

## Region growing for MRI brain tumor volume analysis

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**Abstract:** The tumor volume is a significant prognostic factor in the treatment of malignant tumors. Manual segmentation of brain tumors from MR images is a challenging and time consuming task. A semi-automated region growing segmentation method is proposed to segment brain tumor from MR images. The proposed method can successfully segment a tumor provided that the parameters are set properly. This method is applied to 8-tumor contained MRI slices from 2 brain tumor patients' and satisfactory segmentation results are achieved.

**Keywords:** Brain tumor, MRI, imaging, segmentation.

### Introduction

Tumors can be benign or malignant. Imaging plays a central role in the diagnosis and treatment planning of brain tumor. Tumor volume is an important diagnostic indicator in treatment planning and results assessment for brain tumor. The measurement of brain tumor volume could assist tumor staging for effective treatment surgical planning. Imaging of the tumors can be done by CT scan, Ultrasound and MRI etc. The MR imaging method is the best due to its higher resolution (~100 microns) (Khanpur, 1999; Haney *et al.*, 2001).

The methods to segment brain tumors are snakes segmentation, level set segmentation, watershed segmentation, region-growing segmentation etc. The region growing segmentation is preferred for its wide range of applications and automatic features. Preprocessing experiments are carried out to find which type of filtering will be more beneficial. This reduces the effect of the speckle and preserves the tumor edges: thereby provide the foundation for a successful segmentation. The desired tumor area is selected from the segmented image to calculate the volume.

MR imaging is currently the method of choice for early detection of brain tumor. However, the interpretation of MRI is largely based on radiologist's opinion. Computer aided detection systems can now assist in the detection of suspicious brain lesions and suspicious masses. The task of manually segmenting brain tumors from MR imaging is generally time consuming and difficult. An automated segmentation method is desirable because it reduces the load on the operator and generates satisfactory results (Xie *et al.*, 2005).

After taking the image of the tumorous brain there is a need to process it. The image shows the place of the infected portion of the brain. The image does not give the information

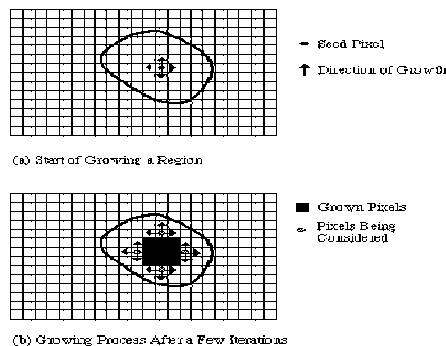
about the numerical parameters such as area and volume of the infected portion of the brain. After preprocessing of the image, first image segmentation is done by using region growing segmentation. The segmented image shows the unhealthy portion clearly. From this image the infected portion (tumor) is selected by cropping the segmented image. From this cropped image, area and volume are calculated (Heath *et al.*, 2001; Moonis *et al.*, 2002; Lu *et al.*, 2003, 2005; Yang, 2004; Salman *et al.*, 2005; Edman, 2007).

Chang *et al.*, (1994) proposed a region-growing framework for image segmentation. This process is guided by regional feature analysis and no parameter tuning or a priori knowledge about the image is required. The image is first divided into many small primitive regions that are assumed to be homogeneous. These primitive regions are then merged to form larger regions until no more merges are possible. Two regions are merged if they pass the homogeneity test and also if the value of the edge connecting them is weak.

The focus of this study is on investigating how different merge criteria affect the quality of segmentation and the processing time. The merge criteria are based on four important aspects of segmentation output, these are region mergeability, boundary accuracy, merge rejections and number of iterations required. The algorithm automatically or manually takes segmentation thresholds based on local feature analysis. The algorithm is robust and produces high quality segmentation on a wide range of textured and grey scale images.

For region growing, seeds can be automatically or manually selected. Their automated selection can be based on finding pixels that are of interest, e.g. the brightest pixel in an image can serve as a seed pixel. They can also be determined from the peaks found in an image histogram. On the other hand, seeds can also be selected manually for every object present in the image. The method is employed to segment an image into different regions using a set of seeds. Each seeded region is a connected component comprising of one or more points and is represented by a set  $S$ . The set of immediate neighbours bordering the pixel is calculated. The neighbour are then examined and if they intersect any region from set  $S$ , then a measure  $\delta$  (difference between a pixel and the intersected region) is computed. If the

Fig.1. Representation of region growth

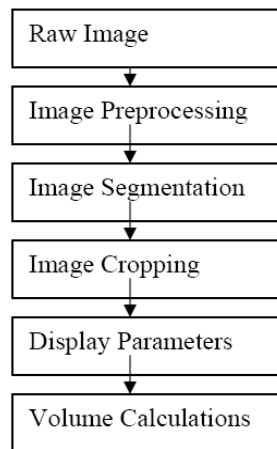


neighbours intersect more than one region, then the set is taken as that region for which difference measure  $\delta$  is maximum. The new state of regions for the set then constitutes input to the next iteration. This process continues until the entire image pixels have been assimilated into regions. Hence, for each iteration the pixel that is most similar to a region that it borders is appended to that region. The SRG algorithm is inherently dependent on the order of processing image pixels. The method has the advantage that it is fairly robust, quick, and parameter free except for its dependency on the order of pixel processing.

Mehnert & Jackway (1997) improved the above seeded region-growing algorithm by making it independent of the pixel order of processing and making it more parallel. Their study presents a novel technique for Improved Seeded Region Growing (ISRG). ISRG algorithm retains the advantages of Seeded Region Growing (SRG) such as fast execution, robust segmentation and no parameters to tune. The algorithm is also pixel order independent. If more than one pixel in the neighbourhood has same minimum similarity measure value, then all of them are processed in parallel. No pixel can be labelled and no region can be updated until all other pixels with the same priority have been examined. If a pixel cannot be labelled, because it is equally likely belong to two or more adjacent regions, then it is labelled as 'tied' and takes no part in the region growing process. After all of the pixels in the image have been labelled, the pixels labelled 'tied' are independently re-examined to see whether or not the ties can be resolved. To resolve the ties an additional assignment criterion is imposed, such as assigning a tied pixel to the largest neighbouring region or to the neighbouring region with the largest mean. ISRG algorithm produces consistent segmentation because it is not dependent on the order of pixel processing. Parallel processing ensures that the pixels with the same priority are processed in the same manner simultaneously.

In case of region detection, each pixel of a digitised image is chosen as a primitive. An ideal region is obtained from a group of pixels of the given image by approximating the grey-level values of these pixels with a linear or quadratic approximation scheme. A set of attributes is calculated for each pixel of the group belonging to the given image as well as for the each pixel of the ideal region. In particular, four attributes, contrast, total variation, global average grey-level value, and representative grey-level value are used. Distance between the group of pixels and the ideal region is obtained as a numerical measure of dissimilarity between them. Pixel assignment to regions is decided according to the distance measure. The authors concluded that there is a noticeable improvement in these results when

Fig.2. The Proposed methodology



semantic information is added. There is no optimal set of attributes that can be used for all of the images. Any image has to be tested with a number of different attribute value combinations in order to obtain the best possible segmentation results. This scheme is found suitable for the class of problems in which fine structural detail of an image is not needed.

Beaulieu & Goldberg (1989) proposed a hierarchical stepwise optimisation algorithm for region merging, which is based on stepwise optimisation and produces a hierarchical decomposition of the image. The algorithm starts with an initial image partition into a number of regions. At each iteration, two segments are merged provided they minimise a criteria of merging a segment to

another. In this stepwise optimisation, the algorithm searches the whole image context before merging two segments and finds the optimal pair of segments. This means that the most similar segments are merged first. The algorithm gradually merges the segments and produces a sequence of partitions. The sequences of partitions reflect the hierarchical structure of the image.

Gambotto (1993) proposed an algorithm that combines the region growing and edge detection methods for segmenting the images. The method is iterative and uses both of these approaches in parallel. The algorithm starts with an initial set of seeds located inside the true boundary of the region. The pixels that are adjacent to the region are iteratively merged with it if they satisfy a similarity criterion. A second criterion uses the average gradient over the region boundary to stop the growth. The last stage refines the segmentation. The analysis is based on cooperation between the region growing algorithm and the contour detection algorithm. Since, adding segments to a region, some pixels that belong to the next region and to the previous region, may be misclassified performs the growing process. A nearest neighbour rule is then used to locally reclassify them.

Hojjatoleslami & Kittler (2002) proposed a new region growing approach for image segmentation, which uses gradient information to specify the boundary of a region. The method has the capability of finding the boundary of a relatively bright/dark region in a textured background. The method relies on a measure of contrast of the region, which represents the variation of the region grey-level as a function of its evolving boundary during segmentation. This helps to identify the best external boundary of the region. The application of a reverse test using a gradient measure then yields the highest gradient boundary for the region being grown. The unique feature of the approach is that in each step at most one candidate pixel will exhibit the required properties to join the region. The growing process is directional so that the pixels join the grown region according to a ranking list and the discontinuity

measurements are tested pixel by pixel. The algorithm is also insensitive to a reasonable amount of noise. The main advantage of the algorithm is that no a priori knowledge is needed about the regions.

### The proposed methodology

'Region growing' is a procedure that groups pixels or sub regions into larger regions based on predefined criteria. The basic approach is to start with a set of "seed" points and from these grow regions by appending to each seed those neighboring pixels that have properties similar to the seed. Selection of the seed depends on the nature of the problem. When a priori information is not available, the procedure is to compute at every pixel the same set of properties that ultimately will be used to assign pixels to regions during the growing process (Fig. 1).

The selection of similarity criteria depends not only on the problem under consideration but also on the type of the image data available. For example, the analysis of land use satellite imagery depends heavily on the use of color. Grouping pixels with the same gray level to form a region without paying attention to connectivity would yield a segmentation result that is meaningless in the context of this discussion.

Another problem in region growing is the formulation of a stopping rule. Basically, growing a region should stop when no more pixels satisfy the criteria for inclusion in that region. Criteria such as gray level, texture and color are local in nature and do not take into account the history of the region growth. Additional criteria that increase the power of a region growing algorithm utilize the concept of size, likeness between a candidate pixel and the pixels grown so far and the shape of the region being grown.

In the region growing segmentation, the first aim is to determine the initial seed points. In this application, it is known that the pixel of defective welds tends to have the maximum allowable digital value. Based on this information, we selected as the starting points all pixels having values of 255. The points thus extracted from the original image (Basu, 1987; Rafael *et al.*, 2003; Sonka *et al.*, 2003; Liu *et al.*, 2004).

#### A. Basic formulation

The objective of the segmentation is to partition an image into regions. Let R represents the entire image region. We may view segmentation as a process that partitions R into 'n' sub regions like  $R_1, R_2,$  and  $R_3, \dots, R_n$  such that

$$a) \bigcup_{i=1}^n R_i = R.$$

b)  $R_i$  is connected region,  $i=1,2,\dots,n$ .

$$c) R_i \cap R_j = \phi \text{ for all } i \text{ and } j, i \neq j.$$

$$d) P(R_i) = TRUE \text{ for } i=1,2,\dots,n.$$

$$e) P(R_i \cup R_j) = FALSE \text{ for } i \neq j.$$

Here,  $P(R_i)$  is logical predicate defined over the points in set  $R_i$  and  $\phi$  is the null set. Condition (a) indicates that the segmentation must be complete; that is every pixel must be in a region. Condition (b) requires that points in a region must be connected in some predefined sense. Condition(c) indicates that the region must be disjoint. Condition (d) deals with the properties that must be satisfied by the pixel in a segmented region. Condition (e) indicates that regions  $R_i$  and  $R_j$  are different in the sense of predicate (Vaidyanathan *et al.*, 1995; Lu *et al.*, 2004; Hwang *et al.*, 2007).

#### B. Region growing

This method takes a set of seeds as input along with the image. The seeds mark each of the objects to be segmented. Comparing all unallocated neighboring pixels to the regions iteratively grows the regions. The difference between a pixel's intensity value and the region's mean,  $\delta$ , is used as a measure of similarity. The pixel with the smallest difference measured this way is allocated to the respective region. This process continues until all pixels are allocated to a region.

Seeded region growing requires seeds as additional input. The segmentation results are dependent on the choice of seeds. Noise in the image can cause the seeds to be poorly placed. Unseeded region growing is a modified algorithm that doesn't require explicit seeds. It starts off with a single region  $A_1$  the pixel chosen here does not significantly influence final segmentation. At each iteration it considers the neighboring pixels in the same way as seeded region growing. It differs from seeded region growing in that if the minimum  $\delta$  is less than  $A_1$  then a predefined threshold T is added to the respective region  $A_j$ . If not, then the pixel is considered significantly different from all current regions  $A_i$  and a new region  $A_{n+1}$  is created with this pixel ([http://en.wikipedia.org/wiki/Segmentation\\_\(image\\_processing\)](http://en.wikipedia.org/wiki/Segmentation_(image_processing))).

First, we search the maximum intensity  $I_{max}$  and the minimum intensity  $I_{min}$  in the image. We can obtain the initial threshold by following equation (Bu *et al.*, 2005). Secondly, we calculate the mean intensities of the background and foreground on the basis of threshold  $T_{old}$ , with the following equations (2) and (3).

$$T_{old} = \frac{I_{max} + I_{min}}{2} \quad (1)$$

$$I_{bm} = \frac{\sum_{I(x,y) < T_{old}} I(x,y)}{\sum_{I(x,y) < T_{old}} N(x,y)} \quad (2)$$

$$I_{fm} = \frac{\sum_{I(x,y) \geq T_{old}} I(x,y)}{\sum_{I(x,y) \geq T_{old}} N(x,y)} \quad (3)$$

$$T_{new} = \frac{I_{bm} + I_{fm}}{2} \quad (4)$$

Where,  $I_{bm}$  is the mean intensity of the background,  $I_{fm}$  is the mean intensity of the foreground,  $I(x, y)$  is intensity of pixel and  $N(x, y)$  is the number of pixels. Now the new threshold  $T_{new}$  is computed by equation (4).

If  $T_{new} = T_{old}$ , then  $T_{new}$  is the proper threshold value.

The range of image segmentation algorithms is based on region growing. Region growing algorithms take one or more pixels, called seeds and grow the regions around them based upon a certain homogeneity criteria. If the adjoining pixels are similar to the seed, they are merged with them within a single region. The process continues until all the pixels in the image are assigned to one or more regions (Ma *et al.*, 1991; Lu *et al.*, 2004).

**Implementation**

Implementation of this approach contains various processing steps, like raw image collection, image preprocessing, image segmentation, image cropping, volume calculation and parameters display. There are many input parameters such as value of standard deviation for Gaussian filtering, value of threshold to convert the intensity adjusted image into the binary image, initial value of seed point, threshold value for region growing segmentation etc. The sequence of the processing steps can be arranged in a meaningful manner and is shown in Fig.2.

**Raw Image Collection:** MR images of brain tumor are collected from website ([www.med.harvard.edu/AANLIB/home.html](http://www.med.harvard.edu/AANLIB/home.html)). Here the data sets of two patients are available with the specifications: Image type-T1 (axial), thickness of image slice-0.5cm, number of images per data set -23 and image format Gif.

**Image preprocessing:** Image preprocessing is the very first step in the image processing. In this process the image is converted into the accessible form. Also image ‘intensity adjustment’ and ‘noise reduction’ processes are carried out. After this the image filtering is performed. Filtering is necessary because it reduces the noise present in the image. Here Gaussian filtering is used. These filters are characterized by narrow bandwidths, sharp cutoffs, and low overshoots. A key feature of Gaussian filters is that the Fourier transform of a Gaussian is also a Gaussian, so the filter has the same response shape in both the time and frequency domains. The Gaussian filter has the minimum possible group delay. The input parameter of the Gaussian filter is the standard deviation. After filtering the intensity adjustment of the image is done. After the intensity adjustment the image format is changed from ‘intensity’ image to ‘binary’ image. After this the image ‘dilatation’ is done. This image is used as an input image for the segmentation process.

**Image segmentation:** Here the region growing segmentation is used to segment the MR image of brain tumor. A detail of the region growing segmentation is covered in the respective section. The algorithm takes an initial threshold value and seed point as input parameters. It is based on the measurement of mean value of the pixel intensity. The segmented image shows the tumor portion without any undesired portion of the image. This segmented image is used in the next step to detect the

Fig. 3. Data set 1

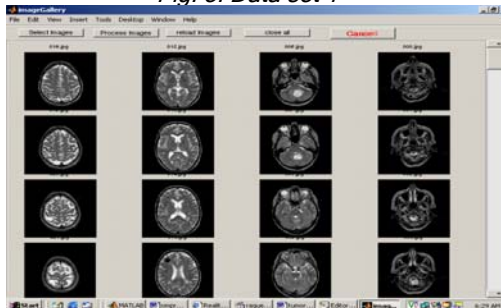
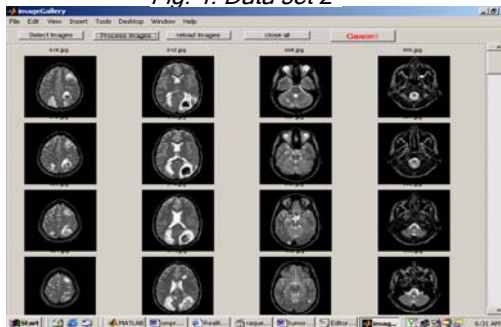


Fig. 4. Data set 2



desired tumor region.

**Image cropping:** Cropping is the process of selecting desired region from an image that is to be processed. The

image shows the desired tumor portion. This cropped image is used to calculate the tumor volume.

**Area and volume calculation:** Area of an image is the total number of the pixels present in the

Table 1. Various parameters setting

S. No.	Data Set	Infected image	Parameters setting															
			Gaussian filter standard	Binary image (Q)	For SE 90 dilation of binary image		SE 0 dilation of binary		Seed point for region growing		Threshold for region growing		SE 90 for dilation of cropped image		SE 0 for dilate-on of cropped image			
				s	t	u	v	x	y	w	a	g	h	e	f			
1	1	15	0.9	0.102	1	10	1	0	10	220	0.5	371.1250	20	40	20	0		
2	1	16	1.3	0.102	1	10	1	0	10	20	0.5	502.7500	20	40	20	0		
3	1	17	1.3	0.102	1	10	1	0	60	100	0.45	309	14	20	14	0		
4	2	12	0.9	0.102	1	10	1	0	10	220	0.5	371.1250	20	40	20	0		
5	2	13	0.9	0.5	1	10	1	0	80	50	0.5	1.2289e+003	20	25	20	0		
6	2	14	0.9	0.45	1	10	1	0	80	30	0.4	1.0506e+003	16	20	16	0		
7	2	18	0.9	0.3	1	10	1	0	80	30	0.4	565	15	20	15	0		
8	2	19	0.9	0.5	1	10	1	0	80	30	0.2	1.4343e+003	14	20	14	0		

image. Area can be calculated in the length units by multiplying the number of pixels by the dimension of the pixel. Here the dimension of the pixel is  $0.035 \times 0.034 \text{ cm}^2$ ; the pixel area is  $0.001190 \text{ cm}^2$ . To calculate the number of pixels in the cropped image the function Bwarea is used. This function calculates the on pixels present in the image. But in this process the desired portion of the image is black i.e. the pixels are off. To count the off pixels first calculate the on pixels in the cropped image after that dilate the cropped image completely. From this dilated image calculate the total number of pixels present in the dilated image by using the same function. Total

Fig. 5: (a) Input MR image (b) Gaussian filtered image (c) Intensity adjusted image (d) Output binary image (e) Dilated gradient mask (f) Region growing segmented image (g) Cropped image (h) Completely dilated cropped image

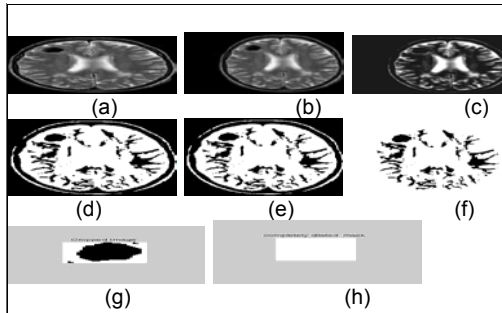
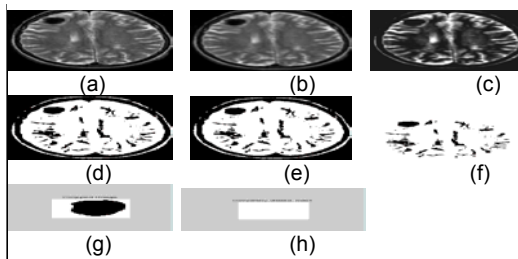


Fig. 6: (a) Input MR image (b) Gaussian filtered image (c) Intensity adjusted image (d) Output binary image (e) Dilated gradient mask (f) Region growing segmented image (g) Cropped image (h) Completely dilated cropped image



These data sets show the tumorous images. Data set 1 has the tumor in the images 15, 16, 17 and the data set 2 has the tumor in the images 12, 13, 14, 18, 19. Table 1 shows the various parameter settings for processing of infected images of data set 1 and data set 2.

The results of processing for raw input images 15, 16 and 17 of data set 1 are shown in Fig. 5, 6 and 7 respectively. When input images 12, 13, 14, 18 and 19 of data set 2 are processed its outcomes are shown in Fig. 8- 12.

Table 2 shows the tumor parameters in the data set 1. Data set 2 has tumor at two places. Table 3 shows the tumor parameters at one place and Table 4 shows tumor parameters at the other place. Table 5 shows the total tumor area and volume of the brain tumor in the data sets.

Table 2. Tumor volume of data set 1

S. No.	Infected Image	Tumor Area (cm <sup>2</sup> )	Tumor volume (cm <sup>3</sup> )
1	15	0.4561	0.2280
2	16	0.5099	0.2549
3	17	0.2086	0.1043
	Total	1.1746	0.5872

number of pixel of the desired region can be calculated by subtracting the number of on pixels of the cropped image from that of the dilated image. Assume the number of on pixels in the cropped image is  $A_1$ ; the number of on pixels in the dilated image is  $A_2$ . So the total number of pixels in the desired region are  $A$ . Mathematically 'A' can be written as  $A' = A_2 - A_1$ .

Where, A is the number of pixels area to be analyzed. After multiplying it by the pixel dimension we can get the area in the length units. Here the pixel dimension is  $0.035 \times 0.034 \text{ cm}^2$ . So the area in the length unit can be written as:  $A = A' \times 0.035 \times 0.034$  OR  $A' \times 0.001190 \text{ cm}^2$ . Volume can be calculated by multiplying the area by the thickness of the image slice. The thickness of the one slice of the image is 0.50 cm. So the volume of the tumor present in the image slice is given as:  $V = A \times 0.50 \text{ cm}^3$ . Where 'V' is the volume of the tumor present in one slice and 'A' is the area of tumor present in the one slice.

**Parameters display:** Displayed parameters are the area and volume of the brain tumor present in the particular slice of the MR image.

**Results**

When the algorithm executes the following things are come out. The data sets are shown in Fig.3 & Fig.4.

**Conclusions**

In this study an automated system for brain tumor volume measurements is developed based on MR imaging. This method is applied to 8-tumor contained MRI slices from 2 brain tumor patients' data sets and satisfactory segmentation results are achieved.

The result shows that this approach can successfully segment a tumor if the desired parameters are set correctly. The developed algorithm is

Table 3. Tumor volume data set 2

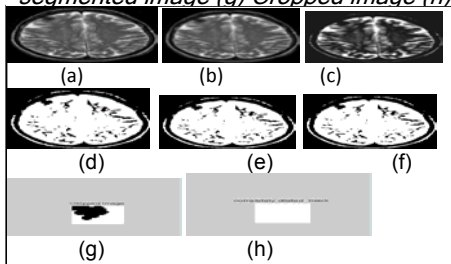
S. No.	Infected Image	Tumor area (cm <sup>2</sup> )	Tumor volume (cm <sup>3</sup> )
1	12	0.6313	0.3156
2	13	0.9941	0.4971
3	14	0.5604	0.2802
	Total	2.1858	1.0929

Table 4. Tumor volume of data set 2

S. No.	Infected Image	Tumor Area (cm <sup>2</sup> )	Tumor Volume (cm <sup>3</sup> )
1	18	0.1954	0.0977
2	19	0.1040	0.0520
	Total	0.2994	0.1597

useful to locate the tumor with its size. It takes the user defined input parameters for analytical calculations with one image at a time for processing and shows the output image at every step. Data sets (1, 2) have many infected images; these tumorous images are processed one by one. The numerical values of area and volume of the tumor in each image are shown in the Table 2-4. Table 5 shows the total numerical value of the tumor area

Fig. 7: (a) Input MR image (b) Gaussian filtered image (c) Intensity adjusted image (d) Output binary image (e) Dilated gradient mask (f) Region growing segmented image (g) Cropped image (h) Completely dilated cropped image



and volume. Further work is in progress to improve the segmentation.

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Table 5. Total tumors volume of data set 1 & 2

S.No	Data set	Tumor Area (cm <sup>2</sup> )	Tumor Volume (cm <sup>3</sup> )
1	1	1.1746	0.5872
2	2	2.1858	1.0929
Total		0.2994	0.1597

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Fig. 9. (a) Input MR image (b) Gaussian filtered image (c) Intensity adjusted image (d) Output binary image (e) Dilated gradient mask (f) Region growing segmented image (g) Cropped image (h) Completely dilated cropped image

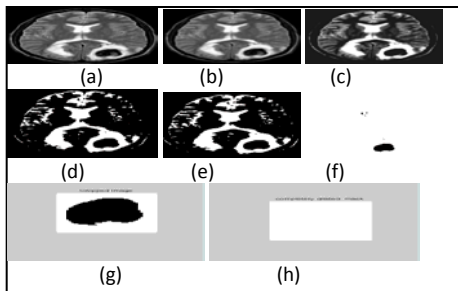


Fig. 10. (a) Input MR image (b) Gaussian filtered image (c) Intensity adjusted image (d) Output binary image (e) Dilated gradient mask (f) Region growing segmented image (g) Cropped image (h) Completely dilated cropped image

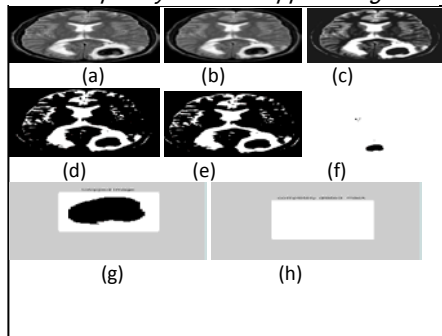
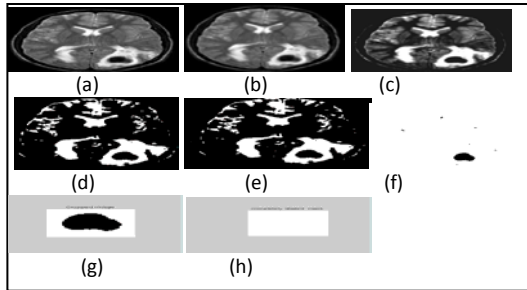


Fig. 8. (a) Input MR image (b) Gaussian filtered image (c) Intensity adjusted image (d) Output binary image (e) Dilated gradient mask (f) Region growing segmented image (g) Cropped image (h) Completely dilated cropped image



7. Beaulieu JM and Goldberg M (1989) Hierarchy

Fig. 11. (a) Input MR image (b) Gaussian filtered image (c) Intensity adjusted image (d) Output binary image (e) Dilated gradient mask (f) Region growing segmented image (g) Cropped image (h) Completely dilated cropped image

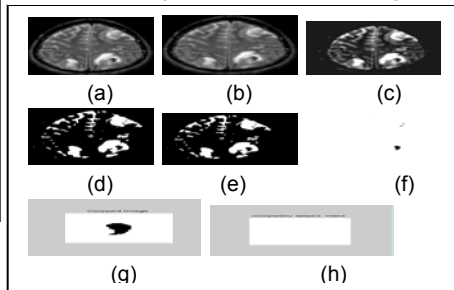
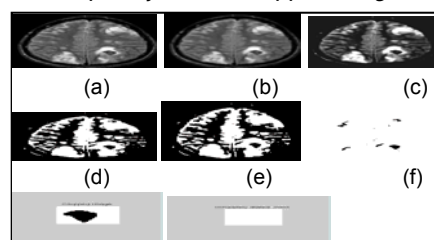


Fig. 12. (a) Input MR image (b) Gaussian filtered image (c) Intensity adjusted image (d) Output binary image (e) Dilated gradient mask (f) Region growing segmented image (g) Cropped image (h) Completely dilated cropped image



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