Brain Tumor Detection on MRI image

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Abstract—Brain tumor detection is crucial in medical imaging for timely and accurate diagnosis, impacting patient treatment and prognosis. This project focuses on developing a computer-aided diagnosis (CAD) system for automated brain tumor detection in magnetic resonance imaging (MRI) images. The system integrates image processing techniques using classical methods to preprocess, analyze, and classify MRI images. Key steps include enhancing image quality, extracting features to characterize tumor regions, and employing segmentation algorithms like thresholding, watersheding segmentation for precise localization. Experimental evaluation using diverse MRI datasets demonstrates the system's ability to accurately detect brain tumors with high sensitivity and specificity. This project contributes to medical imaging technology by providing a reliable tool for early tumor detection, improving patient outcomes and treatment strategies.

I. Introduction

The detection and diagnosis of brain tumors using medical imaging techniques such as magnetic resonance imaging (MRI) play a crucial role in the early detection and treatment planning of brain-related diseases. Brain tumors are abnormal growths of cells within the brain that can have severe consequences if not detected and treated in a timely manner. In recent years, the development of computer-aided diagnostic systems for brain tumor detection has garnered significant attention due to their potential to assist healthcare professionals in accurately identifying and analyzing tumor regions in MRI images. These systems utilize advanced image processing and machine learning techniques to automatically segment and classify tumor regions, thereby aiding in early diagnosis and treatment planning. This project aims to develop a robust and efficient brain tumor detection system using MRI images, leveraging image processing techniques to enhance the accuracy and reliability of tumor detection. Through the implementation of various preprocessing, segmentation, and morphological algorithms, the proposed system aims to provide a valuable tool for healthcare professionals in the diagnosis and treatment of brain tumors.

II. METHODOLOGY

A. Input Image Acquisition:

MRI images of the brain, including the input image and ground truth image, are selected through a user interface for file selection. These images are then loaded into MATLAB for processing.

B. Data Processing:

The input MRI image is converted to grayscale and undergoes skull stripping to remove non-brain tissue. This involves thresholding, hole filling, and morphological operations to isolate the brain region.

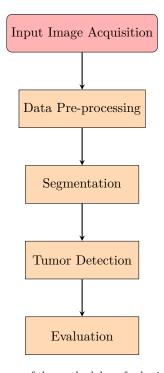


Fig. 1. Flow diagram of the methodology for brain tumor detection using MRI images.

C. Segmentation:

Skull-stripped images are filtered using high-pass and median filtering techniques to enhance quality. Threshold and watershed segmentation partition the image into regions based on intensity levels, delineating potential tumor areas.

D. Tumor Detection:

Segmented images are analyzed to identify tumor regions. Small areas are filtered out, and closing operations ensure complete detection. The resulting tumor outline is overlaid on the original image for visualization and comparison.

E. Evaluation:

The accuracy of tumor detection is assessed using performance metrics like the Dice coefficient, IoU score, and F1 score. These metrics quantify algorithm performance and its ability to detect brain tumors from MRI images.

III. Methods

A. Input Acquisition

The input acquisition stage is pivotal in the brain tumor detection project, facilitating the gathering of MRI images and their corresponding ground truth data. Using a file selection dialog, users interactively choose input MRI and ground truth images. The code validates the selection, ensuring exactly two files are chosen. File paths are constructed, and images are read into memory. Displaying

the input MRI image confirms the selected data. This process initializes the detection process and prepares for subsequent preprocessing and analysis.

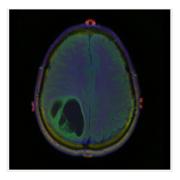


Fig. 2. Input image

B. Data Preprocessing

The preprocessing stage encompasses a series of essential steps aimed at preparing the input MRI images for subsequent analysis and tumor detection. This stage is crucial for enhancing the quality of the images, removing irrelevant information, and isolating the brain region for accurate segmentation. The preprocessing steps include:

1. Grayscale Conversion: The input MRI images are converted from color to grayscale using the . This conversion simplifies subsequent processing steps by reducing the dimensionality of the images and focusing solely on intensity values.

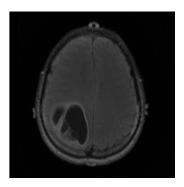


Fig. 3. Gray image

- 2. Skull Stripping: Skull stripping aims to remove non-brain tissues, such as the skull and scalp, from MRI images to isolate the brain region for analysis. This enhances the accuracy of subsequent processing steps like tumor segmentation and classification. Thresholding and morphological operations, including erosion and dilation, refine the binary mask to eliminate remaining non-brain structures. Region filling techniques, such as hole filling and connected component analysis, ensure the inclusion of the entire brain region. The resulting skull-stripped image, obtained by applying the binary mask to the original MRI image, serves as input for noise reduction, image enhancement, and tumor segmentation.
- 3. Noise Reduction: One of the most commonly used noise reduction techniques is filtering, which involves applying linear or nonlinear filters to the MRI images to suppress noise while preserving image details. In the methodology above, both high-pass and median filters are applied to the preprocessed MRI images to reduce

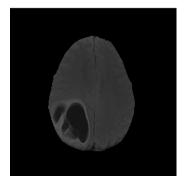


Fig. 4. Brain without skull

noise and enhance image quality. The high-pass filter, implemented using a Gaussian kernel, is used to emphasize high-frequency components in the image, effectively sharpening edges and enhancing image contrast. This helps to remove high-frequency noise while preserving important image features, such as tumor boundaries and tissue structures. Additionally, the median filter is applied to

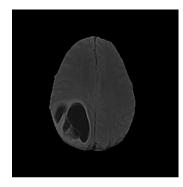


Fig. 5. Sharpened image

the sharpened image to further reduce noise and smooth out image artifacts. The median filter replaces each pixel value with the median value of its neighboring pixels, effectively removing outliers and reducing the impact of random noise on the image.



Fig. 6. Median filtered image

By combining these noise reduction techniques, the methodology effectively enhances the quality of the MRI images while minimizing the impact of noise on subsequent tumor segmentation and analysis. The resulting images are cleaner and more visually interpretable, facilitating more accurate and reliable tumor detection results.

C. Threshold segmentation

Threshold segmentation partitions an image based on pixel intensity values, a fundamental technique in image processing. In brain tumor detection from MRI images, threshold segmentation isolates potential tumor regions from surrounding brain tissue. Preprocessing steps, including noise reduction and image enhancement, precede threshold segmentation to enhance MRI image quality. This segmentation identifies regions of interest indicative of potential tumors.

First, the preprocessed MRI image undergoes multilevel thresholding to determine optimal threshold values based on the image histogram. This approach maximizes the separation between foreground and background intensity distributions, resulting in distinct intensity levels. These thresholds partition the image into regions, highlighting potential tumor regions with varying intensity characteristics.

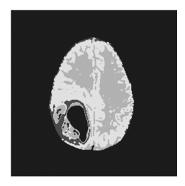


Fig. 7. After thresholding

Next, segmented regions are quantized into a fixed number of intensity levels, assigning each pixel to a specific level based on its intensity value. This simplifies the segmentation output complexity. The image is then converted to color representation, assigning each segmented region a unique color for easy visualization and interpretation of results.



Fig. 8. After thresholing 2

To further refine the segmentation output, the color image is converted back to grayscale to simplify processing, resulting in a single intensity channel. The grayscale segmented image is then thresholded to isolate intensity ranges corresponding to potential tumor regions. Pixels within the desired range are retained, while others are set to background values. This binary image serves as the final segmentation output, highlighting potential tumor regions for further analysis.

D. Watersheding segmentation

The watershed segmentation technique separates distinct regions in the grayscale image by treating it as a topographic surface, with intensity values representing elevations. Watershed lines form along minima in the surface, dividing it into catchment basins. In the code, watershed transformation is applied to the negative Euclidean distance transform of the binary image obtained through thresholding. This transform assigns high values to regions near object boundaries, aiding accurate identification and separation of individual structures. The resulting segmented image delineates different regions, facilitating tumor detection and analysis. Prior



Fig. 9. After watersheding

to transformation, the binary image is inverted to create a topographic representation, and the negative Euclidean distance transform assigns higher intensities to pixels near object boundaries. Visualization using pseudocolor aids in interpreting segmentation outcomes. The watershed algorithm effectively segments the image into distinct regions, enabling further analysis such as morphological operations for tumor detection.

E. Deleting small areas and Closing

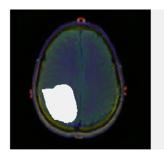
Morphological operations refine the binary image obtained after watershed segmentation, particularly for tumor detection. Morphological closing, involving dilation and erosion, bridges small gaps and smooths irregularities in the binary image. A disk-shaped structuring element with a radius of 100 pixels is used for this closing operation. Dilation expands binary region boundaries, filling narrow gaps and connecting nearby structures. Erosion trims binary region edges. Adjusting the structuring element size controls the extent of morphological closing. This step enhances tumor segmentation accuracy and completeness, ensuring accurate representation of underlying tumor structures in medical images.



Fig. 10. Closed image

F. Overlaying

The detected tumor region is overlaid on the original MRI image for visualization and comparison. Using a binary representation of the tumor, the code sets the alpha (transparency) values of tumor pixels to zero, making them transparent while leaving the rest of the image unaffected. This transparency effect preserves the original image features while highlighting the tumor region. A similar overlay is applied to the original ground truth mask for comparison. The side-by-side display of the detected tumor and ground truth facilitates qualitative assessment of segmentation accuracy by visually comparing algorithm output to known tumor regions. This overlaying aids in evaluating and validating the tumor detection process.



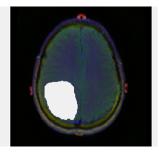


Fig. 11. Detected Tumor vs Original mask

G. Result analysis and Evaluation

1) Dice Coefficient:: The Dice coefficient, a widely used metric in image segmentation, quantifies the spatial overlap between the predicted tumor region and the ground truth. Computed as twice the intersection divided by the sum of the sizes of the predicted and ground truth regions, the Dice coefficient ranges from 0 (no overlap) to 1 (perfect overlap). The formula is expressed as:

$$Dice = \frac{2 \times Intersection}{Predicted\ Area + Ground\ Truth\ Area} \quad \ (1)$$

The resulting coefficient provides a concise measure of segmentation accuracy, with higher values indicating better alignment between the predicted and ground truth tumor regions.

Dice Coefficient for a sample image: 0.96756

2) Intersection over Union (IoU) Score:: The Intersection over Union (IoU) score, also known as the Jaccard index, evaluates the similarity between the predicted and ground truth tumor regions by calculating the ratio of their intersection to their union. The IoU score is computed as:

$$IoU = \frac{Intersection}{Union} \tag{2}$$

where the union is the sum of the predicted and ground truth areas minus their intersection. The IoU score ranges from 0 to 1, with higher values indicating better spatial alignment. This metric provides a robust measure of how well the predicted tumor region aligns with the ground truth, offering insights into the segmentation accuracy.

IoU score for a sample image: 0.93715

3) F1 Score:: The F1 score, a harmonic mean of precision and recall, offers a balanced assessment of the algorithm's performance. Precision measures the accuracy of positive predictions, while recall gauges the ability to

capture all positive instances. The F1 score is computed as:

$$F1 = \frac{2 \times Precision \times Recall}{Precision + Recall}$$
 (3)

This metric ranges from 0 to 1, with higher values indicating a better balance between precision and recall. The F1 score is particularly useful in scenarios where both false positives and false negatives are critical, as it considers the trade-off between these two factors, providing a comprehensive evaluation of the segmentation performance.

The F1 score for a sample image:0.97521

These three evaluation metrics collectively contribute to a thorough quantitative assessment of the tumor detection algorithm, offering valuable insights into its accuracy and effectiveness. For the best accuracy, trial and error method have been used to get Dice coefficient, IOU score, F1 score approximately 150 images in order to decide the threshold values for these evaluation techniques.

IV. FINAL EVALUATION

TABLE I
MEAN AND STANDARD DEVIATION

Evaluation Methods	Mean	Standard Deviation
Dice Coefficient	0.87286	0.21149
IOU Score	0.81865	0.24288
F1 Score	0.90371	0.13449

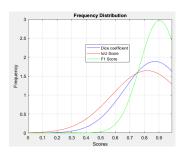


Fig. 12. Frequency distribution graph

The evaluation metrics for brain tumor detection using MRI images show strong performance of the segmentation model. The Dice Coefficient averages 0.87286, indicating high similarity between predicted and actual segmentations. The IOU score averages 0.81865, demonstrating good overlap between predicted and ground truth segmentations. The F1 score averages 0.90371, indicating a commendable balance between precision and recall in the model's predictions. Standard deviations across metrics highlight performance variability across different test samples. Overall, these metrics collectively suggest a robust and accurate brain tumor segmentation model based on MRI images.

V. Comparison

TABLE II EVALUATION COMPARISON

Model Description	Dice Coefficent	IOU Score	F1-Score
Classical Method(ours)	0.8728	0.8186	0.9037
UNet++ and MobileNetv2	0.9245	0.8965	
UNetPlus	0.9061	0.84257	0,9576

Here, we have shown a comparison that shows us a comparison of accuracy between our work and other's work.

Here, every work that we have shared in the tables have used the same dataset that we have used, although usage of Machine Learning has been seen in others' working procedures. While the classical method shows respectable performance, Machine Learning and Deep Learning Models exhibit superior segmentation accuracy in brain tumor detection.

VI. CONCLUSION

This paper explored brain tumor detection on MRI images, comparing classical segmentation methods with the potential of Machine Learning and Deep Learning approaches. While classical techniques like thresholding and watershed segmentation demonstrate respectable performance, this research highlights the superior segmentation accuracy achievable through machine learning models. Our project successfully implemented a system for early brain tumor detection from MRI scans using classical methods. This showcases the technical skills of our undergraduate team and the potential for technology to revolutionize healthcare. As future professionals committed to excellence and innovation, we aim to contribute to the ongoing progress at the intersection of technology and medicine, ultimately leading to positive impacts on healthcare outcomes.

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