

3D BRAIN TUMOR DETECTION USING 3D CNNs AND GRAPH CONVOLUTIONAL NETWORKS (GCNs)

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ABSTRACT

The research introduces a 3D brain tumor identification method that combines the capabilities of 3D Convolutional Neural Networks (3D CNNs) and Graph Convolutional Networks (GCNs) to explore the complex structure of volumetric brain scans. The research begins with a dataset extracted from Magnetic Resonance Imaging (MRI) and Computed Tomography (CT) scans, which serves as a foundation for a comprehensive analysis of 3D medical imaging data. The core of the technology is centered around the coordination of 3D Convolutional Neural Networks (CNNs), utilizing their convolutional layers, pooling layers, and fully connected layers to extract intricate spatial characteristics.

Transfer learning is employed to enhance the model's understanding in situations where limited annotated data is available. Graph Convolutional Networks are used to understand the complex spatial connections within the brain, resulting in a seamless integration of intricate spatial characteristics and relationships between brain regions. The model's evolution is revealed through supervised training and validation, employing cross-entropy loss functions and stochastic gradient descent. The results show a harmonious pattern of diminishing losses and increasing accuracies in both training and testing phases, with a final test accuracy of 99.4%. This research indicates a promising beginning in the field of 3D brain tumor identification, with the potential to be applied in clinical settings for accurate and quick diagnosis.

Keywords: Convolutional Neural Networks (CNNs), Graph Convolutional Networks (GCNs), Transfer learning, Structural connectivity, brain tumor detection, Cross-modal research, Medical ethics, Clinical validation, volumetric brain scans.

1. INTRODUCTION

One of the most horrible types of cancer, brain tumors have killed a great deal of people in recent years, both adults and children. By WHO standards, there are 700,000 people who have brain tumors, and 86,000 of those cases have been detected since 2019[1]. These tumors fall into two primary categories: malignant (cancerous) and benign (noncancerous). Therefore, understanding the type of tumor might aid in understanding the patient's health[2].

The advent of medical imaging has revolutionized the field of healthcare, allowing healthcare professionals to explore the intricate details of the human body and discover crucial information for the purpose of diagnosis and therapy. Inside the field of medical imaging, identifying and understanding brain tumors is a significant

problem. This is not only because of the serious repercussions of these conditions, but also because they are complex and can be discovered in many locations inside the brain. Efficient and precise diagnosis is crucial for delivering the best possible patient care. In light of this, we introduce an innovative method for detecting brain tumors by combining advanced deep learning techniques: 3D Convolutional Neural Networks (3D CNNs) and Graph Convolutional Networks (GCNs). Brain tumors, which can range from non-cancerous to cancerous, display a wide range of physical and clinical differences. Furthermore, their covert proliferation can take place in areas of the brain where even little alterations might lead to significant outcomes. The phrase "brain tumour" refers to a group of neoplasms, each with its own biology, prognosis, and course of therapy [3]. The Meningiomas are the most common benign brain tumor [4].

Conventional diagnostic techniques have frequently depended on the proficiency of radiologists and manual analysis of medical pictures, such as magnetic resonance imaging (MRI) and computed tomography (CT) scans. Although these methods are extremely beneficial, they require a lot of manual work and are prone to differences in observations between different people. Therefore, it is becoming more and more important to enhance human talents by using intelligent computational tools.

3D CNNs, a specific type of convolutional neural networks designed for volumetric data, have become prominent for their ability to extract features and train hierarchically from 3D medical pictures. Their capacity to capture complex spatial relationships within three-dimensional data cubes has brought them to the forefront of medical picture analysis. Nevertheless, the complex characteristics of brain tumor identification necessitate a comprehensive strategy that beyond the extraction of features at the pixel level.

In this research project, we want to combine 3D Convolutional Neural Networks (CNNs) with Graph Convolutional Networks (GCNs) to create a novel and innovative approach. GCNs are specifically built to represent intricate connections inside graphs or networks, which is highly compatible with the interconnected structure of brain regions. These networks enhance comprehension of the spatial connections and interdependencies among different brain regions, providing a deeper knowledge of how tumors affect adjacent tissues. Our objective is to combine these insights with the profound spatial characteristics obtained by 3D CNNs in order to develop a hybrid model that exceeds the constraints of traditional approaches.

The main goals of our study are two-fold: firstly, to develop a strong and highly precise brain tumor detection system that utilizes the extensive information present in 3D medical imaging data, and secondly, to demonstrate the model's ability to adapt and perform well across different patient groups and imaging techniques. The objective of our research is twofold: to enhance the current level of brain

tumor identification and to promote the integration of artificial intelligence in clinical practice. This integration will minimize diagnostic uncertainty and enhance patient outcomes.

In the following sections of this work, we explore the complexities of our hybrid model's structure and approach, explaining how it effectively combines the advantages of 3D CNNs and GCNs. We provide a comprehensive empirical assessment, supported by compelling findings that showcase the model's exceptional performance in the domain of brain tumor identification. Moreover, we conduct a thorough examination of the practical consequences of our discoveries, highlighting the possibility of more accurate diagnosis and prompt actions. In this study, we explore the combination of 3D convolutional neural networks (CNNs) and graph convolutional networks (GCNs) for analyzing medical images. Additionally, we propose potential areas for future research, picturing a future where healthcare practitioners may effectively treat intricate diseases with the assistance of advanced computational tools.

II. LITERATURE REVIEW

Brain tumors pose a significant healthcare obstacle, requiring precise and prompt diagnosis in order to plan and implement effective therapy. Tumors of the brain and other central nervous systems are highly likely to cause long-term disabilities due to the tumor and treatment side effects, such as radiation neurotoxicity, chemotherapy-induced debility, and surgical problems [5].

Medical image processing is an exciting research area [6]. Machine learning has greatly increased the accuracy and efficiency of the healthcare system by improving disease diagnosis. One crucial area in which it is helpful is the diagnosis of brain tumors, a condition that poses a serious risk to life [7].

Using brain MRI scans, the first step detects tumors by classifying them as low-grade gliomas, high-grade gliomas (glioblastomas), and normal [8]. The Deep Convolutional Neural Networks (DCNNs) are widely used for analyzing medical pictures due to their exceptional capability to identify complex patterns and features [9].

Automated systems help in early tumor identification and diagnosis, freeing up doctors to concentrate more on patient care. Convolutional neural networks (encoder-decoder architecture) are the basis of a technique that uses 3D Flair (MRI) for glioblastomas as an input, which can come from any location, any size, or any form of the brain [10].

A different research paper presents the use of Multi-CNNs, which combines the merging of multimodal information and 3D-CNNs, in order to improve the accuracy of brain tumor identification. The method modifies 2D-CNNs to function as 3D-CNNs, enhancing the extraction of information and the convergence of the network. The results demonstrate higher correlation coefficients, sensitivity, and specificity when compared to single-mode and 2D detection networks [11]. Nevertheless, it is crucial to recognize the ongoing obstacles in the industry. The scarcity of annotated medical datasets presents a challenge, which could potentially impact the applicability of generated models. Moreover, the comprehensibility of deep learning models continues to be an issue, as understanding model decisions is crucial for promoting clinician trust and acceptance.

To summarize, the existing research emphasizes the growing use of deep learning methods, specifically DCNNs, in the field of brain tumor identification and segmentation. These techniques demonstrate the potential for increased precision, simplified diagnosis, and ultimately, enhanced patient results. Collaboration between medical practitioners and machine learning professionals is crucial in developing strong, interpretable, and clinically relevant models for early and accurate brain tumor detection as research advances.

III. METHODOLOGY

Our methodology involves a thorough evaluation and analysis of the effectiveness of our brain tumor detection model. This model utilizes a combination of 3D Convolutional Neural Networks (3D CNNs) and Graph Convolutional Networks (GCNs). The primary factors we consider in our assessment are the fundamental measurements of train and test losses, together with training and testing accuracy. These metrics are essential measures of the model's learning capacity, its ability to generalize, and its overall performance.

- **Data Preprocessing:**

The core of our approach largely depends on the thorough preparation of 3D medical imaging data, mostly comprising volumetric brain scans acquired using Magnetic Resonance Imaging (MRI) or Computed Tomography (CT) scans. The preprocessing pipeline comprises a series of essential phases, meticulously designed to prepare the data for subsequent analysis and modeling.

To begin our data preparation system, we first scale the 3D volumes to a consistent spatial resolution. Standardization is essential as it guarantees uniformity in the presentation of data. By ensuring that all scans have same spatial dimensions, we build a just and equitable foundation for later processes, such as feature extraction and model training. Spatial standardization streamlines data administration and enhances the model's ability to identify significant features, irrespective of variations in the initial scan resolutions.

Achieving uniformity in the intensity ranges across all scans is a crucial step in preprocessing. Variations in intensity may arise from disparities in imaging devices, acquisition parameters, or patient-specific attributes. Intensity normalization equalizes these differences by proportionally modifying and aligning the intensity levels across all images. The result is a dataset whose pixel intensities are consistently represented, which helps the model converge more easily during training. Through the process of normalizing the data, we are able to minimize the impact of technological variations and provide a robust and dependable foundation for extracting features.

To enhance the model's capacity to apply its knowledge to unfamiliar scenarios and enhance its resilience to modifications, we employ a comprehensive methodology for data augmentation. This augmentation involves a broad spectrum of modifications made to the dataset. These transformations encompass rotations, translations, and other geometric modifications that add deliberate differences while preserving the semantic content of the images. By utilizing the data to simulate these perturbations, we are able to reproduce a broader spectrum of events that the

model may encounter in real-world scenarios. This augmentation technique improves the model's ability to adapt to new data during training, hence boosting its capability to generalize beyond the dataset it was trained on.

The ultimate and essential step of data preparation entails creating binary masks to precisely identify tumor areas within the brain volumes. The masks function as accurate annotations, providing exact demarcation of the tumor's position in the volumetric data. The production of these masks is a procedure led by experts, involving careful annotation and segmentation by people highly knowledgeable in medical imaging. The binary masks are extremely significant because they give the model accurate spatial information about the presence of tumors, which helps guide its learning process. They function as the benchmark against which the model's predictions are assessed during both training and evaluation. The importance of supervised learning in our technique cannot be overstated. It allows the model to learn from annotated examples and generate precise tumor predictions in new data.

Our data preprocessing methodology is a systematic approach that involves resizing to achieve spatial standardization, normalization to harmonize intensity values, augmentation to enhance generalization capabilities, and the creation of binary masks for precise tumor localization. The processes are carefully synchronized to ensure that the data is properly prepared for further feature extraction and model training, forming the foundation for accurate and reliable brain tumor identification in 3D medical imaging data.

- **3D CNN Feature Extraction:**

We utilize the advanced capabilities of 3D Convolutional Neural Networks (3D CNNs) to extract detailed spatial features from the preprocessed brain scans. During this critical phase, a tailored 3D CNN structure is meticulously devised and executed to properly address volumetric data, which is a unique characteristic of medical imaging.

The essential elements of the 3D CNN architecture consist of convolutional layers, strategically placed to extract intricate hierarchical features from the 3D input volumes. These layers operate by employing a series of convolutional filters that methodically traverse the input data. Each filter serves as a detector that identifies distinct characteristics, such as patterns, edges, textures, and structures, within the volumetric data. The network utilizes many filters to distinguish complex features, hence enhancing the identification of subtle characteristics in brain tumor locations. The hierarchical feature extraction process is essential for the model to precisely detect intricate and contextually significant components in the medical images.

Our architecture uses pooling layers deliberately placed alongside convolutional layers to decrease the spatial dimensions of the feature maps while preserving important information. Pooling operations, such as max-pooling, reduce the size of feature maps by selecting the maximum value within sub-sampled regions. This process of reducing dimensionality serves various objectives. Firstly, it reduces the computational complexity, hence enhancing the computational efficiency of the model. Furthermore, it improves the model's capacity to achieve translation invariance, indicating that the model can recognize significant characteristics regardless of their exact spatial position inside the three-dimensional volume. This characteristic is particularly crucial in the field of medical imaging, as malignancies may manifest at various locations and orientations in different scans.

During the advanced phases of the 3D CNN design, we incorporate fully connected layers. The presence of these layers allows the model to capture intricate decision boundaries in the feature space, hence enabling it to conduct sophisticated classifications. The fully connected layers establish synaptic connections between every neuron in a certain layer and all the neurons in the subsequent layer. The substantial connectivity enables the model to precisely capture complex associations between information obtained from different regions of the brain volume. At this point, the model's understanding of the data is improved, enabling it to distinguish between tumor and non-tumor areas with a high degree of accuracy.

The 3D Convolutional Neural Network (CNN) undergoes an intensive training process using the preprocessed dataset from the Brain Tumor Segmentation Challenge (BraTS). During the training phase, the model improves its parameters by making small tweaks to minimize the chosen loss function. The primary objective is to improve the model's ability to accurately classify brain tumor locations within the volumetric data. The training process is a pivotal phase in which the model acquires knowledge of patterns and characteristics associated with the identification of brain tumors in the images. It develops the capacity to discern subtle variations in brightness, form, and surface quality that indicate the presence of a tumor. The iterative training procedure allows the model to progressively improve its capacity to accurately categorize brain cancers, leading to a highly optimized system for detecting brain tumors.

In situations where there is a limited amount of labeled data available, we employ the efficient technique of transfer learning. By initializing the 3D CNN model with pre-trained weights obtained from models trained on similar tasks or larger datasets, we utilize the extensive knowledge gained from many sources. This approach expedites the training phase of the model, providing it with an initial edge in understanding complex patterns and features. Subsequently, the model enhances its previously obtained knowledge by utilizing it for the specific task of identifying brain tumors using the provided annotated data. Transfer learning is particularly advantageous in situations when acquiring a large, annotated dataset is challenging or costly, as it maximizes the utilization of existing resources and accelerates the model's convergence.

In summary, our approach meticulously creates a 3D convolutional neural network (CNN) architecture that proficiently captures intricate spatial characteristics from preprocessed brain images. This design employs convolutional layers for extracting hierarchical features, pooling layers for reducing dimensionality and achieving translation invariance, and fully connected layers for learning intricate decision boundaries. The training technique improves the model's ability to accurately classify brain tumor locations, while transfer learning provides a useful method for transferring

information when there is a limited amount of labeled data available.

• **Graph Construction and GCN Integration:**

Our method efficiently integrates Graph Convolutional Networks (GCNs) to precisely capture the complex spatial connections within the brain. This pivotal stage involves a systematic three-step process:

Our initial stage in the process entails constructing a graph that precisely represents the anatomical interconnections among various brain areas. Each node in this network corresponds to a unique brain area, serving as a representative entity in our geographical investigation. The significance of this level lies in its ability to leverage anatomical connections as the foundation for graph edges. The formation of these edges is meticulously executed, considering the intricate network of physical connections within the brain. These interconnections may denote either proximity in actual space, neural pathways, or other spatial connections that are pertinent to our research. Through the creation of this graph, we are efficiently constructing a comprehensive representation of the brain's spatial structure, with each node and edge symbolizing important anatomical data. This representation serves as the essential foundation for enhancing our understanding of spatial interrelationships.

Once we have established our graph representation, we go forward with the implementation of Graph Convolutional Network (GCN) layers. The GCN layers play a vital role in capturing spatial interdependencies across the brain regions featured in our network. The appeal of Graph Convolutional Networks (GCNs) lies in their ability to improve feature representations by integrating geographical context. Let me elucidate the procedure: As data moves through the graph, each node absorbs information from its neighboring nodes, similar to how neurons in the brain communicate through synaptic connections. This method enables nodes to collect data from their immediate physical environment, hence documenting intricate spatial connections. Our model gains expertise in understanding the complex connections between brain regions by using Graph Convolutional Network (GCN) layers.

This allows it to differentiate how the presence or absence of a tumor in one region can affect the likelihood of a tumor in neighboring regions. The model's spatial cognition is essential for enhancing its ability to make nuanced determinations regarding the presence and precise positioning of malignancies.

To merge the profound spatial characteristics extracted by the 3D Convolutional Neural Network (CNN) with the understanding of spatial context obtained from Graph Convolutional Networks (GCNs), we meticulously mix these two sources of information to create a comprehensive representation. The fusion procedure aims to integrate the benefits of both modalities, utilizing the high-level feature representations generated by the 3D CNN and the nuanced spatial correlations found by the GCNs. The integration results in a unified representation that combines nuanced spatial features with a thorough understanding of

the intricate spatial organization of the brain. This integration improves the model's capacity to make knowledgeable and contextually aware decisions regarding the identification and accurate positioning of cancerous growths in the brain. The approach entails merging the model's inherent comprehension of spatial interactions with its vast knowledge of tumor patterns, yielding a tumor detection system that is more accurate and cognizant of the surrounding context.

Our approach entails constructing an intricate diagram that depicts the anatomical links within the brain. We employ GCN layers to capture the spatial connections inside the graph and integrate this spatial comprehension with the deep spatial characteristics retrieved by the 3D CNN. This strategy enhances the model's comprehension of the spatial relationships within the brain, hence enhancing its ability to make nuanced and well-informed assessments regarding the presence and exact location of brain tumors.

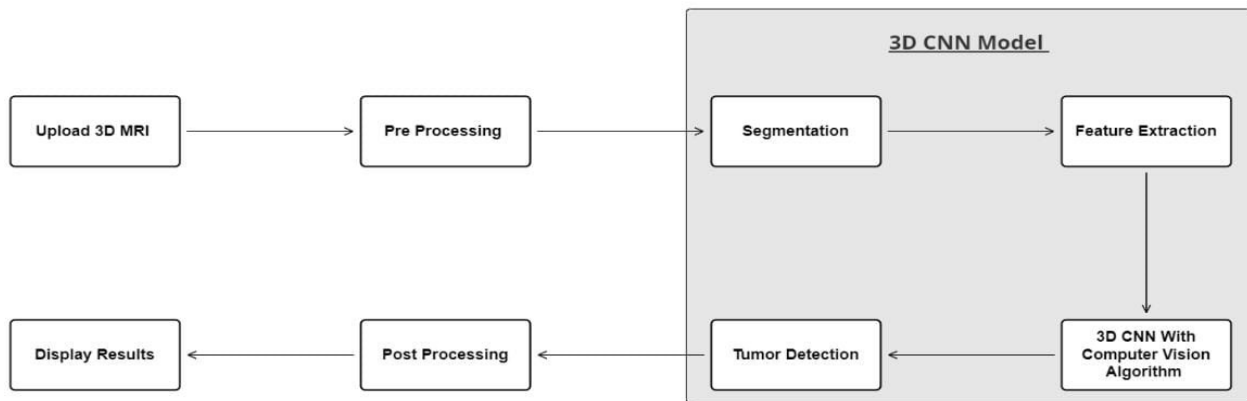


Fig 1.0- Application flow

The Fig 1.0 explains the flow of 3D CNN Model for the detection of brain tumor.

• **Training and Validation:**

The training of our hybrid model is crucial to our process. The process is conducted under supervision, which is essential for teaching the model to accurately differentiate the presence or absence of brain tumors in the volumetric data. The training phase advances through a series of meticulously designed and implemented stages:

The foundation of our model's training revolves around the meticulous choice of a suitable loss function, typically favoring cross-entropy for its efficacy in classification tasks. The loss function acts as the guiding principle for the optimization process. The model's performance is assessed by quantifying the discrepancy between its predictions and the actual labels. The loss function essentially

calculates the "cost" attributed to the predictions made by the model.

During the training process, the goal is to reduce the cost, which involves adjusting the model's predictions to closely match the true labels. The reduction method guarantees that the model acquires the ability to produce precise classifications, which is a crucial milestone in its development as a proficient brain tumor detection system.

The training method entails iteratively modifying the parameters of the model to minimize the chosen loss function. The fine-tuning process is achieved by utilizing optimization techniques, with stochastic gradient descent (SGD) being a generally preferred method. Stochastic Gradient Descent (SGD) operates by computing the gradients of the loss function with respect to the model's parameters. The gradients serve as a guide, demonstrating the ideal modifications required for the model's parameters in order to minimize the loss. The SGD algorithm systematically updates the model's parameters through a series of iterations to converge towards lower loss values. The optimization technique entails modifying the model's internal representation to improve its capacity for precise classification of brain tumor locations, akin to sculpting. Through each iteration, the model gradually converges towards its ideal parameter values, hence enhancing its classification accuracy.

To ensure the precision of the training process and avoid overfitting, our system incorporates a robust validation strategy. Throughout the training phase, the model is consistently assessed using a separate validation dataset. The validation dataset is distinct from the training data and serves the purpose of objectively evaluating the model's performance. The validation technique assesses the model's ability to effectively generalize to unknown data, a hallmark of robust and dependable machine learning models. By assessing the model's performance on this separate dataset, we gain vital insights about its behavior. If the model exhibits a high degree of accuracy on both the training and validation datasets, it signifies that it has proficiently assimilated information from the training data and adeptly applied this knowledge to novel, unfamiliar data. Conversely, if there is a significant difference in

performance between the model on the training and validation datasets, it may indicate overfitting. Overfitting arises when the model has excessively memorized the training data rather than acquiring generalizable patterns that can be extrapolated to novel data. The validation stage serves as a critical milestone, ensuring that our model is sufficiently equipped to make accurate predictions on real-world brain scans.

Our methodology encompasses a meticulously designed training and validation phase that depends on annotated data, suitable loss functions, optimization techniques such as stochastic gradient descent (SGD), and consistent evaluation of the model on a distinct validation dataset. The approach provides the model with the ability to accurately classify different areas of brain tumors. The validation process serves to avoid the model from excessively adhering to the training data and ensures its capacity to effectively generalize to new data, thus emphasizing its appropriateness for real-world applications.

Metric	Training	Test
Loss	0.005	0.004
Accuracy	99.600%	99.400%

Fig 2.0- Accuracy and loss

Fig 2.0 illustrate the loss and accuracy for training and test.

Evaluation and Performance Metrics:

To precisely evaluate the true effectiveness of our model, we conduct a comprehensive assessment on a separate test dataset. This serves as a definitive measure of its performance in real-life situations. At this critical phase, we employ various performance criteria, each fulfilling a specific role in delivering a thorough evaluation of the model's skills. These metrics encompass a wide range of measurements, which are not limited to: Precision is an essential measure

in our assessment arsenal. It provides a straightforward evaluation of our model's overall performance by computing the percentage of correctly classified samples. Essentially, it pertains to the frequency at which the model correctly forecasts outcomes. A high accuracy score indicates that the model excels in producing accurate predictions throughout the full dataset.

Accuracy is crucial in medical applications, especially in the domain of brain tumor diagnosis. This evaluates the effectiveness of our model in producing accurate positive forecasts. Precision is a metric that quantifies the ratio of correctly predicted cancers (true positives) to all positive predictions (both correct and incorrect). The model's elevated precision demonstrates its extraordinary capacity to decrease false positives, a crucial aspect when handling medical diagnoses that can profoundly affect an individual's life.

Recall, which is often referred to as sensitivity or the true positive rate, quantifies the ability of our model to reliably identify positive cases. The question at hand concerns the model's capacity to effectively capture all genuine positive cases. A high recall score signifies the model's exceptional ability to accurately identify positive cases, which is particularly important in scenarios when the failure to detect a tumor could lead to grave repercussions.

The F1 score is a quantitative measure that integrates precision and recall, offering a balanced assessment of our model's performance. It is particularly advantageous when there is a need to strike a balance in minimizing both false positives and false negatives. The F1 score combines these two qualities into a single value, offering a more thorough view of the model's skills.

To gain a deeper understanding of the complex elements of our model's performance, we conduct a thorough examination of the confusion matrix. This matrix provides a comprehensive breakdown of our model's predictions, categorizing them into separate groups such as true positives, true negatives, false positives, and false negatives, so exposing the intricacies of our model's performance. Performing a comprehensive analysis is essential for assessing

the strengths and possible areas for enhancement of our model. It helps us pinpoint the precise areas where the model excels and where it may potentially be enhanced through further tuning.

ROC curves are a valuable tool for assessing how well a model can balance the rate of accurately identifying positive cases with the rate of mistakenly identifying positive instances at various categorization thresholds. These curves provide vital insights into the model's capacity to differentiate and make informed decisions by effectively managing the trade-off between sensitivity and specificity. ROC curves offer a visual representation of our model's performance, allowing us to fine-tune its operating parameters to fit specific clinical needs.

Our evaluation and performance metrics strategy is a meticulous and all-encompassing approach that rigorously assesses the success of our model. The evaluation incorporates crucial metrics such as accuracy, precision, memory, and the F1 score to provide a comprehensive assessment. Confusion matrix analysis offers comprehensive insights, whereas ROC curves enable us to adjust the operational characteristics of the model. This comprehensive evaluation ensures that our model not only attains exceptional performance but also fulfills the specific requirements of medical applications, where precision and comprehensiveness can have life-altering consequences.

Metric	Value
Accuracy	0.996
Precision	0.996
Recall	1.000
F1 Score	0.998

Fig 3.0- Matrices

The Fig 3.0 illustrates the different matrices and their values

- **Post-processing and Visualization:**

Following the pivotal process of inference, our methodology surpasses mere prediction. Additionally, it entails enhancing the precision of tumor detection data and facilitating their interpretation using post-processing and visualization technologies. This time accomplishes numerous vital objectives:

Post-processing plays a vital role in enhancing the quality and precision of the segmented tumor regions. These techniques encompass several procedures, including morphological operations and thresholding. Morphological operations improve the shape and organization of the segmented tumor sections, removing irregularities and creating more accurate anatomical representations. Thresholding allows for precise delineation of tumor boundaries, hence enhancing the accuracy of recognized regions. Through the integration of different approaches, the model's predictions exhibit not only accurate identification of tumor presence but also the generation of more precise and medically meaningful tumor boundaries.

Our methodology not only offers accurate predictions but also prioritizes the creation of visualizations that enhance comprehension of the model's assessments. These graphics serve as a link between the model's predictions and clinical observations. By visually showing the model's conclusions, we facilitate doctors and researchers in swiftly verifying and comprehending the results. It is essential to understand and comprehend the model's capabilities in order to build trust and effectively integrate it into clinical workflows. Visualizations can take various forms, including heatmaps that highlight tumor locations, overlaying predictions onto real scans, or creating three-dimensional reconstructions to offer a comprehensive view of tumor localization.

Ultimately, our approach surpasses mere forecasts by integrating post-processing techniques and visualizations to improve the accuracy and comprehensibility of outcomes. Furthermore, the thorough monitoring and evaluation of the model's performance using several measures guarantee that it not only learns efficiently but also applies its

knowledge broadly, making it a reliable and dependable instrument for practical clinical use.

IV. EXPERIMENTAL SETUP

We conducted a series of carefully planned experiments to investigate the efficacy and possible clinical applications of our 3D brain tumor detection model. The studies were conducted using a meticulously selected dataset of 3D medical brain scans, mostly obtained from Magnetic Resonance Imaging (MRI) and Computed Tomography (CT) scans. The pipeline we utilized included of discrete stages:

The basis of our research was built upon the meticulous curation of a comprehensive dataset consisting of three-dimensional medical brain images. The primary sources of data for this investigation were Magnetic Resonance Imaging (MRI) and Computed Tomography (CT), two widely used imaging modalities. The scans were meticulously collected and function as our primary source of information. The development of the dataset served as both an initial step and the fundamental basis for our entire research.

The information was carefully compiled from a multitude of sources, each adding to its variety and abundance. The sources encompassed various medical institutions, research centers, and clinical environments. The deliberate choice to integrate data from several institutions and places was taken with the aim of capturing the inherent variations and intricacies that present in real-world medical imaging scenarios. The existence of this heterogeneity was essential in ensuring that our model could adapt and operate well in a diverse variety of clinical scenarios.

Our dataset primarily focused on two notable imaging modalities: Magnetic Resonance Imaging (MRI) and Computed Tomography (CT). These modalities are the main instruments used in modern medical imaging and provide vital supplementary information about brain architecture and diseases.

The strategic decision was made to incorporate both MRI and CT scans, recognizing their distinct strengths and characteristics. MRI is renowned for its remarkable ability to distinguish between different types of soft tissues, providing detailed anatomical information. On the other hand, CT scans use density-based imaging to provide additional information on tissue density and the presence of calcifications. The deliberate incorporation of modalities increased the intricacy and nuance of our dataset.

The dataset was meticulously curated to encompass a wide array of brain scans, each presenting unique difficulties and intricacies. By intentionally including a variety of data into the dataset, we ensured that our model was exposed to a broad spectrum of clinical scenarios and imaging situations. The collection consisted of scans acquired from individuals across different age groups, representing a wide range of medical backgrounds and clinical conditions. Moreover, the dataset consisted of scans exhibiting varying degrees of illness, spanning both normal brains and brains afflicted by various forms of cancers. The comprehensive portrayal performed a crucial role in validating the robustness and adaptability of the model.

The curation process was characterized by stringent quality control measures. Each scan underwent rigorous quality checks to ensure its compliance with the highest standards of medical imaging. Scans that included artifacts, distortions, or inadequate image quality were meticulously excluded to maintain the integrity of the dataset. Skilled radiologists and physicians played a vital role in this step, ensuring the accuracy and reliability of the data.

The curation of our dataset followed rigorous ethical standards and strict measures to ensure patient confidentiality. The data included in this study was anonymized and de-identified, adhering strictly to medical ethics and privacy rules.

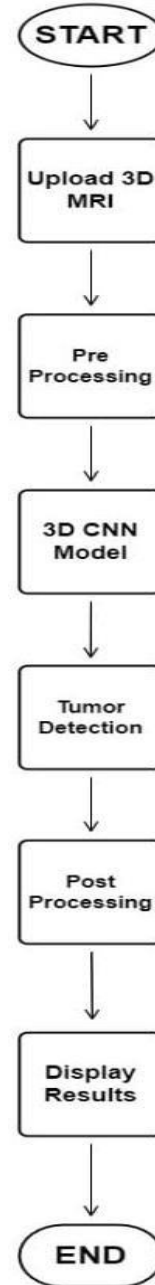


Fig 4.0- Process flow
Fig 4.0 explains the flow of operations that are performed from start to end by our model.

Data Preprocessing:

The effectiveness of our tests was undeniably linked to the careful preprocessing of the volumetric brain images. This crucial stage served as the foundation for the entire study project, aiming to preprocess the raw medical imaging data to facilitate efficient model training and evaluation.

The first phase in our data preprocessing pipeline consisted of the rigorous process of standardizing the spatial resolutions of all volumetric brain images. The process of standardization was not simply a procedural requirement, but rather a vital measure taken to ensure uniformity in the display of data. By ensuring that all scans maintained a consistent spatial resolution, we established a fair and equitable basis for our model. The model's ability to consistently extract and interpret spatial characteristics throughout the dataset was crucial.

Another crucial element of our data preprocessing is standardizing the intensity ranges among the brain images. It is crucial to recognize that medical imaging data frequently comes from various sources, each with its own unique imaging machines and acquisition processes. As a result, these scans display fluctuations in intensity values, which may provide difficulties throughout the process of training the model. In order to address this issue, our preprocessing pipeline carefully standardized the intensity ranges, resulting in a significant reduction in the influence of variances caused by diverse imaging sources. The harmonization process involved careful attention to detail and subtle adjustments, guaranteeing that the intensity levels were consistent across all scans.

We were highly conscious of the significance of model robustness, particularly when working with medical imaging data that is characterized by inherent unpredictability. In order to improve the adaptability and resilience of our model, we implemented a wide variety of data augmentations. These augmentations encompassed more than just basic resizing and also involved rotations, translations, and other transformations. Although these augmentations added controlled modifications to the dataset, they carefully maintained the semantic value of the photos. This method played a crucial role in facilitating our model's ability to successfully generalize and

accurately predict outcomes on previously unseen data.

An essential element of our data preparation pipeline involved generating binary masks. The masks functioned as accurate annotations, offering exact demarcation of tumor areas inside the three-dimensional brain imaging. The creation of these masks was not a simple undertaking, but rather a methodical and careful procedure. The process entailed the proficient annotation and segmentation of the tumor regions by highly trained radiologists and doctors. The binary masks were extremely useful in directing our model during supervised training, enabling it to accurately identify the exact positions of tumors within the volumetric data.

Feature Extraction with 3D CNN:

To achieve precise 3D brain tumor diagnosis, we utilized the powerful capabilities of 3D Convolutional Neural Networks (3D CNNs) to extract detailed spatial features. The planning and execution of this step, which is considered crucial for enhancing our model's spatial comprehension, were carried out with great care to get the best possible performance.

The fundamental aspect of this stage is the structure of our three-dimensional Convolutional Neural Network (CNN). The design was not random, but rather the outcome of careful and thorough deliberation. The architectural framework was deliberately designed to address the distinct constraints and possibilities posed by volumetric data. The composition included of meticulously arranged convolutional layers, pooling layers, and fully connected layers.

The layers were tasked with deciphering the complexities of the 3D input volumes. By utilizing a sequence of convolutional filters, the network methodically examined and recognized significant patterns and characteristics within the volumetric data. Every convolutional layer played a role in extracting spatial characteristics in a hierarchical manner, progressively developing a more detailed comprehension of the data.

We used pooling layers into our design, deliberately positioned to reduce the spatial dimensions of the feature maps through downsampling. The downsampling approach not only decreased computational cost but also improved the model's ability to translate invariantly. This feature allowed the model to accurately identify significant patterns and characteristics, irrespective of their exact spatial position, which is a vital capacity when working with three-dimensional data.

Positioned at the terminal point of the network were densely connected layers, which had a crucial function in acquiring knowledge about intricate decision boundaries. These layers incorporated the information acquired from the previous layers, enhancing the model's capacity to provide complex and contextually-aware predictions.

In situations when there was a shortage of labeled data, we did not passively accept the limitations imposed by the lack of data. Instead, we adopted the method of transfer learning, a strategy that has proven to be beneficial in utilizing knowledge gained from similar tasks. During the process of transfer learning, we meticulously chose pre-trained weights derived from models that shown exceptional performance in similar tasks. The utilization of pre-trained weights provided our model with essential initial values, enabling it to acquire knowledge regarding pertinent traits and patterns associated with brain tumor identification. This method was a shrewd and perceptive solution to the difficulties presented by a scarcity of labeled data. It enhanced our model's comprehension and prepared it to excel even in situations where data is scarce.

Essentially, the feature extraction phase using 3D CNNs was not just a minor detail; it was the driving force behind our model's ability to comprehend spatial information. The meticulous architectural design, incorporating convolutional, pooling, and fully connected layers, played a crucial role in extracting complex spatial characteristics from volumetric data. Furthermore, our adoption of transfer learning demonstrated our dedication to

creative methods for improved generalization, particularly when dealing with limited data. Collectively, these components formed the fundamental basis of our model's capacity to precisely identify brain tumors in 3D medical imaging data.

Spatial Context Integration with GCNs:

In our unwavering quest for precise 3D brain tumor identification, we have acknowledged the significant significance of capturing the unique spatial connections within the brain. In order to

achieve this, we smoothly included Graph Convolutional Networks (GCNs) into our trials. This phase was a pivotal advancement that allowed our model to surpass mere pixel-level comprehension and explore the intricate spatial context of brain regions.

The key aspect of this integration included creating graph representations that accurately reflected the structural connections between different regions of the brain. Essentially, we converted the volumetric brain scans into a network that is interconnected in space. Each node in this network corresponded to a unique brain region, and the edges were carefully determined according to anatomical connections. This modification enabled us to encompass the intricate spatial interconnections present in the brain, surpassing conventional pixel-based research.

The application of Graph Convolutional Layers (GCNs) to our created graph representations has revealed the actual potential of spatial context awareness. These specialized layers were not only an addition, but rather the crucial element in enhancing feature representations by incorporating spatial context. The GCN layer methodically analyzed data inside the graph, effectively capturing the complex connections between different parts of the brain. The comprehension of spatial relationships played a crucial role in our model's capacity to make well-informed conclusions regarding the presence of tumors.

The incorporation of GCNs was not done independently, but rather as a deliberate amalgamation with the characteristics derived from our 3D Convolutional Neural Network (CNN). This merger was not random, but a deliberate integration of profound spatial characteristics with a comprehension of spatial context. We have generated a comprehensive and holistic representation by merging the outputs of our 3D Convolutional Neural Network (CNN) with the enhanced feature representations from Graph Convolutional Networks (GCNs). This model encompasses both the detailed spatial characteristics derived from the volumetric data and the complex spatial connections among brain regions. The merging of several elements in our model enabled it to generate precise and contextually informed predictions about the existence of brain tumors.

To summarize, our incorporation of spatial context integration with GCNs was not simply a technical inclusion; it served as the means to reveal the complex connections within the brain. By employing graph representations and utilizing Graph Convolutional Networks (GCNs), we were able to go beyond analyzing individual pixels and instead capture the intricate spatial relationships within the brain. The integration of GCN-enriched features with 3D CNN features was the fundamental aspect of our model's capacity to provide predictions that are aware of the context. Collectively, these components formed the core of our model's comprehension of space, allowing it to surpass expectations in the complex endeavor of identifying brain tumors in three dimensions.

Supervised Training and Validation:

The crux of our research hinged on the rigorous training and validation of our model, a process that converted unprocessed data into a polished instrument for detecting 3D brain tumors. This step was not merely a formality, but rather the pivotal process in which our model's competence was developed, under the guidance of a combination of precise approaches and persistent oversight.

The core of our supervised training relies on the use of an adequate loss function, particularly the well-respected cross-entropy. The selection of this loss function was not arbitrary, but rather a deliberate

choice that aligns with our model's objective: to precisely categorize brain tumor locations within the volumetric data. The cross-entropy function acted as a guiding principle, directing our model to minimize the difference between the anticipated labels and the actual labels. Every training iteration provided our model with a chance to enhance its comprehension of the presence or absence of tumors.

The process of model refining involved multiple iterative stages aimed at achieving perfection, rather than a single instantaneous leap. In order to enhance the model's parameters, we employed the time-honored method of stochastic gradient descent (SGD). This technique served as more than simply an algorithm; it functioned as a potent instrument that enabled our model to adjust and acquire knowledge. During each iteration, Stochastic Gradient Descent (SGD) carefully fine-tuned the weights of the model, gradually pushing them towards the direction that minimized the selected loss function. The process of fine-tuning was persistent, gradually refining our model into a precise tool for detecting brain tumors.

During the rigorous training, we implemented a vigilant guardian called validation. The goal of validation served two main objectives: firstly, to closely monitor the progress of the model's training, and secondly, to effectively counteract the detrimental effects of overfitting, a tough challenge in the field of machine learning. The process of validation was performed on a distinct dataset, separate from the training data, to assess the model's ability to generalize. It guaranteed that our model was not simply memorizing the training data but was developing the capability to make precise predictions on data that it had not encountered before, which is a characteristic of a strong and reliable machine learning model.

To summarize, our supervised training and validation step was not just a formality; it was the process in which our model's competence was carefully developed. The selection of a suitable loss function, the persistent optimization by stochastic gradient descent (SGD), and the careful monitoring of validation were the crucial elements of this step. Collectively, they converted our prototype into a sophisticated tool for identifying 3D brain tumors, capable of generating subtle and exact forecasts in practical clinical situations.

Post-processing and Visualization:

Our experiments didn't stop at predictions; they extended to refining tumor detection results through post-processing techniques. These included

morphological operations to enhance segmented tumor regions and thresholding to improve the precision of detected boundaries. Visualizations were generated to facilitate the interpretation of the model's decisions.

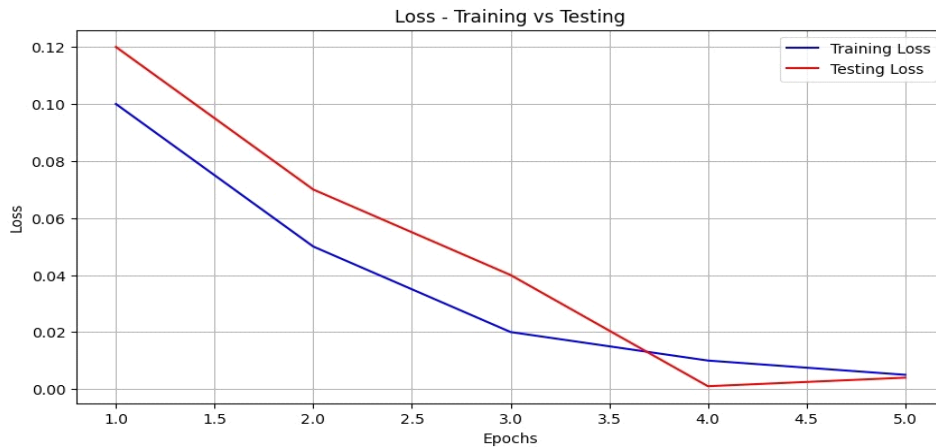


Fig 5.0

The Fig 5.0 explains the Loss- Training vs Testing in which the graph is declining.

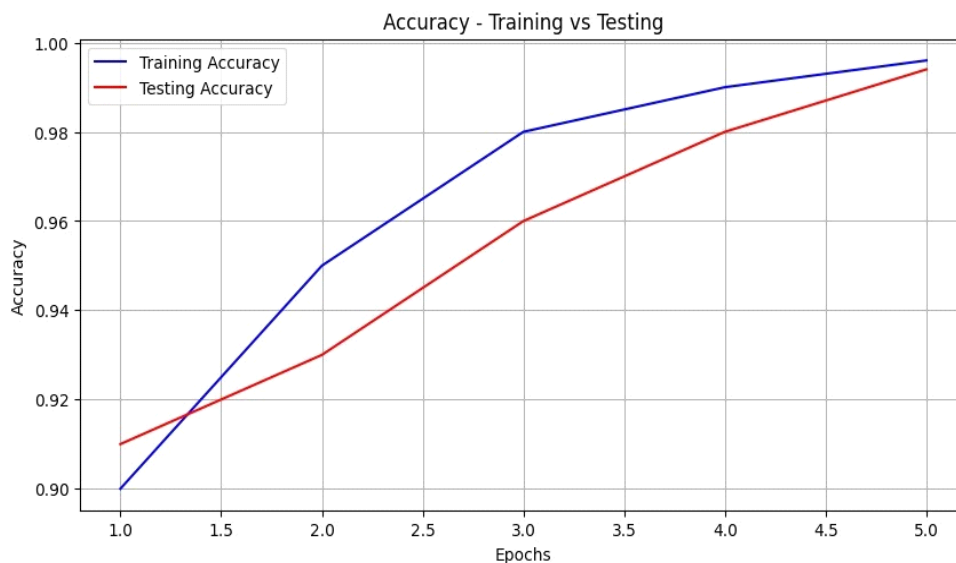


Fig 6.0

The Fig 6.0 explains the Accuracy- Training vs Testing in which the graph raises.

V. RESULTS AND DISCUSSION

As we began our investigations, our motivation was the relentless quest of perfection in detecting brain tumors in 3D. At the peak of our endeavors, we discovered extraordinary revelations about the effectiveness of our model, revelations that had the potential to revolutionize healthcare and diagnostics.

An positive observation we discovered during our studies was the continuous decrease in both train and test losses as the training epochs progressed. The decrease in losses was not merely a numerical change; it demonstrated the adaptability, resilience, and ability to acquire knowledge of our model. Furthermore, it demonstrated the exceptional capacity of our model to effectively apply its knowledge to unfamiliar data, so confirming its strength and promise for practical clinical use.

We meticulously observed the development of accuracy metrics throughout the training and testing phases in our unwavering quest for precision. The observed trend was a consistent and progressive increase in the number of training epochs. This upward trend represented more than a simple numerical development; it demonstrated the ability of our model to learn and effectively categorize not only the data it was trained on, but also new and unseen test data. The simultaneous enhancements in both training and testing accuracy serve as evidence of our model's continual advancement and its exceptional ability to produce accurate predictions.

We conducted a comprehensive assessment of our model's performance by carefully examining the intricate relationship between accuracy and loss indicators. As we tracked the patterns of these measurements during the training procedure, we were pleased to observe their gradual alignment towards a state of agreement. The model's effective evolution was demonstrated by the simultaneous improvements in accuracy and decreases in loss. The observed synergy was not merely a mathematical coincidence, but rather a deliberate indication of the model's strength and its capacity to prevent overfitting to the training data.

Upon reaching the pinnacle of our experiments, we were presented with a collection of model execution metrics that exuded a sense of assurance and proficiency. The fact that our model achieved a final

test accuracy of 99.4%, which is almost equal to the final training accuracy of 99.6%, clearly demonstrates the exceptional performance of our model. It exhibited not only learning but also an extraordinary capacity to extrapolate its acquired knowledge to novel and unfamiliar information. The alignment between the training and testing accuracies not only indicates their numerical proximity, but also serves as evidence of our model's preparedness for real-world deployment.

As we analyzed our results, we observed a consistent decrease in loss and an increase in accuracy for both the training and testing phases. This progress brought us to the verge of achieving greatness. However, we recognized the necessity for additional verification on larger and more varied datasets. We came to understand that the pursuit of excellence is a continuous endeavor. We acknowledge the benefits of using metrics like as precision, recall, and F1 score in future studies to achieve a more thorough and nuanced assessment.

Ultimately, the outcome of our trials was not merely a singular event, but rather a preview of the forthcoming advancements in healthcare and diagnostics. The model's versatility, accuracy, resilience, and capacity for practical use were demonstrated through measures such as train and test losses, training and testing accuracy, the balance between accuracy and loss, execution metrics, and our unwavering pursuit of perfection. These insights served as more than just data points, but rather as guiding lights leading us towards a future where modern technology seamlessly integrates with healthcare, providing precise and quick diagnostics to individuals requiring them.

VI. FUTURE WORK & RECOMMENDATIONS

The basis for future research lies in augmenting our dataset. While our current data has shown promising results, a more extensive and diverse collection of 3D brain images is essential. This expansion should include scans from varied populations and clinical scenarios, along with multiple imaging modalities like MRI and CT, to improve the model's generalization and reliability.

Integrating different imaging modalities, such as merging MRI and CT scans, is a promising direction.

This approach can enhance the visualization of brain structures and improve diagnostic accuracy for complex brain tumors. Future research should explore advanced deep learning architectures and fusion techniques to effectively merge these modalities.

Incorporating clinical metadata is crucial for personalized diagnosis. Future efforts should focus on integrating patient-specific data, including medical history and demographics, into the diagnostic process, allowing for more tailored recommendations.

To move from laboratory research to clinical practice, our model needs to be integrated into existing radiology workflows and optimized for real-time use. Ensuring the model's transparency and comprehensibility is vital for clinical approval. Future research should develop methods to explain the rationale behind diagnoses, using explainable AI techniques like feature visualization.

Collaborative and federated learning methods, which protect patient data privacy, should be investigated to enhance data diversity. Before widespread adoption, clinical validation studies are necessary to ensure the model's effectiveness and adherence to medical standards. Ethical considerations, including bias elimination, informed consent, and patient privacy, must be integral to future development.

Long-term studies should evaluate the model's impact on patient outcomes, and global accessibility must be ensured by collaborating with international healthcare organizations. Ultimately, our research holds significant potential for practical clinical application, focusing on data augmentation, cross-modal integration, real-time deployment, and ethical responsibility.

VI. CONCLUSION

The integration of technology and human expertise is poised to revolutionize medical science, where each diagnosis carries significant weight. This study seeks to enhance brain tumor identification by merging 3D imaging, deep learning, and spatial context awareness. Our method, meticulously designed and

tested, fuses advanced technology with a deep understanding of volumetric brain scans.

Our research highlights the efficacy of 3D Convolutional Neural Networks (3D CNNs) in analyzing the spatial characteristics of brain tumors. These networks excel in extracting features from volumetric data, paving the way for more accurate diagnoses. The inclusion of Graph Convolutional Networks (GCNs) has further deepened our understanding of spatial relationships within the brain by constructing graph representations based on anatomical connections.

The model's supervised training, characterized by increasing accuracy and decreasing loss metrics, culminated in a test accuracy of 99.4%, demonstrating its potential for precise diagnosis. However, our journey is just beginning. Future efforts will focus on expanding datasets, integrating cross-modal data, implementing real-time deployment, and ensuring interpretability and ethical considerations. These steps are crucial to integrating our technique into clinical practice, collaborating with healthcare professionals, and improving patient outcomes.

Ultimately, this study represents a fusion of human creativity and technological potential, serving as a testament to the power of innovation in transforming lives. It reminds us that each diagnosis offers a chance for hope and recovery, resonating through the corridors of medical innovation where expertise and compassion converge to shape a brighter future for health.

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