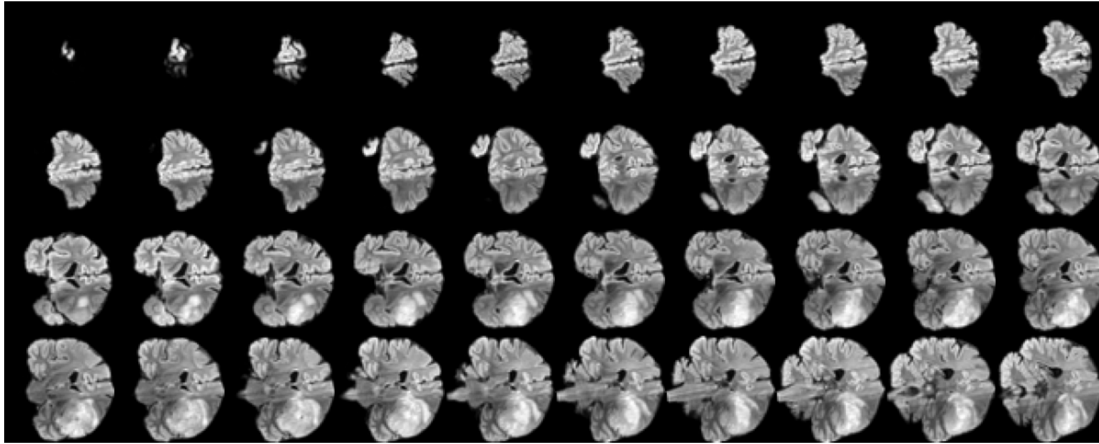
Figure 7: Visualization of Slices in an NifTi Model

4.6. Model Architecture:

One factor of the CNN model used for brain tumor classification is the design of the model, which pre-determines its ability to identify features from MRI scans. The proposed model structure involves 3D convolutional layers for feature extraction, max-pooling layers for dimensionality reduction, batch normalization layer for zero mean and unit variance layers for a network input distribution, and dropout to reduce the likelihood of the model being reliant on a particular feature. The final layers involve dense layers. The convolution layers aim at extracting feature pyramids from the given 3D MRI volumes, and the max-pool layers downsample feature maps and decrease spatial extent. Batch normalization aids the model maintaining its stability and accelerates convergence through normalizing layer activations. Cross entropy loss reduces overfitting of the model since it sums the logarithm of the probability of the ground truth along with the predicted classes, while dropout sets a percentage of neurons to zero during training to improve generalization of the model. Classification is then

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conducted after the application of global average pooling as it sums up the spatial information. Through regularization of the second language features added to the convolutional layers, the model reduced cases of overfitting while improving the capacity to learn on and predict results from new data. Altogether, the design of the CNN model is well-planned to perform feature extraction from cerebral MRI scans and enhance the power of discrimination of tumor class types.

4.6.1. Convolution Operation:

The convolution operation is the core building block of a CNN. It involves applying a filter (also called a kernel) to an input volume to produce an output volume.

Given an input volume X of shape $W,H,D)$ where W is the width, H is the height, and D is the depth (number of channels), and a filter W of shape (F,F,F) where F is the spatial extent of the filter, the convolution operation at a single spatial position (i,j,k) in the output volume Y is computed as follows:

$$Y_{i,j,k} = {}_{m=0}\sum^{F-1} {}_{n=0}\sum^{F-1} {}_{p=0}\sum^{F-1} X_{i+m,j+n,k+p} \cdot W_{m,n,p}$$

Here, $X_{i+m,j+n,k+p}$ represents the value of the input volume at position $(i+m,j+n,k+p)$, and $W_{m,n,p}$ represents the value of the filter at position (m,n,p). The output $Y_{i,j,k}$ is the result of summing the element-wise multiplication of the input volume and the filter at each position.
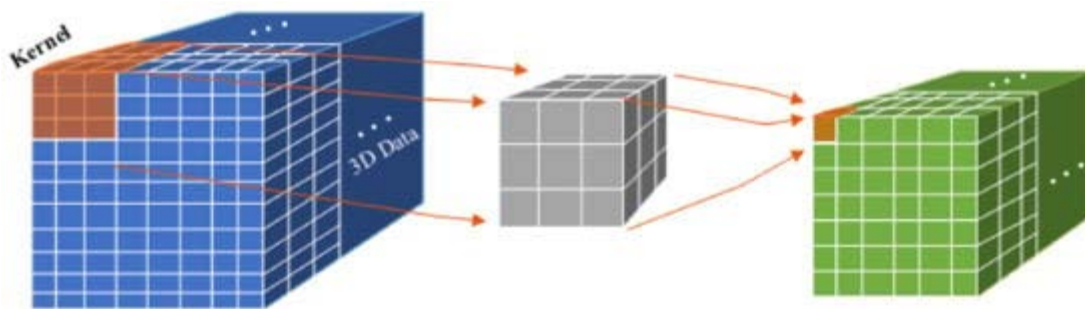

Figure 8: Mechanism of 3D Convolutional Layer

4.6.2. Max Pooling Operation:

Max pooling is a downsampling operation that reduces the spatial dimensions of the

input volume by taking the maximum value within each local region of the volume.

Given an input volume *X* of shape (*W,H,D*) and a pooling size *P*, the max pooling operation at position (*i,j,k*) in the output volume *Y* is computed as follows:

$$Y_{i,j,k} = \max_{m,n,p}\{X_{i \times P + m, j \times P + n, k \times P + p}\}$$

Here, *P*×*P*×*P* is the size of the pooling window, and we take the maximum value within each window.
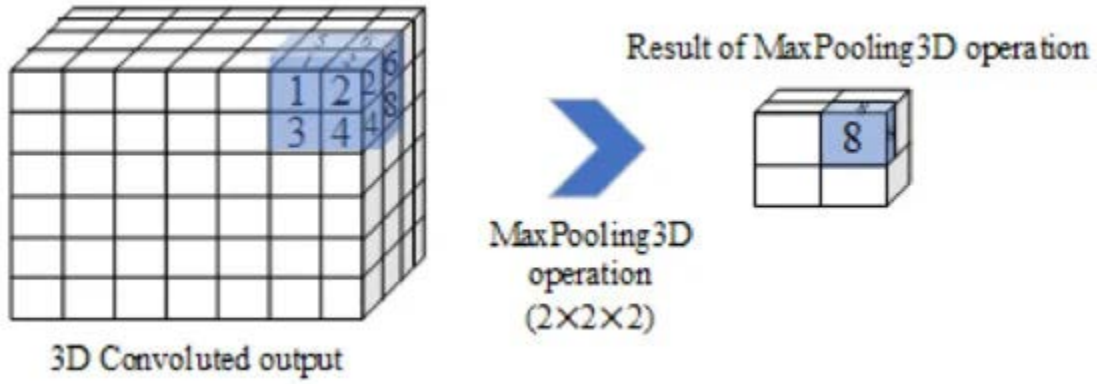
Figure 9: Mechanism of MaxPool 3D
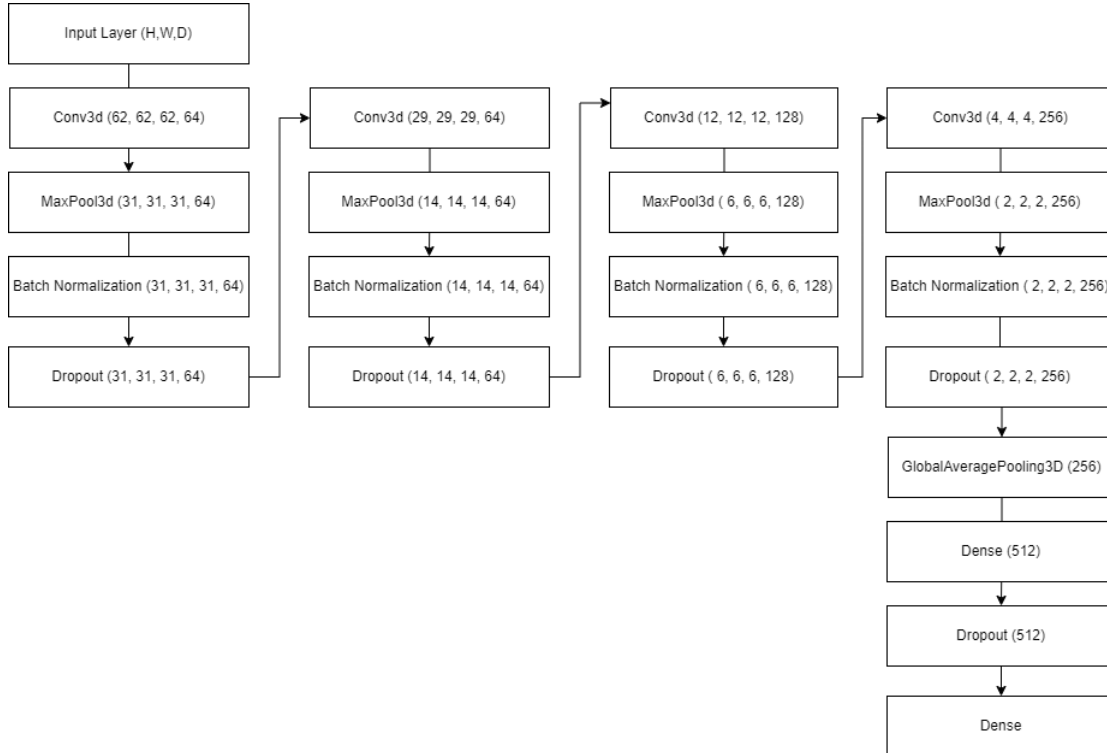
Figure 10: Model Architecture

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4.6.3. Loss Calculation and Optimization:

Loss calculation and optimization constitute essential components of the training process, influencing the model's ability to learn and generalize from the data. For binary classification tasks such as brain tumor detection, binary cross-entropy loss is commonly employed. This loss function measures the dissimilarity between predicted probabilities and ground truth labels, providing a quantitative measure of model performance. Optimization of the CNN model is achieved through the Adam optimizer, which adapts the learning rate to the gradients' magnitude, facilitating efficient convergence. Additionally, a learning rate schedule is implemented, wherein the learning rate exponentially decays over epochs, aiding in fine-tuning and stabilizing the training process. Callbacks such as ModelCheckpoint are utilized to save the best-performing model weights, ensuring reproducibility and facilitating model evaluation.

4.7. GAN Architecture

The generator and the discriminator are the two primary parts of generative adversarial networks, or GANs. The discriminator's goal is to discern between created and actual data samples, while the generator's goal is to produce realistic data samples in order to trick the discriminator. Both of these networks are configured in an adversarial framework. During the training process, the discriminator works to sharpen its ability to discern between real and synthetic data, while the generator aims to provide more compelling material.

4.7.1. Generator

The generator in our GAN architecture is a neural network that transforms random noise into structured data resembling the target dataset (3D brain MRI scans). The generator starts with a fully connected layer, which reshapes the input noise vector into a small 3D volume. Subsequent layers are 3D transposed convolutional layers (also known as deconvolutional layers), which upsample the volume to the desired output size. The generator's architecture can be described as follows:

1. Input Layer: A random noise vector z of size 100.

2. Dense Layer: A fully connected layer that transforms z into a volume of shape (8, 8, 8, 256).

3. Reshape Layer: Reshape the output into a 3D volume.

4. Conv3DTranspose Layers: Three 3D transposed convolutional layers to upsample the volume:

5. Output Layer: Produces a 3D volume of shape (64, 64, 64, 1).

The generator aims to map a random noise vector \(z \) from a latent space to a data space that resembles the training data. This mapping involves multiple layers to upsample and transform the noise into a structured output. The first layer is a fully connected (dense) layer that converts the 100-dimensional noise vector z into a volume with dimensions (8, 8, 8, 256). This is achieved through a linear transformation followed by batch normalization and LeakyReLU activation to introduce non-linearity and stabilize training. The formula for this transformation is:

$$h\_1 = LeakyReLU(BatchNorm(W_1 z + b_1))$$

Next, the volume is reshaped into a 3D format suitable for further processing by convolutional layers. The reshaped volume undergoes a series of 3D transposed convolutions (deconvolutions), which progressively increase the spatial dimensions while reducing the depth. These layers also use batch normalization and LeakyReLU activation to maintain the stability of the gradient flow and introduce non-linearity. The final layer uses the tanh activation function to ensure the output values are in the range [-1, 1], matching the normalized range of the input data.

4.7.2. Discriminator

A neural network known as the discriminator receives a 3D volume as input and produces a single scalar value that indicates the likelihood that the input is real—that is, from the training dataset—as opposed to coming from the generator. The discriminator's architecture consists of several 3D convolutional layers, followed by fully connected

layers. The discriminator's architecture can be described as follows:

1. Input Layer: A 3D volume *x* of shape (64, 64, 64, 1).

2. Conv3D Layers: Three 3D convolutional layers with LeakyReLU activations and dropout:

3. Flatten Layer: Flatten the 3D volume into a 1D vector.

4. Dense Layer: A fully connected layer that outputs a single value with a sigmoid activation function, representing the probability that the input is real.

The discriminator's task is to classify 3D volumes as real (from the training set) or fake (generated by the generator). It uses a series of 3D convolutional layers to extract spatial features from the input volume. The input volume *x* is first processed by a 3D convolutional layer, which applies a convolution operation to capture local patterns in the data. This is followed by a LeakyReLU activation to introduce non-linearity and a dropout layer to prevent overfitting.

This process is repeated for additional convolutional layers, progressively increasing the number of filters and using dropout to reduce overfitting. After the convolutional layers, the 3D volume is flattened into a 1D vector, which is then passed through a dense layer with a sigmoid activation function. This final layer outputs a single probability value indicating whether the input volume is real or fake.

$$y = \sigma(W_5 h_4 + b_5)$$

4.7.3. Feature Scaling

The results achieved when visualized through TSNE- visualization showed a lot of difference between real and synthetic images. In order to minimize the difference, feature scaling was applied. Feature scaling is an essential preprocessing step in training

GANs (Generative Adversarial Networks) as it normalizes the data range, improving training stability and performance. In this context, feature scaling is applied to both real and fake images to ensure they have a consistent range, crucial for the discriminator to distinguish effectively between real and generated images. For real images, the normalization process involves subtracting the minimum value of the batch and dividing by the range (maximum value - minimum value) to scale the data to [0, 1]. The same process is applied to fake images generated by the generator. This consistent data range ensures both real and fake images have values within the same range, improves training stability, facilitates faster and more stable convergence, and mitigates the impact of outliers. Overall, feature scaling transforms the real and fake images to a normalized range, enhancing the GAN's learning efficiency and performance.

The dataset was divided into two; one with label0 that holds nifty models with no tumor and the other with label1 that has glioblastoma infected brain models. GAN architecture was applied separately on both of these datasets. The new results plotted through TSNE-visualization showed great overlap between the real and synthetic data. The results are summarized in table 2.
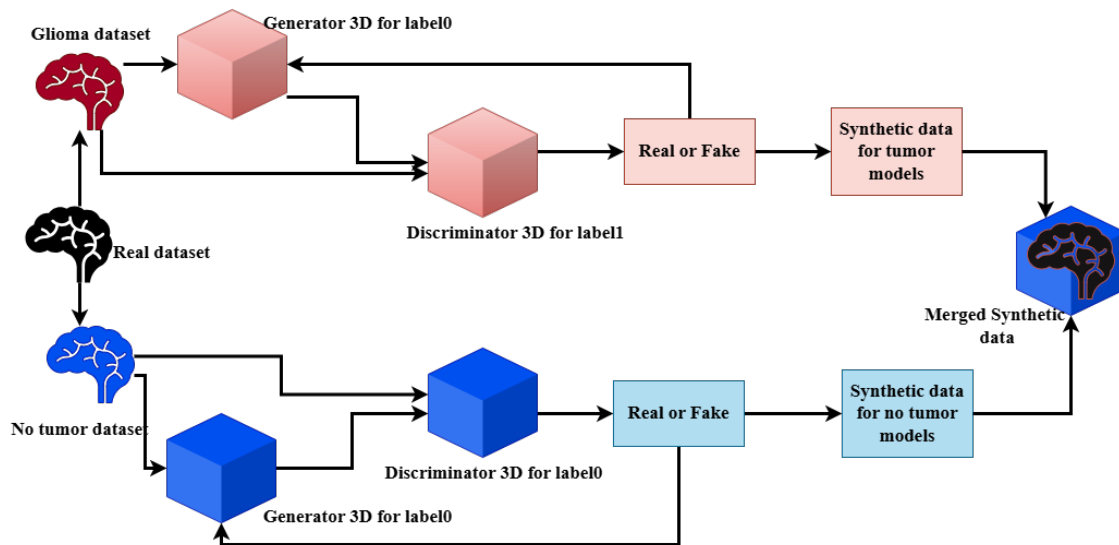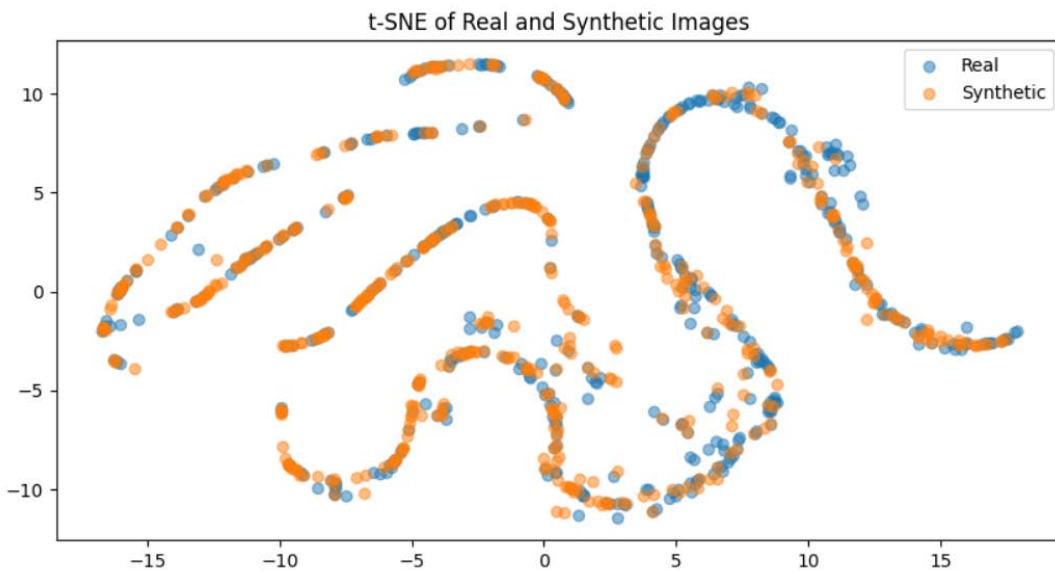

Figure 20: GAN Architecture

Table2: GAN metrics

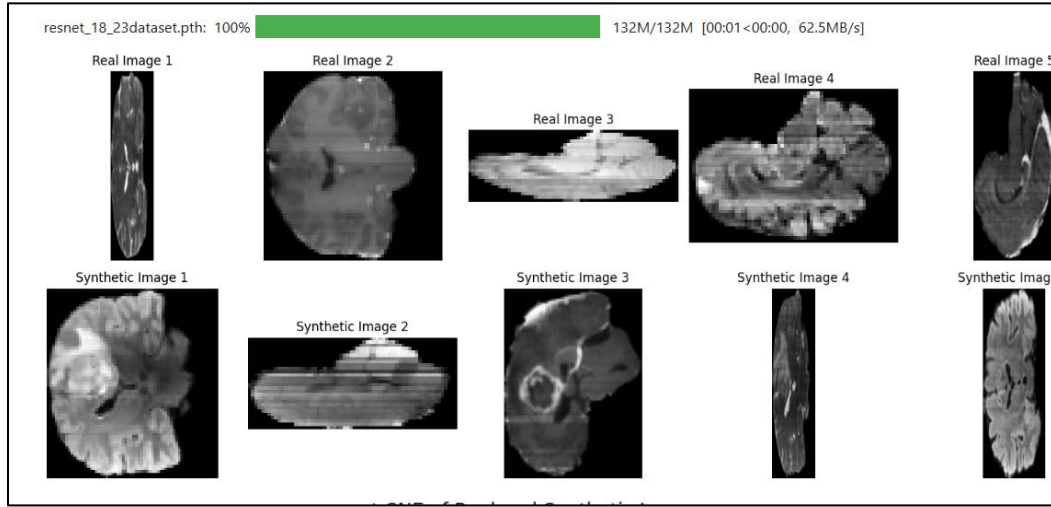| GAN	Generator Loss	Discriminator Loss
Label 0	3.9198	0.1511
Label 1	3.6544	0.5155
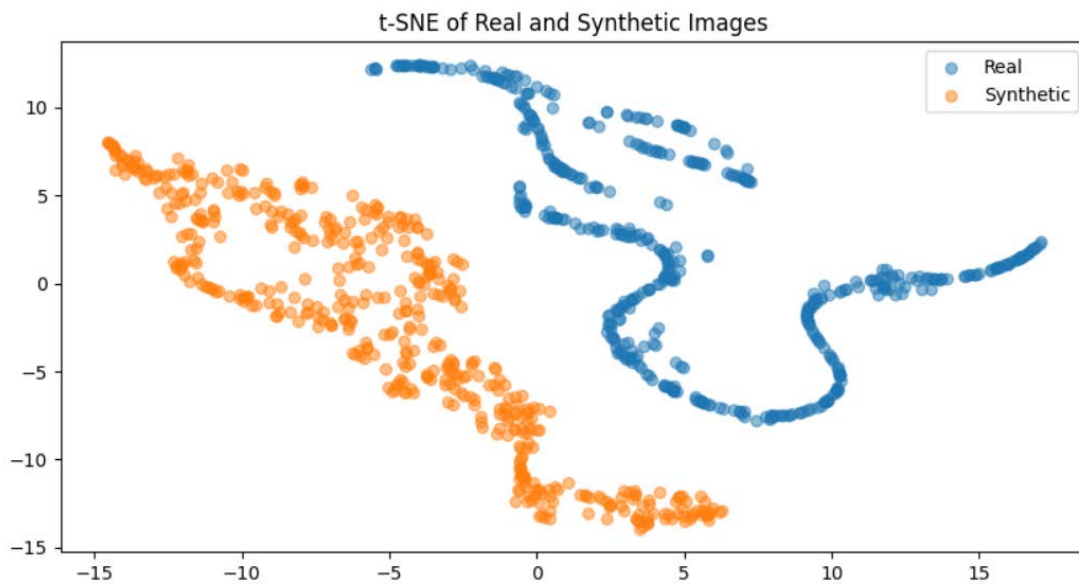
Figure 21: GAN Before Feature Scaling


Figure 22: GAN After Feature Scaling

Figure 23: Synthetic and Real Images

4.8. Hyperparameter Tuning

Hyperparameter is a process of tuning consisting of finding a comprehensive set of values for various hyperparameters which include the number of filters in the convolutional layers, the total number of convolutional layers, the use of kernel regularizer, dropout rate, batch size and type of loss function. RandomSearch tuner from the k-two Keras Tuner library was used to search through these hyperparameter combinations by creating and testing the various model versions within the set number of trials. The above parameters make sure that the validation accuracy is optimized, and from these aspects, the best configuration of the model is considered. The tuner iterates over the hyperparameter space and tries different values, trains models on the given data, and finds the set of hyperparameters that produce the best results for a set of performance metrics; the best hyperparameter set is used to compile and train a final model for evaluation on a separate test set. The code was set for 50 trials with 100 epochs each. Figure 20 and 21 shows that despite hyperparameter tuning, significant validation accuracy was not achieved.

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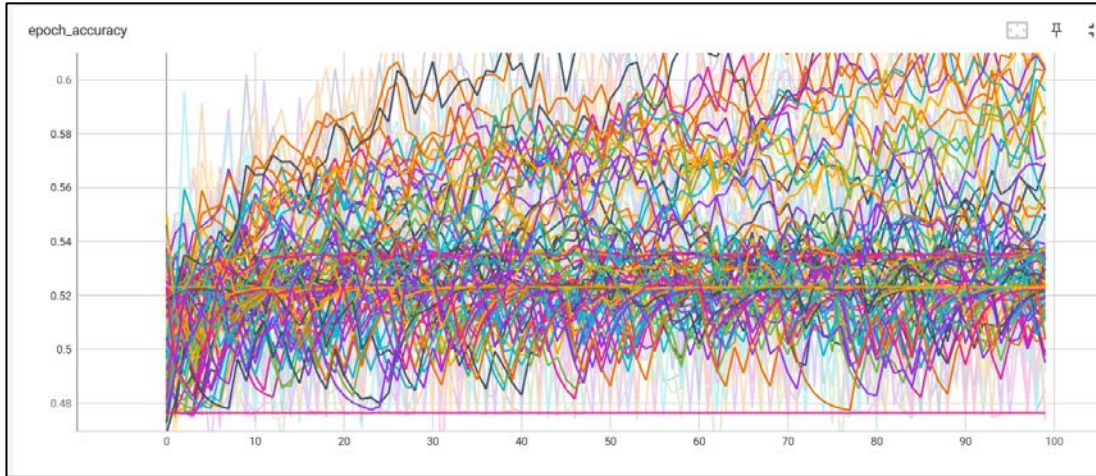
Figure 11: Epoch Accuracy over 50 Trials
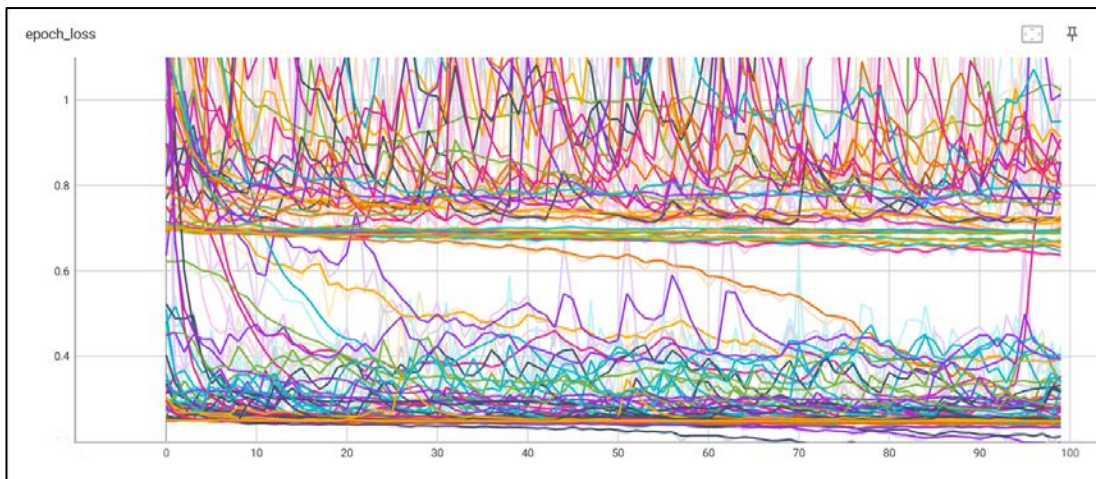
Figure 12: Epoch Loss over 50 Trial

4.9. ResNet18 in MONAI for 3D Applications:

ResNet18, a variant of the Residual Network (ResNet) architecture, has been adapted for 3D applications within the MONAI framework to address the unique challenges of medical imaging and other volumetric data tasks. The original ResNet18, developed by He et al., introduced the concept of residual learning to tackle the problem of vanishing gradients in deep networks. This architecture comprises 18 layers, including convolutional layers, batch normalization layers, ReLU activation functions, and identity shortcuts. The 3D version of ResNet18 extends this architecture by replacing the 2D convolutional and pooling layers with their 3D counterparts, enabling the network to process three-dimensional data volumes effectively.

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The architecture of 3D ResNet18 in MONAI can be described as follows:

1. Input Layer: Takes a 3D input volume, typically a medical image with dimensions $(D \times H \times W \times C)$, where (D) is depth, (H) is height, (W) is width, and (C) is the number of channels.

2. Initial Convolution and Pooling: A 3D convolution layer with a kernel size of $(7 \times 7 \times 7)$ stride of 2, and padding of 3, followed by a 3D batch normalization layer, a ReLU activation, and a 3D max-pooling layer with a $(3 \times 3 \times 3)$ kernel, stride of 2, and padding of 1.

3. Residual Blocks: Four sets of residual blocks, each consisting of two 3D convolutional layers (with kernel sizes of \(3 \times 3 \times 3\)), batch normalization layers, and ReLU activations. The first convolution in each block reduces the spatial dimensions, except in the identity connections where a 3D convolution with a stride of 2 is used to match the dimensions.

4. Fully Connected Layer: After the final residual block, a global average pooling layer reduces the spatial dimensions to 1, followed by a fully connected layer that maps the features to the desired output classes.

Mathematically, the core of the residual learning approach can be expressed as:

$$[y_l = \mathcal{F}(x_l, \{W_l\}) + x_l]$$

Where (x_l) and (y_l) are the input and output of the (l)-th layer, F represents the residual function (composed of convolution, batch normalization, and ReLU), and W_l denotes the weights of the layer. The identity shortcut connection (x_l) allows the network to learn residual functions more effectively, mitigating issues like vanishing gradients.

The ResNet18 in MONAI is developed for medical imaging tasks like MRI, CT, and PET scans where the architectural layout in 3D is vital. As a result of this, the network can be deeper while avoiding such issues from afflicting the learning process such as gradient degradation. This is particularly the case in an application such as medical imaging where minutiae of different structures in the body need to be learned in order

to distinguish between normal and abnormal tissues.

MONAI improves ResNet18 for 3D use cases in medical imaging through data augmentation and loaders which focuses on medical images as well as pre-trained weights using medical data. These are the improvements that allow the 3D ResNet18 to have high accuracy at such processes as tumor segmentation, organ classification, and identification of abnormalities. The modularity of MONAI makes it possible for researchers and practitioners to customize the architecture for certain tasks depending on the required performance in the clinical environment. The integration with PyTorch guarantees that users can take advantage of all the PyTorch tools in training deep learning models thereby easing the transition from research to production in medical AI applications.
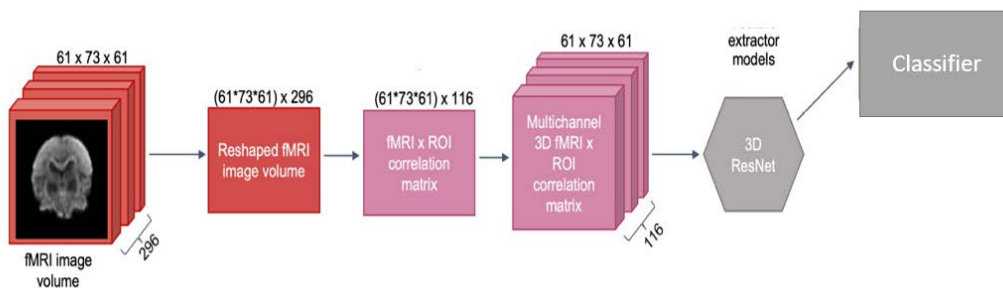
Figure 13: Basic model architecture of RESNET-18

4.10. TRANSFER LEARNING:

During the training from the scratch and hyperparameter tuning, the best solutions were not achieved; therefore, transfer learning was applied using a pretrained model. This classification is performed using a 3D ResNet-based model on glioma MRI scans to estimate MGMT promoter methylation status. Before feeding the images to the model, few data set processing steps include reading image paths and their labels from the CSV file, performing data augmentations using MONAI's Compose with operations that include loading the images, checking if they had the channel dimension, scaling the

intensity of the images, randomly flipping the images and resizing them to a size that is suitable for model training, in this case 64×64×64. For the training of the model, the data is divided into training and validation sets and these sets are wrapped in to `DataLoader`. The `GliomaDataset` class is introduced for loading individual image files and translating them into the desired format and scale.

The model that has been employed here is a 3D ResNet18 which is a deep convolution neural network which has been modified for binary classification by setting `num_classes=1` and a sigmoid function is later applied to the output for binary classification. For the loss function, training process employs binary cross-entropy with logits BCEWithLogitsLoss and the weight updates are made by the Adam optimizer. The training loop of the model involves moving through epochs, initializing forward and backward pass to reduce the loss while testing the model on the validation dataset from time to time. Some of the metrics that are calculated during validation include ; accuracy, precision, recall, F1 score. The selected model as per the validation accuracy is stored. Transfer learning is applied by using the base on the ResNet18 architecture which is pre-trained with glioma MRI data, share features learned from other domain (for instance ImageNet) in order to enhance the model performance and the convergence rate of the medical imaging data.

With regard to transfer learning in the code, there is a pre-trained ResNet18 model with the MONAI and with 3D data capable of using 1 channel (`resnet18(spatial_dims=3, n_input_channels=1, num_classes=1)`). This approach takes advantages of the hierarchical feature extraction which has been built into the ResNet architecture from the large-scale database. What transfer learning means here therefore is that while ResNet was trained to detect general features in images, we are going to use the weights protruding from ResNet and retrain them on the specific glioma classification task. First, this method helps to improve the model's capacity for learning relevant patterns from a smaller sample, second, increases the model's ability to generalize and accelerates convergence during the training process. The model's parameters are updated using the Adam optimizer, following the equation:

$$[\theta_{t+1} = \theta_t - \eta \cdot \widehat{g_t}]$$

where θ represents the model parameters, η is the learning rate, and g_t is the gradient estimate at time (t). The training loop periodically evaluates model performance on the validation set to ensure that the model generalizes well and saves the best model based on validation accuracy, incorporating metrics like precision, recall, and F1 score for a comprehensive performance assessment.
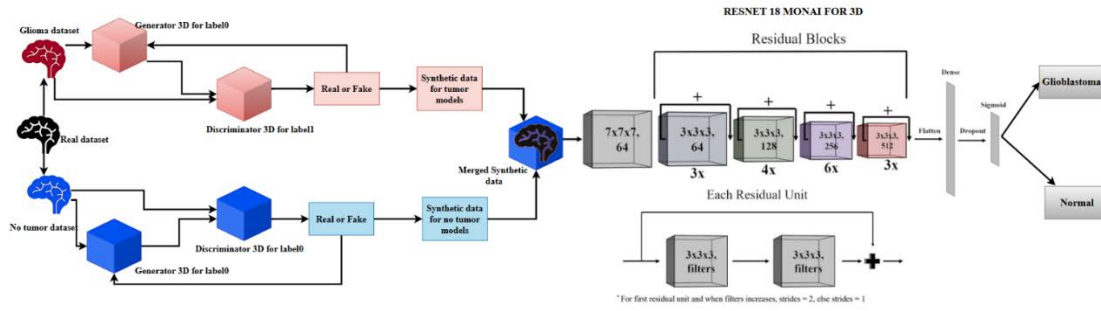
Figure 27: Complete model architecture with GAN and RESNET-18

4.11. Training and Evaluation:

The training and evaluation phase involve iteratively feeding batches of preprocessed MRI scans into the CNN model, adjusting its parameters to minimize the defined loss function. During training, the model's performance is monitored on both the training and validation datasets, allowing for the assessment of training progress and detection of overfitting. Evaluation metrics such as accuracy and loss are computed and visualized over epochs, providing insights into the model's learning dynamics and convergence behavior. Through iterative training and evaluation, the CNN model learns to accurately classify brain tumor presence, leveraging the diverse set of augmented MRI scans for robust performance.

4.12. Model Evaluation and Prediction:

Following model training, the best-performing model weights are loaded for evaluation and prediction tasks. The model evaluates its performance on unseen data from the validation dataset, allowing for an assessment of its generalization capability. Additionally, the model predicts the class probabilities for individual MRI scans,

providing insights into the likelihood of brain tumor presence. These predictions are interpreted in terms of confidence scores, quantifying the model's certainty regarding the classification decision. By leveraging the trained CNN model for evaluation and prediction tasks, healthcare practitioners can gain valuable insights into the presence of brain tumors in MRI scans, facilitating timely diagnosis and treatment decisions. After 60 epochs, a validation accuracy 0f 95.93% was achieved while loss decreased to 0.02%. Precision was calculated around 0.9665 and recall around 94.45 percent. The f1 score achieved was 95.54%. Confusion matrix diagram shows true positive as 2119 samples and false negatives as 2099 samples.
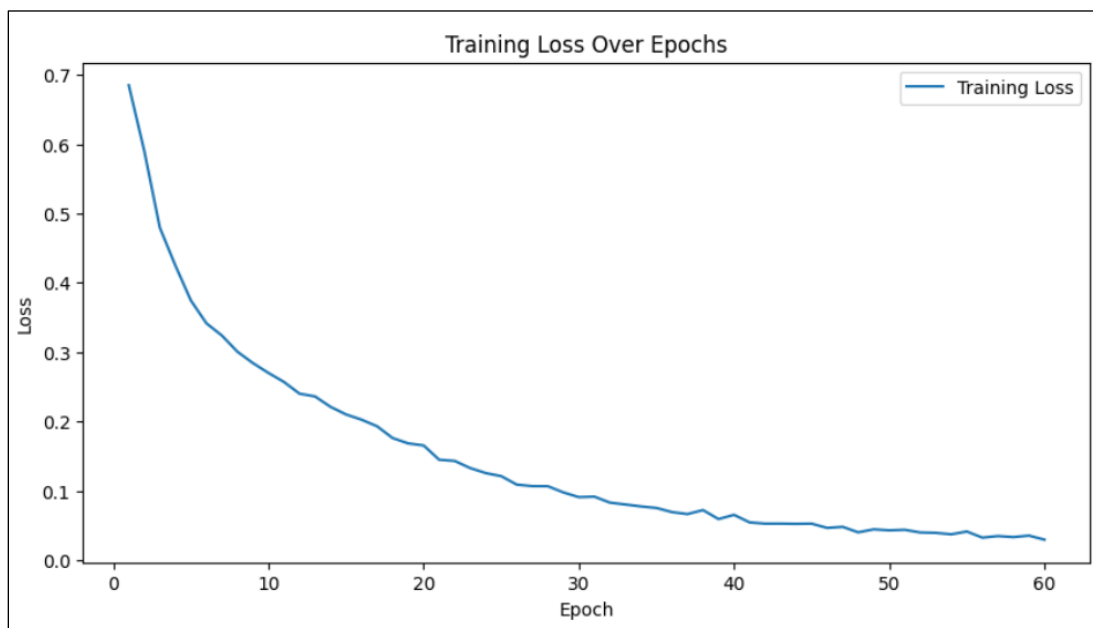
Figure 14: Training Loss over Epochs
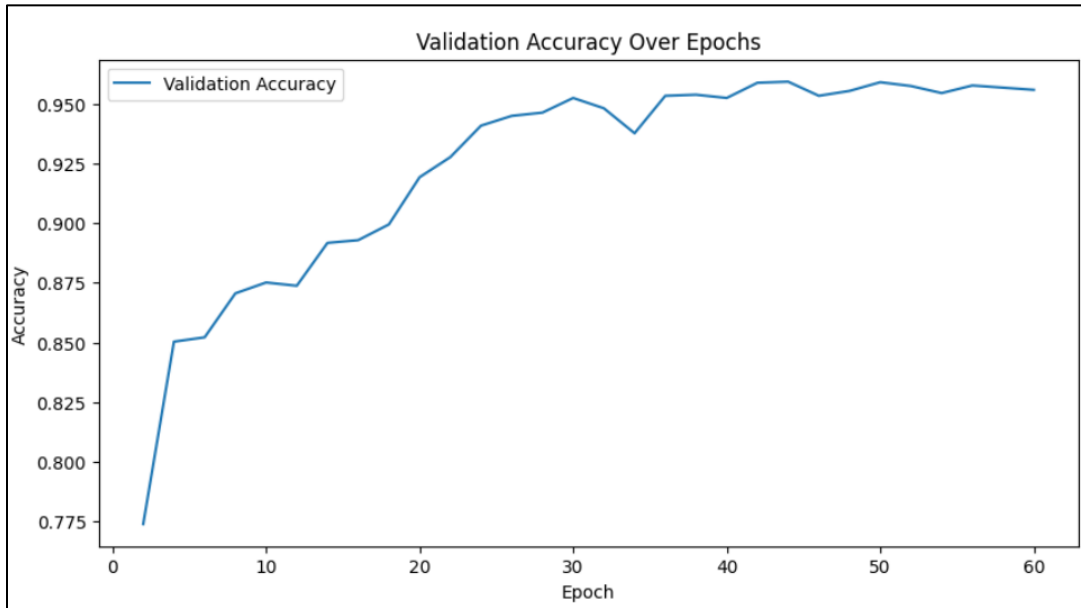
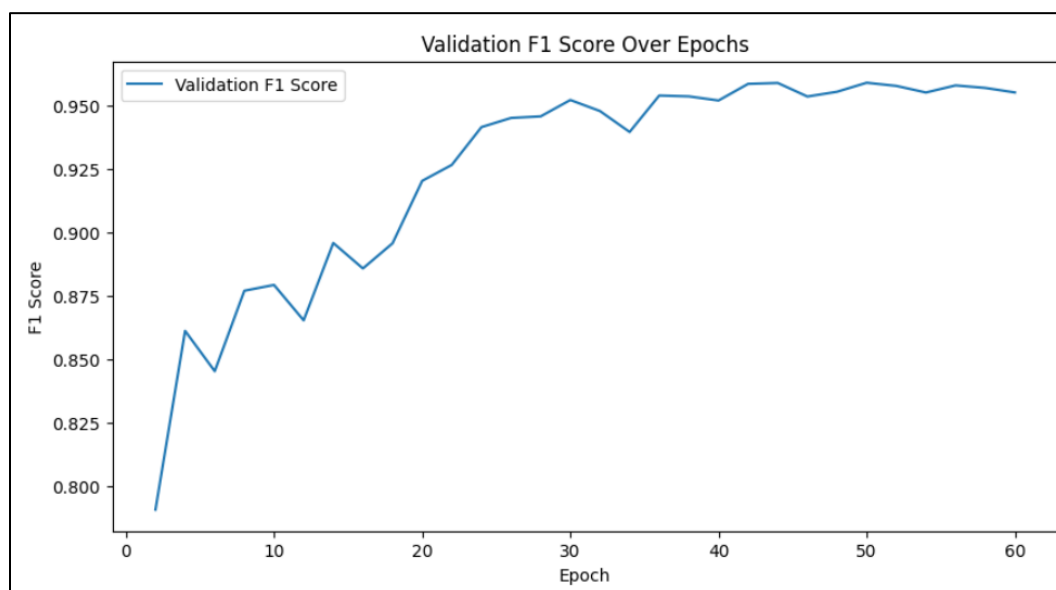**Figure 15: Validation Accuracy over Epochs**
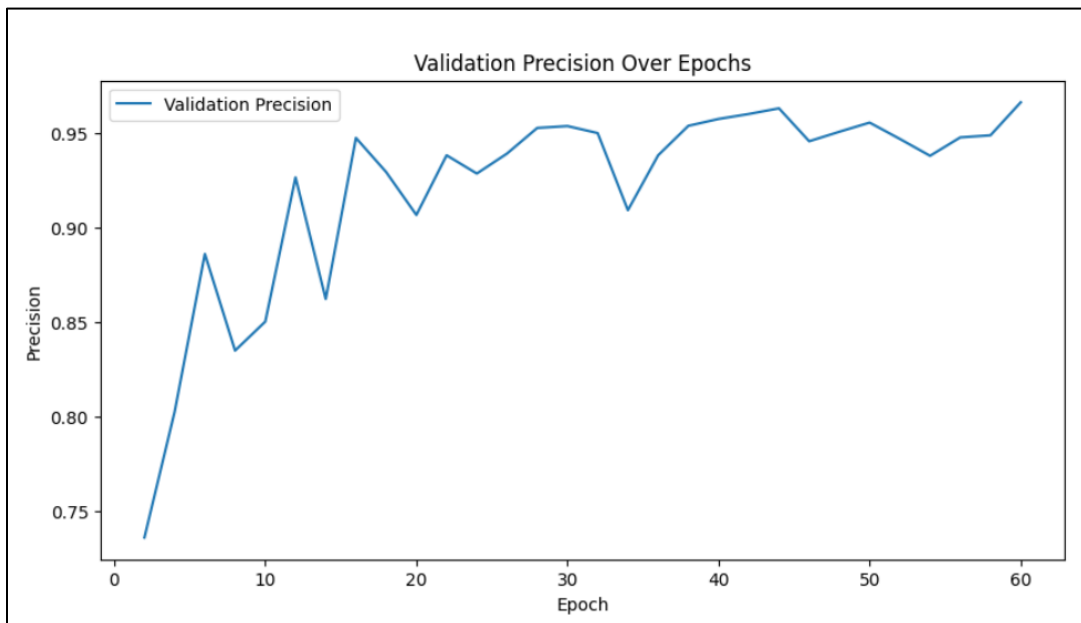
Figure 30: Validation Precision over Epochs
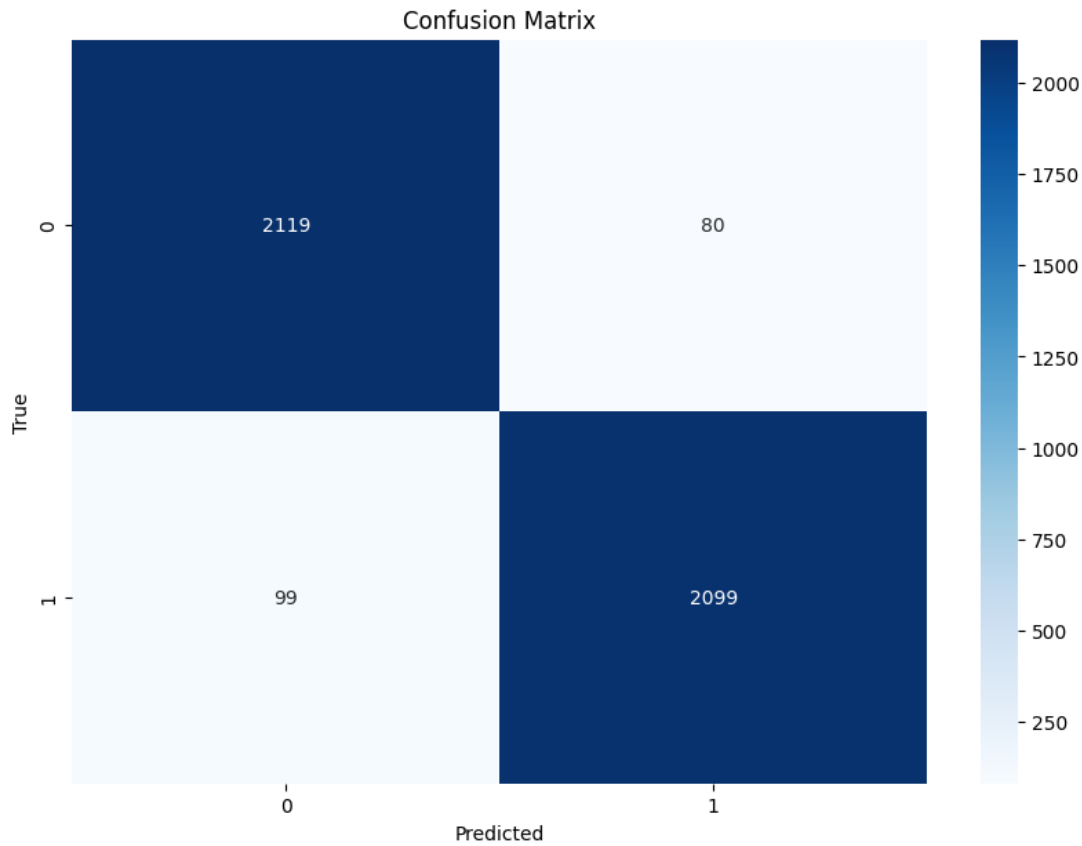
Figure 31: Recall over Epochs

Figure 32: F1 Score over Epochs

Figure 33: Confusion Matrix

4.12. Summary

In summary, our project focuses on developing an AI-based solution for the detection of glioblastoma using 3D CNN applied to DICOM MRI images. We start by converting the DICOM images to PNG format, followed by preprocessing steps to enhance image quality and consistency. The preprocessed images are then transformed into 3D NIfTI format to facilitate volumetric analysis.

To improve the robustness of the model, we employ data augmentation techniques such as rotation to increase the diversity of the training dataset. Additionally, hyperparameter tuning is utilized to optimize the performance of the 3D CNN model. Through extensive experimentation and evaluation, we aim to demonstrate the effectiveness of our approach in accurately detecting glioblastoma from medical imaging data.

Overall, our project represents a promising step towards the development of advanced AI tools for brain tumor detection and diagnosis, with the potential to significantly impact clinical practice by enabling early detection, precise localization, and personalized treatment planning for patients with glioblastoma.

Chapter 5

User Interface

5.1. Introduction

In this chapter, we delve into the frontend development of the Glioblastoma Detection web application, highlighting the crucial aspects that enable an intuitive, responsive, and user-friendly interface. The frontend, built using a combination of HTML, CSS, and JavaScript, works seamlessly with Flask to provide real-time predictions and advanced visualization capabilities. By exploring the integration of Flask for model prediction, the user interface design, and the 3D model rendering functionalities, we aim to showcase how these elements come together to create a robust tool for glioblastoma detection and visualization. This chapter illustrates the journey from uploading MRI scans to visualizing complex brain structures, emphasizing the importance of user experience in medical diagnostic applications.

5.2. Flask Integration for Model Prediction

The Glioblastoma Detection web application employs Flask; a WSGI web application framework in Python that combines a trained machine learning model for identifying glioblastoma from MRIs. Due to the simplicity and flexibility of Flask, it is viable to use this framework to develop this application. The general initialization of the app is done by creating an instance of the Flask class, and the trained model using a defined function load_model(model_path), where model_path directed to the location of the model. Two main routes are defined within the Flask application: two routes: the home route with path `/` and the predict route with path ` /predict`. The home route eliminates the variable of the `upload. A STP `MRI_file_uploader.html` is the template file used which is a front end through which a user uploads his MRI files. The predict route handles POST requests only for file uploads, the file received is processed and then passed through the model to get the prediction. As a result, the returned response is in the JSON format. This integration makes it easy for frontend and backend to communicate, meaning real-time prediction based on operation entered by the user is made possible.

The conversion of DICOM to NIfTI is a process that follows certain sequential steps in order to get final and correct outputs from the analysis of medical images. First of all, the DICOM images are delivered in zip format and upon the uploading, they are unzipped. Black images are usually non-informative images and after the DICOM files are extracted, these images are removed from the set. The conversion is done for the rest of the DICOM files to the PNG format to make manipulation easier. After this, the images are cropped and resized to the particular dimensions of PNG format among the images. After that, the PNG images are than inverted back into 3D volume and save in NIfTI format for the next processing. This NIfTI file after aggregating and the pre-processing of the collected imaging data is than fed to a pre-trained ML model for analysis or prediction. This pipeline guarantees that the data is preprocessed properly regarding cleaning and formatting to other medical imaging processes

.
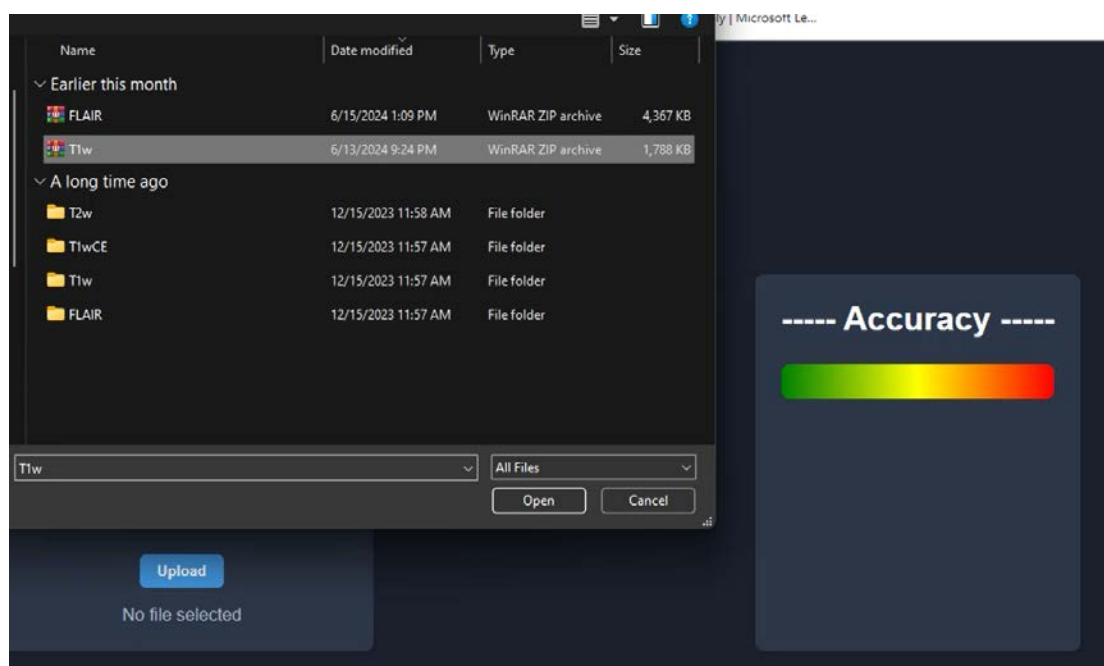
Figure 34: Loading Dicom Zip to Frontend
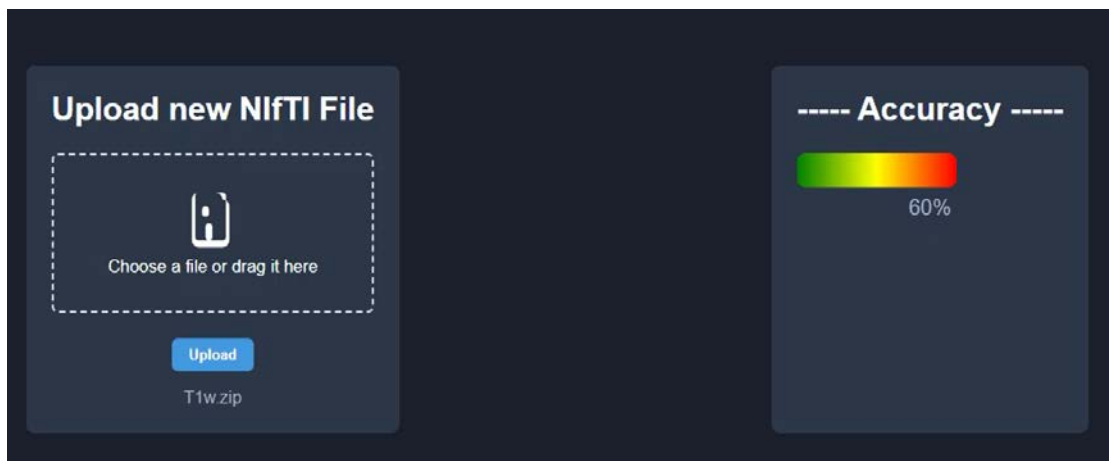
Figure 16: Color Bands Highlighting the Risk of Glioblastoma

5.3. Frontend User Interface

The frontend of the Glioblastoma Detection web application is designed with user experience in mind, using HTML, CSS, and JavaScript for a modern, responsive, and visually appealing interface. The `upload.html` template is divided into two main sections: the hero section and the upload section. The hero section features a full-screen video background that creates an engaging introduction to the application. The content within this section includes a title, a brief description of glioblastoma, and a button that links to an external visualization tool. The upload section provides a user-friendly interface for uploading MRI scans. A well-styled form allows users to select or drag-and-drop DICOM files for analysis. The section is designed with clean, modern aesthetics, including hover effects and transitions that enhance the overall user experience. The interface ensures that users can easily navigate and interact with the application, facilitating smooth and efficient file uploads.
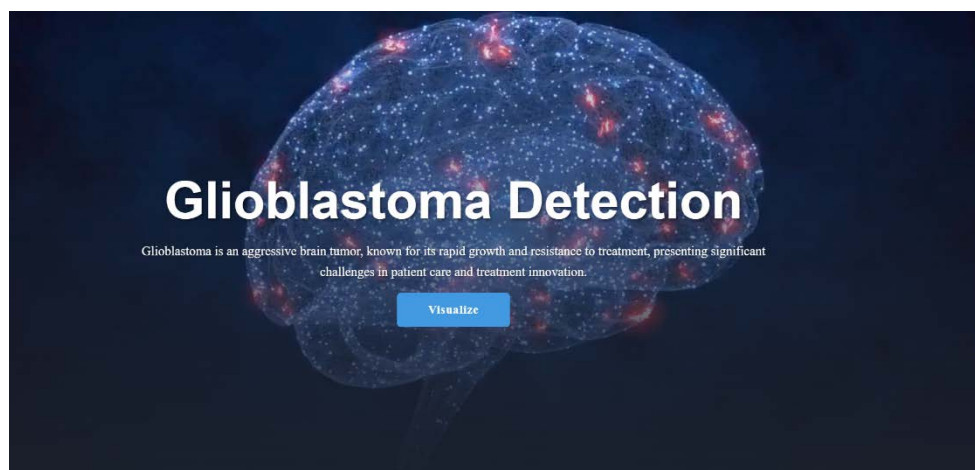

Figure 17: Front End User Interface

5.4. 3D Model Rendering

The provided HTML and JavaScript files collectively create a web-based application for 3D rendering and visualization of medical imaging data, specifically NIfTI files commonly used in neuroimaging. The HTML structure defines a basic interface with a navigation menu and a canvas for rendering 3D images. The menu offers options for File, View, Color, and Shader settings, each containing sub-options for interacting with the visualization. JavaScript files `nifti-reader.js`, `FileSaver.js`, and `volume-renderer.js` are integral to the application's functionality, handling tasks such as reading NIfTI files, saving screenshots, and rendering the 3D images.

The 3D rendering process begins with initializing WebGL on the canvas element and setting up various shaders for processing the volume data. The `loadVolume` function reads and parses NIfTI files, extracting the necessary data for rendering. The `glDraw` function manages the rendering, including setting up view and projection matrices, handling lighting, and drawing the 3D volume using WebGL. User interactions are facilitated through menu options that allow changes in view orientation, color schemes, and shaders. Additionally, users can adjust opacity and quality through keyboard inputs and capture screenshots of the current rendering. This application provides a robust framework for neuroimaging visualization, enabling interactive exploration of 3D volumes with a range of customization options directly within a web browser.

This integration is particularly valuable for visualizing the complex structures within MRI scans, providing insights that are critical for medical analysis and decision-making. In the hero section of the `upload.html` template, a button is included that directs users to Visualize.html, allowing them to explore and visualize their MRI data in 3D. This feature significantly enhances the application's functionality, making it not only a tool for prediction but also a platform for detailed data visualization. By leveraging this, the application provides users with a robust and interactive means of understanding their medical data, thereby supporting better-informed healthcare decisions.
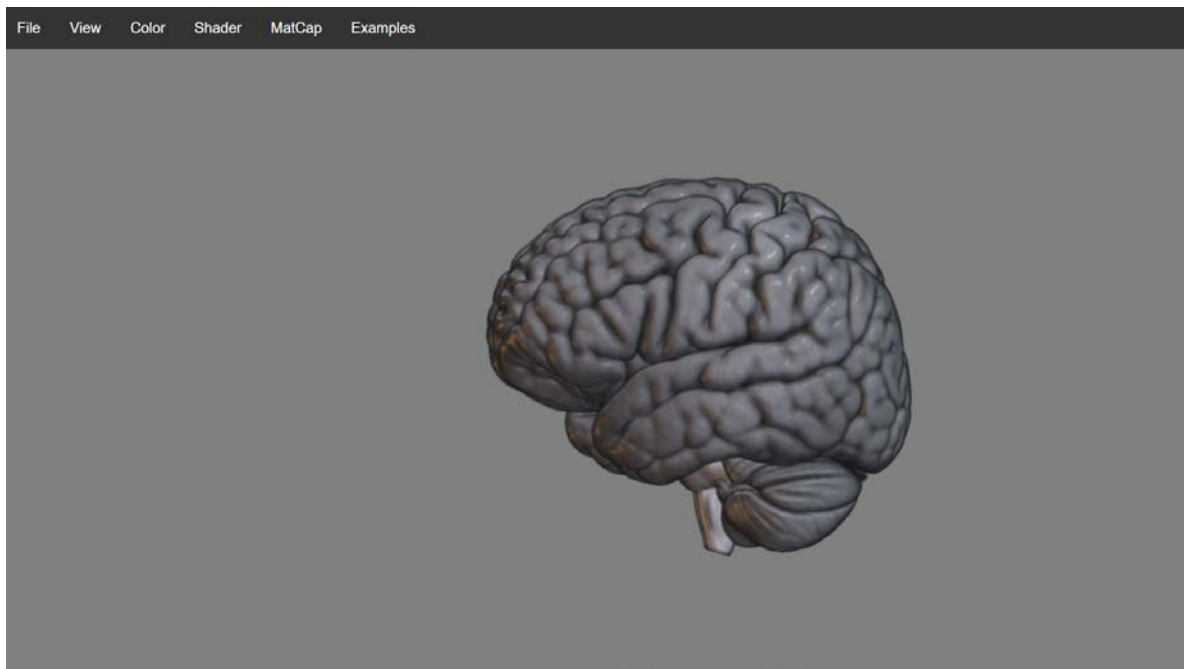
Figure 18: 3D Model Rendering
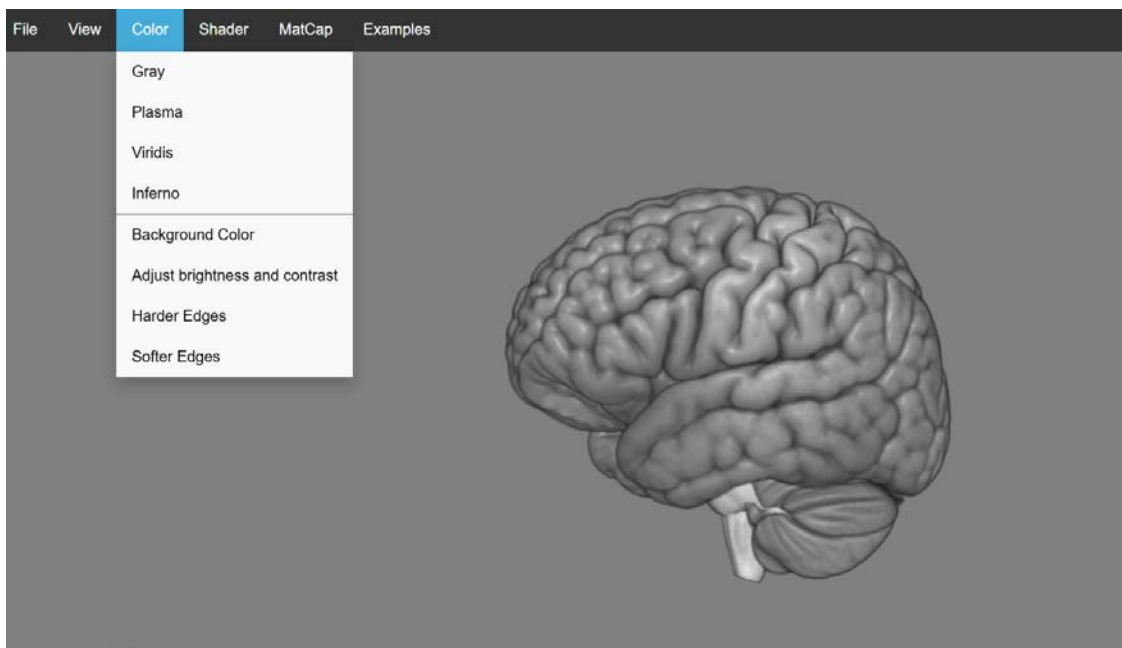
Figure 38: Color, Contrast and Lighting adjustments

5.5. Summary

The Glioblastoma Detection web application effectively combines Flask's backend capabilities with a modern and user-friendly frontend to deliver a powerful tool for medical diagnosis. The seamless integration of a trained machine learning model with

Flask allows for real-time prediction of glioblastoma from MRI scans. The thoughtfully designed frontend ensures an engaging and intuitive user experience, while the integration of MRIcroWeb offers advanced 3D visualization capabilities. Together, these components create a comprehensive application that enhances the process of glioblastoma detection and supports medical professionals and patients in making informed decisions

Chapter 6

Conclusion

6.1. Summary

The main idea of the project is to improve current approaches to the diagnosis and treatment of glioblastoma, a fatal type of brain tumor, using radiogenomics and AI technologies. By designing AI algorithms to predict the genetic subtypes of glioblastoma from MRI scans, the project aims to offer minimally invasive stratification for tailored treatment regimens. This approach can enhance patient prognosis and increase survival rates.

This undertaking is crucial given its potential to improve medical diagnosis and treatment, have direct clinical applications, promote research in medical imaging and AI, facilitate data sharing, and make a positive global impact on healthcare, especially in resource-scarce regions. By leveraging the trained CNN model for evaluation and prediction tasks, healthcare practitioners can gain valuable insights into the presence of brain tumors in MRI scans, facilitating timely diagnosis and treatment decisions.

After 60 epochs of training, the model achieved a validation accuracy of 95.93%, with the loss decreasing to 0.02%. Precision was calculated at approximately 96.65%, and recall was around 94.45%. The f1 score achieved was 95.54%. The confusion matrix showed 2119 true positives and 2099 false negatives.

The methodology involves data collection and preprocessing, 3D object creation, model selection, training, assessment, interpretability, clinical validation, and fine-tuning. The stakeholders include medical personnel, technical industries, organizations such as the NIH and FDA, and most crucially, glioblastoma patients and their families.

6.2. Recommendations or Future Work

Moving forward, several areas of future work can be identified to enhance the project's outcomes.

- Addition of more similar datasets to increase data for better accuracy. More datasets can be of Brats 2017 till 2020 and other MRI datasets.
- Similar methodology can be adapted for other cancer and tumors such as breast cancer, various type of gliomas etc. Better accuracy may help in early detection of the cancer as well.

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