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DETECTION OF BRAIN TUMOURS USING IMPROVED PILLAR K-MEANS ALGORITHM

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ABSTRACT

This paper presents a new approach to image segmentation using improved 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 algorithm considers the placement of pillars should be located as far from each other to resist the pressure distribution of a roof, as same as the number of centroids between the data distribution. This algorithm is able to optimize the K-means clustering for image segmentation in the aspects of accuracy and computation time. This algorithm distributes all initial centroids according to the maximum cumulative distance metric. This paper evaluates the proposed approach for image segmentation by comparing with K-means clustering algorithm and fuzzy c-means clustering and pillar k-means algorithm. Experimental results clarify the effectiveness of our approach to improve the segmentation quality and accuracy aspects of computing time.

Index terms: K-means, Centroids, Fuzzy, Clustering, Segmentation.

INTRODUCTION

Brain is the center of human Central nervous system. The brain is a complex organ as it contains 50-100 billion neurons forming a gigantic neural network. Detection of anatomical brain structures with their exact location is important for treatments lke radiation therapy and surgery. Radiologists perform the diagnosis of brain tumour manually on MRI images but it being time consuming and error prone as large no of image slices and the large variations between them. DICOM (Digital Imaging and Communications in Medicine) plays a key role as it is the standard for handling, storing, reading, viewing and writing, printing information for medical Imaging. The techniques like MRI (Magnetic Resonance Imaging), NMRI (Nuclear Magnetic Resonance Imaging), MRT (Magnetic Resonance Tomography) and CT (Computed Tomography) Scan are being widely used to get the images for processing to detect the tumour, out of which MRI is widely used as it provides much greater contrast between the different soft tissues of the body compared to Segmentation techniques like K means clustering, Fuzzy C means, Hierarchical, Watershed Algorithms, and Self Organizing Maps are widely implemented depending on which methodology is required as it can be Region growing, frequency domain based or thresholding based which classifies the MRI Images. A tumour is an acronym for a neoplasm or a solid lesion formed by an abnormal growth of cells (termed neoplastic) which looks like a swelling. Brain Tumours are composed of the cells that exhibit abnormal and unrestrained cell division. Brain tumour can be benign or malignant, benign being non-cancerous and malignant are cancerous. Malignant tumours are classified in to two types like Primary and Secondary tumours. Benign tumour is less harmful compared to malignant as in malignant tumour it spreads rapidly invading other tissues of brain, progressively worsening the condition causing death. MRI images to detect brain tumour classifies the tumour depending on whether the brain is an abnormal tissue containing normal volume brain tissues like white matter, gray matter and CSF (cerebro-spinal fluid) but also have some slices contain pathology like edema and necrosis hence making them abnormal brain tissues. Based on the CSF Symmetry on the vertical axis through the brain center a normal volume brain tissue and an abnormal volume brain tissue could be classified. The MRI images can be of T1, T2 weighted type of which T2 weighted Images are being widely used in Medical Imaging as in this case of cerebral and spinal study, the CSF (cerebrospinal fluid) are lighter in T2 weighted images as they are acquired using fast echo spin sequence whereas the T1 weighted images are acquired using a spin echo sequence. Primary focus on exact brain tumours location and its extraction with parameters like area and time to yield faithful and error free output.

Segmentation is process of partitioning the image into different parts having similar features. The pre-processing stages needs to done on the image initially, followed by clustering algorithms and towards the fag end thresholding be done for the extraction of the tumour which is the region of interest (ROI) from the entire image. The features for thresholding being intensity based, area based Thresholding is the vital part of segmentation as the tumour must be isolated from the brain image. The below is a flowchart (sequence) of exactly how a tumour is detected in our system.

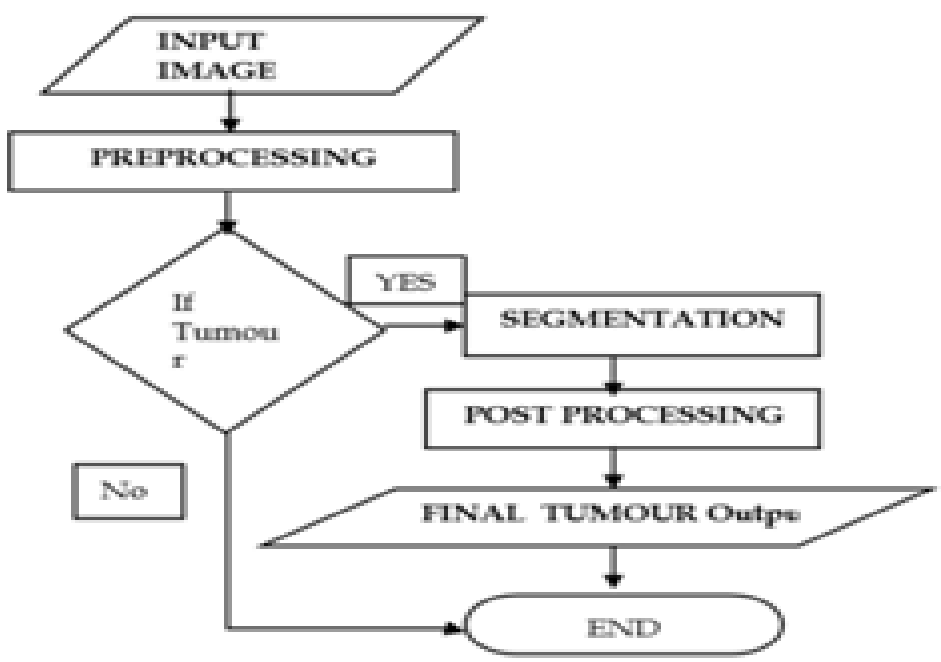


Fig:1 Flowchart for brain tumour detection

EXISTING METHODS

Cluster analysis

Clustering is a set of data with similar characteristics. In dividing the data into groups of similar objects are used, here the distance functions are used to determine the similarity of the two objects in the data set. Cluster analysis or clustering is the assignment of a set of observations into subsets (called clusters) so that observations in the same cluster are similar in some sense. Clustering is a method of unsupervised learning, and a common technique for statistical data analysis used in many fields, including machine learning, data mining, pattern recognition, image analysis and bioinformatics.

A. K-means clustering

One of the most popular and widely studied clustering algorithms to separate the input data in the Euclidian space is the K-Means clustering.

It is a non hierarchical technique that follows a simple and easy way to classify a given dataset through a certain number of clusters (we need to make an assumption for parameter k) that are known a priori.

The K-Means algorithm is built using an iterative framework where the elements of the data are exchanged between clusters in order to satisfy the criteria of minimizing the variation within each cluster and maximizing the variation between clusters.

When no elements are exchanged between clusters, the process is halted.

The K-means algorithm is an iterative technique that is used to partition an image into K clusters. The basic algorithm is:

- Pick K cluster centers , either randomly or based on some heuristic
- Assign each pixel in the image to the cluster that minimizes the distance between the pixel and the cluster center
- Re-compute the cluster centers by averaging all of the pixels in the cluster.
- Repeat steps 2 and 3 until convergence is attained (e.g. no pixels change clusters)

In this case, distance is the squared or absolute difference between a pixel and a cluster center. The difference is typically based on pixel color, intensity, texture, and location, or a weighted combination of these factors. K can be selected manually, randomly, or by a heuristic. This algorithm is guaranteed to converge, but it may not return the optimal solution. The quality of the solution depends on the initial set of clusters and the value of K.

A1.Fuzzy c-means clustering:

The fuzzy logic is a way to processing the data by giving the partial membership value to each pixel in the image. The membership value of the fuzzy set is ranges from 0 to 1. Fuzzy clustering is basically a multi valued logic that allows intermediate values i. e. , member of one fuzzy set can also be member of other fuzzy sets in the same image. There is no abrupt transition between full membership and non membership. The membership function defines the fuzziness of an image and also to define the information contained in the image.

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 , the given sensitivity threshold).
- Compute the centroids for each cluster.
- For each point, compute its coefficients of being in the clusters.

Disadvantage

- K-means does not yield the same result with each run, since the resulting clusters depend on the initial random assignments (the k - means algorithm addresses this problem by seeking to choose better starting clusters).
- K-means minimizes intra - cluster variance, but does not ensure that the result has a global minimum of variance.
- Another disadvantage is the requirement for the concept of a mean to be definable which the case is not always.
- Fuzzy c-means produces better result than k-means but not robust to noisy images.

PROPOSED METHODS

A. Pillar k-means algorithm:

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 $X=\{xi \ |i=1,\ldots,n\}$ be data, k be number of clusters, $C=\{ci \mid i=1,\ldots,k\}$ be initial centroids, $SX \subseteq X$ be identification for X which are already selected in the sequence of process, $DM=\{xi \ |i=1,\ldots,n\}$ be accumulated distance metric, $D=\{xi \mid i=1,\ldots,n\}$ be distance metric for each iteration, and m be the grand mean of X. The proposed algorithm is described below: Pillar Algorithm

Step1. Initialize Number of Pillars (K=3)

Step2. Assign Random Centers to each pillar

Step3. Initialize Null Matrix C = [ ] , SX = [ ]

Step 4. Calculate the mean of Pixel values and the maximum value from the set of pixels

Step 5. Calculate the distance between Mean and Pixels of Input Image

Step 6. Find the pixels which are neighboring to the pillar and estimate the neighboring boundary distance (Nbds).

Step7. Initialize i = 1 : K and Calculate the Maximum Value using Step 4

Step8. If the maximum value equal to the distance between mean and pixels of image

Step9: Then SX = Union of SX, Maximum value of distance else Go to Step 4

Step10. Now Calculate Minimum Distance of D and Move the Pixel to the relevant pillar

Step11. Now i= i+1;

However, the high resolution MRI Image data points take longer time for computation.

B. Improved pillar k-means algorithm:

It is one of the proposed algorithm which is similar to pillar algorithm. However, the computation time may take long time if we apply the Pillar algorithm directly for all elements of high resolution image data points. In order to solve this problem in this, we reduce the image size to 5%, and then we apply the algorithm. After getting the optimized initial centroids, we apply clustering using the K-means algorithm and then obtain the position of final centroids. We use these final centroids as the initial centroids for the real size of the image, and then apply the image data point clustering using K-means. This mechanism is able to improve segmentation results and make faster computation for the image segmentation.

APPLICATION

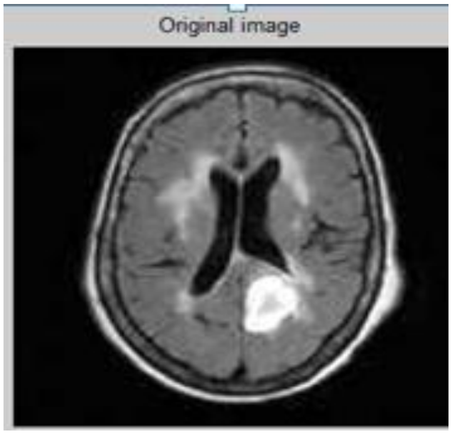
1. In medical image processing.

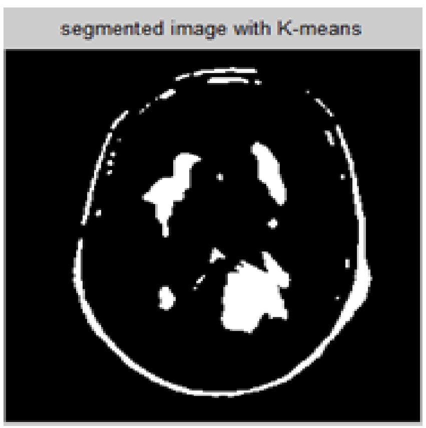
CONCLUSION

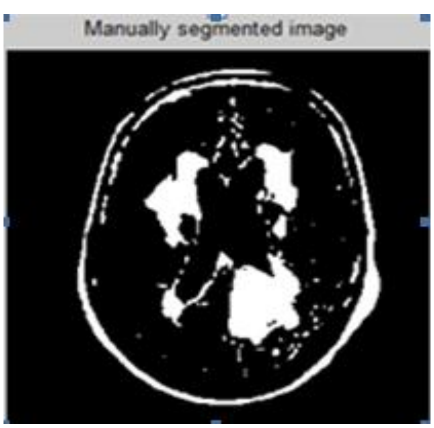
In this Paper, we proposed a new approach to image segmentation using Pillar K-means algorithm and improved pillar k-means algorithm. The system applies the k-means algorithm optimized after Pillar. This algorithm is able to optimize the K-means clustering for image segmentation in the aspects of accuracy and computation time. The experimental results show that our proposed approach for image segmentation using Pillar-k-means algorithm and improved pillar k-means is able to improve the accuracy and enhance the quality of image segmentation. We also made the computation time faster than K-means and maintaining the quality of result. In future 3D assessment of brain using 3D slices with matlab can be developed.

SIMULATION RESULTS

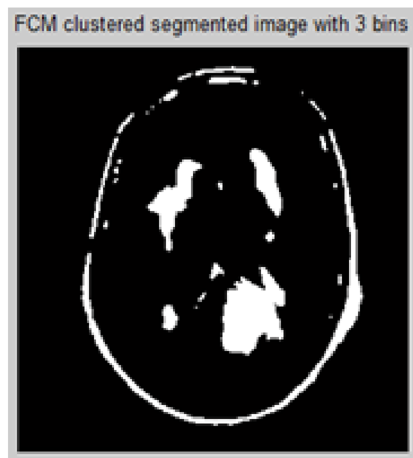
K-means clustering:

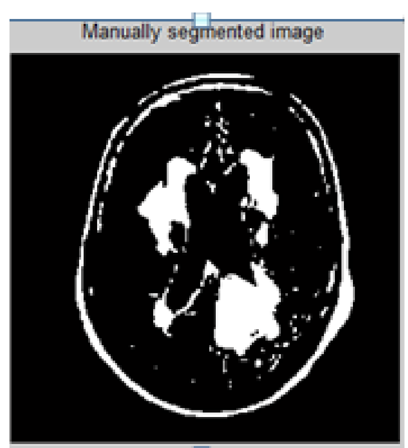




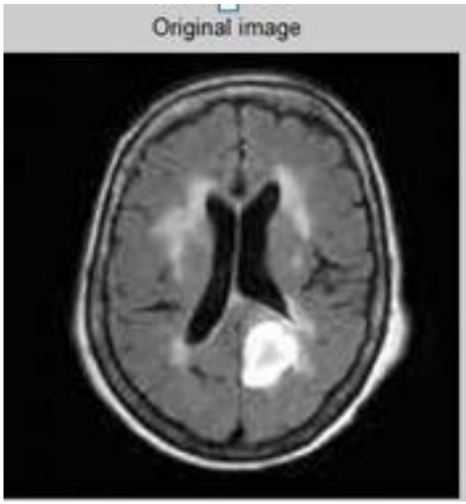


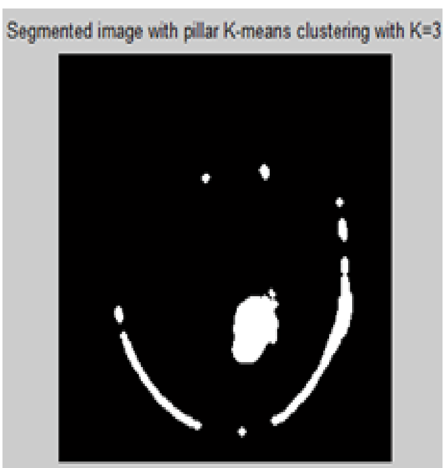
Fuzzy c-means clustering:

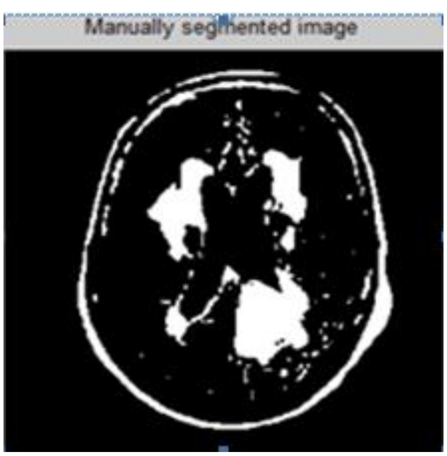




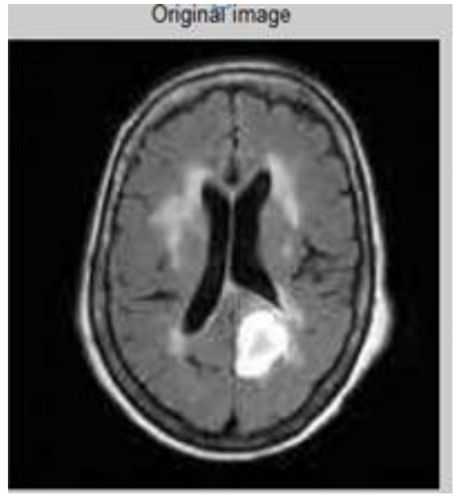
Pillar k-means algorithm:

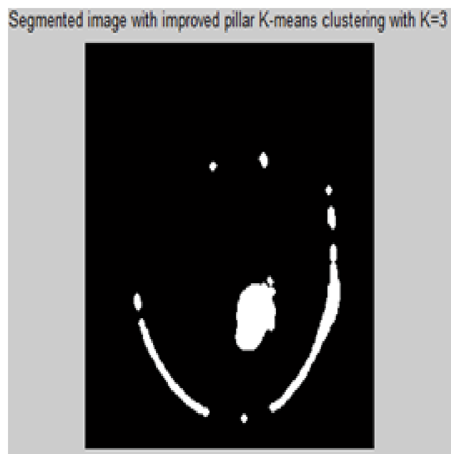


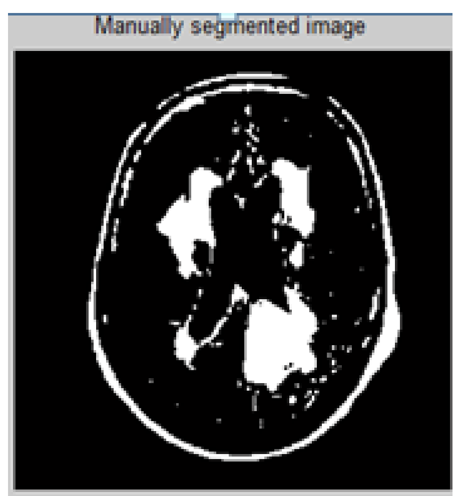




Improved pillar k-means algorithm:







COMPARISON TABLE FOR K-MEANS, FCM, PILLAR K-MEANS, IMPROVED PILLAR K-MEANS

K-means	FCM	Pillar k-means	Improved pillar k-means
SI=0.7855	SI=0.7793	SI=0.4954	SI=0.4954
EF=0.6709	EF=0.6612	EF=0.3428	EF=0.1121
OF=0.0372	OF=0.0358	OF=0.0411	OF=0.0244
TM=0.3594	TM=1.9688	TM=0.1875	TM=0.0781

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