



## An Automated Method for Detection of Brain Abnormalities and Tumor from MRI Images

**Pabitra Roy**

Computer Science and Engineering  
University of Calcutta  
Kolkata, India

**Sudipta Roy, Prof. Samir Kumar Bandyopadhyay**

Computer Science and Engineering  
University of Calcutta  
Kolkata, India

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**Abstract**— This paper presents an automated method for detection of brain abnormalities and tumor edema segmentation from MRI images. The objective in segmentation is outlining the tumor including its subcompartment and surrounding tissues. Usually tumor occupies the locations of normal tissues and their intensity characteristics differ from the surrounding normal tissues. Though the intensity characteristics of tumor region and surroundings normal tissues differs but in T2 scan the tumor intensity characteristics are very close to CSF. So it is very difficult to segment tumor from CSF without proper threshold value selection in intensity based method. We propose a method to find appropriate threshold intensity value which is near the intensity value of the tumor border using standard deviation and the average intensity. We first compute the standard deviation of the intensity values in the image then using this standard deviation an intensity map is performed. We recomputed the standard deviation of the processed image. Using this standard deviation we compute the average intensity of the pixels those are above the standard deviation. The computed average intensity is taken as threshold value to process the original MRI images. This method allows the segmentation of tumor tissue with accuracy and location of abnormal region is also clearly identified. We have computed the tumor border with centroid. At the end of the process the tumor is extracted from MRI images and the shape also determined.

**Keywords**— MRI of Brain Scans, Segmentation, Brain Tumor, standard deviation, Binarization, brain abnormalities.

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### I. INTRODUCTION

In recent years it has been seen that the cancer patient have increased radically day by day. It is very hard to detect tumor in early stage, since accurate measurements in brain tumor diagnosis are quite difficult because of diverse shapes, sizes, appearances of tumor, position of tumor in the brain but once it gets identified the treatment can be done and is curable with technique like chemotherapy, radiotherapy. During the last few years brain tumor segmentation in MRI has become an emergent research field of medical image processing. MRI is an effective tool that provides detailed information about the targeted brain tumor anatomy, which in turn enables effective diagnosis and treatment. A brain tumor is cluster of abnormal cells growing in the brain. They are created by abnormal and uncontrolled cell division, usually in the brain itself. The MRI detects signals emitted from normal and abnormal tissue, providing clear images of most tumors. In Medical image processing segmentation plays a vital role to locate objects and boundaries in images or more precisely assign label to every pixels in an image such that every pixels with the same label share certain visual characteristics. Segmentation subdivides an image into its constituent regions or objects. Segmentation stops when the objects or region of interest in an application have been detected. So main objective of segmentation is to study anatomical structure, identify region of interest i.e. locate tumor, other abnormalities, measure tissue volume to measure growth of tumor.

From MRI images the information such as tumor location provides radiologists an easy way to diagnose the tumor and plan the surgical approach for its removal.

The rest of the paper is organised as follows. In section 2 related works are discussed, proposed method and algorithm is discussed in section 3. Result and discussion is discussed in section 6. Finally we give conclusion and references in section 7 and section 8.

### II. RELATED WORK

The existing tumor detection methods broadly classified into three categories: (A) atlas-based methods [1], [2], (B) symmetry property-based methods and (C) feature-based methods [3]–[6]. Most of the methods are semi-automatic and require user intervention either to initiate or to refine the results. A binarization is an essential preprocessing step for tumor detection purpose [7] and kapur [8] methods for better performance than the well known Otsu [9] have been discussed but a new standard deviation based binarization [10] also very useful for MRI of brain image. Prastawa et. al. [11] describes a framework for automatic brain tumor and edema segmentation from MRI images which does not require contrast enhanced image channels. The presence of abnormal tissues in the CSF class can be detected by measuring the vertical symmetry of the CSF image [12]. An important step in most medical imaging analysis systems is to extract the boundary of an area we are interested in. Many of the methods are there for the MRI segmentation [13 – 19]. Pham, Chenyang Xu, L. Prince represented that ANNs show a paradigm for machine learning and can be used in a variety of ways for image segmentation [20]. The segmentation & edge detection approaches were studied under 5 categories.

These are as follows- 1) Thresholding approaches, 2) Region growing approaches, 3) Genetic Algorithm approaches, 4) Clustering approaches, 5) Neural network approaches. Several authors suggested several algorithms for image segmentation. The segmentation of brain tumor from magnetic resonance images is an important but time-consuming task performed by medical experts. The digital image processing community has developed several segmentation methods [ 23] , many of them ad hoc. Four of the most common methods are: a.) amplitude thresholding, b.) texture segmentation c.) Template matching and d.) region-growing segmentation. Brain Tumor Detection and Segmentation Using Histogram Thresholding is described in [21]. Jianping Fan, Yau Elmagarmid & Aref's [22] paper presents an automatic image segmentation method using thresholding technique. The increased sensitivity of MRI relative to CT for detection of many forms of brain injury as well as brain abnormality has been well-documented [24]. Detection and Quantification of Brain Tumor from MRI of Brain and its Symmetric Analysis is discussed in [26].

### III. PROPOSED METHOD

Images are obtained using MRI scan and these scanned images are displayed in a 2D matrix having pixel as its intensity values. The entries of a gray scale image are ranging from 0 to 255, where 0 represents black colour and 255 represents white colour .If it is a colour image then conversion to gray image is needed. Image is processed to remove any noise present using median filter. Median filters are quite popular because for certain types of random noise, they provide excellent noise reduction capabilities, with considerably less blurring than linear smoothing filters of similar size. Then a standard deviation is computed from the filtered image. The standard deviation is computed as follows. An image  $f(x,y)$  and mean intensity of an image is obtained by summing the values of all its pixels and dividing the sum by total number of pixels in the image.

$$I_{mean} = \frac{1}{MN} \sum_{x=0}^{M-1} \sum_{y=0}^{N-1} f(x,y)$$

Where M is the number of row pixels and N is the number of column pixels. MN is the total number of pixels in the image.

The standard deviation  $S_d$  of the intensity within an image is defined as

$$S_d = \sqrt{\frac{1}{MN} \sum_{x=0}^{M-1} \sum_{y=0}^{N-1} (f(x,y) - I_{mean})^2}$$

Usually the intensity value of the tumor and its surroundings are relatively high with respect to other tissue. Thus when standard deviation of the image is computed it will give low standard deviation, which indicates that they are clustered closely around the mean i.e. data points tend to very close to the mean. But the intensity values of the pixels of the tumor are far from the mean. Using this standard deviation it is impossible to segment the tumor section from its surroundings. Using this standard deviation an intensity map is performed i.e. intensity values greater than standard deviation is set to 255 and less than is set to 0.

Intensity map is defined as

$$L(x, y) = \begin{cases} 255 & \text{if } f(x, y) \geq S_d \\ 0 & \text{if } f(x, y) < S_d \end{cases}$$

Then standard deviation of the processed image is recomputed as.

$$S_{dnew} = \text{standard deviation } [L(x, y)]$$

It gives large standard deviation, which indicates that the data points are far from the mean i.e. data points are spread out over the large range of values. Our aim is to set the threshold value in such a way that it is relatively close to the intensity values of the tumor boundaries. Using the newly computed standard deviation an average intensity is computed of the pixels those are above the standard deviation of the original image.

$$I_{average} = \frac{\text{sum of the intensity values of all the pixels above } S_{dnew}}{\text{total number of pixels having intensity above } S_{dnew}}$$

$$= \frac{\sum_{x=0}^{M-1} \sum_{y=0}^{N-1} (f(x,y) | f(x,y) > S_{dnew})}{n}$$

Where n is the total number of pixels having intensity values greater than  $S_{dnew}$  .

The computed average intensity is taken as threshold value to process the entire original image to segment the tumor section from MRI. The intensity value greater than or equal to the threshold value is set to 255 and less than set to 0. This segments the tumor from MRI.

$$I(x, y) = \begin{cases} 255 & \text{if } f(x, y) \geq I_{average} \\ 0 & \text{if } f(x, y) < I_{average} \end{cases}$$

Label the connected components of image  $I(x, y)$  with 8 connected neighbourhoods. Then remove the components from the labelled image those are not a member and having pixels less than some predefined value. This gives the tumor region.

To find the border of tumor region 'Sobel' edge emphasizing filter (2-D) is used and is given by

$$I_x = \frac{\delta f}{\delta x} = (z_7 + 2z_8 + z_9) - (z_1 + 2z_2 + z_3)$$

$$I_y = \frac{\delta f}{\delta y} = (z_3 + 2z_6 + z_9) - (z_1 + 2z_4 + z_7)$$

$z_1$	$z_2$	$z_3$
$z_4$	$z_5$	$z_6$
$z_7$	$z_8$	$z_9$

-1	-2	-1
0	0	0
1	2	1

-1	0	1
-2	0	2
-1	0	1

Sobel operator (mask)

Where  $I_x$  and  $I_y$  are images of same size as the original is obtained by filtering image by Sobel mask. Due to better smoothing characteristics Sobel masks are used. Using  $I_x$  and  $I_y$  gradient magnitude is calculated as follows.

Gradient magnitude =  $\sqrt{(I_x^2 + I_y^2)}$  is the value of the rate of change in the direction of the gradient vector. Using Gradient magnitude tumor border is detected.

#### IV. Algorithm for Abnormal Region Identification and Its Centroid detection.

**Input:** A MRI image of Brain.

**Output:** Abnormal region identification with centroid

Step1: Read Image (Gray image or Colour Image)

Step2: Convert it to Gray Image ( $I_{GRAY}$ ) form RGB.

Step3: Remove noise by using median filter of image  $I_{GRAY}$ . The processing Image is  $I_{pro}$ .

Step4: Set  $L=I_{pro}$

Step5: Compute standard deviation of  $I_{pro}$  using formula above. Let it  $S_d$ .

Step6: Using this  $S_d$  perform intensity map as follows.

$[m, n]= \text{size}[L]$  // size of image is calculated

**For**  $i=1$  to  $m$

**For**  $j=1$  to  $n$

**If**  $L(i,j) > S_d$  **Then**

**set**  $L(i,j)=255$

**Else**

**set**  $L(i,j)=0$

**End If**

**End For**

**End For**

Step7: Recompute the standard deviation of image  $L$ . Let it  $S_{dnew}$ .

Step8: Compute average intensity of the pixels those are above the  $S_{dnew}$  as follows.

**Set**  $\text{count} \leftarrow 0$

**Set**  $I_{\text{sum}} \leftarrow 0$

**For**  $i=1$  to  $m$

**For**  $j=1$  to  $n$

**If**  $I(i,j) \geq S_{dnew}$  **Then**

**set**  $\text{count} = \text{count} + 1$  // pixel count.

**set**  $I_{\text{sum}} = I_{\text{sum}} + I(i,j)$  // sum of intensity values.

End If

End For

End For

Step9: Average intensity,  $I_{\text{average}} = I_{\text{sum}} / \text{count}$ . // average intensity calculation.

Step10: Take this average intensity as Threshold value to find tumor section.

For i=1 to m

For j=1 to n

If  $I(i,j) > I_{\text{average}}$  Then

set  $I(i,j)=255$

Else

set  $I(i,j)=0$ ;

End If

End For

End For

Step11: Label the connected components of image I with 8 connected neighbourhoods. Let it be  $I_{\text{label}}$ .

Step12: Measure properties of image regions of labelled image  $I_{\text{label}}$  and compute number of pixels in regions.

Step13: Remove the components from Labelled image  $I_{\text{label}}$  is not a member and having pixels less than some predefined value. Let the processed image is H.

Step14: Create 'Sobel' horizontal edge emphasizing filter (2-D filter) predefined as a correlation kernel.

Step15: Compute the gradient magnitude of image H as follows.

$$\text{Gradient magnitude} = \sqrt{I_x^2 + I_y^2}$$

Where  $I_x$  is obtained by filtering the image H by 'Sobel' filter created in Step14.  $I_y$

is obtained by filtering image H by transpose of 'Sobel' filter created in step14.

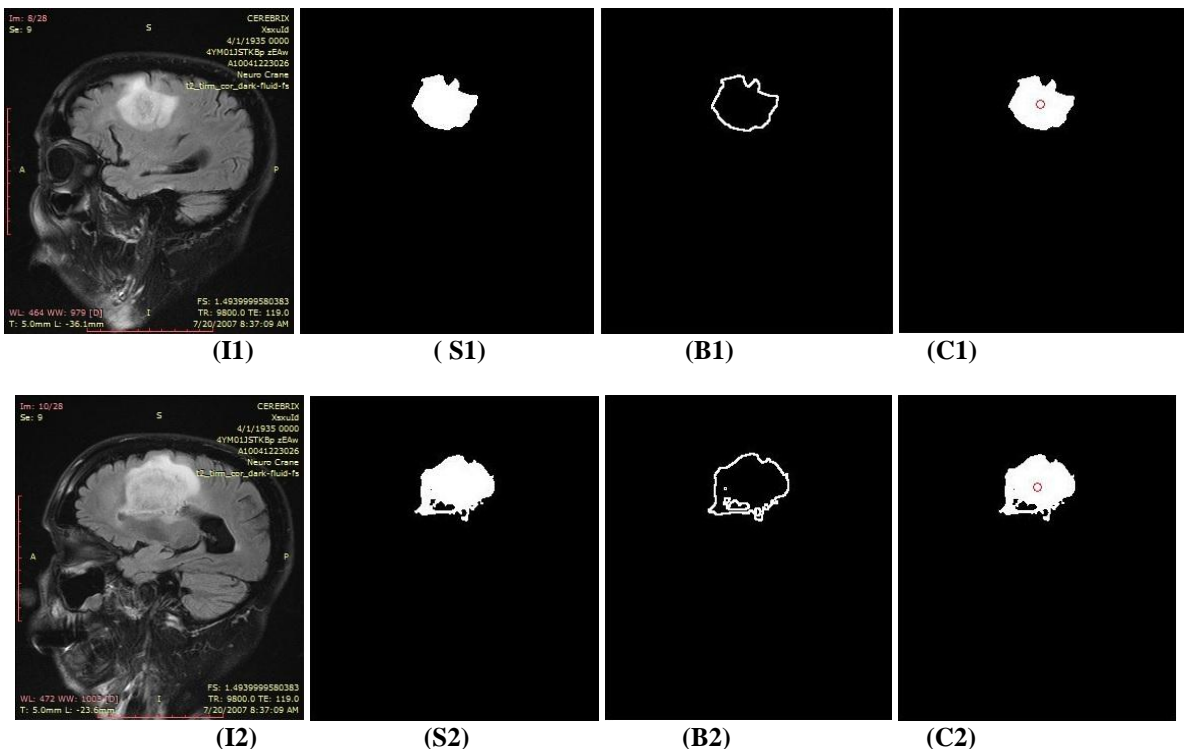
Step16: The step 13 gives the Tumor region and Step15 gives the border of Tumor region.

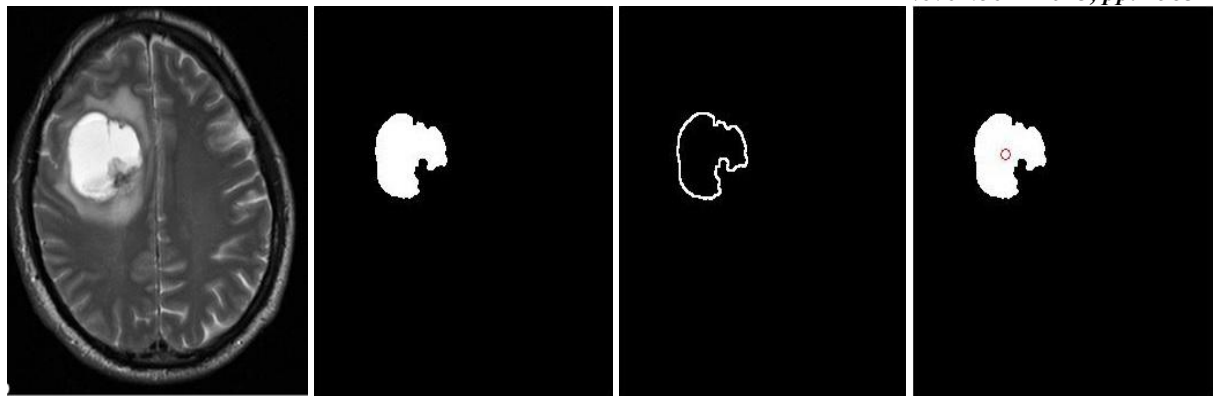
## V. Complexity Analysis:

To calculate the standard deviation, it required  $O(mn)$  time. The step 8 and step 9 required  $O(mn)$  time. To label the connected components it required  $O(mn)$  time. Hence total time complexity =  $O(mn) + O(mn) + O(mn) = O(mn)$ .

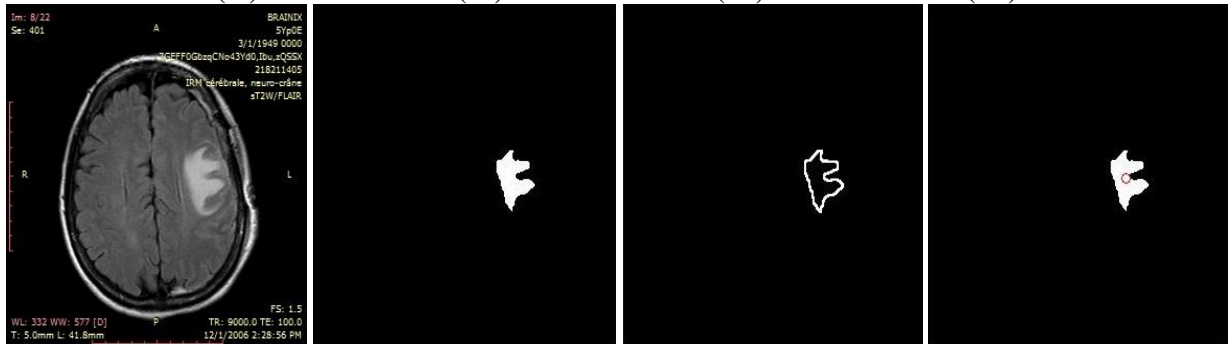
## VI. Results and Discussion

The proposed algorithm is used to detect the location or position the abnormal regions, centroid of the abnormal regions, and border of the abnormal regions and the perimeter of the detected abnormal regions. The output of the segmented abnormal regions and border of the Abnormal regions are plays a vital role in the diagnosis and treatment planning of brain abnormal regions. The proposed method gives very reasonable results for different kind of MRI images.

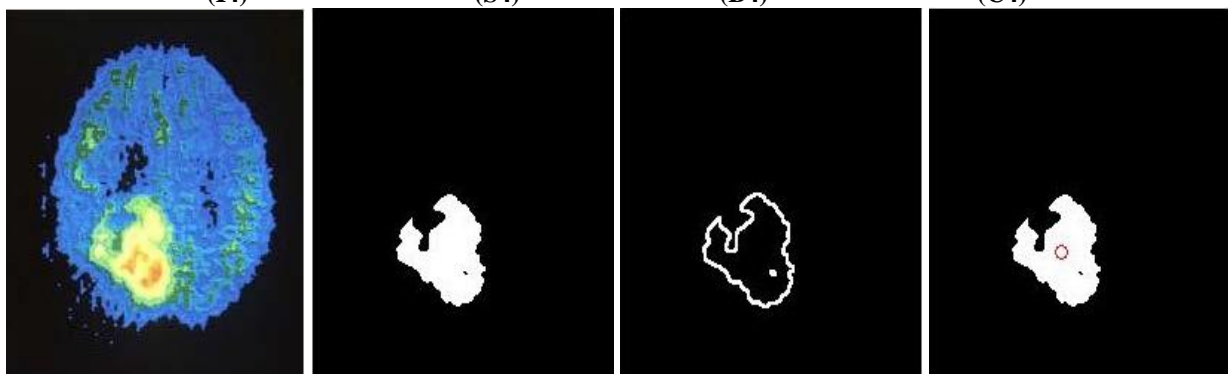




(I3) (S3) (B3) (C3)



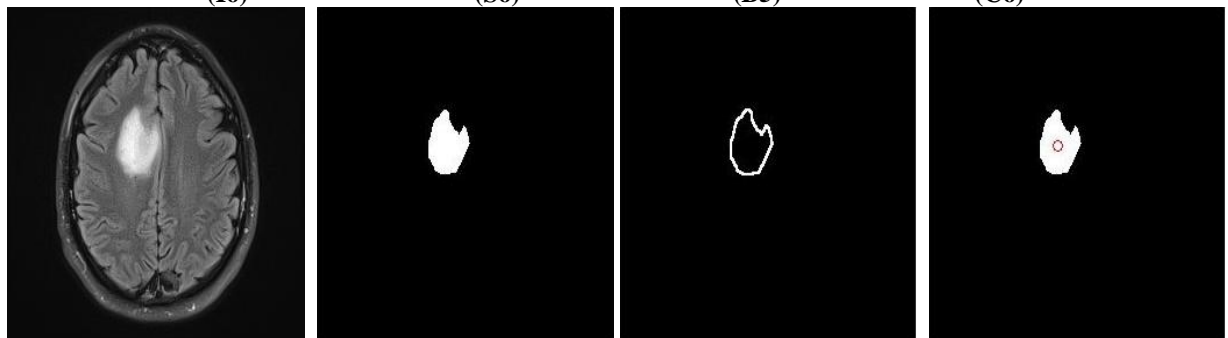
(I4) (S4) (B4) (C4)



(I5) (S5) (B5) (C5)



(I6) (S6) (B6) (C6)



(I7) (S7) (B7) (C7)



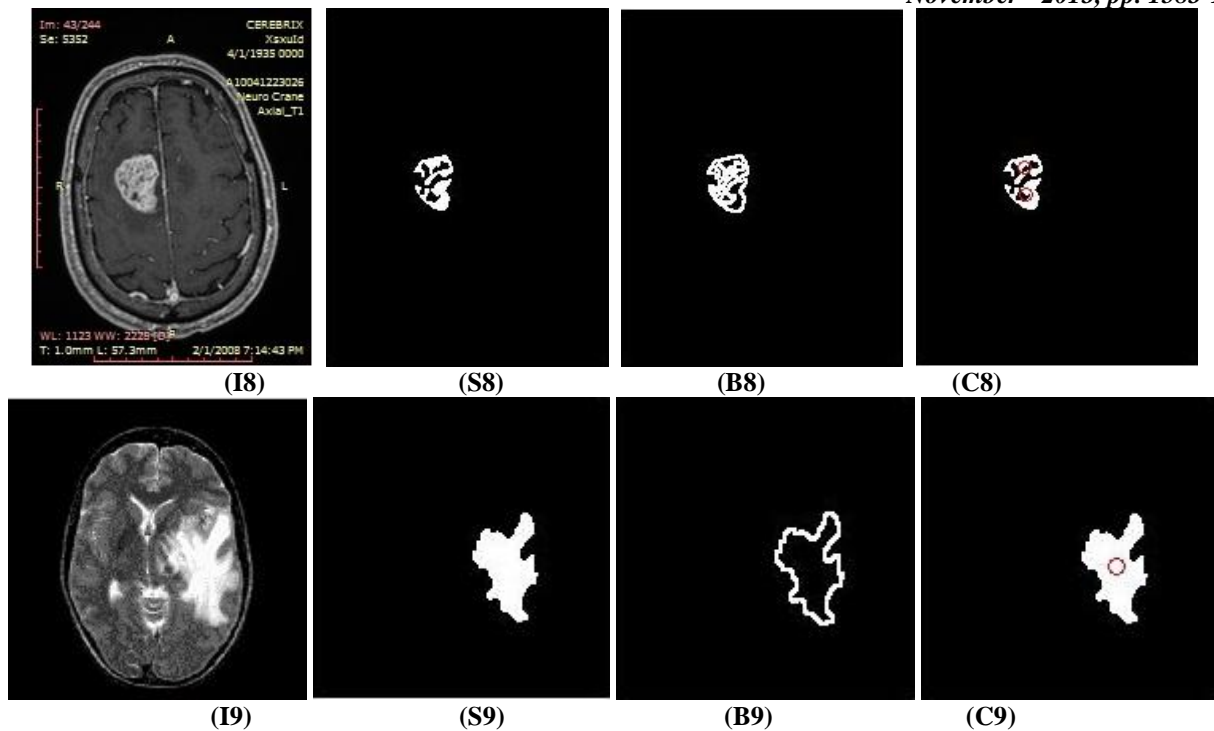


Figure1: **I1-I7** in the column1 are the input MRI Brain Image; **S1-S9** in the column2 are the outputs (Segmented Abnormal Regions); **B1-B9** in the column3 are the border of the abnormal region; **C1-C9** in the column4 are the Abnormal Region with Centroid marked with red circle.

## VII. Conclusion

The proposed algorithm shows an effective method for segmentation of the brain tumors from the 2 dimensional MRI images. We have proposed to detect presence of brain tumor based on thresholding technique. The segmentation of the brain is also being done while detecting the presence of the tumor. We also find the centroid of the tumor and perimeter of the tumor. In this paper we have developed an automatic image based method to detect tumors in 2-D MRI head scans. Experimental results on 30 data sets show that the proposed method performed Automatic Detection of Brain Tumor from MRI Scans .Future research scope in segmentation of medical MRI image will lead towards improving the accuracy , minimizing the computational procedure also minimize the manual interaction.

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