

An Automated Brain Tumor Detection and Size Estimation System Using MRI Images

Aryan Sharma¹, Renu²

¹PG Student, Department of CSE, Sat Kabir Institute of Technology and Management, Ladrawan, Haryana, India

²Assistant Professor, CSE, Sat Kabir Institute of Technology and Management, Ladrawan, Haryana, India

ABSTRACT

Brain tumor detection and accurate size estimation are crucial for early diagnosis, treatment planning, and monitoring disease progression. Manual analysis of Magnetic Resonance Imaging (MRI) scans is time-consuming and prone to human error, underscoring the need for automated systems. This paper presents an automated brain tumor detection and size estimation system using MRI images, implemented with image processing techniques and a graphical user interface (GUI). The proposed method begins with image preprocessing, including resizing, grayscale conversion, contrast enhancement, and Gaussian filtering for noise reduction. Segmentation is performed using Otsu's thresholding to convert the image to binary, followed by morphological operations to remove noise and refine tumor regions. Connected component analysis is then applied to identify potential tumor regions, and validation criteria based on area, solidity, and intensity are used to eliminate false detections. The most prominent valid region is selected as the tumor. Experimental results demonstrate that the proposed system effectively detects tumors in MRI images and accurately distinguishes non-tumor cases, producing appropriate results. The method is computationally efficient, easy to implement, and suitable for preliminary diagnostic support. This work highlights the potential of image processing techniques for developing low-cost, accessible medical image analysis tools and lays a foundation for future improvements through advanced machine learning.

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KEYWORDS: Brain Tumor Detection, MRI Imaging, Image Segmentation.

INTRODUCTION

Brain tumors represent a serious medical condition characterized by abnormal cell growth within the brain, often leading to significant neurological impairments and, in severe cases, life-threatening complications. Early detection and accurate assessment of tumor size are essential for effective treatment planning and improving patient outcomes. Among various medical imaging techniques, Magnetic Resonance Imaging (MRI) is widely preferred due to its high-resolution visualization of soft tissues and its non-invasive nature, making it highly suitable for brain analysis. In contrast, other imaging modalities, such as Computed Tomography (CT), involve exposure to ionizing radiation, which raises health concerns with repeated use [7], while Positron Emission Tomography (PET) is primarily used for metabolic imaging and is less detailed for structural analysis [6].

Traditionally, brain tumor detection relies on manual examination of MRI scans by radiologists, which is both time-consuming and subject to inter-observer variability. To address these limitations, automated techniques based on image processing and artificial intelligence have been increasingly explored. Classical image processing methods, including filtering, thresholding, and morphological operations, have shown promising results in enhancing image quality and isolating tumor regions. For example, techniques involving anisotropic diffusion and morphological processing have been used to improve segmentation accuracy by reducing noise and preserving important structural details [2]. Similarly, region-based segmentation approaches such as region growing and region merging provide improved delineation of tumor boundaries by grouping pixels with similar characteristics [3]. A broader review of

segmentation techniques highlights their importance in medical image analysis, along with challenges such as noise sensitivity and intensity variations [4].

In recent years, machine learning and deep learning approaches have significantly advanced the field of brain tumor detection. Machine learning techniques use feature extraction and classification algorithms to distinguish between tumor and non-tumor regions, achieving greater accuracy than traditional methods [1]. Deep learning models, particularly those based on transfer learning, have demonstrated superior performance by automatically learning complex features from MRI images, reducing the need for manual feature engineering [5]. Additionally, advanced projection-based classification techniques have contributed to more precise tumor localization [8].

Despite these advancements, several challenges remain in the development of reliable automated systems. Variability in MRI data, similarity between tumor and normal tissues, and limited availability of annotated datasets continue to hinder performance. Furthermore, accurate diagnosis is crucial not only for treatment but also for understanding the cognitive impact of brain tumors on patients, as highlighted in recent clinical studies [9].

In this context, the present work focuses on developing an automated system for brain tumor detection and size estimation using MRI images. The proposed approach leverages image processing techniques combined with a graphical user interface (GUI) to provide an efficient, user-friendly, and cost-effective solution for tumor detection and quantitative analysis. This system aims to support early diagnosis and serve as a foundation for future advancements in intelligent medical imaging applications.

RESEARCH BACKGROUND: The field of brain tumor detection and segmentation has witnessed significant advancements over the past decades, driven by the availability of benchmark datasets, improved imaging techniques, and the evolution of computational methods. One of the major milestones in this domain is the introduction of the BRATS (Brain Tumor Segmentation) dataset by the Multimodal Brain Tumor Image Segmentation Benchmark (BRATS) [10], which provides standardized multimodal MRI data for evaluating segmentation algorithms. This dataset has played a crucial role in enabling fair comparison and validation of various methods. Further enhancements to such datasets, including expert annotations and radiomic features, have been introduced by Advancing the Cancer Genome Atlas glioma MRI collections with expert segmentation labels and

radiomic features [11], facilitating more accurate and clinically relevant research. Open-access biomedical repositories, such as The Virtual Skeleton Database [12], have also enabled collaborative research and data sharing in medical imaging.

Early research in brain tumor analysis primarily focused on classical segmentation techniques. Studies such as MRI segmentation of the human brain: challenges, methods, and applications [14] and Survey on brain tumor segmentation and feature extraction of MR images [15] provide comprehensive insights into traditional approaches, highlighting challenges such as noise, intensity inhomogeneity, and tumor appearance variability. Techniques based on thresholding, region growing, and feature extraction have been widely used, with improvements such as binomial thresholding and multi-feature selection enhancing segmentation performance [16]. Additionally, early work on 3D segmentation methods emphasized the importance of volumetric analysis for better tumor characterization [17]. Advanced deep learning techniques have also significantly improved segmentation performance. For example, a deep learning-enhanced tumor segmentation approach for MR brain images [24] demonstrated improved accuracy in delineating tumor regions. These methods outperform traditional approaches by effectively handling complex tumor structures and MRI data variations.

With the increasing complexity of medical imaging data, hybrid and machine learning-based approaches have gained prominence. For instance, a brain tumor classification based on a hybrid approach [13] proposed combining multiple techniques to improve classification accuracy. Similarly, feature-based classification methods integrated with machine learning models have shown improved performance in distinguishing tumor types by leveraging statistical and texture features [20]. In recent years, deep learning has emerged as a dominant approach in brain tumor detection and segmentation. Reviews such as Review of MRI-based brain tumor image segmentation using deep learning methods [18] highlight the effectiveness of deep neural networks in automatically learning complex features from MRI images. Convolutional Neural Networks (CNNs) have been widely adopted for classification tasks, as demonstrated in studies like Classification of brain tumors from MRI images using a convolutional neural network [19] and Brain tumor classification using a convolutional neural network [22]. Hybrid deep learning models combining CNNs with other techniques, such as extreme learning machines, have further improved classification performance [21].

Moreover, multi-phase and multi-model systems have been proposed to enhance diagnostic accuracy and robustness [23].

PROPOSED METHODOLOGY

Figure 1 presents the complete methodology of brain tumor detection and analysis implemented in the system, showing a step-by-step pipeline from image input to final result and visualization.

Step 1. Image Acquisition: The process begins of acquiring a brain MRI image via the graphical user interface (GUI). The input image $I(x,y)$ represents the spatial intensity distribution of brain tissues, where x and y denote pixel coordinates. The image may be in RGB or grayscale format and is resized to a standard dimension (e.g., 256×256) to ensure uniform processing. This step ensures consistency and prepares the image for further analysis.

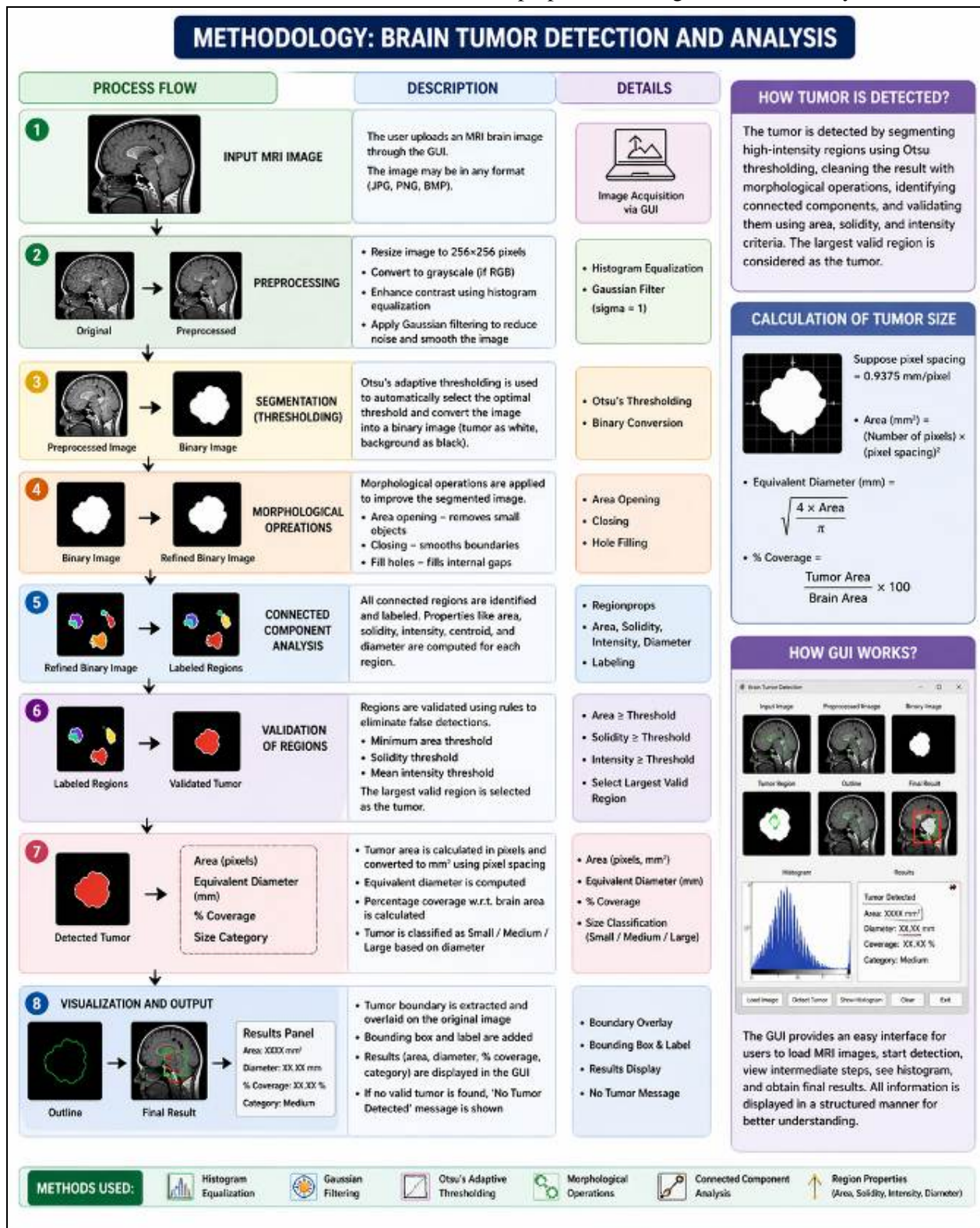


Figure 1: Methodology for Brain Tumor Detection and Analysis

Step 2. Image Preprocessing: Preprocessing enhances image quality and reduces noise. The RGB image is converted into grayscale using:

$$I_g = 0.2989R + 0.5870G + 0.1140B \quad (1)$$

Then, contrast enhancement is applied using intensity transformation:

$$I_e(x, y) = \frac{I_g(x, y) - I_{min}}{I_{max} - I_{min}} \quad (2)$$

Gaussian filtering is used for noise removal:

$$G(x, y) = \frac{1}{2\pi\sigma^2} e^{-\frac{x^2+y^2}{2\sigma^2}} \quad (3)$$

This improves clarity and highlights tumor regions.

Step 3. Image Segmentation: Segmentation separates the tumor from the background using Otsu's thresholding. The optimal threshold T is selected by maximizing inter-class variance: The binary image is obtained as:

$$B(x, y) = \begin{cases} 1, & I(x, y) > T \\ 0, & \text{otherwise} \end{cases} \quad (4)$$

This converts the image into tumor (white) and background (black).

Step 4. Morphological Operations: Refine the binary image. Area opening removes small objects:

$$B'(x, y) = B(x, y) \ominus S \quad (5)$$

Closing operation smooths boundaries:

$$B''(x, y) = (B' \oplus S) \ominus S \quad (6)$$

Hole filling ensures internal continuity. These operations improve segmentation accuracy.

Step 5. Connected Component Analysis: Identifies distinct regions in a binary image. Each region R is labeled and analyzed. The area is calculated as:

$$A_i = \sum_{(x,y) \in R} 1 \quad (7)$$

Properties such as centroid and solidity are computed:

$$C = \left(\frac{1}{A_i} \sum x, \frac{1}{A_i} \sum y \right) \quad (8)$$

This step identifies candidate tumor regions.

Step 6. Validation of Tumor Region: The validation of the tumor region is a crucial step in the detection process, as it ensures that only meaningful and clinically relevant regions are considered while eliminating false positives caused by noise, artifacts, or normal brain structures. After performing connected component analysis, multiple candidate regions R_i are obtained from the binary image. However, not all these regions correspond to a tumor. Therefore, a set of validation criteria is applied to filter out invalid regions based on their geometric and intensity properties. First, an area threshold is applied to remove very small regions that are likely to be noise. The area of each region is calculated as in equation 7.

Only regions satisfying $A_i > A_{th}$ are retained. Next, the solidity of each region is evaluated, which measures how compact or solid a region is compared to its convex hull:

$$\text{Solidity} = \frac{\text{Area}}{\text{Convex Area}} \quad (9)$$

Regions with low solidity are typically irregular or fragmented and are therefore discarded. Additionally, an intensity-based validation is performed, where the mean intensity of the region is computed:

$$\mu_i = \frac{1}{A_i} \sum_{(x,y) \in R_i} I(x, y) \quad (10)$$

Since tumors generally appear brighter on MRI, regions with mean intensity below a threshold are rejected. After applying all these conditions, only the regions that satisfy area, solidity, and intensity thresholds are

considered valid tumor candidates. If multiple valid regions remain, the region with the maximum area is selected as the tumor:

$$R_t = \arg \max (A_i) \quad (11)$$

This validation step significantly improves the accuracy of the system by reducing false detections and ensuring that the identified region truly corresponds to a tumor.

Step 7. Tumor Detection Decision: The tumor detection decision stage is a critical step in the overall system, where the algorithm determines whether a tumor is present in the MRI image using the validated regions from the previous stage. After applying area-, solidity-, and intensity-based filtering, a set of candidate regions, R_i , remains. If no region satisfies all validation criteria, the system concludes that no tumor is present in the image. Mathematically, this can be expressed as:

$$\sum_{i=1}^n R_i = 0 \Rightarrow \text{No Tumor Detected} \quad (12)$$

In such cases, the system stops further processing, clears any intermediate outputs, and displays a message such as “No Tumor Detected” in the GUI. This prevents false positives and ensures reliable results. On the other hand, if one or more valid regions are identified, the system proceeds by selecting the most probable tumor region. Since tumors typically appear as the most prominent abnormal structure in the brain, the region with the maximum area is chosen using Equation 11. This selected region is then considered as the detected tumor and is passed to subsequent stages for further analysis, such as size estimation and visualization. This decision-making mechanism acts as a logical checkpoint in the pipeline, ensuring that only meaningful detections are processed further, thereby improving the robustness and accuracy of the system.

Step 8. Tumor Analysis: Tumor analysis is the stage in which the detected tumor region is quantitatively evaluated to extract meaningful medical information. Quantitative analysis is performed on the detected tumor. The tumor area in real units is calculated as:

$$\text{Area}(\text{mm}^2) = A \times (s)^2 \quad (13)$$

where s is pixel spacing. Tumor coverage is:

$$\% = \frac{\text{Tumor Area}}{\text{Brain Area}} \times 100 \quad (14)$$

This provides clinical insights into tumor size and severity. Based on the computed area or diameter, the tumor can be further categorized into different classes such as small, medium, or large, providing a quick assessment of severity. This quantitative analysis enhances the usefulness of the system by not only detecting the presence of a tumor but also providing detailed measurements that can assist in diagnosis, monitoring, and treatment planning.

Step 9. Tumor Visualization: The final stage of the system, where the detected tumor is graphically represented on the MRI image to make the results easier to interpret. After identifying the tumor region R_t , its boundary is extracted using perimeter detection. This is typically achieved by subtracting the eroded version of the tumor region from the original region:

$$P = R_t - \text{erode}(R_t) \quad (15)$$

where P represents the boundary pixels of the tumor. This step highlights the exact shape and extent of the tumor. To further enhance visualization, a bounding box is drawn around the tumor using the coordinates obtained from region properties. The bounding box is defined by: (x,y,w,h) . where (x,y) represents the top-left corner, and w and h denote the width and height of the box. This provides a clear indication of the tumor’s location within the brain. Additionally, a label such as “Tumor” is placed near the centroid of the region:

$$(x_c, y_c) = \left(\frac{1}{A} \sum x, \frac{1}{A} \sum y \right) \quad (16)$$

This helps in clearly identifying the detected region. The tumor boundary or region is then overlaid on the original grayscale MRI image, often using a distinct color (e.g., red or yellow) to differentiate it from normal tissues. Overall, tumor visualization transforms the analytical output into an intuitive and interpretable format, allowing users to easily understand the location, size, and shape of the tumor, thereby enhancing the practical usability of the system.

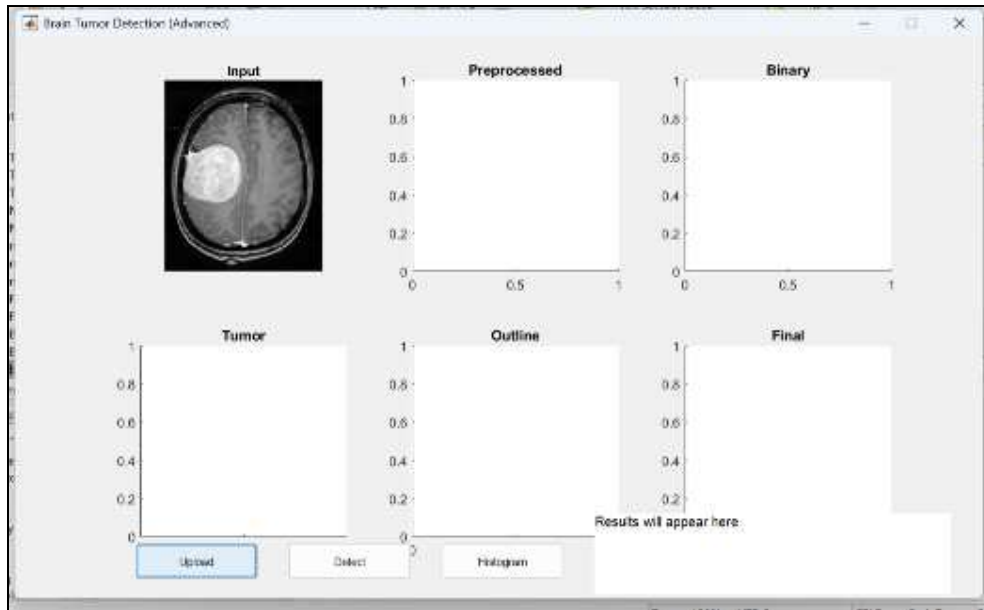
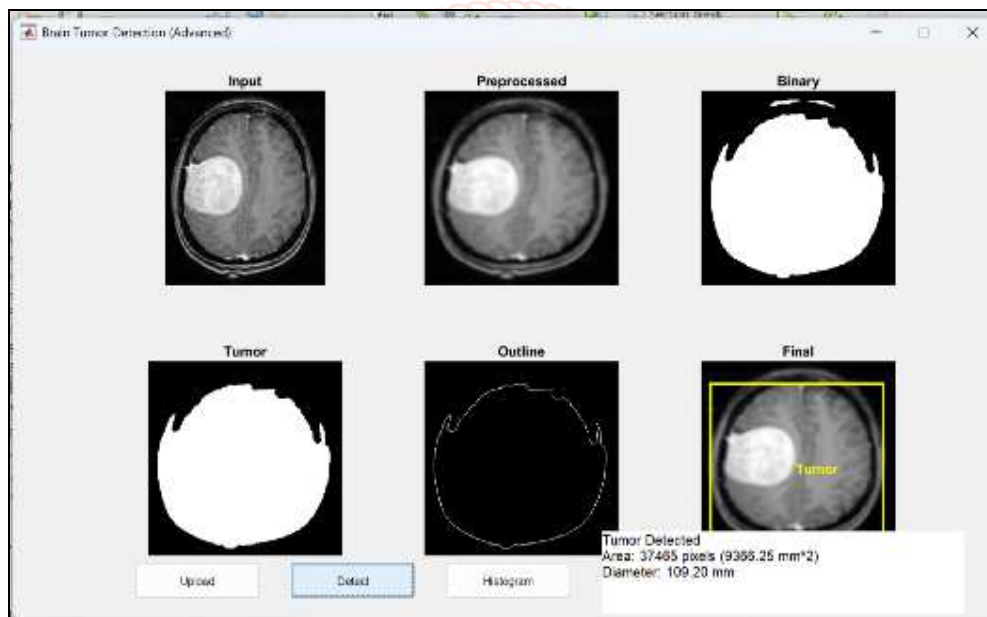
SIMULATIONS OUTPUTS**Figure 2: Input Image in GUI****Figure 3: Tumor Detected**

Figure 3 explains that the Input image represents the original MRI scan containing a bright abnormal region on the left side of the brain, which is likely the tumor. The Preprocessed image shows the result after applying grayscale conversion, contrast enhancement, and Gaussian filtering. These steps improve visibility and reduce noise, making the tumor region more distinguishable. The Binary image is obtained using Otsu's thresholding, where the image is converted into black and white; here, the white region represents high-intensity areas, including the tumor and some surrounding structures. In the bottom row, the Tumor image displays the extracted region after applying morphological operations and connected component analysis. However, in this case, the segmentation has captured a large portion of the brain along with the tumor, indicating slight over-segmentation. The Outline image shows the boundary of the detected region using perimeter extraction, highlighting the shape of the segmented area. The Final image overlays the detected tumor on the original MRI, where a yellow bounding box and the label "Tumor" indicate the location of the detected region. At the bottom of the GUI, quantitative results are displayed. The system calculates the tumor area in pixels and converts it into real-world units (mm^2), along with the equivalent diameter in millimeters. These measurements provide useful information about the size of the tumor.

The figure 4 shows the histogram of a brain MRI image, representing the distribution of pixel intensity values across the image. The horizontal axis ranges from 0 (black) to 255 (white), while the vertical axis shows the

frequency or number of pixels at each intensity level. This graphical representation helps in understanding how pixel values are distributed within the MRI image. A prominent peak on the left side of the histogram indicates a large number of low-intensity (dark) pixels, which correspond to the background and non-brain regions. The middle portion of the histogram, typically between intensity values of 80 to 150, represents normal brain tissues such as gray matter and white matter. These regions show a relatively smooth distribution due to gradual intensity variations within the brain structure.

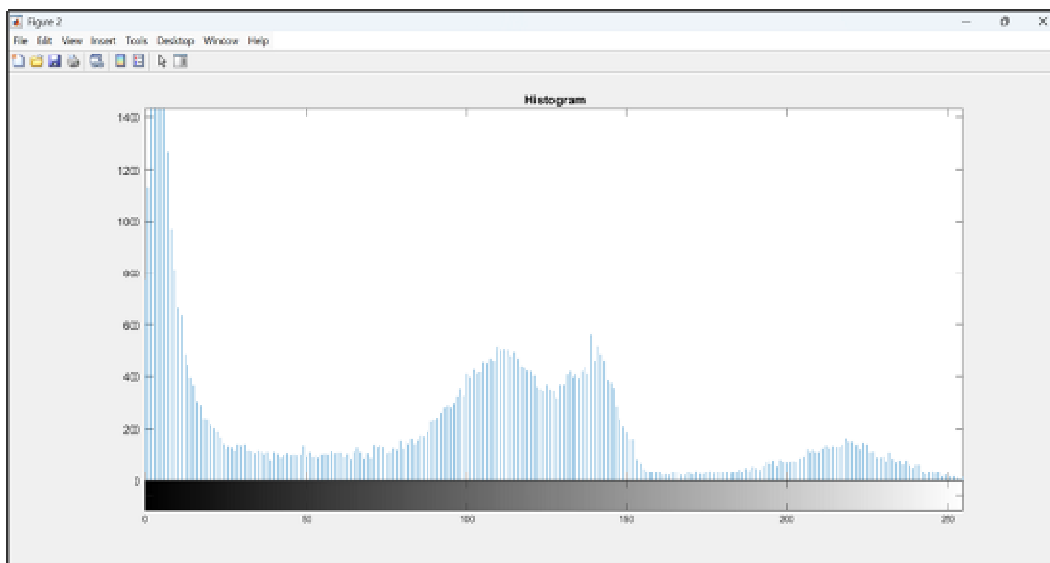


Figure 4: Histogram Representation of MRI Brain Image Intensity Distribution

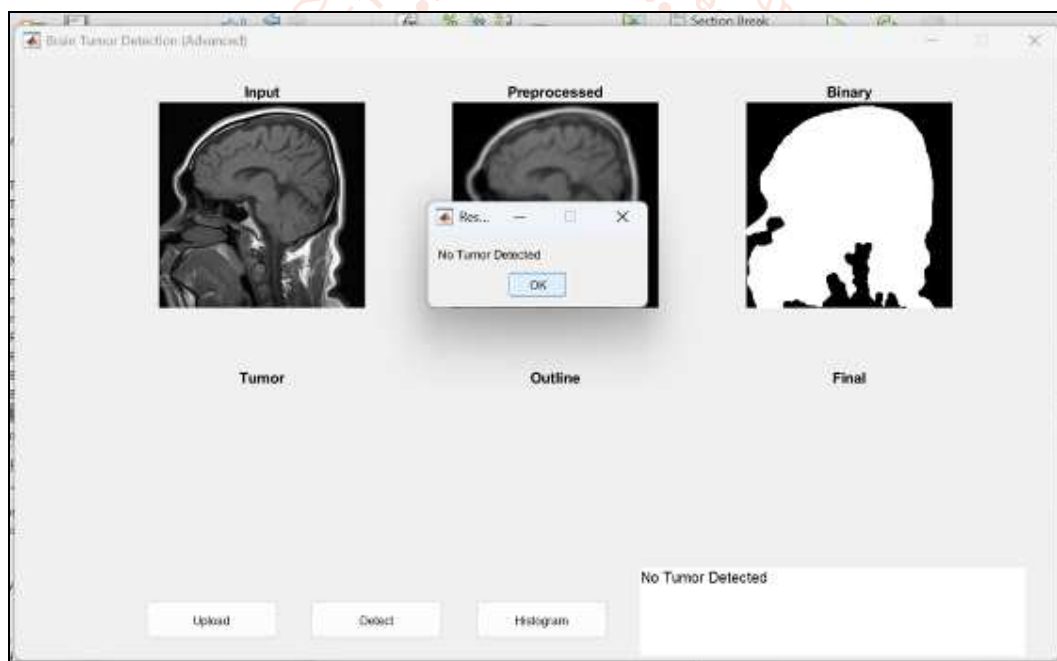


Figure 5: GUI Output for Brain MRI Image Showing No Tumor Detection

Figure 5 illustrates the output of the developed brain tumor detection system when a normal MRI image (without a tumor) is processed. In the input image, a sagittal view of the brain is shown, with normal anatomical structures and no visible abnormality. The preprocessed image shows the result of applying image enhancement techniques, such as grayscale conversion, contrast adjustment, and Gaussian filtering, which improve image clarity and reduce noise. The binary image, obtained through Otsu's thresholding, converts the grayscale image into a black-and-white format. In this case, the white regions correspond to normal brain structures rather than any abnormal tumor region. Since these regions do not meet the validation criteria (e.g., sufficient area, solidity, and intensity), they are not classified as tumors. As a result, the system correctly identifies that no tumor is present. This is confirmed by the pop-up message "No Tumor Detected" and the same message displayed in the results panel at the bottom of the GUI. The tumor, outline, and final output sections remain empty, indicating that no region has been selected for further analysis or visualization.

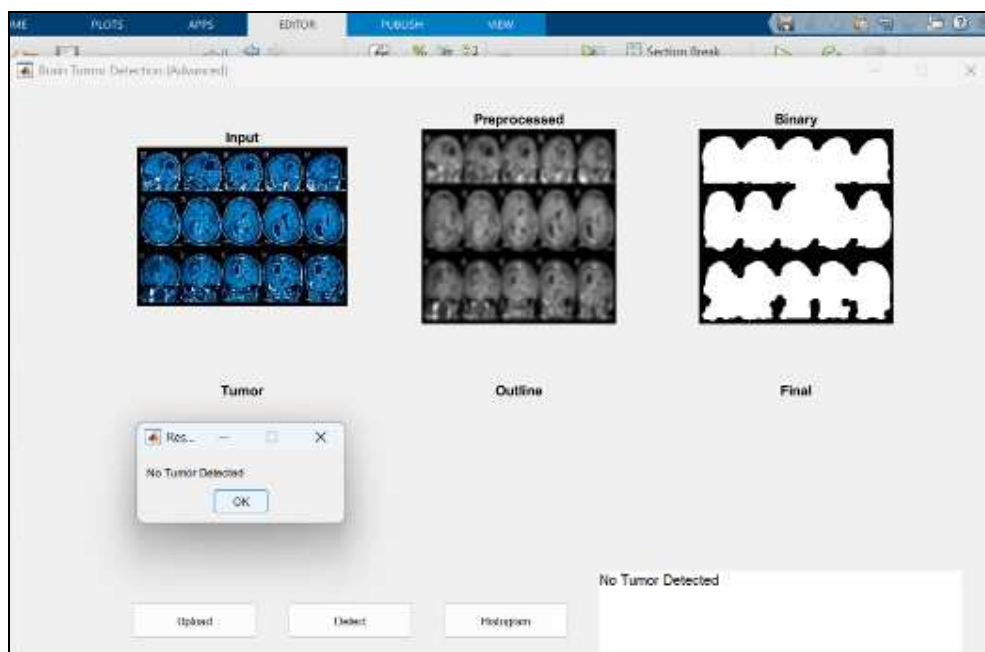


Figure 6: GUI Output for Multi-Slice MRI Input Showing No Tumor Detection

Figure 6 illustrates the output of the brain tumor detection system when a multi-slice MRI image (composite image) is provided as input instead of a single MRI slice. In the input image, multiple brain MRI scans are arranged in a grid format. While this type of image is useful for visualization, the developed system is designed to process only a single MRI slice at a time, which affects the accuracy of subsequent processing steps.

CONCLUSION

This work presents an automated brain tumor detection and size estimation system using MRI images, implemented through image processing techniques and a user-friendly graphical user interface (GUI). The proposed approach integrates multiple stages, including preprocessing, Otsu's thresholding for segmentation, morphological refinement, connected component analysis, and validation based on region properties such as area, solidity, and intensity. This structured pipeline enables effective identification of tumor regions while minimizing false detections. The system not only detects the presence of a tumor but also performs quantitative analysis by estimating tumor area and equivalent diameter, providing meaningful clinical insights. The inclusion of a GUI enhances usability by allowing users to visualize each stage of processing, from input image to final tumor localization with bounding box and labeling. Additionally, the system demonstrates robustness by correctly identifying non-tumor cases and avoiding false positives through strict validation criteria. However, certain limitations exist, such as sensitivity to input image type (e.g., multi-slice images) and dependence on intensity-based segmentation, which may affect performance in complex cases with low contrast or heterogeneous tumor structures. Despite these challenges, the proposed method offers a computationally efficient, cost-effective, and easy-to-implement solution suitable for preliminary diagnostic support.

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