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Supervised and Unsupervised Image Clustering for Brain Tumor (MRI) Image Segmentation

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Manuscript Details	Abstract
	Image segmentation is the classification of an image into different groups. Many researches have been done in the area of image segmentation using clustering. There are different methods and one of the most popular methods is k-means clustering algorithm. K-means clustering algorithm is an unsupervised algorithm and it is used to segment the interest area from the background. This proposed research uses K-means clustering algorithm and Simple Linear Iterative Clustering for brain tumour medical image segmentation for early diagnosis. This research also discusses supervised clustering methods such as segmentation using manual thresholding, otsu, niblack and sauvola thresholding as well as Active Contour Segmentation methods. **Keywords:** Supervised Clustering, Unsupervised Clustering, Machine Learning, Image Segmentation, Brain Tumor.
	## Introduction Image segmentation stands as a widely employed technique to accurately categorize image pixels in decision-focused applications. This process involves dividing an image into discrete regions, where pixels within each region exhibit substantial similarity, while maintaining high contrast between regions. It holds immense value across various domains, including healthcare, image processing, traffic analysis, and pattern recognition. Diverse strategies exist for image segmentation, encompassing threshold-based, edge-based, cluster-based, and neural network-based approaches [1]. Among these methods, clustering emerges as notably efficient, with variants such as K-means clustering, Fuzzy C-means clustering, mountain clustering, and subtractive clustering [2]. K-means clustering, in particular, gains prominence due to its simplicity, computational efficiency, and applicability to datasets with numerous variables. However, it does exhibit

sensitivity to the number of clusters and the initial centroid selection, necessitating careful consideration [2].

In today's medical landscape, image segmentation plays a pivotal role by isolating regions of interest from backgrounds. Medical images, often represented as numerical arrays in computers, embody crucial diagnostic information through variations in relevant physical quantities [3]. Processing and analyzing these images enable their transformation into quantifiable symbolic representations, facilitating diagnosis, integration of multi-modal data, and extraction of qualitative insights. Within medical image analysis, a core challenge is image segmentation, which entails identifying object boundaries, such as organs or anomalies. Successful segmentation enables shape analysis, volume change detection, and precise radiation therapy planning, contributing significantly to medical treatment protocols. In upcoming work, the segmentation results will be assessed through evaluation metrics like PSNR and RSME, thereby enhancing the comprehensiveness of the study [4].

2 Related Work

2.1 Radiography and Fluoroscopy

Numerous studies have been conducted in the field of image segmentation employing diverse methodologies, often tailored to specific application contexts. Among these techniques, the K-means algorithm stands out as a straightforward clustering approach, exhibiting various adaptations for center initialization. Concurrently, researchers are actively developing novel methods aiming for improved efficiency and enhanced segmentation outcomes. Several recent works in this domain are explored below [5].

Purohit and Joshi [4] introduced an innovative and efficient approach to the K-means clustering algorithm. Their method focuses on optimizing cluster center generation by minimizing mean square error while maintaining manageable execution times. Notably, it achieved reduced mean square error without incurring significant execution time increments. Comparative evaluations revealed that higher accuracy is achieved for dense datasets compared to sparse ones. [6].

Jose et al. [5] proposed a comprehensive Brain Tumor Segmentation process utilizing K-means Clustering and Fuzzy C-means Algorithm, coupled with area calculation. Their workflow comprises pre-processing, advanced K-means clustering, fuzzy c-means clustering, and subsequent feature extraction. Pre-processing involves image enhancement through filtering, while the advanced K-means and fuzzy c-means algorithms contribute to effective image clustering. Extracted segmented images are then subjected to feature extraction, particularly focused on tumor regions in MRI images [7].

Yedla et al. [6] presented an improved K-means clustering algorithm enhanced by a novel initial center determination approach. This novel method optimizes data point assignment to clusters with reduced time complexity. Their proposed algorithm showcases heightened accuracy while maintaining computational efficiency, surpassing the original K-means clustering algorithm. Notably, their approach obviates the need for additional input like threshold values, contributing to its practicality.

Nazeer and Sebastian [7] put forth an advanced algorithm designed to enhance both accuracy and efficiency within the K-means clustering paradigm. Their enhanced K-means approach integrates a systematic framework encompassing two core facets: initial centroid determination and data point cluster assignment. By experimenting with varied initial centroids, they achieved reduced time complexity while preserving clustering accuracy. The proposed algorithm offers promising potential for optimizing clustering tasks without sacrificing precision.

In summary, these recent studies exemplify the ongoing efforts within the field of image segmentation, particularly in the realm of K-means clustering, to devise novel methodologies that enhance accuracy, efficiency, and practicality.

3 Unsupervised Clustering Algorithm

3.1 K-means Clustering

Clustering serves as a technique to partition a dataset into distinct groups, a prominent example being the k-means clustering approach. The k-means method segregates a dataset into k distinct clusters [11] [12]. It involves categorizing a given dataset into k non-overlapping clusters. The k-means algorithm operates through two distinct phases. Initially, it computes the k centroids, and subsequently, it assigns each data point to the cluster with the nearest centroid. Various techniques exist to determine the distance to the closest centroid, with the widely used Euclidean distance. After the initial grouping, the centroids of each cluster are recalculated. Based on these new centroids, a new Euclidean distance is computed between each center and data point, followed by the assignment of points to clusters based on minimum Euclidean distance. Each cluster is identified by its constituent objects and centroid. The centroid for a cluster minimizes the sum of distances from all objects in that cluster. Consequently, the k-means process is iterative, iteratively minimizing the sum of distances from each object to its respective cluster centroid across all clusters. Consider an image with dimensions x×y that needs to be divided into k clusters. Given an input pixel p(x, y) and cluster centers ck, the k-means clustering algorithm unfolds as follows [13]:

1. Commence by setting the number of clusters, k, and initializing the cluster centers.
2. For each pixel within the image, compute the Euclidean distance, denoted as d, between the center and the pixel using the provided formula.
1. d = ||p(x, y) − ck||
2. Assign all pixels to the nearest center based on the calculated distance, d.
3. Once all pixels are assigned, recalculate the new positions of the cluster centers using the provided formula.

$$c_k = \frac{1}{k} \sum_{y \in c_k} \sum_{y \in c_k} p(x, y)$$

4. Iterate through the process until the specified tolerance or error value is met.
5. Restructure the clustered pixels to form the resultant image.

While k-means boasts simplicity in implementation, it is not without its limitations. The effectiveness of the ultimate clustering outcome hinges on the arbitrary choice of the initial centroids. If these starting points are selected randomly, varying results may emerge across different initializations. Thus, it becomes imperative to meticulously select initial centroids to align with the desired segmentation outcome. Additionally, the computational complexity of k-means clustering warrants attention during its design. This complexity is influenced by factors including the volume of data elements, the number of clusters, and the number of iterations involved [13].

3.2 Simple Linear Iterative Clustering

This approach involves amalgamating pixels within the image plane by considering both their color similarity and spatial proximity, resulting in the creation of superpixels. The most contemporary method for superpixel segmentation is Simple Linear Iterative Clustering, renowned for its minimal computational demands. In essence, this technique clusters pixels in a five-dimensional space encompassing color and spatial coordinates, yielding compact and nearly uniform superpixels.

Superpixels are crafted through the aggregation of pixels within the image plane, guided by their color resemblance and spatial proximity. This process occurs within a five-dimensional space where XY represents pixel coordinates. Given that the distance between colors in the CIELAB space has an upper limit, whereas spatial distances on the XY plane are contingent on image dimensions, normalizing spatial distances becomes imperative for employing Euclidean distance within this 5D space. Consequently, a novel distance metric, factoring in superpixel dimensions, has been formulated to facilitate pixel clustering within this five-dimensional realm [13].

4 Supervised Clustering Algorithms

4.1 Segmentation by Thresholding – Manual Input

An external pixel value, spanning from 0 to 255, serves to distinguish the foreground from the background within the image. Consequently, a transformed image is generated, either surpassing or falling short of the designated threshold. The initial phase of this thresholding process involves the normalization of an image's intensity range from 0 to 255 to a normalized scale of 0 to 1. Following this, a fixed threshold value is employed for comparison. If the comparison holds true, the outcome is recorded as 1; otherwise, it is recorded as 0. This binary image on a global scale is instrumental for edge detection, as well as facilitating contrast and color variation analysis 4.2 Segmentation by Thresholding Using Niblack, Sauvola and Otsu's thresholding. The Niblack and Sauvola thresholding methods are specifically tailored to enhance the quality of microscopic images. These techniques operate on a local level, adjusting the threshold based on the local mean and standard deviation for each pixel within a sliding window. In contrast, Otsu's thresholding technique involves an iterative process wherein it evaluates various threshold values and quantifies the dispersion between sample points on either side of the threshold – foreground and background. The objective is to identify the optimal foreground and background distributions.

These localized thresholding methods primarily rely on mean and standard deviation as fundamental computational parameters. However, the determination of the final local pixel value takes into account additional positive factors as well. This comprehensive approach ensures an effective separation between the object and its background.

$$\text{Sauvolavalue} = x * (1 + k * (\sigma r - 1))$$
$$\text{Niblackvalue} = x + k * \sigma - c$$

Where x and σ symbolize the mean and standard deviation of pixel intensities, respectively.

4.3 Active Contour Segmentation

The foundation of the active contour method lies in the reduction of energy functional. Active contour, also known as snakes, constitutes a segmentation strategy that leverages energy forces and constraints to isolate pixels of significance from the rest of the image, enabling subsequent processing and analysis. The term "active contour" pertains to a model within the segmentation process.

The active contour model stands as a dynamic approach to image segmentation, harnessing the energy constraints and pressures present in the image to demarcate regions of interest. In this method, an active contour delineates distinct boundaries or curvatures for each segment of the targeted object. The primary objective of the active contour model involves minimizing the energy function, arising from a combination of external and internal forces. The external force takes shape as curves or surfaces, while the internal force draws from image data. This external force facilitates the automatic adaptation of initial outlines to conform to the shapes of objects depicted in images.

5 Results

Various categories of medical images were employed for our analysis. Within medical image analysis, the focus predominantly lies on segmenting the infected areas or regions of interest from the background. Specifically, we utilized MRI images of brain tumours afflicted by infections for our investigation. The proposed algorithm was implemented using the Python programming language. A comparative assessment was conducted, contrasting the outcomes of the k-means algorithm with those of alternative algorithms, and these findings are visually presented in Figure 1-3.
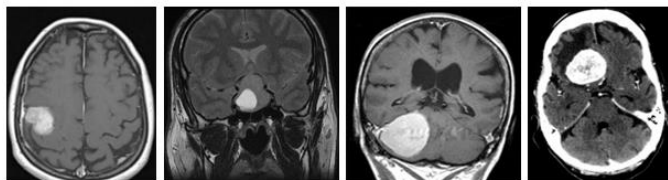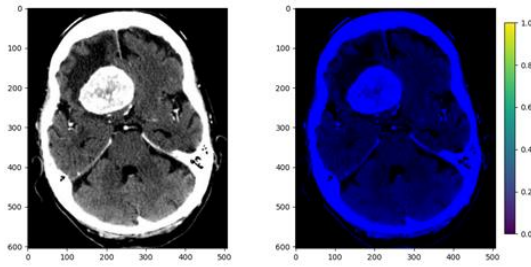

Fig. 1. Sample MRI images affected by tumor

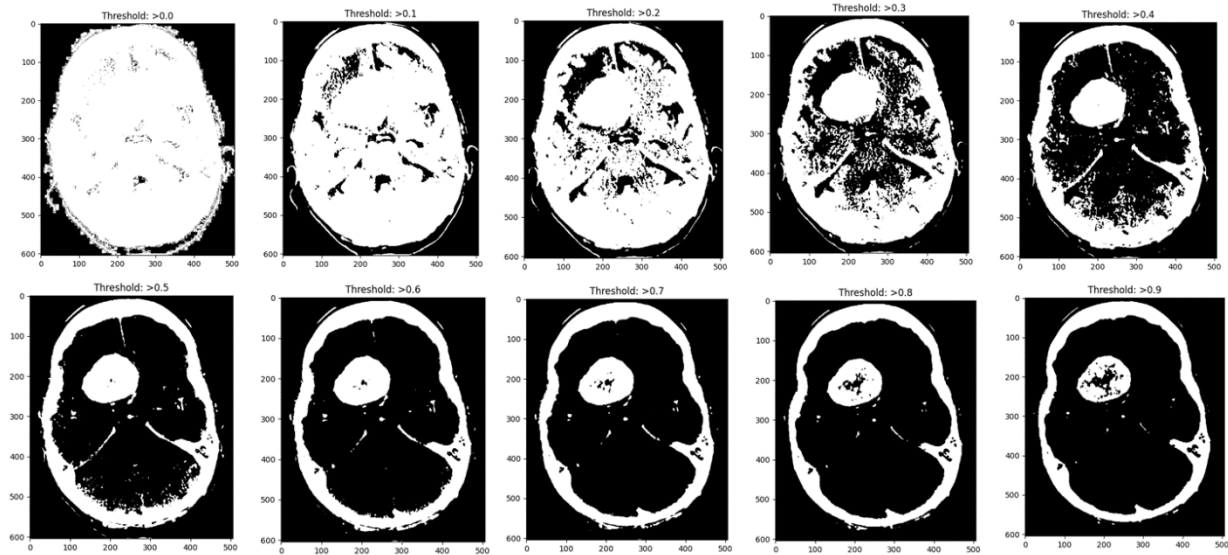**Fig. 2. RGB to HSV conversion of the input image**

Fig. 3. Segmentation by Thresholding – manual input from t=0.1 to t=0.9
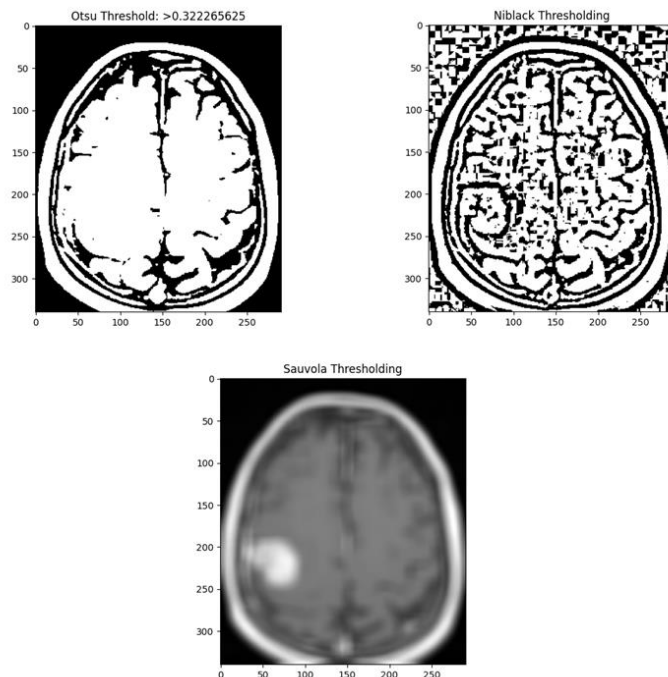

Fig. 4. Results for a) Otsu Thresholding (left upper) b) Niblack Thresholding (right upper) c) Sauvola Thresholding (last)
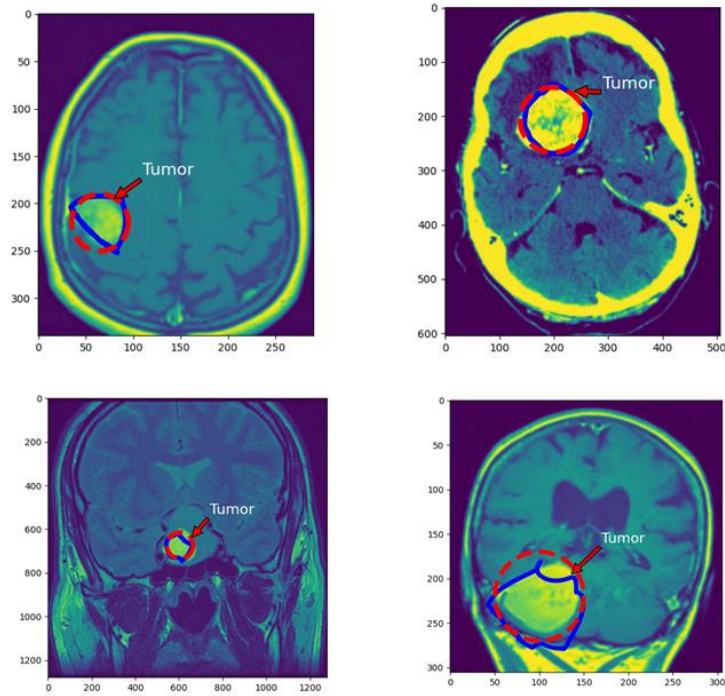
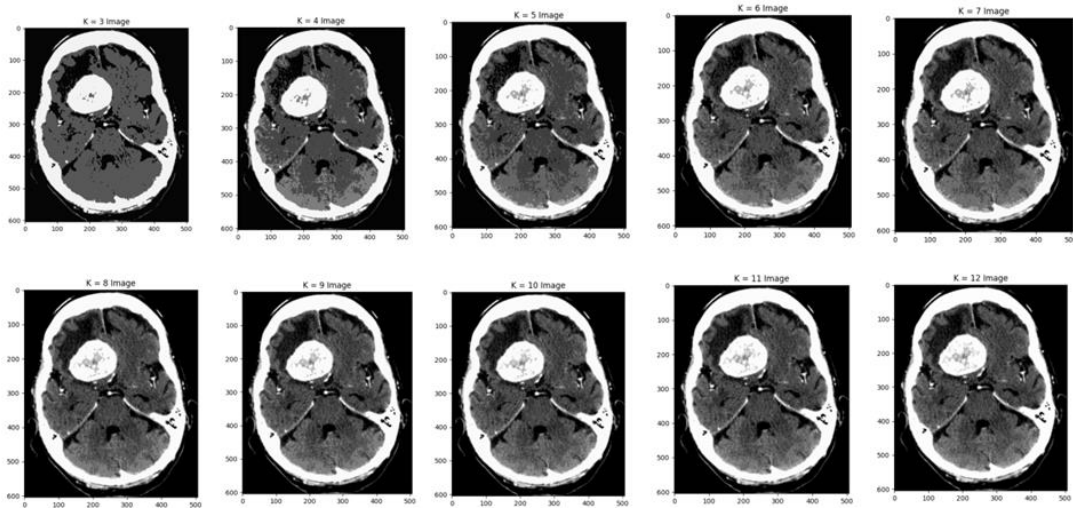**Fig. 5. Output for MRI image segmentation using contour segmentation**

Fig. 6. Results of k-means clustering algorithm for k=3 to k=12
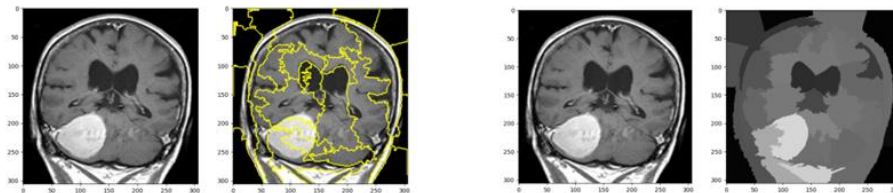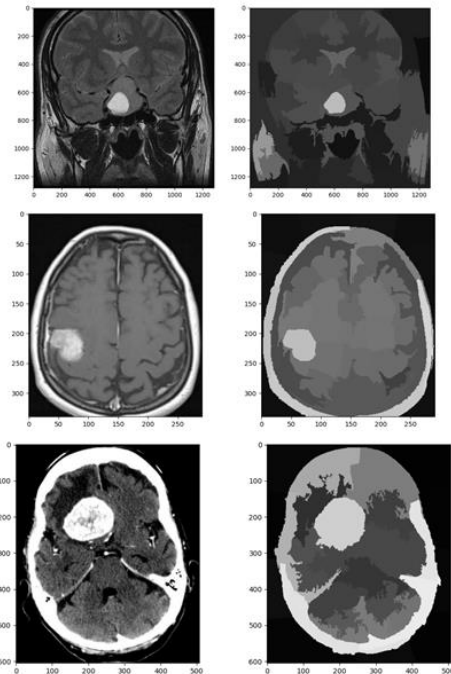

Fig. 7. Results of Iterative Clustering Algorithm for MRI images

Fig. 8. More results with unsupervised clustering, where tumor can be detected easily

Conclusion

Image segmentation refers to the process of categorizing distinct sections within an image. Numerous investigations have been conducted in the domain of image segmentation through clustering techniques. Diverse approaches exist, with one of the widely embraced techniques being the k-means clustering algorithm. Operating in an unsupervised manner, the k-means algorithm serves to differentiate regions of interest from the image background. In the context of this study, the utilization of the k-means clustering algorithm and the Simple Linear Iterative Clustering technique is proposed for the segmentation of medical images related to brain tumors. This endeavor also delves into supervised clustering strategies, encompassing methodologies like manual thresholding, Otsu's method, Niblack's method, and Sauvola's method, along with the incorporation of Active Contour Segmentation techniques. Additionally, we employed an unsupervised active contour segmentation technique

to perform image segmentation, yielding exceptional outcomes. In forthcoming stages, a comparative analysis of evaluation metrics like PSNR and RSME will be conducted to assess these results.

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