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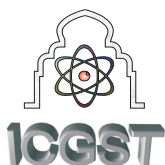
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Brain Tumor Detection based on Multi-parameter MRI Image Analysis

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Abstract

Segmentation of anatomical regions of the brain is the fundamental problem in medical image analysis. While surveying the literature, it has been found out that no work has been done in segmentation of brain tumor by using watershed in MATLAB Environment. In this paper, a brain tumor segmentation method has been developed and validated segmentation on 2D & 3D MRI Data. This method can segment a tumor provided that the desired parameters are set properly. This method does not require any initialization while the others require an initialization inside the tumor. The visualization and quantitative evaluations of the segmentation results demonstrate the effectiveness of this approach. In this study, after a manual segmentation procedure the tumor identification, the investigations has been made for the potential use of MRI data for improving brain tumor shape approximation and 2D & 3D visualization for surgical planning and assessing tumor. Surgical planning now uses both 2D & 3D models that integrate data from multiple imaging modalities, each highlighting one or more aspects of morphology or functions. Firstly, the work was carried over to calculate the area of the tumor of single slice of MRI data set and then it was extended to calculate the volume of the tumor from multiple image MRI data set.

Keywords: Brain tumor, Magnetic resonance Imaging (MRI), Image segmentation, watershed segmentation, MATLAB.

1. Introduction

The body is made up of many types of cells. Each type of cell has special functions. Most cells in the body grow and then divide in an orderly way to form new cells as they are needed to keep the body healthy and working properly. When cells lose the ability to control their growth, they divide too often and

without any order. The extra cells form a mass of tissue called a tumor. Tumors are benign or malignant. There are three methods of segmentation. These are Snakes (Gradient Vector Flow), Level Set Segmentation and Watershed Segmentation [1].

The aim of this work is to design an automated tool for brain tumor quantification using MRI image data sets. This work is a small and modest part of a quite complex system. The whole

system will when completed visualize the inside of the human body, and make surgeons able to perform operations inside a patient without open surgery. More specifically the aim for this work

is to segment a tumor in a brain. This will make the surgeon able to see the tumor and then ease the treatment. The instruments needed for this could be ultrasound, Computer Tomography (CT Scan) and Magnetic Resonance Imaging (MRI). In this Paper, the technique used is Magnetic Resonance Imaging (MRI).

Watershed segmentation uses the intensity as a parameter to segment the whole image data set. Moreover, the additional complexity of estimation imposed to such algorithms causes a tendency towards density dependent approaches.[2]. Three dimensional segmentation is a reliable approach to achieve a proper estimation of tumor volume. Among all possible methods for this purpose, watershed can be used as a powerful tool which implicitly extracts the tumor surface. Watershed segmentation based algorithm has been used for detection of tumor in 2D and in 3D.

For detection of tumor in 2D the software used is MATLAB. But for detection of tumor in 3D, the software used were MATLAB and 3D Slicer. 3D Slicer was used to create the 3D image using axial, sagittal and coronal images. This 3D image was then used by MATLAB to detect the tumor in 3D.

Also, a Graphical User Interface (GUI) has been designed, which is user friendly environment to understand and run the work done by the one click of



a mouse. This user friendly graphical user interface (GUI) was developed with the help of MATLAB. The rest of the paper is organized as follows. Section-2 presents the methodology of the problem, section 3 & 4 gives materials and implementation of the problem and section 5 gives the result and section 6 discusses the conclusion.

2. Methodology

2.1 Methodology (Theoretical)

A conceptually simple supervised block-based and image-based (shape, texture, and content) technique has been used to analyze MRI brain images with relatively lower computational requirements. The process flow of our proposed methodology may be shown as figure 1.

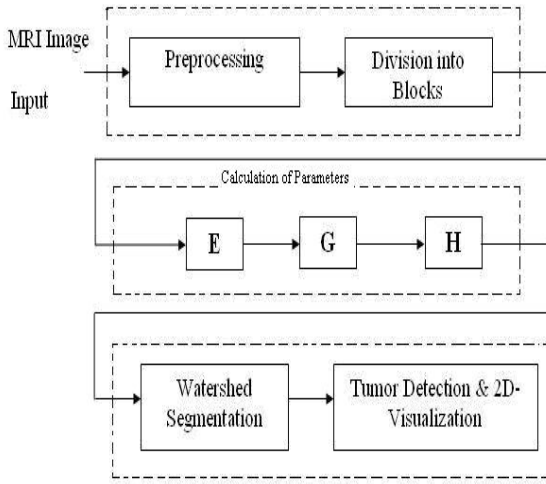


Figure 1. Methodology

The first section discusses how images are divided into regions using a block-based method. The second section shows how each classified block is studied individually by calculating its multiple parameter values. In this instance, the multiparameter features refer to the following three specific features: the edges (E), gray values (G), and local contrast (H) of the pixels in the block being analyzed [7].

Input Image

The images we got from MRI are of three types: axial Images, sagittal Images, coronal Images. The numbers of images depend on the resolution of the movement of the MRI magnets.

2.1.1. Preprocessing

The Preprocessing is used for loading the Input MRI images to the MATLAB Environment and also it removes any kind of noise present in the input images. In preprocessing the first step is to load the MRI image data set on to the MATLAB workspace and after loading they will be processed in such a way that instead of processing 128 images in one

direction a whole clip of 128 images is processed by one command, otherwise it would have been very hectic situation for processing each and every image independently. Thus after this processing there are only three clips instead of 384 separate images, i.e. one clip for axial images, one clip for sagittal images and one clip for coronal images. After that all the clips are combined to get the single clip for further processing. Then the noises are filtered out from MRI images using the Wiener filter which is a type of linear filter. The MRI image after removal of noise is further used for parameter calculation. [3], [4].

2.1.2. Multiparameter Calculations

Recent advances in medical image analysis often include processes for an image to be segmented in terms of a few parameters and into smaller sizes or regions, to address the different aspects of analyzing images into anatomically and pathologically meaningful regions. Classifying regions using their multiparameter values makes the study of the regions of physiological and pathological interest easier and more definable. Here, multiparameter features refer to the following three specific values for the edges (E), gray values (G), and local contrast (H) of the pixels[18],[19],[20].

2.1.2.1. Edge (E) Parameter

Edge information is often used to determine the boundaries of an object. This is mainly used for analysis to derive similarity criterion for a pre-determined object. The incidences of cerebral compression reduce the edge. Given this understanding, we use the Sobel edge detection method to detect image edges (I_E) is obtained by filtering an input image with two convolution kernels concomitantly, one to detect changes in vertical contrast (h_x) and the other to detect horizontal contrast (h_y), shown in equation (1). Image output (I_E) is obtained by calculating the gradient magnitude of each pixel, as shown in equation (2). Subsequently, the edge parameter (E) is calculated, whereby E (r, c) is increased by one each time when $I_E(x, y) = '1'$ in a supervised block, as shown in equation (3)

$$H_x = \begin{bmatrix} -1 & 0 & 1 \\ -2 & 0 & 2 \\ -1 & 0 & 1 \end{bmatrix}, H_y = \begin{bmatrix} -1 & -2 & -1 \\ 0 & 0 & 0 \\ 1 & 2 & 1 \end{bmatrix} \quad (1)$$

$$I_E(x, y) = \sqrt{I_x^2(x, y) + I_y^2(x, y)} \quad (2)$$

$$E_{(r,c)} = \sum_{(x,y) \in B} (I_E = 1) \quad (3)$$



2.1.2.2. Gray (G) Parameter

Gray parameter avoids the need to scale the data-to-color mapping, which would be required if we used a color map of a different size. The gray parameter (G) for each block of the brain is accumulated, and controlled by a binary image (I_T) using the G_D value as a threshold, as shown in equation (6). G_D value is calculated using the average pixel value (I_{av_s}) of each image slice (S) for total image slices (T) of an image dataset, shown in equation (4) and (5).

$$I_{av_s} = \frac{1}{65536} \sum I_p(x, y) \quad (4)$$

$$G_D = \frac{\sum_{s=0}^T I_{av_s}}{T} \quad (5)$$

$$G_{(r,c)} = \sum_{(x,y) \in B} I_p(x, y), \forall I_T(x, y) = 1 \quad (6)$$

The pixels intensity for each slice was calculated to establish the threshold values and thus provide the basis for analysis of clinical MR images from patients with brain tumors[10],[11].

2.1.2.3. Contrast (H) Parameter

An intensity image is a data matrix, I , whose values represent intensities within some range. MATLAB stores an intensity image as a single matrix, with each element of the matrix corresponding to one image pixel. The matrix can be of class double, uint8, or uint16. While intensity images are rarely saved with a color map, MATLAB uses a color map to display them. In essence, MATLAB handles intensity images as indexed images. Contrast (H) is often used to characterize the extent of variation in pixel intensity. In the present technique, the computational program analyses the differences, especially in instances of strong dissimilarity, between entities or objects in an image $I(x, y)$.

We adopt the minimum/maximum stretch algorithm for the 8-neighborhood connectivity, where $\min H$ and $\max H$ represent the minimum and maximum intensity values of the neighborhood pixel $C_8(I_H)$, as shown in equation (7). In the previous studies, tumor cells are often associated with higher value of contrast (H) parameter [9]. H_d is obtained by totaling the contrast of a supervised block, as shown in equation (8).

$$I_H(x, y) = \left(\frac{I(x, y) - \min H}{\max H - \min H} \right) \times \max H \mid H \in C_8(I_H) \quad (7)$$

$$H_d(r, c) = \sum_{(x, y) \in B} I_H(x, y) \quad (8)$$

2.1.2.4. Watershed Segmentation

By interpreting the gradient map of an intensity image as height values, we get lines which appear to be ridges. If the contours were a terrain, falling rain would find the way from the dividing lines towards the connected catchments basin. These dividing lines are called watersheds. As illustrated in Fig. 5.1 steep edges cause high gradients which are watersheds [12]-[16]. Image segmentation by mathematical morphology is a methodology based upon the notations of modification. The watershed transformation can be built up by flooding process on a gray tone image and may be shown as shown in figure 2.

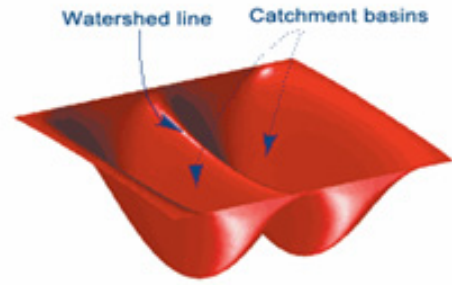


Figure 2. Watershed segmentation simplified to 2 Dimensions

2.1.2.5. Watershed Segmentation (Pros & Cons)

It has been found that among the segmentation methods investigated in this work, the watershed segmentation, a classic in image segmentation, marked out as the most automatic method of the three.

As watershed segmentation technique segregates any image as different intensity portions and also the tumorous cells have high proteinaceous fluid which has very high density and hence very high intensity, therefore watershed segmentation is the best tool to classify tumors and high intensity tissues of brain. Watershed segmentation can classify the intensities with very small difference also, which is not possible with snake and level set method.

It has been found that the snake and the level set method were best initialized from the inside of the tumor. The program needs to be extending to handle segmentation with a probe through the tumor. This can be done by segmenting the probe or in combination with tracking information which provides the position of the probe.

Improved robustness can be gained by segmenting the blood vessels inside the brain during preoperative image analysis. With the use of image registration the vessels can be found in the operative images and eliminate them from the feature map used in tumor segmentation. Such an extension also contributes to added complexity and there is no



guarantee the added feature will increase the robustness of the complete system.

The watershed method did not require an initialization while the others require an initialization inside the tumor.

The limitation of watershed segmentation is that its algorithms produce a region for each local minimum. This will normally lead to over segmentation. We can say the algorithm has solved the problem but detrains the result as a puzzle. Obviously there is a need for post processing these numerous regions. One way to face this problem is to recognize the regions in a hierarchy.

2.2. Methodology (Practically)

The computational analysis is implemented on a IBM Think Centre Pentium IV 2.80GHz computer with 512 MB RAM. The support analysis software used is MATLAB and 3D Slicer. In order to evaluate the performance of our algorithms and methodology, the experiments were conducted on MRI data set.

2.2.1 Preprocessing

Load and View Axial Images in MATLAB Environment as shown in figure 3(a).

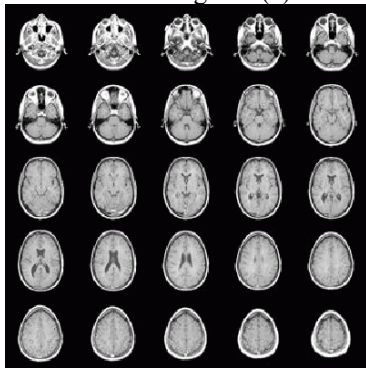


Figure 3(a). Axial Slices

Load and View Saggital Images in MATLAB Environment as shown in figure 3(b).

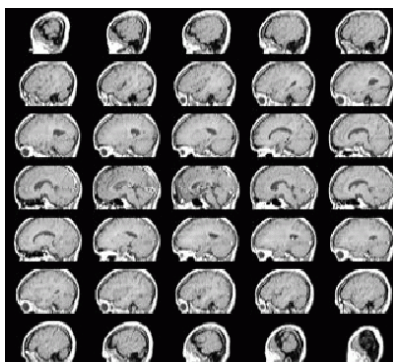


Figure 3(b). Saggital Slices

Load and View Coronal Images in MATLAB Environment as shown in figure 3(c)

Now all the clips were combined together to produce a single clip and then any noise present in the MRI images had been removed by using the algorithm which is based on Weiner filter.

2.2.2. Multiparameter Calculations

Recent advances in medical image analysis often include processes for an image to be segmented in terms of a few parameters and into smaller sizes or regions, to address the different aspects of analyzing images into anatomically and pathologically meaningful regions. Classifying regions using their multiparameter values makes the study of the regions of physiological and pathological interest easier and more definable. Here, multiparameter features refer to the following three specific values for the edges (E), gray values (G), and local contrast (H) of the pixels.

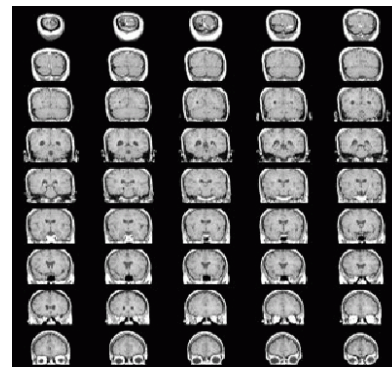


Figure 3(c). Coronal Slices

Extract Axial, saggital and coronal slices & create Movie clip as shown in figure 3(d).

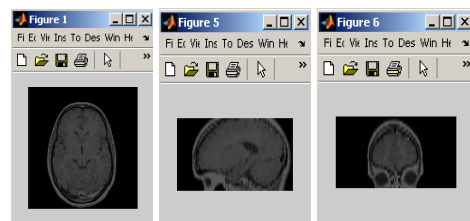


Figure 3(d). Movie clips of axial, saggital and coronal slices



Figure 4. Edge Image of MRI Data Set



2.2.2.1. Edge Parameter Calculation (E)

We will be using Sobel edge detection for detecting edges as explained in the theoretical section. This can be achieved by executing the algorithms and the result obtained may be shown as figure 4.

2.2.2.2. Gray Parameter (G) Calculation

The gray parameter (G) for each block of the brain is accumulated, and controlled by a binary image using the value as a threshold. Pixels intensity for each slice was calculated to establish the threshold values and thus provide the basis for analysis of clinical MR images from patients with brain tumors. This can be achieved by executing the algorithm and the result obtained may be shown as figure 5.



Figure 5. Binary Image of MRI Data Set

2.2.2.3. Contrast Parameter (H) Calculation using morphological watersheds

Contrast (H) is often used to characterize the extent of variation in pixel intensity. A computational program analyses the differences, especially in instances of strong dissimilarity, between entities or objects in an image using Watershed Segmentation. As we know that malignant tumor cells contain highly proteinaceous fluid, which is represented as high signal intensity on MRI images of the brain [12],[13]. Usually the watershed transformation is applied to a boundary map, which is a gray scale function, derived from the input image, that has low values within the regions and high values along region boundaries. The gradient magnitude of an intensity based image is oftenly used as the boundary map, as well as higher order features such as curvature [18].

Watershed segmentation can be used for segregating the different intensity portions and this can be achieved by executing the algorithm in MATLAB and the result obtained may be shown as figure 6.

2.2.3. Tumor Block Detection & Visualization

2.2.3.1. Segmentation of brain tumor using Region of Interest (ROI) Command

As it has been seen from the above result that high density images have been separated from the MRI images using Watershed Segmentation. Here main aim is to segment the tumor from the MRI images.

This can be done by using the ROI command in MATLAB. After the application of the ROI command, the tumor may be segmented.

This can be achieved by executing the algorithm in MATLAB and the result obtained may be shown as figure 7.

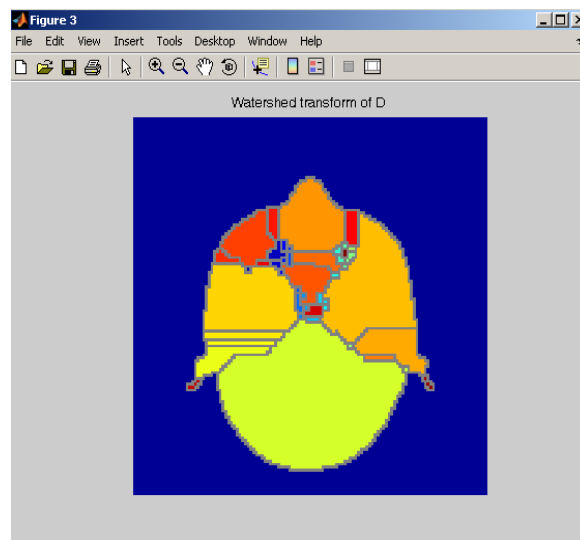


Figure 6. Intensity Image of MRI Data Set using Watershed Segmentation

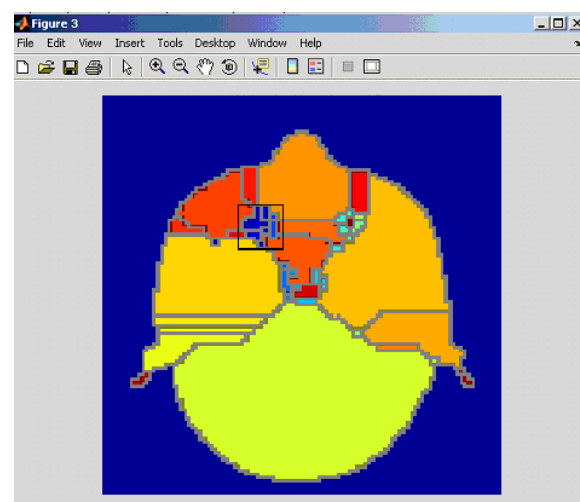


Figure 7. Constructed Image after Application of ROI Command on MRI intensity image

The image after the application of the ROI command may be shown as figure 8:

2.2.3.2 Formation of 3D image of MRI Data Set using 3D Slicer

As the MRI Image date set is collection of 2D images. The tumor can not be segmented in 3D unless and until we have 3D MRI image data set. Therefore, a software 3D SLICER has been used to get a 3D image from a collection of 2D MRI data set of axial, saggital & coronal images. Then, applying watershed segmentation (3D) in MATLAB to this 3D image, the segmented tumor in 3D with all its dimensions can be obtained using 3D Slicer.



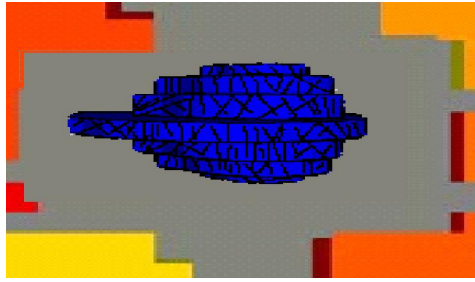


Figure 8. Enhanced image of the area after application of the ROI command

3D image of MRI data set using 3D SLICER may be shown as figure 9.

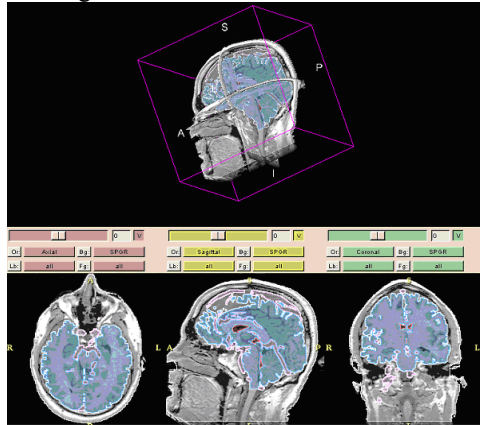


Figure 9. Viewer of 3D Slicer

2.2.3.4. Segmentation & Visualization of Brain tumor in 3D

Now applying watershed segmentation (3D) by executing algorithm to the above MRI 3D image, we will get the image of tumor as Tumor image in 3D may be shown in figure 10.

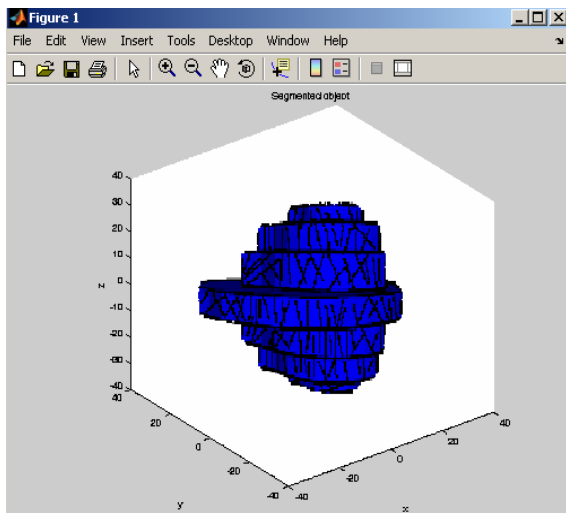


Figure 10. Segmented Tumor Image-3D

2.2.4. Designing of Graphical User Interface (GUI):

The MATLAB Graphical User Interface development environment, provides a set of tools for creating

graphical user interfaces (GUIs). These tools greatly simplify the process of designing and building GUIs.

Designing of GUI for Tumor Detection & Visualization

Using the above technique a GUI has been designed which is a user friendly approach to understand this project and to make calculations without any hectic practice while diagnosing a tumor.

This GUI may be shown as figure 11.

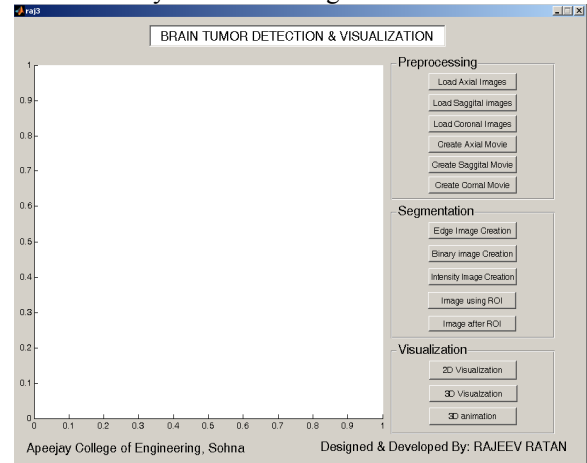


Figure 11. Tumor Detection & Visualization GUI

By clicking on the push buttons we can check the results sequentially without any knowledge of MATLAB. Thus a user friendly environment has been designed which is helpful in understanding the work.

3. Results

3.1. Dimensions of Segmented Tumor

The figure gives the result of 3D in the form of pixels in X, Y and Z directions respectively. As display settings are 1028 X 768 pixels on the monitor of the computer being used for the work and the dimensions of the monitor are 280mm X 210mm, thus the dimensions of the one pixel comes out to be 0.2734mm X 0.2734mm. By viewing the tumor from different angles, we may give the dimensions of tumor as under. The tumor shown may be considered to be made up of seven different layers. As viewed from upside the tumor's layer may be given the names as: 1st upper layer, 2nd upper layer, 3rd upper layer, middle layer, the layer below middle layer, the second last layer, the last layer.

The dimensions of the different layers of detected tumor of Data Set 1 may be tabulated as under.

Thus we see that the total approximate volume of tumor of data set 1 comes out to be 4075.65 mm³ (4.07565 cm³)

The dimensions of the different layers of detected tumor of Data Set 2 may be tabulated, see table 2.



| S.N. | Name of Layer | Dimensions (Max) (pixels) | Dimensions (Max) (mm-mm-mm) | App. Volume (mm ³) |
|------|------------------------------|---------------------------|-----------------------------|--------------------------------|
| 1 | 1 st Upper Layer | 33*23*7 | 9.02*6.29*1.91 | 108.37 |
| 2 | 2 nd Upper Layer | 54*38*11 | 14.76*10.39*3.01 | 461.60 |
| 3 | 3 rd Upper Layer | 63*48*14 | 17.22*13.12*3.83 | 865.29 |
| 4 | Middle Layer | 87*68*12 | 23.79*18.59*3.28 | 1450.60 |
| 5 | The Layer Below Middle Layer | 62*46*13 | 16.95*12.58*3.55 | 756.97 |
| 6 | The Second Last Layer | 52*34*10 | 14.22*9.29*2.73 | 360.64 |
| 7 | The Last Layer | 31*19*6 | 8.48*5.19*1.64 | 72.18 |
| | | | Total | 4075.65 |

Table 1 The dimensions of the different layers of detected tumor

| S.N. | Name of Layer | Dimensions (Max) (pixels) | Dimensions (Max) (mm-mm-mm) | App. Volume (mm ³) |
|------|------------------------------|---------------------------|-----------------------------|--------------------------------|
| 1 | 1 st Upper Layer | 26*18*5 | 7.10*4.92*1.37 | 47.86 |
| 2 | 2 nd Upper Layer | 32*26*6 | 8.75*7.10*1.64 | 101.89 |
| 3 | 3 rd Upper Layer | 41*31*9 | 11.20*8.48*2.46 | 233.64 |
| 4 | Middle Layer | 54*46*7 | 14.76*12.58*1.91 | 354.65 |
| 5 | The Layer Below Middle Layer | 41*32*6 | 11.20*8.75*1.64 | 160.72 |
| 6 | The Second Last Layer | 30*24*8 | 8.20*6.56*2.19 | 117.80 |
| 7 | The Last Layer | 28*14*7 | 7.66*3.83*1.91 | 56.04 |
| | | | Tota3.831 | 1072.60 |

Table 2. The dimensions of the different layers of detected tumor

Thus we see that the total approximate volume of tumor of data set 2 comes out to be 1072.60 mm³ (1.0726 cm³).

As it is clear from the above two results that tumor can be segmented out from the MRI image data set very efficiently and effectively and 3D image can be visualized in MATLAB environment. After visualizing it becomes very easy to calculate the tumor dimensions.

4. Conclusion

The results show that Watershed Segmentation can successfully segment a tumor provided the parameters are set properly in MATLAB environment. Watershed Segmentation algorithm performance is better for the cases where the intensity level difference between the tumor and non tumor regions is higher. It can also segment non homogenous tumors providing the non homogeneity is within the tumor region. This paper proves that

methods aimed at general purpose segmentation tools in medical imaging can be used for automatic segmentation of brain tumors. The quality of the segmentation was similar to manual segmentation and will speed up segmentation in operative imaging.

Among the segmentation methods investigated, the watershed segmentation is marked out best out of all others. The user interface in the main application must be extended to allow activation of the segmentation and to collect initialization points from a pointing device and transfer them to the segmentation module. Finally the main program must receive the segmented image and present the image as an opaque volume. It has only one limitation that the method is semi-automatic. Further work can be carried out to make this method automatic so that it can calculate the dimensions of the segmented tumor automatically.

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