

Comparison of Segmentation based on Threshold and KMeans Method

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Abstract

The segmentation, detection, and extraction of infected tumour area from magnetic resonance (MR) images are a primary concern but a tedious and time taking task performed by radiologists or clinical experts, and their accuracy depends on their experience only. So, the use of computer aided technology becomes very necessary to overcome these limitations. In this study, to improve the performance and reduce the complexity involves in the medical image segmentation process, we have investigated many algorithm methods are available in medical imaging amongst them the Threshold technique brain tumour segmentation process gives an accurate result than other methods for MR images. The proposed method compare with the K-means clustering methods, it gives a cluster of images. The experimental results of proposed technique have been evaluated and validated for performance and quality analysis on magnetic resonance brain images, based on accuracy, process time and similarity of the segmented part. The experimental results achieved more accuracy, less running time and high resolution.

Keywords:

Threshold, k-means clustering

1. Introduction

The uncontrolled growth of cancerous cells in the brain is called as tumours. The brain tumour is identified by benign or malignant. Malignant is the active cancerous cells with rapid growth in the brain. The benign cell has not the dangerous cancerous cells. The benign cells can be converted into malignant cells but the malignant cells never become benign cells. This study addresses the problems of segmentation of abnormal brain tissues among normal tissues such as gray matter (GM), white matter (WM), and cerebrospinal fluid (CSF) from magnetic resonance (MR) images using Threshold technique [1, 2].

To detect infected tumour tissues from medical imaging modalities, segmentation is employed. Segmentation is necessary and important step in image analysis; it is a process of separating an image into different regions, blocks

or clusters sharing common and identical properties, such as contrast, patterns of pixels, and distance around the boundary of the region, and gray level.

2. Literature Survey

Automatic identifying and extraction of brain tumour has proposed techniques like Threshold, K-Means Clustering, Fuzzy Clustering Means (FCM), Pulse Couple Neural Network(PCNN) algorithm, Expectation Maximization (EM) segmentation algorithm, Watershed and Hierarchical Clustering (WHC) algorithm, support vector machine (SVM), artificial neural network (ANN) algorithm . The above literature survey has revealed that some of the techniques are invented to obtain segmentation only; some of the techniques are invented to obtain feature extraction and some of the techniques are invented to obtain classification only^[3,4]. K-means clustering algorithm gives effective segmentation of infected tumour region and analysis on combined approach could not be conducted in all the published literature.

3. Threshold

In Threshold technique is based on histogram to identify the infected areas by deep and sharp valley between two peaks representing objects and background respectively.

The threshold can be chosen at the bottom of this valley. However, for most MR images, it is often difficult to detect the valley bottom precisely when the valley is flat and broad, imbued with noise, or when the two peaks are extremely

unequal in height, often producing no traceable valley. The threshold method can choose the value and separate the object from its background:

Let N be the set of natural numbers, (x, y) be the spatial coordinate of a digitized image, and $G = \{0, 1, \dots, I - 1\}$ be a set of positive integers representing gray levels. Then, an image function can be defined as the mapping $f: N \times N + G$. The brightness (i.e., gray level) of a pixel with coordinate (x, y) is denoted as $f(x, y)$.^[5]

Let $t \in G$ be a threshold and $B = \{b_0, b_1\}$ be a pair of binary gray levels and $b_0, b_1 \in G$. The result of threshold an image function $f(.,.)$ at gray level t is a binary image function $f_t: N \times N \rightarrow B$, such that

$$f_t(x, y) = b_0 \text{ if } f(x, y) < t \\ b_1 \text{ if } f(x, y) \geq t.$$

In general, a threshold method is one that determines the value t^* of t based on a certain criterion.^[5] If t^* is determined solely from the gray level of each pixel, then the threshold method is point-dependent. If t^* is determined from the local property (e.g., the local gray level distribution) in the neighbourhood of each pixel.^[6] Threshold technique is one that thresholds the entire image with a single threshold value, whereas a local threshold technique is one that partitions a given image into sub images and determines a threshold for each of these sub images.^[7,8] Let the number of pixels with gray level i be n_i . Then the total number of pixels in a given image is

$$n = \sum_{i=0}^{i-1} n_i$$

The probability of occurrence of gray level i is defined as

$$p_i = \frac{n_i}{n}$$

Also, by convention the gray level 0 is the darkest and the gray level $l - 1$ is the lightest.^[9,10]

Threshold algorithm applied on the dataset which is in the DICOM method that has converted into JPEG images then apply the Threshold level of 75. The value of threshold will set by the contrast of an image.

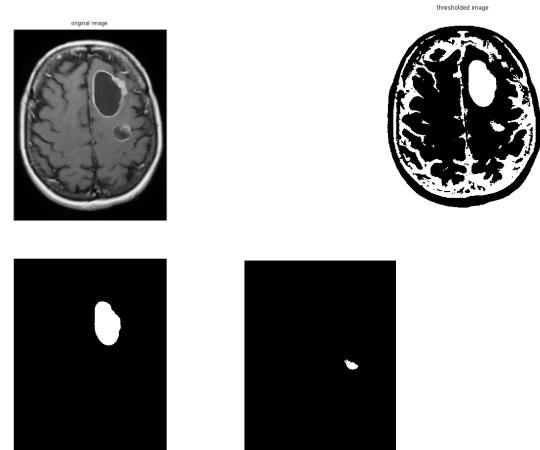


Figure 1 Segmented image by Threshold technique

4. The k-means algorithm

Since the simplest form of K-means clustering algorithm, it is used by most of the researchers in the field of data mining. The process of k-Means follows eminent and simple way to classify a given data set by means of a certain number of clusters.^[11,12] The k-means clustering is a method used to divide n patterns $\{x_1, x_2, \dots, x_n\}$ in d dimensional space into k clusters (assume k clusters). The result is a set of k clusters based on k centres, each of which is located at the centroid of the separated dataset. This algorithm can be shortened in the following steps:

- Step 1: Give the number of cluster value as k .
- Step 2: Randomly choose the k cluster centres.
- Step 3: Calculate mean or centre of the cluster.
- Step 4: Calculate the distance between each pixel to each cluster centre.
- Step 5: If the distance is near to the centre then move to that cluster.
- Step 6: Otherwise move to next cluster.
- Step 7: Re-estimate the centre.
- Step 8: Repeat the process until the centre doesn't move.

The k-means clustering algorithm fixes the k value as 5 in MR image.

In this research work, tumour detection by identifying the pixel values in MRI brain images

are taken for analysis. The source code is written in MATLAB software. The k-Means algorithm is applied to find the clusters of MRI images by dividing the image into 5 groups. The various stages of images are given in the Figure 2.

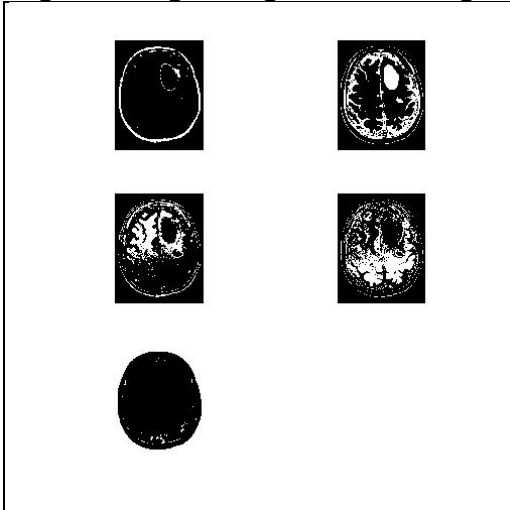


Figure 2. K means algorithm output when k=5

The steps involved in clustering the MRI brain images by k-Means algorithm are given below.

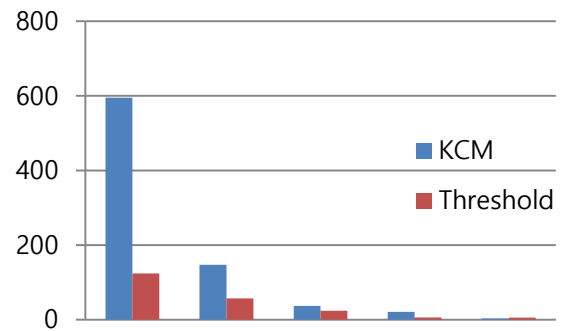
- Step 1: Insert the original images as input.
 - Step 2: Convert the fetched MRI DICOM format file into .JPG
 - Step 3: Cluster dataset images.
 - Step 4: Find out the ‘k’ in image by algorithm itself.
 - Step 5: Get the clustered objects.
- Result of segmented image in Figure 3.



Figure 3 Segmented tumour by K-means clustering

The above figures from figure-1 and figure-3 were calculated and isolated brain tumour by two proposed methods. The first stage is to determine the area of segmented image. The second stage is to determine the process time, perimeter, minimum axis and maximum axis of the segmented image. Segmented areas are automatically calculated from MR images. The segmented images compare by the two methods.

Methods	Area	Perimeter	Major Axis	Minor Axis	Pocess Time
KCM	595	147	37	21	3.3252
Threshold	124	57	24	6	5.5813



5. Conclusion

In this paper, a fully automated tumour detection method based on Threshold technique and k-means methods are proposed. Threshold is identified by its intensity value which is used as a method to find the region that contains tumour in brain MR images. The K-means clustering gives an exact image representation of segmented images by the clustering methods. The K-means clustering has minimum processing time and also gives an accurate infected area. Therefore, the entire tumour area identification approach is extendable to 3D to convert into volumetric data. The K-means clustering method is a suitable method to segment brain MR images. This method can also be applied to other medical images, e.g., heart or liver MRI.

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