



ISBN	978-81-929866-5-4
Website	icca.co.in
Received	14 – March– 2016
Article ID	ICCA011

VOL	05
eMail	icca@asdf.res.in
Accepted	02 - April – 2016
eAID	ICCA.2016.011

An Image Segmentation and Classification for Brain Tumor Detection using Pillar K-Means Algorithm

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Abstract – Human brain is the most complex structure where identifying the tumor like diseases are extremely challenging because differentiating the components of a brain is complex. In this paper, pillar k-means algorithm is used for segmentation of brain tumor from magnetic resonance image (MRI). Generally, the brain tumor is detected by radiologist through analysis of MR images which takes longer time. The pillar k-means algorithm's experimental results clarify the effectiveness of our approach to improve the segmentation quality, accuracy, and computational time. Classify, the tumor from the brain MR images using Bayesian classification.

Keywords – Pillar k-means algorithm, Magnetic resonance image (MRI), Brain tumor, Bayesian classification.

I. INTRODUCTION

Each cell in the human body has its special function and will grow and divide in an order to keep the body healthy. When cells lose the ability to control their growth the cell division starts without any order. The extra cells form as a mass of tissue called as tumor. Tumors that originate within brain tissue are known as primary brain tumor. Brain tumor will be differentiated by grade I to grade IV. Cells from higher grade tumors are more abnormal and grow faster than grade I tumors. The amount of drug to be pumped into the human body to cure the tumor cells depends on the size of the tumor and this can be obtained accurately by Magnetic Resonance imaging (MRI) scan or a CT scan (Computed Tomography). However, in this paper, MRI scan images are used for the analysis. MRI is a very powerful tool to diagnose the brain tumors. It gives pictures of the brain and requires no radiation. The acquired image is analyzed using image processing methods. Image segmentation and clustering procedure are introduced to estimate the area of the tumor. Image segmentation is classified into Pixel based methods, regional methods and edge based methods. In this paper the brain tumor images are partitioned into multiple segments as sets of pixels using pixel based segmentation. The MRI Image represents white and grey color pixel elements. White color pixel data points are related to tumor cells and the Gray color pixel data points relate to normal cells. Collection of data points of the pixels that belongs to the same color will be quantified using Euclidian distance method. The clusters may contain large number of pixels. The pixels may be either close or far from the cluster center. If the cluster centers are known, allocate each pixel point to the closest cluster center. Each center is the mean of the points allocated to that cluster. In order to estimate the area of the tumor, Manual segmentation, Fuzzy C-Means, K-Means and Pillar K-Means clustering algorithms are used to obtain the true area of the tumor.

II. Existing Overview

Markov random field is used along with the CS algorithm to find the optimum values for a function. Threshold for the segmentation process is obtained by calculating centre pixel intensity from the label's kernel. The existing method is based on the threshold and region growing. In case of the region growing based segmentation it needs more user interaction for the selection of the seed. Seed is nothing but the center of the tumor cells the regional growing method ignored the spatial characteristics. Normally spatial characteristics are important for malignant tumor detection. This is the main problem of the current system.

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III. Proposed Algorithm

The proposed method is a combination of two algorithms. In the literature survey many algorithms were developed for segmentation. But they are not good for all types of the MRI images. This paper proposes a new approach for MRI brain tumor detections that utilizes Pillar Algorithm to optimize K-means clustering. The Pillar algorithm performs the pillars placement which should be located as far as possible from each other to withstand against the pressure distribution of a roof, as identical to the number of centroids amongst the data distribution. It designates the initial centroids positions by calculating the accumulated distance metric between each data point and all previous centroids, and then selects data points which have the maximum distance as new initial centroids. The segmentation process by this approach includes a new mechanism for clustering the elements of high-resolution images in order to improve precision and reduce computation time. It can improve significantly performance of the information extraction, such as color, shape, texture, and structure.

The Pillar algorithm is described as follows. Let $X = \{x_i \mid i=1, \dots, n\}$ be data, k be number of clusters, $C = \{c_i \mid i=1, \dots, k\}$ be initial centroids, $SX \subseteq X$ be identification for X which are already selected in the sequence of process, $DM = \{x_i \mid i=1, \dots, n\}$ be accumulated distance metric, $D = \{x_i \mid i=1, \dots, n\}$ be distance metric for each iteration, and m be the grand mean of X . The following execution steps of the proposed algorithm are described as:

1. Set $C = \emptyset$, $SX = \emptyset$, and $DM = []$
2. Calculate $D \square \text{dis}(X, m)$
3. Set number of neighbors = $\alpha * n / k$
4. Assign $\square (D)$
5. Set neighborhood boundary = $\beta *$
6. Set $i=1$ as counter to determine the initial centroids
7. $DM = DM + D$
8. 8. Select $\mathcal{K} \square \text{xargmax}(DM)$ as the candidate for initial centroids
9. $SX = SX \cup \mathcal{K}$
10. Set D as the distance metric between X to \mathcal{K} .
11. Set $no \square$ number of data points fulfilling $D \leq$
12. Assign $DM(\mathcal{K}) = 0$
13. If $no <$, go to step 8
14. Assign $D(SX) = 0$
15. $C = C \cup \mathcal{K}$
16. $i = i + 1$
17. If $i \leq k$, go back to step 7
18. Finish in which C is the solution as optimized initial centroids.

Steps involved in this system are: pre-processing, feature extraction, association with segmentation and classification. The pre-processing step has been done using the median filtering process and features have been extracted using adaptive histogram equalization technique. This paper presents a new approach to image segmentation using Pillar K-means algorithm. This segmentation method includes a new mechanism for grouping the elements of high resolution images in order to improve accuracy and reduce the computation time. The system uses K-means for image segmentation optimized by the algorithm after Pillar.

The Bayesian algorithm is a set of rules for using evidence (data) to change your beliefs, an algorithm is a set of rules for doing a calculation. Here we using Bayesian algorithm for classification of tumor (i.e) stage I, stage II, stage III, or stage IV.

Block Diagram

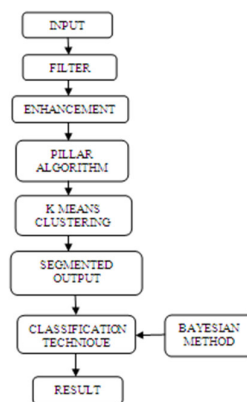


Figure 1.1. block diagram of brain tumor segmentation using pillar k-means algorithm

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Feature Extraction

The feature extraction is extracting the cluster which shows the predicted tumor at the FCM output. The extracted cluster is given to the thresholding process. It applies binary mask over the entire image. It makes the dark pixel become darker and white become brighter. In threshold coding, each transform coefficient is compared with a threshold. If it is less than the threshold value then it is considered as zero. If it is larger than the threshold, it will be considered as one. The thresholding method is an adaptive method where only those coefficients whose magnitudes are above a threshold are retained within each block. Let us consider an image 'f' that has the k gray level. An integer value of threshold T, which lies in the gray scale range of k. The thresholding process is a comparison. Each pixel in 'f' is compared to T. Based on that, binary decision is made. That defines the value of the particular pixel in an output binary image 'g': $g(n) = „0“$ if $f(n) \geq T$ „1“ if $f(n) < T$

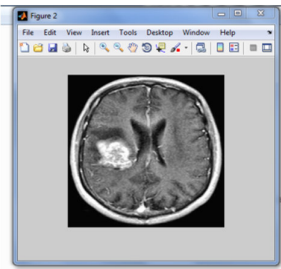
Approximate Reasoning In the approximate reasoning step the tumor area is calculated. That is the image having only two values either black or white (0 or 1). Here 256x256 jpeg image is a maximum image size. The binary image can be represented as a summation of total number of white and black pixels.

Where, P = number of white pixels 1 Pixel = 0. 264 mm

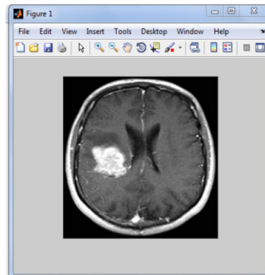
The area calculation formula is

$$\text{Size_of_Tumor}, S = (\sqrt{P}) * 0.264$$

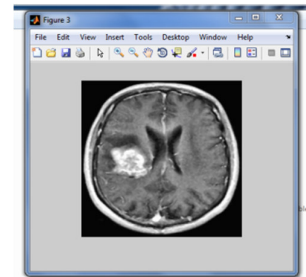
IV. Comparison and Results



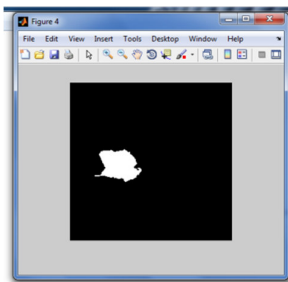
Input MRI



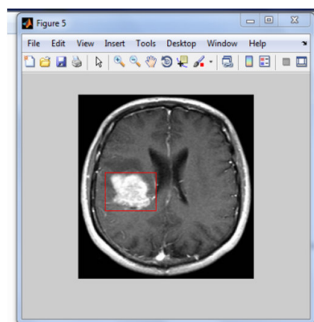
Filter output



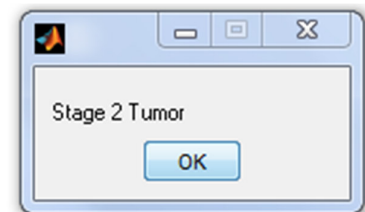
Enhancement output



Pillar output



Segmentation output



Bayesian classification output

The above pictures are the step by step output of pillar k-means algorithm.

```

Time for Segmentation:
Pillar K Mean:

eptime =

        6.1098

Cuckoo Search:

ectime =

       10.3453

Finding keypoints...
59 keypoints found.
Stage 2 Tumor

```

Here, from above figure we show computation time comparison between pillar k-means algorithm and cuckoo search algorithm. Where, cuckoo search takes 10.3 seconds for segmentation but pillar k-means algorithm takes just 6.1 seconds for segmentation and additionally it describes the classification of tumor (i.e) stages of tumor like stage I, stage II, stage III, or stage IV.

V. Conclusion

For treatment of Brain tumor, size and location of the tumor is to be determined. K-Means and Pillar K-Means Algorithms are used to estimate the area of the tumor. The proposed Pillar K-Means algorithm has shown better results than the other methods and is able to optimize the computation time and hence improved the precision and enhanced the quality of image segmentation. And also location of the tumor may be determined in addition with the size i.e. area of the tumor and the location of the tumor is very important for applying the radiation or chemo therapy.

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