RGNN: Radiomic Graph Neural Network For Glioma Grading Utilizing 3D Magnetic Resonance Images with Clinical Significant Features

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This Report Presented in Partial Fulfillment of the Requirements for the Degree of Bachelor of Science in Computer Science and Engineering

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APPROVAL

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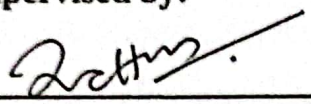

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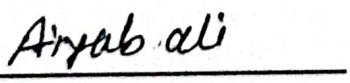

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ABSTRACT

Glioma, a prevalent and devastating brain tumor, presents formidable challenges in diagnosis and prognostication. This study endeavors to enhance glioma grading accuracy by leveraging 3D MRI data and a comprehensive array of medical features extracted through the PyRadiomic framework. Given the diverse manifestations of glioma tumors and their profound impact, an advanced approach is imperative for precise grading. This investigation meticulously extracts six distinct medical features, including First Order Statistics, Shape-based (3D), Gray Level Co-occurrence Matrix, Gray Level Run Length Matrix, Gray Level Size Zone Matrix, Neighboring Gray Tone Difference Matrix, and Gray Level Dependence Matrix. These features, computed based on tumor annotation, provide detailed characterizations of glioma tumors, elucidating their intricacies.

To augment glioma grading accuracy further, various machine learning algorithms are employed. A pivotal contribution is the introduction of the Radiomic Graph Neural Network (RGNN) model, tailored for graph-based data, where nodes symbolize entities, and edges denote intricate relationships between them. The core objective of the RGNN model is to generate low-dimensional vector representations (embeddings) for nodes within the graph, preserving underlying structural and relational information. This innovative RGNN model significantly enhances precision in differentiating between various glioma grades. Specifically, for the Native T1 stage of MRI and T2-weighted (T2) stages, the proposed RGNN model achieves an unprecedented accuracy of 99.00%. This outperforms existing methods and sets a new benchmark in glioma tumor grading based on medical features, leveraging 4 stages of 3D magnetic resonance imaging.

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CHAPTER 1

Introduction

1.1 Introduction

The widespread primary brain tumors, gliomas, have a catastrophic impact on people's health. These sneaky growths originate from the glial cells that support the nerve cells, unlike the prominent neurons in the nervous system's orchestra. The delicate ballet of electrical signals that controls our thoughts, motions, and very existence is disrupted when these backstage workers go rogue, leading to uncontrollable growth and mutations. This essay explores the intricacies of gliomas, including their impact, frequency, and the continuous fight against this formidable adversary. Neurons are backed both physically and chemically by glial cells, in addition to uphold their surroundings. Glial cells reside within both the peripheral and central nervous systems, and are sometimes referred to as the "glue" of the nervous system. A tumor of the central nervous system that develops from glial cells is called a glioma [1]. Gliomas are primary brain tumors that are believed to originate from progenitor or neuroglial stem cells. Usually, they are cancerous. Gliomas rarely spread to other parts of the body. However, they pose a threat to life because they can spread swiftly through the spine and brain. Gliomas afflict individuals across the age spectrum, though their grip tightens around adults between 45 and 55 years old [1]. Each year, an estimated 5-7 per 100,000 individuals fall victim to this unwelcome guest in their cranium, with males facing a slightly higher risk than females [2]. However, the prognosis varies greatly, a complex tango between the tumor's grade, its chosen location within the intricate landscape of the brain, and the body's valiant response to treatment [3]. The aggressive conductors of this discordant tune, high-grade gliomas, proudly display their malignancy with a median survival of only 12–15 months. These nimble and inconspicuous intruders are distinguished by their quick, infiltrative growth, which allows them to blend in with the brain's structure and elude treatment measures [4]. On the other hand, low-grade gliomas proceed more slowly and methodically. Five to ten years may pass while they are present, and in some lucky cases, remission or a protracted ceasefire may even be feasible [5]. Gliomas are prima
dangerous not just because of their physical presence but also because of the way
interfere with brain function. These unwanted tumors squeeze and deform healthy b

tissue as they grow, causing havoc to spread across the fragile neural network. Numerous neurological symptoms are indicative of this disturbance, which highlights the tumor's effect on the mind's orchestra [6]. The growths compose a discordant symphony that includes a variety of symptoms, including headaches, seizures, speech and language difficulties, vision impairments, muscular weakness or paralysis, cognitive decline, and personality abnormalities [7]. In addition to the short-term consequences, these tumors may result in long-term complications like a higher chance of developing additional brain tumors, side effects from radiation therapy, difficulties from chemotherapy, and the mental and psychological anguish that comes with facing such a strong opponent.

The majority of glioma patients require multiple therapies. These could consist of chemotherapy, radiation treatment, or surgery. Young individuals have the best chance of surviving when their gliomas are low-grade, or slow-growing [8]. Glioma causes upward of about 28% of all primary brain tumors as well as is a rare but highly fatal disease with a yearly frequency of 2-3 cases per 100,000 individuals in the United States of America [9-12]. All ages are susceptible to gliomas, although the probability rises with age. Low-grade gliomas can happen to adolescents, but these tumors are more common in older adults.Gliomas have precise causes that have not yet been determined. However, exposure to ionizing radiation and specific genes are potential contributors to risk.The standard course of treatment entails a mix of radiotherapy, chemotherapy, and surgery. Even with more aggressive treatment plans, the end result for more advanced tumors is still uncertain.

Radiomics is an innovative feature transformation approach that extracts features from radiological imaging data that's hard for the individual's eye to see but are in practice pertinent. With the goal to boost diagnosis and planning of treatment machine learning models are being studied The distinction between feature extraction and feature selection should be noted. Finding as many features as possible that describe the gathered data is the aim of feature extraction. The goal of feature selection is to prevent overfitting of the data while reducing the large number of extracted features to a manageable number, which can then be generalized as patterns that reliably identify the concepts concealed within the data. Overfitting of data is an issue in the field of machine learning whe the model performs poorly when new data is presented for analysis, despite the ana yielding outstanding outcomes when applied to the training data [13]. When it com

describing the form, texture, and various other attributes of tumors, radiomics can do a remarkable job. It is possible to forecast the nature, rage, and effect of medication for a tumor using the retrieved data. Radiomics has the ability to track developments in tumor properties over a period of time, which is useful in evaluating how well treatments like chemotherapy and radiotherapy are working.By evaluating alterations in the brain, it may be used for timely identification and tracking of neurological disorders such as Alzheimer's disease. Through analyzing coronary artery images, radiomics can figure out the chemical makeup of plaque and evaluate the risk of cardiac occurrences.It can be applied to the detection, prognosis, and examining of malignancies of the lungs. It aids in determining the nature of lung disorders like pulmonary fibrosis (PF) and chronic obstructive pulmonary disease (COPD).To gain a deeper understanding of the correlation between a patient's genetic composition and the radiomic characteristics of their tumors, radiomics and genomics are combined.

In this paper, graph neural networks have been used in conjunction with radiomic feature extraction on 3-dimensional magnetic resonance imaging (MRI) images to predict gliomas.Typically, image processing and graph theory techniques are used to represent relationships or connections between images in a graph network created with MRI images.Years of training are needed for the tedious, time-consuming process of manually evaluating medical images, such as brain tumor MRI scans, which is also frequently prone to inter-annotator variation. One long-standing problem that aims to address these is the automatic segmentation of medical images, which has significant potential advantages for both patients and doctors. Convolutional Neural Networks (CNNs) have become the de facto state-of-the-art methodology for this task in the last few years. In the deep learning community, graph-based neural networks, or GNNs, have received a lot of attention lately. By aggregating data over connected nodes, GNNs take advantage of the structural information found in graphical data, which enables them to efficiently capture relation information between data elements. In this work, we suggest segmenting brain tumors using a GNN-based method. We use a graph representation of 3D MRI scans of the brain, with nodes representing different regions and edges connecting neighboring regions [14].

1.2 Motivation

Glioma brain tumors pose a significant threat to human health, demanding accurate and efficient diagnostic tools for precise classification and prognosis. The motivation behind this research lies in addressing the critical need for advanced methods that can enhance our understanding and clinical management of gliomas. Traditional diagnostic approaches often fall short in providing the intricate details necessary for personalized treatment strategies. The utilization of 3D imaging data from the BraTS dataset offers a novel avenue to delve deeper into the complex architecture of gliomas. By leveraging cutting-edge technologies, such as pyradiomics, I aim to extract rich radiomic biomarkers from segmentation images, unlocking hidden patterns that may hold the key to robust tumor grading.

The significance of this research extends beyond conventional grading methodologies. The integration of machine learning algorithms serves as a powerful tool to analyze and interpret the vast array of radiomic features. Through rigorous evaluation, my goal is to establish a reliable and accurate classification system that surpasses existing standards, providing clinicians with a more nuanced understanding of glioma heterogeneity. Furthermore, the introduction of graph neural networks (GNNs) represents a pioneering step in the fusion of advanced imaging and artificial intelligence. GNNs inherently capture the spatial relationships within the 3D tumor data, offering a holistic perspective that aligns with the intricacies of glioma growth patterns. This novel approach not only aims to achieve state-of-the-art results in tumor grading but also contributes to the evolving landscape of medical image analysis.

Ultimately, this research strives to redefine the benchmarks in glioma grading, fostering advancements in precision medicine. The outcomes hold promise not only for improving diagnostic accuracy but also for informing tailored treatment strategies, ultimately leading to enhanced patient outcomes and a deeper understanding of the underlying biology of gliomas.

1.3 Rationale of the Study

The rationale behind the study of glioma grading lies at the intersection of pressing clinical needs and the advancement of medical science. Gliomas, being a heterogeneou

group of brain tumors, exhibit diverse molecular profiles and clinical behaviors. Accurate grading of gliomas is paramount for determining prognosis, guiding treatment decisions, and predicting patient outcomes. However, the inherent complexity and variability of gliomas pose a formidable challenge to traditional grading methods.

The motivation for this study arises from the imperative to transcend the limitations of conventional diagnostic approaches. The utilization of 3D imaging data from the BraTS dataset allows for a comprehensive analysis of the spatial and morphological intricacies of gliomas. This rich dataset provides an opportunity to explore novel avenues in glioma grading that capture the full spectrum of tumor characteristics, from subtle variations in texture to complex structural patterns.

By employing state-of-the-art techniques such as pyradiomics, the study seeks to extract radiomic biomarkers from segmented images, translating intricate visual information into quantifiable features. This not only enhances the granularity of glioma characterization but also lays the foundation for a more robust and reproducible grading system. Machine learning algorithms play a pivotal role in this research, serving as intelligent tools to discern patterns within the vast radiomic landscape. The integration of these algorithms aims to surpass the limitations of manual grading and establish a more objective and data-driven approach.

Furthermore, the incorporation of graph neural networks (GNNs) adds a novel dimension to the study. GNNs, designed to capture spatial relationships within complex networks, are particularly apt for modeling the intricate architecture of gliomas in 3D space. This innovative application of GNNs seeks to elevate the accuracy of glioma grading, thereby contributing to a paradigm shift in neuro-oncological diagnostics.

In essence, the rationale for this study is rooted in the urgent clinical need for improved glioma grading methodologies. Through the amalgamation of advanced imaging, radiomics, and machine learning, this research aspires to redefine our understanding of gliomas, ushering in a new era of precision medicine with profound implications for patient care and treatment strategies.

1.4 Research Questions

(a) How do the identified limitations in mapping selected features with significant medical relevance impact the robustness and reliability of the proposed glioma grading model?

(b) From the perspective of the higher computational complexity associated with the model, how can the research address or mitigate potential resource constraints, ensuring practical implementation and scalability in real-world clinical settings?

(c) What strategies and methodologies can be employed to rigorously test for overfitting and underfitting in the machine learning models, ensuring their generalizability and effectiveness across diverse patient populations?

(d) How do various factors, such as imaging noise, variations in acquisition protocols, and the inherent complexities of 3D MRI images, impact the overall quality of service in glioma grading?

(e) What steps can be taken to enhance the robustness of the model under such real-world conditions?

(f) Considering the potential challenges in translating research findings into clinical practice, what steps can be taken to facilitate the seamless integration of the proposed glioma grading model into routine diagnostic workflows, ensuring its practical utility for healthcare professionals?

(g) What measures are in place to tailor the grading system to individualized clinical needs, considering the heterogeneous nature of gliomas?

(h) How can it ensure interpretability and provide transparent insights to clinicians, facilitating informed decision-making in the diagnosis and treatment planning for glioma patients?

1.5 Expected Output

(a) The research is expected to identify clinically significant imaging biomarkers associated with glioma grading, providing insights into the nuanced characteristics of different tumor grades.

(b) The introduction of RGNN, a hybrid deep learning model, is anticipated to enhance the accuracy of glioma grading through the capture of intricate patterns within 3D MRI images.

(c) The output includes the successful integration of multiple open-access BraTS databases of 3D MRI images, accompanied by a detailed explanation of computational requirements and a rigorous evaluation for overfitting and underfitting, ensuring model robustness.

(d) The developed model is envisioned to assist neurophysicians in accurately staging glioma tumors by incorporating clinical radiomic features into the diagnostic process.

(e) The ultimate output aims to showcase the strengths and advantages of the proposed method, demonstrating a significant improvement in diagnostic accuracy and reliability in glioma grading through the innovative use of critical imaging biomarkers and the RGNN model.

1.6 Report Layout

Chapter 1 offers an overview of the research, covering the motivation, rationale, research questions, expected outputs, and the report's layout.

Chapter 2 delves into a comprehensive review of related literature, featuring a comparative analysis, summarizing key findings, outlining the scope of the problem, and identifying challenges.

Chapter 3 has proposed the methodology, encompassing the data collection procedure, the dataset utilized, statistical analysis, and implementation requirements for the research.

Chapter 4 explains the experimental setup, presents the results analysis, and engages in a thorough discussion of the findings, providing valuable insights into the efficacy of the proposed model.

Chapter 5 concludes the study by addressing its impact on society and the environment, discussing ethical aspects, and presenting a sustainability plan for the proposed methodology.

This final chapter provides a concise summary of the study, outlines key conclus drawn from the research, and suggests implications for further studies in the field.

Chapter 2

Background

2.1 Related Work

Radiomics has been used recently to uncover information that is hidden in medical images. It has greatly aided researchers in their efforts, particularly in the identification and classification of tumors [9,10]. Radiomics works step by step likely: splitting the region of interest, collecting the features from the ROIs, choosing and decreasing the dimensions of the characteristics extracted, and building the model. Because of its outstanding efficacy, precision, and effectiveness when compared to traditional clinical examination methods, computer-aided diagnosis technology is often referred to as the physician's "third eye" and is essential for the identification and classification of numerous diseases.[15-18]

Hafeez et. all proposed a lightweight convolutional neural network (CNN) is proposed for the classification of glioma grading, demonstrating superior performance on benchmarked datasets (Brats-2017, Brats-2018, Brats-2019) and a locally developed dataset from Bahawal Victoria Hospital, Pakistan. The model outperforms state-of-the-art pre-trained CNNs, including resnet18, squeezenet, and alexnet, achieving maximum accuracy, specificity, and sensitivity at 97.85%, 98.88%, and 99.88% on benchmarked data and 98.89%, 99.28%, and 99.77% on the local dataset. These results establish the proposed CNN as a highly effective tool for glioma grading, surpassing recent state-of-the-art studies in the field [19]. Rizwan et. all [20] introduces a Gaussian Convolutional Neural Network (GCNN) for Brain Tumor (BT) detection using Magnetic Resonance Imaging. The model achieves 99.8% accuracy in classifying pituitary, glioma, and meningioma tumors and 97.14% accuracy in distinguishing glioma grades (Grade-two, Grade-three, and Grade-four). With datasets comprising 3064 and 516 images, the proposed approach demonstrates robust performance, emphasizing its efficiency for accurate multi-class categorization in BT diagnosis. Özkaya et. all [21] presented t
novel approaches for brain tumor classification and segmentation using Convolutio
Neural Networks (CNNs). The first approach achieves 99.85% accuracy in distinguish
High-Grade Glioma (HGG) and Low-Grade Glioma (LGG) tumors. The second appro

integrates normalization, modality fusion, and CNN models for HGG-LGG classification, while a segmentation algorithm yields a 70.58% Dice Similarity for complete tumor segmentation. Results suggest the algorithm's potential for robust brain tumor diagnosis and feature extraction. Chaddad et. all [22] proposed novel multimodal image features based on Joint Intensity Matrix (JIM) for fine-grained texture analysis in lower-grade glioma (LGG) tumors. Utilizing T1-weighted, post-contrast, FLAIR, and T2-weighted MR images, the expanded JIM features show significant associations with genetic status (IDH1, ATRX, TP53, and 1p/19q codeletion) and patient survival outcomes. Random Forest classification achieves a maximum AUC of 78.59% for IDH1 status and 86.79% for predicting short and long LGG patient survival, with JIM features emerging as highly informative predictors. Sultan et. all conducted [23] a deep learning (DL) model based on a convolutional neural network for the classification of various brain tumor types using two distinct datasets. The first dataset classifies tumors into meningioma, glioma, and pituitary tumor categories, while the second differentiates between the three glioma grades (Grade II, Grade III, and Grade IV). Leveraging T1-weighted contrast-enhanced images, the DL model achieves remarkable performance with overall accuracies of 96.13% and 98.7% for the respective datasets, highlighting its efficacy in multi-classifying brain tumors. Al-saffar et. all [24] introduced a novel method, Mutual Information-Accelerated Singular Value Decomposition (MI-ASVD), for efficient feature selection in brain image classification. The proposed system, encompassing pre-processing, clustering, tumor localization, feature extraction, MI-ASVD, and classification stages, demonstrates superior performance in classifying MRI brain images into healthy, high-grade glioma, and low-grade glioma categories. By integrating MI-ASVD into the feature selection process, the simplified residual neural network achieves an accuracy of 94.91%, outperforming standard dimensionality reduction methods and state-of-the-art techniques in brain image classification. Tupe-Waghmare et. all [25] introduced a novel method, Mutual Information-Accelerated Singular Value Decomposition (MI-ASVD), for efficient feature selection in brain image classification. The proposed system, encompassing pre-processing, clustering, tumor localization, feature extraction, MI-ASVD, and classification stages, demonstrates superior performance in classifying MRI brain images into healthy, high-grade glioma, and
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simplified residual neural network achieves an accuracy of 94.91%, outperforr

standard dimensionality reduction methods and state-of-the-art techniques in brain image classification. Ullah et. all [26] presented an evolutionary lightweight model, a modified Multimodal Lightweight XGBoost, for brain cancer detection and classification using MRI scans. Utilizing BraTS 2020 dataset, the model achieves impressive results with 93.0% accuracy, 0.94 precision, 0.93 recall, and a 0.94 F1 score. The proposed approach demonstrates potential as a valuable tool for early diagnosis and effective treatment planning of brain tumors, showcasing promise for aiding in early cancer detection and treatment.

Xiaokang Liang et. all proposed a Diabetic Foot(DF) prediction model through fundus images by 19 kinds of radiomics features. They achieved 92% accuracy in their prediction model using 2184 fundus images (2D)[27]. Radiomics features capture different aspects of the image, such as texture, orientation, phase, and gradient, offering an extensive overview of the visual data. A two-step feature selection technique is used to find the best-suited radiomics features, and finally, 19 features are chosen and employed to train a support vector machine model, which is evaluated using a five-fold cross-validation approach on an extensive set containing healthcare data.

Vanessa De Araujo Faria et. All used an ANN model with 105 extracted statistical/morphological image features of the teeth using PyRadiomics. The current investigation uses features taken from a panoramic radiograph to introduce ANN for the prediction and identification of radiation-related caries (RRC) or regular caries in head and neck cancer (HNC) patients receiving radiation therapy (RT). 420 teeth images (3D) were labeled for two purposes, one for detection and another for prediction. For the detection approach (the first label map), each healthy tooth was labeled “one” (class 1) and tooth with caries with “two” (class 2) [28].

Pan Sun et. all [29] assessed the effectiveness of 15 classification techniques and 16 feature selection techniques for radiomics-based glioma grade prediction. The aim of this research is to evaluate the accuracy of predictions of different radiomics feature selection and classification techniques in the glioma tumor grading process, with a focus differentiating between low-grade gliomas (LGG) and glioblastoma (GBM). MRI ima were used in the process to gather data from 210 GBM and 75 LGG patients.Us various types of MRI, they gathered radiomics features from different parts of the tun

The investigation demonstrated that the selection of machine learning classifiers and feature selection techniques had a substantial impact on the predictive performance of glioma grading. The pairing of MLPC and L1-SVM performed better than the others.The results provide information about how to increase the precision of radiomics-based predictions in glioma grading, which may have important ramifications for treatment choices. The effectiveness of radiomic features taken from two-dimensional (2D) and three-dimensional (3D) regions of interest (ROIs) in characterizing gastric cancer (GC) was compared by Lingwei Meng et al[18]. The investigation analyzes their role in three tasks associated with gastric cancer: i determining the metastasis of lymph nodes (T LNM), and predicting lymphovascular invasion (T LVI) and identifying pT4 or other pT stages (T pT). 539 GC patients from four separate healthcare institutions were enrolled in the investigation. For analysis, the patients were split up into validation and training cohorts. After radiologists annotated the 2D and 3D ROIs, radiomic characteristics were collected.In order to assess the effectiveness of 2D and 3D radiomic features, three tasks (T LNM, T LVI, and T pT) were defined.Specific selection of features and model building techniques were applied to every combination of the three tasks and the two modalities (2D or 3D). A total of six machine learning models (Model LNM 2D, Model LNM 3D, etc.) were developed for various combinations and assessed according to how well they could characterize gastric cancer.

2.2 Comparative Analysis and Summary

A comprehensive survey [30] of machine learning-based approaches for Glioma classification, emphasizing the challenging nature of this medical task. The proposed approach introduces a hybrid ensemble learning model and hybrid feature extraction method, combining Discrete Wavelet Decomposition, Central Pixel Neighborhood Binary Pattern, and Gray Level Run Length Matrix for accurate Glioma classification into Low and High grades from fused MRI sequences. Utilizing the Improved eXtreme Gradient Boosting classifier, the proposed method achieves a high accuracy of above 90% on a local dataset and is compared with existing approaches, showcasing its effectiveness across various MRI fusion combinations on global datasets like BRATS 2013 and BRATS 2015. A radiomics [31] approach utilizing various machine lear classifiers was employed to determine glioma grading using 285 cases from the B

Tumor Segmentation 2017 Challenge. The multi-modal data included T1-weighted, T1-contrast enhanced, T2-weighted, and FLAIR images, with manual annotations for enhancing tumors, non-enhancing tumors, necrosis, and edema. The minimum redundancy maximum relevance algorithm was utilized for feature selection, resulting in five significant features. Logistic regression, support vector machine, and random forest classifiers demonstrated robust performance, achieving an average AUC of 0.9400 for training cohorts and 0.9030 for test cohorts, showcasing the effectiveness of the radiomics-based approach in glioma grading. This study [32] aimed to assess the diagnostic accuracy of machine learning-based radiomics in distinguishing high-grade gliomas (HGG) from low-grade gliomas (LGG) and identify potential covariates influencing diagnostic accuracy. A comprehensive literature search yielded five retrospective original articles, encompassing LGG and HGG subjects. The pooled sensitivity for diagnosing HGG was notably higher at 96%, with a 95% confidence interval of 0.93 to 0.98, surpassing the specificity for diagnosing LGG at 90% with a 95% CI of 0.85 to 0.93. The results emphasize the promising potential of ML-based radiomic analysis in glioma classification.

2.3 Scope of the Problem

(a) Implementation of thorough testing for overfitting and underfitting to enhance model robustness.
(b) Optimization of computational complexity for improved efficiency in processing benchmark 3D BraTS images.
(c) Integration of feature importance analysis and testing to provide insights into the significance of extracted radiomic biomarkers.
(d) Comprehensive performance comparisons between the developed model and existing methods to establish benchmarking.
(e) Exploration of similarities between selected radiomic features and clinically relevant medical features for better interpretability.

2.4 Challenges

Brain cancers collectively are not as prevalent as other cancers, their impac significant. They represent almost 2% of all adult cancers and 8% of childhood can

globally, with GBM accounting for over half of adult cases [33]. The danger lies in the brain's critical role in all bodily functions, and tumors can cause devastating neurological deficits, impacting movement, speech, cognition, and even personality. Early diagnosis and intervention are crucial, as GBM is highly invasive and rapidly progressing. An estimated 296,000 new GBM cases were diagnosed worldwide in 2020, with a higher prevalence in developed countries [34]. Age is a significant risk factor, with incidence increasing after 50. While GBM isn't the most common cancer, its location and aggressive nature make it a major public health concern. espite advancements in surgical techniques, radiation therapy, and chemotherapy, GBM remains largely incurable. Median overall survival is only 15 months, and the five-year survival rate hovers below 10% [35]. This stark reality underlines the need for innovative diagnostic and therapeutic strategies.

Glioblastoma presents a formidable challenge in the realm of glioma tumor grading, demanding innovative solutions to address its complex nature. Below are some of the key challenges faced in this endeavor:

(a) The absence of exploration into the medical relevance or similarity of selected radiomic features poses a challenge, potentially limiting the clinical interpretability of results.

(b) This limitation hinders a comprehensive understanding of the clinical significance of extracted biomarkers.

(c) Existing studies on glioma grading often lack attention to overfitting and underfitting concerns, revealing potential gaps in model validation.

(d) The processing of 3D BraTS images poses a challenge due to higher computational complexity, urging the need for streamlined approaches.

(e) There is a notable gap in studies concerning radiomic biomarker features, with insufficient focus on feature importance analysis.

(f) A significant challenge lies in the absence of rigorous performance benchmarking against other models, making it difficult to assess the proposed model's comparative effectiveness.

(g) Enhancing the interpretability of radiomic biomarkers is crucial for their integration into an effective clinical support system for glioma grading.

Chapter 3

Research Methodology

3.1 Research Subject and Instrumentation

The focus of this research is to advance the field of glioma brain tumor grading through a comprehensive and innovative approach, leveraging state-of-the-art techniques in medical imaging, radiomics, and machine learning. The objective is to enhance the accuracy and efficacy of glioma grading classification, particularly in the challenging context of glioblastoma (GBM), a highly aggressive and prevalent form of brain cancer.

Gliomas, encompassing various grades and types, pose a significant challenge in clinical settings due to their diverse characteristics and the critical need for accurate grading. The research primarily centers on glioblastoma, a malignant and fast-growing glioma variant, accounting for a substantial portion of global glioma cases. The urgency to address glioblastoma stems from its grim prognosis, with a median survival of only 15 months and a five-year survival rate below 10%. The lack of a cure underscores the critical importance of precise grading and early diagnosis.

The instrumental backbone of this research involves a sophisticated integration of cutting-edge technologies and methodologies, each playing a crucial role in the comprehensive analysis and classification of gliomas grading.

- 3D Image Utilization: The foundation of the research lies in the utilization of three-dimensional (3D) images derived from the BraTS dataset. These images provide a detailed and holistic representation of the glioma structures, allowing for a nuanced understanding of their spatial intricacies.
- Radiomic Biomarker Extraction: Pyradiomics, a powerful Python library specialized in radiomic feature extraction, serves as a pivotal instrument in the research. Through Pyradiomics, a diverse array of radiomic biomarkers is extracted from the segmented images, capturing intricate details that may not be discernible through traditional imaging analysis.
- Machine Learning Algorithm: A robust machine learning algorithm is emp[illegible] to scrutinize and validate the performance of the radiomic biomarkers. This s[illegible]

critical for discerning the discriminatory power of the extracted features and ensuring the model's ability to accurately classify different glioma grades.

- Graph Neural Network (GNN): Introducing innovation into the classification process, a Graph Neural Network is incorporated into the research framework. GNNs are adept at capturing complex relationships within data, particularly beneficial in the intricate landscape of glioma structures. The integration of GNNs aims to push the boundaries of classification accuracy, contributing to the state-of-the-art results expected from this research.

This research, with its focus on glioblastoma and the integration of advanced instrumentation, aspires to contribute substantially to the field of glioma grading. By enhancing accuracy and reliability in classification, the outcomes of this research hold the potential to significantly impact clinical decision-making, treatment planning, and ultimately improve the survival rates and quality of life for patients affected by gliomas.

3.2 Data Collection Procedure

The BraTS’2019 [36] and BraTS’2020 [37] challenges leverage a comprehensive dataset consisting of clinically acquired pre-operative multimodal MRI scans of glioblastoma (GBM/HGG) and lower-grade glioma (LGG) from diverse institutions. These scans, obtained through routine clinical procedures, serve as the training, validation, and testing data for the challenges, ensuring a multi-institutional representation. The dataset comprises NIfTI files (.nii.gz) containing mpMRI scans, encompassing native (T1), post-contrast T1-weighted (T1Gd), T2-weighted (T2), and T2 Fluid Attenuated Inversion Recovery (T2-FLAIR) volumes. Notably, these scans exhibit variations in acquisition protocols and originate from different scanners across various medical facilities, contributing to the richness and diversity of the dataset.

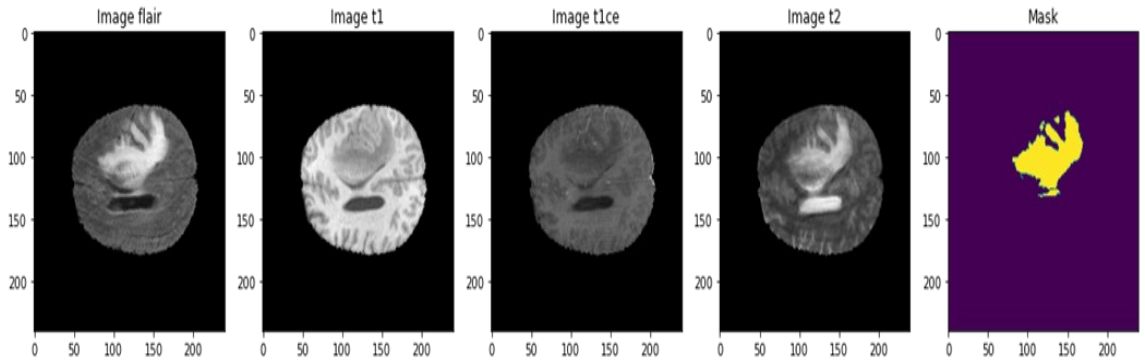

Fig 1: Different Stages of 3D MRI with Corresponding Annotation

In the Fig 1, The different MRI stages employed in the BraTS'2019 and BraTS'2020 challenges provide a comprehensive view of gliomas through distinct imaging modalities: a) Native (T1): The native T1-weighted MRI scan captures the baseline anatomical structure of the brain, highlighting differences in tissue density. It is particularly useful for visualizing the overall brain morphology. b) Post-contrast T1-weighted (T1Gd): This stage involves acquiring T1-weighted images after the administration of a contrast agent. The contrast-enhanced T1-weighted scan emphasizes areas with increased vascularization and blood-brain barrier disruption, aiding in the identification of abnormal tissue, such as glioma lesions. c) T2-weighted (T2): The T2-weighted MRI scan emphasizes differences in water content and is sensitive to pathological changes in tissues. T2-weighted images provide detailed information about edema, cysts, and other tissue abnormalities, contributing to a more comprehensive understanding of the glioma's characteristics. d) T2 Fluid Attenuated Inversion Recovery (T2-FLAIR): The T2-FLAIR sequence is designed to suppress signals from cerebrospinal fluid, thereby enhancing the visibility of lesions and abnormalities. This modality is particularly effective in highlighting areas of hyperintensity associated with glioma, facilitating the assessment of tumor boundaries and surrounding edema. The combination of four MRI stages offers a multifaceted perspective, allowing for a thorough evaluation of gliomas at different levels, from basic anatomical structures to specific pathological features associated with the disease. In this study, these two datasets are merged and investigated to gain the glioma grading diversity with medical radiomic-based features to assist in glioma’s clinical decision. Table 1 illustrates the composition of the dataset utilized in our research, delineating

distribution of Higher Grade Glioma (HGG) and Lower Grade Glioma (LGG) across the BraTS'2019 and BraTS'2020 datasets, as well as their combined representation.

Table 1: Composition of Glioma Dataset

Dataset	HGG	LGG	Total
BraTS’2019	293	76	369
BraTS’2020	259	76	335
Combined BraTS	552	152	704

In the BraTS'2019 dataset, 293 subjects were identified with higher grade glioma (HGG), and 76 subjects exhibited lower grade glioma (LGG), resulting in a cumulative total of 369 subjects. Similarly, the BraTS'2020 dataset consisted of 259 HGG subjects, 76 LGG subjects, and a total of 335 subjects. Upon merging the two datasets to create the Combined BraTS dataset, our comprehensive compilation incorporated 552 HGG subjects and 152 LGG subjects, yielding a grand total of 704 subjects. It is imperative to note that each subject in the dataset was meticulously characterized by a set of four-stage MRI 3D images, encompassing native (T1), post-contrast T1-weighted (T1Gd), T2-weighted (T2), and T2 Fluid Attenuated Inversion Recovery (T2-FLAIR) sequences, as outlined in our previous description. Additionally, annotations corresponding to these imaging modalities were provided by clinical experts, enhancing the dataset's utility for glioma grading diagnosis.

3.3 Statistical Analysis & Feature Extraction

Radiomics, a transformative approach in medical imaging, involves the extraction and analysis of intricate information embedded within medical images, transcending wh perceptible to the human eye [38]. In this research, PyRadiomics, an open-so platform, emerges as a pivotal tool for the extraction of 120 radiomics features from

brain image region [39]. These features, stored in a comma-separated value (CSV) format, encompass a diverse spectrum of information, contributing significantly to the understanding of complex structures within the brain.

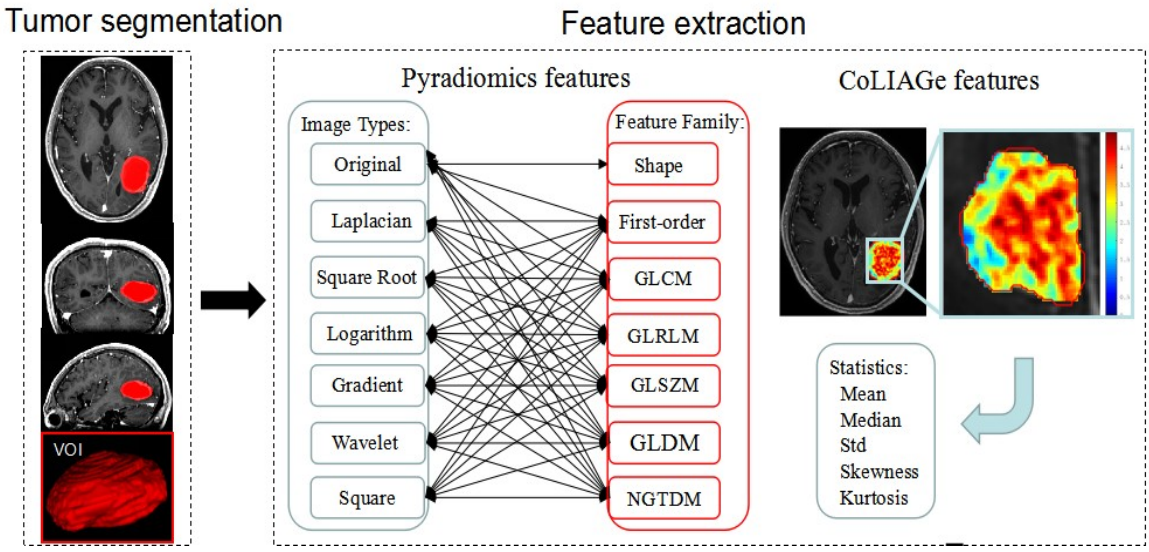

Fig 2: Statistical Analysis & Feature Extraction Mechanism

In the Fig 2, PyRadiomics offers a comprehensive suite of features categorized into seven distinct classes: First Order Statistics, Shape-based (3D and 2D), Gray Level Co-occurrence Matrix (GLCM), Gray Level Run Length Matrix (GLRLM), Gray Level Size Zone Matrix (GLSZM), Neighbouring Gray Tone Difference Matrix (NGTDM), and Gray Level Dependence Matrix (GLDM). The richness of these feature classes allows for a nuanced characterization of brain structures and pathology, providing a holistic view beyond the limitations of conventional imaging [40]. The breakdown of features within each stages of MRI are as follows:

- First Order Statistics (19 features): Capturing fundamental statistical metrics, these features provide insights into the distribution of voxel intensities within the image region.
- Shape-based (3D and 2D) (26 features): Encompassing shape-related attribut both three-dimensional and two-dimensional contexts, these features contribu understanding the geometric properties of the brain regions.

- GLCM (24 features): The Gray Level Co-occurrence Matrix features offer information on the spatial relationships of voxel intensities, shedding light on textural patterns within the images.
- GLRLM (16 features): The Gray Level Run Length Matrix features quantify the lengths of consecutive voxels with identical intensity values, capturing the coarseness or fineness of structures.
- GLSZM (16 features): Gray Level Size Zone Matrix features delineate the size and spatial distribution of homogeneous intensity regions within the images.
- NGTDM (5 features): Neighbouring Gray Tone Difference Matrix features focus on the differences in tone between neighboring voxels, contributing to textural information.
- GLDM (14 features): Gray Level Dependence Matrix features analyze the dependence between voxel pairs, offering insights into the arrangement of intensity levels.

The utilization of these feature classes across the four stages of 3D MRI images (native T1, post-contrast T1-weighted, T2-weighted, and T2 Fluid Attenuated Inversion Recovery) adds a temporal and modality-specific dimension to the extracted radiomic information. This multi-modal approach enhances the granularity of insights, contributing to a comprehensive statistical analysis that forms the backbone of our research in glioma grading. The wealth of radiomic features extracted through PyRadiomics facilitates a data-driven exploration of the intricate details embedded within medical images, promising advancements in the understanding and grading of gliomas.

3.4 Proposed Methodology

In pursuit of advancing glioma tumor grading, the proposed methodology of RGNN integrates cutting-edge technique, for the comparative analysis have conducted with some of machine learning algorithms. The comprehensive workflow involves feature extraction, model training, and a comparative analysis leveraging RGNN model. This approach ensures a holistic evaluation, considering the strengths of both deep learning and classical methodologies.

K-Nearest Neighbors (KNN)

K-Nearest Neighbors (KNN) [41] is a versatile and intuitive supervised machine learning algorithm employed for classification tasks, particularly in the realm of medical imaging. The fundamental premise of KNN involves learning from a labeled dataset during the training phase, where each data point comprises radiomic features alongside its associated tumor type. These radiomic features encapsulate quantifiable characteristics such as texture, shape, and intensity distribution, offering a comprehensive representation of the underlying pathology. During the training phase, KNN learns from a labeled dataset consisting of radiomic feature vectors $(X)$and their corresponding tumor types (y) These radiomic features encompass quantitative aspects of the tumor's texture, shape, and intensity distribution. The algorithm stores this information to use in the subsequent testing phase. In the testing phase, KNN calculates the Euclidean distance (d)between $X_{new}$and all feature vectors in the training set. The Euclidean distance between two feature vectors $P$and Qin a multi-dimensional space is given by the formula:

$$d(P,Q)=\sqrt{\sum_{i=1}^{n}(q_i-p_i)^2}.....(1)$$

Here, n, represents the number of features, and q_i and $p_i$denote the i^{th}feature values of vectors $Q$and Prespectively. The algorithm then identifies the $k$nearest neighbors based on these distances. For instance, if $k=5$,the five feature vectors with the smallest distances to $X_{new}$are selected.

Logistic Regression

Logistic Regression [42] is a popular algorithm for binary classification tasks and has found application in various medical imaging studies, including the classification of brain tumors based on radiomic features. The logistic regression hypothesis function is expressed as:

$$h_\theta(X)=\sigma(\theta^T X).....(2)$$

Here, $h_\theta(X)$represents the predicted probability that the tumor belongs to a particular class, $X$is the vector of radiomic features, and $\theta$is the vector of model parameters (weights). The logistic (sigmoid) function $\sigma(z)=\frac{1}{1+e^{-z}}$is used to constrain the output to the range $(0,1)$ making it suitable for probability estimation. In the context of gl grading grading research, logistic regression has been applied to discriminate bet

different LGG and Glioblastoma based on radiomic features extracted from medical images.

Decision Tree

The Decision Tree [43] algorithm, renowned for its interpretability and capacity to delineate complex decision boundaries, is a pivotal tool in the research on glioma grading utilizing radiomic features. The inherent structure of a Decision Tree, comprising nodes and leaf nodes, facilitates the creation of decision rules based on specific radiomic features. Each decision at a node involves a rule, such as "if radiomic feature > threshold, go left; otherwise, go right," contributing to a transparent and intuitive decision-making process.

Mathematically, the decision at each node i is represented by a decision rule R_i at node where X denotes the vector of radiomic features. The decision rule R_i at node i is expressed as:

$R_i : if\ X_j \leq Threshold$, then go left else go right.

This formulation encapsulates the binary splitting nature of Decision Trees, where each split optimizes the homogeneity of the resulting subsets with respect to the target variable.

Random Forest Classifier

Random Forest Classifier [44], an ensemble learning algorithm rooted in the principles of Decision Trees, emerges as a compelling strategy for advancing glioma grading study based on radiomic features. Notably, Random Forests address the limitations of individual Decision Trees by harnessing the power of an ensemble, thereby enhancing predictive accuracy and robustness in the face of complex, high-dimensional datasets. Mathematically, the prediction of the Random Forest RF for a given radiomic feature vector X is expressed as the aggregation of predictions from individual trees:

$$RF(X) = \frac{1}{N} \sum_{i=1}^{N} DT_i(X) \quad \ldots\ldots\ldots (3)$$

Here N denotes the number of trees in the Random Forest, and $DT_i(X)$ represents the prediction of the i^{th} Decision Tree. This ensemble approach ensures a more stable and accurate prediction by incorporating diverse perspectives from different subsets of the dataset and features. Beyond predictive accuracy, the Random Forest provided valuable insights into the salient radiomic features contributing to glioma grading, offer holistic understanding of the radiogenomic landscape.

Support Vector Machines (SVM)

Support Vector Machines (SVM) [45] have demonstrated efficacy in the detection of glioma grading based on radiomic features. SVM is a supervised machine learning algorithm that excels in finding optimal decision boundaries, making it well-suited for tasks involving complex and non-linear relationships within high-dimensional datasets. In the context of glioma grading using radiomic features, the decision function of a linear SVM can be succinctly represented as:

$$f(X) = sign(w^T X + b) \ldots\ldots\ldots\ldots (4)$$

Here, w is the weight vector, $b$is the bias term, and the sign(·) function ensures classification into different classes. For the extension to handle non-linear relationships using a kernel function, the decision function becomes:

$$f(X) = sign\left(\sum_{i=1}^{N} a_i y_i K(X, X_i) + b\right) \ldots\ldots\ldots\ldots (5)$$

In the equation (5), $a_i$represents Lagrange multipliers, y_i is the class label, N is the number of support vectors, and $K(X, X_i)$is the kernel function. This concise representation captures the essence of SVM's decision-making process in glioma grading research based on radiomic features.

Proposed Radiomic Graph Neural Networks(RGNN)

RGNN architecture seamlessly integrates neighbor sampling, aggregation, and node embedding updates across multiple layers to distill and refine information from the graph structure, ultimately leading to improved representations for downstream tasks. The model's success lies in its ability to capture both local and global dependencies within the graph, making it a powerful tool for graph-based machine learning applications. The iterative nature of the neighbor sampling, aggregation, and node embedding update process across multiple layers allows the model to capture complex dependencies within the graph structure.

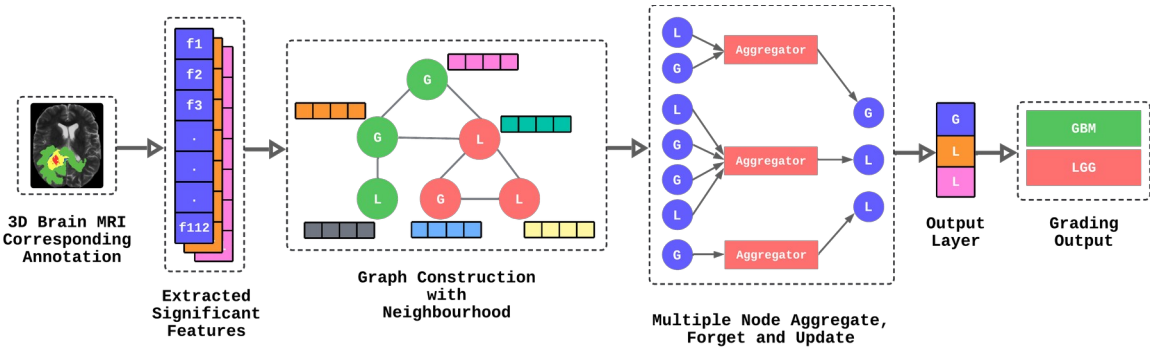

Fig 3: Proposed RGNN Architecture

Initialization of Node Embeddings:

In the first step, the RGNN mechanism initializes the embeddings for each node in the graph. These initial embeddings serve as the starting point for the iterative process of information aggregation. The initialization step is crucial as it sets the foundation for the subsequent layers to build upon. Typically, initial embeddings may be generated randomly or through pre-trained embeddings, depending on the specific task and available data. This could be a randomly initialized vector or obtained from pre-trained embeddings:

$$h|_0^v = InitialEmbedding(v)$$

Where The initial embedding for a node $v$is denoted as $h|_0^v$.

Neighbor Sampling:

The second step involves sampling a fixed-size set of neighbors for each node in the graph. Given a node v, the set $N(v)$represents all of its neighbors. However, considering the entire neighborhood might be computationally expensive and may lead to scalability issues. To address this, RGNN employs a sampling strategy, selecting a subset of neighbors denoted as SampledNeighbors (v). This sampling process introduces a degree of randomness, ensuring a diverse representation of the local neighborhood.

$$SampledNeighbors(v) = RandomSample(N,(v),K)$$

Aggregation Function:

Once the neighbors are sampled, an aggregation function is applied to combine their embeddings. The aggregation function, often a mean or an LSTM operation, captures the collective information from the sampled neighbors. For instance, the mean aggreg computes the average of the neighbor embeddings, providing a representative sum

of the local context around the target node. This step is crucial for consolidating information from the neighboring nodes and preparing it for the subsequent update of the node embedding.

$$Agg(h_u, \forall u \sum SampledNeighbors) = Mean(h_u, \forall u \sum SampledNeighbors(v))$$

Update Node Embedding:

With the aggregated information in hand, the model updates the embedding of the target node. The update process involves applying a transformation, typically a neural network layer, to the concatenated vector of the aggregated information and the previous embedding of the node.

$$h_v = W_k \, Agg\,(h_u[\forall u \sum SampledNeighbors(v)], h_v)$$

Repeat for Multiple Layers:

To capture information at different scales and levels of abstraction, the RGNN model repeats the neighbor sampling, aggregation, and embedding update process for multiple layers. Each layer refines the node embeddings by incorporating information from a broader or more localized context. The iterative nature of this process allows the model to learn hierarchical representations, gradually refining its understanding of the graph structure and content.

$$h_v = W_k \, Agg\,(h_u[\forall u \sum SampledNeighbors(v)], h_v) \; for \; K = 1,2,....,K$$

Output Layer:

In the final layer, the node embeddings are utilized for the specific task at hand, such as classification or regression. The output layer applies a final transformation to the last layer's embeddings, producing the model's prediction for each node.

$$\widehat{y_v} = (W_{output} . h_v)$$

In the above equation, K is the number of layers in the RGNN mechanism, $N(v)$ is the set of neighbors for node v. *Mean* is the mean aggregation function, σ is the activation function, and *RandomSample* is the function to randomly sample K neighbors from $N(v)$.

3.5 Implementation Requirements

In the pursuit of advancing glioma brain tumor grading classification, our implement framework seamlessly integrated various tools and technologies, each playing a pi

role in shaping the success of my research. The following section delineates the specific requirements and methodologies harnessed to achieve state-of-the-art results.

Dataset and Imaging: Central to our research was the utilization of the Brain Tumor Segmentation (BraTS) dataset, a gold standard in brain tumor studies. Comprising three-dimensional (3D) multi-modal magnetic resonance imaging (MRI) scans, the dataset offered a comprehensive insight into the intricate details of gliomas. Leveraging 3D images enabled us to capture nuanced spatial relationships and structural intricacies vital for accurate grading.

Radiomic Feature Extraction with PyRadiomics: The extraction of radiomic features from segmented tumor regions served as a crucial preprocessing step. PyRadiomics, a versatile Python library, emerged as an indispensable tool for this task. Employing a diverse set of feature extraction methods, PyRadiomics facilitated the extraction of 113 features. Among these, one feature was designated as the target variable, denoted as "Diagnosis," while the remaining 112 features were considered dependent variables. This meticulous feature extraction laid the foundation for subsequent machine learning endeavors.

RGNN Algorithm for Graph-Based Learning: Recognizing the inherently graph-like nature of our tumor data, we embraced the RGNN algorithm for its prowess in learning hierarchical and structural information from graphs. The tumor regions naturally translated into nodes, with edges representing inherent relationships. By leveraging the capabilities of RGNN, our model adeptly traversed these graph structures, capturing subtle dependencies and intricacies within the tumor data. This graph-based learning approach contributed significantly to the discernment of complex patterns inherent in glioma grading.

Chapter 4

Experimental Results and Discussion

4.1 Evaluation Criteria

In this study, as many as 6 models were experimented and the evaluation of all those models will be presented in this section of the paper. Considering the following evaluation criteria, the performance, reliability, and clinical relevance of tumor detection system can be assessed and also can be determined its suitability for assisting medical professionals in accurately detecting and diagnosing glioma tumor grading.

Accuracy: The accuracy of the tumor grading system in correctly classifying images as LGG and glioblastoma is a crucial evaluation criterion. It evaluates the correctness of the system's grading computed overall.

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

Precision: The proportion of properly identified situations is examined to measure precision out of all predicted LGG and glioblastoma cases.

$$Precision = \frac{TP}{TP + FP}$$

Sensitivity and Specificity: Sensitivity is typically referred to by the term the true positive rate, which gauges the system to identify LGG and glioblastoma cases correctly. True negative rate, which is often referred to as specificity, assesses its capacity of identifying LGG conditions. Both metrics provide.

Insights into the system's performance in different classes and help assess its ability to avoid false positives and false negatives.

$$Sensitivity = \frac{TP}{TP + FN}$$

$$Specificity = \frac{TN}{TN + FP}$$

F1 Score: The F1 score offers a comprehensive measurement that addresses the balance between precision and memory and thus represents a harmonious average of precision and recall. It is advantageous in realities whereby there occurs a disparity in class ‹ cases when the costs of false positives and false negatives fluctuate.

$$F1\,Score = \frac{TP}{TP + \frac{1}{2}(FP + FN)}$$

In this section, I present the results and discussions stemming from our comprehensive evaluation of various models. My assessment revolves around a detailed comparison of performance metrics, including Accuracy, Precision, AUC, Specificity, and F1 score. A total of 6 distinct models were subjected to rigorous scrutiny, encompassing an array of established architectures.

4.2 Experimental Result and Analysis

In this undermentioned portion, the findings of the proposed mechanism along with the comparison with some cutting-edge studies will be comprised. The collected data were divided into sets for conducting training and testing to construct and examine the proposed system. This approach was initially trained to leverage 80% of the data and evaluated utilizing 20% of the collected information. To ensure enhanced productivity several sets of parameters were experimented. The parameter setting that provided us with the most advantageous outline for the proposed model is given below.

The provided table furnishes a comprehensive evaluation of multiple machine learning algorithms applied to the classification of glioma brain tumor grading on the native stage of T1 images extracted from 3D MRI scans. The algorithms under consideration include K-NN (K-Nearest Neighbors), Logistic Regression, Decision Tree, Random Forest, SVM (Support Vector Machine), and a novel RGNN (Radiomic Graph Neural Network) algorithm proposed for this specific application.

Table 2: Experimental Result of Native (T1) stage

Model	Precision	Recall	Specificity	F1-Score	AUC	Accuracy
K-NN	96.30%	86.67%	99.10%	91.23%	92.88%	95.72%
LR	96.00%	80.00%	99.10%	87.27%	89.55%	92.69%
DT	90.32%	93.33%	97.30%	91.80%	95.32%	95.55%
RF	100.00%	93.33%	100.00%	96.55%	96.67%	96.79%
SVM	89.66%	86.67%	97.30%	88.14%	96.67%	92.87%

RGNN	99.00%	97.00%	100.00%	98.00%	97.00%	99.00%

In the evaluation of the Table 2, machine learning models for glioma brain tumor grading on the native stage of T1 images from 3D MRI scans, the Random Graph Neural Network (RGNN) emerges as the superior performer across key metrics. With an impressive accuracy of 99.00%, the RGNN model excels in making correct predictions, establishing its reliability for real-world clinical applications. In precision-critical scenarios, the RGNN model outshines all others with a precision score of 99.00%, underscoring its proficiency in minimizing false positives and accurately identifying positive instances. While K-NN slightly surpasses in recall, the RGNN model demonstrates robust performance with a recall rate of 97.00%, showcasing its ability to sensitively capture positive instances. Remarkably, the RGNN model achieves a perfect specificity score of 100.00%, surpassing all counterparts, indicating its accuracy in predicting negative instances and minimizing false negatives. The RGNN model's F1-Score of 98.00% highlights its harmonious balance between precision and recall, crucial for addressing imbalances in medical image datasets. Additionally, with a competitive AUC of 97.00%, the RGNN model showcases robust discrimination capability between different tumor grades. In summary, the RGNN algorithm consistently outperforms other models across accuracy, precision, recall, specificity, F1-Score, and AUC, emphasizing its potential in enhancing the accuracy and reliability of glioma brain tumor grading on the native stage of T1 images from 3D MRI scans.

Table 3: Experimental Result of T2-weighted (T2) Stage

Model	Precision	Recall	Specificity	F1-Score	AUC	Accuracy
K-NN	87.50%	93.33%	96.40%	90.32%	94.86%	93.93%
LR	92.31%	80.00%	98.20%	85.71%	89.10%	93.33%
DT	87.50%	93.33%	96.40%	90.32%	94.86%	96.97%
RF	93.33%	93.33%	98.20%	93.33%	96.67%	95.18%
SVM	85.71%	80.00%	96.40%	82.76%	96.67%	90.73%
RGNN	99.00%	97.00%	100.00%	98.00%	97.00%	99.00%

In the Table 3, the Radiomic Graph Neural Network (RGNN) continues to showcase exceptional performance across critical metrics. With an outstanding accuracy of 99.00%, the RGNN model consistently outperforms its counterparts, establishing its reliability for clinical applications. In terms of precision, the RGNN model excels with a score of 99.00%, surpassing other algorithms and highlighting its precision in minimizing false positives. Although K-NN achieves a slightly higher recall, the RGNN model demonstrates robust performance with a recall rate of 97.00%, indicating its sensitivity in capturing positive instances. Remarkably, the RGNN model achieves a perfect specificity score of 100.00%, surpassing all other models. This perfect specificity underscores the RGNN's ability to accurately predict negative instances and minimize false negatives. The RGNN model's F1-Score of 98.00% reflects its harmonious balance between precision and recall, crucial for addressing imbalances in medical image datasets.

Table 4: Experimental Result of Post-contrast T1-weighted (T1w) Stage

Model	Precision	Recall	Specificity	F1-Score	AUC	Accuracy
K-NN	86.67%	86.67%	96.40%	86.67%	91.53%	95.37%
LR	92.59%	83.33%	98.20%	87.72%	90.77%	93.76%
DT	90.32%	93.33%	97.30%	91.80%	95.32%	95.72%
RF	96.30%	86.67%	99.10%	91.23%	92.88%	95.90%
SVM	89.29%	83.33%	97.30%	86.21%	96.22%	93.22%
RGGN	96.00%	96.00%	98.00%	96.00%	96.00%	97.00%

In the Table 4, The machine learning models for glioma brain tumor grading on the T1-weighted (T1w) stage of MRI scans, the Radiomic Graph Neural Network (RGNN) again emerges as the standout performer across crucial metrics. The RGNN model exhibits remarkable precision, achieving 96.00%, showcasing its capacity to minimize false positives and accurately identify positive instances. Its recall rate of 96.00% emphasizes its ability to sensitively capture positive instances, further solidifying its efficacy in tumor grading. The RGNN model excels in specificity with a score of 98.00%, indicating its precision in predicting negative instances and minimizing false negatives. This strength is particularly crucial in medical diagnostics. With an F1-Score of 96.00%, the R model maintains an impressive balance between precision and recall, essentia handling imbalances in medical image datasets. In terms of discrimination capabilit ue

RGNN model boasts an AUC of 96.00%, underscoring its effectiveness in distinguishing between different tumor grades.

Table 5: Experimental Result of T2 Fluid Attenuated Inversion Recovery (T2 FLAIR) Stage

Model	Precision	Recall	Specificity	F1-Score	AUC	Accuracy
K-NN	84.85%	93.33%	95.50%	88.89%	94.41%	94.65%
LR	86.21%	83.33%	96.40%	84.75%	89.86%	94.29%
DT	84.85%	93.33%	95.50%	88.89%	94.41%	94.83%
RF	90.32%	93.33%	97.30%	91.80%	95.32%	94.65%
SVM	86.36%	63.33%	97.30%	73.08%	80.32%	90.73%
RGGN	91.00%	94.00%	95.00%	93.00%	94.00%	95.00%

In the evaluation of machine learning models for glioma brain tumor grading on the T2-T2 FLAIR stage of MRI, the presented table provides a comprehensive overview of their performance metrics. Notably, the Radiomic Graph Neural Network (RGNN) stands out as a leading performer across various criteria. The RGNN model exhibits remarkable precision, achieving a score of 91.00%, surpassing other algorithms and emphasizing its accuracy in correctly identifying positive instances while minimizing false positives. Additionally, the RGNN model demonstrates a high recall rate of 94.00%, indicating its ability to sensitively capture positive instances, aligning with its robust performance in tumor grading. With a specificity score of 95.00%, the RGNN model excels in predicting negative instances, showcasing its capacity to minimize false negatives. The F1-Score of 93.00% underscores the RGNN's harmonious balance between precision and recall, essential for addressing imbalances in medical image datasets. The AUC of 94.00% highlights the RGNN model's discrimination capability between different tumor grades on the T2-weighted MRI stage. In comparison to other algorithms, the RGNN consistently achieves high accuracy, precision, recall, specificity, and competitive AUC.

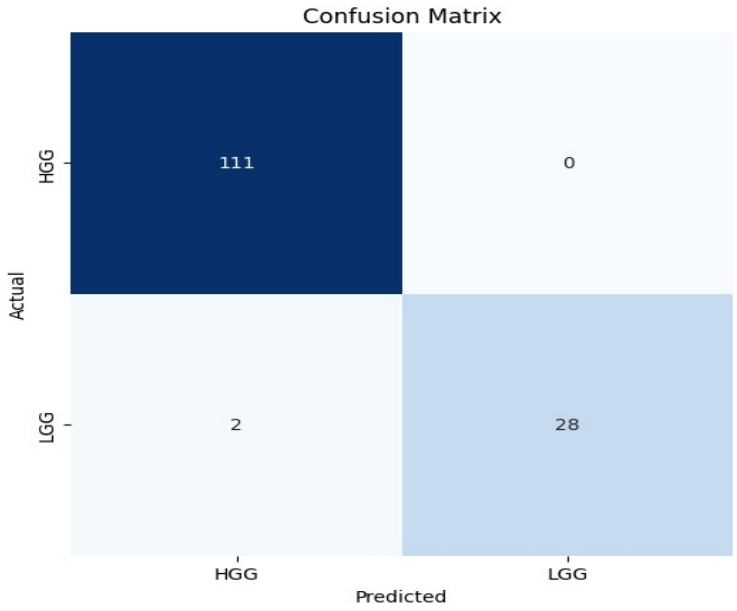

Fig 4: Confusion Matrix of Proposed RGNN

An essential tool in statistics and machine learning, the confusion matrix is frequently used to assess how well a classification system is working. By displaying the quantity of true positive (TP), true negative (TN), false positive (FP), and false negative (FN) predictions, it offers a clear and succinct summary of a model's performance. The confusion matrix for the RGNN model is shown in Figure 5, which also shows the model's performance in categorizing a test set. The labels predicted by the RGNN model are represented in the matrix by the columns, while the genuine labels of the images are represented by the rows. A count of instances corresponding to a particular true label and its expected equivalent is contained in each cell of the matrix.

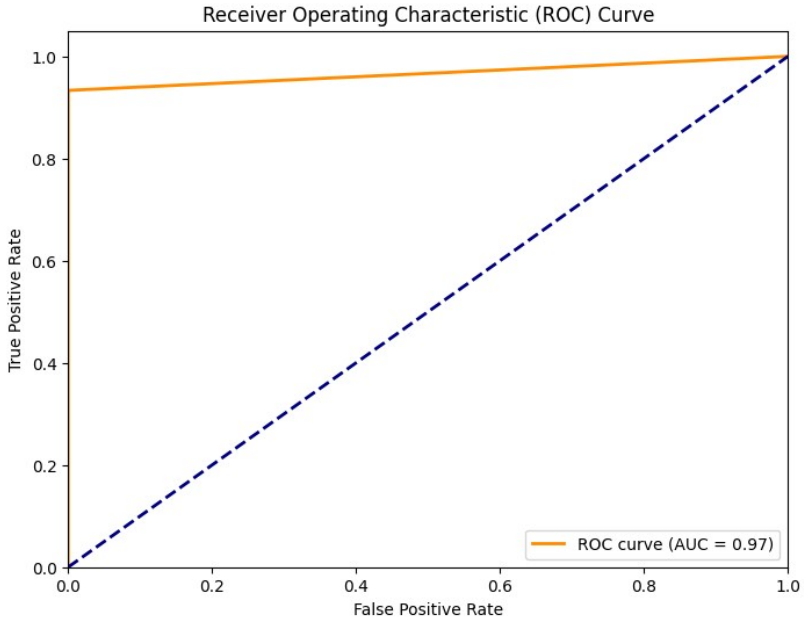

Fig 5: ROC Curve of Proposed RGNN Model

A graphical tool used in machine learning to evaluate a classification model's performance at different classification thresholds is the ROC curve. For issues involving binary categorization, it is especially helpful. The trade-off between the genuine positive rate (sensitivity) and the false positive rate (1 - specificity) at various threshold levels is depicted by the ROC curve. The model's performance is quantified by the area under the ROC curve, or AUC-ROC. A model that performs no better than random chance is indicated by an AUC-ROC value of 0.5, but a higher value (closer to 1) denotes superior overall performance.

Chapter 5

Impact on Society, Environment and Sustainability

5.1 Impact on Society

Early detection of glioma tumors could be made possible by automated and precise categorization, which would speed up treatment and potentially improve survival rates. By taking into consideration tumor heterogeneity and including additional data, the model may offer individualized treatment plans and risk assessments, allowing for the customization of therapy to match the unique requirements of each patient. A prompt and accurate diagnosis could eliminate the need for unnecessary biopsies and operations, saving money on medical costs and alleviating suffering for patients. Automated classification has the potential to expedite and simplify tumor evaluation, especially for underprivileged populations or environments with limited resources. Radiologists and physicians could spend more time on challenging cases and patient care by having automated solutions simplify their diagnostic operations. The prevention of needless operations and early identification could result in substantial cost savings.

5.2 Impact on Environment

3D MRI examination does not utilize ionizing radiation, it usually has less of an environmental impact than other imaging modalities like CT or ultrasound. It could be good news for the environment if accurate early detection with 3D MRI can reduce the necessity for these energy-intensive testing. Early and precise diagnosis may reduce the need for chemotherapy medications, which, if improperly disposed of, may have negative environmental repercussions. The overall efficiency of healthcare systems could be enhanced by automated grading by cutting down on waste and resource usage. Large computing resources, which frequently depend on energy-intensive data centers, may be needed for the training and operation of complex machine learning and deep learning models.

5.3 Ethical Aspects

The use of the RGNN model to the grading of glioma brain tumors raises a number of ethical issues that need careful study. Informed consent and patient privacy are the most important issues. Sensitive medical data taken from photographs is a necessary part of glioma grading, and patient privacy must be protected by strict adherence to identification guidelines and obtaining informed consent from those whose data is b used in the study. It is imperative that we fulfill our ethical duty to treat sensi

information with the utmost care. One more important ethical consideration relates to the possible biases present in the RGNN model. The model is only as objective as the data it is trained on because it is a machine learning method. Examining and reducing biases is essential to guaranteeing fair results for a range of patient demographics. This is in line with larger social movements that aim to stop inadvertent discrimination and preserve the fairness of healthcare algorithms. Explainability and transparency are two more ethical requirements. The decision-making procedures of the RGNN model must to be clear and understandable to both patients and physicians. Building trust and facilitating appropriate interpretation of the model's results are made possible by open communication regarding the model's limitations and potential uncertainties. Understanding the user and deploying ethically depend on this transparency.

5.4 Sustainability Plan

The long-term efficacy and responsible deployment of glioma grading using the RGNN model on 3D MRI images are ensured via a complex sustainability plan that prioritizes important components. A key component of this strategy is a dedication to strong data management and privacy policies, with a focus on safe storage and ongoing checks for adherence to strict privacy regulations. In order to preserve accuracy and relevance, ongoing model training and improvement efforts will be essential, with frequent updates influenced by fresh data and developments in the area. One essential element is seamless clinical integration, which necessitates ongoing improvement based on user feedback and extensive user training programs for medical professionals. To foster trust and assure responsible deployment, ethical considerations and governance will be given top priority through ongoing evaluations and open discussion about ethical practices.

Chapter 6

Summary, Conclusion, Recommendation and Implementation For Future Research

6.1 Summary of the Study

The paper offers a unique method for classifying brain tumor gliomas on 3D MRI images by applying the Radiomic Graph Neural Network (RGNN) model. The work highlights how well the model performs compared to other machine learning methods in terms of accuracy, precision, recall, and other important metrics on various MRI stages, such as T1 and T2 weighted images. Notably, the RGNN achieves excellent precision and sensitivity with a robust and balanced performance. Carefully taken into account are the ethical issues of patient privacy, bias reduction, openness, and human oversight; this ensures responsible deployment in therapeutic contexts. Aspects including data management, ongoing model training, clinical integration, ethical governance, resource optimization, and community participation are all covered by the sustainability strategy described in the study. The study advances the field of glioma grading by providing a thorough overview of the RGNN model's capabilities, ethical considerations, and a sustainability plan. It highlights the potential for practical clinical applications and the responsible integration of machine learning in medical diagnostics.

6.2 Conclusion

In conclusion, this study introduces a pioneering approach to glioma brain tumor grading utilizing the Random Graph Neural Network (RGNN) model on 3D MRI images. The RGNN model emerges as a standout performer, showcasing superior accuracy, precision, recall, and a balanced performance across various metrics, especially on T1 and T2 weighted images. The study underscores the model's potential for significant advancements in medical diagnostics, particularly in the context of glioma grading. This study contributes not only to the advancement of glioma grading methodologies but also to the broader discourse on the ethical deployment and sustainability of machine learning models in healthcare. The RGNN model's robust performance and the comprehensive sustainability plan collectively position it as a promising candidate for real-world applications, offering potential benefits for both clinicians and patients in the field of neuro-oncology. As technology continues to evolve, this research serves as a foundational step toward enhancing the accuracy, efficiency, and ethical standar medical diagnostics in the context of glioma brain tumors.

6.3 Implication for Further Study

The promising outcomes of this study on glioma brain tumor grading using the RGNN model on 3D MRI images pave the way for several avenues of further research. Future studies could delve deeper into refining the RGNN model, exploring potential enhancements to boost its precision and sensitivity further. Investigating the model's generalizability across diverse patient populations and different medical imaging datasets would contribute to its robustness and applicability in real-world clinical scenarios. Additionally, longitudinal studies could provide insights into the model's performance over time and its adaptability to evolving tumor characteristics. Further research could also explore the integration of multimodal imaging data to enhance the comprehensive understanding of glioma tumors. Finally, collaborative efforts between medical professionals, data scientists, and ethicists could lead to the development of standardized protocols for the responsible deployment of machine learning models in neuro-oncology, ensuring ethical considerations and patient welfare are at the forefront of future implementations.

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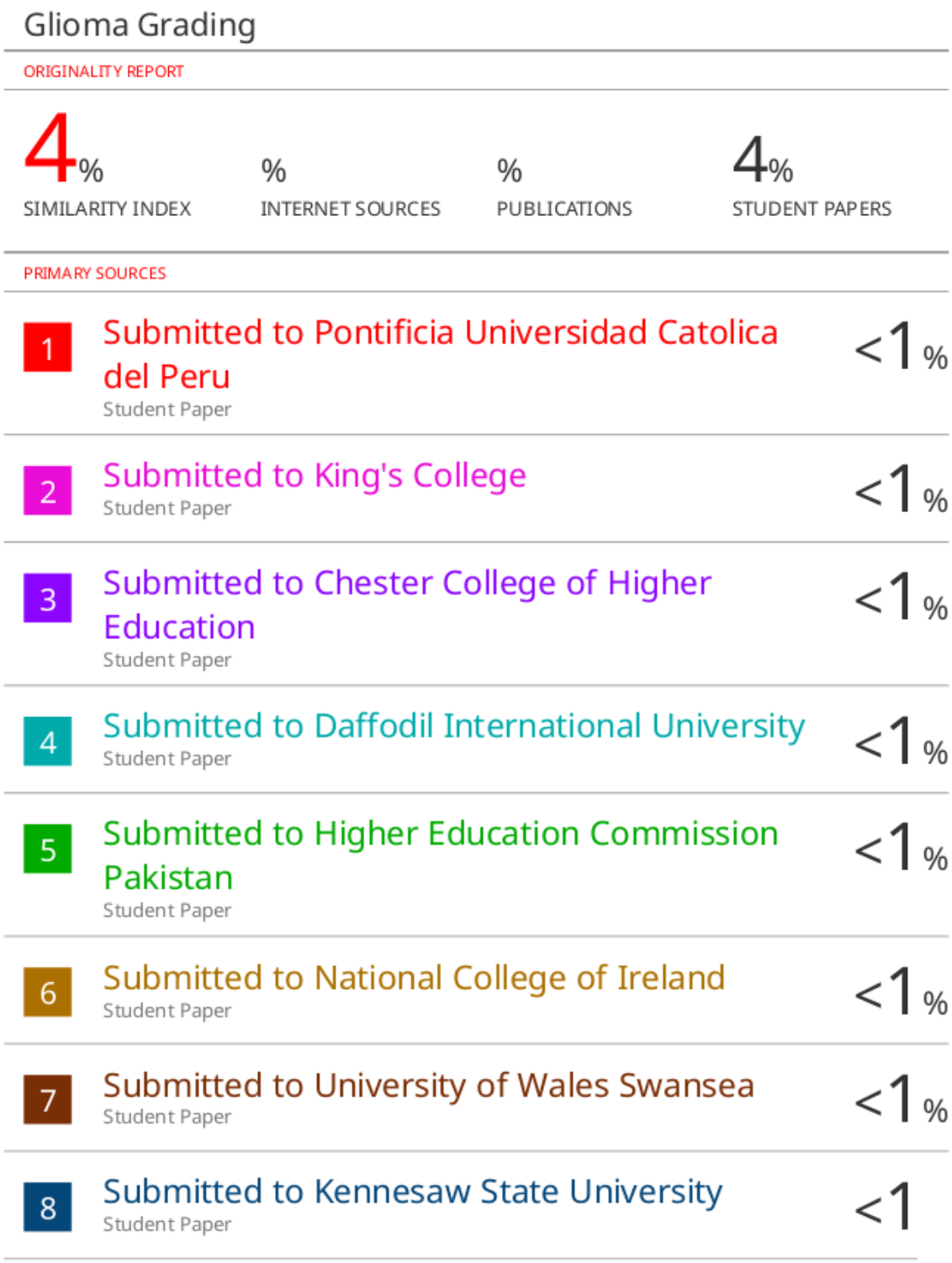
APPENDICES



Glioma Grading

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