Evaluation Of Hybrid Segmentation Technique For Pre-Operative Brain MR Images

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Abstract: Tumor diagnosis with accurate evaluation of brain MR images is crucial as the shape, size and location varies accordingly. Brats 2015 database comprises variety of sequences like T2, T1, T1-ce and FLAIR are considered for the analysis of glioma tumor. The proposed technique incorporates hybrid combination of algorithms namely active contour and expectation maximization to merge the desired feature of each technique to improve the performance better in comparison with the individual techniques. The performance criteria used for evaluating the tumor extraction mainly rely on the dice similarity coefficient (DSC), tumor area, sensitivity and specificity. Gaussian filter is used for enhancing the raw MR image. The proposed hybrid system shows superior results in terms of tumor area, sensitivity, specificity and DSC but takes more time compared to individual methods. The result shows that proposed algorithm provides convincing DSC value of average 0.91 and sensitivity of average 0.93, evaluated on the overlapping of tumor extracted image with the ground truth specified manually by the experts. A higher value of sensitivity and specificity (probability near to1) shows the performance of an algorithm in segmenting the tumor and non-tumor region effectively.

Index Terms: Active contour, DSC, Expectation maximization, Hybrid method, Gaussian filter, sensitivity, specificity.

1. INTRODUCTION

Brain tumor image segmentation using MR images is crucial and difficult task to diagnose the brain tumor because of the various characteristics like size, shape, orientation, location and image intensity levels. Brain tumors are due to glial tissues which spread rapidly and needs proper diagnosis and treatment [1]. Magnetic resonance (MR) imaging provides finer details of the soft tissues of human brain and used widely in biomedical applications due to invasive approach [2]. For the better diagnosis and planning the treatment, it is necessary to identify the tumors in the early stage by the radiologists. Low grade glioma and high grade glioma are the primary tumors referred as benign and malignant tumors. Benign tumors usually have uniformity structure and don't spread but malignant tumors grow rapidly affecting healthy tissues and have heterogeneous structure. Location of the tumor helps to find exact size and shape of the tumor [3],[4]. Brain image segmentation involves mainly two techniques namely manual and automatic segmentation. Manual segmentation is based on the user knowledge and very time consuming process whereas the automatic segmentation depends on the probability of the intensity values of the image [5],[6]. Multimodal sequences are considered for the study like T1 weighted (T1W), T2 weighted (T2W), T1 contrast enhanced (T1ce) and Fluid attenuation inversion recovery (FLAIR) viewed in different plane such as axial, sagittal and coronal respectively. Meningiomas and oligodendroglioma are referred as grade I and grade II tumors respectively (usually benign). Anaplastic astrocytoma and Glioblastoma are considered as grade III and grade IV tumors respectively (usually malignant) [7]. Chances of survival prediction of glioma patients significantly increase if tumor diagnosed at the early stage. Image segmentation helps to separate the tumor affected regions (edema and dead cells) from the normal healthy tissues. Analysis of conventional MR images preferred by experts is complicated which may lead to inaccurate results and takes more computation time Manual procedures like identification and segmentation of the tumor provides inaccurate results because of the noise induced in the machine while acquiring the images results in poor quality of the image, so it is necessary to use the automatic segmentation technique to yield better performance. The segmentation algorithm applied to MR image needs to be evaluated by the expert's opinion. One such evaluating parameter is dice similarity coefficient which compares segmented image with ground truth obtained from the experts. The rest of the paper is organized as section 2 presents the methods used in image segmentation, section 3 explains the methodology incorporated, section 4 presents results and discussion and section 5 concludes the paper and future work.

2 RELATED WORKS

Kong et al. [8] described clustering and selection of features for extracting tumor in automatic process using MR brain tumor scan images. Aljahdali et al. [9] explained an automatic segmentation which works on modified fuzzy clustering, improves the accuracy of the segmentation but computational time is of great interest and still an open problem in medical segmentation. T Logeshwari et al. [10] proposed a detection of brain tumor using hierarchical self-organizing map (HSOM) approach, where T2 weighted sequences were extracted with an average computation time of 29.9708s. S Bauer et al. [11] presented various automatic approaches for the detection of tumor, MR images are processed on the intensity levels of voxels with the information of neighboring pixels. These methods provide good results without any human interaction. Chaddad et.al [12] presented a Gaussian mixture model (GMM) technique to extract the features automatically. Wavelet features depends on principal component approach for feature reduction and hence the better performance of the GMM is achieved. Zanaty et. al [13] proposed a method to segment the tumor using hybrid approach combining Fuzzy C means, region growing and evaluated based on Jaccard similarity index parameter using MR brain images. Wang et al. [14] explained semi-automatic segmentation technique based on active contour method to cope up with the problem of intensity values. Sachdeva et al. [15] suggested a new approach to the active contour model consisting gradient vector flow (GVF) and vector fluid flow (VFF) patterns used to analyze the performance of MR brain tumor. Zou et al. [16] proposed systematic methods to evaluate the overall accuracy of the results of automatic segmentation. He developed EM algorithm which interprets the pixels based on the probability of intensity values. Zikic et al. [17] uses difference between the intensities of multimodal MR sequences to develop Gaussian Mixture Model (GMM) works on probability of intensity values with average DSC scores of 70% and 71% for extracting edema and tumor core in HGG, 44% and 62% for segmenting LGG respectively. Festa et al. [18] extract the information about MRI intensities, context information and textural features for developing the Random Forest method to achieve average DSC scores of 83% and 70% for segmenting the entire abnormal region and the tumor core in HGG where as in LGG its 72% and 47% respectively. Demirhan et al. [19] developed a tissue segmentation approach based on wavelets and neural networks, there by extracting the tumors effectively from the normal tissues. Torheim et al. [20] proposed automatic approach which provides better predictions and improved clinical factors like volume of the tumor, and stage of the brain tumor when compared with first-order statistical features.

3 METHOD AND MATERIALS

The proposed hybrid method consists of preprocessing stage, segmentation techniques like active contour and expectation maximization, evaluation parameters as shown in fig 1. Brats 2015 dataset with multimodal sequences such as T1w, T2w, T1ce and FLAIR is considered for the study.

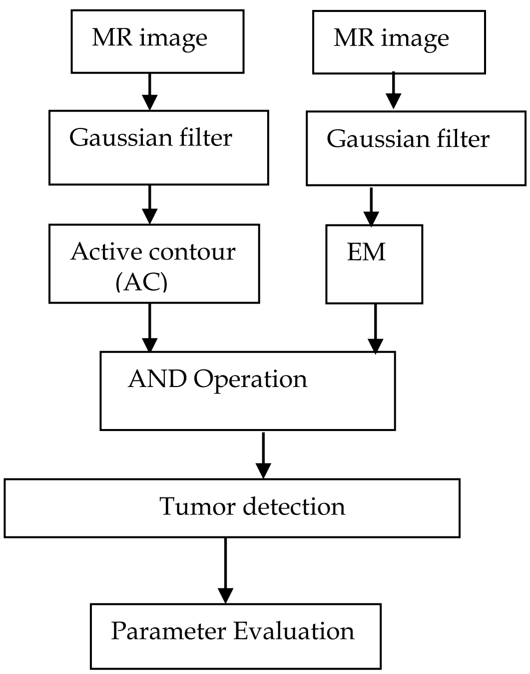


Fig .1 *Flow chart of Proposed Method*

3.1 Preprocessing

Gaussian filter is used as a denoising filter to enhance the quality of the image to extract the boundary or edge of the tumor accurately which helps for the accurate segmentation of the tumor.

3.1 Segmentation Techniques

The proposed hybrid technique consists of two algorithms namely active contour and expectation maximization. The binary images obtained from each algorithm are ANDed together to reduce the number of false positive rates.

3.2 Active Contour

The main objective of the active contour is to minimize the energy function which consists of internal energy and external energy. Following are the steps to extract tumor using active contour.

1. MR images are converted to gray level from RGB level as gray levels can compute pixel intensity levels effectively. Gaussian filter is applied to enhance the image based on the gradient of the image given by,

$$g = \frac{1}{1 + (\left|G_{\sigma} * I\right|)^{2}} \tag{1}$$

Where g is edge function, G_{σ} denotes Gaussian function with standard deviation.

2. Consider the initial contour points to extract the region based on center derivation of neighboring eight pixels to apply boundary conditions for better segmentation.

3. For a Set Function, $\Omega \rightarrow R$ we define an energy functional $E(\phi)$ by

$$E(\phi) = \mu R_{p}(\phi) + \lambda L_{g}(\phi) + \alpha A_{g}(\phi) \tag{2}$$

Where λ >0 and $\alpha \in$ R are the coefficients of the energy functional $L_{g}(\phi)$ and $A_{g}(\phi)$ defined by Equ (3) and Equ (4) respectively,

$$L_{g}(\phi) = \int_{\Omega} g\,\delta(\phi)\left|\nabla \phi\right| dx \tag{3}$$

$$A_{g}(\phi) = \int_{\Omega} gH(-\phi)\,dx \tag{4}$$

Where δ = Dirac delta function, H= Heaviside function, $L_{g}(\phi)$ = line integral function, $A_{g}(\phi)$ = weighted area of the region.

Direct delta function is expressed as $\delta_{\varepsilon}(x)$ and is given by

$$\delta_{\varepsilon}(x) = \begin{cases} \frac{1}{2\varepsilon}\left(1 + \cos\left(\frac{\pi x}{\varepsilon}\right)\right), & \left|x\right| \le \varepsilon \\ 0, & \left|x\right| > \varepsilon \end{cases} \tag{5}$$

Heaviside function is given by,

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

4. Calculate the curvature by considering the divergence of the new boundary condition described in step 2.
5. Let $\phi : \Omega \rightarrow R$ defined on domain Ω and energy functional E(ϕ) is given by,

$$E(\phi) = \mu R_p(\phi) + E_{ext}(\phi) \tag{7}$$

Where R_p is distance regularization given by,

$$R_p(\phi) = \int_{\Omega} P(|\nabla \phi|)dx \tag{8}$$

Where p is considered as double potential for distance regularization and is expressed as $P_2(S)$ and

is given by, $$P_2(S) = \begin{cases} \frac{1}{(2\pi)^2}(1 - \cos(2\pi s)), & s \le 1 \\ \frac{1}{2}(s-1)^2, & s \ge 1 \end{cases} \tag{9}$$

6. The final energy functional is expressed as

$$E(\phi) = \mu \int_{\Omega} p(|\nabla \phi|dx + \lambda \int_{\Omega} g\delta_{\varepsilon}(\phi)|\nabla \phi|dx + \alpha \int_{\Omega} gH_{\varepsilon}(-\phi)dx$$

(10)

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

3.3 Expectation Maximization (EM)

EM algorithm is used to find the probability of the intensity of the pixel belonging to the particular class based on the histogram of the image. Following steps are considered for extracting the region.

1. Define the number of classes for the given MR image
2. The initial parameter ϕ is calculated based on the histogram of the image and is represented by

$$\phi = \{p_1, ... p_k, \mu_1, ... \mu_k, \sigma_1, ..., \sigma_k\}$$

Where k= number of classes, p= probability of pixels, μ =mean, σ = variance

3. E-step: Calculate the membership probability of data belonging to each class in the expectation step based on the current estimation of ϕ and is given by,

$$P_k(x \mid \theta_k) = P_k(x \mid \mu_k, \varepsilon_k) = \frac{0.5}{\sqrt{\det(2\pi\varepsilon_k)}} e^{-(x-\mu_k)^T \varepsilon_k^{-1}(x-\mu_k)} \tag{11}$$

Where θ_k is represented in terms of $[\mu_k, \varepsilon_k]$, P_k is the mixing proportion of class k, x is the intensity of the pixel.

4. M-step: Mean and variation calculates the new estimation based on the probability of the intensity values estimated in expectation step and is given by,

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

(12)

$$\varepsilon_k^{t+1} = \frac{\sum_{i=1}^{N} x_i P(k \mid x_i, \theta^t)(x_i - \mu^{t+1})(x_i - \mu_k^{t+1})^T}{\sum_{i=1}^{N} P(k \mid x_i, \theta^t)} \tag{13}$$

5. E-step and M-step is repeated until convergence occurs.

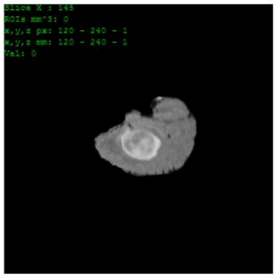
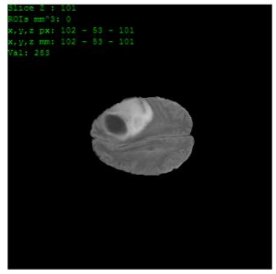
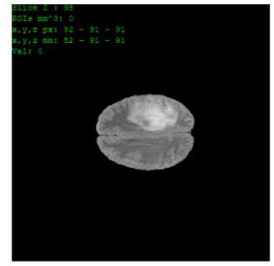
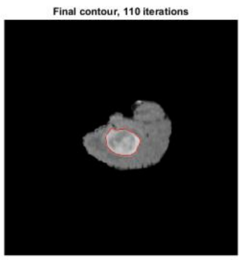
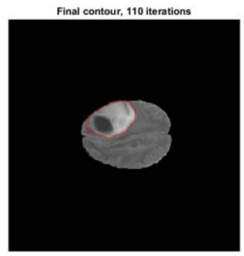
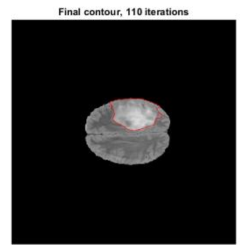
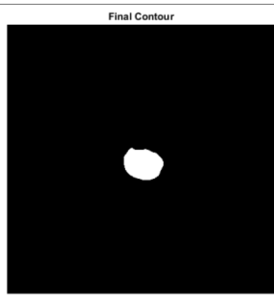
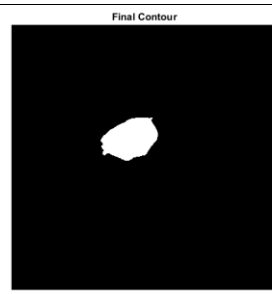
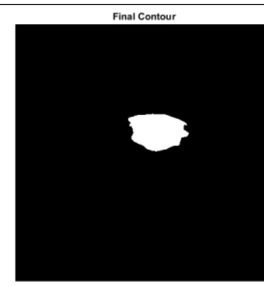
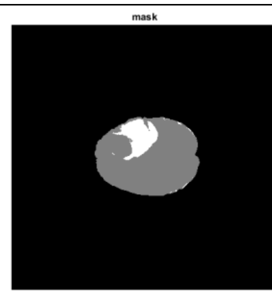
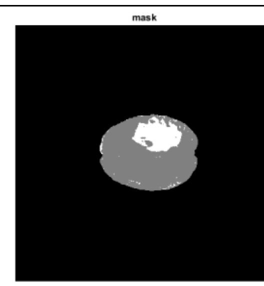
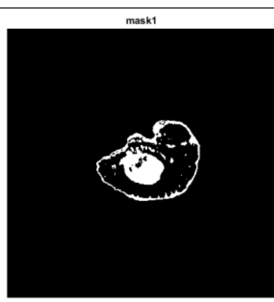
3.4 Hybrid Method (Proposed)

To enhance the overall performance of the proposed method two algorithms such as active contour and expectation maximization are fused together to solve the same problem more efficiently by considering the features of individual techniques, thereby reducing the false positive rates gradually. Following steps for proposed system is as follows,

1. Consider the brain MR images in all the three planes for processing.
2. Convolution is performed to enhance the image using Gaussian filter.
3. Apply the active contour algorithm for the enhanced image to extract the tumor in the form of binary image.
4. Apply EM algorithm for the enhanced image in step 2 to segment the tumor and get the binary image.
5. Perform the masking (ANDing) operation between two binary images obtained in step 3 and step 4, merging the features of both active contour and EM algorithm, hence improves the performance better than the individual techniques.

4 RESULTS AND DISCUSSIONS

To evaluate and validate the performance of the segmentation algorithms Brats benchmark 2015 is used which mainly contains multimodal sequences like T1W, T2W, T1CE, and FLAIR in all the 3 planes with the ground truth. Segmentation results are shown in fig 2 and fig 3 respectively. EM works well only if the intensity levels of background and object is differentiable as it extracts the tumor based on the probability of the intensity values but the computation time taken is less. Active contour works fine for all kinds of images but takes more time because of iterative process. The proposed hybrid technique performs the ANDing operation and thereby merging the features of both algorithms and provided better results compared to individual technique as shown in the fig 2 and 3 respectively. The table 1 shows the statistical measures for evaluating the performance of the algorithm and proposed method gives convincing average DSC value of 0.915. In the proposed method the area of the extracted tumor is significantly improved as the hybrid values are nearer to the ground truth (GT) values provided by the experts. The average sensitivity and specificity values of proposed method are 0.93 and 0.99 respectively which is better compared to other techniques. The dice similarity coefficient ranges from probability 0 to 1 and is expressed as,

	Image 1	Image 2	Image 3
a) Original Image			
b) Active contour			
c) Active contour B/W			
d) EM			
e) EM B/W			

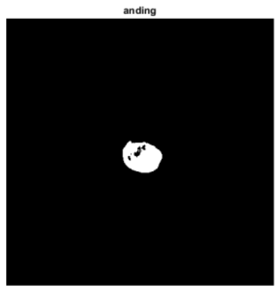
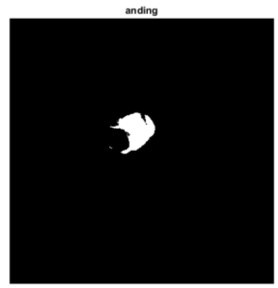
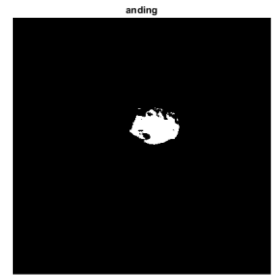
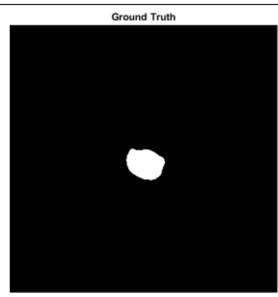
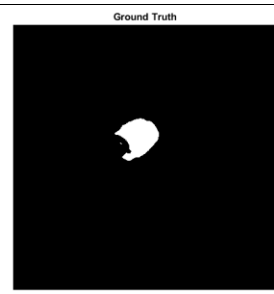
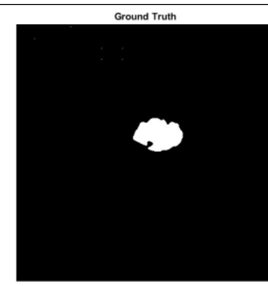
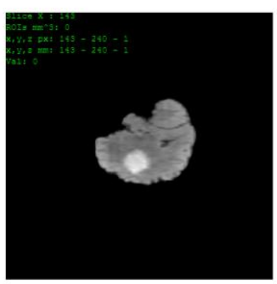
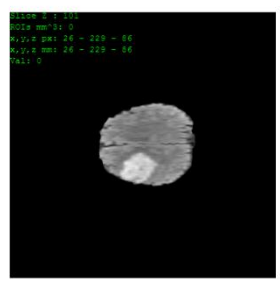
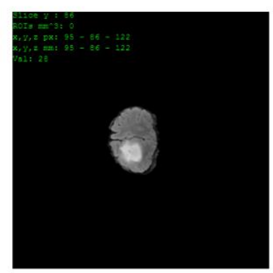
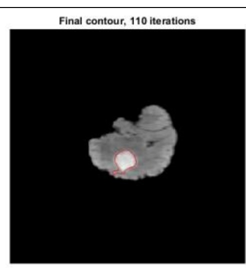
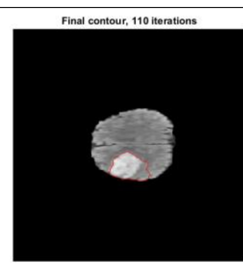
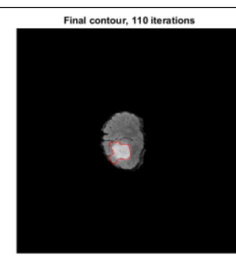
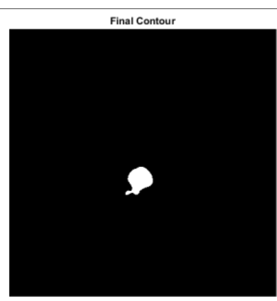
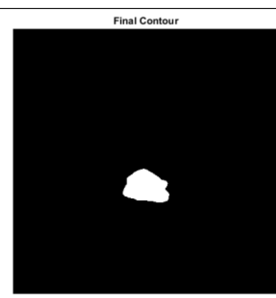
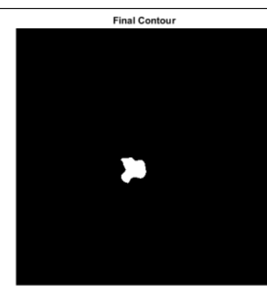
f) HYBRID			
g) GROUND TRUTH			

***Fig .2** Results of segmentation techniques, a) shows original MR raw image, b) and c) shows active contour results in gray level and binary level, d) and e) shows EM results in gray and binary level, g) ground truth.*

	Image 4	Image 5	Image 6
a) Original Image			
b) Active contour			
c) Active contour B/W			

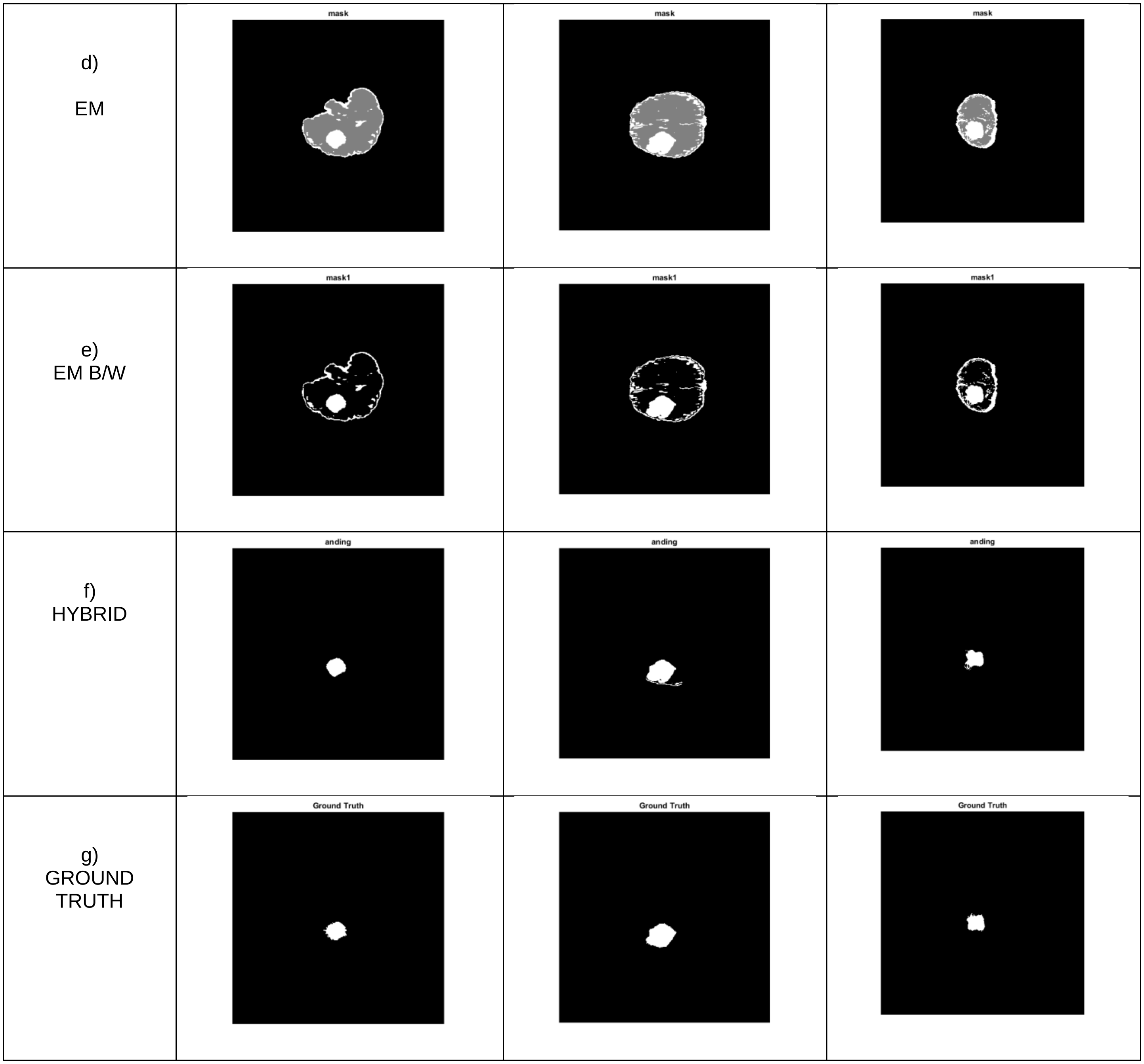


Fig .3 *Results of segmentation techniques, a) shows original MR raw image, b) and c) shows active contour results in gray level and binary level, d) and e) shows EM results in gray and binary level, g) ground truth.*

Table .1 *Evaluation of Segmentation techniques*

Images	Dice coefficient			Sensitivity			Area				Specificity		
	Active	EM	Hybrid	Active	EM	Hybrid	GT	Active	EM	Hybrid	Active	EM	Hybrid
Image 1	0.96	0.58	0.93	0.93	0.42	0.93	2045	2167	4446	2012	0.9999	0.9991	0.999
Image 1	0.76	0.88	0.90	0.62	0.96	0.99	2521	3948	2145	2081	0.9998	0.9972	0.997
Image 1	0.81	0.91	0.93	0.69	0.91	0.96	2799	3979	2802	2643	0.9998	0.9985	0.998
Image 1	0.89	0.48	0.94	0.86	0.32	0.98	999	1093	2813	923	0.9996	0.9995	0.9994
Image 1	0.81	0.57	0.92	0.69	0.41	0.92	1783	2537	4008	1788	0.9999	0.9992	0.9992
Image 1	0.83	0.44	0.87	0.77	0.29	0.85	925	1082	1788	967	0.9994	0.9996	0.9994
Average	0.84	0.64	0.91	0.76	0.55	0.93					0.9997	0.998	0.998

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

Sensitivity measures how likely the pixel of the tumor region is segmented correctly and the probability range lies between 0 and 1. For better segmentation value should be near to 1 and is expressed as,

$$Sensitivity = \frac{TP}{TP + FN}$$
(15)

Specificity measures how likely the pixel of the non-tumor region is segmented correctly and the probability range lies between 0 and 1. For better segmentation value should be near to 1 and is expressed as,

$$Specificity = \frac{TN}{TN + FP}$$
(16)

Where TP is true positive describes the intersection of delineated image with ground truth.
TN is true negative indicates part of the image beyond the union of the delineated image with ground truth.
FN is false negative measures the values of missed region of ground truth.
FP is false positive describes the delineated image not overlapped with the ground truth.

CONCLUSION

Ten patients suffering from glioma tumor obtained from Brats benchmark 2015 standard with T1W, T2W, T1ce and FLAIR is considered for the study. Gaussian filter is used to enhance the quality of the image. The proposed technique shows that dice similarity coefficient with average of 0.915 is better than the other existing algorithms. The average value of sensitivity (how exactly the tumor is segmented correctly) is 0.93 and specificity (indicates non tumor segmented correctly) is 0.99 which outperforms the existing methods. The extracted area of tumor for the proposed system is superior compared to other techniques but the drawback of proposed system is increase in overall computational time. Future work is concentrated on the features extracted by these algorithms especially shape, location and statistical values for the proper classification of glioma into LGG or HGG at the early stage.

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