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Robust Brain Tumor Segmentation in MRI Using Spatial FCM with Bias Field Correction and GLCM-Based Texture Analysis

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Abstract-*An improved and stronger automatic system for identifying brain tumors in MRI scans was created by making changes to the traditional Fuzzy C-Means (FCM) clustering method used before. While basic FCM works well for handling uncertain pixel classifications, it is very sensitive to noise, uneven image brightness, and doesn't consider the spatial relationships between pixels, which can lead to incorrect tumor outlines. To fix these problems, the new method uses advanced steps before processing the images, such as removing skull parts, reducing noise, improving contrast, and correcting for brightness inconsistencies. Then, an enhanced version of the Spatial Fuzzy C-Means (SFCM) algorithm is used, which takes into account the surrounding area during the clustering to better distinguish tissues and keep the structure clear. Also, texture features are extracted using Gray Level Co-occurrence Matrix (GLCM) parameters and special post-processing techniques are applied to remove incorrect areas and sharpen the tumor edges. The final segmented tumor area is clearly shown on the original MRI image with detailed boundary information. Tests show that this new method is more accurate, sensitive, and reliable than older FCM methods, which helps reduce the need for manual work and assists doctors in early diagnosis and better treatment planning.*

Key Words: Spatial Fuzzy C-Means (SFCM), Magnetic Resonance Imaging (MRI), Image Preprocessing Techniques, Brain Tumor Segmentation, Bias Field Correction (N4 Algorithm)

1. INTRODUCTION

Brain tumors are among the most critical and life-threatening neurological disorders, making early detection and accurate segmentation essential for effective diagnosis and treatment planning. Traditionally, tumor identification relies on manual inspection of Magnetic Resonance Imaging (MRI) scans by radiologists. However, this process is time-consuming, prone to inter-observer variability, and highly dependent on expert knowledge, which may lead to inconsistent segmentation results [2], [3].

With advancements in medical imaging, MRI has become a powerful tool for detecting brain abnormalities due to its high spatial resolution and soft tissue contrast. Several computer-aided diagnosis systems have been developed to assist clinicians in tumor detection and segmentation. Conventional methods, including thresholding and clustering techniques, have been widely used; however, they often struggle with challenges such as noise, intensity inhomogeneity, and unclear tumor boundaries, limiting their overall performance [4].

In recent years, intelligent computational approaches, particularly fuzzy clustering techniques such as Fuzzy C-Means (FCM) and its variants, have gained significant attention in brain tumor segmentation. These methods effectively handle uncertainty in pixel classification and have shown promising results in segmenting complex tumor regions [1], [5]. Moreover, advanced techniques such as Spatial FCM (SFCM), hybrid models integrating deep features, and bias field correction methods (e.g., N4 correction) have been introduced to improve segmentation accuracy and robustness by incorporating spatial and intensity information [6], [7].

Additionally, feature extraction methods such as Gray Level Co-occurrence Matrix (GLCM) and enhanced preprocessing techniques, including skull stripping, noise filtering, and contrast enhancement, have further improved segmentation quality by capturing texture and structural details of tumor regions [5], [8]. Recent developments also include intuitionistic fuzzy models and hybrid segmentation frameworks that combine clustering with contour-based refinement, providing more precise tumor boundary detection [9], [10].

Despite these advancements, achieving high segmentation accuracy while maintaining robustness against noise and intensity variations remains a challenging task. Therefore, there is a need for an improved and automated framework that integrates advanced pre-processing, enhanced spatial fuzzy clustering, and effective post-processing techniques to ensure accurate and reliable brain tumor segmentation.

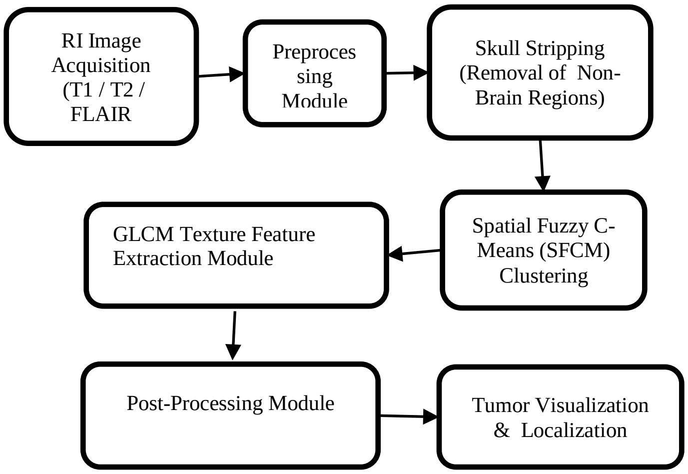

Fig 1: Architecture diagram

2. METHODOLOGIES

The system is made to give a good and automatic way to find brain tumors in MRI images, and it fixes the problems with old methods. It starts with better ways to prepare the MRI data so the images are cleaner and easier to work with. First, it removes parts of the image that are not brain tissue, like the skull and other structures, so the algorithm can focus only on the brain. This makes the process faster and more efficient. Then, it cleans up the image to get rid of unwanted noise and problems while keeping the important edges and details clear. It also makes the image brighter to show tumors better by increasing the difference between healthy and unhealthy tissues. To fix a common issue in MRI images, called intensity inhomogeneity, the system uses N4 bias field correction. This fixes differences in brightness that happen because of the way the images are taken, making sure the same tissues have similar brightness across the image. This helps clustering algorithms work better because they get more reliable information. Once the images are ready, the system uses a clustering method called Spatial Fuzzy C-Means (SFCM) to separate different parts of the brain. Unlike the usual FCM method, SFCM looks at neighboring pixels to improve accuracy, which helps keep the edges of tissue regions clear and reduces errors from noise or mistakes. It also uses a tool called Gray Level Co-occurrence Matrix (GLCM) to look at how pixels relate to each other and find texture features like contrast and energy, which help tell normal tissue apart from tumors. Combining these methods makes the segmentation more accurate and reliable. After that, some shape-based tools are used to clean up the results by removing small areas that are not part of the tumor, filling in gaps, and smoothing the edges. This makes the final image clearer and more accurate. Lastly, the system shows the segmented tumor on top of the original MRI image, making it easier for doctors to see where the tumor is. This helps with diagnosing, planning treatment, and studying the tumor more closely. The system uses a mix of advanced steps like preparing images, spatial clustering, texture checking, and shape fixing to give a fast, accurate, and reliable way to find brain tumors.

2.1 MRI Image Acquisition Module

The MRI Image Acquisition Module is the first stage of the brain tumour segmentation system, responsible for collecting MRI images from scanners or public datasets. It supports multiple modalities such as T1, T2, and FLAIR, which provide detailed information about brain structures and abnormalities. The module standardizes images by ensuring uniform resolution, format, and gray scale intensity representation for consistent processing. It converts raw MRI data into structured digital image matrices for computational analysis and stores them in an organized database along with relevant metadata. This enables efficient data management, retrieval, and scalability. Overall, the module provides high-quality and standardized input data, forming the foundation for accurate pre-processing and tumor segmentation.

The module also ensures data quality by minimizing inconsistencies that may arise during image acquisition, such as variations in intensity, noise, or resolution differences across different scanners. By maintaining standardized inputs, it improves the reliability of subsequent pre-processing and segmentation stages, leading to more accurate tumor detection. Furthermore, the availability of well-organized MRI datasets enables efficient training and testing of segmentation models. This supports the development of robust and scalable systems that can handle large volumes of medical data, ultimately assisting clinicians in faster diagnosis and improved treatment planning.

2.2 Pre-processing & Intensity Normalization Module

The Pre-processing and Intensity Normalization Module enhances MRI image quality before segmentation by removing noise, correcting intensity variations, and improving clarity. Adaptive filtering is used to reduce noise while preserving important structural details, and contrast enhancement improves the visibility of tumor regions. The module also applies N4 bias field correction to eliminate intensity inhomogeneity and ensures uniform tissue representation. Additionally, intensity normalization standardizes pixel values across different MRI scans, improving consistency and model performance. Overall, this module prepares clean, high-quality images, enabling more accurate and reliable tumor segmentation. This module plays a vital role in reducing artifacts and inconsistencies that may affect the accuracy of clustering algorithms. By enhancing image quality and maintaining structural integrity, it ensures that important tumor features are preserved for further analysis. Furthermore, pre-processing improves the robustness and generalization of the system across different datasets. It provides a strong foundation for advanced techniques like spatial clustering and feature extraction, ultimately leading to more precise tumor detection and boundary identification.

2.3 Skull Stripping Module

The Skull Stripping Module is an essential pre-processing step that removes non-brain tissues such as the skull, scalp, fat, and background from MRI images. This helps eliminate irrelevant information that could interfere with accurate tumor segmentation, ensuring that only the brain region is analyzed. By isolating the region of interest, the module improves the reliability and precision of tumor detection.

The module uses techniques such as morphological operations and intensity-based thresholding to separate brain tissues from non-brain regions. Operations like erosion, dilation, opening, and closing help refine the brain mask, while thresholding distinguishes tissues based on intensity differences. These combined methods produce a clean and accurate representation of the brain region. By removing unwanted structures, the module reduces false positives that may occur due to skull edges or background artifacts. It ensures that segmentation algorithms focus only on meaningful brain data, thereby improving detection specificity and accuracy.

Additionally, skull stripping reduces computational complexity by limiting processing to a smaller, relevant area. This enhances efficiency, speeds up processing time, and improves clustering performance, especially when handling large datasets. Importantly, the module preserves essential brain structures while removing non-brain tissues, maintaining anatomical integrity for accurate tumor localization and boundary detection. Overall, it plays a vital role in improving segmentation accuracy, efficiency, and reliability by providing clean and focused input for further processing.

2.4 Spatial Fuzzy C-Means (SFCM) Segmentation Module

The Spatial Fuzzy C-Means (SFCM) Segmentation Module is an advanced clustering technique that improves traditional Fuzzy C-Means (FCM) by incorporating spatial neighborhood information into the segmentation process. Unlike conventional FCM, which classifies pixels based only on intensity, SFCM considers both pixel intensity and surrounding pixel characteristics, making it more suitable for MRI images where neighboring pixels often belong to the same tissue. In this module, the MRI image is divided into clusters representing tumor and non-tumor regions. Each pixel is assigned fuzzy membership values based on intensity similarity and spatial proximity, ensuring that classification is influenced by neighboring pixels. This approach reduces the chances of misclassification, especially for noisy or isolated pixels, leading to more reliable segmentation results. A key advantage of SFCM is its ability to reduce noise sensitivity. By enforcing neighborhood consistency, the algorithm smooths out intensity variations and prevents incorrect classification caused by noise. This is particularly useful in MRI images, where noise and intensity fluctuations are common.

The module also preserves spatial continuity of brain tissues by encouraging similar classification among neighboring pixels. This results in more coherent and realistic segmentation, maintaining the natural structure of brain tissues and improving tumor boundary representation. Additionally, the fuzzy nature of SFCM allows each pixel to belong to multiple clusters with varying degrees of membership. This is important in medical imaging, where tumor boundaries are often unclear. It helps in accurately capturing uncertainty and improves the detection of complex tumor regions. Overall, the SFCM module produces smoother, more accurate, and continuous segmentation outputs compared to traditional methods. By combining intensity and spatial information, it enhances boundary detection, reduces noise effects, and provides a robust framework for precise brain tumor segmentation.

2.5 GLCM-Based Texture Feature Extraction Module

The GLCM-Based Texture Feature Extraction Module analyzes texture properties of MRI images to improve the differentiation between tumor and normal tissues. Since intensity values alone are often insufficient, the module uses the Gray-Level Co-occurrence Matrix (GLCM) to capture spatial relationships between pixel intensities, providing deeper insight into tissue patterns. GLCM computes important texture features such as contrast, homogeneity, energy, correlation, and entropy. These features help identify variations in texture, where tumor regions typically appear more irregular and heterogeneous compared to normal brain tissues. This allows for better highlighting of tumor boundaries and structural differences. By incorporating texture analysis, the module enhances the system's ability to accurately distinguish tumor regions from healthy tissues. It captures subtle variations that are not detectable through intensity-based methods, leading to improved segmentation precision.

Another major advantage is the reduction of false positives. Regions with similar intensity but different textures can be correctly classified, improving the reliability of tumor detection and minimizing incorrect segmentation results. Additionally, the extracted features strengthen the classification process by providing more descriptive information about tissue characteristics. This supports better decision-making and improves the robustness of the segmentation system. Overall, the module enables refined tumor identification by analyzing detailed texture patterns, helping to distinguish different tumor regions such as active areas, necrosis, and edema. This improves accuracy, reliability, and clinical usefulness of the brain tumor segmentation system.

2.6 Post-Processing & Boundary Refinement Module

The Post-Processing and Boundary Refinement Module improves the quality and accuracy of segmented tumor regions by removing imperfections such as noise, small isolated regions, and irregular boundaries. After initial segmentation, this module ensures that the output is clean, smooth, and clinically meaningful. Morphological operations like erosion and dilation are applied to refine the segmentation. Erosion removes small unwanted regions and noise, while dilation fills gaps and expands tumor areas. Combined operations such as opening and closing help produce continuous and well-defined tumor regions.

The module also eliminates false positives by removing small isolated regions that do not belong to the tumor. Additionally, it fills internal gaps and discontinuities within the tumor area, ensuring a complete and coherent segmentation. Boundary refinement is performed to smooth and correct irregular or jagged tumor edges, improving the accuracy of tumor shape and localization. This ensures that the segmented boundaries closely match the actual anatomical structure. Furthermore, the module maintains structural consistency while enhancing visual clarity, making the results easier to interpret. Overall, it produces accurate, smooth, and reliable tumor segmentation outputs that support effective diagnosis and treatment planning.

2.7 Tumor Visualization & Localization Module

The Tumor Visualization and Localization Module is the final stage of the system, responsible for presenting the segmented tumor in a clear and clinically meaningful way. It extracts the refined tumor boundaries and accurately maps them onto the original MRI image, ensuring that the results are easily interpretable by medical professionals. The module overlays the detected tumor region on the original MRI scan using highlighting techniques, allowing simultaneous visualization of brain structures and tumor location. This improves clarity and helps in identifying the exact position, shape, and extent of the tumor.

It also enhances interpretation by clearly marking tumor regions, making it easier to detect even small or complex abnormalities. This visual representation supports radiologists in analyzing tumor characteristics and comparing changes over time. Additionally, the module enables quantitative analysis by calculating important parameters such as tumor size, area, and volume. These measurements assist in evaluating disease severity and tracking tumor progression. Overall, this module provides accurate visualization, precise localization, and meaningful insights, supporting effective diagnosis and treatment planning while delivering reliable final output for clinical use.

RESULT & DISCUSSION

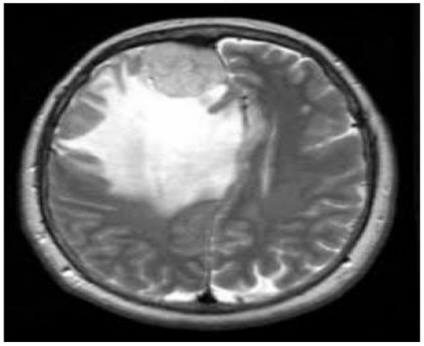

Fig.2. Input image

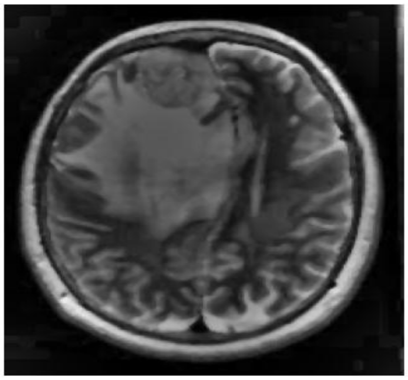

Fig.3. Pre-processing image

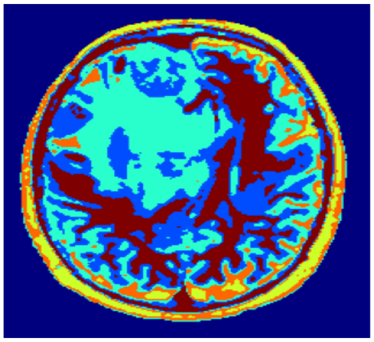

Fig.4. SFCM Clustering image

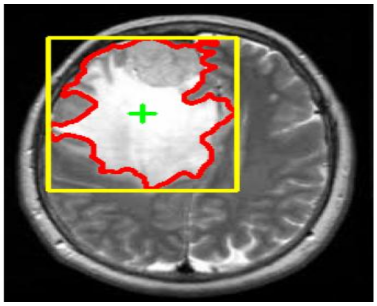

Fig.5. Tumor Location

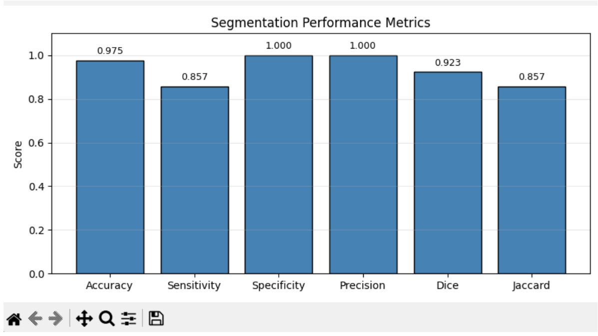

Fig.6. Performance Metrics

Fig. 2 shows the original MRI brain image, which has noise, varying brightness, and other unwanted features that make it hard to see the tumor clearly. Fig. 3 shows the preprocessing step, where methods like removing noise, adjusting brightness, and improving contrast are used to make the image better. These steps make important parts of the brain easier to see and get the image ready for proper analysis. Fig. 4 shows the result of the SFCM (Spatial Fuzzy C-Means) clustering, where the image is divided into different areas based on how bright each pixel is and where it is located. This helps separate the tumor area from healthy tissue by grouping similar pixels together. Fig. 5 shows where the tumor was found, clearly marking the affected part, which helps in accurate identification and study. The results in Fig. 6 show how well the method works, with good accuracy, sensitivity, and specificity. All together, these results show that combining preprocessing with SFCM clustering helps detect tumors more accurately and supports doctors in making reliable diagnoses.

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