

Knowledge Based Brain Tumor Segmentation using Local Maxima and Local Minima

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ABSTRACT

In this work, we have proposed an automatic method to brain tumor segmentation using magnetic resonance imaging (MRI) histogram. In our proposed method input is taken from abnormal slice of the MRI volume. Based on image histogram of the abnormal slice, our algorithm automatically detected the local minima and maxima using histogram smoothing techniques. Threshold value obtained from local minima between the two local maxima and segments the tumor region in T2-W MRI. These proposed works also compared with traditional clustering techniques are K-Means and FCM (Fuzzy C Means). The method yields high segmentation accuracy on various qualitative parameters and taken less computation time.

Keywords :— MRI, Image segmentation, Histogram smoothing, K means, FCM

I. INTRODUCTION

The diagnosis of human being has been improved significantly with the arrival of computed tomography (CT), positron emission tomography (PET) and magnetic resonance imaging (MRI). Medical imaging provides a reliable source of information of the human body to the clinician for use in fields like reparative surgery, radiotherapy treatment planning, stereotactic neurosurgery etc. Several new techniques have been devised to improve the biomedical research. MRI is a non-destructive testing technique for medical imaging that uses the magnetic field and pulses of radio waves [1]. It gives better visualization of soft tissue in human body. MRI is the preferred procedure for diagnosing a large number of potential problems or abnormal conditions in many different parts of the body. In general, MRI creates pictures that can show differences between healthy and unhealthy tissue. Physicians use MRI to examine the brain, spine, joints (e.g., knee, shoulder, hip, wrist and ankle) abdomen, pelvic region, breast, blood vessels, heart and other body parts.

Segmentation plays an important role in biomedical image processing. It is often the starting point for other processes, including registration, shape analysis, visualization and quantitative analysis. In brain diagnostic system it is of increasing interest in the study of many brain disorders, pathologies detection, anatomy delineation, treatment planning and computer-aided neurosurgery. The normal MRI brain slice contains major three tissues as white matter (WM), gray matter (GM) and cerebrospinal fluid (CSF) [2]. The abnormal MRI brain slice having additional one more region as tumor. Tumor intensity characteristics are differing from normal tissue characteristics. This proposed work focused on automatic brain tumour segmentation using image histogram. This all work done by using histogram smoothing on abnormal MRI brain slices. From histogram we can automatically detected top two local maxima and found local

minima between them. Based on the local minima, we automatically fitting threshold value for segmentation.

Somasundaram and Kalaiselvi [3] present comparative study of MR brain image segmentation techniques. The aim of this study is to assess the robustness and accuracy of three most commonly used unsupervised segmentation methods k-means (KM), FCM and EM. Somasundaram and Kalaiselvi [4] proposed a technique to detect the tumor from MRI brain scans. They extract the brain portion by removing the unwanted non brain region and segmented the brain into regions like WM, GM, CSF and background using FCM algorithm. Sabbih et al. [5] summarized that the comprehensive review of the methods and techniques used to detect the brain tumor through MRI image segmentation. Ananthi et al. [6] introduced a new method of clustering algorithm based on interval-valued intuitionistic fuzzy sets (IVIFSs) generated from intuitionistic fuzzy sets to analyze tumor in magnetic resonance (MR) images by reducing time complexity and errors. Janet Light et al. [7] test their idea to fully automated algorithm is implemented to extract the required features from the brain signals and classify them into normal and fall pattern. Kalaiselvi et al. [8] detect brain abnormality using the bilateral symmetry property of hemisphere and histogram similarity measures.

This paper includes section 2 as proposed work which contains segmentation process of histogram smoothing using Gaussian distribution and determine threshold using local maxima and minima. Section 3 describes the various qualitative metrics parameter. Section 4 contains results and discussion. Section 5 concludes the paper.

II. PROPOSED METHOD

The resultant images of existing methods (K-means and Fuzzy C-Means) on abnormal slice are shown in Fig 1. Fig. 1 show that the existing methods are not well to detect the brain

tumor when compared with the gold standard which is given by the medical community.



Fig.1. Existing method results

To overcome this problem the proposed work is a simple histogram based fully automatic brain tumor segmentation method. In our proposed method input is taken from abnormal slice of the T2-W MRI volume. The pre-processing of the proposed method starts from the brain portion extraction. Segmentation part includes the histogram smoothing using Gaussian distribution and finding the local maxima and minima values. The flowchart of the proposed method is given in Fig 2.

A. Histogram Smoothing

For an image I (x, y) with size M × N of and number of gray levels of the histogram can be expressed as:

$$H = \langle h_i \rangle \quad i = 0, 1, \dots, L-1 \quad (1)$$

where, H is the histogram vector, h_i is number of pixels of gray level i in the image and L is maximum number of possible gray level in the image. The normal histogram contains lot of nonstructural peak values as shown in Fig. 3 and doesn't give any information about the abnormal region. Histogram smoothing using Gaussian distribution expressed as:

$$f(x | \mu, \sigma^2) = \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{(x-\mu)^2}{2\sigma^2}} \quad (2)$$

where, μ is the mean and σ^2 is variance with the default values (0, 5) as shown in Fig.3. In this proposed work, the threshold values obtained from the histogram smoothing using Gaussian distribution.

B. Threshold detection

From the Fig. 3, two peaks are raised from the normal and abnormal tissues of the MR image. These two peaks are named as local maxima. Minimum value between these two maxima named as local minima. Threshold value obtained from the local minima for tumor segmentation. The segmentation is done based on the threshold value.

III. QUALITATIVE PARAMETERS

The gold standard compared with proposed method using following qualitative parameters.

A. Dice coefficient

Dice coefficient is used to show the similarity level between extracted tumor and gold standard tumor region. It is mathematically formulated as

$$Dice = \frac{2|A \cap B|}{|A| + |B|} \quad (3)$$

Where, A is gold standard tumor region and B is the tumor region obtained from proposed method. If the Dice coefficient value is 1 it shows perfect overlap between A and B. If value is 0 there is no overlap between A and B.

B. Jaccard coefficient

Jaccard coefficient similarly like Dice coefficient and mathematically formulated as

$$Jaccard = \frac{|A \cap B|}{|A| + |B| - |A \cap B|} \quad (4)$$

C. Mean absolute error

It calculates the mean absolute error between the gold standard and proposed method [6]. MSE decrease with increase similarity among A and B and vice versa.

$$MAE = \frac{1}{P \times Q} \sum_{i=1}^P \sum_{j=1}^Q (A_{ij} - B_{ij}) \quad (5)$$

where P×Q determine size of the image.

D. SNR

High Signal to noise ratio value indicates A and B are similar. SNR mathematically formulated as

$$SNR = 10 \log_{10} \left[\frac{\sum_{i=1}^P \sum_{j=1}^Q (A_{ij})^2}{\sum_{i=1}^P \sum_{j=1}^Q (A_{ij} - B_{ij})^2} \right] \quad (6)$$

Fig.2. Flow chart of proposed method

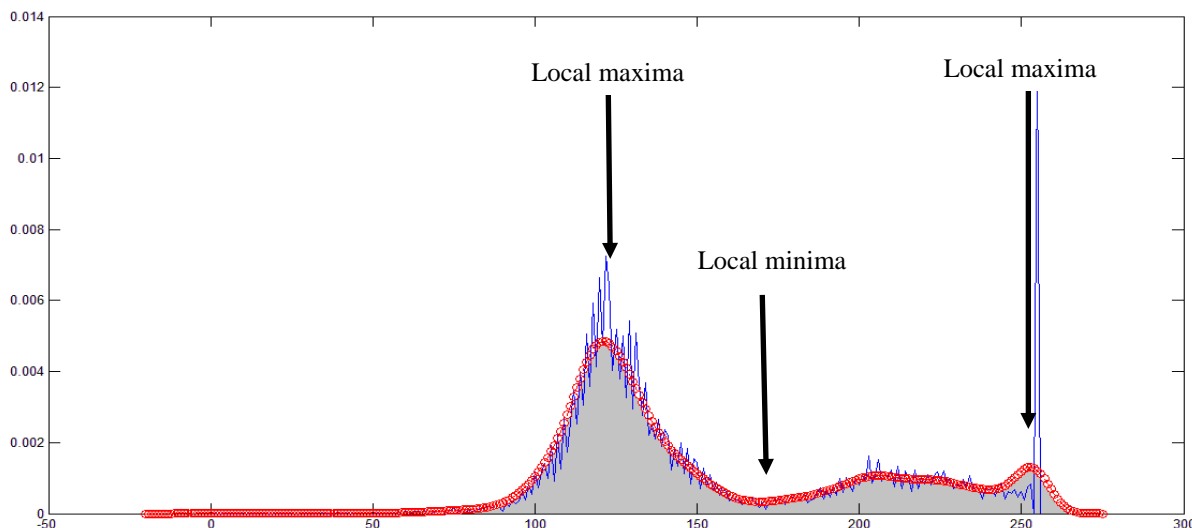
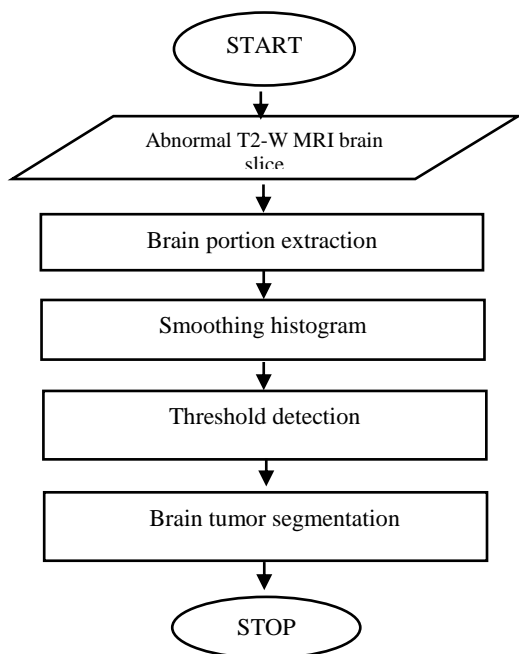


Fig.3. Histogram smoothing using Gaussian distribution and finding local minima and maxima

E. PSNR

Peak signal to noise ratio mathematically formulated as

$$PSNR = 10 \log_{10} \left[\frac{L^2}{\frac{1}{PQ} \sum_{i=1}^P \sum_{j=1}^Q (A_{ij} - B_{ij})^2} \right] \quad (7)$$

Here, L is the count of gray levels in the image. High PSNR value indicate A and B are similar.

F. Universal Quality Index

This measures quantity of data that has been transferred between A and B. The metric range lies between -1 to 1. If the both images are similar QI reached maximal value else minimal value.

$$QI = \frac{(4\sigma_{AB})(\mu_A + \mu_B)}{(\mu_A^2 + \mu_B^2)(\sigma_A^2 + \sigma_B^2)} \quad (8)$$

where $\mu_A = \frac{1}{PQ} \sum_{i=1}^P \sum_{j=1}^Q A_{ij}$ $\mu_B = \frac{1}{PQ} \sum_{i=1}^P \sum_{j=1}^Q B_{ij}$

$$\sigma_A^2 = \frac{1}{PQ-1} \sum_{i=1}^P \sum_{j=1}^Q (A_{ij} - \mu_A)^2$$

$$\sigma_B^2 = \frac{1}{PQ-1} \sum_{i=1}^P \sum_{j=1}^Q (B_{ij} - \mu_B)^2$$

$$\sigma_{AB}^2 = \frac{1}{PQ-1} \sum_{i=1}^P \sum_{j=1}^Q (A_{ij} - \mu_A)(B_{ij} - \mu_B)$$

G. Correlation

The correlation value is one when the A and B are similar and is less than one whenever dissimilarity increase.

$$CORR = \frac{2C_{ab}}{C_a + C_b} \quad (9)$$

where $C_a = \sum_{i=1}^p \sum_{j=1}^q A_{ij}^2$, $C_b = \sum_{i=1}^p \sum_{j=1}^q B_{ij}^2$
 and $C_{ab} = \sum_{i=1}^p \sum_{j=1}^q A_{ij} B_{ij}$.

H. Percentage of pixels detected

The percentage of pixels that were correctly detected P_{co} [9]:

$$P_{co} = TP / Max(N_{PM}, N_{GS}) \quad (10)$$

where, N_{PM} represents number of tumor pixels obtained by the proposed method, N_{GS} represent number of tumor pixels calculated from the gold standard. The metric range lies between 0 and 1. If P_{co} value is 1, then it shows the perfect match between the images. Else if its value is 0, then there is no match between images.

I. Percentage of Pixels not detected

The percentage of pixels that were not detected (P_{nd}) [10]:

L. Specificity

Specificity or true negative rate computes how much percentage of non tumor pixels correctly detected as non tumor pixels. The range of metrics lies between 0 to 1 and maximal value is optimal.

$$Specificity = \frac{TN}{TN + FP} \quad (14)$$

M. Accuracy

Accuracy is the proportion of true results. It is gives percentage of how much tumor and non tumor pixels exactly detected. The range of metrics lies between 0 and 1. If the accuracy value equal to 1 then the output as exactly same as input.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (15)$$

IV. RESULTS AND DISCUSSIONS

Our proposed method using BRATS 2012 data set. Testing system of proposed method used hardware and software configurations are Intel Pentium Processor, 2 GB RAM, Windows 8.1 Pro 32 bit and MATLAB 2013b 32-bit.

Proposed method on sample image in Fig.1 (a) gives the threshold value $T = 174$. Gold standard and proposed method output image using T value as shown in Fig.4 (a) and (b).

$$P_{nd} = FN / Max(N_{PM}, N_{GS}) \quad (11)$$

The metric range lies between 0 and 1. If P_{nd} value is 0, shows all pixels are correctly detected. Else if its value is 0, shows all the pixels are not detected. Here minimal value is optimal.

J. Percentage of false alarm

The percentage of pixels that were erroneously detected as edge pixels defined as (P_{fa}):

$$P_{fa} = FP / Max(N_{PM}, N_{GS}) \quad (12)$$

The metric range lies between 0 and 1. If P_{fa} value is 0 shows there is no pixel erroneously detected as edge pixel else P_{fa} value is 1. Here minimal value is optimum.

K. Sensitivity

Sensitivity defines the percentage of tumor pixels correctly detected as tumor pixel. The range of metrics lies between 0 to 1 and maximal value is optimal.

$$Sensitivity = \frac{TP}{TP + FN} \quad (13)$$

Fused image from (a) and (b) as shown in Fig.4 (c). From the Fig. 4(c) white, red and green pixels intimates that the true positive, false positive and false negative respectively.



Fig. 4 (a) Gold Standard (b) Proposed Method (c) Fused image of a and b

Table 1 shows the results of proposed and existing segmentation methods compared with gold standard using qualitative parameters on sample MRI image. Likewise Table 2 results obtained using average of 61 abnormal slices in BRATS_HG0006 dataset. Table 3 shows proposed and existing methods output on BRATS_HG0006 dataset.

TABLE 1
SEGMENTATION COMPARISON OF GOLD STANDARD WITH PROPOSED AND EXISTING METHODS ON SAMPLE IMAGE FIG.1 (A)

Method	Dice	Jaccard	MAE	SNR	PSNR	QI	CORR
Proposed	0.9303	0.8697	0.0105	8.5767	43.8725	0.9475	0.9304
K-means	0.9287	0.8669	0.0106	8.4962	43.7920	0.9462	0.9287
FCM	0.5685	0.3971	0.0473	2.0364	37.3323	0.8954	0.5685

Method	TP	TN	FP	FN	P _{co}	P _{nd}	P _{fa}	Sensitivity	Specificity	Accuracy	Time (sec)
Proposed	3565	45084	290	245	0.9247	0.0635	0.0752	0.9360	0.9936	0.9891	0.5851
K-Means	3551	45088	304	241	0.9211	0.0625	0.0789	0.9364	0.9933	0.9889	1.5530
FCM	1589	45183	2266	146	0.4122	0.0379	0.5880	0.9158	0.9522	0.9510	0.9110

TABLE 2
SEGMENTATION COMPARISON OF GOLD STANDARD WITH PROPOSED AND EXISTING METHODS ON 61 ABNORMAL IMAGES

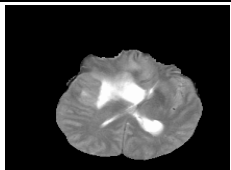
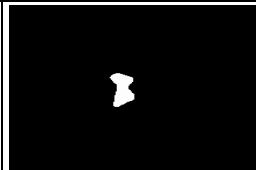


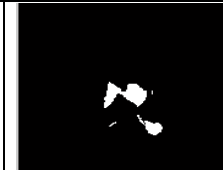
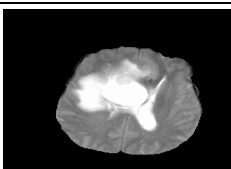


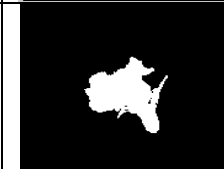

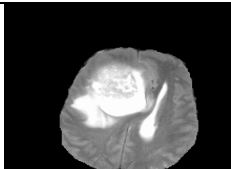




Method Name	Dice	Jaccard	MAE	SNR	PSNR	QI	CORR	P _{co}	P _{nd}	P _{fa}	Sensitivity	Specificity	Accuracy	Time (sec)
Proposed	0.7962	0.6824	0.0246	4.5076	41.3002	0.9279	0.7962	0.7286	0.2407	0.1098	0.7584	0.9923	0.9745	6.605
K-Means	0.7958	0.6816	0.0246	4.4829	41.2756	0.9277	0.7957	0.7274	0.2397	0.1116	0.7593	0.9922	0.9745	85.400
FCM	0.4796	0.3227	0.0473	0.4796	37.6341	0.8983	0.8414	0.3785	0.2441	0.6141	0.6905	0.9628	0.9510	22.637

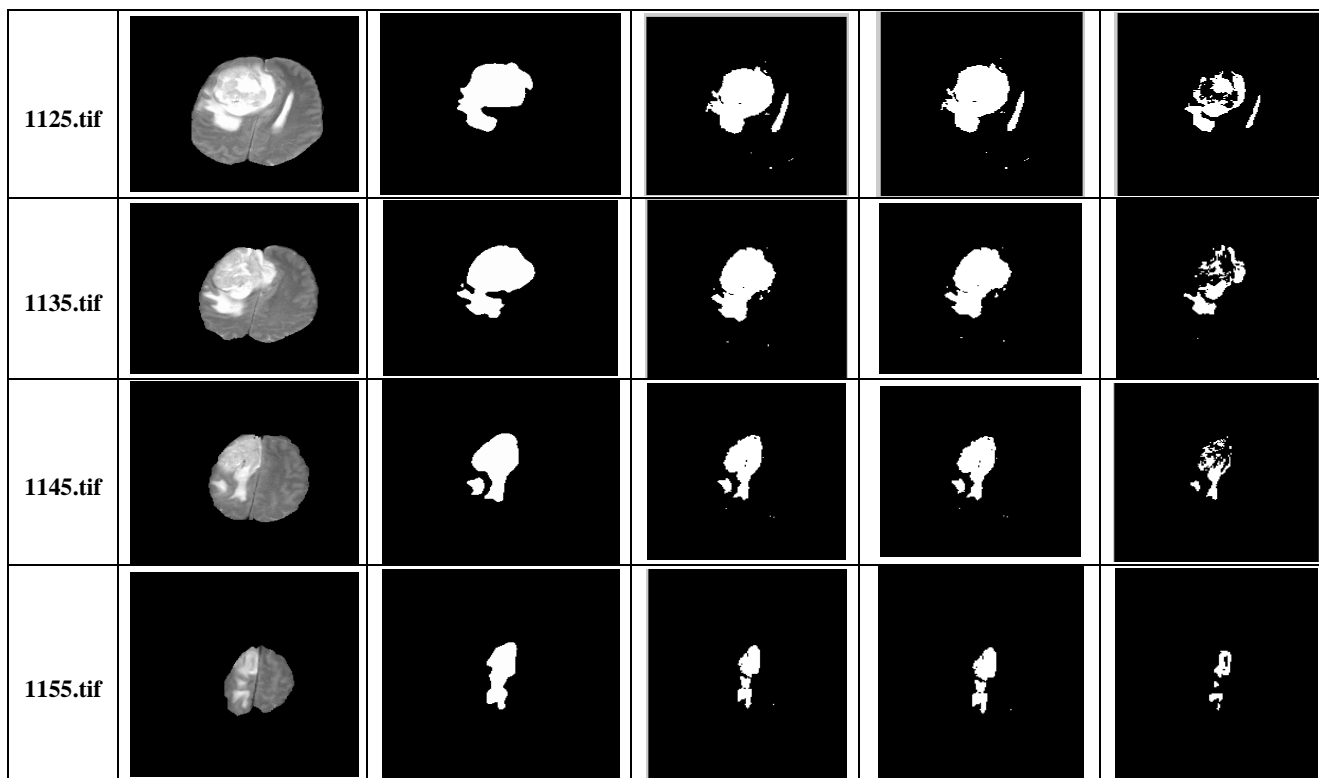
From the Table 1 and Table 2, we observed that K-Means and proposed method almost same values. But compared with Gold standard, proposed method gives very closest segmentation results than the K-Means. Proposed method gives better segmentation than traditional algorithms K-means and FCM. Proposed method detects the optimal threshold value from abnormal MRI slice. Time taken by the proposed method is optimal than other existing methods.

V. CONCLUSION AND FUTURE ENHANCEMENT

The proposed work is knowledge based automatic brain tumor segmentation using image histogram. This work produced the effective result of segmenting the tumor from abnormal MRI brain image. This method gives better results compared with the existing methods. In future we planned reduce computation time using GPU based parallel computing.

TABLE 3
RESULTS OF PROPOSED AND EXISTING METHODS ON BRATS_HG0006 DATASET

Slice No	Original MRI	Gold Standard	Proposed Method	K-Means	FCM
1095.tif					
1105.tif					
1115.tif					



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