

# Detection and Validation of Segmentation Techniques for MR Brain Tumor of Glioma Patients



Akshath M J, H S Sheshadri

**Abstract:** Prediction of brain tumor becomes difficult with respect to the irregular shape, growth, location and volume of the tumor, thus segmentation is highly required for the proper detection of the tumor. Four sequences of MR images like T1, T2, T1 contrast and fluid attenuation inversion recovery (FLAIR) is collected from the BRATS 2015 dataset for the validation of segmentation techniques. In this paper two segmentation techniques like semi-automated active contour and fully-automated expectation maximization (EM) are discussed as both are widely used in the field of brain tumor analysis. The synthetic data obtained is skull stripped and noise free reducing the process time for detecting the tumor. The main objective is to extract the region of interest, validate and improve the accuracy, dice coefficient of the synthetic dataset with the ground truth available. Active contour is an iterative process with the initial contour selected manually and EM works on the probability of the intensity values. The result shows some of the images works better with active contour and some with EM. Time taken is less for EM compared to active contour. Accuracy, dice coefficient, sensitivity is better in EM compared to Active contour. Statistical features and textural features extracted from the above techniques plays vital role for the accurate diagnosis of the tumor. In this context segmentation is vital to further classify images into low grade and high grade glioma's helping radiologists to accurately diagnose the abnormal tissue growth with effective planning of treatment.

**Index Terms:** Active contour, Expectation maximization, Glioma, MR images, Segmentation.

## I. INTRODUCTION

Magnetic resonance imaging is considered most for the brain tumor analysis as it provides the information of the soft tissues and importantly it is a non-invasive technique used for the diagnosis. Detecting the presence of tumor in the brain is difficult due to irregular shape, location and size. Tumors in the brain are caused from glial cells, hence called as gliomas. Gliomas are categorized as low grade gliomas (LGG) and high grade gliomas (HGG). HGG are more aggressive in growth than LGG, if LGG is not diagnosed properly may lead to evolve into HGG over time [1]. Segmentation algorithms help to examine the tissues, shapes and structures of the brain helping the radiologists to diagnose the tumor in a quantitative manner. However,

extracting the tissues of the brain, especially tumor and edema is complicated because of the nonhomogeneous distribution of intensity values [2]. Automatic segmentation techniques are considered and selected based on their capabilities to achieve better results compared to those obtained manually by experts. Four different sequences of MR images are considered like T1-weighted (T1), contrast enhanced T1 weighted (T1ce), T2 weighted (T2) and FLAIR MRI scans. Segmentation is considered as one of the basic problem referring to assign a label to each pixel such that pixels belonging to same label share certain suitable characteristics in biomedical image processing. Manually segmenting the brain MRI is widely used in clinical practice but it is time consuming, to analyze the data in huge number; experts required could be more to analyze the visual appearances of the brain tumor, hence automatic segmentation with more accurate results has emerged in recent years. Segmentation approaches provides the suitable features like volume, identifying the shape and location along with statistical and textural based features helping the classifier to properly categorize the tumor into abnormal ones (LGG and HGG) from the normal images. Visualizing the information from the region of interest in any medical image, segmentation is highly required and considered as crucial step as its output affects the process of analyzing an image. MRI is widely used in interpreting the tumor effects as it is a powerful and noninvasive imaging tool, used to diagnose, characterize the disease. HGG requires more intention to diagnose as the cells grow with rapid rate. Glioblastoma is the most common type of HGG which needs to be diagnosed effectively for the proper treatment and predicting the survival rate of the patients based on the features obtained from the segmentation process [2]. Active Contour is a semi-automated technique having the advantage of identifying multiple region of interest but consumes more time because of iterative process. At the other end EM is a fully automated technique which works on probability of the intensity based on the histogram values [3]. Proper segmentation leads to reduce the false alarms in the classification process. Validation of the segmentation techniques with the ground truth obtained manually by the expert's leads to come up with an accurate automatic detection of the brain tumor with better results leading to accurate classification. The paper is organized as section II explains the methods involved in biomedical image segmentation. Methodology is discussed in section III. In section IV segmentation results of semi-automated and fully automated techniques are described. Conclusion is summarized in section V and future scope in section VI.

Manuscript published on 30 September 2019.

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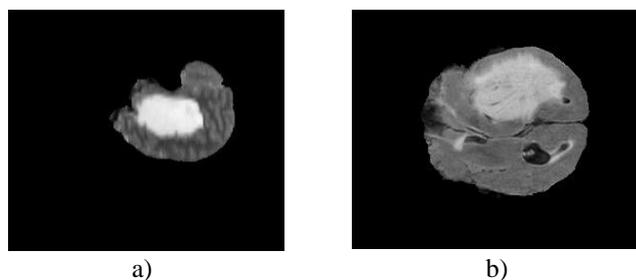
## II. RELATED WORKS

Demirhan et al. [4] presented a new tissue segmentation technique using wavelet transform and neural networks, which provides better segmentation of brain MR images into the tumor, white matter (WM), gray matter (GM), edema, and cerebro spinal fluid (CSF). Kong et al. [5] used discriminative clustering and feature selection for automatic segmentation of brain tumor using MR scan images. C Parmar et al. [6] claims that semi-automatic segmentation is better compared to manual segmentation, in contrast with inter-user variability, which provides better output accuracy. Hence, segmentation becomes necessary to discuss the current methodologies used in recent years in medical image processing; automated algorithms provide accurate results with no user intervention. Wang et al. [7] presented a medical image segmentation technique on active contour model reducing the error rate with non-homogeneous intensity values. Chaddad et al. [8] proposed a technique of automatic feature extraction based on Gaussian mixture model (GMM). In this method, wavelet based features using principal component analysis (PCA) to reduce the dimension and hence the performance of the GMM is enhanced. Ajala Funmilola A. et al. [9] described various methods employed in medical image segmentation like clustering methods, global thresholding, region growing, models especially deformable and markov random etc. They mainly focused on clustering methods, especially k-means and fuzzy c-means clustering. Combination of clustering algorithms to form hybrid technique such as fuzzy k-c means algorithm, providing better results. Yan Li et al. [10] explained a new unsupervised MRI segmentation technique on self-organizing feature map (SOFM). This novel technique contains spatial information of the pixel values using Markov Random Field, Sachdeva et al. [11] explained the intensity of brightness levels and textural patterns to indicate the edges of the boundary using active contour around the tumor in MR imaging methods. S Bauer et al. [12] explained many automatic segmentation techniques for detecting tumor, images are processed on the intensity values of voxels with the information of neighborhood pixels. These methods are flexible providing better results with no human user interaction. Thresholding techniques can be used effectively with clear histograms of the object and the background. These techniques provide inaccurate segmentation result as the distribution of pixel values is complex to analyze the brain tumor. Gray level distribution of GM, WM and CSF pixels lead to incorrect detection of the boundary. Region growing techniques use the homogeneous pixel values and connectivity criteria for segmentation and therefore not suitable for brain tumor segmentation as the brain structure contains irregular shapes. The brain tumor extraction separates raw MR images into region having the tumor glial cells from the normal tissues. Festa et al. [13] extracted intensity, information of the neighborhood pixels, context information and textural features. Random Forest method gives average dice similarity index of 83% and 70% for extracting the complete tumor region in high grade glioma, and with average of 72% and 47% in low grade glioma patients. Zanaty et al. [14] suggested a method to extract tumor using hybrid technique fusing Fuzzy C means, region growing and validated using Jaccard similarity index to measure the gray and white matter segmented tissues from MR brain images.

Reza et al. [15] uses intensity differences along with textural features as input for the random forest classifier achieving the average dice coefficient of 0.92 and 0.91 for segmenting the entire tumor region from the tumor core for high grade glioma and low grade glioma. Ben george et al. [16] produced segmentation outcome of the glioma images with overall processing time of 31.21s based on bacteria foraging optimization method. Processing time of an algorithm plays a vital role for diagnosing the tumor process. Within less computational time helps the radiologist to extract large volumes of clinical data. Aljahdali et al. [17] proposed an automatic segmentation based on modified fuzzy algorithms, improving the segmentation accuracy and computational time remains an open problem in the case of medical image segmentation. Somasundaram et al. [18] explained about the complete automated extraction of brain for T2 axial weighted images. Harati et al. [19] utilized fuzzy connectiveness (FC) for segmentation and identify abnormal part only in T1 contrast weighted sequence. J Yu et al. [20] suggested a generalized FCM (GFCM) technique to find the variations in FCM and then optimality test is processed using parameter selection method. GFCM involves the optimal test only with cluster prototype but not with membership functions. S Shen et al. [21] suggested a novel FCM algorithm, named improved FCM (IFCM). The method is concerned with the difference of features between its neighboring pixels and to calculate the relative location of the neighboring pixel values. T Logeshwari *et al.* [22] proposed a detection brain tumor from MR images using segmentation process based on hierarchical self-organizing map (HSOM) approach, such that T2 weighted images were segmented with an average time period of 29.9708s requiring further minimization.

## III. METHODOLOGY

In this section semi-automatic segmentation technique like active contour and fully automated technique like EM are discussed. Synthetic dataset is collected from the multimodal Brats 2015 along with the ground truth for validation purpose. All the 3 planes like axial, sagittal and coronal with different MRI sequences such as T1 weighted, T1 contrast weighted, T2 weighted and FLAIR with 25 datasets containing both LGG and HGG are considered for the processing. Some of the images are chosen for the results as shown in fig 1 and result is estimated for the set of same images.



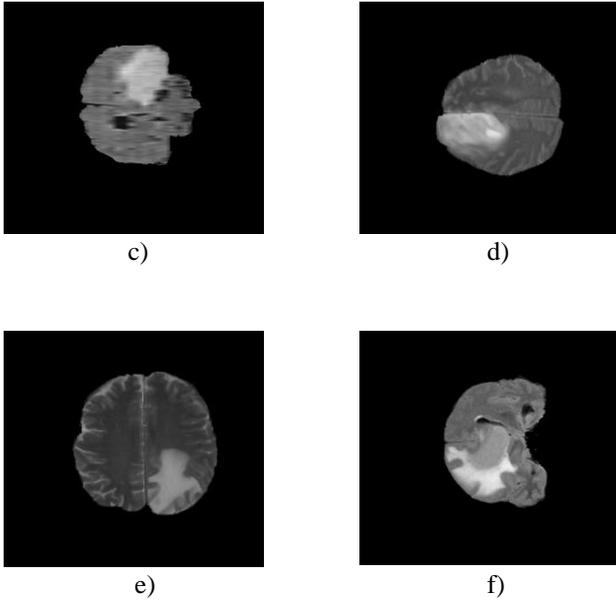


Fig 1. Random samples of Original MR images considered for the study. a) shows T2 sagittal view, b) shows FLAIR axial view, c) shows FLAIR coronal view, d) shows T2 axial view, e) shows T1C axial view, f) shows T1 coronal view.

**A. Edge based Active Contour**

The objective of the level set active contour is minimizing the energy function. Following are the steps considered for the segmentation.

1. MR image is converted to gray scale if image is color. Gray scale is more efficient to compute the homogeneity and in-homogeneity intensity values of image pixels. Gaussian filter is applied to maintain the smoothness of the image by finding the gradient of the image. Let I be an image defining an edge indicator function g given by Eqn. (1),

$$g = \frac{1}{1+(I_{\sigma}+I)^2} \tag{1}$$

$I_{\sigma}$  implies Gaussian function with a standard deviation  $\sigma$ , g is edge indicator function and I is image.

2. Draw the initial contour points to compute the segmentation using center derivation of eight neighboring pixels to apply boundary conditions for proper segmentation of an image.
3. For a Set Function  $\Omega \rightarrow R$  we define an energy functional  $\epsilon(\Phi)$  given by Eqn. (2),

$$\epsilon(\Phi) = \mu R_p(\Phi) + \lambda L_g(\Phi) + \alpha A_g(\Phi) \tag{2}$$

Where  $\lambda > 0$  and  $\alpha \in R$  are the coefficients of the energy functional  $L_g(\Phi)$  and  $A_g(\Phi)$ , which are defined by Eqn. (3) and Eqn. (4) respectively.

$$L_g(\Phi) \triangleq \int_{\Omega} g \delta(\Phi) |\nabla \Phi| dx \tag{3}$$

$$A_g(\Phi) = \int_{\Omega} g H(-\Phi) dx \tag{4}$$

Where,  $\delta$  = Dirac Delta Function and H = Heaviside function respectively.

$L_g(\varphi)$  - Line integral of the function

$A_g(\varphi)$  - weighted area of the region

Dirac delta function is given by Eqn. (5).

$$\delta_{\epsilon}(x) = \begin{cases} \frac{1}{2\epsilon} [1 + \cos(\frac{\pi x}{\epsilon})], & |x| \leq \epsilon \\ 0, & |x| > \epsilon \end{cases} \tag{5}$$

Heaviside function is given by Eqn. (6),

$$H_{\epsilon}(x) = \begin{cases} 0.5(1 + \frac{x}{\epsilon} + \frac{1}{\pi} \sin(\frac{\pi x}{\epsilon})) & , |x| \leq \epsilon \\ 1 & , |x| > \epsilon \\ 0 & , |x| < -\epsilon \end{cases} \tag{6}$$

Heaviside function and Neumann bound constrain is convergence for image segmentation.

4. Calculate the curvature by taking the divergence of the new bound condition mentioned in step 2.
5. Let  $\varphi: \Omega \rightarrow R$  defined on domain  $\Omega$ . We define an energy functional  $\epsilon(\varphi)$  given by Eqn. (7),

$$\epsilon(\Phi) = \mu R_p(\Phi) + \epsilon_{ext}(\Phi) \tag{7}$$

Where  $R_p$  is the distance regularization term given by Eqn. (8)

$$R_p(\Phi) \triangleq \int_{\Omega} p(|\nabla \Phi|) dx \tag{8}$$

6. The final energy function is given by Eqn. (9),

$$E_{\epsilon}(\Phi) = \mu \int_{\Omega} p(|\nabla \Phi|) dx + \lambda \int_{\Omega} g \delta_{\epsilon}(\Phi) |\nabla \Phi| dx + \alpha \int_{\Omega} g H_{\epsilon}(-\Phi) dx \tag{9}$$

Where  $\lambda$  term is the edge term and  $\alpha$  is the weighted area of the region.

7. Repeat the steps until the tumor boundary gets converged.

**B. Expectation Maximization (EM)**

The parameter vector  $\Phi$ , is the missing data that defines the mixture. The EM technique utilizes the maximum likelihood estimation to estimate the value of  $\Phi$ . Following steps are described as follows.

1. The number of classes K is defined and the MR images are given for processing.
2. The initial parameter  $\Phi_{(0)}$  is estimated based on the intensity values obtained from histogram of the image and the number of classes.
3. Estimate the values of Expectation given by Eqn. (10). Calculate the membership probability of each data.

$$P_k(x|\theta_k) = P_k(x|\mu_k, \epsilon_k) = \frac{0.5}{\sqrt{\det(2\pi \epsilon_k)}} e^{-(x-\mu_k)^T \epsilon_k^{-1} (x-\mu_k)} \tag{10}$$



Where  $K$  is number of classes extracted from the image and  $P_k$  term is the probability of pixels belonging to that class based on the histogram values.  $\theta_k \forall K = 1, 2, 3, \dots, K$  is represented in the form of  $[\mu_k, \epsilon_k]$  which defines the mean and variance of the distribution  $K$  respectively.

4. In Maximization, mean and variance of every kernel element is computed based on the probability values estimated in Expectation. Mean and variance are given by Eqn. (11) and Eqn. 12 respectively.

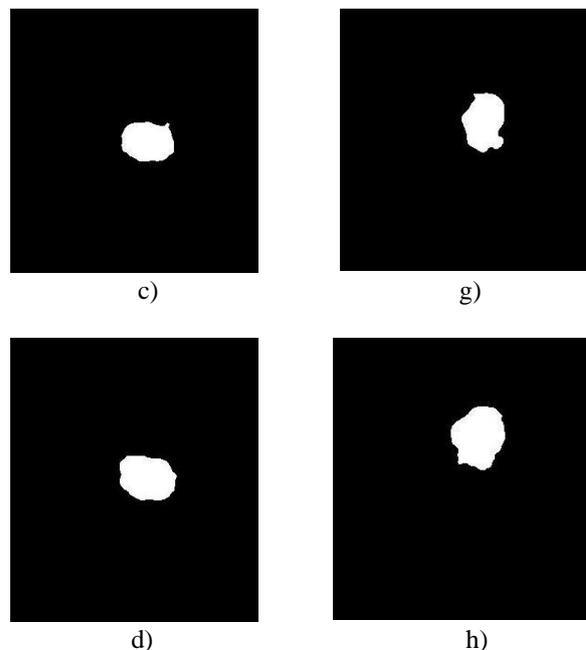
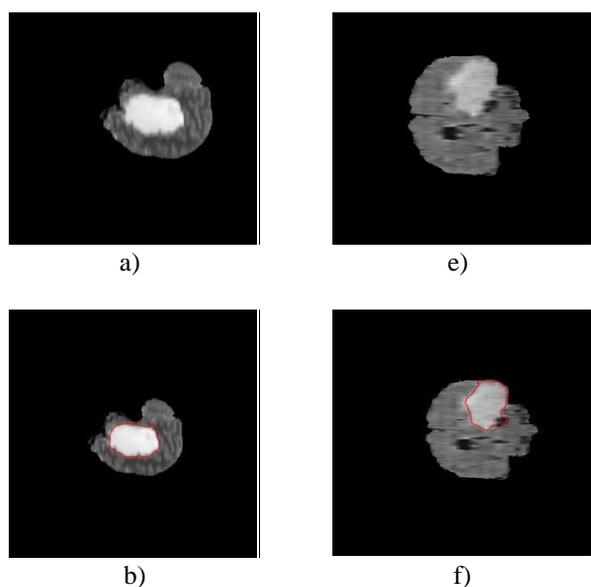
$$\mu_k^{t+1} = \frac{\sum_{i=1}^N x_i P(k|x_i, \theta^t)}{\sum_{i=1}^N P(k|x_i, \theta^t)} \quad (11)$$

$$\epsilon_k^{t+1} = \frac{\sum_{i=1}^N x_i P(k|x_i, \theta^t) (x_i - \mu_k^{t+1}) (x_i - \mu_k^{t+1})^T}{\sum_{i=1}^N P(k|x_i, \theta^t)} \quad (12)$$

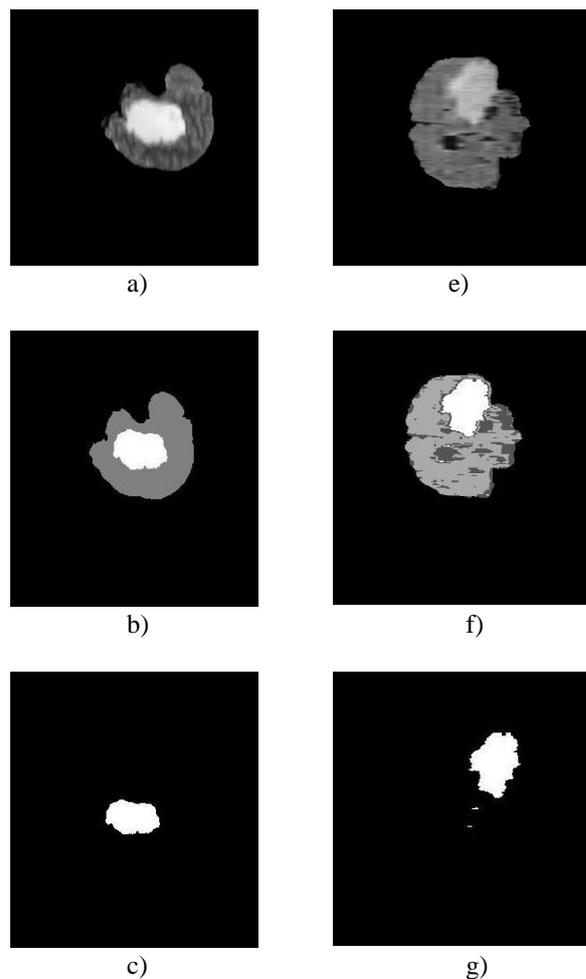
5. Repeat the Expectation and Maximization steps iteratively till the convergence.

### IV. RESULTS AND DISCUSSIONS

The Segmentation techniques like semi-automatic and fully automatic are discussed on the synthetic dataset collected from the multimodal Brats 2015 dataset which is categorized into LGG and HGG. 25 cases of glioma patients are used with MR sequences such as T1W, T2W, T1 contrast enhanced and FLAIR in all the 3 different planes. Validation of each segmentation algorithm is carried out based on the ground truth provided by the experts. Parameters like Dice similarity coefficient, Accuracy, overall time taken are the parameters are considered for evaluating the performance of the algorithm. Results of the segmentation techniques are shown in fig.1 and fig.2 respectively. Performance measures are computed as shown in the table 1.



**Fig. 2 Results of Active Contour, a and e are original MR t2 sagittal and t2 coronal image respectively, b and f are final contour, c and g are mask output, d and h are ground truth obtained by experts.**



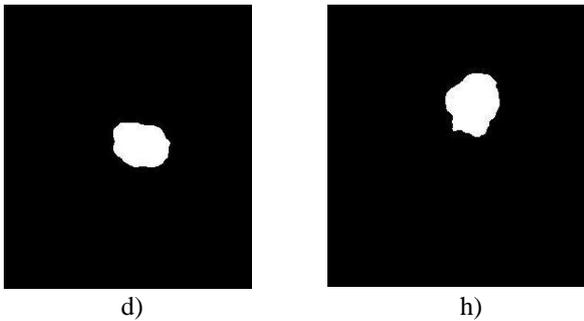


Fig. 3 Results of Active Contour, a and e are original MR t2 sagittal and t2 coronal image respectively, b and f are final class probability regions, c and g are mask output, d and h are ground truth obtained by experts. Statistical performance of the segmentation is evaluated by accuracy and dice similarity coefficient (DSC) ranging from 0 to 1 where 0 means segmentation result mismatched with ground truth and 1 is a perfect match. Accuracy and DSC is given by Eqn. (13) and Eqn. (14) respectively,

$$Accuracy = \frac{TP+TN}{TP+FP+TN+FN} \quad (13)$$

$$Dice = \frac{2*TP}{FP+FN+2TP} \quad (14)$$

Where TP is true positive specifies intersection of segmented image and ground truth  
 TN is true negative indicates part of the image beyond the union of segmented image and ground truth.  
 FN is false positive measuring the values of missed parts of the ground truth.  
 FP is false positive indicating segmented region not overlapped with ground truth part.

As the statistical values shown in table 1 clears that time taken to extract the tumor is less in EM compared to Active contour. In active contour initial points is chosen by the user and therefore based on the iterative process the result varies which is the major drawback of active contour whereas in EM tumor is extracted automatically using the probabilistic value of the pixels that belongs to suitable class without any user intervention, but main drawback of EM method is it can't distinguish the intensity of neighboring pixels belonging to the same class.

**Table 1: Performance measures of segmentation approaches**

Image	Methods	Accuracy	Time taken	DSC
T2 sagittal	Active contour	0.996	127.3sec	0.88
	EM	0.993	<b>3.42sec</b>	0.84
FLAIR axial	Active contour	0.992	168.6sec	0.85
	EM	0.991	<b>25sec</b>	0.82

FLAIR coronal	Active contour	0.995	127sec	0.851
	EM	0.994	<b>17.97sec</b>	0.928
T2 axial	Active contour	0.996	170sec	0.87
	EM	0.993	<b>21.88sec</b>	0.79
T1C axial	Active contour	0.997	137.3sec	0.87
	EM	0.996	<b>27.83sec</b>	0.70

### V. CONCLUSION

Multimodal sequences like T1, T2, T1C and FLAIR are used for detection techniques for glioma patients. Two segmentation techniques are explained having their own advantages and disadvantages. In semi-automatic active contour, more time is consumed because of iterative process and performance keeps on changing each time as the initial points are given by the user. Thus, fully automatic is preferred as the EM works on the probability values of pixels based on histogram with less computation time. The result shown in table 1 shows active contour provides better accuracy but varies each time when the initial points are chosen by the user but the results of EM remains same as user interaction is not required. Thus accuracy, time consumed and dice similarity coefficient index values are concluded better in EM than active contour.

### VI. FUTURE SCOPE

Active contour is an iterative process which consumes much time for validation and EM doesn't work well for all MR brain images, so to overcome these drawbacks hybrid algorithm combining active contour and EM is considered to get the improved performance in extracting the brain tumor.

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