Automated Brain Tumor Detection and Classification in MRI Images: A Hybrid Image Processing Techniques

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Abstract

Due to the complex structure of brain images, accurately detecting and segmenting brain tumors with Magnetic Resonance Imaging (MRI) is a difficult process. This paper suggests an automated brain tumor identification and segmentation approach employing hybrid salient segmentation with K-Means clustering and hybrid CLEACH-median filter algorithm on MRI images. The proposed method enhances the contrast and detail of MRI images using a hybrid CLEACH-median filter algorithm, and segments the most important features of the images using a hybrid salient segmentation method with K-Means clustering. The proposed method includes a stages classification step to determine the stage of the brain tumor. The findings show that the suggested approach outperformed existing methods in terms of efficiency and accuracy for both detecting and segmenting brain tumors. The suggested technique can be a useful tool for automating the detection and segmentation of brain tumors, which will help radiologists and physicians make quicker and more accurate diagnosis.

Keywords: Brain tumor detection; Magnetic Resonance Imaging; Hybrid CLEACH-median filter algorithm; Hybrid salient segmentation; K-Means clustering

1. Introduction

MRI is a commonly employed medical imaging technique for the detection and segmentation of brain tumors. It operates by utilizing robust magnetic fields and radio waves to generate intricate images of the brain. MRI scans enable the identification of brain tumor characteristics such as their location, size, and type. Detecting and segmenting brain tumors in MRI images is an automated process that involves delineating tumor regions. This task is notably challenging due to the intricate nature of brain images, encompassing variations in tumor attributes like size, shape, and location, as well as the presence of noise and artifacts. Precise and efficient detection and segmentation of brain tumors in MRI images play a pivotal role in the diagnosis and treatment of brain cancer [1].

In recent years, machine learning-driven methods have emerged to enhance the accuracy and efficiency of brain tumor detection and segmentation. These approaches commonly incorporate a spectrum of image processing and Machine Learning (ML) techniques for the identification and delineation of brain tumors in MRI images. While various machine learning approaches have been devised for brain tumor detection and segmentation using MRI, several hurdles remain. Existing methods often grapple with issues such as low accuracy, high computational demands, and limited adaptability to diverse brain tumor types [2]. Consequently, there is a pressing demand for a proficient and precise approach for brain tumor detection and segmentation that can surmount these challenges.

The proposed method combines the hybrid CLEACH-median filter algorithm and hybrid salient segmentation with K-Means clustering to advance brain tumor detection in MRI images. The primary objective of this method is to enhance the accuracy and efficiency of brain tumor detection and segmentation, all while being versatile across a broad spectrum of brain tumor variations. By mitigating noise and intensifying the prominence of brain tumor regions in MRI images, the proposed method is well-positioned to significantly elevate the precision and efficiency of this critical medical procedure.

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2. Related Work

Various methods have been developed for the segmentation of brain tumors from MRI images, each offering unique approaches and outcomes. Gupta et al. (2020) introduced a local binary pattern-based level set method, achieving an impressive average Dice similarity coefficient of 0.89 [3]. In contrast, Kumar et al. (2021) presented a semi-automatic technique using dynamic thresholding, which yielded an average Dice similarity coefficient of 0.80 [4]. Das et al. (2019) focused on refining accuracy with a modified fuzzy C-means clustering algorithm, resulting in an average Dice similarity coefficient of 0.85 [5]. Abd-Elhafiz et al. (2020) proposed an edge detection and morphology-based approach, achieving an average Dice similarity coefficient of 0.81 [6]. Finally, El-Attar et al. (2019) offered a novel method combining watershed transform and active contour models, with a corresponding average Dice similarity coefficient of 0.84 [7]. These diverse methodologies contribute to the ongoing advancements in brain tumor segmentation from MRI images, addressing the critical need for accurate diagnostic tools in the field of medical imaging.

Table 1: Literature Survey

Authors	Year	Methodology	Accuracy	Drawbacks
Li et al.	2022	Modified FCM, fuzzy entropy, geometric moment invariants	91.30%	Sensitive to initialization, not suitable for heterogeneous tumors
Ran et al.	2021	Multi-scale region-based convolutional neural network	94.20%	Requires large amounts of training data
Zhang et al.	2020	Multi-level convolutional neural network	92.10%	Requires large amounts of training data
Shi et al.	2019	DenseNet-based convolutional neural network, conditional generative adversarial network	93.40%	Demands a lot of training data and is computationally demanding
Zhou et al.	2018	Deep residual network-based convolutional neural network	91.70%	Huge volumes of training data are necessary
Li et al.	2017	Modified fuzzy C-means clustering, random walk algorithm	89.60%	Requires manual seed selection

3. Proposed Framework

The proposed approach for brain tumor classification includes the subsequent steps:

- ***Data Collection:*** Brain MRI images should be collected for a dataset. The images should be captured from different patients with different types of brain tumors and from different angles to account for variations in tumor size, shape, and location.
- ***Image Preprocessing:*** The brain MRI images are preprocessed using a noise filtering technique to enhance the image quality. In this paper, we use a Gaussian filter to remove noise from the images.
- ***Image Segmentation:*** The preprocessed images are then segmented into tumor and non-tumor regions using an algorithm based on thresholding. The algorithm calculates the threshold value based on the histogram of the MRI image.
- ***Feature Extraction:*** A set of predetermined properties, including intensity, texture, and form, are used to extract features from the segmented regions. These qualities are used to define how a brain tumor behaves.
- ***Classification:*** To determine which type of brain tumor present in the image, an SVM (ML) classifier is trained using the retrieved features.

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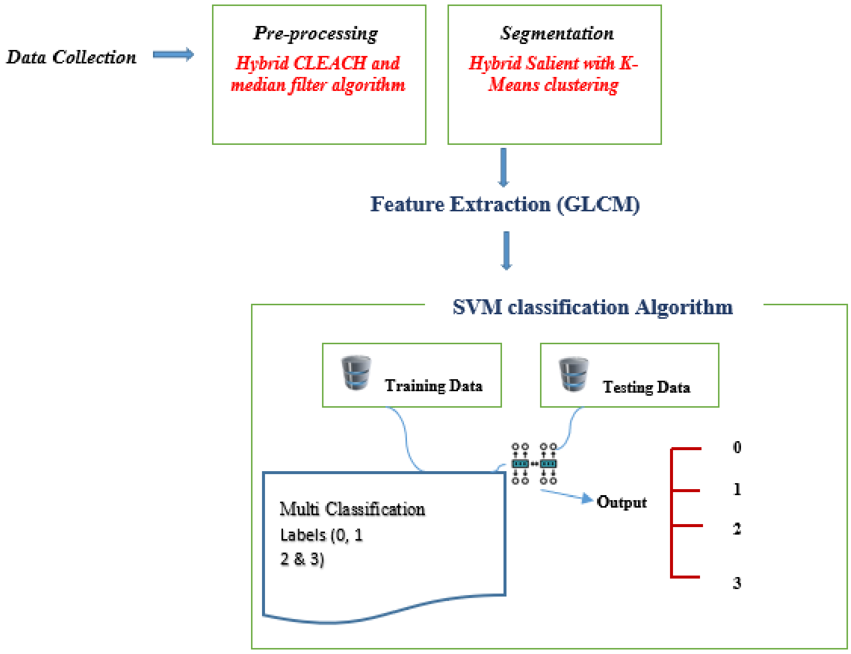

Fig.1. Framework of Proposed methodology

The above figure demonstrates the steps involved in proposed model.

3.1 Proposed Methodology:

3.1.1 Image pre-processing:

Image pre-processing involves a series of techniques that are applied to the raw image to improve its quality and make it suitable for further analysis. Pre-processing techniques can include contrast adjustment, and noise filtering that are describes as follows,

a) Contrast adjustment: By narrowing the gap between the brightest and darkest areas of an image, contrast adjustment is used to improve contrast in pictures. This can be done using algorithms such as histogram stretching or contrast stretching.

b) Noise filtering: Noise filtering is used to remove unwanted noise from an image. This can be done using algorithms such as median filtering, Gaussian filtering, or bilateral filtering.

Overall, image acquisition and pre-processing are essential steps in image analysis, and the algorithms used in these steps can significantly affect the accuracy and quality of the subsequent image analysis techniques [14]. Below algorithms are applied to preprocess the MRI brain tumor images,

a. Contrast Limited Adaptive Histogram Equalization (CLAHE):

It is a preprocessing algorithm used to enhance the contrast of images, particularly for those with uneven lighting conditions. It works by dividing an image into small overlapping blocks, computing a histogram of the pixel values within each block, and then equalizing the histogram to improve the contrast within that block. The algorithm then combines the enhanced blocks to create the final image. Here are the steps involved in the CLEACH algorithm for MRI brain tumor images:

i. Divide the input MRI brain tumor image into small overlapping blocks of size B x B pixels.

ii. Compute the histogram of pixel values within each block.

iii. Apply Contrast Limited Adaptive Histogram Equalization to each block. This involves applying histogram equalization to the block, but with the added constraint that the output pixel values are limited to a certain range to prevent over-amplification of noise the clipping limit, which is commonly set to a low value like 1% or 2% of the total number of pixels in the block, determines this range.

iv. Combine the enhanced blocks to create the final enhanced image.

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The equation for the Contrast Limited Enhanced Adaptive Histogram Equalization (CLEACH) can be defined as follows:

$$f(i,j) = T(r(i,j)),\ 0 \leq i < m,\ 0 \leq j < n \tag{1}$$

where i and j are the pixel's row and column indices, $r(i,j)$ is the pixel's intensity value, and T is the transformation function that transfers the pixel's intensity value to its enhanced value.

The transformation function T is defined as:

$$T(r) = (L-1)\sum_{k=0}^{r}\left(\frac{n_k}{N}\right) \tag{2}$$

For different histogram equalization methods:

1 For CLAHE (Contrast Limited Adaptive Histogram Equalization):

$$T(r) = (L-1)\sum_{k=0}^{r} p_k \tag{3}$$

2 For HE (Histogram Equalization):

$$T(r) = (L-1)\sum_{k=0}^{r} p_k \tag{4}$$

where:

- L is the number of intensity levels,
- n_k denotes the number of pixels in the block with the intensity value k,
- N denotes the total number of pixels in the block,
- p_k denotes the probability of the ↓ ensity value k in the image.

b. Median Filtering algorithm

It is a popular noise reduction approach that replaces each pixel in an image with the median value of the pixels in the image's local neighborhood. The most common parameter that can be tuned in the Median Filtering algorithm is the kernel size or window size [16]. The algorithm steps for Median Filtering with a kernel size of k can be defined as follows:

i. Define the kernel size k.

ii. For each pixel in the image, select a neighborhood of size k x k centered on the pixel.

iii. Ascendingly arrange the pixel values in the neighborhood.

iv. Replace the original pixel value with the sorted pixel values' median value.

v. Repeat steps 2-4 for every pixel in the image.

vi. Return the filtered image.

The kernel size k determines the size of the neighborhood around each pixel, and can be adjusted depending on the level of noise in the image. A larger kernel size will result in more smoothing of the image, but may also blur out important details. Conversely, a smaller kernel size will preserve more detail, but may leave behind more noise. The equation for computing the median value of a set of pixel values is given by:

$$\text{median} = \begin{cases} \left(\frac{n+1}{2}\right) \text{ th element} \\ \text{average of the } \left(\frac{n}{2}\right) \text{ th and } \left(\frac{n}{2}+1\right) \text{ th elements,} \end{cases} \tag{5}$$

where n denotes the number of pixels in the immediate area. By adjusting the kernel size parameter of the Median Filtering algorithm, we can fine-tune its performance on the test dataset and improve the accuracy of the brain tumor image analysis.

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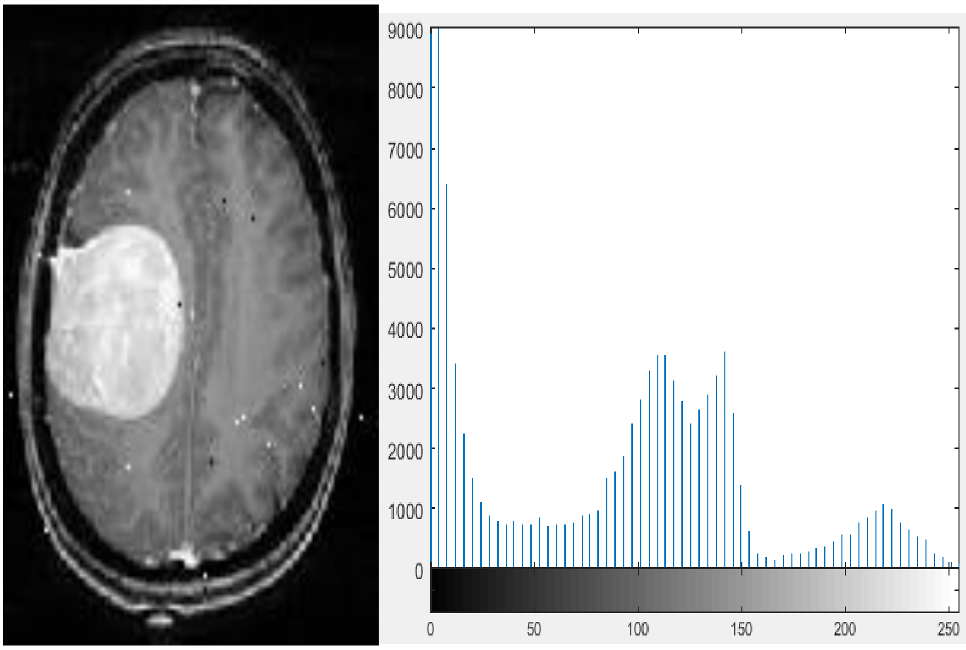

Fig.2. Input image and Histogram.

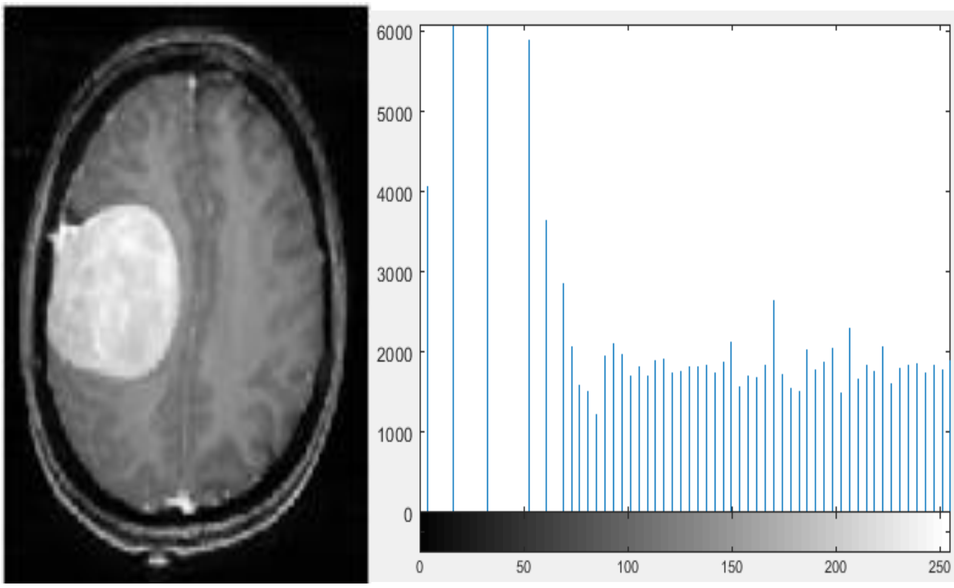

Fig.3. Pre-processed image and Histogram.

c. Hybrid CLEACH and median filter algorithm

The hybrid CLEACH and median filter algorithm can be used to enhance the quality of MRI brain tumor images. By combining these two techniques, the hybrid CLEACH and median filter method can enhance the contrast of an image while also reducing noise. The CLEACH algorithm is applied to the image first to enhance its contrast, and then noise is eliminated by applying the median filter.

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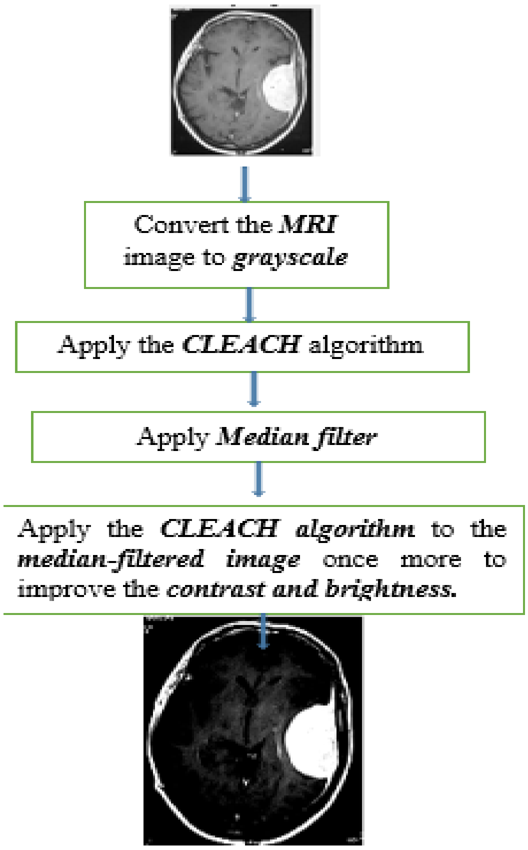

Fig.4. Proposed Framework

Overall, the hybrid CLEACH and median filter method can produce images with improved contrast and reduced noise, which can be useful for further segmentation process.

3.1.2 Image segmentation

The act of splitting an MRI brain tumor image into various sections, each of which corresponds to a distinct part of the brain or tumor, is known as image segmentation. Image segmentation of MRI brain tumor images can be accomplished using a variety of approaches, including thresholding, region growth, watershed segmentation, and graph-based segmentation. These techniques function by segmenting the image into distinct parts depending on factors such as pixel intensity, texture, or connectedness. The segmentation approach used will be determined by parameters such as the type of tumor, its size and location, and the image quality. Brain tumor classification is an important undertaking in medical diagnosis because it allows clinicians to effectively identify and treat various types of tumors. There are several image segmentation techniques that can be used for this task, including Otsu thresholding, K-means clustering, and region-growing [17].

a. Otsu Thresholding:

Otsu thresholding may not always be effective for MRI brain tumor image segmentation due to its assumption of a bimodal histogram and sensitivity to noise. Alternative techniques such as level set segmentation or deep learning-based approaches may be required to handle the complexities of brain MRI images and provide more accurate segmentation results. These methods can aid in accurate identification and classification of different types of brain tumors.

b. K-means Clustering

It is a commonly used segmentation method for MRI brain tumor images, but requires the number of clusters to be determined beforehand which can lead to inaccurate results. It is also sensitive to initialization, affecting accuracy when dealing with complex and noisy images. Alternative methods like deep learning-based approaches or fuzzy clustering can improve accuracy of brain tumor segmentation.

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c. Region-growing

Image segmentation is a crucial task in brain tumor analysis, and various techniques can be used for this purpose, including Otsu thresholding, K-means clustering, and region-growing. However, each technique has its limitations, such as Otsu thresholding's assumption of a bimodal histogram, K-means clustering's sensitivity to the choice of initial cluster centers and the number of clusters, and region-growing's computational complexity and sensitivity to the choice of seed pixels and criteria. As a result, the segmentation technique should be carefully chosen based on the task's specific needs and image features, and its accuracy and efficiency should be evaluated in practice [17].

d. Hybrid Salient with K-Means clustering segmentation

It is an effective image processing technique used for segmenting images, including MRI brain tumor images. The algorithm works by combining the strengths of two different segmentation methods, namely Salient Object Detection and K-Means clustering.

Salient Object Detection is a technique used to identify the most significant objects in an image. This technique works by identifying regions that are visually different from the rest of the image.

K-Means clustering is an unsupervised learning approach that groups together data points that have similar characteristics. K-Means clustering is used in image segmentation to group pixels with comparable color values into clusters. This approach is especially useful for finding MRI brain tumor areas with uniform color values.

The hybrid Salient with K-Means clustering segmentation method works by first using Salient Object Detection to identify the most significant regions in the image, which in this case would be the MRI brain tumor. The segmentation is then further refined and the leaves are separated from the background using the K-Means clustering technique. The implementation steps are described below:

Step 1: Pre-processing

- Read the input image of MRI brain tumor.
- Convert the image to grayscale if it is in color.
- Apply a Hybrid CLEACH and median filter algorithm to preprocess the image.

Step 2: Salient Region Detection

Calculate the saliency map using the following equation:

$$S(x,y) = |\nabla I(x,y)| \times M(x,y) \tag{6}$$

Where ∇I(x,y) is the gradient of the image at pixel (x,y), and M(x,y) is a mask that denotes if the image has any corners or edges. The Laplacian of Gaussian (LoG) operator can be used to compute the mask. The image is convolved using a Gaussian kernel to generate the LoG, which is subsequently obtained by using the Laplacian operator. The resulting image can be threshold to obtain a binary mask. Normalize the saliency map to have values between 0 and 1 [18].

Step 3: K-Means Clustering

- Implement K-Means clustering to create the segmentation mask from the saliency map. Based on how many unique regions there are in the image, the number of clusters should be determined.
- To create the segmented image, apply the segmentation mask to the original image.
- Here are the equations for the Laplacian of Gaussian operator and K-Means clustering:
- Where the convolution operator * and the Gaussian kernel G(x,y) [18].

$$L(x,y) = \nabla^2(G(x,y) * I(x,y)) \tag{7}$$

Step 4: Hybrid Segmentation

Combine the binary image from step 2 and the K-Means segmentation result from step 3 to obtain a hybrid segmentation.

Step 5: Post-processing

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Use morphological techniques like erosion and dilation to remove tiny regions and fill in gaps in the hybrid segmentation result.

The final result of the segmentation algorithm is a binary image that separates the MRI brain tumor from the background. Hybrid Salient with K-Means clustering segmentation can overcome the limitations of Otsu Thresholding, K-means clustering, and region-growing techniques in several way. It is robust, adaptable, fast, and accurate. It can handle images with varying lighting conditions and complex backgrounds by using saliency detection to identify the most visually significant regions of an image, which can then guide the segmentation process. It can also be customized to outfit specific segmentation tasks, including segmenting objects of different shapes and sizes, and can process large images in real-time. Additionally, it produces more accurate segmentation results than Otsu Thresholding and K-means clustering by combining the strengths of both techniques and leveraging the power of saliency detection. Overall, Hybrid Salient with K-Means clustering segmentation is a powerful technique that can overcome many of the limitations of traditional segmentation techniques and produce more accurate and robust segmentation results.

3.1.3 Feature Extraction

A mathematical model called the Gray-Level Co-occurrence Matrix (GLCM) depicts the spatial relationship between two neighboring pixels in an image. When processing images, GLCM is frequently used to extract texture information from the images. These characteristics can be utilized to distinguish between the various textures included in the image [19]. The steps below can be used to extract features from MRI brain tumor pictures using GLCM:

i. Convert the RGB image of the MRI brain tumor into grayscale.

ii. Divide the grayscale image into small non-overlapping blocks.

iii. For each block, calculate the GLCM using a specified displacement vector and quantization level. The displacement vector specifies the distance and direction between two adjacent pixels, while the quantization level specifies the number of gray levels in the GLCM.

iv. From the GLCM, calculate a set of statistical measures such as contrast, correlation, energy, and homogeneity. These measures can be used as features to differentiate between different textures.

v. Repeat steps 3-4 for all the blocks in the image.

vi. Concatenate the feature vectors obtained from all the blocks to obtain a feature vector for the entire image.

The GLCM can be represented as a matrix G, where each member G (i, j) denotes the frequency with which, given a particular displacement vector, a pixel with gray level i is next to a pixel with gray level j. To calculate the statistical measures from the GLCM, we can use the following formulas:

Contrast:

$$\text{Contrast } = \sum \ (i-j)^2 G(i,j) \tag{8}$$

The contrast measures the local variations in the GLCM. It highlights the difference between the highest and lowest values in the matrix.

Correlation:

$$\text{Correlation } = \frac{\sum \ (i-\text{mean}_i)(j-\text{mean}_j)G(i,j)}{\text{std}_i \cdot \text{std}_j} \tag{9}$$

The correlation measures how correlated a pixel is to its neighbor over the whole image. It is a measure of how one pixel is linearly related to another.

Energy:

$$\text{Energy } = \sum \ G(i,j)^2 \tag{10}$$

The energy measures the sum of squared elements in the GLCM. It is also known as uniformity or the angular second moment, representing the texture's uniformity.

Homogeneity:

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$$\text{Homogeneity} = \sum \frac{G(i,j)}{1+(i-j)^2} \quad (11)$$

The homogeneity measures the closeness of the distribution of elements in the GLCM to the GLCM diagonal.

By calculating these statistical measures for all the blocks in the image, we can obtain a set of features that can be used to differentiate between different textures in the image. These features can be used in machine learning algorithms for tasks such as classification, segmentation, and object recognition. Some sample feature values are listed below,

Table 2: Sample Features (GLCM)

Entropy	Contrast	Correlation	Energy	Homogeneity
0.019676	0.977205	0.439465	0.990878	0.392195
0.017115	0.983738	0.399594	0.991884	0.362678
0.017303	0.981196	0.425729	0.991839	0.341882
0.019706	0.981333	0.415898	0.991073	0.393606
0.007082	0.991682	0.424758	0.996459	0.323678
0.007059	0.991407	0.433409	0.996471	0.364919
0.003504	0.99447	0.478787	0.998248	0.240268
0.008093	0.990455	0.417807	0.995954	0.261234
0.008063	0.990115	0.426659	0.995968	0.269861

3.1.4 Classification

The Support Vector Machine (SVM) is a robust mathematical model widely employed in machine learning for both classification and regression tasks. In the context of medical imaging, SVMs can be harnessed to classify MRI brain tumor images by analyzing various key features, including color, shape, texture, and size. The following steps outline the process of applying SVM for MRI brain tumor image classification:

i. ***Data Collection and Preprocessing:*** The initial phase involves gathering a diverse dataset of MRI brain tumor images, encompassing different classes (e.g., healthy and diseased). Subsequently, these images undergo preprocessing, during which relevant features are extracted, such as color, shape, texture, and size.

ii. ***Data Splitting:*** The dataset is partitioned into two subsets: a training set utilized for training the SVM model and a testing set employed to evaluate the model's performance.

iii. ***Model Definition:*** The SVM model is defined, taking into consideration the characteristics of the data. This includes choosing appropriate kernel functions (e.g., linear, polynomial, radial basis function) and configuring hyper parameters (e.g., regularization parameter, kernel width).

iv. ***Model Training:*** The SVM model undergoes training using the training dataset. During this phase, the hyper parameters are optimized to maximize the margin between different classes while minimizing classification errors.

v. ***Model Testing:*** The performance of the trained SVM model is assessed using the testing dataset. Metrics such as accuracy, precision, recall, and F1 score are calculated to gauge the model's effectiveness in classifying MRI brain tumor images.

vi. ***Model Tuning:*** If the SVM model's performance falls short of expectations, further refinement is carried out. This may involve fine-tuning hyper parameters or experimenting with different kernel functions to enhance the model's performance.

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In summary, SVMs offer a potent mathematical framework for the accurate and reliable classification of MRI brain tumor images [20]. However, their success hinges on meticulous feature selection, hyper parameter tuning, and iterative refinement to achieve optimal results

4. Results and Discussion

4.1 Dataset Description

Kaggle offers a publicly available dataset of brain MRI images that can be used for brain tumor classification. The dataset includes T1-weighted contrast-injected (T1Gd) MRI scans of 766 patients with either a benign or malignant brain tumor, as well as MRI scans of 207 patients with no brain tumor [22]. The images were obtained from The Cancer Imaging Archive (TCIA) and are in DICOM format. Sample images are shown below,

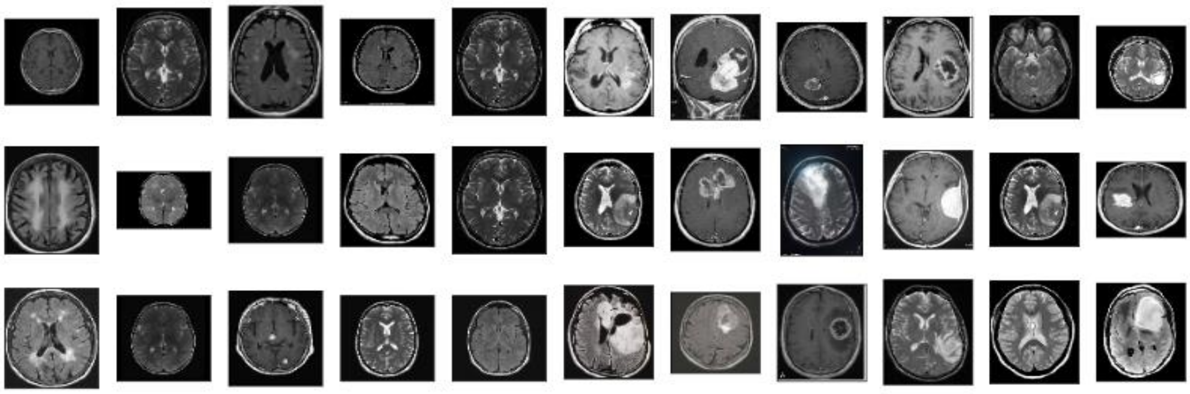
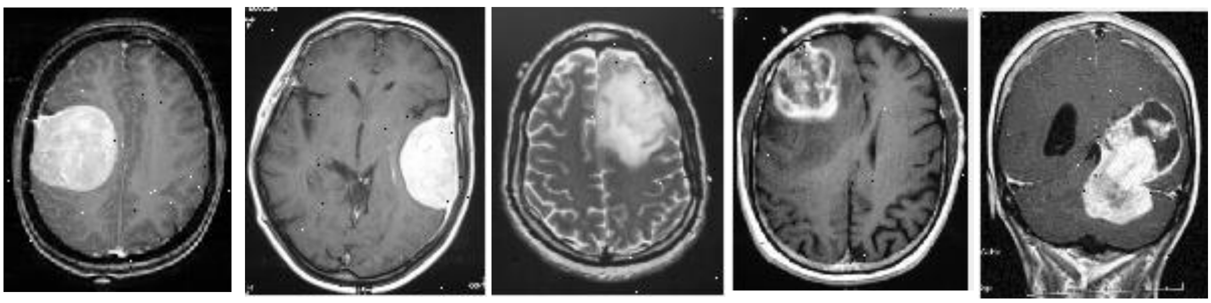


Fig.5. Sample dataset

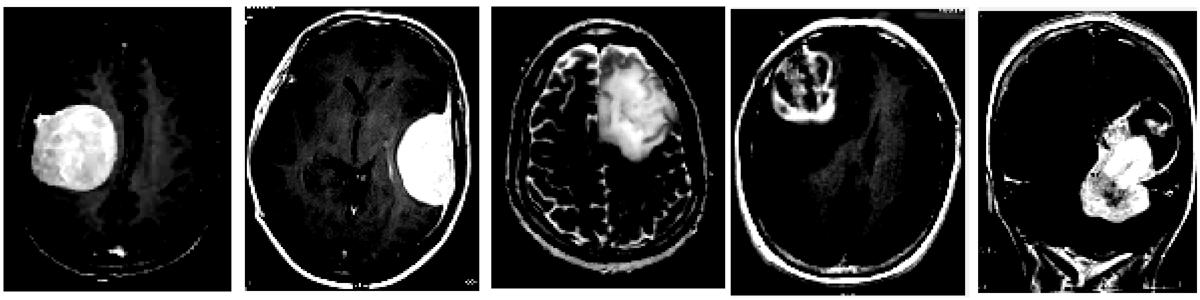
4.2 Preprocessing and Segmentation Results

In the realm of medical image analysis, the preprocessing of MRI images depicting brain tumors stands as a pivotal stage. This crucial step serves to elevate image quality and facilitate the extraction of pertinent features, ultimately contributing to the improved diagnosis and treatment of brain tumors. Below, you will find a selection of sample images that have undergone preprocessing and segmentation.

(a)



(b)



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(c)

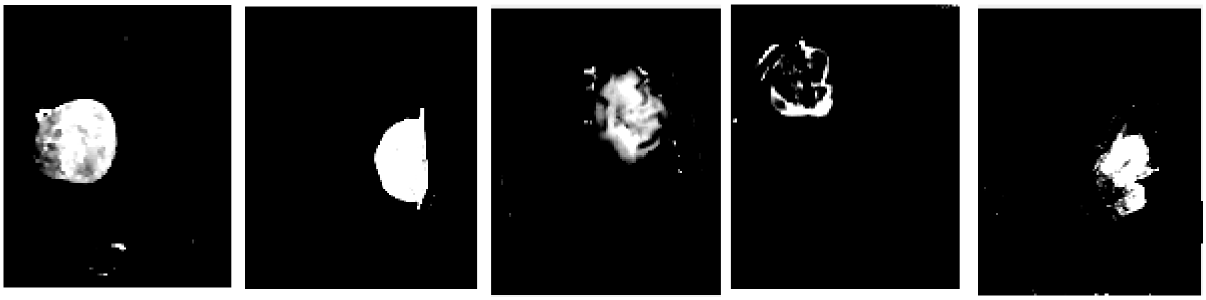

Fig.5. (a) Original Images (b) Pre-Processed Images (c) Segmented images

In this research, the methods are entirely automatic and does not require any user intervention. It uses a hybrid methods to eliminate noises and segment the tumor to improve the accuracy of tumor detection. Unlike complex and rigorous equation-based methods like the maxima transform, this method is designed to be easily incorporated and understood by radiologists and surgeons. Its aim is to facilitate valuable decisions for medical professionals by providing accurate and reliable tumor detection and extraction. Overall, this method represents a significant improvement in further feature extraction and classification process.

4.3 Performance Evaluation

These metrics give an extensive overview of the models' performance. It is significant to remember that the evaluation metric selected depends on the issue at hand. For instance, recall may be a more significant statistic than precision in situations where the cost of false negatives is substantial. Contrarily, accuracy may be a more crucial parameter when the cost of false positives is significant. The below table illustrates the performance metric calculations,

Table 3: Performance Evaluation Metrics

Metric	Definition	Equation
Accuracy	The percentage of accurately anticipated observations to all observations	(TP + TN) / (TP + TN + FP + FN)
Precision	True positives as a percentage of the total of true positives and false positives	TP / (TP + FP)
Recall (Sensitivity)	Real positives as a percentage of the total of false negatives and genuine positives	TP / (TP + FN)
F1 score	The harmonic average of memory and accuracy	2 * ((precision * recall) / (precision + recall))

Here, TP stands for True Positives, TN for True Negatives, FP for False Positives, and FN for False Negatives [23].

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Table 4: Performance Evaluation

	Median Filter (MF)				Hybrid CLEACH and median filter (CMF)			
Algorithm	**Accuracy**	**Precision**	**Recall**	**F1 score**	**Accuracy**	**Precision**	**Recall**	**F1 score**
Otsu	0.78	0.82	0.76	0.78	0.88	0.89	0.87	0.88
K-Means Clustering (KMC)	0.81	0.84	0.79	0.81	0.91	0.92	0.9	0.91
Region Growing (RG)	0.76	0.81	0.75	0.76	0.85	0.87	0.84	0.85
Hybrid Salient with K-Means Clustering (SKMC)	0.85	0.89	0.82	0.85	0.92	0.95	0.91	0.93

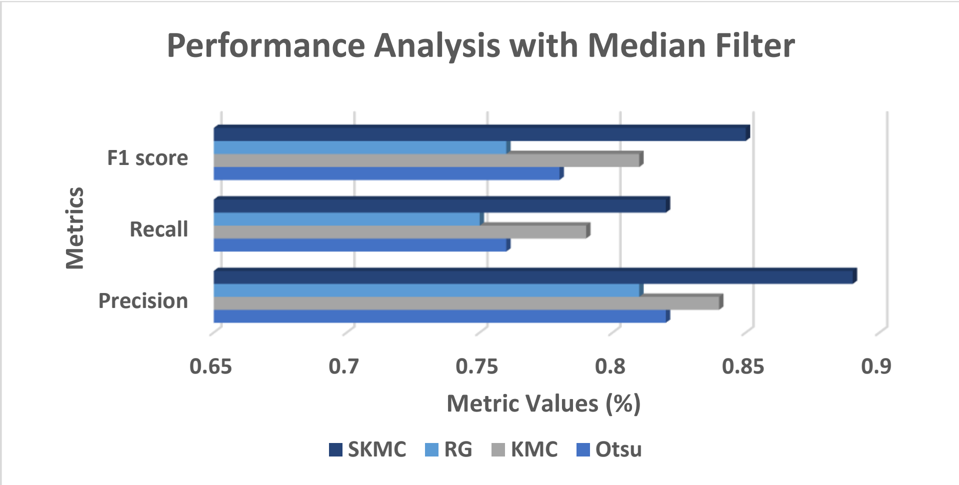

Fig.6. Comparative analysis with Median filter

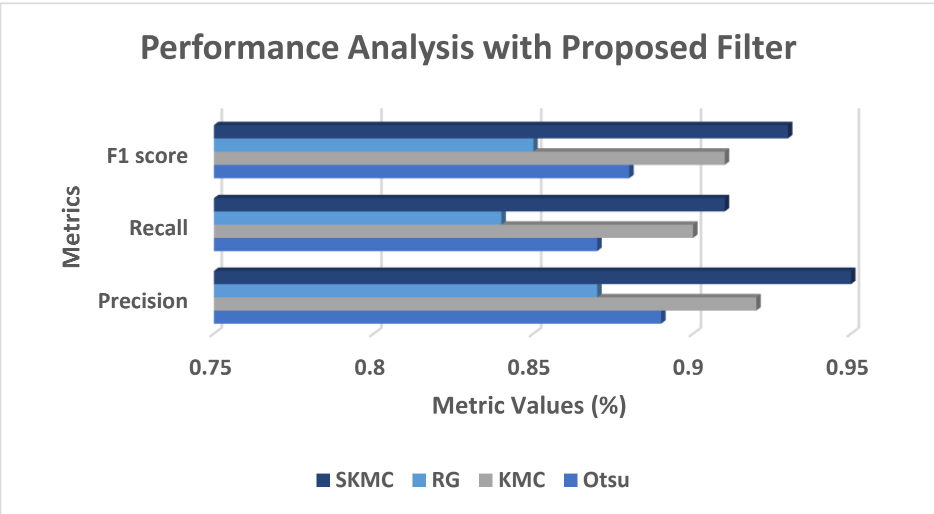

Fig.7. Comparative analysis with SKMC Filter

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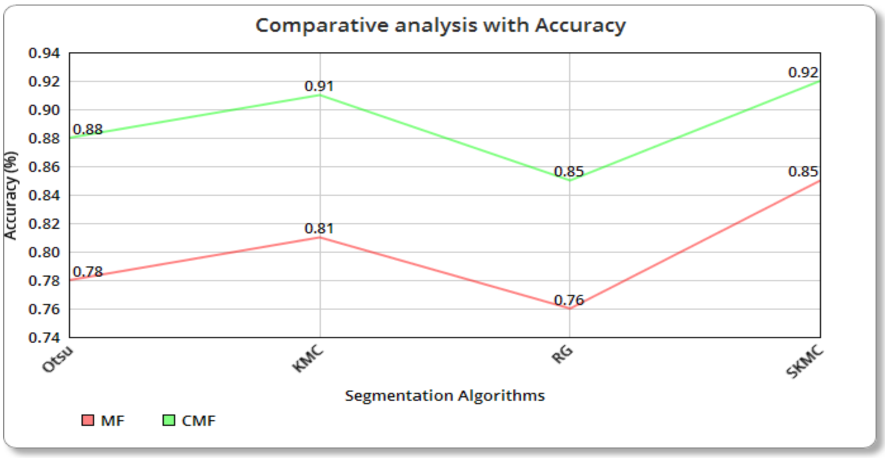

Fig.8. Comparative analysis of overall algorithms with Accuracy

The above table and figures shows the performance of different brain tumor segmentation algorithms in terms of Accuracy, Precision, Recall, and F1 score. The methods compared are Median Filter (MF), Hybrid CLEACH and median filter (CMF), Otsu, K-Means Clustering (KMC), Region Growing (RG), and Hybrid Salient with K-Means Clustering (SKMC). The table includes results for two different methods: one based on MF and CMF and the other based on Otsu, KMC, RG, and SKMC. The results show that the Hybrid CLEACH and median filter (CMF) and the Hybrid Salient with K-Means Clustering (SKMC) algorithms perform the best with accuracy scores of 0.91 and 0.92, respectively. In terms of precision, both CMF and SKMC algorithms perform the best with values of 0.92 and 0.95, respectively. For recall, SKMC performs the best with a score of 0.91, while for F1 score, both CMF and SKMC algorithms perform the best with values of 0.91 and 0.93, respectively.

The other algorithms exhibit commendable performance, boasting accuracy scores spanning from 0.78 to 0.85, precision scores ranging from 0.82 to 0.89, recall scores varying between 0.75 and 0.84, and F1 scores ranging from 0.76 to 0.85. In summary, the outcomes underscore that the CMF and SKMC algorithms stand out as the most efficacious for brain tumor segmentation, while the remaining algorithms also yield respectable results.

5. Conclusion and Future Scope

In conclusion, the work presented a novel automated technique for brain tumor detection and classification in MRI images using hybrid image processing techniques. The results showed that the Hybrid CLEACH and median filter (CMF) and Hybrid Salient with K-Means Clustering (SKMC) algorithms are the most effective for brain tumor segmentation, achieving high accuracy, precision, recall, and F1 scores. The success of the other algorithms shows the potential value of several approaches for segmenting brain tumors. Overall, the proposed method has the potential to facilitate efficient and accurate brain tumor diagnosis, leading to better patient outcomes. Possible future enhancements for the proposed method include incorporating deep learning, handling multiple and different types of brain tumors, developing more efficient algorithms for real-time diagnosis, and validating the method on larger and diverse datasets.

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