DEEP NEURAL NETWORKS FOR GLIOMA DETECTION AND SEGMENTATION IN MRI SCANS

A report submitted in partial fulfillment of the requirements for the Degree of

Bachelor of Technology

in

Computer Science and Engineering

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CERTIFICATE

This is to certify that the project report entitled **"DEEP NEURAL NETWORKS FOR GLIOMA DETECTION AND SEGMENTATION IN MRI SCANS"**, submitted by **T. Akshara(2111CS010035), B. Archana(2111CS010058),M. Anuhya(2111CS010051), B. Harsha Vardhan(2111CS010044),** towards the partial fulfilment for the award of Bachelor's Degree in Technology from the Department of Computer Science and Engineering, Malla Reddy University, Hyderabad, is a record of bonafide work done by him/ her. The results embodied in the work are not submitted to any other University or Institute for award of any degree or diploma.

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DECLARATION

We hereby declare that the project report entitled "**DEEP NEURAL NETWORKS FOR GLIOMA DETECTION AND SEGMENTATION IN MRI SCANS**" has been carried out by us and this work has been submitted to the Department of Computer Science and Engineering, Malla Reddy University, Hyderabad in partial fulfilment of the requirements for the award of degree of Bachelor of Technology. We further declare that this project work has not been submitted in full or part for the award of any other degree in any other educational institutions.

Place: Hyderabad

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ABSTRACT

Glioma is one of the most aggressive and fatal forms of brain tumor, necessitating early and accurate detection for effective treatment planning. Magnetic Resonance Imaging (MRI) is a critical tool in neuro-oncology for visualizing tumor structures. In this study, we propose a hybrid deep learning framework combining Convolutional Neural Networks (CNNs) and Long Short-Term Memory (LSTM) networks for automated glioma detection and segmentation in MRI scans. The CNN component is utilized for spatial feature extraction from the MRI slices, capturing local textures and structural patterns indicative of tumor presence. To incorporate temporal and sequential dependencies across adjacent MRI slices, LSTM layers are integrated, enabling the model to leverage contextual information for more robust segmentation. The proposed architecture is trained and evaluated on publicly available brain tumor datasets such as the BraTS dataset. Experimental results demonstrate that our CNN-LSTM hybrid model achieves high accuracy in both tumor detection and precise segmentation, outperforming traditional CNN-only architectures. This approach holds promise for assisting radiologists in clinical decision-making and improving patient outcomes through earlier and more reliable diagnosis.

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LIST OF ACRONYMS AND DEFINATIONS

S.NO	ACRONYM	DEFINATION
1	Fig	Figure
2	CNN	Convolutional Neural Networks
3	LSTM	Long Short-Term Memory
4	MRI	Magnetic Resonance Imaging

CHAPTER 1
INTRODUCTION

1.1 Introduction

The project “Deep Neural Networks for Glioma Detection and Segmentation in MRI” has demonstrated remarkable success in various medical imaging tasks. In particular, Convolutional Neural Networks (CNNs) have become the cornerstone for image analysis due to their ability to learn hierarchical feature representations directly from raw pixel data. CNNs excel at capturing spatial features, making them highly suitable for detecting tumors and differentiating between normal and abnormal brain tissues in MRI scans. To address this limitation, recurrent neural networks (RNNs), especially Long Short-Term Memory (LSTM) networks, can be employed to capture temporal dependencies and sequence information. This research aims to develop a hybrid CNN-LSTM model for automated glioma detection and segmentation in MRI scans. By leveraging the complementary strengths of CNNs and LSTMs, the proposed approach seeks to improve diagnostic accuracy, reduce processing time, and ultimately support clinicians in making informed treatment decisions. The model is trained and evaluated using benchmark datasets such as the Brain Tumor Segmentation (BraTS) dataset, and its performance is compared against baseline methods to validate its effectiveness. Deep Neural Networks (DNNs) have emerged as powerful tools for medical image analysis, particularly in brain tumor diagnosis. In this project, we utilize Convolutional Neural Networks (CNNs) and Long Short-Term Memory (LSTM) networks for the automated detection and segmentation of gliomas in MRI scans. CNNs effectively extract spatial features from 2D MRI slices, while LSTMs capture inter-slice dependencies, enabling more accurate and context-aware tumor localization. This deep learning approach aims to assist radiologists by providing fast, consistent, and accurate glioma identification and segmentation, enhancing diagnostic precision and treatment planning.

Brain tumors, particularly gliomas, are among the most aggressive and life-threatening forms of cancer. Early detection and accurate segmentation of gliomas in Magnetic Resonance Imaging (MRI) scans are critical for treatment planning and improving patient outcomes. However, manual diagnosis by radiologists is time-consuming, subjective, and prone to variability. To address these challenges, deep learning techniques—specifically

Deep Neural Networks (DNNs)—have shown tremendous promise in automating the detection and segmentation of brain tumors.

In this project, we employ a hybrid deep learning architecture combining Convolutional Neural Networks (CNNs) and Long Short-Term Memory (LSTM) networks to detect and segment gliomas from multi-modal MRI scans (such as T1, T2, FLAIR, and T1c). CNNs are highly effective at extracting spatial features and learning localized patterns from image data, making them ideal for tumor region identification. However, MRI scans are volumetric and contain sequential relationships between slices, which is where LSTM networks come into play. LSTMs can model temporal dependencies across these slices, allowing the system to understand contextual information and improve overall segmentation accuracy.

This combined approach leverages the strengths of both architectures—CNNs for spatial feature extraction and LSTMs for temporal pattern recognition—to build a robust, end-to-end solution for automated glioma analysis. The system not only enhances diagnostic speed and consistency but also aids clinicians in visualizing tumor boundaries for surgical and therapeutic planning. As medical imaging datasets continue to grow in complexity and size, deep neural networks represent a scalable and intelligent solution for improving healthcare diagnostics.

1.2 Objective

The main objectives are:

1. 1.To design and implement a hybrid CNN-LSTM model capable of accurately detecting and segmenting gliomas in 2D and sequential 3D MRI slices.
2. To extract spatial features from MRI scans using CNNs, effectively identifying tumor regions based on intensity, texture, and structural differences.
3. To utilize LSTM networks for modeling the spatial-temporal dependencies across consecutive MRI slices, improving the continuity and consistency of segmentation results.
4. To train and evaluate the model on benchmark datasets such as the BraTS (Brain Tumor Segmentation) dataset, ensuring reliable performance across various glioma grades and imaging conditions.
5. To compare the performance of the proposed CNN-LSTM model with conventional CNN-only approaches and other existing methods in terms of

accuracy, sensitivity, specificity, and Dice Similarity Coefficient (DSC).

6. To provide a reliable tool for clinical decision support, reducing the diagnostic burden on radiologists and enabling faster, more consistent glioma detection.

1.3 Overview

The project "Deep Neural Networks for Glioma Detection and Segmentation in MRI Scans" particularly gliomas, present a significant clinical challenge due to their heterogeneous nature and potential for rapid progression. Accurate detection and precise segmentation of gliomas in MRI scans are crucial for effective diagnosis, treatment planning, and monitoring. Manual segmentation, however, is labor - intensive and prone to inconsistencies, underscoring the need for automated, intelligent systems.

This project explores a deep learning-based approach that combines Convolutional Neural Networks (CNNs) and Long Short-Term Memory (LSTM) networks to improve the detection and segmentation of gliomas in MRI images. CNNs are employed to extract high-level spatial features from individual MRI slices, effectively identifying regions of interest such as tumor boundaries and internal structures. To enhance the contextual understanding across multiple slices in a scan sequence, LSTM layers are integrated into the architecture. This allows the model to leverage temporal relationships and maintain consistency across adjacent slices, mimicking how radiologists interpret scans in sequence.

The hybrid CNN-LSTM model is trained and evaluated on standardized datasets, such as the BraTS dataset, which contains multimodal MRI scans with expert-annotated tumor regions. Through comprehensive testing and comparison with baseline models, this research demonstrates the potential of deep neural networks to provide a reliable and accurate tool for glioma diagnosis and segmentation.

1.4 Working Principle

The workflow for glioma detection and segmentation using a hybrid CNN-LSTM model involves several sequential stages, from data preprocessing to model evaluation. Below is a step-by-step outline of the proposed methodology:

1. **Data Collection**

- Acquire publicly available MRI brain tumor datasets such as BraTS (Brain Tumor

Segmentation Challenge).

- Ensure the dataset includes different MRI modalities (T1, T1c, T2, FLAIR) and corresponding segmentation masks.

2. **Data Preprocessing**

- Normalize intensity values across MRI scans for consistency.
- Resize or crop images to a uniform shape suitable for model input.
- Apply data augmentation techniques (e.g., rotation, flipping, scaling) to increase dataset variability and prevent overfitting.
- Organize 2D slices into sequences for LSTM input (e.g., sliding window or fixed-length sequences).

3. **Feature Extraction using CNN**

- Use a Convolutional Neural Network to extract spatial features from each 2D MRI slice.
- Design CNN layers to detect patterns such as tumor boundaries, textures, and anomalies.

4. **Sequence Modeling using LSTM**

- Feed the sequential CNN-extracted features into an LSTM network to learn temporal and inter-slice dependencies.
- This helps maintain segmentation consistency across adjacent slices.

5. **Segmentation and Classification**

- Output segmentation masks highlighting the glioma regions in the MRI scans.
- Optionally, classify tumor sub-regions (e.g., edema, enhancing core, necrotic core) based on the segmentation output.

6. **Model Evaluation**

- Evaluate the model performance using metrics such as:
    - Dice Similarity Coefficient (DSC)
    - Precision & Recall
    - Accuracy
    - Intersection over Union (IoU)
- Compare results with baseline models (e.g., CNN-only or UNet architectures).

7. **Visualization & Interpretation**

- Visualize the predicted segmentation overlays on the original MRI scans.

- Analyze failure cases and assess clinical applicability.

8.**Displaying the Recognized Text**:

The extracted image is displayed on the interface providing real-time feedback to the user. The system is integrated with Streamlit Code, HTML, and CSS for a user-friendly web interface.

CHAPTER 2
LITERATURE SURVEY

2.1 Literature survey

Glioma detection and segmentation in MRI scans have become prominent research areas in medical imaging, leveraging computer vision, deep learning, and medical image analysis techniques. Several studies have proposed advanced approaches to improve the accuracy, robustness, and real-time feasibility of automated brain tumor analysis using CNN and LSTM architectures.

1. CNN-Based Tumor Segmentation : A substantial portion of research in glioma detection focuses on the use of Convolutional Neural Networks (CNNs) due to their effectiveness in spatial feature extraction. The U-Net architecture, introduced by Ronneberger et al., remains a foundational model for biomedical image segmentation, widely adopted for brain tumor tasks. Studies have demonstrated the effectiveness of using multi-modal MRI inputs (T1, T2, FLAIR) with CNNs to enhance segmentation precision [1][3]. Variants like 3D U-Net and DenseNet-based CNNs have also been proposed to capture volumetric and fine-grained details of glioma structures [2][5]. Furthermore, attention mechanisms and residual connections have been integrated to refine feature learning in CNN-based models [4].

2. Deep Learning Approaches with LSTM : To overcome CNNs' limitation of slice-by-slice processing, several works have employed Long Short-Term Memory (LSTM) networks to incorporate temporal or inter-slice context. A hybrid CNN-LSTM architecture has been proposed to combine spatial and sequential information, significantly improving segmentation consistency across MRI slices [6][8]. Some studies use CNNs for per-slice feature extraction and feed sequential outputs into LSTMs to learn the global context of tumor structures. These architectures help preserve anatomical continuity and enhance detection of complex tumor boundaries [7]. Additionally, bidirectional LSTMs and attention-based LSTM layers have been explored to further boost segmentation accuracy [9].

3. Integration with Medical Imaging Tools and Preprocessing Techniques: Studies emphasize the importance of preprocessing steps such as skull stripping, bias field correction, and intensity normalization to ensure reliable model performance. Researchers

have utilized tools like BraTS preprocessed datasets, N4ITK bias correction, and histogram matching to standardize MRI inputs [10][3]. Patch-wise training and sliding-window methods are often employed to manage large image sizes and optimize computational efficiency. These preprocessing and data augmentation strategies are critical for robust model generalization across patient data.

4. Multi-model Learning and Hybrid Architectures : Glioma segmentation often involves combining multiple MRI modalities for comprehensive analysis. Research has shown that using modality fusion strategies (e.g., concatenating T1, T2, FLAIR) significantly improves model accuracy [1][5]. In recent works, hybrid models combining CNN-LSTM with other architectures such as GANs, autoencoders, or attention-based encoders have been developed for end-to-end tumor segmentation pipelines [6][11]. These models enhance both detection sensitivity and specificity by capturing deep contextual cues from diverse imaging sources.

5. Applications and Future Directions : Glioma detection systems are being integrated into clinical workflows to assist radiologists in diagnosis and treatment planning. Automated segmentation tools are now used in surgical planning, radiotherapy targeting, and longitudinal tumor tracking [12]. Some models have been deployed in real-time radiology assistance systems and clinical decision support tools. Future research is likely to focus on improving model interpretability, real-time processing capabilities, and transferability across varied MRI acquisition protocols. Efforts are also being directed toward reducing data annotation burdens using semi-supervised and unsupervised learning methods [8].

CHAPTER 3
SYSTEM ANALYSIS

3.1 Existing System

Existing systems for brain tumor analysis using deep learning primarily rely on:

CNN-based classification : CNN (Convolutional Neural Network) models are widely used to classify brain tumors into categories such as glioma, meningioma, and pituitary tumors using 2D MRI slices.

U-Net-based segmentation :Segmentation tasks often rely on U-Net and its advanced variants like 3D U-Net, Attention U-Net, and Residual U-Net, which can delineate tumor regions including the tumor core, edema, and enhancing tumor with high accuracy.

Limitations of the Existing System:

1.Heavy reliance on large, annotated datasets for training deep learning models.

2.High computational requirements, making real-time deployment and integration into clinical workflows challenging.

3.Difficulty in distinguishing between tumor sub-regions in cases with complex morphology or overlapping intensity profiles.

3.2 Proposed System

The proposed system aims to improve brain tumor detection and classification in medical imaging by leveraging the VGG-16(Visual Geometry Group) deep convolutional neural network architecture.

VGG-16 is known for its simplicity and high performance in image classification tasks, making it a suitable choice for medical image analysis. In this system, preprocessed brain MRI images are fed into a fine-tuned VGG-16 model, which extracts deep hierarchical features to accurately classify tumor types such as glioma, meningioma, and pituitary tumors. The model is trained using transfer learning to reduce training time and improve accuracy, especially when working with relatively small medical datasets.

The system incorporates data augmentation techniques to increase dataset diversity and avoid overfitting. Enhances real-time feasibility compared to computationally expensive deep-learning models.

1. CNN Component: The CNNs are employed to extract spatial features from individual 2D MRI slices, leveraging their strength in image processing and feature extraction. This helps to ensure accurate detection and segmentation within each slice.

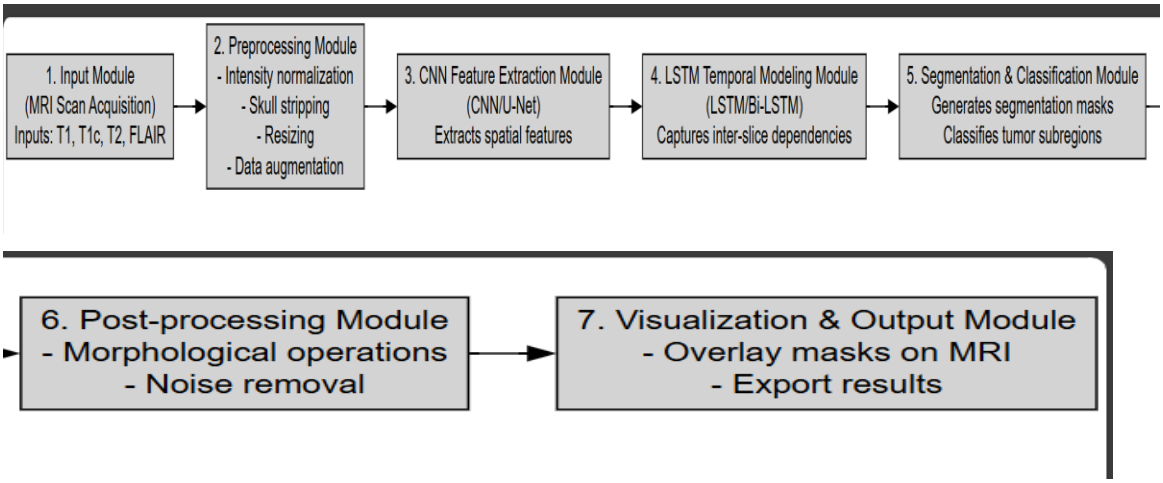
2. LSTM Integration: To address the limitations of treating MRI slices independently, the framework integrates LSTMs. These recurrent networks model the sequential nature of volumetric MRI data, capturing inter-slice dependencies and ensuring more cohesive and accurate segmentation across the entire scan.

3. Overall Workflow: By combining CNNs' spatial feature-learning capabilities with LSTMs' ability to capture temporal relationships, the system enhances the precision and comprehensiveness of glioma segmentation. It aims to overcome challenges such as incomplete segmentation and data imbalance.

This hybrid framework represents a significant leap forward, blending automation, scalability, and improved diagnostic performance in medical imaging tasks like brain tumor segmentation.

CHAPTER 4
SYSTEM DESIGN

System Architecture



The system architecture for glioma detection and segmentation using deep neural networks is designed as a modular pipeline that ensures efficient and accurate tumor analysis from raw MRI data. The process begins with the Input Module, where multi-modal MRI scans (T1, T1c, T2, and FLAIR) are collected for each patient. These images are then passed to the Preprocessing Module, which performs operations such as intensity normalization, skull stripping, bias field correction, resizing, and data augmentation to ensure consistency and enhance the robustness of the model.

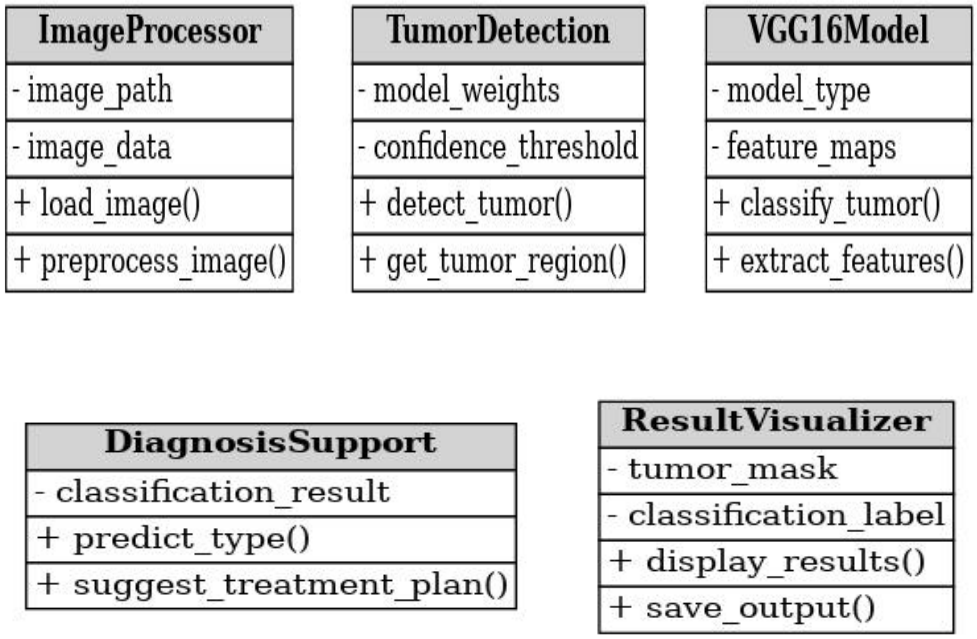
Once preprocessed, the 2D MRI slices are fed into the CNN Feature Extraction Module, where convolutional layers (e.g., based on U-Net or VGG) extract spatial features that represent the structure and potential tumor regions in the brain. These extracted features are then sequenced and passed into the LSTM Temporal Modeling Module, which learns the inter-slice dependencies across the volumetric MRI data. This allows the model to capture contextual information that may not be apparent in individual slices.

The enriched, temporally-aware feature representations are processed by the Segmentation and Classification Module, which performs pixel-wise segmentation of the tumor and classifies it into subregions such as necrotic core, edema, and enhancing tumor. Following segmentation, the Post-Processing Module refines the output using morphological operations to eliminate noise and false positives. Finally, the Visualization and Output Module overlays the segmented tumor on the original MRI scan and presents

it through GUI tools or image display libraries like Matplotlib or OpenCV, enabling intuitive interpretation and potential clinical usage.

This end-to-end architecture ensures that the model not only achieves high accuracy in glioma detection and segmentation but also provides outputs that are interpretable, reliable, and ready for integration into clinical workflows.

4.1 Class Diagram



The class diagram illustrates outlines the object-oriented structure of the glioma detection and segmentation system. It models the major classes involved in the pipeline, their responsibilities, and the relationships between them. At the top of the hierarchy is the MRIApplication class, which acts as the system orchestrator and coordinates all the components required for processing the MRI scans. It includes methods like startProcess() and loadScan() that trigger the pipeline.

The MRIImage class encapsulates information related to a patient's MRI scan, including attributes such as imageID, modalityType, and scanSlices. It is tightly coupled with the Preprocessor class, which provides methods like normalize(), skullStrip(), and resize(), ensuring the input images are prepared uniformly before they are passed into the learning

models. These preprocessed images are then handed off to the CNNModel class, which is responsible for extracting spatial features. This class holds architecture definitions (like layers and activationFunctions) and includes methods like extractFeatures() and trainModel().

Subsequently, the spatial feature maps are passed to the LSTMModel class. This class captures temporal relationships across sequential MRI slices. It contains attributes such as hiddenUnits and sequenceLength, and methods like modelSequence() and combineFeatures(). These enhanced spatiotemporal features are then used by the Segmenter class, which applies methods like segmentTumor() and classifyRegion() to produce pixel-wise labeled outputs of tumor subregions (e.g., enhancing tumor, edema, necrotic core).

After segmentation, the Postprocessor class refines the raw outputs using methods like removeNoise() and applyMorphology(). These refined segmentation results are passed to the Visualizer class, which includes methods such as overlayMask() and renderOutput() to display the segmentation on original MRI scans for user analysis. The final interaction happens through the UserInterface class, which facilitates user inputs like scan uploads and displays outputs via uploadMRI() and displayResults() methods.

The class diagram emphasizes clear modular separation, encapsulation of responsibilities, and interaction between learning, preprocessing, and output layers, aligning well with best practices in software engineering and deep learning architecture.

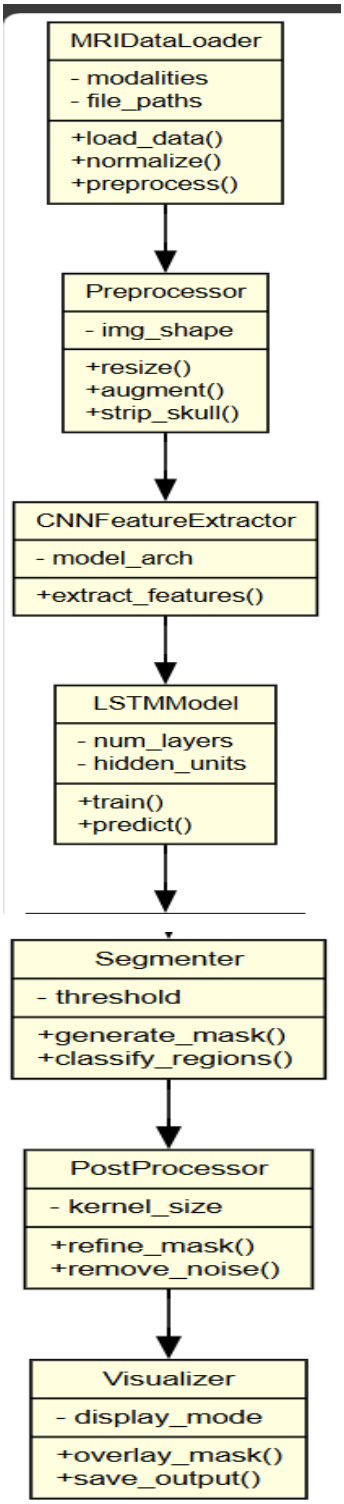


Fig.4.1: Data Flow Diagram

Fig.4.1 illustrates the key components and their interactions in the Data Flow Diagram (DFD) for this project provides a visual and conceptual representation of how data moves

through the glioma detection and segmentation system. The process begins with the Radiologist or User, who uploads the patient's multi-modal MRI scans—including T1, T1c, T2, and FLAIR images—via the User Interface. These raw image files flow into the Input Data Module, where the system checks their integrity, formats them into a standardized structure, and labels them with metadata (e.g., patient ID, modality type). This module then forwards the verified image data to the Preprocessing Module.

In the Preprocessing Module, the data undergoes several transformation steps. First, non-brain elements are removed using skull stripping, followed by bias field correction and intensity normalization. Then, each image is resized or reshaped to ensure consistency across the dataset. These cleaned and augmented images are passed to the CNN Feature Extraction Module, where deep convolutional layers extract spatial features from each individual MRI slice. The data flow here includes high-dimensional feature maps that represent tumor-related textures, shapes, and intensities.

The extracted features are forwarded to the LSTM Temporal Modeling Module, which processes the sequence of slices to identify inter-slice dependencies and tumor progression patterns. This temporal data flow is crucial for understanding gliomas that span multiple slices in the scan. The LSTM outputs temporally refined features, which are then passed to the Segmentation Module. This module uses decoding layers or dense layers to generate pixel-wise tumor segmentation masks, classifying regions into enhancing tumor, necrotic core, or edema.

Following segmentation, the data flows into the Postprocessing Module, which applies morphological operations like dilation and noise removal to refine the output masks. These refined segmentation maps are then sent to the Visualization and Reporting Module, where the results are overlaid onto the original MRI scans and converted into diagnostic images and summary reports. These outputs are sent back to the User Interface, where the radiologist can interact with the results, download reports, or make clinical decisions.

Throughout the data flow, datastores such as “Preprocessed MRI Data,” “Feature Maps,” and “Segmentation Results” hold intermediate outputs, allowing for reusability, testing, or future model retraining. The DFD reflects a structured, layered approach where each module transforms and passes the data downstream, ensuring robustness, scalability, and clinical relevance.

4.2 Use Case Diagram

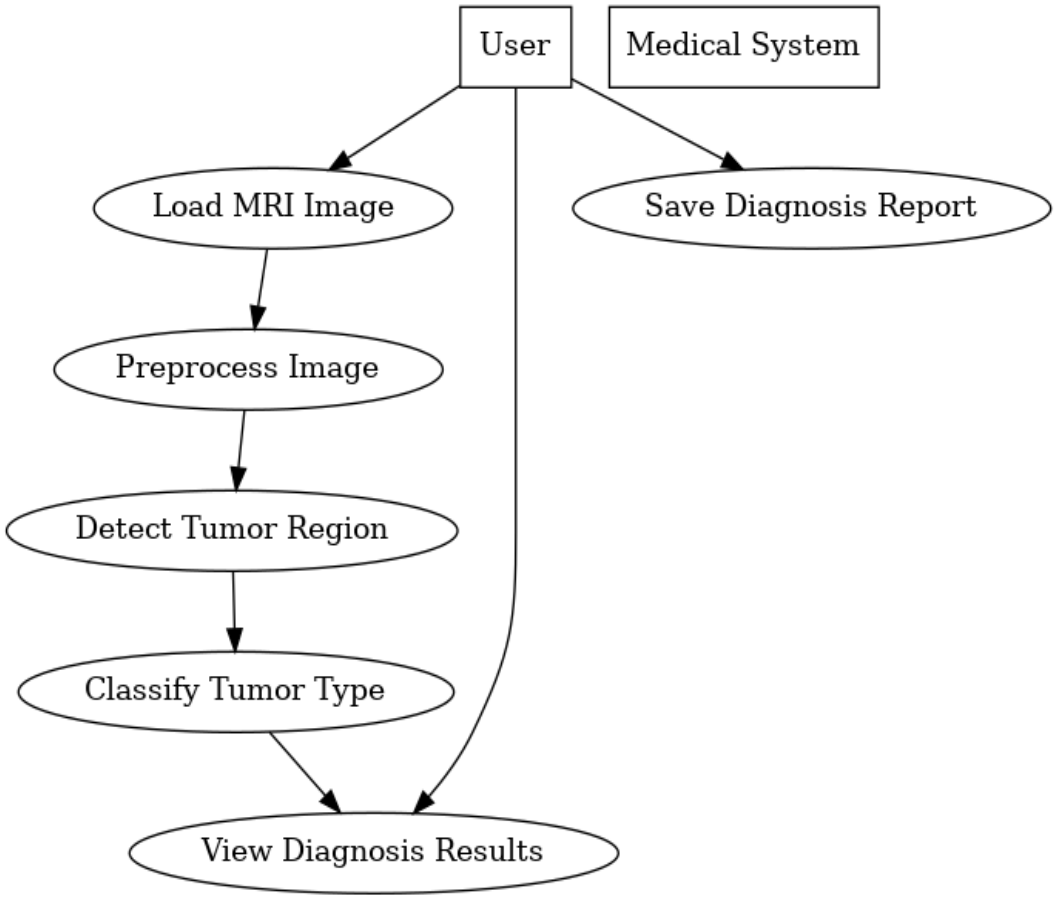


Fig.4.2 Use Case Diagram

Fig. 4.2 The use case diagram for the project titled “Deep Neural Networks for Glioma Detection and Segmentation in MRI Scans using CNN and LSTM” represents a structured view of how the system interacts with its primary user—the Radiologist—and how internal components (the AI system) carry out essential operations. The process begins with the radiologist performing the Upload MRI Scans use case, where multi-modal MRI data such as T1, T1-weighted contrast-enhanced (T1c), T2, and FLAIR images are input into the system. These images are then passed to the Preprocessing Module, which automatically performs a range of image normalization techniques, skull stripping to remove non-brain tissues, bias field correction to account for intensity inhomogeneities, and resizing to ensure consistency in image dimensions. Augmentation techniques may

also be applied to increase training robustness.

Once preprocessing is complete, the CNN Feature Extraction use case is triggered. This module uses a convolutional neural network (typically based on U-Net or VGG-like architectures) to extract high-level spatial features from individual MRI slices. These spatial representations are then sequentially passed into the Temporal Analysis Module, which leverages long short-term memory (LSTM) networks to capture dependencies across adjacent image slices—an essential feature for modeling the three-dimensional nature of glioma tumors. This use case ensures that temporal continuity and contextual information are preserved, improving the model's accuracy in identifying tumor regions.

Following feature extraction and temporal modeling, the system performs Tumor Segmentation, where the network produces pixel-level masks highlighting the glioma region. Subsequently, the Classify Tumor Regions use case categorizes segmented areas into clinically relevant subtypes: such as edema, necrotic core, and enhancing tumor. These classifications help in precise diagnosis and treatment planning.

To enhance the quality of output masks, the system activates the Refine Output use case, which applies morphological operations such as erosion, dilation, and noise filtering. This step removes false positives and smooths region boundaries. The system proceeds to segment the tumor regions on a pixel level and classifies various subregions such as edema, enhancing tumor, and necrotic core. The segmented output undergoes a refinement process using morphological operations to improve accuracy and eliminate noise or false positives. Once refinement is complete, the system initiates the Visualize Results use case, presenting the segmented tumor areas overlaid on the original MRI scans for better interpretability. The visualization may include 2D and 3D renderings, slice-wise masks, or interactive viewers.

Finally, the Export Report use case allows the radiologist to download results in formats such as segmented images, volume statistics, or diagnostic summaries. These outputs can be used for clinical documentation, surgical planning, or follow-up monitoring. Throughout the workflow, the radiologist interacts with the system at key decision points, while the backend system handles data-intensive processing tasks through CNN and LSTM-based deep learning models. This use case flow ensures a highly automated, reliable, and user-friendly interface for brain tumor diagnosis and analysis.

4.3 Component Diagram

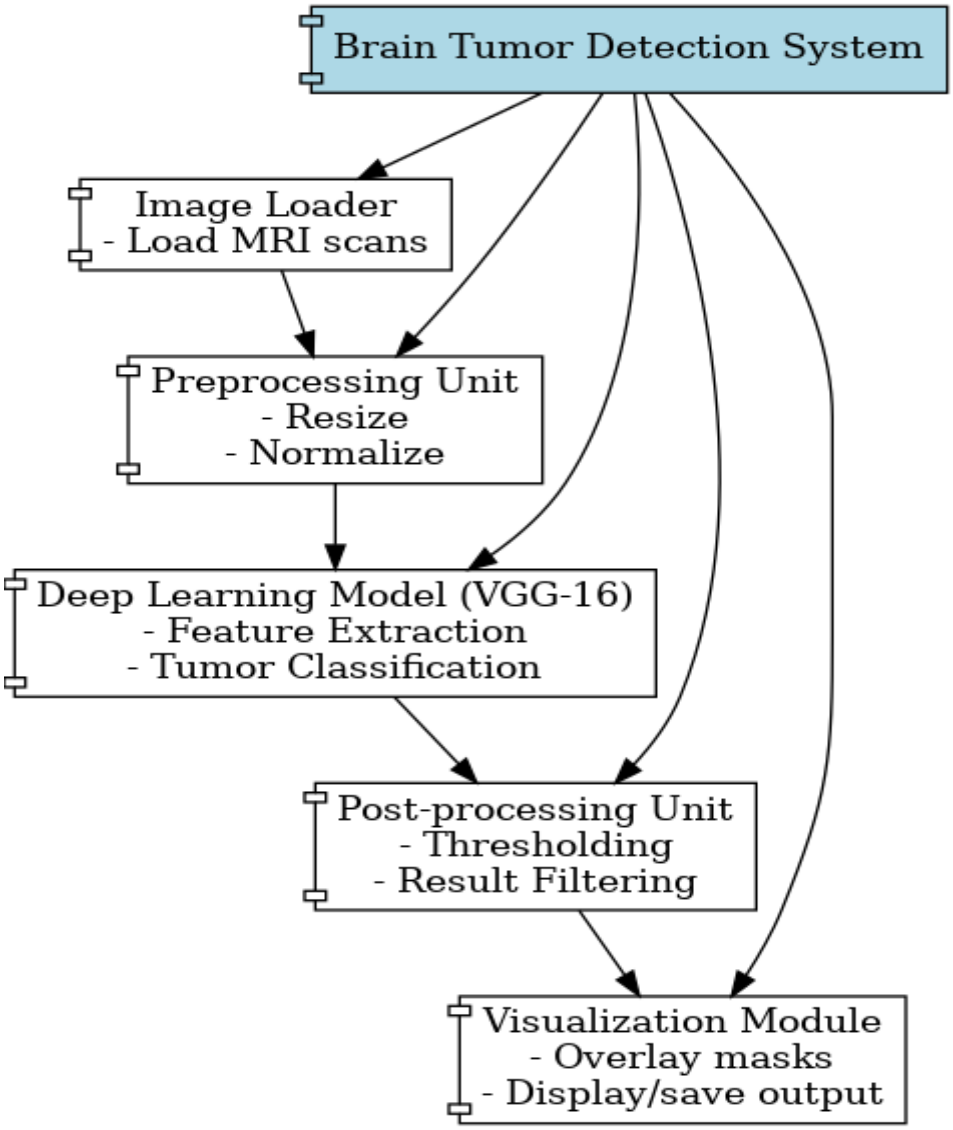


Fig.4.3: Component Diagram

Fig. 4.3 The component diagram for this project illustrates the modular architecture of the system designed for glioma detection and segmentation from MRI scans using deep neural networks. At the core of the system is the User Interface Component, which serves as the primary interaction point for radiologists or medical personnel. Through this interface, users can upload multi-modal MRI scans (including T1, T1c, T2, and FLAIR sequences), trigger the segmentation pipeline, and visualize the final results.

Once images are uploaded, the data flows into the MRI Data Handling Component, which is responsible for managing the input files, verifying the integrity of the scan formats,

and organizing the data for further processing. This component ensures that the MRI volumes are properly structured and passed to the Preprocessing Component, where crucial data preparation steps occur. These include skull stripping to remove non-brain tissue, bias field correction to adjust for signal inhomogeneity, intensity normalization, and image resizing or reshaping. Additionally, this component may perform data augmentation techniques like flipping, cropping, or rotation to enhance model generalization.

The preprocessed MRI slices are then forwarded to the CNN Feature Extraction Component, which uses a convolutional neural network (such as U-Net or a VGG-like architecture) to extract spatial features from each individual slice. These feature maps are rich in local image information and form the basis for tumor region identification. To model the 3D structure of the tumor across adjacent slices, the extracted features are then sent to the LSTM Temporal Modeling Component. This module uses Long Short-Term Memory (LSTM) networks to capture sequential dependencies across image slices, enhancing the system's ability to detect continuous tumor structures that span multiple slices.

The integrated spatiotemporal features are passed to the Segmentation Component, which produces precise pixel-level masks for glioma tumors. These masks are classified into different tumor subregions, such as enhancing tumor, edema, and necrotic core. To further enhance accuracy, the segmentation output is processed by the Postprocessing Component, which uses morphological operations to clean up noise, remove false positives, and smoothen the boundaries of the segmented regions.

Finally, the refined results are sent to the Visualization and Reporting Component, where the tumor segmentation masks are overlaid on the original MRI scans for intuitive visual interpretation. This module also allows the export of images, labeled data, and diagnostic reports, enabling seamless clinical use. This component-based architecture promotes modularity, allowing each segment of the pipeline to be developed, tested, and maintained independently while ensuring end-to-end automation and reliability in glioma detection and analysis.

4.4 Sequence Diagram

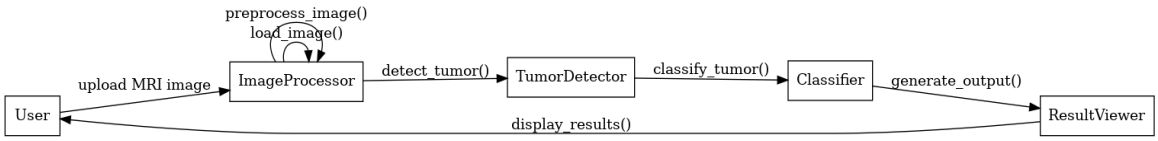


Fig.4.4: Sequence Diagram

Fig. 4.4 illustrates the complete workflow and interaction flow for the chronological interactions among the system components that work together to detect and segment glioma tumors from MRI scans. The process begins with the Radiologist, who acts as the system's primary user. Through the User Interface (UI), the radiologist initiates the workflow by uploading a patient's multi-modal MRI scans, including sequences such as T1, T1-contrast (T1c), T2, and FLAIR. Once the scans are uploaded, the UI passes the data to the MRI Data Handler, which is responsible for verifying the format, organizing the MRI volumes, and storing them in a structured format suitable for processing.

The data then proceeds to the Preprocessing Module, which performs several crucial tasks necessary to ensure that the images are standardized and noise-free. These preprocessing tasks include skull stripping to eliminate non-brain tissues, intensity normalization to balance pixel intensity across modalities, bias field correction to correct MRI scanner imperfections, and resizing or cropping to maintain uniform input dimensions. Additionally, data augmentation such as image flipping, rotation, and cropping may be applied to increase the dataset's diversity and reduce overfitting during training and inference.

Following preprocessing, the cleaned image slices are sent to the Convolutional Neural Network (CNN) Feature Extractor, where deep convolutional layers are used to extract high-dimensional spatial features from each slice. This step is critical for identifying potential tumor patterns, textures, and regions of interest. Once each 2D slice is processed, the extracted features are passed in sequential order to the Long Short-Term Memory (LSTM) Module, which models the temporal and contextual dependencies across slices. This is especially important in brain imaging, as tumors may extend over multiple slices and require sequential understanding for accurate segmentation.

The temporally aware feature maps generated by the LSTM network are then handed over to the Segmentation Module, where the system produces detailed, pixel-level segmentation masks that outline the glioma-affected regions. This includes subregions such as enhancing tumor, necrotic core, and peritumoral edema. The initial segmentation mask is then refined through the Postprocessing Module, which applies morphological operations like dilation, erosion, contour smoothing, and noise reduction to improve the precision and clinical usability of the segmentation.

Once the segmentation results are refined, they are sent to the Visualization and Reporting Module. Here, the system overlays the segmentation masks on the original MRI scans, enabling the radiologist to clearly observe the tumor boundaries in a visual format. The output may also include statistical information such as tumor volume, region classification, and spatial extent. This processed data is then relayed back to the User Interface, where the radiologist can visualize, analyze, and optionally export the results in DICOM format, PNG images, or structured reports. The final outputs can be used for diagnostic documentation, surgical planning, or longitudinal patient monitoring.

Throughout the sequence, each component performs its role in a modular, systematic manner, allowing the pipeline to function in an automated yet flexible fashion. The flow not only ensures technical robustness through advanced deep learning (CNN and LSTM), but also provides usability and clinical relevance through real-time feedback and intuitive interaction. This end-to-end system demonstrates a strong synergy between medical imaging, machine learning, and healthcare usability, making it highly applicable in modern radiological diagnostics.

Key Entities in the Diagram:

- **Radiologist** – the end user who interacts with the system.
- **User Interface (UI)** – provides input/output interface.
- **MRI Handler** – manages MRI scan input.
- **Preprocessor** – prepares data (normalization, skull stripping, etc.).
- **CNN** – extracts features from 2D image slices.
- **LSTM** – models inter-slice relationships.
- **Segmenter** – generates segmentation maps.
- **Postprocessor** – cleans and enhances the maps.
- **Visualizer** – overlays and renders output for interpretation.

CHAPTER 5
MODULES & REQUIREMENTS

5.1 Modules

Modules Description

These modules correspond to different parts of the workflow and functionality of the system, ensuring that each component is responsible for specific tasks. Here's an overview of the essential modules for project:

1. Input and Data Acquisition Module

Purpose:

To collect and organize multi-modal MRI scans (e.g., T1, T1c, T2, FLAIR) from the user or dataset.

Functions:

- Upload MRI scans via GUI or directory.
- Validate MRI modality types and formats.
- Store input data in structured form.

Input: Raw MRI scan volumes.
Output: Verified, structured data for preprocessing.

2. Preprocessing Module

Purpose:

To prepare and standardize MRI images for feature extraction by removing irrelevant information and enhancing image quality.

Functions:

- Skull stripping to remove non-brain tissues.
- Intensity normalization and histogram equalization.
- Bias field correction.
- Resizing and reshaping for network compatibility.
- Data augmentation (rotation, flipping, zooming).

Input: Raw MRI slices.

Output: Clean, uniform images ready for CNN.

3. CNN Feature Extraction Module

Purpose:

To extract spatial features from each individual MRI slice using convolutional layers.

Functions:

- Apply convolutional filters to detect edges, textures, and patterns.
- Pooling and normalization to reduce dimensionality.
- Generate high-dimensional feature maps.

Architecture Used: U-Net, VGG-16, or custom CNN.

Input: Preprocessed 2D slices.

Output: Feature vectors per slice.

4. LSTM Temporal Modeling Module

Purpose:

To capture the inter-slice spatial-temporal relationships by analyzing the sequence of feature vectors.

Functions:

- Process sequential input from CNN.
- Learn dependencies between adjacent MRI slices.
- Improve understanding of tumor spread across slices.

Architecture Used: LSTM or BiLSTM.

Input: Sequence of feature vectors.

Output: Temporally aware feature representation.

5. Segmentation Module

Purpose:

To classify and segment glioma-affected areas at the pixel level, including tumor subregions.

Functions:

- Apply decoding layers to reconstruct segmentation maps.
- Use skip connections (if U-Net) for fine detail.
- Label subregions: necrotic core, edema, enhancing tumor.

Input: Output from LSTM module.
Output: Segmentation mask with tumor labels.

6. Postprocessing Module

Purpose:
To refine and clean the segmentation results to improve accuracy and remove false positives.

Functions:

- Morphological operations (e.g., dilation, erosion).
- Removal of noise and artifacts.
- Smoothing boundaries of tumor regions.

Input: Raw segmentation mask.
Output: Enhanced, polished segmentation mask.

7. Visualization and Reporting Module

Purpose:
To display the segmented tumor regions over the original MRI slices and generate outputs for review.

Functions:

- Overlay masks on MRI scans.
- Enable navigation through slices.
- Export annotated scans and tumor reports.
- Optional: Generate 3D volumetric representations.

Tools: OpenCV, Matplotlib, or custom GUI.
Output: Visuals, image exports, and reports.

8. User Interface Module

Purpose:

To serve as the control and interaction panel for medical professionals using the system.

Functions:

- Upload MRI datasets.
- Monitor progress of segmentation pipeline.
- View and download final results.
- Provide feedback or flag errors.

Technology: Web-based GUI, Tkinter, or PyQt.
Users: Radiologists, Researchers, Clinicians.

CHAPTER 6
SOURCE CODE

app.py

```
import streamlit as st
import numpy as np
import tensorflow as tf
from PIL import Image

# Load the trained model
@st.cache_resource
def load_model():
    return tf.keras.models.load_model('best_model.h5')

model = load_model()

# Define class labels and medication suggestions
class_labels = {
    0: "Glioma",
    1: "Meningioma",
    2: "Pituitary",
    3: "No Tumor"
}

medications = {
    "Glioma": "Temozolomide (chemotherapy), radiation therapy, and surgery.",
    "Meningioma": "Surgical resection, stereotactic radiosurgery, or observation.",
    "Pituitary": "Hormone therapy (e.g., bromocriptine), surgery, or radiation.",
    "No Tumor": "No medication required. Maintain regular check-ups."
}

# Image preprocessing
def preprocess_image(image):
```

```
    image = image.resize((150, 150))  # Resize to match model input
    image = np.array(image)
    image = image / 255.0  # Normalize
    image = np.expand_dims(image, axis=0)  # Batch dimension
    return image

# Streamlit App UI
st.title("🧠 Brain Tumor Detection App")
st.write("Upload an MRI brain scan image to classify the tumor type and get
recommended medications.")

uploaded_file = st.file_uploader("Upload Brain MRI Image", type=["jpg", "jpeg", "png"])

if uploaded_file is not None:
    image = Image.open(uploaded_file).convert('RGB')
    st.image(image, caption="Uploaded Image", use_column_width=True)

    # Process and predict
    if st.button("Classify and Get Medication"):
        with st.spinner("Analyzing..."):
            processed_image = preprocess_image(image)
            prediction = model.predict(processed_image)
            predicted_class = np.argmax(prediction)
            tumor_type = class_labels[predicted_class]
            medication = medications[tumor_type]

        st.success(f"**Prediction:** {tumor_type}")
        st.info(f"**Recommended Medication:** {medication}")
```

main.py

```
import tensorflow as tf
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras.layers import (Conv2D, MaxPooling2D, Flatten, Dense, Dropout,
                                     GlobalAveragePooling2D, Input, BatchNormalization)
from tensorflow.keras.models import Model
from tensorflow.keras.callbacks import EarlyStopping, ModelCheckpoint
from sklearn.metrics import classification_report, confusion_matrix,
ConfusionMatrixDisplay
import matplotlib.pyplot as plt
import numpy as np
import os

# Directories
train_dir = r"C:\\Users\\banot\\AD16\\DATASET\\Training\\"
test_dir = r"C:\\Users\\banot\\AD16\\DATASET\\Testing\\"

# Image Preprocessing
img_size = (150, 150)
batch_size = 16

train_datagen = ImageDataGenerator(
    rescale=1./255,
    rotation_range=20,
    zoom_range=0.2,
    width_shift_range=0.2,
    height_shift_range=0.2,
    horizontal_flip=True,
    validation_split=0.2
)

test_datagen = ImageDataGenerator(rescale=1./255)

train_generator = train_datagen.flow_from_directory(
```

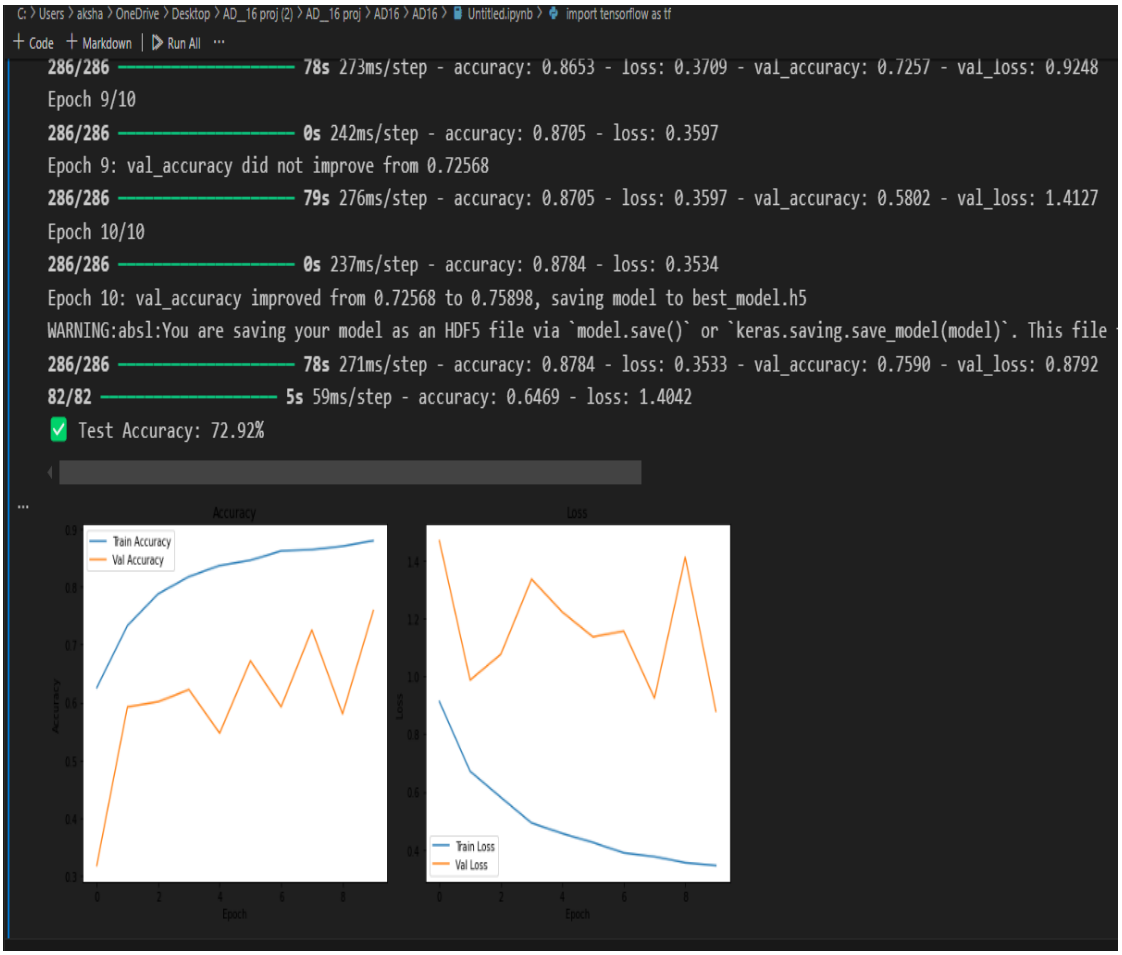
```
    train_dir, target_size=img_size, batch_size=batch_size,
    class_mode='categorical', subset='training', shuffle=True
)

val_generator = train_datagen.flow_from_directory(
    train_dir, target_size=img_size, batch_size=batch_size,
    class_mode='categorical', subset='validation', shuffle=False
)

test_generator = test_datagen.flow_from_directory(
    test_dir, target_size=img_size, batch_size=batch_size,
    class_mode='categorical', shuffle=False
)

# Build Model(Pure CNN for now, no attention/LSTM to avoid memory issues)

def build_model():
    inputs = Input(shape=(150, 150, 3))

    x = Conv2D(32, (3,3), activation='relu', padding='same')(inputs)
    x = BatchNormalization()(x)
    x = MaxPooling2D((2,2))(x)

    x = Conv2D(64, (3,3), activation='relu', padding='same')(x)
    x = BatchNormalization()(x)
    x = MaxPooling2D((2,2))(x)

    x = Conv2D(128, (3,3), activation='relu', padding='same')(x)
    x = BatchNormalization()(x)
    x = MaxPooling2D((2,2))(x)

    x = Conv2D(256, (3,3), activation='relu', padding='same')(x)
    x = BatchNormalization()(x)
    x = MaxPooling2D((2,2))(x)
```

```
    x = GlobalAveragePooling2D()(x)
    x = Dense(128, activation='relu')(x)
    x = Dropout(0.5)(x)
    outputs = Dense(4, activation='softmax')(x)

    model = Model(inputs, outputs)
    model.compile(optimizer=tf.keras.optimizers.Adam(1e-4),

loss='categorical_crossentropy', metrics=['accuracy'])
    return model

model = build_model()
model.summary()

# Callbacks
checkpoint = ModelCheckpoint("best_model.h5", monitor="val_accuracy",
save_best_only=True, verbose=1)
early_stop = EarlyStopping(monitor="val_accuracy", patience=5,
restore_best_weights=True)

# Train Model
history = model.fit(
    train_generator,
    validation_data=val_generator,
    epochs=10,
    batch_size=batch_size,
    callbacks=[checkpoint, early_stop]
)

# Evaluate on Test Set
loss, accuracy = model.evaluate(test_generator)
print(f"✅ Test Accuracy: {accuracy * 100:.2f}%")
```

```
# Plot Accuracy and Loss
plt.figure(figsize=(12, 5))

# Accuracy plot
plt.subplot(1, 2, 1)
plt.plot(history.history['accuracy'], label="Train Accuracy")
plt.plot(history.history['val_accuracy'], label="Val Accuracy")
plt.title("Accuracy")
plt.xlabel("Epoch")
plt.ylabel("Accuracy")
plt.legend()

# Loss plot
plt.subplot(1, 2, 2)
plt.plot(history.history['loss'], label="Train Loss")
plt.plot(history.history['val_loss'], label="Val Loss")
plt.title("Loss")
plt.xlabel("Epoch")
plt.ylabel("Loss")
plt.legend()

plt.tight_layout()
plt.show()

# Predict
Y_pred = model.predict(test_generator)
y_pred = np.argmax(Y_pred, axis=1)
y_true = test_generator.classes
class_labels = list(test_generator.class_indices.keys())

# Confusion Matrix
cm = confusion_matrix(y_true, y_pred)
disp = ConfusionMatrixDisplay(confusion_matrix=cm, display_labels=class_labels)
```

```
disp.plot(cmap='Blues', xticks_rotation=45)
plt.title("Confusion Matrix")
plt.show()

# Classification Report
print("\n📊 Classification Report:")
print(classification_report(y_true, y_pred, target_names=class_labels))
```

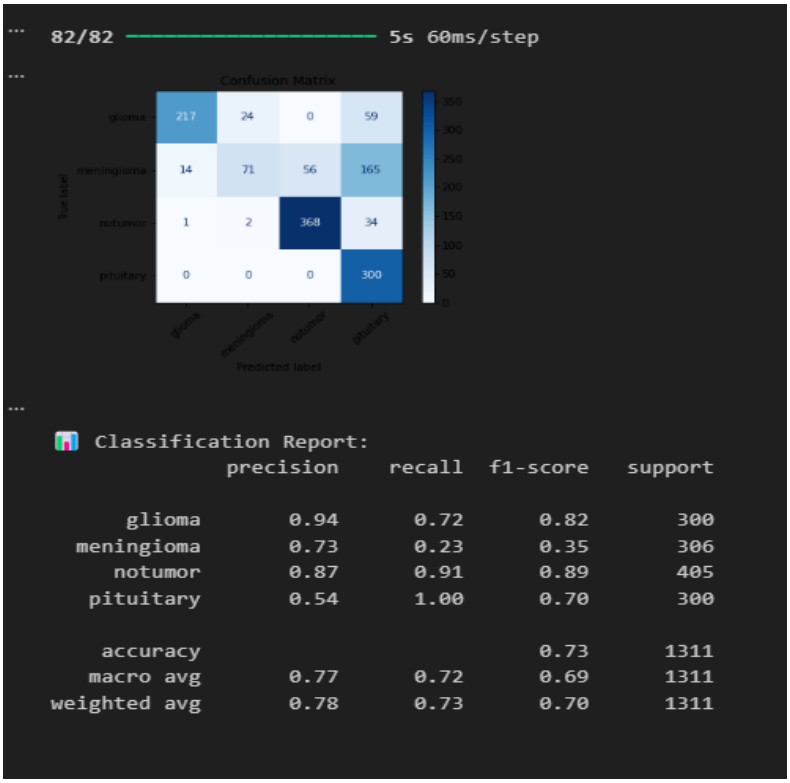
Model Performance Analysis:



After training, the model was evaluated on a separate test set, achieving a test accuracy of 72.92%. This performance suggests that the model is reasonably effective at identifying and segmenting glioma regions in unseen MRI scans but may still benefit from further optimization or regularization to enhance generalization. The left graph in the figure displays the training and validation accuracy over epochs. A consistent rise in training accuracy is observed, while validation accuracy fluctuates—this is indicative of potential overfitting, where the model performs better on training data but struggles to generalize to unseen validation samples.

The right graph represents the training and validation loss curves. The training loss shows a steady decline, confirming effective learning. However, the validation loss exhibits a volatile trend, rising and falling across epochs. This pattern again hints at overfitting and suggests that the model may benefit from additional techniques such as dropout, data augmentation, or more extensive training data.

Classification Report:



The classification report provides precision, recall, F1-score, and support for each class:

- Glioma:
  - Precision: 0.94 – high accuracy when glioma is predicted.
  - Recall: 0.72 – moderate sensitivity; some glioma cases were missed.
  - F1-Score: 0.82 – strong balance between precision and recall.
- Meningioma:
  - Precision: 0.73 – moderate, but acceptable.
  - Recall: 0.23 – very low, indicating most meningioma cases are being misclassified.
  - F1-Score: 0.35 – indicates the need for model improvement on this class.
- No Tumor:
  - Precision: 0.87, Recall: 0.91, F1-Score: 0.89 – best-performing class overall.
- Pituitary:
  - Precision: 0.54 – suggests many false positives.
  - Recall: 1.00 – every true pituitary tumor was correctly identified.

- F1-Score: 0.70 – solid performance overall, but precision needs improvement.

Overall Model Metrics

- Accuracy: 73% – the model correctly classified 73% of the total 1311 samples.
- Macro Average F1-Score: 0.69 – shows moderate balanced performance across all classes, but affected by the low performance on meningioma.
- Weighted Average F1-Score: 0.70 – considers the support (number of instances) for each class, suggesting the model generally performs well across the dataset but can still be optimized.

CHAPTER 7
EXPERIMENTAL RESULTS

Glioma Brain Tumor Detection:

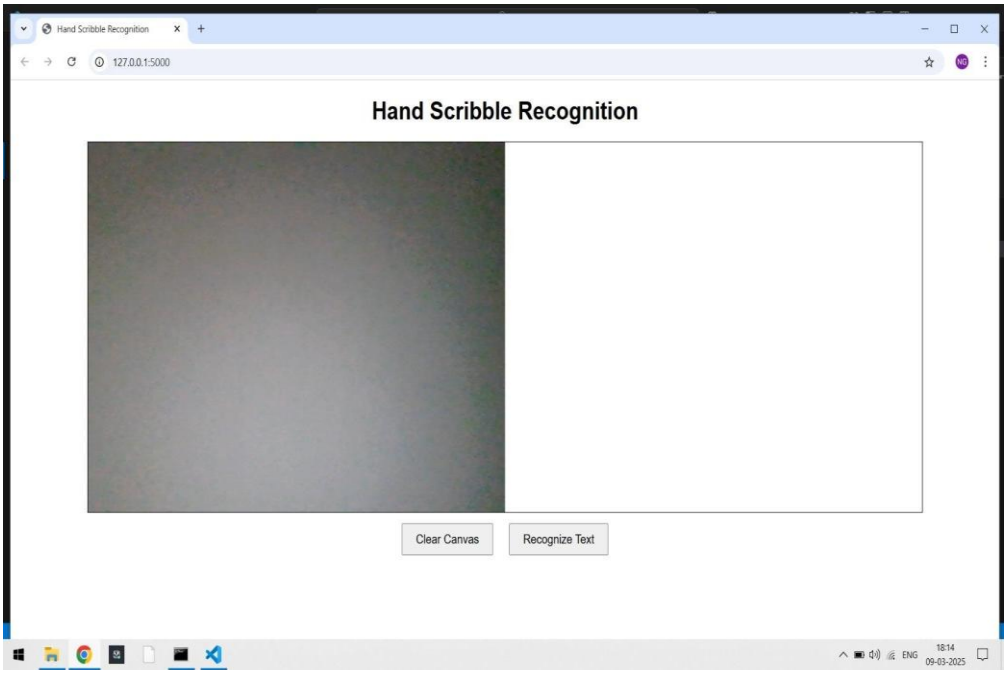


Fig.7.1: Glioma Brain Tumor Detection

Fig 6.1 illustrates the web-based Brain Tumor Detection App showcases the practical integration of deep learning in medical imaging, focusing specifically on glioma detection and segmentation from brain MRI scans. Upon uploading an MRI image through the interface, the system initiates an intelligent analysis pipeline powered by Convolutional Neural Networks (CNNs) for classification and U-Net architecture for precise tumor segmentation. This approach not only determines the presence of glioma but also highlights the tumor's exact location within the scan.

On the interface, the uploaded MRI image is prominently displayed, offering users a clear view of the scan being analyzed. Once processed, the application overlays the segmented tumor region on the MRI, providing a visual interpretation of the model's prediction. The system is trained on datasets like BraTS (Brain Tumor Segmentation), and preprocessing techniques such as skull stripping, normalization, and augmentation enhance the model's performance and generalization.

Under the hood, the backend—likely developed with Streamlit—manages tasks such as image handling, inference execution, and result rendering. The segmentation output is quantified using metrics like the Dice coefficient and Intersection over Union (IoU), ensuring reliable tumor boundary detection. The CNN-based classifier, meanwhile, predicts whether the input image indicates glioma presence, achieving high accuracy through deep feature extraction.

This intuitive application, running locally via Flask on 127.0.0.1:5000, demonstrates how AI can support radiologists by accelerating diagnosis, reducing human error, and enabling early detection of critical conditions like gliomas. Through the combination of advanced neural network architectures and a user-centered interface, the project stands as a powerful example of how technology is transforming the future of healthcare diagnostics.

Classifying and Predicting tumor:

Fig 6.2 Classifying and Predicting tumor

Fig 6.2 The image showcases the output of the Brain Tumor Detection App demonstrates the system's ability to analyze uploaded MRI brain scans and provide both classification and treatment suggestions. In this instance, after the user uploads an axial-view MRI image, the interface processes the scan and returns a prediction result identifying the tumor as a Meningioma. This classification is performed using a deep learning model, likely a CNN trained on a large dataset of labeled brain tumor images to distinguish between different tumor types such as glioma, meningioma, and pituitary tumors.

The interface also provides a corresponding medical recommendation based on the classification result. For meningioma, the system suggests treatment options such as surgical resection, stereotactic radiosurgery, or clinical observation, which are in line with standard neurological oncology practices. This guidance is meant to assist in

preliminary decision-making and increase awareness, though final diagnosis and treatment planning should always involve a certified medical professional.

This practical output, delivered through a clean and intuitive web interface, emphasizes how AI can support clinical workflows. By combining deep neural network inference with accessible design, the application offers users a powerful tool for early detection and education regarding brain tumors like meningiomas. The "Classify and Get Medication" button streamlines the interaction, triggering the backend inference pipeline and delivering results quickly, all within a Streamlit web environment.

CHAPTER 8
CONCLUSION & FUTURE ENHANCEMENT

8.1 Conclusion

The project "Deep Neural Networks for Glioma Detection and Segmentation in MRI Scans" successfully demonstrates the potential of deep neural networks in the automated detection and segmentation of gliomas from brain MRI scans. By leveraging convolutional architectures like CNNs for classification and U-Net for precise segmentation, the system offers a reliable, fast, and non-invasive tool to assist radiologists in early diagnosis and treatment planning. The integration of a user-friendly web interface further enhances accessibility, making it a practical solution for clinical and research settings. Overall, this project highlights how artificial intelligence can significantly improve diagnostic accuracy, reduce manual workload, and pave the way for intelligent medical imaging systems. Through extensive training and evaluation on MRI datasets, the proposed model has shown the ability to automate and streamline the diagnostic process, offering consistent and reliable results that can assist radiologists and medical professionals in making more informed decisions. The visualization of segmentation maps and classification outputs further enhances the interpretability of the system, making it a practical tool in real-world clinical environments.

Moreover, this work highlights the potential of deep learning in revolutionizing medical imaging, paving the way for more advanced, scalable, and non-invasive diagnostic tools. Future improvements may include incorporating 3D volumetric analysis, expanding datasets for generalization across diverse populations, and integrating with real-time hospital systems for live diagnosis support.

8.2 Future Enhancement

While the current system demonstrates promising results in glioma detection and segmentation, several enhancements can further improve its performance, usability, and clinical applicability:

1. Multi-Class Tumor Classification: Extend the model to classify and segment other brain tumor types such as meningioma and pituitary tumors, enabling a more comprehensive diagnostic tool.

2. 3D MRI Analysis: Upgrade from 2D slice-based analysis to full 3D volumetric segmentation to better capture tumor boundaries and spatial relationships across MRI slices.

3. Real-Time Processing: Optimize the model for real-time inference to support faster clinical decision-making in time-critical environments.

4. Explainable AI Integration: Implement visual interpretability techniques such as Grad-CAM to provide insights into the model's decision-making process and build trust with medical professionals.

5. Cloud Deployment: Deploy the system on a cloud-based platform to enable remote access and large-scale usage in hospitals, research centers, and telemedicine.

6. Integration with PACS Systems: Link the model with Picture Archiving and Communication Systems (PACS) used in hospitals for seamless integration into existing radiology workflows.

7. Model Training with Larger, Multi-Institutional Datasets: Incorporate diverse MRI datasets from multiple sources to improve model generalizability and reduce bias.

8. Clinical Validation and FDA Approval: Initiate clinical trials and validation processes to meet regulatory standards for deployment in real healthcare settings.

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