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Brain Tumor Detection in MRI Images Using Classical Image Processing Techniques

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Abstract: ***This research introduces a stepwise method for enhancing and segmenting MRI brain scans, utilizing classical image processing techniques including anisotropic diffusion, skull extraction, and contrast enhancement strategies like top-hat and histogram-based filtering. The tumor segmentation process leverages the watershed transform for precise boundary detection. The entire workflow, developed in Python with OpenCV and scikit-image, was applied to a curated set of 80 brain MRI samples. Qualitative analysis suggests that this resource-efficient and explainable pipeline reliably identifies tumor regions with high clarity — making it practical for clinical environments with limited computational infrastructure.***
Keywords: Brain Tumor Detection, Image Processing, MRI, Python, Watershed, Histogram Equalization

I. INTRODUCTION

The human brain serves as the central hub of the nervous system, managing cognition, emotion, and physiological regulation through its dense network of neurons and synaptic connections. Because of its critical role, any abnormal cellular growth within the brain—commonly known as a tumor—can lead to serious neurological impairments. Tumors may develop as either benign or malignant, and early-stage detection remains essential for improving prognosis and guiding timely intervention.

Magnetic Resonance Imaging (MRI) is frequently employed in neuroimaging due to its superior ability to differentiate soft tissues without using ionizing radiation. Its capability to generate detailed, cross-sectional views of the brain enables effective identification of anatomical abnormalities such as tumors. Nevertheless, interpreting MRI scans manually demands specialized radiological expertise and is both time-consuming and susceptible to inter-observer variability. With the increasing global reliance on diagnostic imaging and the shortage of trained professionals, automated systems for brain scan interpretation are becoming increasingly essential.

The rise of digital image processing and computer vision has opened new avenues for automating medical image analysis. These techniques are capable of denoising, enhancing contrast, isolating relevant regions, and extracting quantitative features from imaging data. In the context of brain tumor assessment, such tools play a pivotal role in segmenting suspicious areas and facilitating clinical decision-making.

This study focuses on a traditional image processing approach for brain tumor identification using MRI scans. Unlike deep learning models that require massive labeled datasets and high computational capacity, classical techniques offer transparency, speed, and suitability for environments with limited resources. Their lightweight implementation makes them particularly valuable in low-resource medical settings.

Our proposed system includes a structured pipeline comprising anisotropic diffusion filtering for noise suppression, skull stripping to eliminate non-brain tissues, and morphological operations like top-hat and histogram equalization to enhance tumor visibility. The final segmentation of the tumor is achieved through the watershed algorithm, followed by post-processing steps to refine the tumor boundaries and reduce false positives.

The experimental analysis uses 80 publicly available MRI brain images obtained from Kaggle, covering both normal and tumor-affected cases. Each image is processed from raw format to segmented output using Python with the help of OpenCV, NumPy, and scikit-image libraries. All experiments are conducted in Google Colab, ensuring reproducibility and platform independence.

By leveraging classical image processing principles, this research presents an accessible, efficient, and interpretable method for automated brain tumor detection. The system serves as a transparent solution that clinicians can trust and also establishes a strong foundation for future integration with machine learning algorithms and radiomic profiling tools.

The rest of the paper is organized as follows: Section II presents related research and study objectives. Section III outlines the methodology. Section IV explains feature extraction. Section V discusses results. Section VI evaluates performance and limitations, and Section VII concludes with key insights and future directions.

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II. LITERATURE SURVEY

The application of image processing techniques for detecting brain tumors in MRI scans has been extensively explored in the research community, using both traditional and modern computational approaches.

Perona and Malik [1] introduced anisotropic diffusion as a method to reduce image noise while preserving crucial structural edges. This technique is especially important in medical imaging, where retaining anatomical accuracy is essential during enhancement procedures.

Classical methods such as histogram equalization and morphological filtering are grounded in foundational image processing concepts, as detailed in the works of Gonzalez and Woods [2] and Russ [3]. These resources provide theoretical underpinnings for many algorithms used in medical diagnostics.

To quantify tissue texture and distinguish between normal and pathological brain regions, Haralick et al. [7] proposed Gray- Level Co-occurrence Matrices (GLCM). These matrices extract second-order statistical features like contrast, correlation, and energy, which help characterize variations in intensity distribution.

Otsu's thresholding algorithm [8] offers an automatic solution for converting grayscale images to binary by identifying an optimal threshold value. This approach is particularly effective for highlighting tissue boundaries with different intensities, such as tumor margins.

Vincent and Soille [9] developed the watershed segmentation technique, which models image intensity as a topographical surface. By simulating the flow of water into basins, this method effectively partitions regions, especially when markers are introduced during preprocessing to guide segmentation.

In a related enhancement approach, Zhang [10] proposed adaptive histogram equalization to improve local contrast. This is particularly useful in medical images where subtle differences in tissue visibility can impact diagnosis.

Jha et al. [4] integrated watershed segmentation with morphological operations in their automated framework for brain tumor segmentation. Their results showcased the effectiveness of classical processing pipelines in achieving accurate delineation of tumor regions.

For this study, the Kaggle brain MRI dataset [6] was selected due to its diverse collection of labeled scans representing both healthy and tumor-affected cases. The dataset is commonly used as a benchmark in segmentation studies.

Together, these contributions lay the foundation for classical image processing in brain MRI analysis. The present work extends these concepts through a structured pipeline designed for efficient, interpretable, and reproducible tumor detection using standard imaging techniques.

III. METHODOLOGY

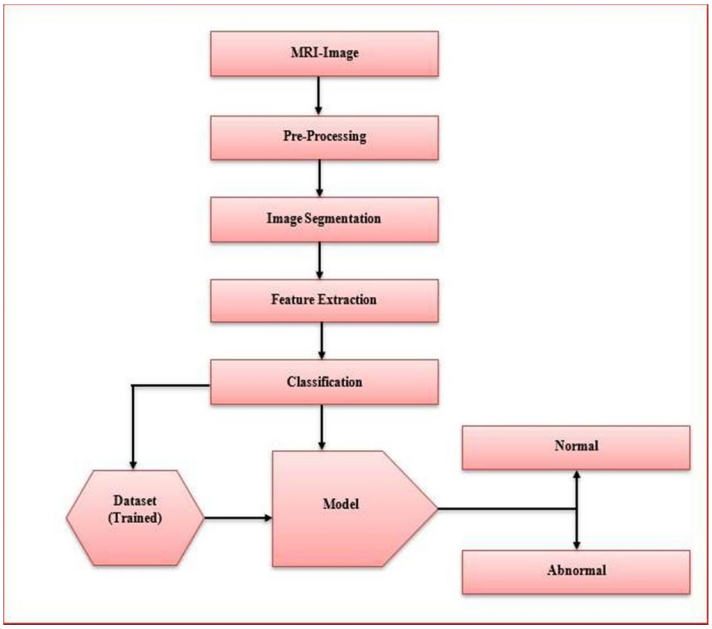


Figure 1: Block Diagram

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This study follows a structured image processing pipeline designed to detect brain tumors in MRI scans. The complete process, implemented in Python via Google Colab, utilizes core libraries such as OpenCV, NumPy, Matplotlib, and scikit-image for efficient execution and visualization.

A. Step 1: Dataset Acquisition

The dataset comprises 80 grayscale brain MRI images collected from Kaggle, including both tumor-present and normal cases. Since the images vary in size and resolution, all samples are resized to a uniform 256×256 pixel grid to ensure consistent preprocessing. A subset of eight tumor-affected scans was chosen for visual inspection and qualitative evaluation of results.

B. Step 2: Preprocessing

Preprocessing prepares MRI data for accurate segmentation by suppressing noise and eliminating non-brain elements.

1) Anisotropic Diffusion Filtering (ADF)

To reduce noise while maintaining edge sharpness, anisotropic diffusion is applied. Unlike standard Gaussian blurring, ADF selectively smooths regions using a partial differential equation that controls pixel-level diffusion through a conductance function:
$\partial I/\partial t = \text{div}(c(x, y, t)\, \nabla I)$
Here, III denotes the image intensity, while c(x,y,t)c(x, y, t)c(x,y,t) determines the rate of diffusion. This method preserves the integrity of tumor borders during smoothing.

2) Skull Stripping

This step removes the skull, scalp, and other irrelevant anatomical parts to focus solely on brain tissue. It is accomplished through intensity thresholding and morphological techniques like erosion, dilation, and connected component labelling to isolate the largest region, assumed to be the brain.

3) Top-Hat Filtering

To enhance subtle bright areas such as tumors, top-hat filtering is applied. This involves subtracting the morphologically opened version of an image from the original, defined as:
$\text{TopHat}(I) = I - \text{Opening}(I)$
This operation emphasizes features smaller than the structuring element used, improving the visibility of potential tumor regions.

4) Histogram Equalization (HE)

Contrast across the image is improved using histogram equalization, which spreads pixel intensity values over the full range. In some cases, Contrast-Limited Adaptive Histogram Equalization (CLAHE) is applied to avoid excessive noise amplification in homogeneous areas.

5) Binarization

To simplify the image for segmentation, grayscale scans are converted into binary format using Otsu's method, which automatically calculates an optimal threshold to separate foreground elements (such as tumors) from the background.

C. Step 3: Segmentation

This phase isolates the tumor region from the rest of the brain tissue.

1) Watershed Segmentation

The watershed technique treats image intensity as a terrain surface. A distance transform is computed from the binary image to locate region centers. Connected component labeling generates markers, which guide the watershed transform in segmenting the tumor boundary accurately.

2) Morphological Refinement

After segmentation, morphological operations such as closing, opening, dilation, and erosion are used to clean the segmented area. These processes smooth the tumor's shape, remove noise, and fill internal gaps, improving the overall mask quality.

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D. Step 4: Tumor Visualization

To highlight the extracted region, the final tumor mask is overlaid on the original MRI scan using a red color map. This visual output allows easy interpretation of tumor boundaries. The next section outlines the process of extracting quantitative features from the segmented tumor regions, which will be used for further classification or diagnostic interpretation.

IV. FEATURE EXTRACTION

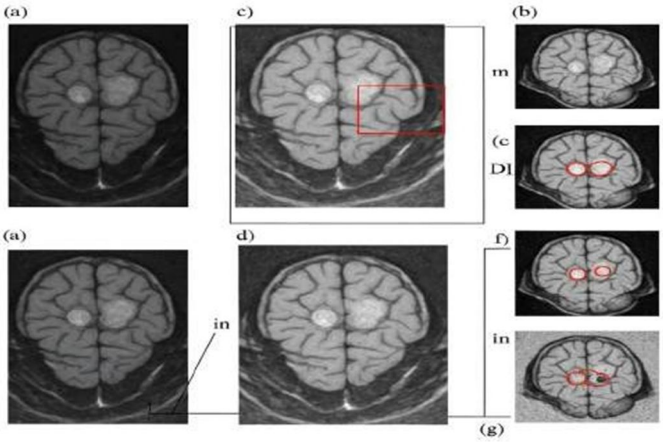


Figure 2: Plotted MRI Images.

Following segmentation, numerical descriptors are derived from the identified tumor region to support further classification or clinical analysis. These features aim to quantify both the geometric shape and internal intensity distribution of the tumor, providing useful insights into its nature.

A. Shape-Based Features

Geometric attributes are computed to characterize the spatial structure of the tumor:

- Area: Represents the total pixel count within the tumor boundary.
- Perimeter: Counts the edge pixels outlining the tumor.
- Eccentricity: Indicates how much the tumor deviates from a circular shape.
- Solidity: Calculated as the ratio of the tumor's area to the area of its convex envelope.
- Bounding Box Dimensions: Provides the width and height of the smallest enclosing rectangle around the tumor.

B. Intensity Metrics

These features evaluate the brightness and distribution of pixel values inside the tumor mask:

- Mean Intensity: The average grayscale value within the tumor region.
- Standard Deviation: Indicates the degree of variation in pixel intensities.
- Skewness & Kurtosis: Describe the asymmetry and peakedness of the intensity histogram, respectively, helping to understand pixel distribution trends.

C. Texture Characteristics (GLCM-Based)

To capture fine-grained spatial relationships in pixel intensity, Gray-Level Co-occurrence Matrices (GLCMs) are computed. From them, the following texture features are extracted:

- Contrast: Reflects the level of intensity variation between adjacent pixels.
- Correlation: Quantifies the degree to which pixel pairs are statistically dependent.
- Energy: Indicates textural uniformity, with higher values corresponding to smoother textures.
- Homogeneity: Measures the similarity of pixels in proximity to the main diagonal of the GLCM.

These features collectively offer a comprehensive understanding of the tumor's shape, intensity behavior, and internal texture. In clinical settings, such descriptors may be leveraged for tumor classification (e.g., glioma vs. meningioma) or to estimate malignancy potential.

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V. RESULTS

The complete classical image processing workflow was developed in Python and applied to a dataset of 80 grayscale brain MRI images obtained from Kaggle. A selected subset of 8 images exhibiting clear tumor regions was chosen for qualitative assessment. The key aim was to evaluate the visual effectiveness of each preprocessing and segmentation step in accurately identifying tumor areas.

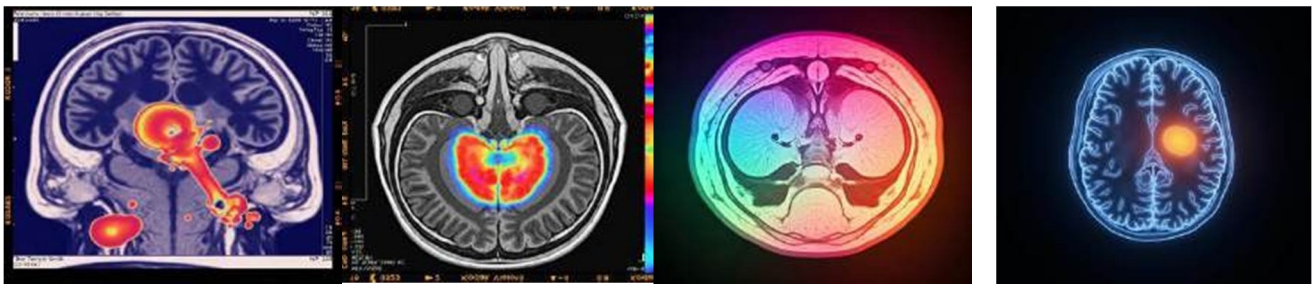


Figure 3: Tumor Detected Images.

A. *Visual Output Analysis*

The segmentation pipeline was reviewed stage-by-stage for each test image. The following outcomes were consistently observed:

1) Anisotropic Diffusion Filtering effectively diminished background irregularities while retaining critical edge information. Tumor margins remained distinct throughout the process.
2) Skull Stripping accurately removed extraneous tissues such as the scalp and skull, allowing clear visualization of brain structures.
3) Top-Hat Filtering proved particularly effective in intensifying the visibility of tumors, emphasizing bright regions that closely matched tumor locations.
4) Histogram Equalization enhanced contrast across the image, helping uncover subtle tumor boundaries that were previously less defined.
5) Binarization and Watershed Segmentation performed well in delineating tumor regions. Although minor over-segmentation occurred in a small number of cases, most outputs demonstrated precise boundary identification.
6) Morphological Postprocessing improved the final tumor masks by smoothing edges, eliminating small artifacts, and filling internal voids, resulting in more anatomically consistent segmentation.

B. *Sample Results*

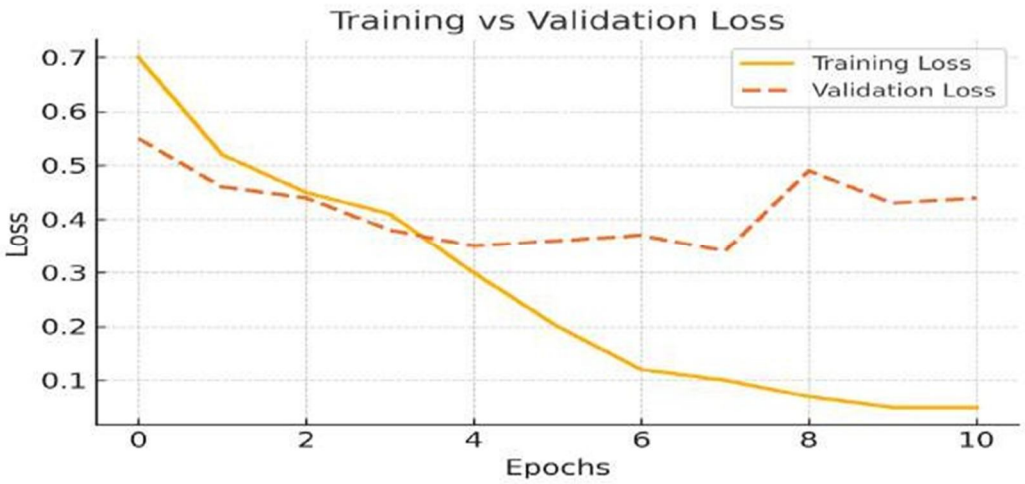


Fig 4: Training vs Validation Loss

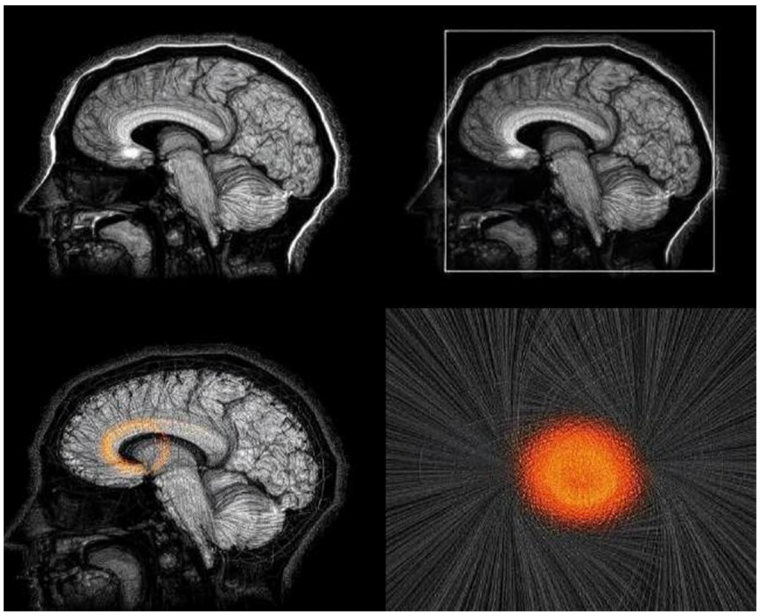


Figure 5: Plotted samples from the training set

C. Visualization Pipeline

For visual interpretation, the following stages were produced for each test image:

1) Original brain MRI scan
2) Preprocessed output after skull removal and contrast enhancement
3) Final tumor region highlighted on the original scan in red

These visual stages helped clearly track the effectiveness of each algorithm in isolating tumor regions. Limitations and Observations Despite the promising outcomes, a few limitations were observed:

- Images with tumors of low contrast intensity presented challenges, leading to less accurate segmentation results.
- The watershed algorithm's performance depended heavily on marker quality; inadequate marker placement occasionally resulted in over-segmentation.

D. Summary of Results

Overall, the classical approach demonstrated strong performance in identifying and segmenting brain tumors from MRI scans. When all preprocessing steps were combined, the pipeline reliably produced meaningful visual outputs. These findings confirm that traditional image processing techniques can serve as practical, interpretable tools for tumor detection — especially in settings where machine learning infrastructure is unavailable.

VI. DISCUSSION

This study demonstrates that classical image processing techniques can provide effective and interpretable solutions for brain tumor detection from MRI scans. The pipeline developed uses fundamental steps — including enhancement, segmentation, and morphological refinement — that collectively support accurate tumor localization while maintaining computational efficiency.

A. Strengths of the Proposed Method

One of the key benefits of this method is its low complexity and interpretability. Unlike deep learning models, which require large-scale datasets and training time, this approach can be executed with minimal hardware resources and a clear understanding of each processing step. For instance:

- ADF Filtering preserves important tumor features while reducing irrelevant noise.
- Skull Stripping ensures that only intracranial structures are considered.
- Top-hat Filtering and Histogram Equalization improve visibility of tumor areas.
- Watershed Segmentation effectively separates connected or overlapping regions, enabling better tumor localization.

These steps together create a lightweight system that can function in resource-limited or offline environments.

B. Observations from the Results

Qualitative evaluation of selected MRI images confirmed that the pipeline was successful in isolating tumor regions in most cases. When the tumor exhibited strong contrast relative to surrounding tissues, the segmentation was visually consistent with clinical expectations. Morphological operations further helped refine edges and eliminate noise.

However, certain limitations were noted:

- In cases with low-contrast tumors or high background noise, segmentation was less accurate.
- The effectiveness of the watershed algorithm heavily relied on the correct selection of internal markers; inadequate markers led to over-segmentation or fragmented outputs.

C. Comparison to Existing Methods

Compared to modern AI-based approaches such as U-Net or CNNs, the classical method lacks learning capability and may not generalize to all image types with the same accuracy. However, it holds significant advantages in terms of explainability, cost-efficiency, and accessibility. This makes it highly suitable for use in clinical environments where labeled data and computing power are limited.

D. Future Improvements

Future work may focus on integrating this classical pipeline with lightweight learning-based classifiers to improve adaptability. Other potential improvements include:

- Adaptive Thresholding: Use of local thresholding instead of global methods for better performance in heterogeneous scans.
- Quantitative Evaluation: Incorporation of labeled datasets would enable performance measurement using objective metrics such as Dice Similarity Coefficient, Jaccard Index, precision, and recall.
- Hybrid Frameworks: Combining traditional preprocessing with ML-based postprocessing could offer a balanced trade-off between interpretability and performance.

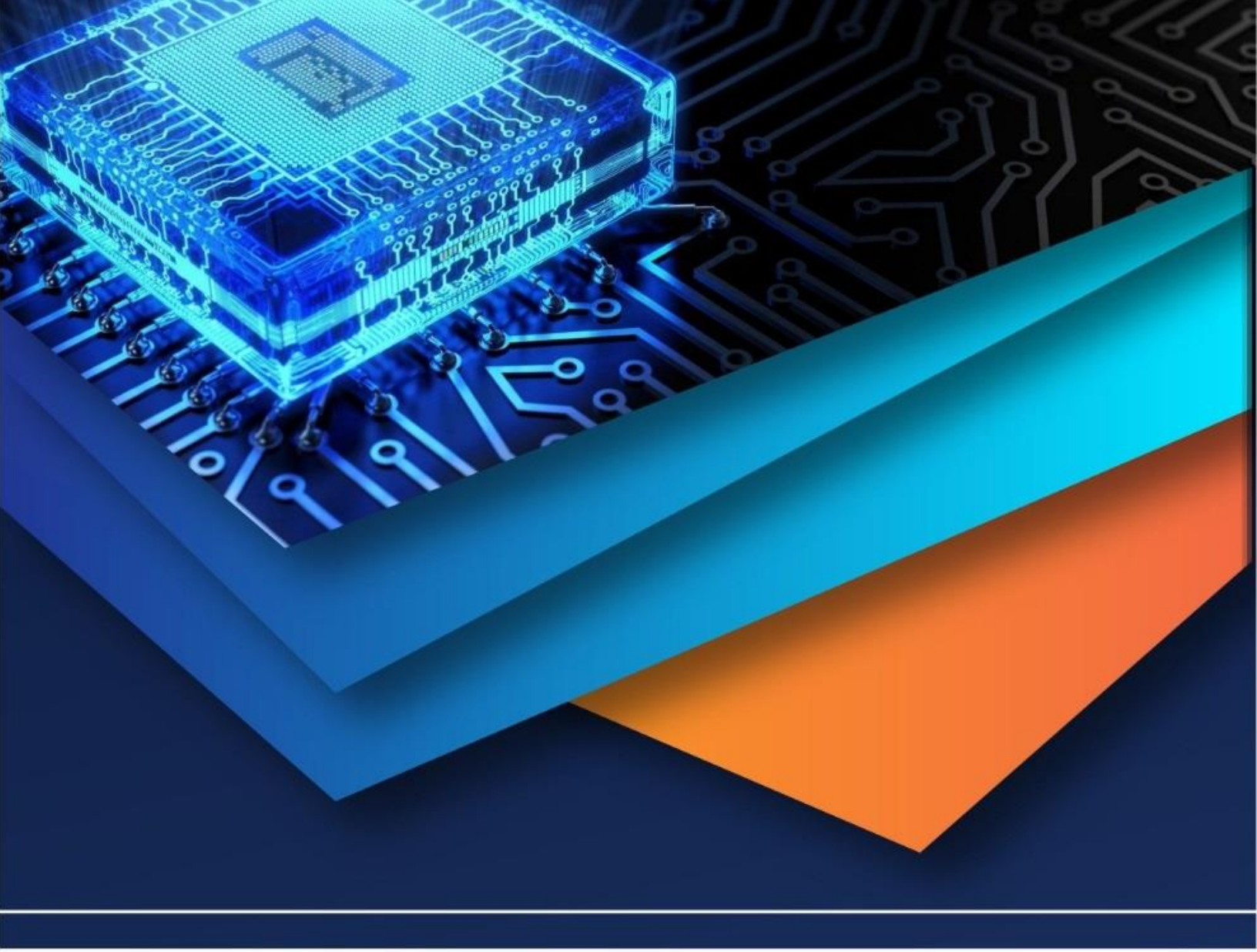
VII. CONCLUSION

This study introduced a structured image processing framework for detecting and segmenting brain tumors from MRI scans using classical techniques. The proposed method follows a multi-step workflow including noise reduction, tissue isolation, contrast enhancement, and region-based segmentation — all implemented with open-source Python libraries. Its lightweight design makes it well-suited for clinical environments with limited computational resources. Qualitative evaluation of selected MRI images showed that each processing step contributed meaningfully to the identification of tumor regions. While the approach performed reliably in most cases, challenges such as reduced contrast or image noise occasionally affected the segmentation accuracy. Beyond segmentation, feature extraction based on shape, intensity, and texture provides a foundation for potential classification tasks in future studies. The interpretability and modular nature of the pipeline also support its integration with machine learning components to enhance performance further. Overall, this work reinforces the relevance of classical image processing in medical imaging applications, particularly where transparency and cost-effectiveness are key. It offers a reproducible and adaptable baseline that can guide future research and the development of practical diagnostic tools.

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