

# DESIGN AND SIMULATION OF EFFICIENT SEGMENTATION OF BRAIN TUMOR FROM MRI IMAGES USING HYBRID FUZZY K-MEANS CLUSTERING ALGORITHM

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*Abstract- Primary goal of grouping a picture is prevailing hues extraction from the pictures. By removing the data from pictures, for example, surface, shading, shape and structure, the picture division can be essential to streamline. In view of the data extraction in any pictures, the division has been utilized in numerous fields, for example, Enhancing the picture, pressure, recovery frameworks i.e., web indexes, object location, and restorative picture preparing. From the previous decades, there are such a significant number of approaches created for the picture division. Among those, Fuzzy c-implys (FCM) is an outstanding strategy and mainstream grouping plan, which will fragment the picture into a few sections dependent on the participation work. After FCM, the K-implys calculation has been proposed to lessen the computational intricacy of FCM. Due to its capacity to bunch tremendous information focuses rapidly, K-implys has been broadly utilized in numerous applications. Later years the Hierarchical grouping is additionally broadly applied for picture division. At that point after, Gaussian Mixture Model has been utilized with its variation Expectation Maximization for fragmenting the pictures.*

- Binary mathematical morphology
- Gray-value mathematical morphology

In the analysis of the objects in images it is essential that we can distinguish between the objects of interest and "the rest." This latter group is also referred to as the background. The techniques that are used to find the objects of interest are usually referred to as segmentation techniques - segmenting the foreground from background. In this section we will two of the most common techniques thresholding and edge finding and we will present techniques for improving the quality of the segmentation result. It is important to understand that:

1. There is no universally applicable segmentation technique that will work for all images, and,
2. No segmentation technique is perfect.

In radiology, magnetic resonance imaging (MRI) [1] is used to investigate the human body processes and functions of organisms. These images can be formed by using the magnetic fields and radio waves. In hospitals, this technique has been using widely for medical diagnosis, to find the disease stage and follow-up without exposure to ionizing radiation. MRI has a broad range of applications in medical diagnosis and in all over world there are over 25,000 scanners to be in use. It has an impact on diagnosis and treatment in many specialties although the effect on improved health outcomes is uncertain. MRT is more preferable over computed tomography (CT) since it does not use any ionizing radiation, when either modality could yield the same information. The sustained increase in demand for MRI within the healthcare industry has led to concerns about effectiveness of cost and over diagnosis. Segmenting an image is an effort to group similar colors or elements of an image into a cluster or group. This can be achieved by clustering, which clusters the number of colors or elements into several clusters based on the similarity of color intensities and gray intensities of an image

## I. INTRODUCTION

In computer vision, segmentation refers to the process of partitioning a digital image into multiple segments (sets of pixels, also known as super pixels). The goal of segmentation is to simplify and/or change the representation of an image into something that is more meaningful and easier to analyze. Image segmentation is typically used to locate objects and boundaries (lines, curves, etc.) in images. More precisely, image segmentation is the process of assigning a label to every pixel in an image such that pixels with the same label share certain visual characteristics.

The result of image segmentation is a set of segments that collectively cover the entire image, or a set of [contours](#) extracted from the image (see [edge detection](#)). Each of the pixels in a region is similar with respect to some characteristic or computed property, such as [color](#), [intensity](#), or [texture](#). [Adjacent](#) regions are significantly different with respect to the same characteristics.

- [Thresholding](#)
- [Edge finding](#)

## II. EXISTING METHODS

The Existing systems had mainly four modules: pre-processing, segmentation, Feature extraction, and approximate reasoning. Preprocessing is done by filtering. Segmentation is carried out by advanced K-means and Fuzzy C-means algorithms. Feature extractions by thresholding and finally, Approximate reasoning

method to recognize the tumor shape and position in MRI image using edge detection method.

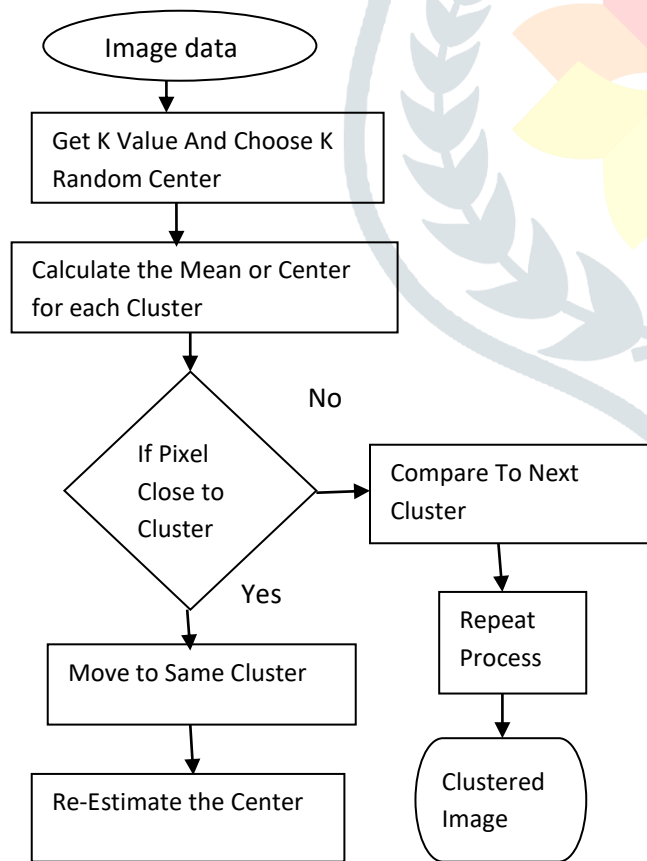
The basic theory of K-means clustering. Let  $A=\{a_i | i=1, \dots, f\}$  be attributes of  $f$ -dimensional vectors and  $X=\{x_i | i=1, \dots, N\}$  be each data of  $A$ . The K-means clustering separates  $X$  into  $k$  partitions called clusters  $S=\{s_i | i=1, \dots, k\}$  where  $M \in X$  is  $M_i=\{m_{ij} | j=1, \dots, n(s_i)\}$  as members of  $s_i$ , where  $n(s_i)$  is number of members for  $s_i$ . Each cluster has cluster center of  $C=\{c_i | i=1, \dots, k\}$ . K-means clustering algorithm can be described as follows

1. Initiate its algorithm by generating random starting points of initial centroids  $C$ .
2. Calculate the distance  $d$  between  $X$  to cluster center  $C$ . Euclidean distance is commonly used to express the distance.
3. Separate  $x_i$  for  $i=1 \dots N$  into  $S$  in which it has minimum  $d(x_i, C)$ .
4. Determine the new cluster centers  $c_i$  for  $i=1 \dots k$  defined as:

$$C_i = \frac{1}{n_i} \sum_{j=1}^{n(s_i)} m_{ij} \in s_i$$

5. Go back to step 2 until all centroids are convergent. The centroids can be said converged if their positions do not change in the iteration. It also may stop in the  $t$  iteration with a threshold  $\epsilon$  if those positions have been updated by the distance below  $\epsilon$ :

$$\left| \frac{c^t - c^{t-1}}{c^t} \right| < \epsilon$$



Flowchart for K-Means Algorithm

### FUZZY C-MEANS CLUSTERING

For each point  $x$  we have a coefficient giving the degree of being in the  $k$ th cluster  $u_k(x)$ . Usually, the sum of those coefficients for any given  $x$  is defined to be 1:

$$\forall x \left( \sum_{k=1}^{\text{num. clusters}} u_k(x) = 1 \right).$$

With fuzzy c-means, the centroid of a cluster is the mean of all points, weighted by their degree of belonging to the cluster:

$$\text{center}_k = \frac{\sum_x u_k(x)^m x}{\sum_x u_k(x)^m}.$$

The degree of belonging is related to the inverse of the distance to the cluster center:

$$u_k(x) = \frac{1}{d(\text{center}_k, x)^m},$$

Then the coefficients are normalized and fuzzyfied with a real parameter  $m > 1$  so that their sum is 1. So

$$u_k(x) = \frac{1}{\sum_j \left( \frac{d(\text{center}_k, x)}{d(\text{center}_j, x)} \right)^{2/(m-1)}}.$$

For  $m$  equal to 2, this is equivalent to normalizing the coefficient linearly to make their sum 1. When  $m$  is close to 1, then cluster center closest to the point is given much more weight than the others, and the algorithm is similar to k-means.

**The fuzzy c-means algorithm is very similar to the k-means algorithm:**

Choose a number of clusters.

- Assign randomly to each point coefficients for being in the clusters.
- Repeat until the algorithm has converged (that is, the coefficients' change between two iterations is no more than  $\epsilon$ , the given sensitivity threshold):
- Compute the centroids for each cluster, using the formula above.
- For each point, compute its coefficients of being in the clusters, using the formula above.

The algorithm minimizes intra-cluster variance as well, but has the same problems as k-means, the minimum is a local minimum, and the results depend on the initial choice of weights. The expectation-maximization algorithm is a more statistically formalized method which includes some of these ideas: partial membership in classes. It has better convergence properties and is in general preferred to fuzzy-c-means.

### III. METHODOLOGY

Here in this section, we described our proposed hybrid fuzzy k-means (FKM) clustering in brief. First, the preprocessing has been done using median filter, which is used to remove the noise from digital images and will improve the quality of the image. Then the output of first stage will be given to the k-means clustering which gives the segmented output of de-noised image. Now, fuzzy clustering will be applied for the k-means segmented output to improve the segmentation accuracy and exact detection of tumor from MR brain images. Finally, binarization will be

used to calculate the size of the tumor based on typography and digital imaging units [21].

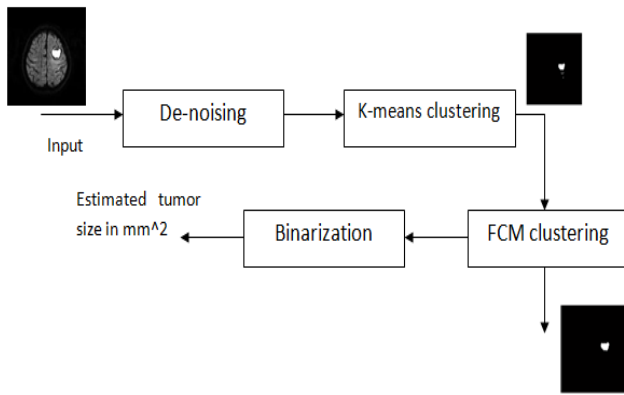


Fig2. Proposed hybrid clustering algorithm

As mentioned in 3.1 sections, while calculating the mean of cluster centroid pixels sometimes we might get the floating values, but the pixel values in an image will always be integers which does not have decimal values. Hence, we proposed a novel algorithm in fig2 to fix this error. In the proposed approach, segmented k-means output will be further segmented by fuzzy clustering for improved accuracy. Then after, the binarization method will be applied to calculate the size of tumor which has been detected by using proposed hybrid clustering algorithm.

#### IV. EXPERIMENTAL RESULTS

In this section, we had given an overview of conventional and proposed segmented results with the area of tumor. All the experiments have been done in MATLAB 2014a 32-bit version with 4GB RAM. We tested five set of images with various sizes such as 400x400, 512x512 and 600x600, which have the different stages of tumors. Then we evaluated the performance of conventional schemes Fuzzy c means, K-means and manually segmented algorithms with the proposed shaft algorithm for characterization of MR Brain tumors. The experimental results of MRI tumor detection using proposed algorithm and existing algorithms will be shown in below figure. By comparing the results our proposed approach for brain tumor detection will be more effective, accurate and reduced computational time. Fig2 shows that the segmented outputs of manually segmented, FCM, K-means and proposed algorithms, we can observe that the proposed algorithm has detected the tumor more effectively with less computational time as shown in table 1

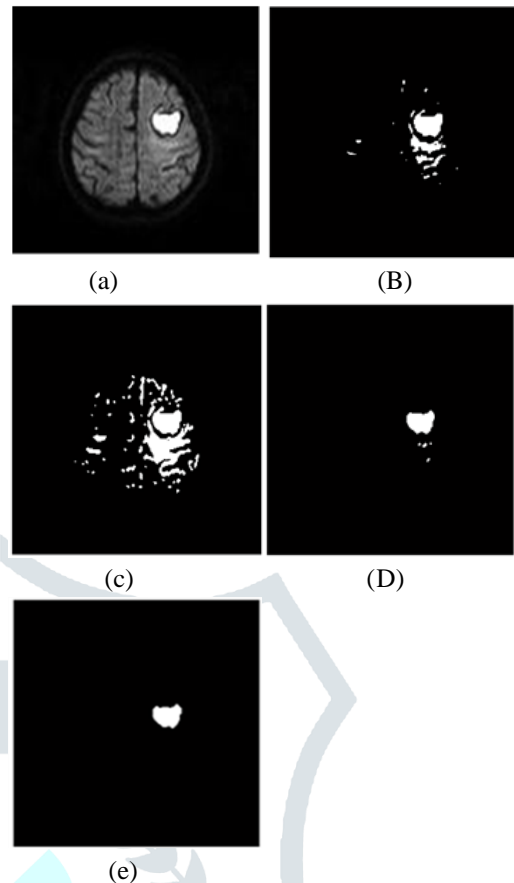


Fig2. (a) Original Image (b) Manually Segmented Image (c) Fuzzy C Means Algorithm (d) K-means segmented image (e) Proposed method

Table I Existing and proposed algorithms computational time (in seconds)

S. No	Cluster algorithm	CPU Computation time (Seconds)				
		Sample 1	Sample 2	Sample 3	Sample 4	Sample 5
1	Fuzzy C Means	11.2633	3.4008	2.9328	2.9172	4.4772
2	K-Means	0.4056	0.5148	0.4368	0.3432	0.9828
3	Proposed	0.2496	0.2340	0.2652	0.2808	0.2496

#### V. CONCLUSION

Here in this paper, we had proposed a novel MR brain image segmentation for detecting the tumor and to find the area of the tumor with improved accuracy and reduced computational time. This paper deals with the new hybrid clustering algorithm for reducing the computational time and binarization method to calculate the area in terms of  $mm^2$  based on the typography and digital imaging units. We compared the simulation results with the existing algorithms with the proposed shaft algorithm then after we found the area of tumor and calculated the CPU computational time. Finally, the proposed algorithm has performed far better than the existing algorithms with reduced computational time.

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