

Efficient Image Segmentation of Brain Tumor Detection Using Clustering Algorithms

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Abstract- Medical image segmentation has become a needed technique in research-oriented applications and clinical purposes. Magnetic Resonance Image (MRI) is used to extract the tumor regions and to map the brain for diagnosing and detect the tumor accurately. In the process of detection of tumor from MRI, segmentation plays vital role for partitioning an image. Clustering approach is widely used in medical applications particularly for brain tumor detection in abnormal MRI images. In this paper to perform well in comparison to other instead of K-means algorithm, Fuzzy C-means (FCM) algorithm and Mean shift is implemented in order to achieve better segmentation. These methods will be used for clustering analysis used to locate the exact tumor area in MRI.

Keywords- Brain Tumor, MRI, Mean-Shift, K-means and FCM.

I. INTRODUCTION

Medical image processing has become an essential part in clinical and research-oriented applications. Brain is the vital part of the human body. Brain tumor is a very serious disease occurs because of uncontrolled growth of cells in the brain. MRI is primarily used in medical imaging to visualize the structure and function of the body it provides detailed images of the body in any plane. Image segmentation is one of the most important steps leading to the analysis of processed image data to retrieve the useful information from the image [10].

Clusters are described by their member objects and by their centers. Usually centroids are used as the centers of clusters. The centroid of each cluster is the point to which the sum of distances from all objects in that cluster is minimized. By using a partitioning clustering algorithm, partitioned Clusters with a goal of obtaining low within-cluster and high between-cluster heterogeneity. That is, a cluster consists of objects which are close to each other as possible, and the objects far from other clusters [6].

The mean shift algorithm used for clustering the dataset. The process starts with defining the spherical window of radius r then calculate the mean points in the window. The spherical window move to the next position by considering next mean and the process is repeated until convergence. In every

iteration the window finds maximum peak and reach at a dense position [7]. Fuzzy sets are used to cluster data, so that each point may belong to two or more clusters with different degrees of membership. In this case, data will be associated to an appropriate membership value. In many situations, fuzzy clustering is more natural than hard clustering Objects on the boundaries between several classes are not forced to fully belong to one of the classes, but rather are assigned membership degrees between 0 and 1 indicating their partial membership. On the contrary, in hard clustering techniques, data are grouped in an exclusive way, so that if a certain datum belongs to a definite cluster then it could not be included in another cluster. Fuzzy C Means (FCM) is a very popular soft clustering technique, and similarly K-means is an important hard clustering technique [8].

The remaining part of the paper is organized as follows: Section 2 states the Mean shift Algorithm, Section 3 states the FCM algorithm is explained in detail in Section 4 states the K-means algorithm. Section 5 illustrates the results of the algorithm with qualitative and quantitative evaluations on MRI data. Finally, a summary and some concluding remarks are given in Section 6.

II. MEAN SHIFT ALGORITHM

In segmentation Mean shift is also one the brain tumor technique. Cluster analysis mainly used in this method. The Mean shift algorithm used for clustering the data. The movement starts with describing the spherical window of radius r then calculate the mean points in the window. The spherical window move to the next position by considering next mean and the process is repeated until convergence. The iteration finds maximum peak and reach at a dense position.

Kernel density estimation is the most popular density estimation method. Given n data points $x_i, i = 1, \dots, n$ in the d -dimensional space R^d , the multivariate kernel density estimator with kernel $K(x)$ and a symmetric positive definite $d \times d$ bandwidth matrix H , computed in the point x is given by [3][12]

$$f(x) = \frac{1}{n} \sum_{i=1}^n k_H(x - x_i),$$

(1)

Where

$$K_H(X) = |H|^{-1/2} K(H^{-1/2} X) \quad (2)$$

The d-variate kernel $K(x)$ is a bounded function with compact support satisfying

$$\int_{\mathbb{R}^d} K(x) dx = 1 \quad \lim_{\|x\| \rightarrow \infty} \|x\|^d K(x) = 0 \quad (3)$$

$$\int_{\mathbb{R}^d} xK(x) dx = 0 \quad \int_{\mathbb{R}^d} xx^T K(x) dx = c_k I$$

where c_k is a constant. The multivariate kernel can be generated from a symmetric univariate kernel $K_1(x)$ in two different ways

$$K^p(x) = \prod_{i=1}^d K_1(x_i) \quad K^s(x) = a_{k,d} K_1(\|x\|) \quad (4)$$

where $K^p(x)$ is obtained from the product of the univariate kernels and $K^s(x)$ from rotating $K_1(x)$ in \mathbb{R}^d , i.e., $K^s(x)$ is radially symmetric. The constant

$$a_{k,d}^{-1} = \int_{\mathbb{R}^d} K_1(\|x\|) dx$$

assures that $K^s(x)$ integrate to one, though this condition can be relaxed in our context. Either type of multivariate kernel obeys, but for our purposes, the radially symmetric kernels are often more suitable [1].

We are interested only in a special class of radially symmetric kernels satisfying

$$K(x) = c_{k,d} k(\|x\|^2) \quad (5)$$

In which case suffices to define the function $k(x)$ called profile of the kernel, only for $x \geq 0$. The normalization constant $c_{k,d}$, which makes $k(x)$ integrate to one, is assumed strictly positive.

Using fully parameterized H increase the complexity of the estimation and, in practice, the bandwidth matrix H is chosen either as diagonal

$$H = \text{diag}[h_1^2, \dots, h_d^2]$$

or proportional to the identity matrix $H=h^2I$. The clear advantage of the latter case is that only one bandwidth parameter $h>0$ must be provided; however, as can be seen from (2), then the validity of a Euclidean metric for feature space should be confirmed first. Employing only one bandwidth parameter, the kernel density estimator (1) becomes the well-known expression [3].

$$f(x) = \frac{1}{nh^d} \sum_{i=1}^n k\left(\frac{x-x_i}{h}\right) \quad (6)$$

The quality of a kernel density estimator is measured by the mean of square error between density and its estimate, integrated over the domain of definition. In practice, however, only an asymptotic approximation of this measure can be computed. Under the asymptotic, the number of data points $n \rightarrow \infty$, while the bandwidth $h \rightarrow 0$ at a rate slower than n^{-1} . For both type of multivariate kernels, AMISE is measure is minimized by Epanechnikov kernel having profile

$$k_E(x) = \begin{cases} 1-x & 0 \leq x \leq 1 \\ 0 & x > 1 \end{cases} \quad (7)$$

Which yields the radially symmetric kernel

$$k_E(x) = \begin{cases} \frac{1}{2} c_d^{-1} (d+2)(1-\|x\|^2) & \|x\| \leq 1 \\ 0 & \text{otherwise} \end{cases} \quad (8)$$

where c_d is a volume of the unit d-dimensional sphere. Note that the Epanechnikov profile is not differentiating at the boundary. The profile

$$k_N(x) = \exp\left(-\frac{1}{2} x\right) \quad x \geq 0 \quad (9)$$

Yields the multivariate normal kernel

$$k_N(x) = (2\pi)^{-d/2} \exp\left(-\frac{1}{2} \|x\|^2\right) \quad (10)$$

For both type composition (4). The normal kernel is often symmetrically truncated to have a kernel with finite support. While these two kernels will suffice for most application we are interested in, all the results presented are below valid for

arbitrary kernels within the condition to be stated [1]. Employing the profile notation, the density estimator (6) can be rewritten as

$$f_{h,k}(x) = \frac{c_{k,d}}{nh^d} \sum_{i=1}^n k \left(\left\| \frac{x - x_i}{h} \right\|^2 \right) \tag{11}$$

III. THE FUZZY C-MEANS (FCM)

The Fuzzy C-Means (FCM) clustering algorithm was first introduced by Dunn and later Bezdek improved in 1981. The FCM algorithm is mainly an iterative clustering method. The fuzzy C-means (FCM) algorithm is a fuzzy clustering method based on the minimization of a quadratic criterion where clusters are represented by their respective centres. The algorithm allows partitioning the data space; As a result, data patterns may be a member of several clusters with different membership values in each cluster. FCM uses fuzzy partitioning such that a given data point can belong to several groups with the degree of belongings specified by membership values between 0 and 1. For a given set of n data patterns, {x= x₁,...,x_k,...,x_n}, the fuzzy clustering technique minimizes the objective function, L. with respect to these centres and membership degrees as follows [2][3]

$$L = \sum_{i=1}^c \sum_{k=1}^N \mu_{ik}^m \|x_k - v_i\|^2 \tag{12}$$

where N is the number of patterns, C is the number of clusters, m is any real number (>1), which controls the fuzziness of the resulting partition, μ_{ik} is the degree of fuzzy membership of pixel x_k in the ith cluster, and ||·|| is any norm expressing the similarity measure.

The objective function is minimized when the large membership values are assigned to input patterns that are close to their nearest cluster centres and low membership values are assigned when they are far from the cluster centres [2][3].

$$\mu_{ik} = \frac{1}{\|x_k - v_i\|^{\frac{2}{m-1}} / \sum_{c=1}^c \|x_k - v_c\|^{\frac{2}{m-1}}} \tag{13}$$

and

$$v_i = \frac{\sum_{k=1}^N \mu_{ik}^m x_k}{\sum_{k=1}^N \mu_{ik}^m} \tag{14}$$

IV. K-MEANS ALGORITHM

K-means clustering groups data vectors into a predefined number of clusters, based on Euclidean distance as similarity measure. Data vectors within a cluster have small Euclidean distances from one another, and are associated with one centroid vector, which represents the "midpoint" of that cluster. The centroid vector is the mean of the data vectors that belong to the corresponding cluster. Hence the k-means algorithm attempts to find the best points in space as the cluster centroids [5].

The standard K-means algorithm is summarized as follows:
 (a) For each data vector, assign the vector to the class with the closest centroid vector, where the distance to the centroid is determined using

$$d(z_p, m_j) = \sqrt{\sum_{k=1}^{N_d} (z_{pk} - m_{jk})^2} \tag{15}$$

where k

subscripts the dimension.

(b) Recalculate the cluster centroid vectors, using until a stopping criterion is satisfied

$$m_j = \frac{1}{n_j} \sum_{\forall z_p \in C_j} z_p \tag{16}$$

N_d denotes the input dimension, i.e. the number of parameters of each data vector; N_o denotes the number of data vectors to be clustered; N_c denotes the number of cluster centroids (as provided by the user), i.e. the number of clusters to be formed; z_p denotes the p-th data vector; m_j denotes the centroid vector of cluster j; n_j is the number of data vectors in cluster j; C_j is the subset of data vectors that form cluster [4].

The K-means clustering process can be stopped when any one of the following criteria are satisfied: when the maximum number of iterations has been exceeded, when there is little change in the centroid vectors over a number of iterations. or when there are no cluster membership changes. For the purposes of this study, the algorithm is stopped when a user-specified number of iterations have been exceeded [5].

V. EXPERIMENTAL RESULTS

The segmentation methods are applied to brain tumor MRI images.

A. Peak-signal-to-noise-ratio (PSNR):

PSNR is the evaluation standard of the reconstructed image quality, it is generally used in measuring the quality and it is important measurement feature. PSNR is measured in decibels (dB) and is given by:

$$PSNR = 10 \log (255^2 / MSE)$$

Where the value 255 is maximum possible value that can be attained by the image. Mean square error (MSE) is defined as $MSE = \frac{1}{M \times N} \sum_{i=1}^M \sum_{j=1}^N (I(i,j) - \hat{I}(i,j))^2$ Where $M \times N$ (4) is the size of the original image. Higher the PSNR value is better than constructed image.

B. Accuracy

The accuracy with the test is its capability to identify the patient and healthy cases accurately. To calculate the accuracy of the test, we have estimate the quantity of true positive and true negative to all evaluated cases. Mathematically, this is state as [3]:

True positive (TP) = the number of case accurately defined as patient

False negative (FN) = the number of case inaccurately defined as healthy

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

Sensitivity:

The sensitivity of the test is its capability to identify the patient cases accurately. To calculate it, we have calculated the quantity of true positive in patient cases. Mathematically, this is state as:

$$\text{Sensitivity} = \frac{TP}{TP + FN}$$

Specificity:

The specificity of the test is its ability to identify the healthy cases accurately. To calculate it, we have calculated the quantity of true negative in healthy cases. Mathematically, this is state as:

$$\text{specificity} = \frac{TN}{TN + FP}$$

Table 1: Performance evaluation

MRI Image	Accuracy			PSNR		
	Mean Shift	FCM	K-means	Mean Shift	FCM	K-means
1	0.8418	0.8314	0.8112	27.8534	23.3765	26.1846
2	0.8517	0.8427	0.8329	29.6295	27.6182	29.3168
3	0.8339	0.8367	0.8214	27.6016	26.7291	26.2145
4	0.8474	0.8329	0.8274	28.9672	27.7192	27.8215

VI. CONCLUSION

In this paper, we presented image segmentation, methods Mean Shift, Fuzzy C-mean and K-Means is presented. The experiments were conducted on multiple tumor images. The tumors are located at various locations. The effectiveness of these algorithms have verified by some experimental results to express its improved performance in detecting the shape and spread of tumor by calculating the parameters of tumor in magnetic resonance image. Mean shift algorithm is an efficient method of clustering, which segments the magnetic resonance image (MRI) into multiple separated regions will support for better therapy.

VII. REFERENCES

- [1]. Dorin Comaniciu, Peter Meer, "Mean Shift: A Robust Approach Toward Feature Space Analysis", IEEE Transactions On Pattern Analysis And Machine Intelligence, vol. 24, no. 5, may 2002.
- [2]. Sudip Kumar Adhikari, Jamuna Kanta Sing, Dipak Kumar Basub, Mita Nasipuri, "Conditional spatial fuzzy C-means clustering algorithm for segmentation of MRI images", Applied Soft Computing, 2015.
- [3]. Mandip kaur, Prabhpreet kaur, "Efficient Image Segmentation Of Brain Tumor Detection Using Fuzzy C-Mean And Mean-

Shift", International Journal of Advanced Research in Computer Science, 2017.

- [4]. Alireza Ahmadyfard, Hamidreza Modares, "Combining PSO and k-means to Enhance Data Clustering", IEEE, 2008.
- [5]. DW van der Merwe, AP Engelbrecht, "Data Clustering using Particle Swarm Optimization", IEEE, 2003.
- [6]. Zeynel Cebeci, Figen Yildiz, "Comparison of K-Means and Fuzzy C-Means Algorithms on Different Cluster Structures", Journal of Agricultural Informatics, 2015.
- [7]. Bhavana B. Ghotekar, K. J. Mahajan, " MRI Brain image Segmentation and Classification: A Review" International Research Journal of Engineering and Technology, 2016.
- [8]. Dibya Jyoti Bora, Dr. Anil Kumar Gupta, "A Comparative study Between Fuzzy Clustering Algorithm and Hard Clustering Algorithm", International Journal of Computer Trends and Technology, 2014.
- [9]. M. Sucharitha, D. Jackson and M. Dev Anand, "Brain Image Segmentation Using Adaptive Mean Shift Based Fuzzy C Means Clustering Algorithm", Procedia Engineering, 2012.
- [10]. Vishal B. Padole, "An Efficient Method for Detection of Brain Tumor in MRI Images", IJARCET, 2014.
- [11]. N Senthilkumaran and J Thimmiraja, "A Study on Histogram Equalization for MRI Brain Image Enhancement", ACEEE, 2014.
- [12]. M.P.W and, M.Jones, "Kernel Smoothing, Chapman and Hall", 1995.