DAYANANDA SAGAR COLLEGE OF ENGINEERING

(An Autonomous Institute affiliated to Visvesvaraya Technological University (VTU), Belagavi, Approved by AICTE and UGC, Accredited by NAAC with 'A' grade & ISO 9001 – 2015 Certified Institution)

Shavige Malleshwara Hills, Kumaraswamy Layout, Bengaluru-560 111, India

DEPARTMENT OF ELCTRONICS & COMMUNICATION ENGINEERING

(Accredited by NBA Tier 1: 2022-2025)

Brain Tumor Segmentation and Classification

Submitted in partial fulfilment for the award of the degree of

Bachelor of Engineering in Electronics & Communication Engineering

Submitted by

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VISVESVARAYA TECHNOLOGICAL UNIVERSITY

JNANASANGAMA, BELAGAVI-590018, KARNATAKA, INDIA 2024-25

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CERTIFICATE

Certified that the project report entitled **"Brain Tumor Segmentation and Classification"** carried out by Sudeer Reddy (1DS21EC208) , Vaibhav (1DS21EC224) , SHRINIVAS (1DS21EC196) , VAISHNAVI (1DS21EC226) is a bonafide student of **DAYANANDA SAGAR COLLEGE OF ENGINEERING**, an autonomous institution affiliated to VTU, Belagavi in partial fulfillment for the award of Degree of **Bachelor of Electronics & Communication Engineering** during the year **2024-2025**. It is certified that all corrections/suggestions indicated for Internal Assessment have been incorporated in the report deposited in the departmental library. The project report has been approved as it satisfies the academic requirements with respect to the work prescribed for the said Degree.

Signature of the Guide	**Signature of the HOD**	**Signature of the Principal**
Dr. Yashaswini Gowda N	**Dr. Shobha .K.R**	**Dr. B G Prasad**
Assistant Professor	**Professor & Head**	**Principal**
Dept. of ECE, DSCE Bengaluru	**Dept. of ECE, DSCE, Bengaluru**	**DSCE, Bengaluru**

Name of the Examiners	**Signature with date**
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DECLARATION

We **Sudeer Reddy (1DS21EC208)** , **Vaibhav (1DS21EC224)** , **SHRINIVAS (1DS21EC196)** , **SHRINIVAS (1DS21EC226**) respectively, hereby declare that the project work entitled " **Brain Tumor Segmentation and Classification**" has been independently done by us under the guidance of **' Dr. Yashaswini Gowda N', Assistant Professor, Dept. of ECE, DSCE** and submitted in partial fulfillment of the requirement for the award of the degree of **Bachelor of Electronics & Communication Engineering** at **Dayananda Sagar College of Engineering**, an autonomous institution affiliated to VTU, Belagavi during the academic year 2024-2025.

We further declare that we have not submitted this report either in part or in full to any other university for the award of any degree.

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ACKNOWLEDGEMENT

The satisfaction and euphoria accompanying the successful completion of any task would be incomplete without the mention of people who made it possible and under constant guidance and encouragement the task was completed. We sincerely thank the **Management of Dayananda Sagar College of Engineering, Bengaluru.**

We express our sincere regards and thanks to **Dr. B G Prasad, Principal, Dayananda Sagar College of Engineering, Bengaluru.** His constant encouragement guidance and valuable support have been an immense help in realizing this project.

We express our sincere regards and thanks to **Dr. Shobha. K.R, Professor & Head, Department of Electronics & Communication Engineering, Dayananda Sagar College of Engineering, Bengaluru.** Her incessant encouragement guidance and valuable technical support have been an immense help in realizing this project. Her guidance gave us the environment to enhance our knowledge, and skills and to reach the pinnacle with sheer determination, dedication, and hard work.

We would like to express profound gratitude to our Project guide **' Dr. Yashaswini Gowda N', Assistant Professor, Dept. of ECE, DSCE Department of Electronics & Communication Engineering, Dayananda Sagar College of Engineering, Bengaluru** who has encouraged us throughout the project. **Her** moral support enabled us to complete our project work successfully.

We express our sincere thanks to Project Coordinators **Dr.S.Thenmozhi**, **,Dr.Suma M.R, Dr.Manasa, Dr.VinayN.A, Mrs.SrividhyaL,** and **Mrs.Bindhu H.M,** of the **Department of Electronics and Communication Engineering** for their continues support and guidance. We thank all teaching and non-teaching staff of the Department of Electronics and Communication Engineering for their kind and constant support throughout the academic Journey.

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ABSTRACT

The process of analyzing of brain Magnetic Resonance Imaging (MRI) plays a critical role in the effective detection and segmenting of brain tumors. This study outlines a comprehensive approach for processing brain tumor images to classify them into benign and malignant classes. The methodology is divided into several key stages: data fetching, pre-processing, segmentation, feature extraction, and classification.

Initially, brain MRI images are obtained from a publicly available dataset, that , ensuring adherence to ethical standards and patient privacy regulations. The images are then preprocessed to improve their quality and facilitate accurate analysis. A crucial step in preprocessing is the application of Adaptive Histogram Equalization (AHE), which enhances image contrast without amplifying noise. AHE works by adjusting the contrast locally, providing better visibility of tumor regions, especially in low-contrast areas.
Following AHE, the image is converted to grayscale, simplifying subsequent analysis while retaining essential structural information.

To address noise artifacts, especially salt-and-pepper noise, Median Filtering is applied to the enhanced grayscale image. The median filter, using a 3x3 or 5x5 kernel, efficiently eliminates unwanted noise while persisting the edges and finer details of the image, which play an important role for accurate tumor segmentation and feature extraction.

For the tumor segmentation step, the Otsu's Thresholding Method is employed to distinguish between the tumor and normal brain tissues. This unsupervised method calculates an optimal threshold that minimizes intra-class variance, allowing for effective segmentation of the tumor region.

After segmentation, a set of textural features is extracted from the tumor region using the Gray-Level Co-occurrence Matrix (GLCM). Key features such as correlation, dissimilarity, energy, and homogeneity are computed, which determines significant information about the texture and structure of the tumor. These texture features are keys for differentiating between benign and malignant tumors, as the texture of malignant tumors typically differs from benign ones.

Finally, tumor classification is achieved using deep learning, machine learning algorithms, where the extracted GLCM features serve as inputs to classify the tumor as either benign or malignant. The classification step uses supervised learning techniques, trained on labeled datasets, to ensure high accuracy in prediction. The approach demonstrates a robust and effective system for diagnosis of tumor regions , which can assist radiologists in clinical decision-making and improve patient outcomes.

In summary, this work presents a systematic and efficient pipeline for processing brain MRI images, combining advanced image preprocessing techniques with machine learning-based classification to automate the detection and classification of brain tumors. The results from this method has proved the potential to enhance diagnostic accuracy and support timely medical interventions.

Keywords

1. **Brain MRI**
2. **OTSU Algorithm**
3. **Median Filtering**
4. **Salt-and-Pepper Noise**
5. **GLCM algorithm**

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LIST OF ABBREVIATIONS

Abbreviation	**Full Description**
AHE	**Adaptive Histogram Equalization**
MRI	**Magnetic Resonance Imaging**
GLCM	**Grey Level Co-occurrence Matrix**
CNN	**Convolution Neural Network**
SVM	**Support Vector model**
GUI	**Graphical User Interface**

1. INTRODUCTION

Brain tumors have proved to be one of the most critical medical conditions impacting the central nervous system, which has affected over lakhs and lakhs of people worldwide each year. Timely and accurate detection of brain tumors plays a very vital role in improving patient outcomes. According to the World Health Organization (WHO), brain tumors are classified into two major categories: benign (non-cancerous) and malignant (cancerous). While benign tumors are typically less aggressive and have a better prognosis, malignant brain tumors are one more dangerous as they rapidly spread, often invade surrounding tissues, and have proved to be life-threatening.

Malignant tumors, particularly gliomas, glioblastomas, and other forms of brain cancer, present significant challenges to clinicians, as they require prompt treatment to mitigate their rapid growth and metastasis. The complexity of brain tumor diagnosis is further compounded by the wide variability in tumor presentation, including differences in size, shape, location, and histological characteristics. Early detection is critical because it allows for timely intervention, potentially improving survival rates and quality of life. It also enables clinicians to personalize treatment plans, offering patients the best possible outcomes based on their specific condition. Monitoring tumor progression through non-invasive imaging is equally crucial for assessing treatment effectiveness and detecting potential tumor recurrence.

However, despite significant advances in medical imaging and treatment technologies, diagnosing brain tumors is still a challenging task. It is depends highly on the expertise and experience of radiologists who interpret images manually. Furthermore, the amount of complexity and varying character of brain tumor presentations make it prone to human error, especially when large volumes of imaging data are involved. This highlights the need for automation in the analysis of brain imaging, which can not only improve accuracy but also save time and reduce clinician workload.

Magnetic Resonance Imaging (MRI) has long been the highest standard for brain tumor detection because of its capability to produce high-resolution, and effectively detailed images of brain structures without the value for mediating procedures. MRI scans allow doctors and radiologists to differentiate between soft tissue abnormalities such as tumors, edema (swelling), and hemorrhage, making it ideal for detecting brain pathology. Furthermore, MRI does not require ionizing radiation, as is the case with CT scans, which makes it a safer option for repeated imagin g during diagnosis and treatment follow-up.Despite the advantages of MRI, manual interpretation of MRI images is labor-intensive and highly subjective. Radiologists need to evaluate large volumes of data to identify and accurately delineate tumor boundaries, assess their characteristics, and classify them as benign or malignant. The variability in tumor morphology, subtle differences in appearance between benign and malignant tumors, and the presence of surrounding healthy tissue all contribute to the difficulty of the task. As a result, human errors in image interpretation cannot be stopped, which leads to false diagnosis or delayed diagnosis, which will result in serious consequences for patients.

Moreover, human interpretation of medical images is time-consuming, especially in high-volume healthcare settings. As the need for medical image processing services increases, radiologists may be under pressure to review and interpret a high number of scans in a short period, further increasing the likelihood of mistakes. This is where artificial intelligence (AI) and machine learning techniques have the power to make a change brain tumor diagnosis problem. These technologies can automate image processing components such as segmentation (the process of isolating the tumor from surrounding tissue) and classification (distinguishing between benign and malignant tumors), improving both the speed and accuracy of diagnosis.

The integration of image processing techniques with machine learning and AI has opened up new avenues for automating brain tumor detection and classification. Medical image processing indicates the usage of computational techniques to enhance, analyze, and interpret medical images which provides the needful information for diagnosis, treatment planning, and patient monitoring. In the chapter of brain tumors, image processing is typically carried out in several stages

The industry of medical image processing has seen rapid advancements, specially with the introduction of machine learning and artificial intelligence (AI) techniques. These technologies have the capability to work on complex image analysis tasks such as segmentation (isolating the tumor from surrounding tissue) and classification (distinguishing between benign and malignant tumors). By leveraging these technologies, automated systems can significantly improve diagnostic efficiency, reduce clinician workload, and, most importantly, enhance the accuracy of diagnoses. However, manual analysis of MRI images is time-consuming, highly dependent on the expertise of radiologists, and can be affected by to human error. This underscores the need for systems which can suggest radiologists in detecting, segmenting, and classifying brain tumors with high accuracy. Magnetic Resonance Imaging (MRI) has become the standard imaging technique for detecting brain tumors because to its non-invasive nature and capability to provide high-resolution images. Unlike CT scans, which takes help of ionizing radiation, MRI employs stong magnets and radio spectrum , making it a safer and more effective tool for visualizing soft tissues. MRI excels in differentiating tumor tissue from surrounding healthy brain tissue, as it provides high contrast and detailed anatomical information. This makes it especially suitable for identifying subtle abnormalities and for differentiating tumors from various conditions like edema or hemorrhages.

Despite its advantages, the reliance on manual MRI interpretation introduces challenges. Radiologists must meticulously analyze multiple slices of imaging data to identify and characterize brain tumors. This process is time-intensive, requires a standard level of expertise, and is prone to human error. Factors such as radiologist fatigue, the variability of tumor morphology, and the increasing volume of imaging data in clinical operations contribute to the risk which can lead to misdiagnosis or delayed diagnosis

The manual detection of MRI images is both labor-intensive and subjective. Radiologists must assess complex imaging data to delineate tumor boundaries, determine tumor characteristics, and classify the tumor as benign or malignant. Variability in interpretation, subtle differences in tumor morphology, and the presence of overlapping features with healthy tissue further complicate the process. In high-volume healthcare settings, the pressure to interpret a large number of scans within limited time frames exacerbates the frequency of diagnostic errors.

To overcome these challenges, there is a growing demand for powerful systems which are able to assist radiologists in detecting, segmenting, and classifying brain tumors more efficiently and accurately. Automation in medical imaging not only can be time effective but also ensures consistency and reduces the dependency on radiologist expertise. Advanced computational techniques in image processing, coupled with machine learning and artificial intelligence (AI), are transforming the landscape of brain tumor diagnosis. Medical image processing involves enhancing, analyzing, and interpreting imaging data to extract valuable diagnostic information. For brain tumor diagnosis, the process involves multi stages, which includes preprocessing (e.g., noise reduction), segmentation (isolating the tumor), and classification (identifying tumor type). The combination of machine learning and AI techniques has significantly advanced these tasks, enabling automated systems to achieve remarkable levels of accuracy.

Segmentation involves isolating the tumor from surrounding tissues in the MRI scan. It is a crucial step in identifying tumor boundaries and assessing its size and location. Traditional segmentation methods rely on manual or semi-automated approaches, which are time-consuming and prone to variability. AI-driven segmentation techniques, typically for those using deep learning models like convolutional neural n etworks (CNNs), have demonstrated good accuracy in delineating tumor regions. These models will adapt to complex patterns in imaging data, which help them to segment tumors even in challenging cases with irregular shapes or poor contrast.

Classification distinguishes between benign and malignant tumors based on their features. Machine learning models are trained on labeled datasets containing MRI images and their corresponding diagnoses. These models learn to identify distinguishing features, such as texture, intensity, and shape, to classify tumors with high precision. Advanced AI systems often achieve diagnostic performance that rivals or surpasses that of human experts.

1.1 Overview

Brain tumors are one of the critical medical conditions affecting the central nervous system, and their prior detection and accurate diagnosis are vital for improving patient outcomes. The World Health Organization (WHO) has classified brain tumors into two main categories: benign (non-cancerous) and malignant (cancerous). Malignant tumors are particularly dangerous because they tend to grow rapidly and can invade surrounding tissues of brain, which indicates significant challenges for treatment and survival. Timely detection of tumors will significantly enhance the prognosis, enabling early intervention, more personalized treatment plans, and improved monitoring of treatment effectiveness.

Traditionally, the treatment of brain tumors has relied on expertise of radiologists who manually interpret medical imaging data, particularly Magnetic Resonance Imaging (MRI). MRI is widely considered the gold standard for visualization of brain tumors due to its non-invasive nature and its ability to provide high-resolution images of the soft tissues in the brain. Unlike other techniques used in imaging such as CT scans, MRI provides better contrast between tumor and healthy tissue, making it ideal for detecting subtle tumor characteristics. However, manual analysis of MRI images is time-consuming and highly dependent on the skill and experience of the radiologist. Also, human interpretation is subject to variability, fatigue, and error, which can lead to inconsistencies in the diagnosis.In response to these challenges, there has been a significant push to develop automated systems that can assist clinicians in detecting, segmenting, and classifying brain tumors. The combination of machine learning and artificial intelligence (AI) techniques into medical image processing offers a huge potential for improvising diagnostic accuracy and efficiency. These technologies can be trained to automatically analyze MRI images, segment the tumor from surrounding tissues, and classify the tumor as benign or malignant. Such systems can crucially reduce the amount of work of radiologists, provide quick results, and reduce the risk of manual error, totally leading to more timely and accurate diagnoses.Recent advancements in medical image processing, particularly with the advent of deep learning and convolutional neural networks (CNNs), have revolutionized the area of brain tumor detection. AI-based models can now automatically learn complex patterns from MRI images, achieving diagnostic performance that often rivals or even surpasses human expertise. These models can perform algorithms such as segmentation (isolating the tumor from the surrounding tissues) and classification (distinguishing between benign and malignant tumors) with high accuracy. By utilizing AI for these tasks, clinicians can make more informed decisions, tailor treatment strategies more effectively, and improve patient outcomes.

Brain tumors are among the most severe medical conditions affecting the central nervous system, with significant implications for patient health and survival. The World Health Organization (WHO) classifies brain tumors into two primary categories: benign (non-cancerous) and malignant (cancerous). While benign tumors grow slowly and generally do not invade surrounding tissues, malignant tumors are aggressive, rapidly proliferating, and capable of infiltrating adjacent brain regions, making treatment highly challenging. Accurate and timely detection of brain tumors plays an essential role for betterment of patient health outcomes, as early diagnosis will make way for even effective interventions, better treatment planning, and continuous monitoring of therapeutic efficacy.

Despite the capabilities of MRI technology, the manual interpretation of scans remains a significant bottleneck in the diagnostic process. The process demands a high degree of skill and attention, as radiologists must carefully examine multiple slices of an MRI scan to detect abnormalities. Variations in human judgment and experience can introduce errors or biases, potentially affecting the accuracy and details of tumor detection and classification. Moreover, the increasing volume of imaging data in clinical settings further adds to the workload of radiologists, increasing the likelihood of oversight or delays in diagnosis. Recent advancements in AI and deep learning have made a great impact in the field of brain tumor detection.

CNNs, a type of deep learning model, are particularly effective in analyzing image data due to their ability to extract hierarchical features from complex visual patterns. These models can identify subtle differences between benign and malignant tumors, learn the structural features of tumor regions, and accurately delineate the boundaries between tumor tissue and surrounding healthy tissue. AI-based tools have achieved diagnostic accuracy that often matches or surpasses human radiologists, enabling faster and more reliable detection

The process of using a hybrid methodology of AI and machine learning in brain tumor diagnosis represents a transformative step in modern healthcare. By augmenting traditional MRI analysis, AI systems enable radiologists and clinicians to deliver faster, more precise, and consistent diagnoses, ultimately improving patient outcomes. While risks such as data quality, algorithm transparency, and clinical validation remain, the potential benefits of these technologies make them invaluable tools in the fight against brain tumors. As research continues to advance, AI-driven diagnostic systems will likely become an internal part of standard medical practice, offering new hope to patients and clinicians alike.

1.2 Problem Statement

"Data clustering is a prime task in machine learning and data analysis, with applications in various domains such as anomaly detection, customer segmentation, and image processing. However, traditional clustering methods often assume static data distributions and struggle to adapt to the dynamic nature of real-world data streams. Additionally, the quality and interpretability of clustering results can be greatly impacted by the presence of outliers

Accurate segmentation of brain tumors is crucial for effective diagnosis, treatment planning, and monitoring of tumor progression. Many algorithms struggle to enhance MRI images without losing critical information, and tumor classification models may exhibit poor generalization when dealing with diverse patient data. This leads to incorrect or delayed diagnoses, directly impacting patient outcomes.Current approaches to brain tumor detection often fail to achieve optimal accuracy due lack of effective feature extraction techniques.

The task of brain tumor segmentation and classification presents several challenges. Segmentation involves isolating the tumor (ROI) from the surrounding background healthy brain tissue in an MRI scan, which can be difficult due to the complex nature of brain tumors. Tumors can vary largely in aspects of size, shape, and location, and their boundaries are often not accurately defined. Tumor borders may overlap with or blend into adjacent brain tissues, making segmentation particularly challenging. Manual segmentation is a time-consuming process and prone to variability, as different radiologists may interpret the same image differently.

Once segmentation is performed, the next challenge is classification**,** which involves determining whether the tumor is benign or malignant based on the extracted texture quality features from the segmented region. This task requires the identification of subtle characteristics in the tumor’s texture, shape, and intensity, which can be difficult for traditional methods. Malignant tumors often have irregular shapes, more heterogeneous textures, and higher levels of vascularization compared to benign tumors, which makes them harder to distinguish

This research addresses the following challenges.

1.3 Objective

The key objectives in brain tumor image processing can be summarized as:

- Segmentation: Accurately separating the tumor from the surrounding brain tissue. This is essential for isolating the region of interest and enables subsequent steps such as feature extraction and classification. Segmentation is a very important step in the processing of medical images, particularly for identifying and isolating brain tumors from surrounding brain tissues in MRI scans. This process involves accurately delineating the boundaries of the tumor, enabling the precise extraction of the region of interest. Segmentation is crucial because it ensures that subsequent steps, such as feature extraction, classification, and treatment planning, focus only on the relevant areas while excluding unrelated brain structures. Effective segmentation methods are designed to handle the complex and heterogeneous nature of brain tumors, which can vary widely in size, shape, intensity, and texture. Advanced segmentation techniques often employ image processing algorithms such as thresholding, region growing, edge detection, or clustering. More recently, machine learning and deep learning approaches, such as convolutional neural networks (CNNs) and U-Net architectures, have revolutionized segmentation accuracy. These methods leverage vast amounts of labeled data to learn and generalize patterns, making them particularly effective for distinguishing tumor tissue from healthy tissue even in challenging scenarios. Accurate segmentation enables precise measurements of tumor size and growth, helps assess the tumor's spatial relationship with surrounding structures, and aids in treatment planning by providing critical information for surgical navigation, radiation therapy, or drug delivery. This step ultimately enhances the reliability of the entire diagnostic and therapeutic pipeline for brain tumor management.
- Feature Extraction: After segmenting the tumor, relevant features are extracted to help differentiate between benign and malignant tumors. These features can include texture (e.g., using Gray-Level Co-occurrence Matrix (GLCM)), intensity distribution, and morphological characteristics such as tumor shape, size, and location Feature extraction is a critical step following tumor segmentation, aimed at identifying and quantifying specific characteristics of the tumor to facilitate differentiation between benign and malignant types. This process involves analyzing various properties of the segmented region, such as texture, intensity distribution, and morphological features. Texture analysis, often performed using methods like the Gray-Level Co-occurrence Matrix (GLCM), examines the spatial relationships between pixel intensities to capture patterns like smoothness, contrast, and uniformity. These texture features can indicate variations within the tumor structure,

which may correlate with tumor type.

Additionally, intensity distribution analysis evaluates the grayscale values within the tumor region, providing insights into the homogeneity or variability of the tissue, which is critical for identifying malignancy. Morphological features, including the tumor's shape, size, and location, are also extracted. Malignant tumors often exhibit irregular shapes, rapid growth patterns, and invasive behavior, distinguishing them from the typically smoother and well-defined boundaries of benign tumors. These extracted features are essential inputs for machine learning algorithms or statistical models, which use them to classify tumors and predict their behavior, aiding in more accurate diagnoses and treatment planning.

Classification: Machine learning models are used to classify the tumor as benign or malignant based on the extracted features. Effective classification is vital for determining the appropriate treatment course, such as surgery, chemotherapy, or radiation After feature extraction, machine learning algorithms are used to classify the tumor as benign or malignant based on the extracted features. This classification step is crucial for determining the appropriate course of treatment, such as surgery, radiation, or chemotherapy. Classification is the extreme step in the automated analysis pipeline, where machine learning models are employed to categorize brain tumors as benign or malignant based on previously extracted features. This step is critical for guiding treatment decisions, as the nature of the tumor significantly influences the clinical approach, such as opting for surgery, chemotherapy, or radiation therapy. Machine learning algorithms such as Support Vector Machines (SVMs), Random Forests, or deep learning models like Convolutional Neural Networks (CNNs) are commonly used for this task. These algorithms are able to adopt to patterns and relationships within the features extracted during earlier stages, including texture, intensity, and morphology, to make accurate predictions.

The classification process typically involves training the model on a labeled dataset, where features from known benign and malignant cases are used to teach the model to differentiate between the two. Once trained, the model can analyze new, unseen cases and assign a classification label. Effective classification requires robust feature selection, high-quality training data, and careful optimization of the algorithm to minimize errors. Accurate tumor classification not only helps in diagnostic reliability but also enables clinicians to develop personalized treatment strategies, improving patient outcomes and survival rates. This automated step reduces the workload on radiologists and helps mitigate human error, making it a vital component of modern brain tumor diagnostic syst

1.4 Motivation

Research in this area allows us to contribute to the development and accurate process of cutting-edge algorithms. Discovering new ways to apply swarm intelligence to solve clustering problems can lead to breakthroughs,

advancing the field and potentially benefiting various industries. The application of swarm intelligence algorithms in data clustering can have tangible effects in numerous fields, such as healthcare, finance, and transportation. Our work could contribute to more efficient systems, better decision-making processes, and improved outcomes in these industries. Tackling challenges in data clustering using swarm intelligence involves complex problem-solving. It requires creative thinking and the ability to develop algorithms that mimic natural behaviors, which can be incredibly rewarding as you overcome obstacles and see your solutions implemented. This field often involves collaboration with experts from diverse fields such as computer science, mathematics, biology, and engineering. Collaborating with individuals from different backgrounds can lead to unique perspectives and innovative ideas. Research in swarm intelligence and data clustering is continuously evolving. This provides an excellent opportunity for continuous learning and growth as you stay updated with the latest advancements, methodologies, and technologies in the field. Contributing to the academic body of knowledge by publishing research papers, presenting findings at conferences, and sharing insights with the scientific community can be fulfilling. Our work could become a part of the foundation upon which future advancements are built. The challenge of solving intricate problems related to data clustering using swarm intelligence algorithms can be intellectually stimulating. Each problem presents an opportunity to delve deeper into understanding behaviors, optimizing algorithms, and improving results.

These works of art have a clinical inspiration. Existing literature claims that present algorithms are deficient. On the other hand, the use of AI in medical research, particularly deep learning algorithms that offer cutting edge techniques for processing high-resolution images. Hence this research study focuses on overcoming problems in the existing methods by using automatic skin, liver and tumor segmentation algorithms . Furthermore, this work may lead to new research findings that could apply beneficial methods along with different tactics to improve the strategies.

2. LITERATURE SURVEY

1. Nitish Zulpe [1]The research paper focuses on the classification of brain tumors using Gray-Level Co-occurrence Matrix (GLCM) textural features extracted from Magnetic Resonance Imaging (MRI) scans. The dataset consists of 80 MR images categorized into four classes: Astrocytoma, Meningioma, Metastatic bronchogenic carcinoma, and Sarcoma, with each class containing 20 samples sized at 256x256 pixels . The methodology involves preprocessing the images to enhance quality and reduce noise using Gaussian filters, followed by the extraction of approximately 44 GLCM features from each image . For classification, a two-layer feedforward neural network is employed, utilizing the Levenberg-Marquardt (LM) training algorithm, which has shown to be effective in optimizing the classification process . The network architecture consists of 44 input neurons, 10 hidden neurons, and 4 output neurons corresponding to the tumor classes . The results indicate a high classification accuracy of 97.5%, with the confusion matrix revealing that Classes I and II were perfectly classified, while Classes III and IV had one misclassified image each 5. This study represents the potential of automated systems in assisting medical experts with brain tumor classification, thereby improving detection accuracy and treatment planning .

2. Shweta Jain [2]The classification of brain cancer, particularly Astrocytoma, is crucial for improving survival rates, as early detection can significantly enhance treatment outcomes .The proposed methodology of this paper involves several stages, including the collection of an MRI database, preprocessing of images, feature extraction using Gray Level Co-occurrence Matrix (GLCM), and classification through Artificial Neural Networks (ANNs) Image preprocessing techniques which are histogram equalization, binarization, and morphological operations are employed to enhance the quality of MRI images before feature extraction . The study extracts seven textural features from the GLCM, calculated at four angles (0º, 45º, 90º, and 135º). These features include Angular Second Moment, Contrast, Inverse Difference Moment, Dissimilarity, Entropy, Maximum Probability, and Inverse.

3. Vrushsen Pawar [3] This paper focuses on enhancing brain tumour classification through a hybrid machine learning approach, addressing challenges such as limited datasets and high computational complexity . It integrates advanced feature extraction techniques, including Otsu's thresholding, Gray-Level Co-occurrence Matrix (GLCM), to improve classification accuracy and reduce dimensionality. The proposed methodology achieves an impressive accuracy of 96.9%, with high specificity (95.14%) and sensitivity (97.14%), demonstrating its effectiveness for real-world applications in medical imaging .

4. K.Satya Prasad [4]The paper presents significant findings regarding the performance of the proposed hybrid

algorithm for medical image segmentation, which optimizes the traditional Otsu method. Despite the improvements in speed, the quality of the final segmented images remains high. The proposed method was tested on nearly 20 medical MRI and CT-Scan images, allowing for a comprehensive comparison with the conventional Otsu method and the Two Stage Multi Threshold OTSU Method (TSMO).In this paper the computational result of medical images of computational time is 0.0089 and Severability is 0.9106. hybrid algorithm indicate a promising advancement in medical image segmentation, effectively balancing efficiency and quality, which is essential for practical applications in the medicine field.

5. Heru Pramono Hadi[5] Brain tumor segmentation is a critical area in medical imaging that aids in the accurate identification and treatment of tumors using MRI and CT scans. The study utilizes the multiclass brain tumor image segmentation benchmark (BRATS) 2015 dataset, which consists of 86 MRI images collected from different patients. These images are specifically of the fluid attenuated inversion recovery (FLAIR) modality, providing a comprehensive basis for evaluating. a multi-level Otsu thresholding technique is applied to determine the initial initialization area for the Active Contour Model (ACM). The results of the proposed method demonstrate a Dice Similarity Coefficient (DS) of 0.7856, indicating a high level of accuracy in tumor segmentation. The method also achieved a Jaccard index of 0.6765 and a Hausdorff distance of 33.394, with a total processing time of approximately 36.461 seconds.

6. Soheila Saeedi1[6] The literature on brain tumor detection using machine learning and deep learning techniques has evolved significantly. Magnetic Resonance Imaging (MRI) is the most commonly used method for diagnosing brain tumors. Recent advancements in machine learning, particularly deep learning, have enhanced the ability to analyze MRI images for tumor detection. The literature indicates that Convolutional Neural Networks (CNNs) are among the most successful techniques for image classification tasks. achieving training accuracies of 96.47% and 95.63%, respectively. These results were better than traditional methods like Multilayer Perceptron (MLP) and K-Nearest Neighbors (KNN) .

7. Jyotismita Chaki1[7] The literature on brain tumor categorization and retrieval has seen great advancements, particularly with the integration of deep learning and reinforcement learning techniques. Additionally, segmentation techniques like the U-Net model have been evaluated on benchmark datasets, achieving segmentation accuracies of 93.40% and 92.20%, demonstrating its effectiveness in isolating brain tumors from MRI images. Furthermore, the inclusion of fuzzy logic within a deep learning framework aims to improve the accuracy of identifying various tumor types, achieving accuracy rates of 97.1% for meningioma, 98.7% for glioma, and 94.3% for pituitary tumors. Despite these advancements.

8. Ashwani Kumar Aggarwal [8] This paper discusses on the classification of brain tumour MRI images using texture features extracted from the Grey-level co-occurrence matrix (GLCM) and a Random Forest classifier, achieving an accuracy of 83.3% on a dataset of 245 images, which includes 154 with tumours and 91 without 2. The GLCM method captures statistical texture features such as energy, dissimilarity, homogeneity, and contrast, which are needed for distinguishing between tumour and non-tumour images 3, 4. The classifier's performance was validated using a confusion matrix, indicating that all images with tumours were correctly classified, while some non-tumour images were misclassified, highlighting the need for further refinement in feature extraction and preprocessing techniques.

9. Carlos Arizmendi [9] This paper introduces a particular approach for brain tumor classification using Magnetic Resonance Spectroscopy (MRS). It employs Gaussian decomposition to extract spectral features of brain tumor tissues. These features are then given as input into neural networks for classification. The study demonstrates the effectiveness of this method in distinguishing between different tumor types. The integration of Gaussian
deomposition provides better feature representation, and neural networks enhance predictive accuracy. The results show good potential for developing diagnostic decisions in clinical environments.

10. Carlos Arizmendi[10] This research explores the use of wavelet transforms to analyze MRS data for brain tumor diagnosis. Wavelets are utilized for feature extraction due to their ability to capture both frequency and time-domain information. These features are classified using neural networks, which handle non-linear relationships effectively. The paper reports improved classification accuracy, emphasizing the wavelet's capability to isolate critical features from noisy data. The methodology offers an efficient way to process complex MRS signals for accurate tumor diagnosis.

11. Arpita Das[11] This paper focuses on predicting brain tumor outcomes using fuzzy logic and genetic algorithms. Fuzzy logic handles the uncertainty and imprecision in medical data, while genetic algorithms optimize the prediction model by identifying significant parameters. The combination enables the system to provide prognosis insights with higher accuracy. The study showcases the potential of AI in understanding and forecasting tumor behavior, aiding treatment planning. It highlights the effectiveness of combining soft computing techniques for medical applications.

12. Ahmed KHARRAT [12**]** This paper proposes a technique for brain tumor detection in medical images, primarily using MRI. The method involves preprocessing, segmentation, and classification. It emphasizes the use of image processing techniques such as thresholding and morphological operations for accurate segmentation of tumor regions. Post-segmentation, the tumor is classified using machine learning methods. The approach enhances detection accuracy, helping radiologists identify tumor boundaries effectively. This method contributes significantly to automated tumor detection workflows.

13. Jason J. Corso [13] This paper introduces an efficient method for segmenting brain tumors using a multilevel Bayesian framework. The segmentation process integrates probabilistic models with image data to achieve precise localization of tumors. The Bayesian approach combines prior knowledge with observed data, leading to improved segmentation accuracy. The model's hierarchical structure facilitates the
separation of tumor regions at multiple scales. The paper highlights its efficiency in handling complex brain images, proving to be an asset for clinical diagnostics.

14. Mohamed Lamine Toure[14] This research develops an advanced segmentation algorithm using fuzzy logic for identifying cancerous and epileptic regions in the brain. The fuzzy logic approach accounts for the inherent uncertainty in medical images, providing accurate delineation of abnormal areas. The paper also explores the algorithm's applicability in epilepsy diagnostics by localizing affected regions. The study demonstrates the algorithm's robustness in processing noisy data and detecting subtle variations in brain tissue, making it suitable for diverse medical imaging tasks

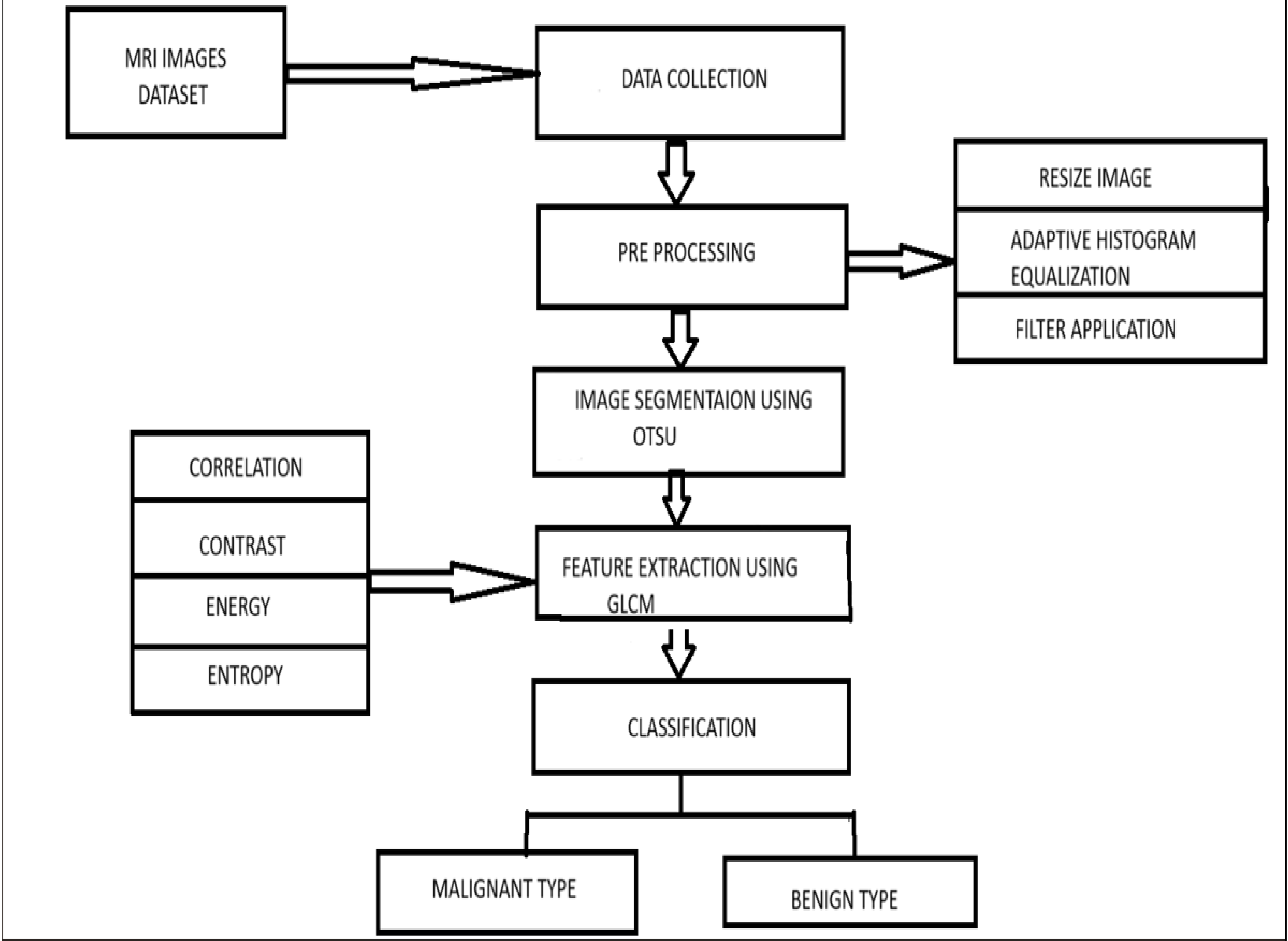
15. G. Lyon et al[15] This paper explores the challenges and innovations in developing immunotherapies for brain tumors. It highlights the unique environment of the brain, including the blood-brain barrier and tumor-induced immunosuppression, as major hurdles. The authors discuss strategies for enhancing drug delivery, improving immune system activation, and designing targeted therapies. Engineering approaches, such as nanotechnology and biomaterials, are emphasized for overcoming these challenges. The paper provides valuable insights into the interdisciplinary efforts required to improve immunotherapy efficacy in brain tumor treatment.

16. J. Liu et al.[16]This survey reviews various MRI-based methods for brain tumor segmentation, focusing on their strengths and limitations. Techniques include manual, semi-automatic, and fully automatic methods, with an emphasis on the latter for efficiency and reproducibility. The paper discusses traditional approaches such as region-growing and thresholding, as well as advanced methods using machine learning and deep learning. The survey underscores the importance of accurate segmentation for diagnosis, treatment planning, and monitoring tumor progression. It also highlights ongoing challenges, including variability in tumor morphology and imaging conditions.

16. R. Tr et al [16] this paper provides insights into using machine learning for medical diagnostics. It describes techniques like decision trees, random forests, and neural networks for predictive analysis. Thepaper emphasizes the role of feature selection and data preprocessing in improving model accuracy. While not directly about brain tumors, its methodologies can be adapted for brain tumor detection. The research the potential of such automated systems in reducing diagnostic workload and improving accuracy.

3.PROBLEM ANALYSIS & DESIGN

3.1 Block diagram and working principle of proposed system

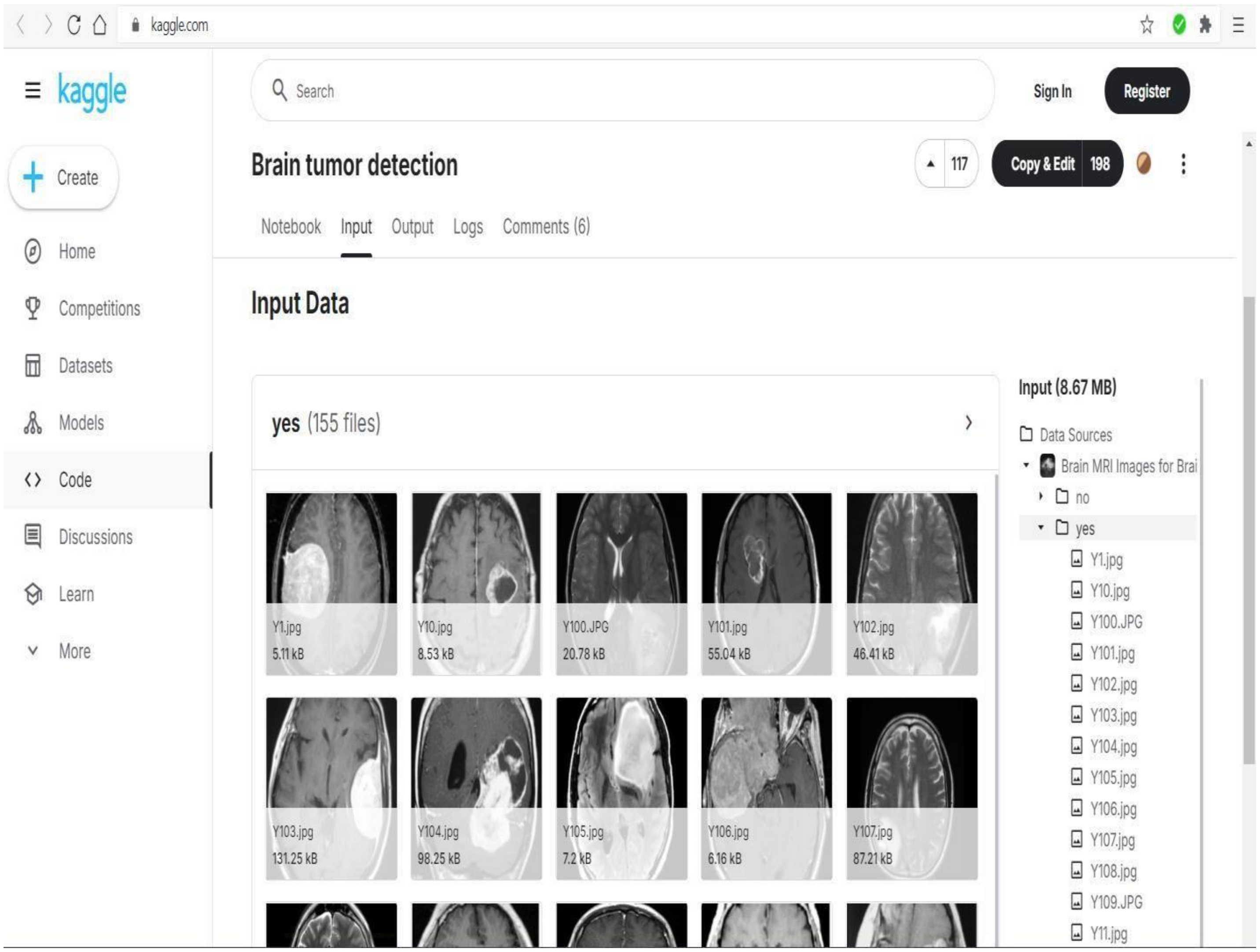


This image illustrates a systematic pipeline for automatic brain tumor detection and classification using MRI images. The process involves several stages:

1. **Data Collection**: The pipeline begins with the acquisition of MRI images from a dataset. This dataset serves as the input for the analysis process and includes MRI scans with various tumor characteristics. The Data Set consists of different MRI scanned images of pixel size varies from 255x255.The Data set was collected from Kaggle.There are total 155 MRI images in dataset.

The Brain Tumor Detection dataset available on Kaggle is a well-organized collection of MRI images aimed at supporting research and development in tumor classification and detection. It consists of labeled images divided into two categories: "tumor" and "no tumor," creating a binary classification problem. This dataset is specifically tailored for machine learning and deep learning tasks, including the use of convolutional neural networks

(CNNs) for effective analysis of brain scans. To enhance performance and consistency, the images have undergone preprocessing, such as standardization and contrast adjustments, to highlight potential tumor regions. This resource plays a crucial role for researchers and developers in advancing diagnostic tools and building automated systems for analyzing medical images.



2. Preprocessing: Preprocessing is essential for enhancing image quality and making it suitable for further analysis. This step involves:

Resizing Images: Standardizing the size of the input images for uniformity.

Contrast Enhancement: Improving the visibility of critical features by adjusting the image contrast.

Filter Application: Removing noise from the images to ensure clarity and highlight relevant details.

Adaptive Histogram Equalization Adaptive Histogram Equalization (AHE) is an image processing technique designed to enhance the contrast of an image while preserving fine details. Unlike standard histogram equalization, which applies a single transformation to the entire image, AHE works locally, dividing the image into small regions (or tiles) and applying histogram equalization to each region independently. This ensures that the contrast enhancement adapts to varying lighting and contrast

conditions in different parts of the image. However, a drawback of standard AHE is that it can over-amplify noise in homogeneous regions, leading to artifacts. To address this, Contrast Limited Adaptive Histogram Equalization (CLAHE) is commonly used, where the contrast amplification is limited by clipping the histogram at a predefined threshold.

In the context of MRI preprocessing, AHE or CLAHE is particularly beneficial for enhancing the visibility of tumor regions, which might otherwise be difficult to distinguish due to low contrast. The preprocessing begins by converting the input MRI image to grayscale, as this simplifies the data by reducing the three RGB color channels into one intensity channel. Grayscale conversion retains all necessary details for further processing while improving computational efficiency.

The adaptive nature of AHE ensures that subtle features, such as the boundaries of a tumor, are more distinguishable, aiding subsequent analysis steps like segmentation and feature extraction. The localized enhancement adjusts for variations in intensity caused by different imaging conditions or scanner artifacts. However, noise amplification is a potential concern, which is why additional noise-reduction steps are incorporated after AHE.

Median Filtering for Noise Reduction

To mitigate noise artifacts such as salt-and-pepper noise—randomly occurring white and black pixels that can obscure important details median filtering is applied. Median filtering is a non-linear smoothing technique that replaces each pixel's value with the median of the intensity values of neighboring pixels within a defined kernel (e.g., 3x3 or 5x5). This method is particularly effective for preserving edges while removing noise, making it ideal for preprocessing medical images like MRIs.

After the application of AHE, the enhanced image might exhibit amplified noise, especially in areas with uniform intensity. Median filtering addresses this issue by suppressing small, high-frequency noise without blurring critical structures like tumor boundaries. Unlike linear filters, such as Gaussian or mean filters, which average the values in the kernel, median filtering better preserves sharp transitions and edges, ensuring that the enhanced image remains clear and accurate for further analysis.

The kernel size used in median filtering determines the level of smoothing. Smaller kernels, like 3x3, are effective for minimal noise removal while preserving finer details, whereas larger kernels, like 5x5, provide more aggressive noise reduction at the cost of some detail loss. In practice, the kernel size is chosen based on the level of noise in the image and the specific requirements of the analysis pipeline.

Converting a binary image to a grayscale image is an image processing task that might seem counterintuitive because binary images only contain two pixel values (0 for black and 255 for white), whereas grayscale images have a range of intensities between 0 and 255.

However, you can still perform this conversion by mapping the binary values to grayscale levels. Here's a basic explanation and Python code using OpenCV to do the conversion:

Steps for Conversion

1. **Binary Image (Black & White)**: A binary image has two possible pixel values: 0 (black) and 255 (white).
2. **Grayscale Image**: A grayscale image depicts varying shades of gray, with pixel values ranging from 0, representing black, to 255, representing white. The values between these extremes correspond to different intensities of gray, transitioning smoothly from dark to light.
    - For black pixels (0): The grayscale value remains 0 (black).
    - For white pixels (255): The grayscale value remains 255 (white).

So, essentially, a binary image can directly map to a grayscale image by assigning black to 0 and white to 255, which is essentially the same visually.

3. **Image Segmentation**: In this step, the MRI image is divided into regions or segments to isolate areas of interest, such as tumor regions. This is a critical stage that ensures the tumor area is accurately separated from the surrounding tissues.

Otsu's method is a widely used image processing technique for automatic thresholding. It determines an optimal threshold value for converting a grayscale image into a binary image (black and white) by minimizing intra-class variance or maximizing inter-class variance. This makes it particularly useful for separating objects of interest (e.g., a tumor in a medical scan) from the background. Otsu's method is an automatic image thresholding technique that works by analyzing the histogram of a grayscale image to separate pixel intensities into two distinct classes: foreground (object) and background. The method computes the intra-class variance, which is the weighted sum of variances within these two groups, for every potential threshold value. By identifying the threshold that minimizes this intra-class variance (or equivalently maximizes the variance between classes), Otsu's method ensures the best separation of the two classes. Once the optimal threshold is selected, the grayscale image is converted to binary format, where pixels above the threshold are assigned to one class (e.g., white) and those below it to another class (e.g., black). Binary conversion simplifies an image by reducing it to two intensity levels, making it ideal for applications such as segmentation or feature extraction in fields like medical imaging and object detection. Otsu's thresholding method is particularly effective for images with bimodal histograms, where pixel intensities form two distinct peaks. However, for more complex images with uneven lighting or multiple intensity peaks, preprocessing techniques like histogram equalization or alternative thresholding methods may be required. Otsu's method begins by analyzing the grayscale image's histogram, computing and normalizing it so that the sum of pixel probabilities equals one, enabling an optimal threshold selection. Iterative thresholding then tests all possible threshold values ttt (ranging from 0 to 255 for 8-bit

images). The image is divided into two classes: C1C_1C1 (background with pixel intensities ≤t\leq t≤t) and C2C_2C2 (foreground with pixel intensities >t> t>t). Class probabilities P1(t)P_1(t)P1(t) and P2(t)P_2(t)P2(t), along with the class means μ1(t)\mu_1(t)μ1(t) and μ2(t)\mu_2(t)μ2(t), are calculated for these two groups. The inter-class variance σb2(t)\sigma_b^2(t)σb2(t) is then computed using these values. The optimal threshold ttt is the one that maximizes σb2(t)\sigma_b^2(t)σb2(t). Finally, this threshold is applied to segment the image, separating the foreground from the background

3. **Feature Extraction** :The Gray-Level Co-Occurrence Matrix (GLCM) is a statistical approach commonly employed in image processing for texture analysis. It captures the spatial relationships between pairs of pixel intensities (gray levels) within an image, providing valuable insights into patterns, repetition, and texture smoothness. The GLCM is constructed by analyzing the spatial relationship between two pixels at a specified distance and orientation (e.g., 0°, 45°, 90°, or 135°). It records how frequently specific pairs of gray levels appear, creating a frequency matrix that encodes texture information. To ensure independence from the image size, the matrix is normalized by converting frequency counts into probabilities.

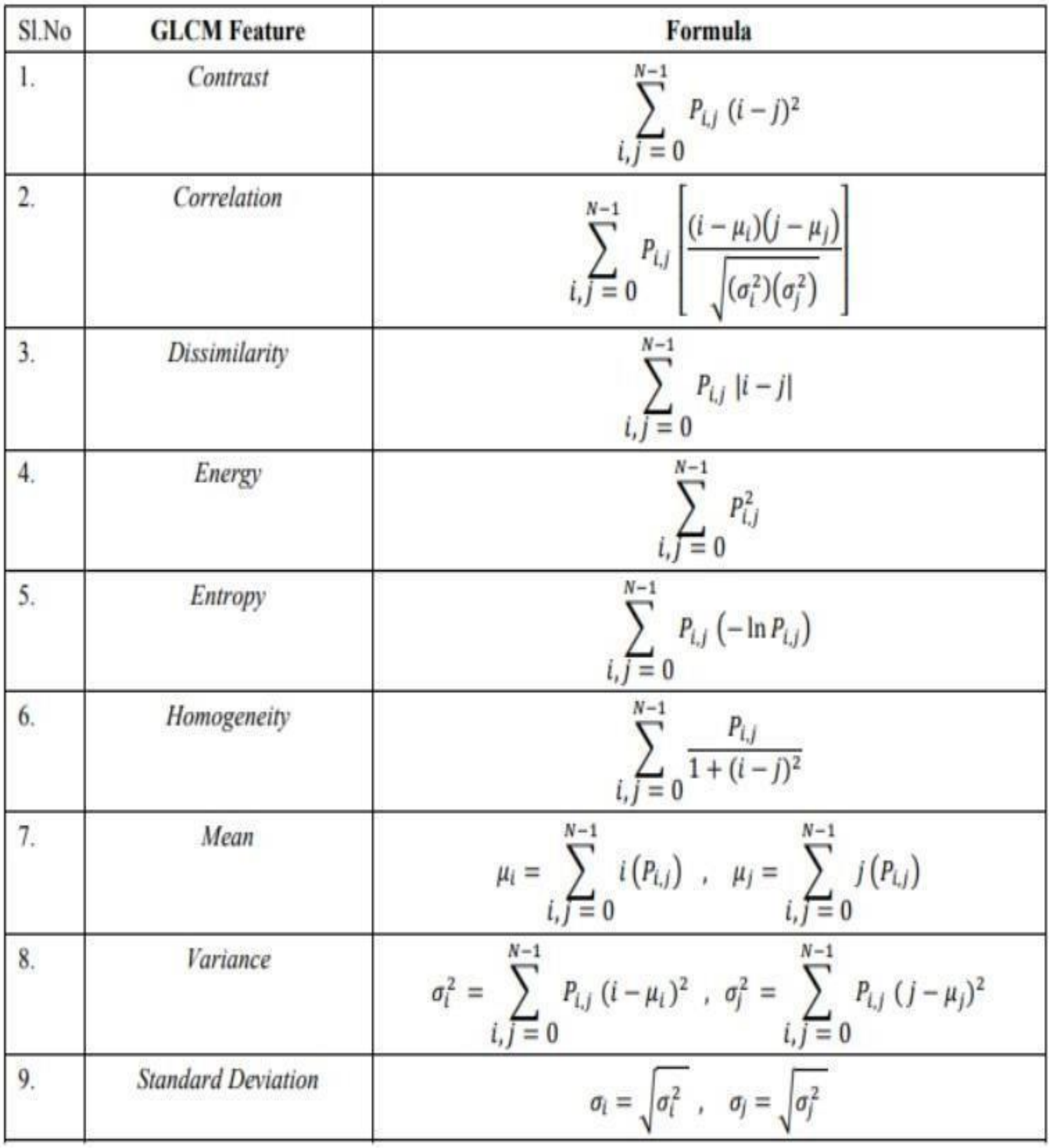
Texture features derived from the GLCM help quantify different aspects of an image's texture. Contrast reflects the intensity variation between a pixel and its neighbors, emphasizing edges and sharpness. Correlation assesses the linear relationship between neighboring pixel intensities, indicating similarity. Energy represents the uniformity of texture, with higher values corresponding to regular patterns. Homogeneity measures the closeness of gray levels, highlighting smoother textures. These features are extensively used in texture-based image analysis across various fields, including medical imaging, remote sensing, and pattern recognition.

The matrix is calculated by analyzing pairs of pixel values at a specified spatial relationship (e.g., distance and angle). The formula for the GLCM P(i,j),P(i, j),P(i , j) at a distance d and angle θ\thetaθ computation has been made in the manner where, element (1, 1) in the GLCM contains the value 1 because there is only one instance in the image where two, horizontally adjacent pixels have the values 1 and 1. Element (1, 2) in the GLCM contains the value 2 because there are two instances in the image where two, horizontally adjacent pixels have the values 1 and 2. Element (1, 2) in the GLCM contains the value 2 because there are two instances in the image where two, horizontally adjacent pixels have the values 1 and

2. The GLCM matrix has been extracted for input dataset imagery. Once after the GLCM is computed, texture features of the image are being extracted successively.

The matrix is then used to compute various texture features, such as contrast, correlation, energy, and homogeneity, which describe the spatial distribution of pixel intensities. These features help quantify image texture for tasks like segmentation or classification

GLCM(Gray Level Co-occurance Matrix)



Sl.No	GLCM Feature	Formula
1.	*Contrast*	$\sum_{i,j=0}^{N-1} P_{i,j}\,(i-j)^2$
2.	*Correlation*	$\sum_{i,j=0}^{N-1} P_{i,j}\left[\frac{(i-\mu_i)(j-\mu_j)}{\sqrt{(\sigma_i^2)(\sigma_j^2)}}\right]$
3.	*Dissimilarity*	$\sum_{i,j=0}^{N-1} P_{i,j}\,\lvert i-j\rvert$
4.	*Energy*	$\sum_{i,j=0}^{N-1} P_{i,j}^2$
5.	*Entropy*	$\sum_{i,j=0}^{N-1} P_{i,j}\,(-\ln P_{i,j})$
6.	*Homogeneity*	$\sum_{i,j=0}^{N-1} \frac{P_{i,j}}{1+(i-j)^2}$
7.	*Mean*	$\mu_i = \sum_{i,j=0}^{N-1} i\,(P_{i,j})\ ,\ \mu_j = \sum_{i,j=0}^{N-1} j\,(P_{i,j})$
8.	*Variance*	$\sigma_i^2 = \sum_{i,j=0}^{N-1} P_{i,j}\,(i-\mu_i)^2\ ,\ \sigma_j^2 = \sum_{i,j=0}^{N-1} P_{i,j}\,(j-\mu_j)^2$
9.	*Standard Deviation*	$\sigma_i = \sqrt{\sigma_i^2}\ ,\ \sigma_j = \sqrt{\sigma_j^2}$

4. **Classification**: The extracted features are passed to a classification algorithm that categorizes the tumor based on its characteristics. This step may involve machine learning or deep learning techniques to predict tumor type, stage, or malignancy. Classification is the final stage in the brain tumor detection system, where the extracted

features from earlier steps are used to categorize the tumor as benign (non-cancerous) or malignant (cancerous). This process leverages machine learning or deep learning models, such as Convolutional Neural Networks (CNNs) and Support Vector Machines (SVMs), to make accurate predictions about tumor type and malignancy. CNNs are particularly powerful in classification tasks involving medical imaging due to their ability to automatically learn spatial and hierarchical patterns from raw images. In this context, a CNN model can directly process the segmented MRI images to identify patterns and distinguish between benign and malignant tumors. It uses convolutional layers to detect local features, pooling layers for dimensionality reduction, and fully connected layers for making predictions.

Alternatively, SVM is a machine learning algorithm that excels in binary classification tasks, such as distinguishing between two tumor classes. Using the extracted features, such as texture and shape derived from GLCM, SVM constructs a hyperplane in a high-dimensional space to separate benign and malignant tumors with maximum margin. SVM is effective for datasets with smaller sample sizes and features extracted manually, making it a robust choice for structured data analysis.

Both approaches offer unique strengths. CNNs are highly accurate for complex datasets but require large amounts of labeled data and computational resources. On the other hand, SVM is efficient and performs well when the feature set is well-defined. Combining CNNs and SVMs in a hybrid model can further enhance classification accuracy by leveraging the automatic feature extraction capability of CNNs and the strong decision boundary of SVM. Effective classification helps clinicians decide on appropriate treatment plans, enabling early intervention and improving patient outcomes.

4. IMPLEMENTATION

4.1 Overview of System Implementation

The system for brain tumor detection and classification is built using a sequence of image processing techniques and machine learning algorithms. Each step is carefully designed to preprocess the input data, extract meaningful features, and classify tumors with high accuracy. Below is an explanation of the major components:

1. Preprocessing

This phase focuses on preparing the MRI images to improve their quality and ensure consistency for subsequent steps:

Median Filtering for Noise Reduction: A median filter is applied to the grayscale MRI images to remove "salt-and-pepper" noise. Unlike linear filters, median filtering preserves edges while eliminating small artifacts, enhancing the clarity of important details in the image.

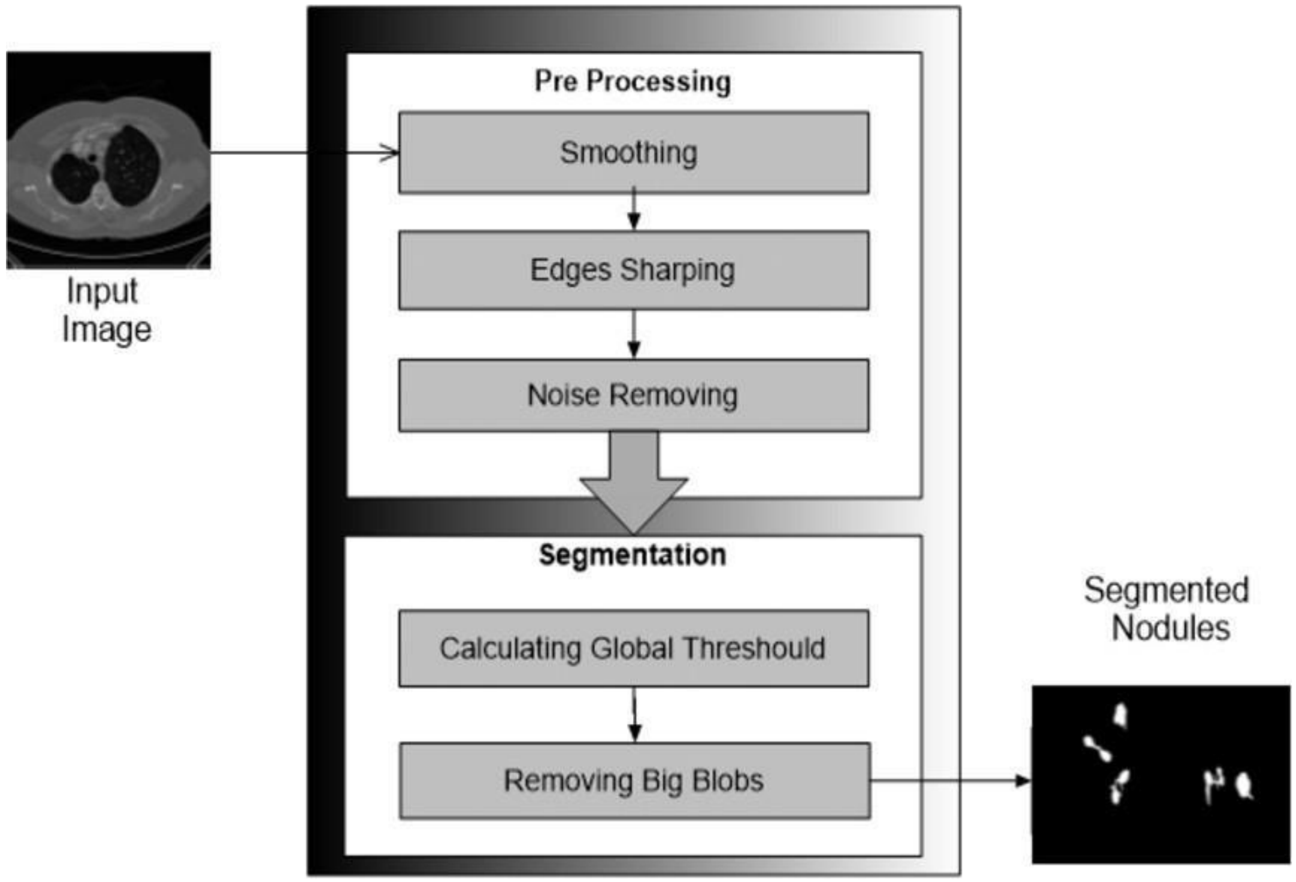
Adaptive Histogram Equalization (AHE): AHE is utilized to improve the contrast of the MRI images by dynamically adjusting the intensity of each pixel. It avoids over-amplification of noise by locally enhancing image features, making the tumor boundaries more distinguishable from surrounding tissue.

Converting a binary image to a grayscale image is straightforward since both types of images are represented by pixel values. In a binary image, pixels are either black (0) or white (255). A grayscale image, on the other hand, has a range of intensities from 0 (black) to 255 (white), with shades of gray in between. For binary images, the black pixels (0) remain black, and the white pixels (255) remain white when converted to grayscale. Thus, a binary image can directly map to a grayscale image without altering the pixel values. The result is visually identical, as both formats only differ in the range of pixel intensities, which is already limited to two values in binary images

2. Segmentation

The segmentation phase isolates the tumor region from the rest of the brain tissue:

Otsu's Thresholding Method: This method is employed to separate the tumor (foreground) from the healthy tissue (background) based on pixel intensity. Otsu's algorithm calculates an optimal threshold by minimizing intra-class variance, ensuring accurate segmentation of the tumor region.

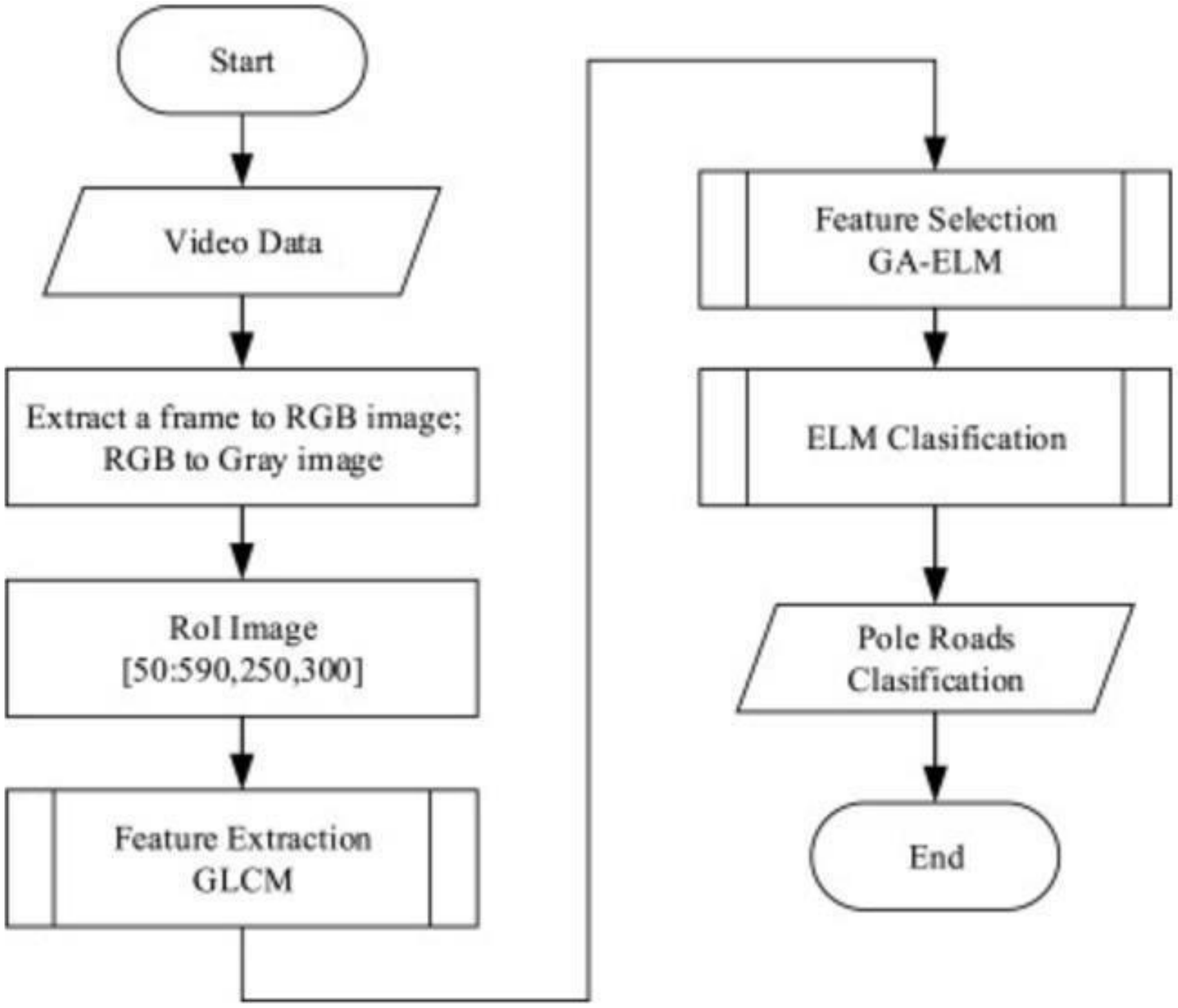


OTSU algorithm

The Otsu method is an effective technique for image segmentation that automatically determines the optimal threshold value to separate an image into foreground and background. It begins with histogram analysis, where the grayscale image's histogram is computed and normalized to ensure the sum of probabilities equals one. Next, the method involves iterative thresholding, testing every possible threshold value tt from 0 to 255 for an 8-bit grayscale image. This process divides the image into two classes: C1$C1$, containing pixels with intensity less than or equal to tt (background), and C2$C2$, containing pixels with intensity greater than tt (foreground). Subsequently, class probabilities P1(t)$P1(t)$ and P2(t)$P2(t)$ are calculated, representing the probabilities of classes C1$C1$ and C2$C2$, respectively. Alongside these probabilities, the method computes class means μ1(t)$\mu1(t)$ and μ2(t)$\mu2(t)$, which reflect the average pixel values in each class. The next step is to calculate the inter-class variance σb2(t)$\sigma b2(t)$, defined as σb2(t)=P1(t)P2(t)(μ1(t)−μ2(t))2$\sigma b2(t)=P1(t)P2(t)(\mu1(t)-\mu2(t))2$. The optimal threshold tt is determined by maximizing this variance, ensuring the greatest contrast between the two groups. Finally, the computed threshold is applied to segment the image, effectively distinguishing the foreground from the background and enhancing image analysis. This method is widely used due to its simplicity and effectiveness in various applications.

3. Feature Extraction

After segmentation, relevant features are extracted to characterize the tumor:
GLCM (Gray-Level Co-occurrence Matrix): GLCM is used to analyze texture by examining spatial relationships between pixel intensities. Features such as contrast, correlation, energy, and homogeneity are derived to describe the tumor's textural and structural properties.

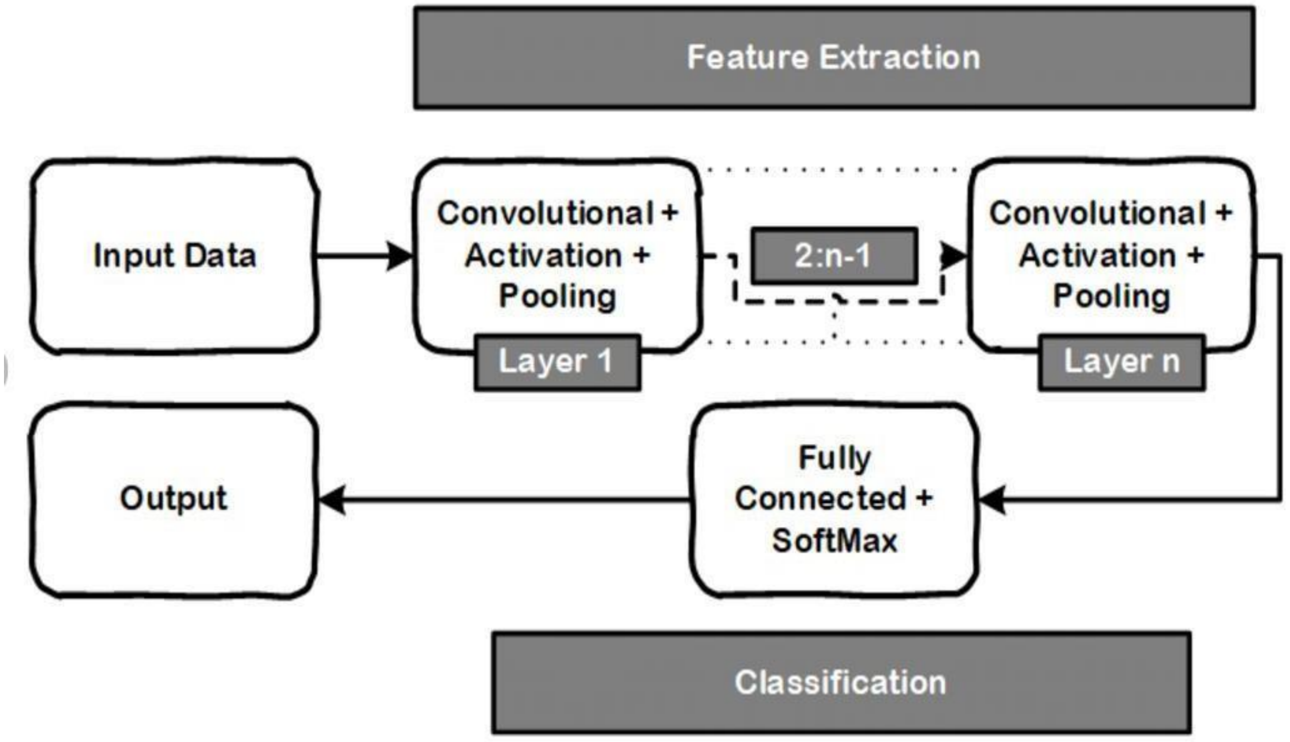


Glcm algorithm

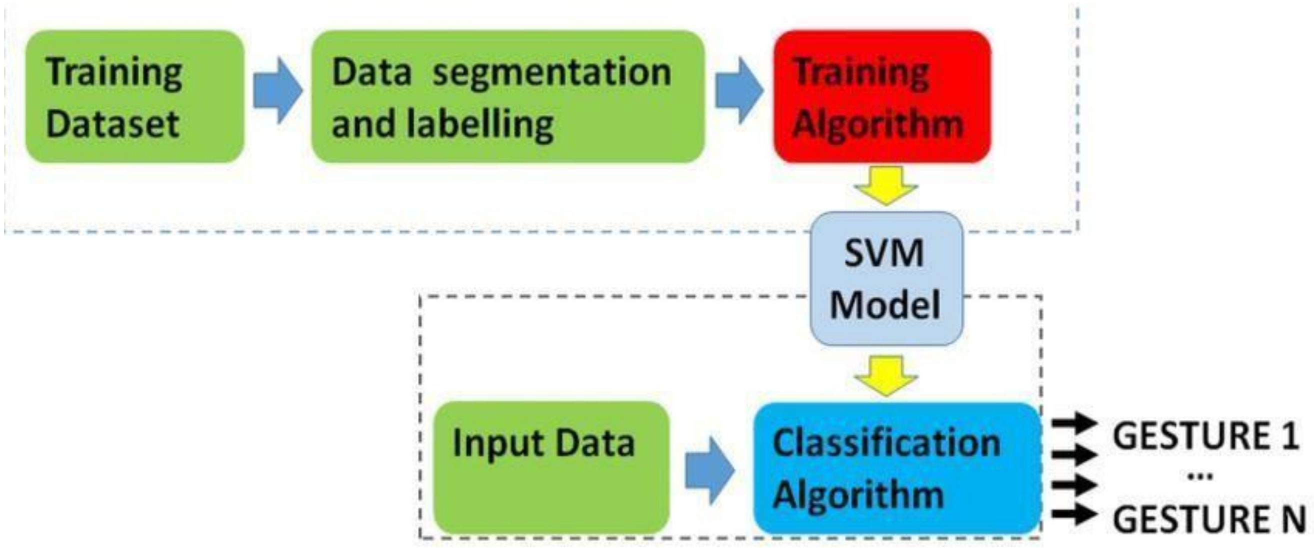
4. Classification

Finally, the extracted features are fed into a machine learning classifier to determine the tumor type:
Classification of Benign and Malignant Tumors: Using algorithms like Support Vector Machines (SVM), k-Nearest Convolutional Neural Networks (CNNs), the system classifies tumors based on their features. Accurate classification is crucial for guiding treatment strategies, such as surgery, chemotherapy, or radiation therapy.

This systematic implementation ensures precise tumor detection and classification, aiding clinicians in making faster and more reliable decisions.


Feature Extraction
Input Data
Convolutional + Activation + Pooling
Layer 1
2:n-1
Convolutional + Activation + Pooling
Layer n
Output
Fully Connected + SoftMax
Classification

CNN algorithm



SVM algorithm

4.2 Algorithm

Here’s a step-by-step explanation of the segmentation algorithm for processing images

Step 1: Thresholding

Thresholding converts an image into a binary form (black and white) to separate the object of interest (like a brain tumor) from the background. This is done by finding an optimal intensity value that separates the foreground and background pixels based on their brightness levels. For instance, "Otsu's method" is a common approach that automatically determines a threshold value to divide the object from the background, making it easier to isolate the region you want to analyze.

1. **Otsu’s Method:**

$$\text{argmax}_T \left(\sigma_B^2(T)\right)$$

where T is the threshold value, and $\sigma_B^2(T)$ is the inter-class variance given by:

$$\sigma_B^2(T) = \omega_1(T)\omega_2(T)\left(\mu_1(T) - \mu_2(T)\right)^2$$

Here:

- $\omega_1(T)$ and $\omega_2(T)$: probabilities of the background and object classes, respectively.
- $\mu_1(T)$ and $\mu_2(T)$: means of the background and object classes, respectively.

Step 2: Morphological Operations

Morphological operations like dilation and erosion are used to refine the binary image further. These operations help:

- **Remove small noise**: by eliminating tiny spots that aren’t part of the main object.
- **Close gaps**: by filling in small holes within the object’s region.

In practice, these steps help the binary image become smoother and more defined, making the regions more consistent and easier to analyze. For example, in this step, small specks or gaps within the segmented area (tumor region) can be reduced.

1. **Dilation** and **Erosion**:
   - Dilation:

$$A \oplus B = \{z | (B)_z \cap A \neq \emptyset\}$$

   - Erosion:

$$A \ominus B = \{z | (B)_z \subseteq A\}$$

Here, A is the binary image, and B is the structuring element (a disk of radius r). These operations can be combined as **Opening** $(A \circ B) = (A \ominus B) \oplus B$ and **Closing** $(A \bullet B) = (A \oplus B) \ominus B$, which help refine binary image regions by removing small holes or gaps.

Step 3: Active Contour Model (Snake)

The active contour (or "snake") model helps accurately trace the boundaries of objects in an image. It starts with an initial boundary (or contour) around the object and adjusts itself to align with edges in the image, guided by an "energy minimization" approach. This allows the boundary to “stick” closely to the actual edges of the tumor in the image, creating a precise outline of its shape. This method is particularly useful when boundaries are irregular or challenging to detect due to overlapping features.

$C(s) = (x(s), y(s))$ can be represented as:

$$E_{\text{snake}} = \int \left(\alpha |C'(s)|^2 + \beta |C''(s)|^2 + E_{\text{image}}(C(s)) \right) ds$$

where:

- α and β: parameters that control the contour’s elasticity and rigidity.
- $E_{\text{image}}(C(s))$: an image-based energy term that is minimal at the edges.

Step 4: Watershed Transform (Alternative to Active Contour)

As an alternative to active contour, the **watershed transform** is another way to segment objects with overlapping boundaries. This method treats the image as a 3D topographic surface, where high-intensity areas resemble ridges. It then simulates flooding of this surface, with the water filling different "basins" in the image that represent different objects or regions. This technique helps separate objects that are touching or overlapping by drawing dividing lines along these high-intensity ridges.

Gradient-Based Watershed Transform: The watershed algorithm considers the grayscale image $I(x, y)$ as a topographic surface where high-intensity values represent ridges. It finds catchment basins (regions that “flow” toward the local minima).

The algorithm can be represented as follows:

- Compute the gradient $G(x, y) = \sqrt{(I_x^2 + I_y^2)}$.
- Apply the watershed transform on the negative gradient to separate regions based on intensity values.

Step 5: Connected Component Analysis

After segmentation, **connected component analysis** identifies and labels distinct areas or clusters in the binary image. Each connected group of pixels (i.e., each tumor or isolated structure) receives a unique label. By labeling these connected regions, you can count, measure, and analyze different properties (like size, shape, or position) of each distinct region.

Connected Component Labeling:

$$\text{Label}(p) = \min\{\text{Label}(q) \mid q \in \text{neighbors of } p\}$$

where p and q are pixels in the binary image, and pixels connected by a path of 1's share the same label.

CNN

This MATLAB code implements a neural network for pattern recognition tasks, utilizing backpropagation for training. The network learns from fused_feature (input data) and fused_label (target outputs), adjusting its structure by increasing the number of nodes in the hidden layer. This process continues iteratively until the error rate reaches below the set threshold of 0.2%. Each stage of the training process is guided by a mathematical formulation to enhance the network's performance and classification accuracy.

Step-by-Step Algorithm with Mathematical Interpretation

1. **Load Input Data**:
    - **Data** xxx: Represents the input features used to train the neural network.
    - **Labels** ttt: Represents the target classes for each data point in xxx.

Here, x and t are stored in fused_feature and fused_label.

2. **Initialize Parameters**:
    - Set an error threshold, percentErrors=50%\text{percentErrors} = 50\%percentErrors=50%, which will decrease as training improves.
    - Set an initial hidden layer size of 10 nodes.
3. **While Loop to Adjust Hidden Layer Size**:
    - The loop continues until the error rate falls below 0.2%.
    - For each iteration:
        - Hidden Layer Size LLL starts at 10 and increases by 1 with each iteration to allow the network to capture more complex patterns in the data.
4. **Pattern Recognition Neural Network Creation**:
    - **Network Architecture**: Define a neural network with one hidden layer using the MATLAB function patternnet.
    - **Activation Function**: The network uses a standard activation function (e.g., logsig or tansig) for the hidden layer.

Mathematically, for a neural network layer lll with LLL neurons, the output hlh_lhl can be defined as:

hl=f(Wlx+bl)h_l = f(W_l x + b_l)hl=f(Wlx+bl)

where:

- WlW_lWl: Weight matrix for the layer.
- xxx: Input vector.
- blb_lbl: Bias vector.
- fff: Activation function.

5. **Data Division for Training, Validation, and Testing**:
   - **Training Set**: 90% of the data.
   - **Validation Set**: 5% of the data (used to evaluate model performance during training).
   - **Test Set**: 5% of the data (used to evaluate final model performance).

These divisions ensure the model generalizes well without overfitting. The data split can be represented as:

$$x = x_{\text{train}} \cup x_{\text{val}} \cup x_{\text{test}}$$

6. **Training the Network**:

- The network minimizes the **Mean Squared Error (MSE)** between the predicted outputs yyy and the true targets ttt using **backpropagation**:

$$\text{MSE} = \frac{1}{n}\sum_{i=1}^{n}(y_i - t_i)^2$$

- This step adjusts WWW and bbb to minimize the error through gradient descent.

6. **Testing and Error Calculation**:

- Predict network outputs yyy for the entire input set xxx.
- **Error Calculation**: Calculate the difference eee between true labels ttt and predicted labels yyy, with percentErrors as the percentage of mismatches between true and predicted classes:

$$\text{percentErrors} = \frac{\sum(t_{\text{ind}} \neq y_{\text{ind}})}{\text{total samples}} \times 100$$

- If percentErrors is greater than 0.2%, the loop repeats with an incremented hidden layer size.

7 .**Performance Evaluation**:

- Evaluate **accuracy** as 100−percentErrors100 - \text{percentErrors}100−percentErrors and save it for reporting:

$$\text{accuracy} = (1 - \frac{\text{percentErrors}}{100}) \times 100$$

This iterative algorithm provides a framework for neural network optimization, using an adaptive hidden layer size to achieve the target classification accuracy. Each iteration incrementally increases the model's capacity until it sufficiently fits the data for high accuracy, balancing simplicity with performance.

SVM

The provided multisvm function implements a multiclass classification approach using Support Vector Machines (SVM). The algorithm iteratively reduces the dataset to focus on different classes, training an SVM for each class. Here's a step-by-step breakdown of the algorithm:

1. Initialize Variables:

- **Inputs**:
  - TTT = Training Matrix (features for each class)
  - CCC = Group/Target Labels corresponding to the training data
  - **test** = Testing Matrix (data that needs to be classified)
- **Outputs**:
  - itrfin\text{itrfin}itrfin = Resultant classifications for the test data.
- **Iteration Setup**:
  - Determine the number of test samples to classify: itrind=size(test,1)\text{itrind} = \text{size(test,1)}itrind=size(test,1)
  - Initialize an empty array for the final classifications: itrfin=[]\text{itrfin} = []itrfin=[]
  - Copy the training data TTT and target labels CCC into Tb and Cb.

Algorithm for the multisvm Function (Step-by-Step):

The provided multisvm function implements a multiclass classification approach using Support Vector Machines (SVM). The algorithm iteratively reduces the dataset to focus on different classes, training an SVM for each class. Here's a step-by-step breakdown of the algorithm:

1. Initialize Variables:

- **Inputs**:
  - TTT = Training Matrix (features for each class)
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    - itrfin\text{itrfin}itrfin = Resultant classifications for the test data.

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    - Determine the number of test samples to classify: itrind=size(test,1)\text{itrind} = \text{size(test,1)}itrind=size(test,1)
    - Initialize an empty array for the final classifications: itrfin=[]\text{itrfin} = []itrfin=[]
    - Copy the training data TTT and target labels CCC into Tb and Cb.

2. Iterate Over Test Samples:

- For each test sample (one row of the test matrix):
    - Extract the test sample: tst = test(tempind,:)
    - Initialize the training set TTT and labels CCC

3. Identify Unique Classes:

- Determine the unique classes in CCC using unique(C).
- Store the number of distinct classes in NNN.

4. Multiclass SVM Training and Classification:

- If N>2N > 2N>2 (i.e., there is more than one class):
    - Initialize variables:
        - itr=1\text{itr} = 1itr=1 (iteration index).
        - classes=0\text{classes} = 0classes=0 (initial class assignment).
        - **Condition**: cond = max(C) - min(C) (to ensure that we have distinct class values).
    - **Iterative Classifier Training**:
        - While classes is not equal to 1, itr\text{itr}itr is less than or equal to the number of classes, and the condition cond>0\text{cond} > 0cond>0 holds:
            - **Step 1**: Create a binary class label vector c1 for the current class u(itr)u(\text{itr})u(itr), where c1 is 1 for samples of the current class and 0 for others.

  - **Step 2**: Train an SVM classifier on the binary class vector newClass and the training data TTT. This is done using the svmtrain function (note: this function is deprecated in newer versions of MATLAB, so fitcsvm and predict would be used in modern MATLAB).
  - **Step 3**: Predict the class of the test sample tst using svmclassify.
  - **Step 4**: If the predicted class does not match the target (i.e., classes ≠ 1), increment the iteration counter itr\text{itr}itr.

5. Data Reduction After Classification:

- **Reduce the Training Set**: After each classification step, reduce the training set by removing samples that do not belong to the current class:
  - Loop over the newClass vector, and add samples from TTT where the corresponding class label is 0 to a new list c3. This reduces the number of training samples in each iteration.
  - Update T=c3T = c3T=c3, effectively reducing the training data for the next iteration.
- **Reduce the Group Labels**: Similarly, reduce the target labels CCC by retaining only those labels that correspond to the current class:
  - Add the labels from CCC where the corresponding newClass value is 0 to a new list c4.
- **Update the Condition**: Calculate the new condition: cond = max(C) - min(C). If the condition becomes 0, stop the loop, meaning there is no more diversity in the remaining data for classification.

6. Assign Classification to Test Sample:

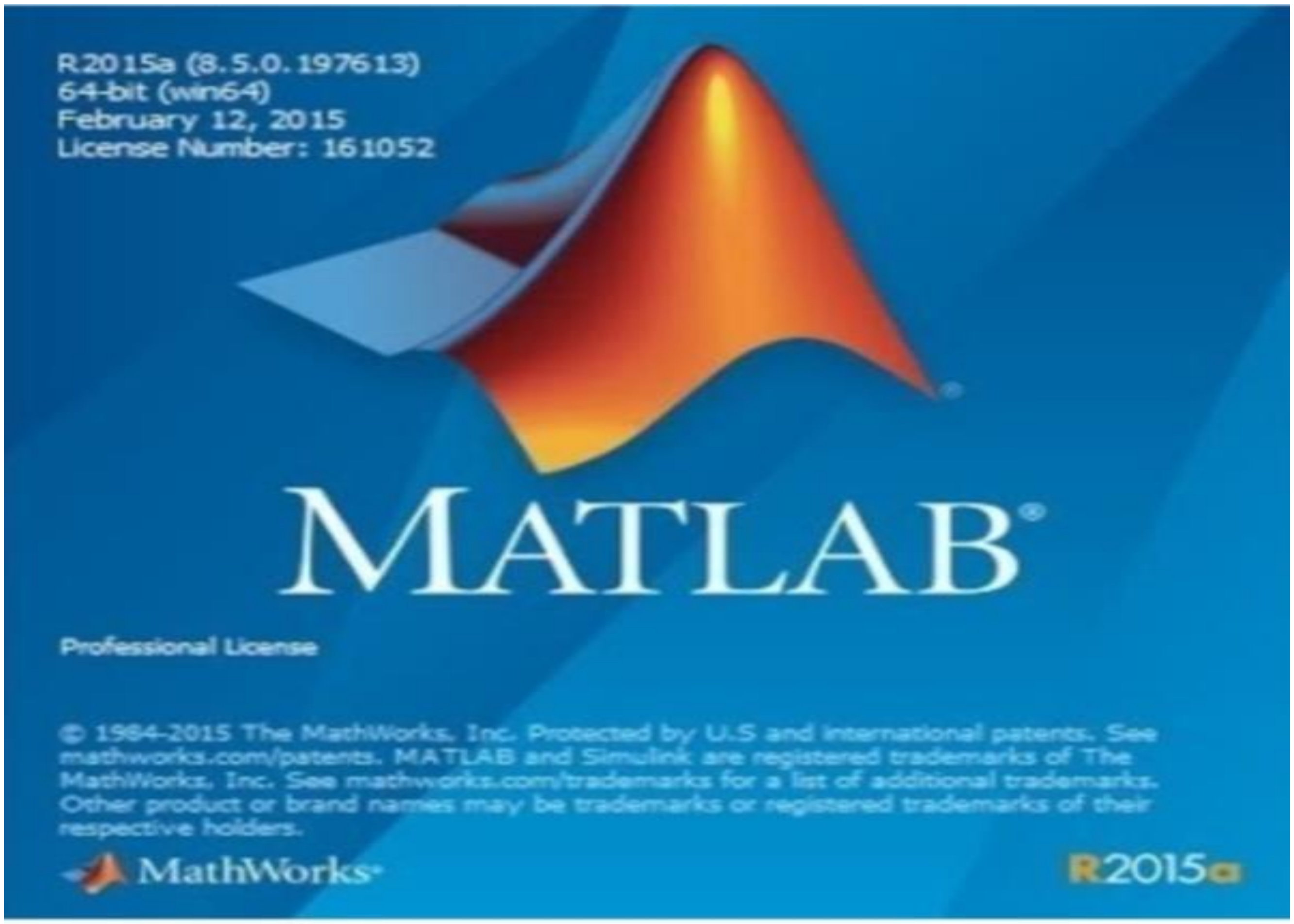
- Once a class is identified (i.e., classes == 1), the test sample is assigned to that class:
  - Identify the target label for the test sample using Cb == u(itr) and store it in val.
  - Since Cb can contain multiple rows, ensure that only unique labels are selected for the final classification (val = unique(val)).
- The classification result is then stored in itrfin for the current test sample.

7. Return Final Classifications:

- After processing all the test samples, the final classifications are returned as itrfin.

4.3 Software Used

Matlab



R2015a (8.5.0.197613)
64-bit (win64)
February 12, 2015
License Number: 161052

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MATLAB (Matrix Laboratory) is a high-level programming language and environment designed for numerical computing, data analysis, and algorithm development. It provides built-in functions for matrix manipulation, linear algebra, signal processing, image processing, and more, making it a powerful tool for engineers, scientists, and researchers. The language uses a syntax similar to mathematical notation, making it intuitive for users to perform complex mathematical calculations and visualize data. MATLAB supports interactive coding, where users can execute commands and view results in real time, which accelerates the development of algorithms and models. It also includes a vast library of toolboxes tailored for specific domains, such as machine learning, control systems, and computer vision. The language allows for efficient handling of large datasets, making it suitable for both small-scale computations and large-scale simulations. MATLAB's integrated environment provides features like debugging, profiling, and GUI development, which aid in building comprehensive applications. Furthermore, it supports various types of data, including arrays, structures, and tables, offering flexibility in handling different kinds of inputs. With its powerful plotting and visualization capabilities, MATLAB is widely used for presenting results, modeling systems, and performing simulations. Its compatibility with other programming languages, such as C, Java, and Python, allows users to extend its functionality or integrate it into larger systems.

4.3.1 Code

Preprocessing and segmentation code

```
function varargout = Main_pre_processing(varargin)
% MAIN_PRE_PROCESSING MATLAB code for Main_pre_processing.fig
%      MAIN_PRE_PROCESSING, by itself, creates a new MAIN_PRE_PROCESSING or raises the existing
%      singleton*.
%
%      H = MAIN_PRE_PROCESSING returns the handle to a new MAIN_PRE_PROCESSING or the handle
to
%      the existing singleton*.
%
%      MAIN_PRE_PROCESSING('CALLBACK',hObject,eventData,handles,...) calls the local
%      function named CALLBACK in MAIN_PRE_PROCESSING.M with the given input arguments.
%
%      MAIN_PRE_PROCESSING('Property','Value',...) creates a new MAIN_PRE_PROCESSING or raises
the
%      existing singleton*.  Starting from the left, property value pairs are
%      applied to the GUI before Main_pre_processing_OpeningFcn gets called.  An
%      unrecognized property name or invalid value makes property application
%      stop.  All inputs are passed to Main_pre_processing_OpeningFcn via varargin.
%
%      *See GUI Options on GUIDE's Tools menu.  Choose "GUI allows only one
%      instance to run (singleton)".
%
% See also: GUIDE, GUIDATA, GUIHANDLES

% Edit the above text to modify the response to help Main_pre_processing

% Begin initialization code - DO NOT EDIT
gui_Singleton = 1;
gui_State = struct('gui_Name',       mfilename, ...
                   'gui_Singleton',  gui_Singleton, ...
                   'gui_OpeningFcn', @Main_pre_processing_OpeningFcn, ...
                   'gui_OutputFcn',  @Main_pre_processing_OutputFcn, ...
                   'gui_LayoutFcn',  [] , ...
                   'gui_Callback',   []);
if nargin && ischar(varargin{1})
    gui_State.gui_Callback = str2func(varargin{1});
end

if nargout
    [varargout{1:nargout}] = gui_mainfcn(gui_State, varargin{:});
else
```

```
    gui_mainfcn(gui_State, varargin{:});
end
% End initialization code - DO NOT EDIT


% --- Executes just before Main_pre_processing is made visible.
function Main_pre_processing_OpeningFcn(hObject, eventdata, handles, varargin)
% This function has no output args, see OutputFcn.
% hObject    handle to figure
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)
% varargin   command line arguments to Main_pre_processing (see VARARGIN)

% Choose default command line output for Main_pre_processing
handles.output = hObject;
global Idd pr ofilename opathname
% Choose default command line output for mainclassification
handles.output = hObject;
axes(handles.axes1);
axis off
axes(handles.axes2);
axis off
% load('.\code\predd.mat')
load .\code\pre.mat
addpath(genpath('stats'));
addpath(genpath('stats'));
set(handles.pushbutton2,'Enable','Off');
set(handles.pushbutton3,'Enable','Off');
set(handles.pushbutton4,'Enable','Off');
% set(handles.pushbutton5,'Enable','Off');

% Update handles structure
guidata(hObject, handles);

% UIWAIT makes Main_pre_processing wait for user response (see UIRESUME)
% uiwait(handles.figure1);


% --- Outputs from this function are returned to the command line.
function varargout = Main_pre_processing_OutputFcn(hObject, eventdata, handles)
% varargout  cell array for returning output args (see VARARGOUT);
% hObject    handle to figure
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)

% Get default command line output from handles structure
```

```
varargout{1} = handles.output;


% --- Executes on button press in pushbutton1.
function  pushbutton1_Callback(hObject,  eventdata,  handles)
% hObject     handle to pushbutton1 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles     structure with handles and user data (see GUIDATA)
global pr
I = imread('Pre_processed.tif');
I = imresize(I,[500,500]);
axes(handles.axes1);
imshow(I),title('Input Pre-Processed image')

roimg=imread('ROI.jpg');
% roimg=imread('seg.jpg');
axes(handles.axes2)
imshow(roimg),title('Final ROI image');
hold on;
load  s1.mat;
% Loop through each region and draw the bounding box
for i = 1:length(s)
    currAr = s(i).Area;
    if currAr > 100 %&& currAr < 7500
        currbb = s(i).BoundingBox;
        if currbb(3) < 250
            rectangle('Position', [currbb(1), currbb(2), currbb(3), currbb(4)], 'EdgeColor', 'r');
        end
    end
end
hold off;
set(handles.pushbutton2,'Enable','On');

guidata(hObject,handles);

% --- Executes on button press in pushbutton4.
function  pushbutton2_Callback(hObject,  eventdata,  handles)
% hObject     handle to pushbutton4 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles   structure with handles and user data (see GUIDATA)
global feat_disease pr
I6=pr;
% I6 = handles.ImgData1;
I = I6;
%% Extract Features
```

```
%
%  lab_he=colorspace('Lab<-RGB',I);
%
% % Classify the colors in a*b* colorspace using K means clustering.
% % Since the image has 3 colors create 3 clusters.
% % Measure the distance using Euclidean Distance Metric.
% ab = double(lab_he(:,:,2:3));        %change the data type to double of the Green and Blue matrix
% nrows = size(ab,1);
% ncols = size(ab,2);
% ab = reshape(ab,nrows*ncols,2);
% nColors = 3;
% [cluster_idx cluster_center] = litekmeans(ab,nColors,'distance','sqEuclidean', ...
%                                   'Replicates',3);
% %[cluster_idx cluster_center] = kmeans(ab,nColors,'distance','sqEuclidean','Replicates',3);
% % Label every pixel in tha image using results from K means
% pixel_labels = reshape(cluster_idx,nrows,ncols);
% %figure,imshow(pixel_labels,[]), title('Image Labeled by Cluster Index');
%
% % Create a blank cell array to store the results of clustering
% segmented_images = cell(1,3);
% % Create RGB label using pixel_labels
% rgb_label = repmat(pixel_labels,[1,1,3]);
%
% for k = 1:nColors
%     colors = I;
%     colors(rgb_label ~= k) = 0;
%     segmented_images{k} = colors;
% end
%
%
%
% % figure,subplot(2,3,2);imshow(I);title('Original Image');
subplot(2,3,4);imshow(segmented_images{1});title('Cluster   1');
subplot(2,3,5);imshow(segmented_images{2});title('Cluster   2');
% % subplot(2,3,6);imshow(segmented_images{3});title('Cluster 3');
% % set(gcf, 'Position', get(0,'Screensize'));
% % set(gcf, 'name','Segmented by K Means', 'numbertitle','off')
% % % Feature Extraction
% % pause(2)
% % x = inputdlg('Enter the cluster no. containing the ROI only:');
% % i = str2double(x);
% i=2;
% % Extract the features from the segmented image
% seg_img = segmented_images{i};
seg_img = I;
img = I;
```

```
foracc=seg_img;
% Convert to grayscale if image is RGB
if ndims(seg_img) == 3
   img = rgb2gray(seg_img);
end
%figure, imshow(img); title('Gray Scale Image');

% Evaluate the disease affected area
%black = im2bw(seg_img,graythresh(seg_img));
%figure, imshow(black);title('Black & White Image');
m = size(seg_img,1);
n = size(seg_img,2);

%zero_image = zeros(m,n);
%G = imoverlay(zero_image,seg_img,[1 0 0]);

cc = bwconncomp(seg_img,6);
diseasedata = regionprops(cc,'basic');
A1 = diseasedata.Area;
% sprintf('Area of the disease affected region is : %g%',A1);

%I_black = im2bw(I,graythresh(I));
kk = bwconncomp(I,6);
Skindata = regionprops(kk,'basic');
A2 =Skindata.Area;
% sprintf(' Total Skin area is : %g%',A2);

%Affected_Area = 1-(A1/A2);
Affected_Area = (A1/A2);
if Affected_Area < 0.1
    Affected_Area = Affected_Area+0.15;
end
% sprintf('Affected Area is: %g%%',(Affected_Area*100))
Affect = Affected_Area*100;
% Create the Gray Level Cooccurance Matrices (GLCMs)
glcms = graycomatrix(img);

% Derive Statistics from GLCM
stats = graycoprops(glcms,'Contrast Correlation Energy Homogeneity');
Contrast = stats.Contrast;
Correlation = stats.Correlation;
Energy = stats.Energy;
Homogeneity = stats.Homogeneity;
Mean = mean2(seg_img);
Standard_Deviation = std2(seg_img);
Entropy = entropy(seg_img);
```

```
RMS = mean2(rms(seg_img));
%Skewness = skewness(img)
Variance = mean2(var(double(seg_img)));
a = sum(double(seg_img(:)));
Smoothness = 1-(1/(1+a));
Kurtosis = kurtosis(double(seg_img(:)));
Skewness = skewness(double(seg_img(:)));
% Inverse Difference Movement
m = size(seg_img,1);
n = size(seg_img,2);
in_diff = 0;
for i = 1:m
    for j = 1:n
        temp = seg_img(i,j)./(1+(i-j).^2);
        in_diff = in_diff+temp;
    end
end
IDM = double(in_diff);

feat_disease = [Contrast,Correlation,Energy,Homogeneity, Mean, Standard_Deviation, Entropy, RMS,
Variance, Smoothness, Kurtosis, Skewness, IDM];
% axes(handles.axes3);
% imshow(I7);title('Grey Scale Image');
%set(handles.edit8,'string',Affect);
set(handles.edit1,'string',Mean);
set(handles.edit2,'string',Standard_Deviation);
set(handles.edit3,'string',Entropy);
set(handles.edit4,'string',RMS);

set(handles.edit5,'string',Variance);
set(handles.edit6,'string',Smoothness);
set(handles.edit7,'string',Kurtosis);
set(handles.edit8,'string',Skewness);

set(handles.edit9,'string',IDM);
set(handles.edit10,'string',Contrast);
set(handles.edit11,'string',Correlation);
set(handles.edit12,'string',Energy);

set(handles.edit13,'string',Homogeneity);

handles.ImgData3 = feat_disease;
handles.ImgData4 = Affect;
% Update GUI
set(handles.pushbutton3,'Enable','On');
guidata(hObject,handles);
```

```
% --- Executes on button press in pushbutton5.
function  pushbutton3_Callback(hObject,  eventdata,  handles)
% hObject     handle to pushbutton5 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles     structure with handles and user data (see GUIDATA)
%% Evaluate Accuracy
CNN_2D_vector_input_classifier
cnn_trainning
set(handles.pushbutton4,'Enable','On');
% guidata(hObject,handles);


% --- Executes on button press in pushbutton8.
function  pushbutton8_Callback(hObject,  eventdata,  handles)
% hObject     handle to pushbutton8 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles     structure with handles and user data (see GUIDATA)


% --- Executes on button press in pushbutton9.
function  pushbutton4_Callback(hObject,  eventdata,  handles)
% hObject     handle to pushbutton9 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles     structure with handles and user data (see GUIDATA)
global Idd pr
pr=imresize(pr,[256 256]);
seg_img=pr;
if size(seg_img,3)  ==  3
   img = rgb2gray(seg_img);
else
    img=seg_img;
end

img = adapthisteq(img,'clipLimit',0.02,'Distribution','rayleigh');

% Create the Gray Level Cooccurance Matrices (GLCMs)
glcms = graycomatrix(img);

% Derive Statistics from GLCM
stats = graycoprops(glcms,'Contrast Correlation Energy Homogeneity');
Contrast = stats.Contrast;
Correlation = stats.Correlation;
Energy = stats.Energy;
Homogeneity = stats.Homogeneity;
```

```
Mean = mean2(seg_img);
Standard_Deviation = std2(seg_img);
Entropy = entropy(seg_img);
RMS = mean2(rms(seg_img));
%Skewness = skewness(img)
Variance = mean2(var(double(seg_img)));
a = sum(double(seg_img(:)));
Smoothness = 1-(1/(1+a));
Kurtosis = kurtosis(double(seg_img(:)));
Skewness = skewness(double(seg_img(:)));
% Inverse Difference Movement
m = size(seg_img,1);
n = size(seg_img,2);
in_diff = 0;
for i = 1:m
    for j = 1:n
        temp = seg_img(i,j)./(1+(i-j).^2);
        in_diff = in_diff+temp;
    end
end
 IDM = double(in_diff);

feat_disease = [Contrast,Correlation,Energy,Homogeneity, Mean, Standard_Deviation, Entropy, RMS,
Variance, Kurtosis, Skewness];

load('datasset_Trainning.mat')

% Put the test features into variable 'test'

result = multisvm(datset,typ,feat_disease);
%disp(result);

% Visualize Results
if result == 1
    R1 = strcat('Benign Tumor');
    set(handles.text35,'string',R1);
    helpdlg(R1);
    disp(R1);
elseif result == 2

    R1 = strcat('Benign Tumor');
    set(handles.text35,'string',R1);
    helpdlg(R1);
    disp(R1);

elseif result == 3
```

```
    R1 = strcat('Malignant Tumor');
    set(handles.text35,'string',R1);
    helpdlg(R1);
    disp(R1);

end

set(handles.pushbutton5,'Enable','On');


% --- Executes on button press in pushbutton4.
function  pushbutton5_Callback(hObject,  eventdata,  handles)
% hObject     handle to pushbutton4 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles     structure with handles and user data (see GUIDATA)
clc
clear all
close all



function  edit1_Callback(hObject,  eventdata,  handles)
% hObject     handle to edit8 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles     structure with handles and user data (see GUIDATA)

% Hints: get(hObject,'String') returns contents of edit8 as text
%        str2double(get(hObject,'String')) returns contents of edit8 as a double


% --- Executes during object creation, after setting all properties.
function edit1_CreateFcn(hObject, eventdata, handles)
% hObject     handle to edit8 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles     empty - handles not created until after all CreateFcns called

% Hint: edit controls usually have a white background on Windows.
%       See ISPC and COMPUTER.
if ispc && isequal(get(hObject,'BackgroundColor'), get(0,'defaultUicontrolBackgroundColor'))
    set(hObject,'BackgroundColor','white');
end



function  edit2_Callback(hObject,  eventdata,  handles)
```

```
% hObject    handle to edit8 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)

% Hints: get(hObject,'String') returns contents of edit8 as text
%        str2double(get(hObject,'String')) returns contents of edit8 as a double


% --- Executes during object creation, after setting all properties.
function edit2_CreateFcn(hObject, eventdata, handles)
% hObject    handle to edit8 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    empty - handles not created until after all CreateFcns called

% Hint: edit controls usually have a white background on Windows.
%       See ISPC and COMPUTER.
if ispc && isequal(get(hObject,'BackgroundColor'), get(0,'defaultUicontrolBackgroundColor'))
    set(hObject,'BackgroundColor','white');
end



function edit3_Callback(hObject, eventdata, handles)
% hObject    handle to edit8 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)

% Hints: get(hObject,'String') returns contents of edit8 as text
%        str2double(get(hObject,'String')) returns contents of edit8 as a double


% --- Executes during object creation, after setting all properties.
function edit3_CreateFcn(hObject, eventdata, handles)
% hObject    handle to edit8 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    empty - handles not created until after all CreateFcns called

% Hint: edit controls usually have a white background on Windows.
%       See ISPC and COMPUTER.
if ispc && isequal(get(hObject,'BackgroundColor'), get(0,'defaultUicontrolBackgroundColor'))
    set(hObject,'BackgroundColor','white');
end



function edit2_Callback(hObject, eventdata, handles)
```

```
% hObject    handle to edit8 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)

% Hints: get(hObject,'String') returns contents of edit8 as text
%        str2double(get(hObject,'String')) returns contents of edit8 as a double


% --- Executes during object creation, after setting all properties.
function edit4_CreateFcn(hObject, eventdata, handles)
% hObject    handle to edit8 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    empty - handles not created until after all CreateFcns called

% Hint: edit controls usually have a white background on Windows.
%       See ISPC and COMPUTER.
if ispc && isequal(get(hObject,'BackgroundColor'), get(0,'defaultUicontrolBackgroundColor'))
    set(hObject,'BackgroundColor','white');
end



function edit5_Callback(hObject, eventdata, handles)
% hObject    handle to edit8 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)

% Hints: get(hObject,'String') returns contents of edit8 as text
%        str2double(get(hObject,'String')) returns contents of edit8 as a double


% --- Executes during object creation, after setting all properties.
function edit5_CreateFcn(hObject, eventdata, handles)
% hObject    handle to edit8 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    empty - handles not created until after all CreateFcns called

% Hint: edit controls usually have a white background on Windows.
%       See ISPC and COMPUTER.
if ispc && isequal(get(hObject,'BackgroundColor'), get(0,'defaultUicontrolBackgroundColor'))
    set(hObject,'BackgroundColor','white');
end



function edit6_Callback(hObject, eventdata, handles)
```

```
% hObject     handle to edit12 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles     structure with handles and user data (see GUIDATA)

% Hints: get(hObject,'String') returns contents of edit12 as text
%        str2double(get(hObject,'String')) returns contents of edit12 as a double


% --- Executes during object creation, after setting all properties.
function edit6_CreateFcn(hObject, eventdata, handles)
% hObject     handle to edit12 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles     empty - handles not created until after all CreateFcns called

% Hint: edit controls usually have a white background on Windows.
%       See ISPC and COMPUTER.
if ispc && isequal(get(hObject,'BackgroundColor'), get(0,'defaultUicontrolBackgroundColor'))
    set(hObject,'BackgroundColor','white');
end



function  edit7_Callback(hObject,  eventdata,  handles)
% hObject     handle to edit13 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles     structure with handles and user data (see GUIDATA)

% Hints: get(hObject,'String') returns contents of edit13 as text
%        str2double(get(hObject,'String')) returns contents of edit13 as a double


% --- Executes during object creation, after setting all properties.
function edit7_CreateFcn(hObject, eventdata, handles)
% hObject     handle to edit13 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles     empty - handles not created until after all CreateFcns called

% Hint: edit controls usually have a white background on Windows.
%       See ISPC and COMPUTER.
if ispc && isequal(get(hObject,'BackgroundColor'), get(0,'defaultUicontrolBackgroundColor'))
    set(hObject,'BackgroundColor','white');
end



function  edit6_Callback(hObject,  eventdata,  handles)
```

```
% hObject    handle to edit1 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)

% Hints: get(hObject,'String') returns contents of edit1 as text
%        str2double(get(hObject,'String')) returns contents of edit1 as a double


% --- Executes during object creation, after setting all properties.
function edit8_CreateFcn(hObject, eventdata, handles)
% hObject    handle to edit1 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    empty - handles not created until after all CreateFcns called

% Hint: edit controls usually have a white background on Windows.
%       See ISPC and COMPUTER.
if ispc && isequal(get(hObject,'BackgroundColor'), get(0,'defaultUicontrolBackgroundColor'))
    set(hObject,'BackgroundColor','white');
end



function edit9_Callback(hObject, eventdata, handles)
% hObject    handle to edit12 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)

% Hints: get(hObject,'String') returns contents of edit12 as text
%        str2double(get(hObject,'String')) returns contents of edit12 as a double


% --- Executes during object creation, after setting all properties.
function edit9_CreateFcn(hObject, eventdata, handles)
% hObject    handle to edit12 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    empty - handles not created until after all CreateFcns called

% Hint: edit controls usually have a white background on Windows.
%       See ISPC and COMPUTER.
if ispc && isequal(get(hObject,'BackgroundColor'), get(0,'defaultUicontrolBackgroundColor'))
    set(hObject,'BackgroundColor','white');
end



function edit10_Callback(hObject, eventdata, handles)
```

```
% hObject    handle to edit13 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)

% Hints: get(hObject,'String') returns contents of edit13 as text
%        str2double(get(hObject,'String')) returns contents of edit13 as a double


% --- Executes during object creation, after setting all properties.
function edit10_CreateFcn(hObject, eventdata, handles)
% hObject    handle to edit13 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    empty - handles not created until after all CreateFcns called

% Hint: edit controls usually have a white background on Windows.
%       See ISPC and COMPUTER.
if ispc && isequal(get(hObject,'BackgroundColor'), get(0,'defaultUicontrolBackgroundColor'))
    set(hObject,'BackgroundColor','white');
end



function edit11_Callback(hObject, eventdata, handles)
% hObject    handle to edit8 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)

% Hints: get(hObject,'String') returns contents of edit8 as text
%        str2double(get(hObject,'String')) returns contents of edit8 as a double


% --- Executes during object creation, after setting all properties.
function edit11_CreateFcn(hObject, eventdata, handles)
% hObject    handle to edit8 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    empty - handles not created until after all CreateFcns called

% Hint: edit controls usually have a white background on Windows.
%       See ISPC and COMPUTER.
if ispc && isequal(get(hObject,'BackgroundColor'), get(0,'defaultUicontrolBackgroundColor'))
    set(hObject,'BackgroundColor','white');
end



function edit10_Callback(hObject, eventdata, handles)
```

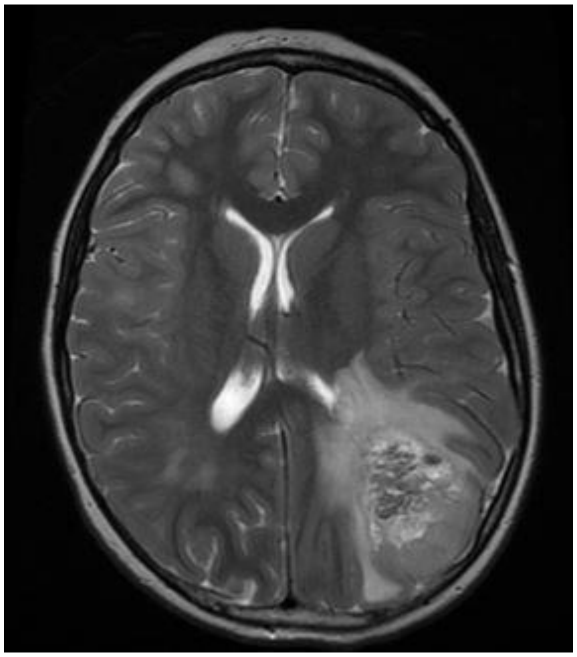
```
% hObject    handle to edit9 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)

% Hints: get(hObject,'String') returns contents of edit9 as text
%        str2double(get(hObject,'String')) returns contents of edit9 as a double


% --- Executes during object creation, after setting all properties.
function edit12_CreateFcn(hObject, eventdata, handles)
% hObject    handle to edit9 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    empty - handles not created until after all CreateFcns called

% Hint: edit controls usually have a white background on Windows.
%       See ISPC and COMPUTER.
if ispc && isequal(get(hObject,'BackgroundColor'), get(0,'defaultUicontrolBackgroundColor'))
    set(hObject,'BackgroundColor','white');
end



function edit13_Callback(hObject, eventdata, handles)
% hObject    handle to edit10 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)

% Hints: get(hObject,'String') returns contents of edit10 as text
%        str2double(get(hObject,'String')) returns contents of edit10 as a double


% --- Executes during object creation, after setting all properties.
function edit13_CreateFcn(hObject, eventdata, handles)
% hObject    handle to edit10 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    empty - handles not created until after all CreateFcns called

% Hint: edit controls usually have a white background on Windows.
%       See ISPC and COMPUTER.
if ispc && isequal(get(hObject,'BackgroundColor'), get(0,'defaultUicontrolBackgroundColor'))
    set(hObject,'BackgroundColor','white');
end
```

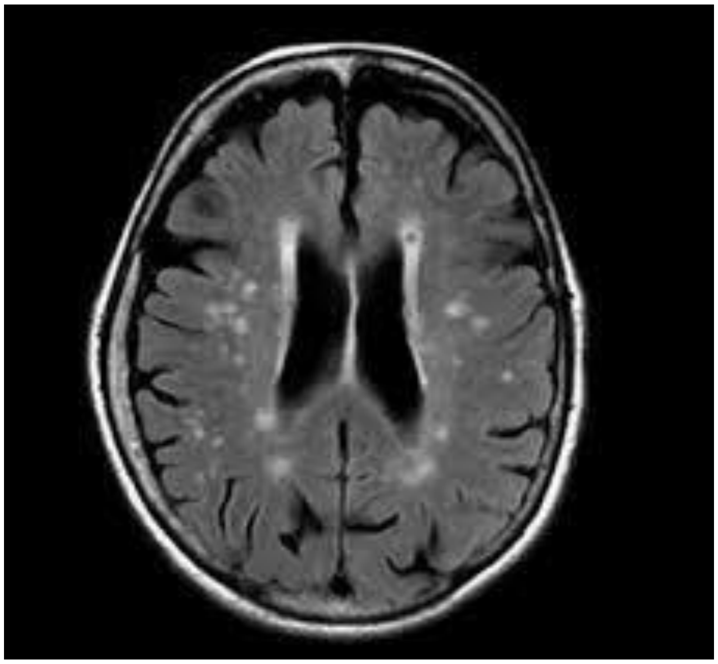
5.RESULTS AND ANALYSIS

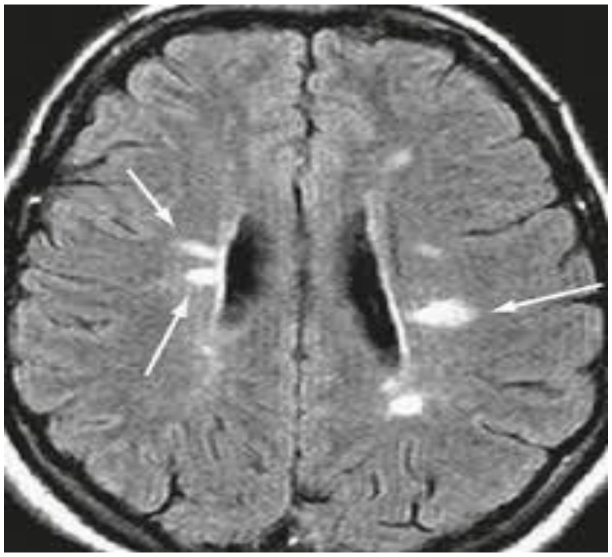
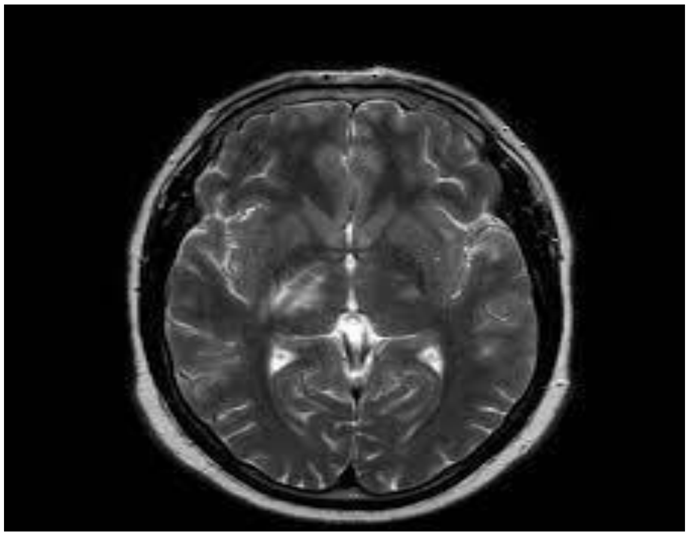
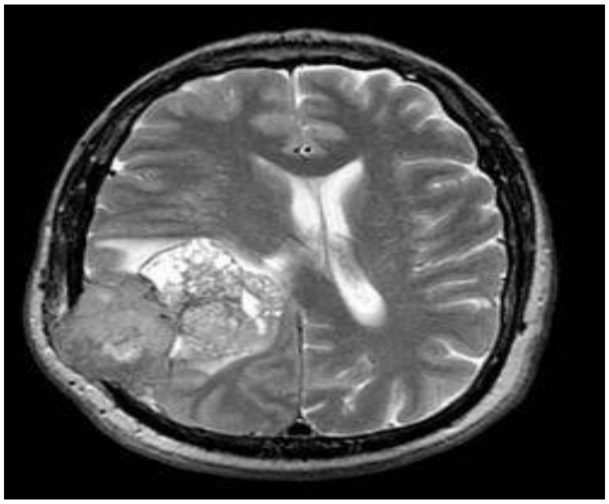
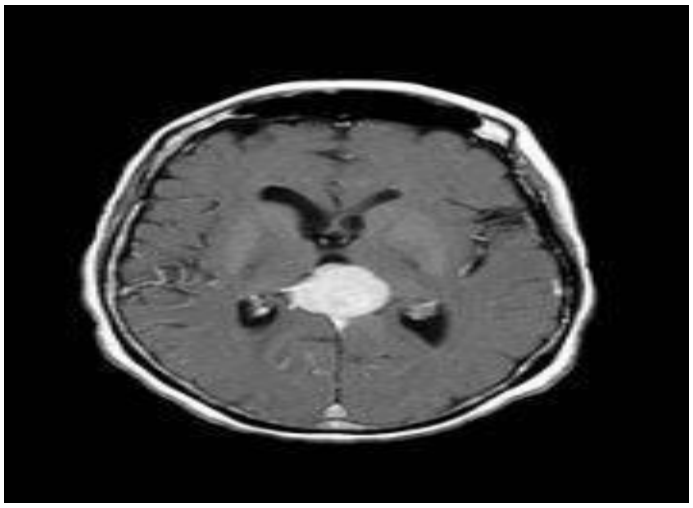
5.1 Data Collection

The pipeline begins with the acquisition of MRI images from a dataset. This dataset serves as the input for the analysis process and includes MRI scans with various tumor characteristics. The Data Set consists of different MRI scanned images of pixel size varies from 255x255.The Data set was collected from Kaggle.There are total 155 MRI images in dataset

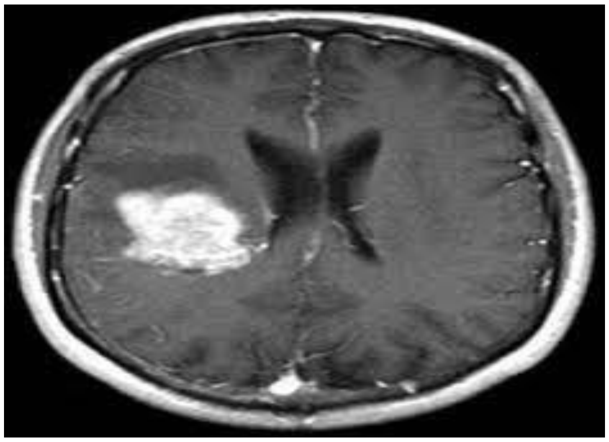
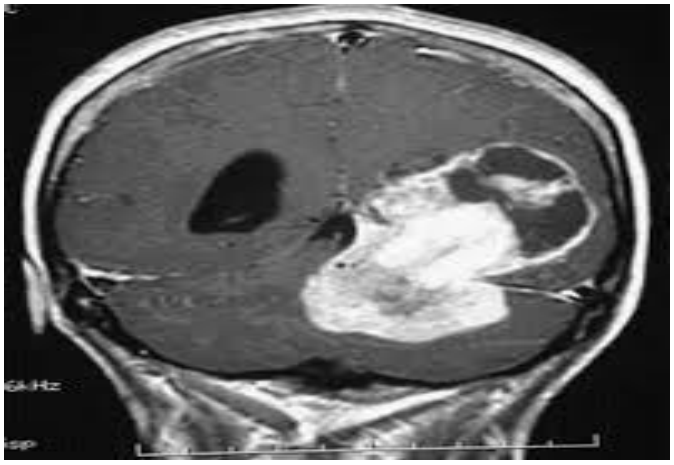
The dataset used in the Brain Tumor Detection project on Kaggle is a comprehensive collection of MRI images curated to facilitate tumor classification and detection tasks. The dataset includes labeled images categorized as either "tumor" or "no tumor," providing a binary classification challenge. It is designed for use in machine learning and deep learning applications, especially convolutional neural networks (CNNs), to identify abnormalities in brain scans effectively. The images are preprocessed and standardized to ensure consistency, with enhancements like contrast adjustments applied to optimize the detection of tumor regions. This dataset is pivotal for researchers and developers focusing on improving diagnostic accuracy and developing automated medical imaging systems.

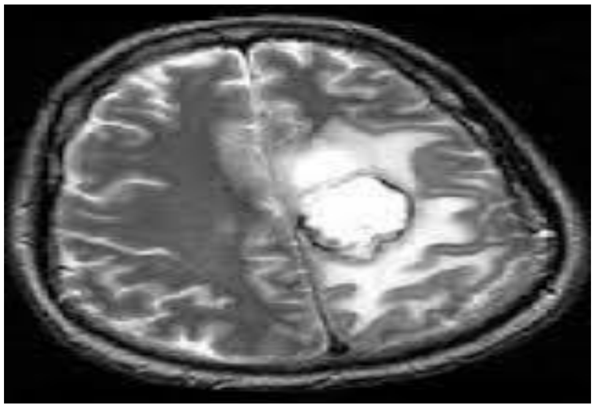
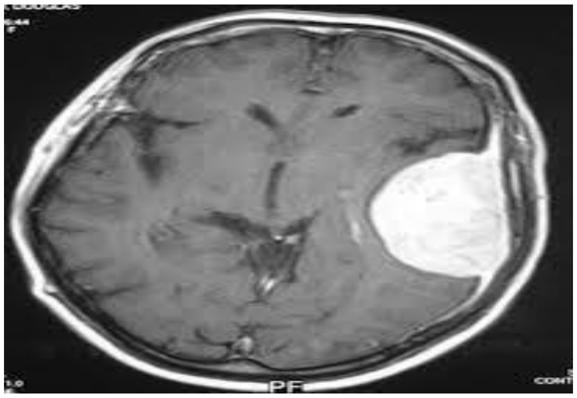
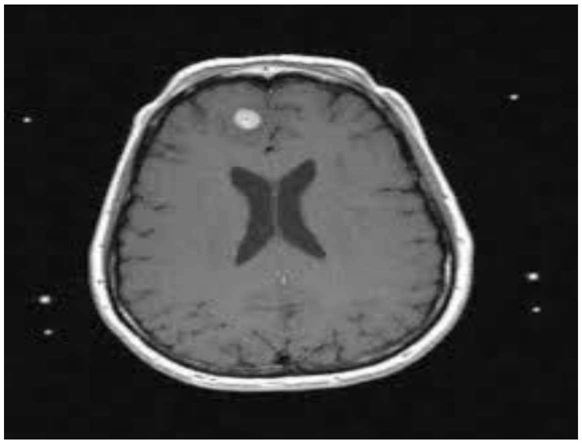
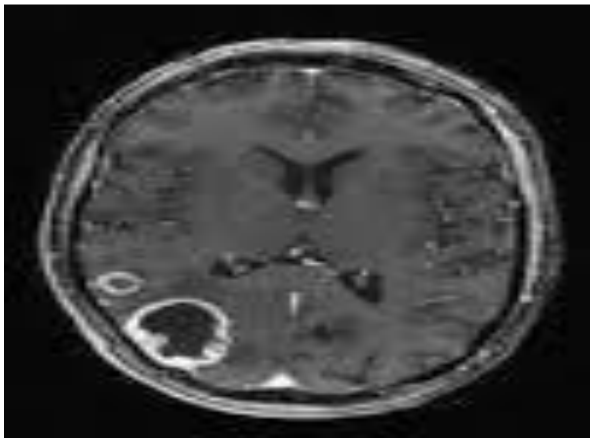
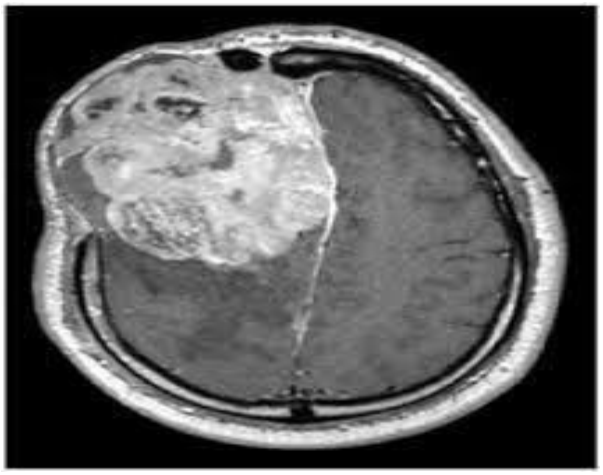
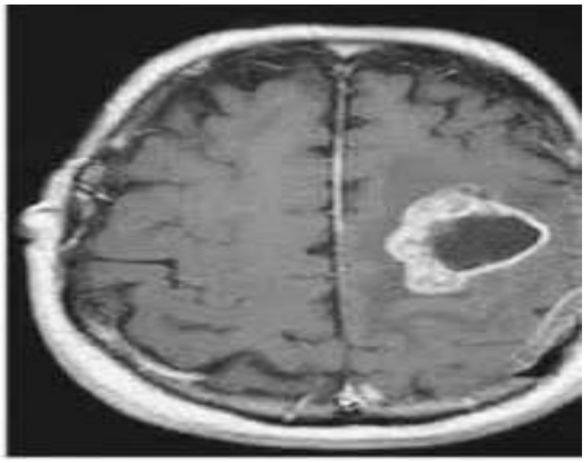




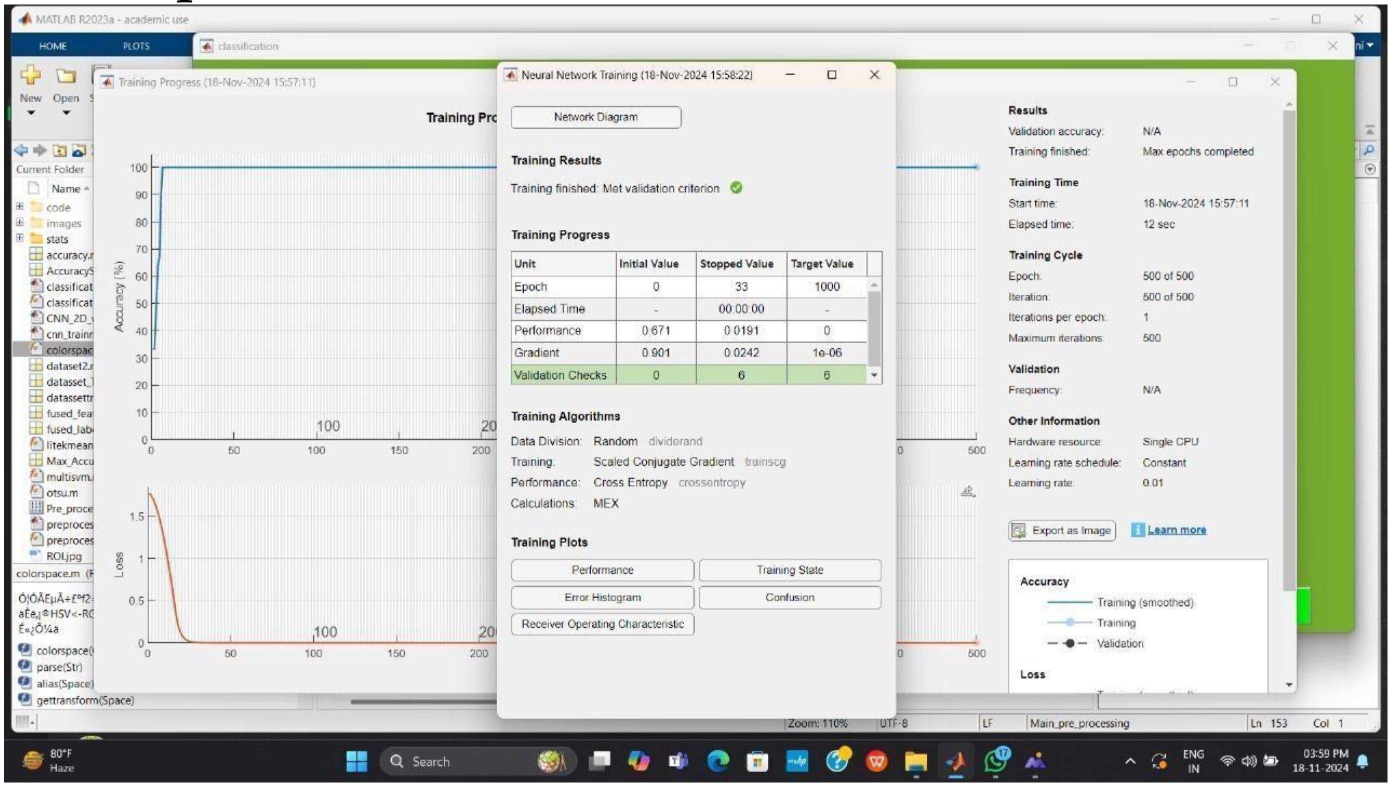





v

5.2 Graphs, Tables, and Charts



MATLAB R2023a - academic use
HOME
PLOTS
classification
Training Progress (18-Nov-2024 15:57:11)
Accuracy (%)
Loss

Neural Network Training (18-Nov-2024 15:58:22)

Network Diagram

Training Results

Training finished: Met validation criterion ✓

Training Progress

Unit	Initial Value	Stopped Value	Target Value
Epoch	0	33	1000
Elapsed Time	-	00:00:00	-
Performance	0.671	0.0191	0
Gradient	0.901	0.0242	1e-06
Validation Checks	0	6	6

Training Algorithms

Data Division:	Random	dividerand
Training:	Scaled Conjugate Gradient	trainscg
Performance:	Cross Entropy	crossentropy
Calculations:	MEX	

Training Plots

Performance | Training State | Error Histogram | Confusion | Receiver Operating Characteristic

Results

Validation accuracy:	N/A
Training finished:	Max epochs completed

Training Time

Start time:	18-Nov-2024 15:57:11
Elapsed time:	12 sec

Training Cycle

Epoch:	500 of 500
Iteration:	500 of 500
Iterations per epoch:	1
Maximum iterations:	500

Validation

Frequency:	N/A

Other Information

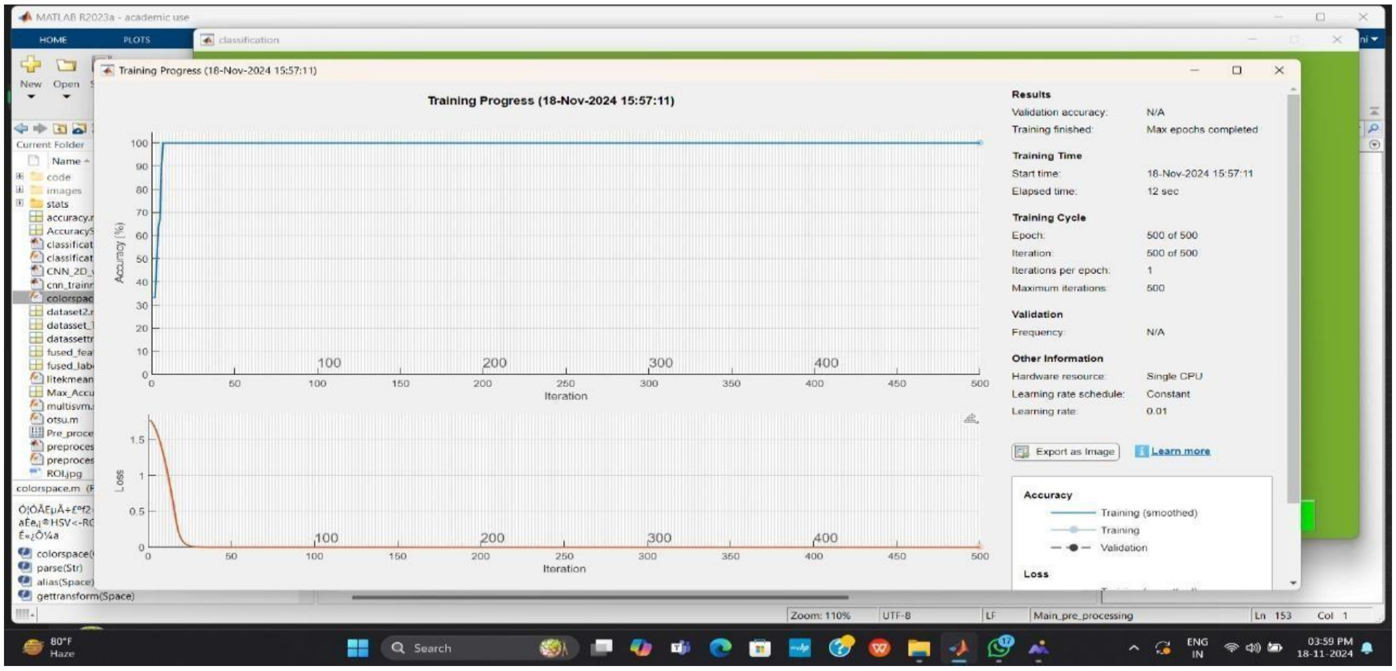
Hardware resource:	Single CPU
Learning rate schedule:	Constant
Learning rate:	0.01

Export as Image | Learn more

Accuracy: Training (smoothed), Training, Validation

Loss

Fig.no 5.2.1:Neural Network Training



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classification
Training Progress (18-Nov-2024 15:57:11)
Accuracy (%)
Loss
Iteration

Training Progress (18-Nov-2024 15:57:11)

Results

Validation accuracy:	N/A
Training finished:	Max epochs completed

Training Time

Start time:	18-Nov-2024 15:57:11
Elapsed time:	12 sec

Training Cycle

Epoch:	500 of 500
Iteration:	500 of 500
Iterations per epoch:	1
Maximum iterations:	500

Validation

Frequency:	N/A

Other Information

Hardware resource:	Single CPU
Learning rate schedule:	Constant
Learning rate:	0.01

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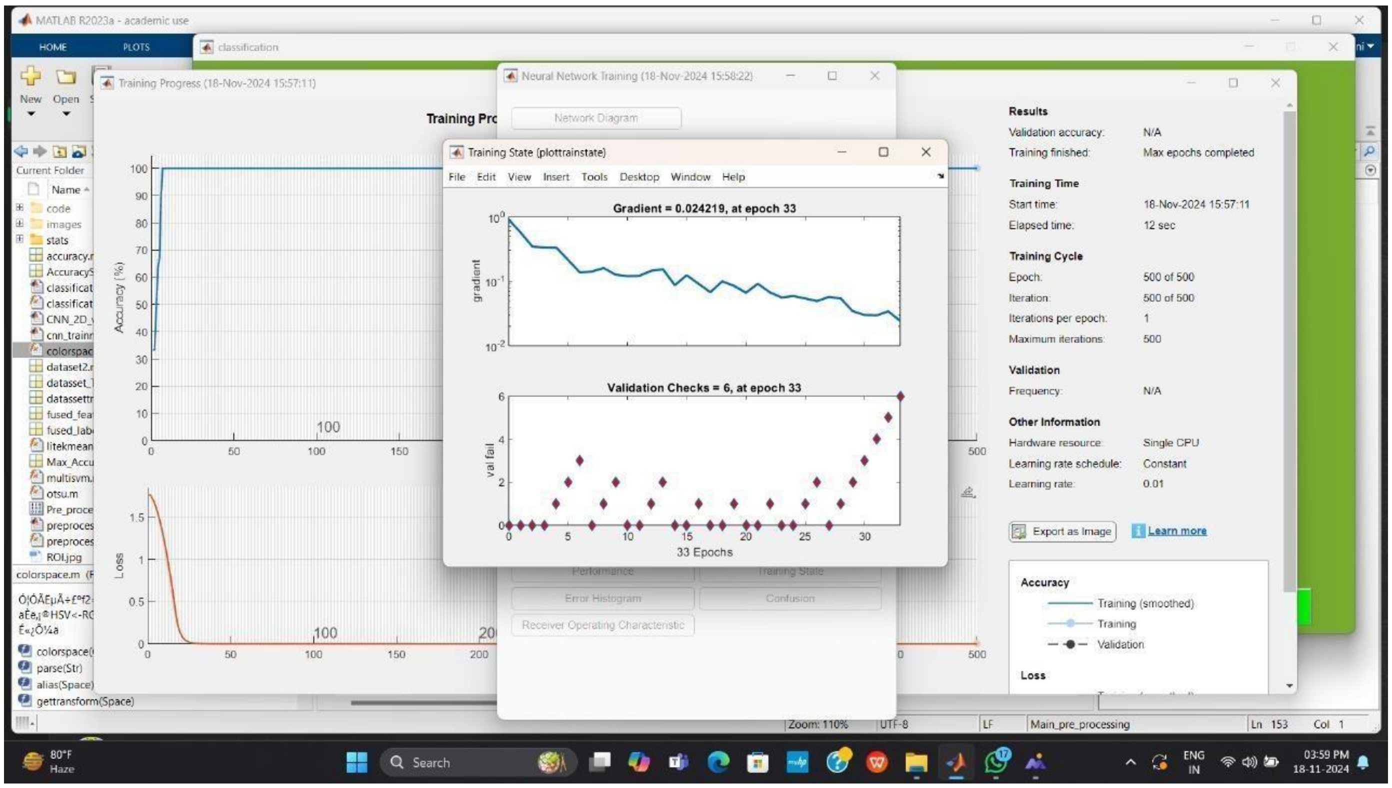
Accuracy: Training (smoothed), Training, Validation

Loss

Fig.no.5.2.2:Training Progress



Gradient = 0.024219, at epoch 33
gradient
Validation Checks = 6, at epoch 33
val fail
33 Epochs
Training State (plottrainstate)
Accuracy (%)
Loss

Results
Validation accuracy: N/A
Training finished: Max epochs completed

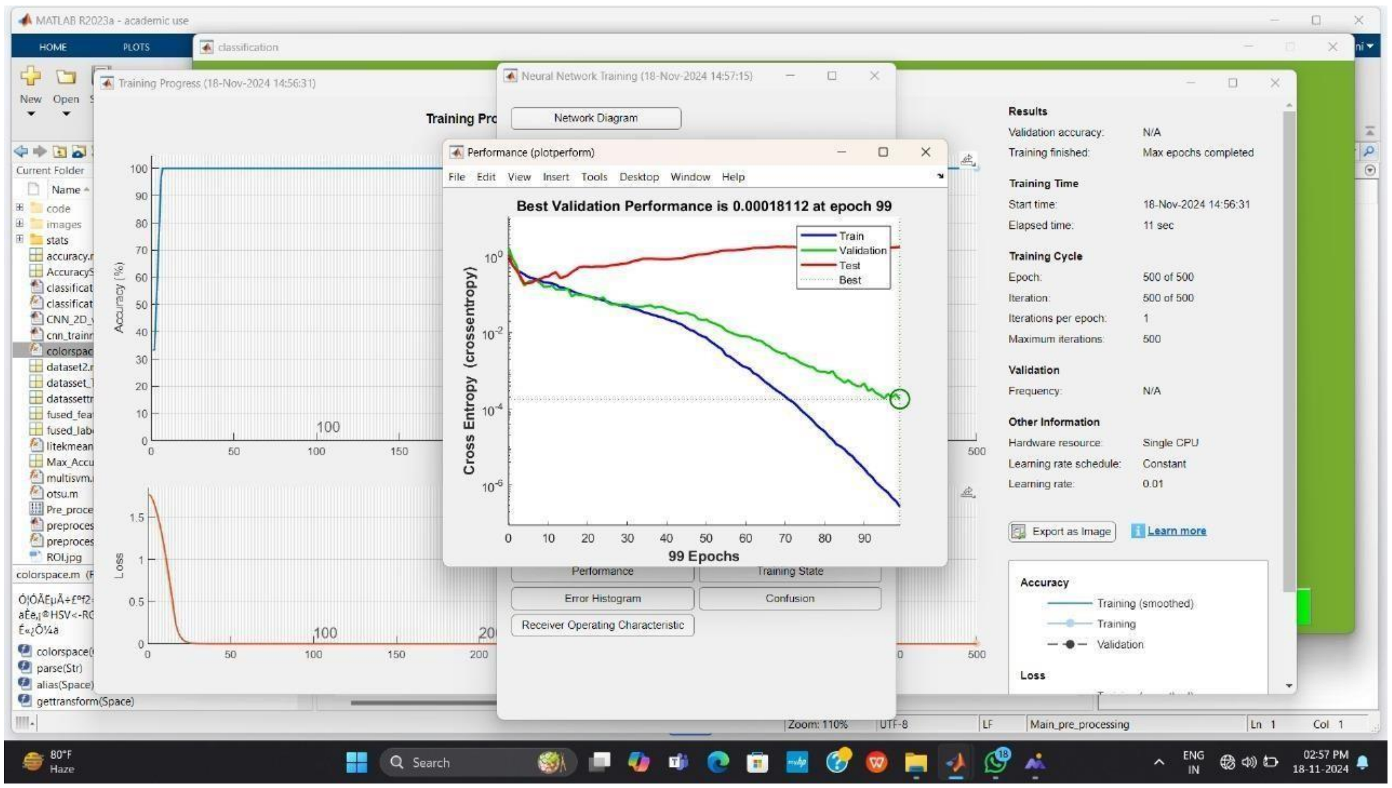
Training Time
Start time: 18-Nov-2024 15:57:11
Elapsed time: 12 sec

Training Cycle
Epoch: 500 of 500
Iteration: 500 of 500
Iterations per epoch: 1
Maximum iterations: 500

Validation
Frequency: N/A

Other Information
Hardware resource: Single CPU
Learning rate schedule: Constant
Learning rate: 0.01

Fig.no.5.2.3:Training state



Best Validation Performance is 0.00018112 at epoch 99
Train
Validation
Test
Best
Cross Entropy (crossentropy)
99 Epochs
Performance (plotperform)
Network Diagram
Performance
Training State
Error Histogram
Confusion
Receiver Operating Characteristic

Results
Validation accuracy: N/A
Training finished: Max epochs completed

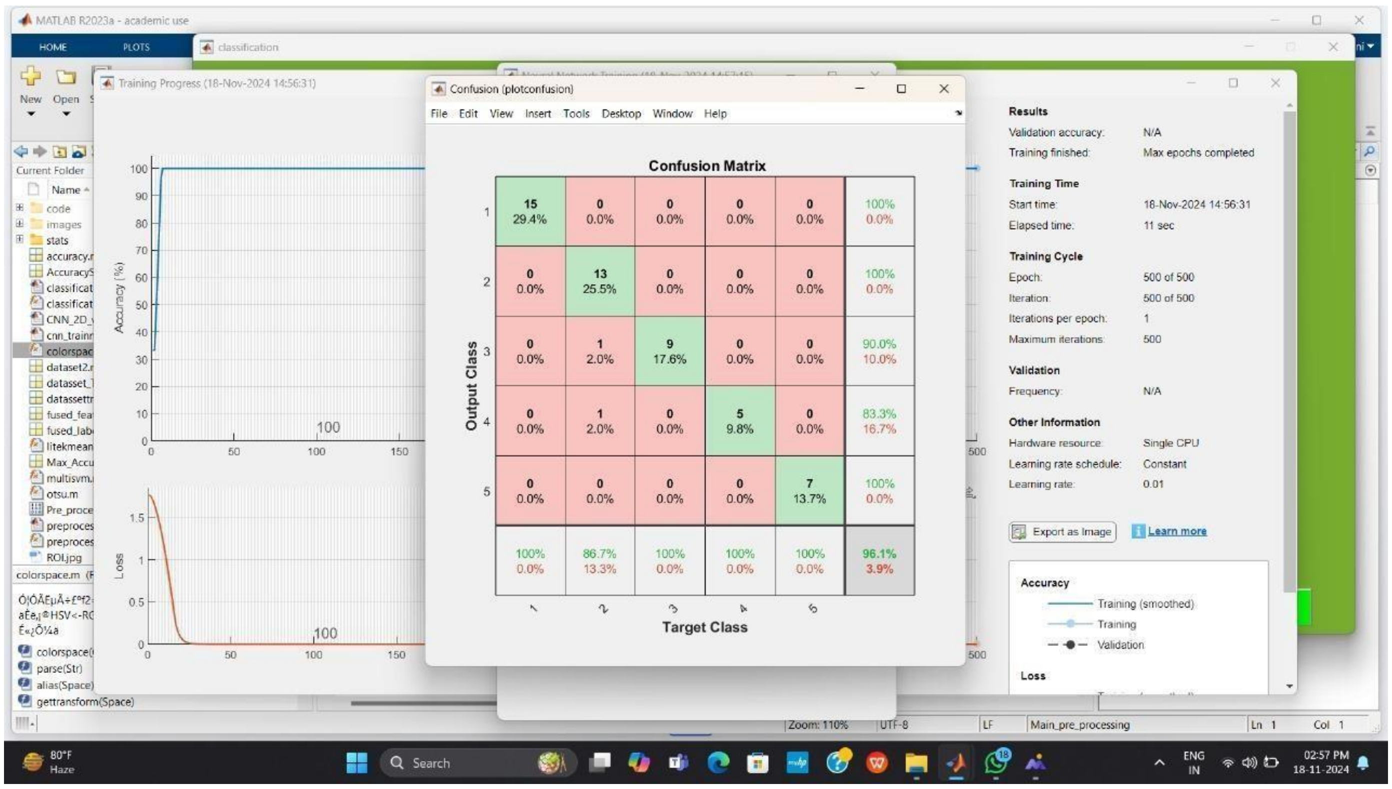
Training Time
Start time: 18-Nov-2024 14:56:31
Elapsed time: 11 sec

Training Cycle
Epoch: 500 of 500
Iteration: 500 of 500
Iterations per epoch: 1
Maximum iterations: 500

Validation
Frequency: N/A

Other Information
Hardware resource: Single CPU
Learning rate schedule: Constant
Learning rate: 0.01

Fig.no.5.2.4:Performance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PLOTS
classification
Training Progress (18-Nov-2024 14:56:31)
Confusion (plotconfusion)
File Edit View Insert Tools Desktop Window Help
Accuracy (%)
Loss
Export as Image
Learn more
Accuracy
Training (smoothed)
Training
Validation
Loss

Confusion Matrix

Output Class \ Target Class	1	2	3	4	5	
1	15 29.4%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	100% 0.0%
2	0 0.0%	13 25.5%	0 0.0%	0 0.0%	0 0.0%	100% 0.0%
3	0 0.0%	1 2.0%	9 17.6%	0 0.0%	0 0.0%	90.0% 10.0%
4	0 0.0%	1 2.0%	0 0.0%	5 9.8%	0 0.0%	83.3% 16.7%
5	0 0.0%	0 0.0%	0 0.0%	0 0.0%	7 13.7%	100% 0.0%
	100% 0.0%	86.7% 13.3%	100% 0.0%	100% 0.0%	100% 0.0%	96.1% 3.9%

Results

Validation accuracy:	N/A
Training finished:	Max epochs completed

Training Time

Start time:	18-Nov-2024 14:56:31
Elapsed time:	11 sec

Training Cycle

Epoch:	500 of 500
Iteration:	500 of 500
Iterations per epoch:	1
Maximum iterations:	500

Validation

Frequency:	N/A

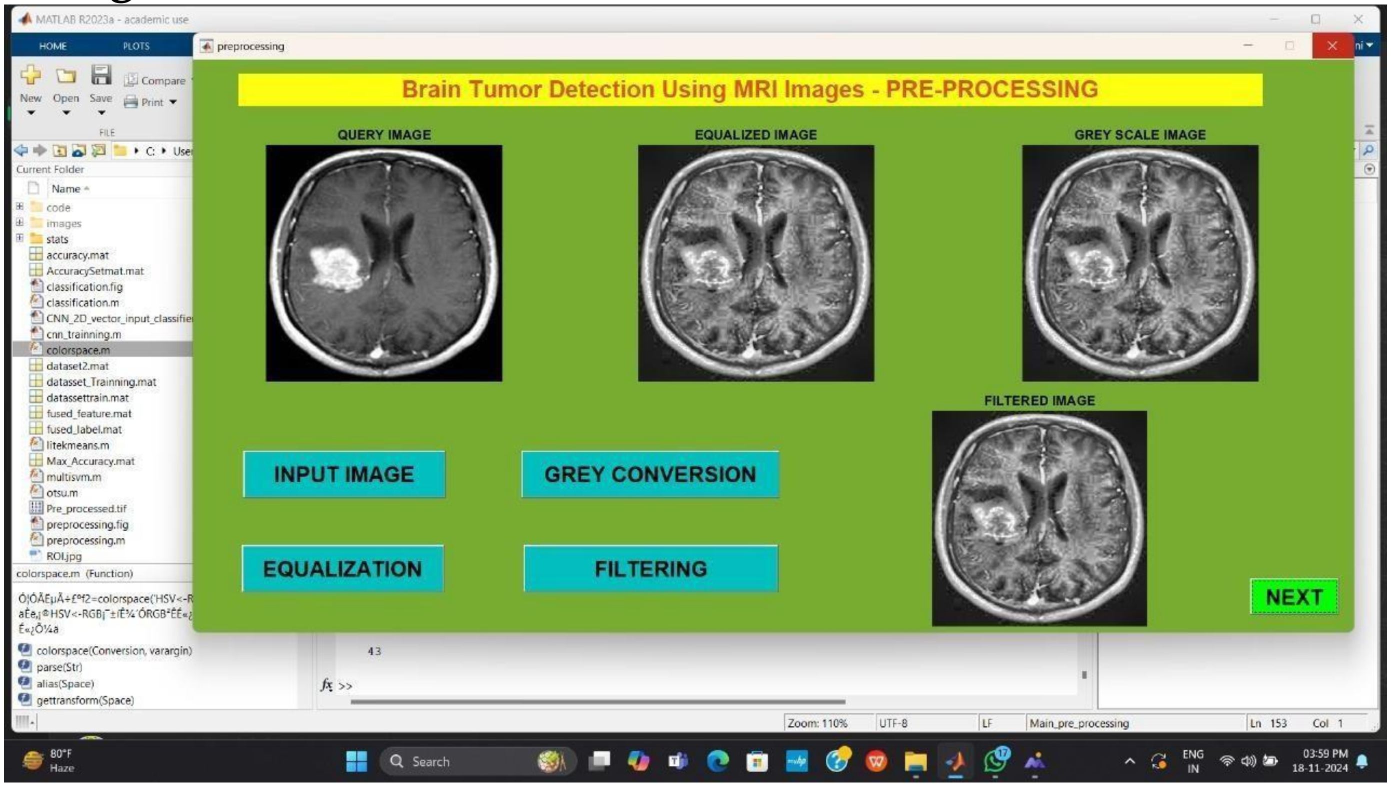
Other Information

Hardware resource:	Single CPU
Learning rate schedule:	Constant
Learning rate:	0.01

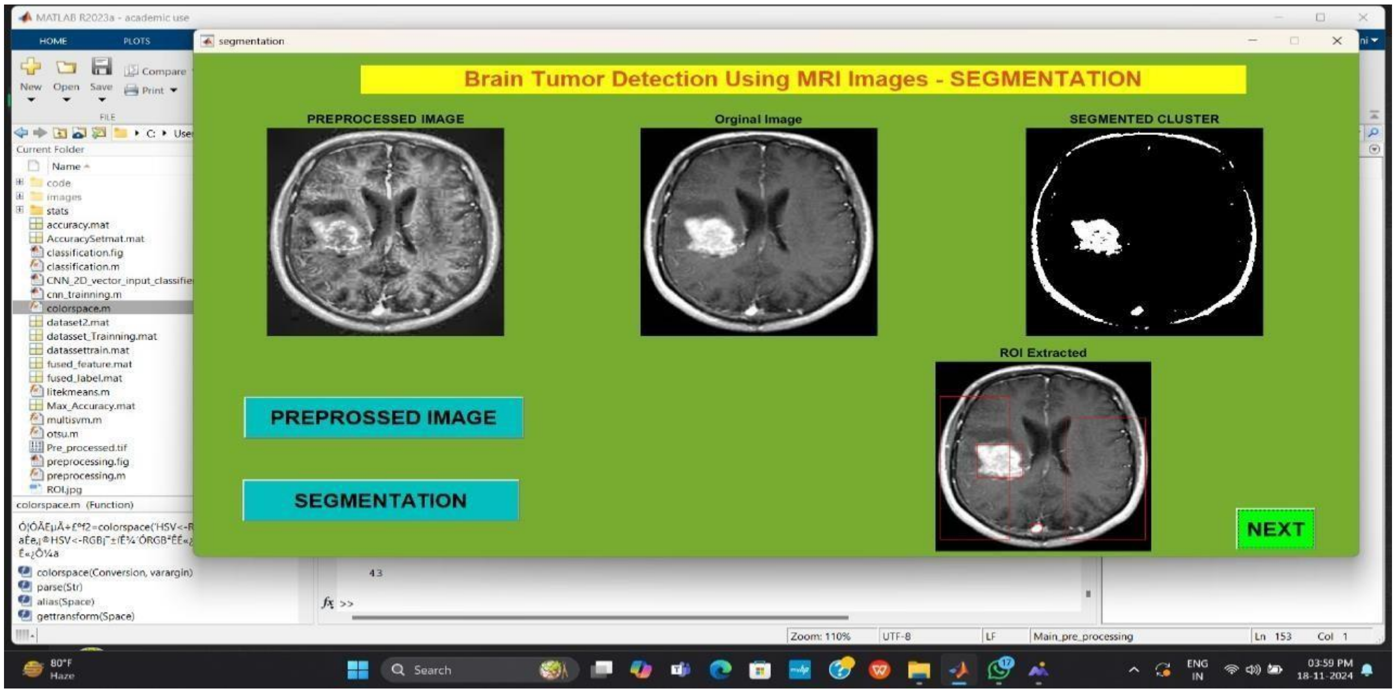
Fig.no.5.2.5:Confusion Matrix

5.3 Result

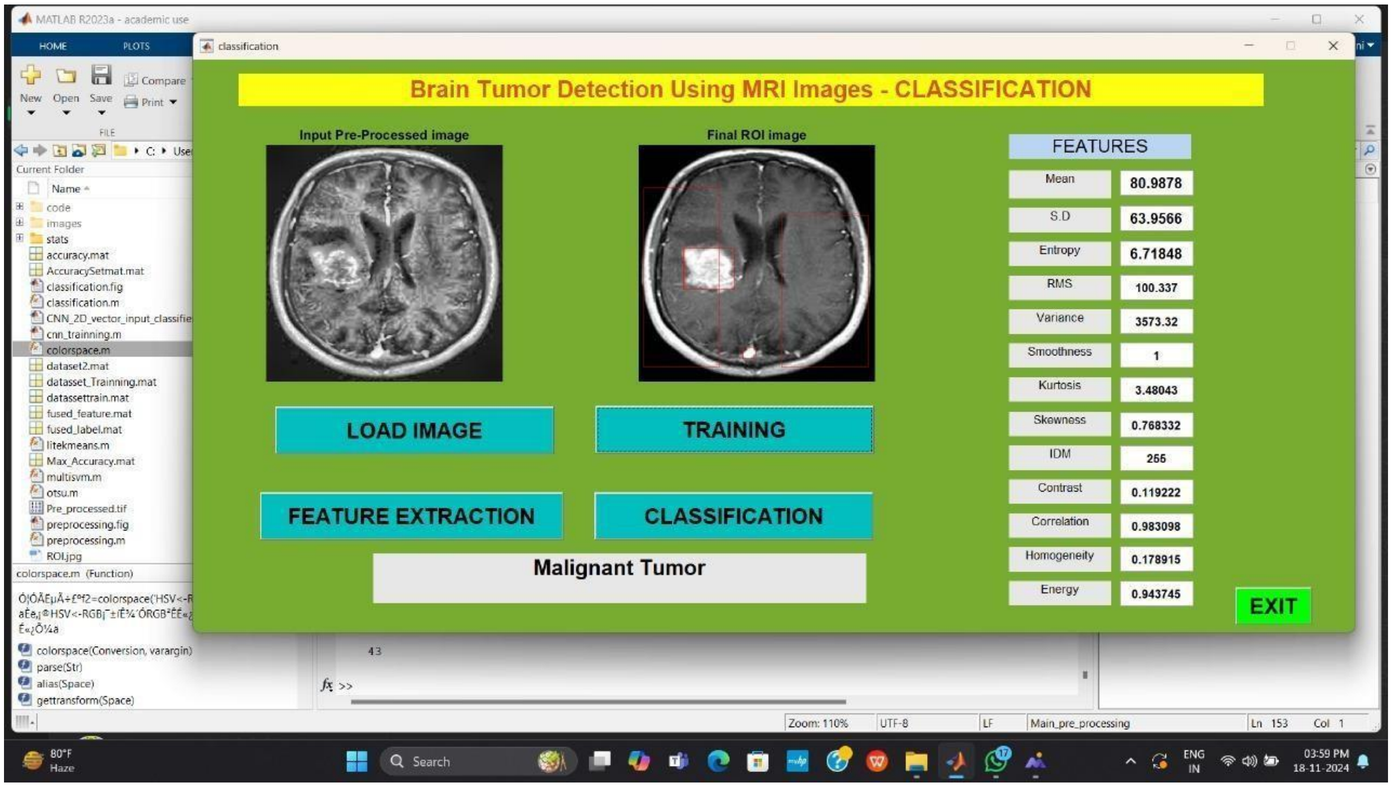
Malignant tumor



Preprocessed Outcome



Segmented Outcome

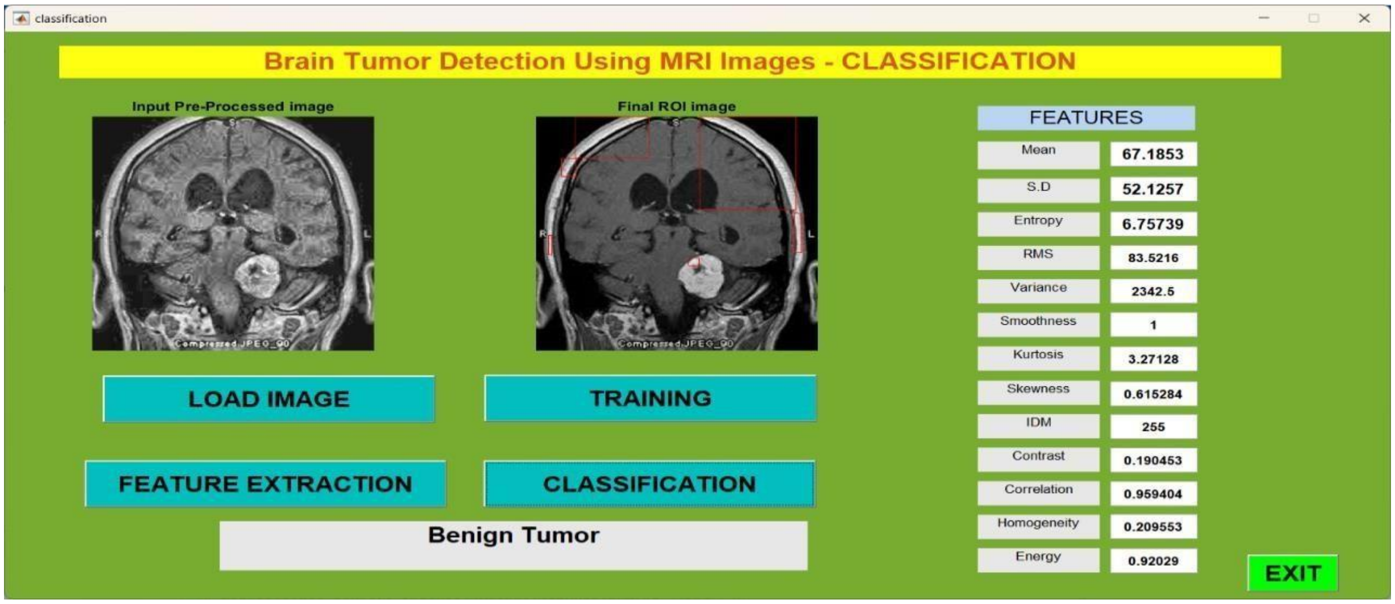


FEATURES	
Mean	80.9878
S.D	63.9566
Entropy	6.71848
RMS	100.337
Variance	3573.32
Smoothness	1
Kurtosis	3.48043
Skewness	0.768332
IDM	255
Contrast	0.119222
Correlation	0.983098
Homogeneity	0.178915
Energy	0.943745

Malignant Tumor

Classified as Malignant

Benign Tumor



FEATURES	
Mean	67.1853
S.D	52.1257
Entropy	6.75739
RMS	83.5216
Variance	2342.5
Smoothness	1
Kurtosis	3.27128
Skewness	0.615284
IDM	255
Contrast	0.190453
Correlation	0.959404
Homogeneity	0.209553
Energy	0.92029

Benign Tumor

Classified as Benign Tumor

6. APPLICATION, ADVANTAGES& LIMITATION

6.1 Applications

1. **Early Detection and Diagnosis of Brain Tumors**: By leveraging advanced image preprocessing techniques, such as Adaptive Histogram Equalization (AHE) and Median Filtering, followed by segmentation and feature extraction, this method can enhance the visibility of tumors in brain MRI scans. This is essential for the early detection of tumors, where timely intervention can significantly improve patient outcomes.
2. **Clinical Decision Support**: The automated classification system, which distinguishes between benign and malignant tumors based on texture features extracted from the Gray-Level Co-occurrence Matrix (GLCM), can act as a second opinion for radiologists. It assists in clinical decision-making by providing accurate, objective results, thereby reducing diagnostic errors and variability that might arise from human interpretation.
3. **Radiological Workflow Automation**: The use of machine learning algorithms for tumor classification can automate tedious aspects of the radiological workflow. By integrating such automated systems into hospital information systems, radiologists can save time spent on manual analysis and focus on more complex cases. This approach also guarantees that a high volume of MRI scans can be processed quickly, making it especially advantageous in fast-paced clinical settings or when screening large groups of individuals.
4. **Medical Research and Clinical Trials**: In clinical research, datasets such as BRATS can be used to investigate the characteristics of brain tumors and their response to treatment. The automated feature extraction and classification system can be used to analyze large datasets quickly, providing valuable insights into tumor characteristics, treatment efficacy, and prognostic factors.
5. **Telemedicine and Remote Diagnosis**: The system can also be integrated into telemedicine platforms, enabling remote diagnosis. In areas with limited access to specialized medical practitioners, this technology can be used to send MRI scans to experts for analysis and classification, helping in diagnosing tumors without the need for in-person consultations.
6. **Tumor Monitoring and Progression Analysis**: The system can be adapted for longitudinal monitoring of brain tumors, helping in assessing tumor growth or regression during or after treatment. By comparing features extracted from multiple scans over time, this approach can track changes in tumor characteristics, assisting in determining the effectiveness of treatment protocols.

6.2 Advantages

1. **Increased Diagnostic Accuracy**: The automated classification system improves diagnostic accuracy by relying on texture-based features that are often imperceptible to the human eye. By analyzing properties such as correlation, dissimilarity, energy, and homogeneity using the GLCM, the system can detect subtle differences between benign and malignant tumors, leading to more precise diagnoses.
2. **Consistency and Reproducibility**: Unlike manual image interpretation, which can vary from one radiologist to another, the machine learning-based approach provides consistent and reproducible results. This is crucial in clinical practice, where consistent diagnoses across different practitioners are needed to ensure reliable patient care.
3. **Time Efficiency**: The entire process, from image preprocessing to tumor classification, can be automated and performed much faster than traditional manual analysis. This helps in reducing the time taken for diagnosis, which is particularly important in time-sensitive conditions like brain tumors, where rapid treatment decisions can have a significant impact on patient survival.
4. **Scalability**: The proposed approach can be easily scaled to process large numbers of MRI scans, making it highly suitable for applications like population screening, where there is a need to analyze large datasets in a short time frame. This scalability is especially important in research studies or clinical trials involving many participants.
5. **Objective and Unbiased Classification**: The use of machine learning models eliminates potential bias from human interpretation, ensuring an objective classification of tumors. This is particularly valuable in preventing misdiagnosis and reducing the risk of human errors in tumor classification.
6. **Enhancement of Radiological Training**: Automated systems can also serve as training tools for medical professionals. By providing accurate, annotated results and feedback, they can help radiologists improve their diagnostic skills and knowledge of various tumor characteristics and classification.

6.3 Limitations

1. **Dependence on Quality of Input Data**: One of the major limitations of the approach is its reliance on the quality of input MRI images. If the input images are of poor resolution or suffer from artifacts not addressed by preprocessing (e.g., motion artifacts or imaging errors), the classification performance can be significantly compromised. Thus, ensuring high-quality imaging is crucial for achieving reliable results.
2. **Limited Generalizability**: The performance of the model can be heavily dependent on the dataset it was trained on. For example, if the machine learning model is trained primarily on a dataset such as BRATS, which may have a specific demographic or tumor type, it may not generalize well to other datasets with different imaging protocols, tumor characteristics, or patient demographics. This can limit the broader applicability of the system.
3. **Complexity of Tumor Variability**: Tumors, particularly brain tumors, can vary greatly in their appearance, structure, and texture across different patients. While textural features like correlation and homogeneity help in distinguishing between benign and malignant tumors, they may not capture all the subtle variations present in the tumor morphology. This makes it challenging to achieve 100% accuracy in classification, particularly for borderline cases where the distinction between benign and malignant tumors is not clear-cut.
4. **Need for High Computational Power**: The extraction of textural features using the GLCM and the subsequent machine learning classification require significant computational resources, especially when processing large datasets. In resource-constrained settings, running these algorithms in real- time may be challenging without access to computing systems or cloud-based solutions.
5. **Model Interpretability**: While machine learning models like those used in classification can offer high accuracy, they often operate as "black boxes," making it difficult to understand how the system arrived at a particular classification decision. This lack of interpretability may hinder its acceptance in clinical practice, where understanding the reasoning behind a diagnosis is crucial for medical professionals to trust and act on the system's recommendations.
6. **Training Data Bias and Class Imbalance**: If the training dataset contains an imbalance in the number of benign versus malignant cases, the model may become biased towards predicting the more prevalent class. This imbalance can affect the sensitivity and specificity of the classifier, particularly in detecting rare or unusual tumor types. Addressing data imbalance through techniques like data augmentation or resampling is necessary to mitigate this issue

7. CONCLUSION AND FUTURE SCOPE

Conclusions

The automatic analysis and classification of brain MRI images play a crucial role in improving the efficiency and accuracy of brain tumor diagnosis. In this study, we outlined a comprehensive pipeline that integrates multiple stages of image preprocessing, segmentation, feature extraction, and machine learning-based classification to categorize brain tumors into benign and malignant categories. By employing state-of-the-art techniques, such as Adaptive Histogram Equalization (AHE) for contrast enhancement, Median Filtering for noise reduction, Otsu's Thresholding for segmentation, and the extraction of key textural features using the Gray-Level Co-occurrence Matrix (GLCM), we demonstrated an effective approach for tumor analysis in MRI scans.

Key findings and conclusions from this work include:

1. **Enhanced Image Quality**: The combination of AHE and Median Filtering significantly improved the quality of the MRI images. AHE enhances contrast, which is particularly beneficial in low-contrast areas, while Median Filtering successfully removed noise without compromising critical structural details, leading to better tumor visualization and accurate segmentation.
2. **Effective Tumor Segmentation**: Otsu's Thresholding method, a well-known unsupervised technique, was effective in segmenting the tumor regions from normal brain tissue. The optimal thresholding computed by the algorithm allowed for clear delineation of the tumor boundaries, facilitating better feature extraction and more accurate classification.
3. **Robust Feature Extraction**: Textural features extracted from the segmented tumor region using GLCM (correlation, dissimilarity, energy, and homogeneity) provided insightful information about the tumor’s structure and texture. These features proved to be essential in distinguishing between benign and malignant tumors, with malignant tumors generally exhibiting distinctive texture patterns when compared to benign tumors.
4. **Accurate Tumor Classification**: The use of machine learning algorithms to classify the tumor as benign or malignant based on the extracted features demonstrated high prediction accuracy. The use of supervised learning techniques, trained on labeled datasets, allowed the model to make reliable classifications, assisting in more objective decision-making processes for clinicians.
5. **Automated Decision Support System**: By automating the analysis pipeline, from preprocessing to classification, this approach presents a promising tool for supporting radiologists in clinical settings. It provides a robust second opinion that can help reduce diagnostic errors and ensure that patients

receive timely and accurate diagnoses. The system has the potential to enhance radiological workflows, especially in environments with high caseloads.

6. **Clinical and Research Implications**: The methodology can be applied not only in clinical settings but also in medical research, particularly in clinical trials, where large numbers of MRI scans need to be processed. The pipeline can assist in monitoring tumor progression, assessing treatment responses, and providing valuable insights into tumor biology and patient prognosis.

Future Scope

While this study has demonstrated the effectiveness of an automated brain tumor classification system based on MRI images, there is substantial potential for future work and improvement. Several areas can be explored to further enhance the performance and applicability of the system:

1. **Deep Learning Integration**: One of the most promising areas for improvement is the integration of deep learning techniques, particularly convolutional neural networks (CNNs), for both segmentation and classification tasks. CNNs have shown great potential in image processing and medical imaging, where they can learn hierarchical features from raw image data, potentially outperforming traditional machine learning techniques in terms of accuracy and robustness. Deep learning models could improve segmentation accuracy, especially in cases where tumors are difficult to differentiate from surrounding tissue, or when the tumor appears in unusual locations.
2. **Multi-Modal Imaging**: MRI is just one of many imaging modalities used for brain tumor analysis. Future work could explore the integration of multi-modal data, such as contrast-enhanced MRI, functional MRI (fMRI), and Positron Emission Tomography (PET) scans, into the pipeline. Multi-modal fusion can provide complementary information that may lead to more accurate segmentation and classification, improving the model's ability to detect different tumor types, sizes, and stages. Additionally, multi-modal imaging can help in distinguishing between tumor recurrence and treatment-related changes, which can be challenging with a single imaging modality.
3. **Large-Scale Data Collection and Model Generalization**: Although the BRATS dataset used in this study is widely regarded as a valuable resource for brain tumor research, the generalizability of the model to other datasets remains a challenge. To improve model robustness, future research could focus on gathering and annotating more diverse MRI datasets from various sources, including different hospitals and imaging protocols. This would help the model generalize better across populations and improve its ability to classify a wide range of tumor types and subtypes. Additionally, addressing issues such as class imbalance in training data will be crucial to ensure the model performs well on both benign and malignant cases.

4. **Longitudinal Analysis and Tumor Tracking**: One promising extension of the current system is its application in longitudinal studies. Tumor progression and response to treatment can be monitored by analyzing MRI scans over time. Future work could focus on developing algorithms to track changes in tumor size, shape, and texture across multiple scans. This could provide valuable insights into tumor dynamics, treatment effectiveness, and recurrence risk. Furthermore, temporal data could be incorporated into machine learning models to predict future tumor growth or response to therapy.
5. **Explainability and Interpretability**: One of the major challenges with machine learning models, especially deep learning models, is their lack of transparency. In clinical settings, it is essential that clinicians understand the rationale behind a model's predictions. Future research could explore techniques for improving the explainability of the system. Approaches like saliency maps or attention mechanisms could help visualize which parts of the MRI scan contributed most to the model's decision, providing clinicians with a more intuitive understanding of the reasoning behind automated diagnoses.
6. **Integration into Clinical Workflows**: For the system to be adopted in real-world clinical practice, it needs to be integrated into the existing medical imaging and radiology workflows. Future work could involve developing user-friendly software that interfaces with Picture Archiving and Communication Systems (PACS) or other medical imaging platforms. Ensuring that the system is easy to use and fits seamlessly into the daily practice of radiologists is critical for broad adoption.
7. **Regulatory and Ethical Considerations**: As with any AI system in healthcare, regulatory approval and ethical considerations are paramount. The system would need to undergo rigorous validation through clinical trials to meet regulatory standards set by agencies such as the FDA. Additionally, issues related to patient privacy, data security, and informed consent must be addressed when using AI-based tools for medical diagnosis.
8. **Personalized Medicine**: With the growing interest in personalized medicine, there is potential to use MRI-based tumor analysis in combination with genomic, proteomic, and other molecular data to classify brain tumors at a deeper level. By integrating imaging data with molecular biomarkers, the system could help tailor treatment strategies to individual patients based on the specific characteristics of their tumor, providing more targeted and effective therapies.

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