Tuhin Utsab Paul, Samir Kumar Bandhyopadhyay / International Journal of Engineering Research and Applications (IJERA) ISSN: 2248-9622 www.ijera.com
Vol. 2, Issue 3, May-Jun 2012, pp. 226-231

Segmentation of Brain Tumor from Brain MRI Images Reintroducing K – Means with advanced Dual Localization Method

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Abstract—
Detection and segmentation of brain tumors in Magnetic Resonance Images (MRI) is an important but very time-consuming task that required to be completed manually by medical experts. Automation of this process is a challenging task due to the occurrence of the high degree of intensity and textural similarity between normal areas and tumor areas in Brain MRI images. In this paper we propose a fully automated two step segmentation process of brain MRI images. Firstly, the scull is stripped from the MRI images by generating a scull mask from the original MRI image. Finally, an advanced K – means algorithm improvised by two level granularity oriented grid based localization process based on standard local deviation is used to segment the image into gray matter, white matter and tumor region. Finally, the length and breadth of the tumor is assessed.

Keywords- *MRI; segmentation; K – means; brain tumor;*

I. INTRODUCTION

The past decade had witnessed a rapid and multi faced increase in the applications of image processing. In today's digital era, capturing, storing and analysis of medical image had been digitized [1]. Even with state – of – the – art techniques, detailed interpretation of medical image is a challenge due to the constraint of time and accuracy. The challenge gets more demanding especially in regions with abnormal color and shape which needs to be identified and interpreted by radiologists for future studies [1]. The key task in designing such image processing and computer vision applications is the accurate segmentation of medical images. Image segmentation is the process of partitioning different regions of the image based on different criteria [1].

Surgical planning, post-surgical assessment, abnormality detection, and many other medical applications require medical image segmentation [2]. The main challenges in medical image segmentation are unknown and irregular noise, inhomogenity, poor contrast and weak boundaries. MRI and other medical images contain complicated anatomical structures that require precise and most accurate segmentation for clinical diagnosis [3].

Brain image segmentation from MRI images is complicated and challenging but its precise and exact segmentation is necessary for tumors detection and their classification, edema, hemorrhage detection and necrotic tissues. For early detection of abnormalities in brain parts, MRI imaging is the most efficient imaging technique. Unlike computerized Tomography (CT), MRI image acquisition parameters can be adjusted for generating high contrast image with different gray level for various cases of neuropathology [4]. Therefore, MRI image segmentation stands in the upcoming research limelight in medical imaging arena.

In the field of neuroscience, mapping of functional activation onto brain anatomy, the study of brain development, and the analysis of neuron atomically variability in normal brains requires the identification of brain structures in MRI images [5]. Apart from this, segmentation of MRI images is essential in clinical diagnosis of neurodegenerative and psychiatric disorders, treatment evaluation, and surgical planning [5].

In this paper we have propose a fully automated and elegant method of segmentation brain MRI images. The segmentation process runs in two discrete steps, initially scull striping and then segmentation using K - means and dual localization. Finally the dimension of the tumor in 2 - D is analyzed. The upcoming sections of the paper follow with related research done and in describing the methodology of the algorithms devised in doing the processing of segmentation on an MRI image.

II. RELATED WORK

The image segmentation is the process of separation of image areas based on different attribute such as texture, gray value range etc. The main objective in image processing applications is extraction of important image features from image data which will eventually lead to automatic computerized description, interpretation and analysis of the scene. Segmentation by the medical experts manually from the magnetic resonance images of the brain tumor is very much __time-consuming task, tiresome, susceptible to error,. Several segmentation methods had been proposed by the digital image processing community, many of which are ad - hoc [6]. Four of the most common methods are: 1) amplitude thresholding, 2) texture segmentation 3) template matching, and 4) region-growing segmentation. This is very much important for detecting necrotic tissues, edema and tumors.

Various algorithms for segmentation [16:17:18:19:20:21:22] had been suggested by several authors. Siyal et al described a new method on "Fuzzy C-means for segmentation purpose" [7]. Phillips, W.E et al described "Application of fuzzy C-Means

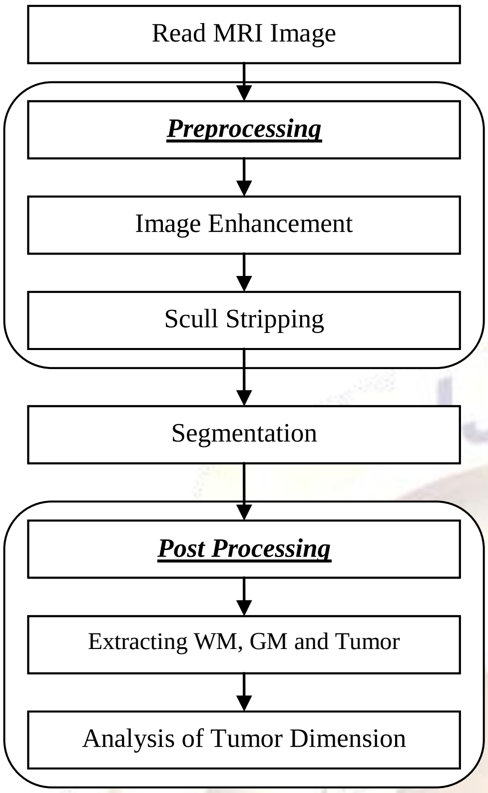
Segmentation Technique for tissue Differentlation in MR Images of a hemorrhagic Glioblastoma Multiforme"[15]. S. Murugavalli1 et al, proposed "A high speed parallel fuzzy c-mean algorithm for brain tumor segmentation" [14]. S. Murugavalli1, proposed "An Improved Implementation of Brain Tumor Detection Using Segmentation Based on Neuro Fuzzy Technique" [13], Vaidyanathan M et al described "Comparison of Supervised MRI Segmentation methods for Tumor Volume Determination during Therapy"[12]. Jayaram K et al described "Fuzzy Connectedness and Image Segmentation"[11].Kannan et aln describe "Segmentation of MRI Using New Unsupervised Fuzzy C mean Algorithm"[10] Ruspini, E Described "Numerical methods for fuzzy clustering"[9]. Dunn, J.C., described "A fuzzy relative of the ISODATA process and its use in detecting compact, well Separated clusters"[6]. Bezdek, J.C., described "Cluster validity with fuzzy sets"[8]. Some other methods such as Learning vector quantization, Watershed, Hybrid SOM or graph cut based approach had also been proposed in different literatures.

III. PROPOSED METHOD

Detection and segmentation of Brain tumor accurately is a challenging task in MRI. Magnetic resonance imaging (MRI) is a medical imaging technique used in radiology to visualize detailed internal structures in different body parts. MRI creates apply of the possessions of nuclear magnetic resonance (NMR) to image nuclei of atoms within the human body. In experimental observation, MRI is used to differentiate pathologic tissue (such as a brain tumor) from usual normal tissue. [23] One of the benefits of an MRI scan is that it is safe to the patient. It applied by strong magnetic fields and non-ionizing emission in the radio frequency range, unlike CT scans and traditional X-rays, which both use ionizing radiation. The MRI image is an image that produces a high contrast images indicating regular and irregular tissues that help to distinguish the overlapping.

In the domain of image processing segmentation of images has a significant position in present days. The aim of segmentation is to make straightforward and/or change the illustration of an image is impressive that has additional important and easier to examine. Image segmentation is typically used to position objects and boundaries in images [24]. In computer vision, segmentation refers to the process of separation a digital image into multiple segments (sets of pixels, also known as super pixels). More specifically, image segmentation is the procedure of transmission a label to each pixel in an image such that pixels with the similar label share convinced visual characteristics. Every of the pixels in a section are similar with respect to some computed property or characteristic, such as color, intensity, or texture. Neighboring regions are appreciably dissimilar with compare to the similar characteristic(s). The effect of image segmentation is a set of segments that communally cover the entire image, or a set of contours remove from the image. [24] It becomes more vital while usually production with medical images where pre-surgery and post surgery announcement are necessary for the meaning of initiating and speeding up the improvement process. Labor-intensive segmentation of these abnormal tissues cannot be measure up to with recent day's high speed computing machines which allow us to visually watch the volume and location of not needed tissues. Computer aided recognition of abnormal enlargement of tissues is mostly motivated by the requirement of achieving maximum possible truthfulness. The improvement in the application of information technology has totally changed the world. The observable motive for the opening of computer systems is: simplicity, accuracy, ease of use and reliability. An image is captured in medical imaging, digitized and progression for segmentation and extracting vital information. [25]Therefore, there is a well-built algorithms need to have some well-organized computer based structure that accurately classify the boundaries of brain tissues along with minimizing the chances of user communication with the system. Additionally, manual segmentation procedures need at least three hours to complete. According to the conventional methods for compute tumor volumes are not dependable and are error susceptible.

The Proposed workflow in this paper is as follows:



Proposed Work Flow

The steps in the proposed workflow go as follows:

A. *Pre – Processing : Image Enhancement*

The image enhancement is done by using a 3 – by – 3 ‘unsharp’ contrast enhancement filters. An ‘unsharp’ filter is created from the negative of the laplacian filter with parameter 'alpha'. Here, the 'alpha' controls the shape of the laplacian and must be in the range 0.0 to 1.0. Default value is 0.2. The image is sharpened by subtracting a blurred version of the image from itself. A two dimensional array H is created as the filter. Each element of the output image is computed using double precision floating point. Since the input image pixel values are integer so output elements that exceed the range of the integer are truncated and fractional values are rounded.

B. *Pre – Processing : Scull Stripping*

For scull stripping, firstly a mask is generated from the original image. For the purpose of mask generation, Otsu's method is used to automatically perform histogram shape – based image thresholding,[26:27] i.e., to reduce the graylevel image to a binary image. OTSU method for thresholdding assumes that the image to be thresholded has two classes of pixels or has a bi-modal histogram (e.g. foreground and background) then it calculates the optimum threshold separating those two classes so that their combined spread i.e. intra-class variance is minimal. For the image, we calculate {(weight of foreground* variance of foreground) + (weight of background* variance of background)} and subsequently the minimum value is accepted for thresholding.

On successful thresholding, we get a binary image with scull as the main outline and some small island of dark zone consisting of cerebra – spinal fluid. To remove those patches of cerebra – spinal fluid, we fill the region encased by the scull in the binary image using flood fill algorithm. Finally the negative of the binary image is used as the scull mask.

This generated scull mask is used over the original image to remove the scull. The original image is masked by the generated scull mask and thereby the scull gets removed from the original image giving a scull stripped image as output.

C. *Automatic Segmentation*

The segmentation process proposed here is a three step refining segmentation process. The three steps are:

1. K - Means algorithm based segmentation.
2. Local standard deviation guided grid based coarse grain localization.

3. Local standard deviation guided grid based fine grain localization.

The problem of image segmentation is nothing but a classical clustering problem where the range of image gray values is clustered in some fixed number of clustered gray values. One of the easiest unsupervised learning algorithms that explain the well acknowledged clustering problem is the K-means [28]. The process follows a straightforward and easy way to categorize a given data set during a definite number of clusters (assume k clusters) fixed a priori. These centroids must be located in a wiliness way because of dissimilar location cause dissimilar outcome, so locate them as much as possible far away from each other. The most important application is to label k centroids, one for every cluster. The next step is to obtain every point be in the right location to a particular (given) data set and relate it to the adjacent centroid. If there are no point is waiting, the first step is finished and an early groupage done. In this point we want to re-calculate k new centroids of the clusters resultant from the earlier step. After calculate these k new centroids, a new binding has to be done between the equivalent data set points and the neighboring new centroid. A repetition has been produce. As a effect of this loop we may well notice that the k centroids alter their position step by step until no additional changes are done, in other words centroids do not shift any more.

Finally, the algorithms aspire at the minimizing of objective function, in that case a squared error function where the square is calculated of the distance measured between a data point and the cluster centre, which is the pointer of the distance of the n data points from their own bunch centre.

The algorithm runs through the following steps:

1. Position K points into the room characterize by the objects that are being clustered. These points simply signify initial group centroids.
2. Closest centroides are assigning each object in to a group.
3. After assigning each object then recalculation of the positions of the K centroids is done.
4. Until the centroids no longer move repeat Steps 2 and 3. This is done due to create a disconnection of the objects from the groups from which the metric to be minimized can be calculated.

Although it can be establish that the method will always come to an end, the k-means algorithm does not essentially locate the best possible arrangement, equivalent to the global objective function minimum. The algorithm is also appreciably responsive to the initial arbitrarily chosen cluster centers.

So, to obtain an optimal segmentation cluster configuration we propose a standard local deviation guided grid based coarse grain localization after the K - means algorithm segmentation. Here, we first calculate the local standard deviation of the k - means segmented image. Here the image is mapped on large grid layout, ideally each grid is of size 8 – by – 8 i.e. 64 pixels. Local standard deviation of each pixel is calculated based on the pixel values of these 64 pixel of that grid. Then the histogram of each grid id calculated and based on the local standard deviation and histogram in each grid, the segmentation boundaries in that grid are reevaluated to generate more optimal segmentation. Choosing a large grid dimension helps us reduce the effect of noise in segmenting the grid. But, conversely, the large grid dimension also ignores the finer anatomic details such as twists and turns in the boundary of the tumor or overlapping region of gray and white matters in the brain.

So, finally to obtain the most optimal segmentation, we once more process the above segmented image using the same concept of standard local deviation guided grid based fine grain localization. Here we chose the grid size ideally to be 3 – by – 3. So, choosing a small grid helps in zeroing on the finer anatomical details of the MRI image that needs to be preserved. This helps in restoring the acute details of the tumor boundary and finer analysis of the overlap region of gray matter and white matter.

D. Post – processing: Extracting WM, GM and Tumor

After the successful completion of the above mentioned three step segmentation process, the histogram of the segmented image is calculated. The analysis of the image histogram shows the distinct peaks in three different image pixel gray value corresponding to gray matter, white matter and tumor. Based on this histogram, the corresponding gray matter, white matter and tumor is extracted.

E. Post – processing: Analysis of Tumor Dimension

A line scan method is applied to the image of the extracted tumor after the segmentation process and the maximum breadth and length of the tumor along the x – axis and y – axis is estimated.

IV. TEST RESULTS AND ANALYSIS

We have got 3 types of MRI images they are:

- Saggital view images (Side view)

- Coronal view images (Back view)
- Axial view images (Top view)

The quality of images, i.e. intensity, gradient, brightness, presence of noise etc, is totally depend on the resolution of the association of the MRI magnets. Our proposed system works on MRI images taken from these entire three axes.

The computational analysis is implemented on a DELL Inspiron system Intel® Core™ i3 CPU @2.13GHz processor and 4.00GB RAM with Windows (C) 7 Home Basic 64 – bit Operating System. The support analysis software used is MATLAB © R2010a 64 – bit version. In order to evaluate the performance of our algorithms and methodology, the experiments were conducted on MRI data set. Test case MRI images are downloaded from MRI image Data Bank of Radiopedia©.

The results of the test case are as follows:

The MRI is in Coronal View:

Figure 1. Input image. Figure 2. Image sharpened. Figure 3. Skull Mask. Figure 4. Skull stripped. Figure 5. Segmented Image. Figure 6. Local Standard Deviation.

Figure 7. White Matter. Figure 8. Gray Matter. Figure 9. Tumor .

Time taken: 12.36 seconds.

Tumor Diamension:

Width: 206 Pixel

Height: 182 Pixel

In the next case, the MRI image is in Saggital view:

Figure 10. Input image. Figure 11. Image sharpened. Figure 12. Skull Mask. Figure 13. Skull stripped. Figure 14. Segmented Image.

Figure 15. Local Standard Deviation. Figure 16. White Matter. Figure 17. Gray Matter. Figure 18. Tumor.

Time taken: 12.40 seconds.

Tumor Diamension:

Width: 206 Pixel

Height: 198 Pixel

Similar results are also available in axial view MRI Images. Test Cases has been done in nearly hundred MRI images and successful tumor detection has been found in more than 96% cases.

V. Conclusion

The method for segmentation proposed here overcomes the drawbacks of the conventional K – means algorithm and gives very satisfactory result both from qualitative and quantitative perspective. The results of segmentation as given above are at par with the recent medical standard. Moreover the success rate of the segmentation in images of brain MRI taken from all the three angles is quite high and satisfactory. The real time execution time in the test cases is less than 9 seconds in almost all the cases and thus can be said to be good as per the current industry standard ad is also very less as compared to manual process. So, based on the above discussion it can be claimed to be a noble segmentation approach in its family of unsupervised clustering approach. This is future scope for 3 – D modeling and volume analysis of brain and tumor and classification of tumor based on this segmentation approach.

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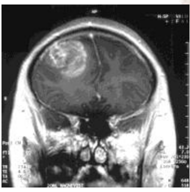
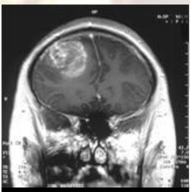
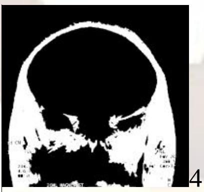
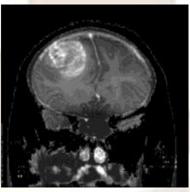
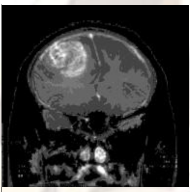
VII. FIGURES

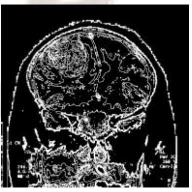
1. 

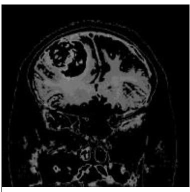
2. 

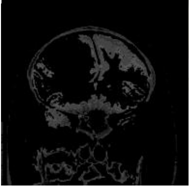
3. 

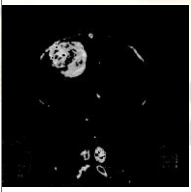
4. 

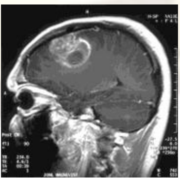
5. 

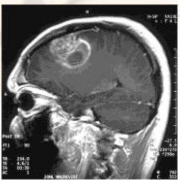
6. 

7. 

8. 

9. 

10. 

11. 

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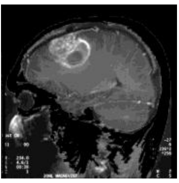
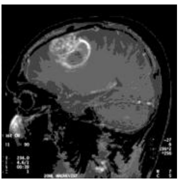
13. 

14. 

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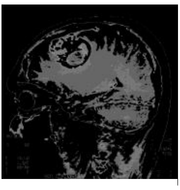
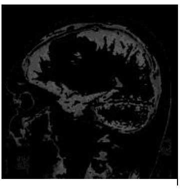
16. 

17. 

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