THE SEGMENTATION OF HIPPOCAMPUS FROM MID-SAGITTAL T2-WEIGHTED MAGNETIC RESONANCE IMAGES OF HUMAN BRAIN USING MORPHOLOGICAL OPERATIONSAND THRESHOLDING

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Abstract

The segmentation of hippocampus from the human brain is a significant task in the medical field for the identification of abnormalities in the brain functions. However, the segmentation of hippocampus is a challenging task because of its complex shape, small size, fuzzy boundaries and anatomical variability. In this paper, we propose a method to segment the hippocampus from clinical magnetic resonance imaging (MRI) of human head. The proposed method uses morphological operations and k-means clustering. The connected component analysis is then used to extract the region of interest (ROI). The jaccard (J) and dice (D) indices are calculated to quantify the performance of proposed method as well as the semi-automatic method ITK-SNAP. The results show that the proposed method works better than the existing ITK-SNAP.

Keywords : Hippocampus; Segmentation; Morphological operations; MRI; K-means; ITK-SNAP.

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I. Introduction

The medial temporal lobe of a human brain consists of hippocampus (Hc) – a paired structure located on either side of a cerebral hemisphere. The Hc plays an important role in memory processing [1] which involves in sending messages to the cerebral hemisphere for long term storage and retrieving them when necessary. The shrinkage and loss of neurons in Hc lead to neurodegenerative diseases such as Alzheimer's disease (AD) [2] [3]. The Fig. 1 shows the normal and diseased brain image where the brain tissue shrinks and ventricles become larger. The neuron loss to Hc affects person's ability to form new memories and also fail to recollect old memories. The Magnetic Resonance Imaging (MRI) is the frequently used imaging tool by the clinicians since it provides valuable information about atrophy to Hc [4].

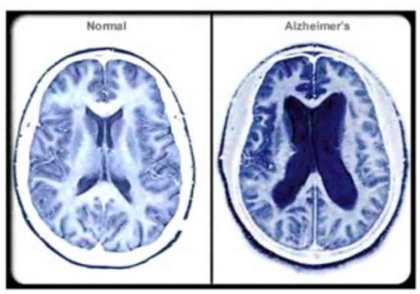

Figure 1. The normal and AD affected brain image

Most of the volumetric studies have used manual segmentation of Hc to analyze the atrophy rate and to identify the disease progression [5]. The manual segmentation is considered to be the gold standard for measuring Hc but is time consuming and requires trained operators. Also, it takes approximately 30-60 min to segment each Hc manually [6].To address these problems, a reliable segmentation methods are needed for the automatic delineation of Hc. However, the segmentation of Hc automatically is more difficult than any other structures in brain because large part of its border with amygdala is is highly indistinguishable [7]. Some of the automatic and semi-automatic methods developed to segment Hc from MRI of human brain are described below.

The automatic method is proposed to segment Hc using multiscale shape information and multi-atlas initialization along with local image features [8] but, the atlas based segmentation method is computationally expensive [9]. The method is developed by empirically-derived deformable model of the hippocampus [10] to maximize the overlap with the corresponding anatomical structure. In another method, the deformable model evolved from the ellipsoid to hippocampal surface with 2562 vertexes is proposed to analyze left and right hippocampus shapes [11].

Gronenschilda et al. [12] developed a time-saving semi-automatic approach for segmentation of cortical regions such as hippocampus using anatomical knowledge. This method involves manual drawing of the border of a region of interest (ROI), supported by three-dimensional (3D) visualization techniques such as rendering, and a automatic tracing of the gray matter voxels inside the ROI using automatic tissue classifier.

Kim et al. [13] segmented hippocampus from 66 patients using a region-growing algorithm. The algorithm is constrained by segmentation using anatomical priors (SACHA), manual segmentation software (FreeSurfer) and ANIMAL (Automatic Nonlinear Image Matching and Anatomical Labeling). To measure malrotation, 3D models are generated from manual hippocampal labels.

In this paper, a semi-automatic method is proposed to segment Hc from MRI of human brain. The proposed method comprises of morphological top-hat and bottom-hat filters [14] [15] to differentiate alveus i.e., the white matter fibers that covers Hc [16]. The filtered image is then binarized using Otsu thresholding technique [17] [18]. The binary dilation is applied to retain the pixels that are lost due to thresholding. Finally, the connected component analysis (CCA) [19] is done to segment the Hc alone.

The remaining part of the paper is organized as follows. In section 2, the method developed to segment Hc from MRI of human brain is presented. In section 3, the materials used in the experiment are given. Result and discussions are given in section 4 and the conclusion is given in section 5.

II. Proposed Method

Several image processing techniques are used to segment Hc from MRI of human brain. There are mainly four steps involved in the proposed algorithm: 1. smoothing anterior and posterior border of Hc using morphological top-hat and bottom-hat filters, 2. detecting the rough Hc region using iterative Otsu thresholding technique, 3. obtaining refined boundary of Hc using binary dilation, 4. segmenting Hc structure alone using CCA. The flow chart of the proposed method is shown in Fig. 2.

A. Differentiating the head and tail of Hc from alveus

The Hc is laterally covered by the alveus which contains white matter fibers. The alveus also plays an important role in describing the boundary of Hc. The sagittal MRI of human brain used in the experiment consists of alveus where it is not clearly visible in most of the images. This feature limits the separation of Hc from alveus. Hence, the morphological top-hat and bottom-hat filters are applied to the input image for the precise separation of Hc.

Morphological operations are conventionally used to expand or to shrink an image. In the proposed method, the morphological operations (top-hat and bottom-hat filters) are applied to the grey-scale image to make lighter part in the image as darker and vice-versa. The top-hat filtering and bottom-hat filtering are given as:

$$I_T = f - (A \circ B) \qquad (1)$$

$$I_B = f - (A \bullet B) \qquad (2)$$

where, f is the original image, $A \circ B$ and $A \bullet B$ are the morphological opening and morphological closing of an image A by a structuring element B. Since the hippocampus is a small sized region, structuring element B of size 3x3 is sufficient for computation. The resultant image is obtained by combining top-hat and bottom-hat filters as:

$$I_{res} = (f + I_T) - I_B \qquad (3)$$

After applying the filters, the region of interest (ROI) is differentiated from its neighboring structures.

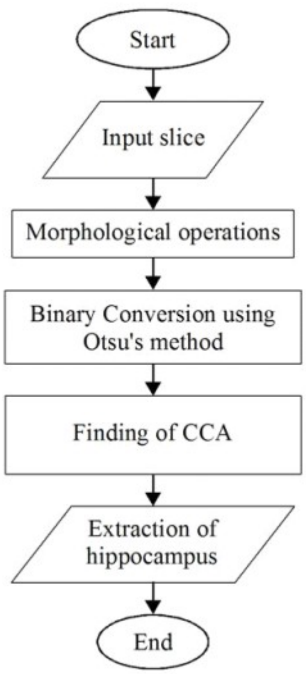

Figure 2. Flow chart of the proposed method

B. Image binarization using Otsu thresholding

The filtered image is converted into binary image using Otsu thresholding technique to detect the rough Hc region. This method automatically finds the threshold using the histogram of a grayscale image based on the idea of finding the threshold that maximizes the between-class variance $\sigma_B^2(t)$ (or minimizes the weighted within-class variance), which is expressed as follows:

$$\sigma_B^2(t) = \frac{[m_G P(t) - m(t)]^2}{P(t)[1 - P(t)]} \qquad (4)$$

where, m_G is the average intensity of the entire image, $m(t)$ is the cumulative mean up to level t, $P(t)$ is the cumulative sum of probability assigned to object. The value which maximizes $\sigma_B^2(t)$ is taken as optimum threshold T and the binary image I_{bin} is obtained as:

$$I_{bin}(x, y) = 1 \quad \text{if } I_{res}(x, y) >= T \qquad (5)$$
$$= 0 \quad \text{otherwise}$$

C. Refining the boundary of Hc using binary dilation

Some of the pixels belong to Hc are lost at the boundary due to thresholding. They are recovered by performing dilation operation on the binary image I_{bin} using the same structuring element B. The binary dilation I_{dil} is given as:

$$I_{dil} = I_{bin} \oplus B \qquad (6)$$

The Hc is then extracted from the I_{dil} using CCA.

III. Materials Used

For the experiment, five volumes of MRI of human head scans in sagittal orientation are taken. The volumes are HFH_002, HFH_006, HFH_007, v02 and 1_24. All the images in the volume are T2 weighted and the resolution is 124 x 256. Each volume consists of 256 images. But, hippocampus is found clearly in 18-22 slices in each volume.

The images are taken from Department of Diagnostic Radiology at Henry Ford Hospital [20], Internet Brain Segmentation Repository (IBSR) [21] developed by Centre for Morphometric Analysis (CMA) at Massachusetts General Hospital and Whole Brain Atlas (WBA) [22], More details about the datasets are given in Table 1.

HFH_002, HFH_006 and HFH_007 datasets are collected from Department of Diagnostic Radiology at Henry Ford Hospital. 1_24 datasets of normal subjects were obtained from the Internet Brain Segmentation Repository (IBSR) and v02 is taken from WBA. A T2-W sagittal image is shown in Fig. 3 to know about the location of hippocampus.

Table 1. Details of T2-W datasets used in this study

S.No	Volume-Id	No. of Slices used for experiment	Clinical
1	HFH_002	12	Normal
2	HFH_006	11	Normal
3	HFH_007	11	Normal
4	v02	12	Normal
5	1_24	10	Normal

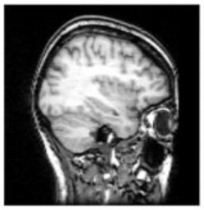

Figure. 3 Location of hippocampus in sagittal MRI

IV. Result and Discussions

We carried out experiments by applying our scheme on the material pool (slices containing hippocampus) and extracted hippocampus Hc. The sample images of the datasets are given in Fig. 4. The Hc extracted from the original slices is shown in Fig. 5.

To evaluate the performance of our method, we also extracted the portion of hippocampus using ITK-SNAP 2.4.0 [23]. For visual comparison the results obtained by manual segmentation, our proposed method and ITK-SNAP 2.4.0 are shown in Fig. 6.

From Fig. 6, we note that over segmentation is produced by ITK-SNAP for some slices. But our proposed method segmented the hippocampus which is closer to the manual segmentation.

For quantitative evaluation we computed the similarity measures Jaccard coefficient (J) [24], and Dice coefficient (D) [25], sensitivity (S), Specificity (Sp), Predictive accuracy (PA), false positive rate (FPR) and false negative rate (FNR) and are given in Table 2.

From Table 2, we observe that our method produced an average value of 0.9075 for J and 0.9480 for D. The average value of J, D, S, Sp, PA, FPR and FNR for the ITK-SNAP 2.4.0 is given in Table 3.

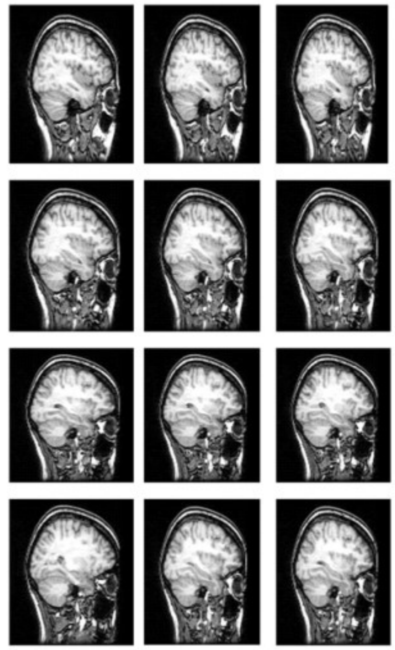

Figure. 4 The original slices of the dataset

Table 2. The computed values of J, D, S, Sp, PA, FPR and FNR for five volumes using proposed method

Volume	J	D	S	Sp	PA	FPR	FNR
HFH_002	0.9079	0.9429	0.9576	0.9831	97.2	0.051	0.044
HFH_006	0.9067	0.9457	0.9587	0.9822	97.1	0.050	0.041
HFH_007	0.9028	0.9414	0.9556	0.9832	98.1	0.061	0.049
v02	0.9099	0.9590	0.9641	0.9809	98.4	0.069	0.039
1_24	0.9102	0.9511	0.9703	0.9840	98.0	0.062	0.025
AVG	**0.9075**	**0.9480**	**0.9612**	**0.9826**	**97.7**	**0.058**	**0.039**

Table 3. Average values of J, D, S, Sp, PA, FPR and FNR of ITK-SNAP for five volumes

Method	J	D	S	Sp	PA	FPR	FNR
ITK-SNAP	0.6525	0.7552	0.9121	0.9574	91.6	0.624	0.711
Proposed	**0.9075**	**0.9480**	**0.9612**	**0.9826**	**97.7**	**0.058**	**0.039**

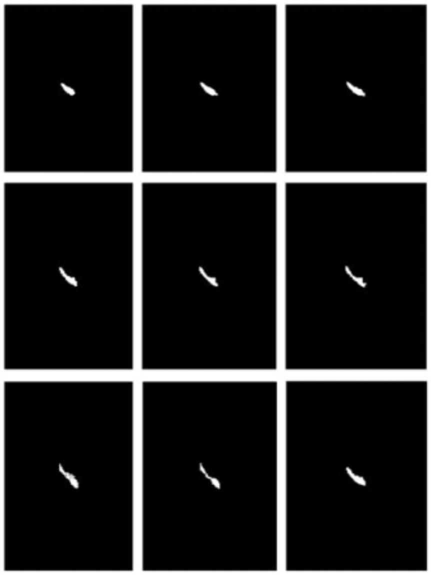

Figure 5. Extracted hippocampus from slices shown in Figure 4

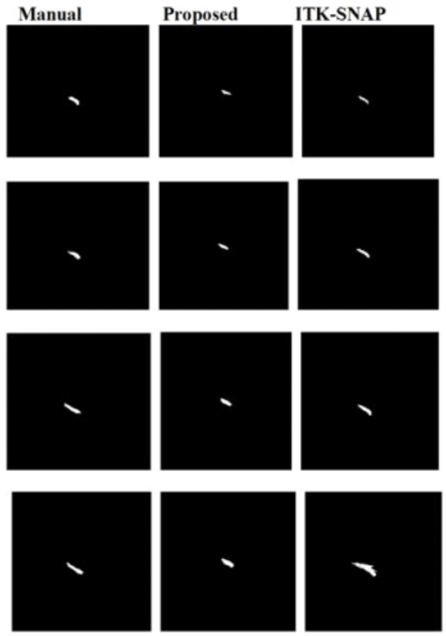

Figure. 6. Column 1 shows the manual segmentation. The extraction of Hc by the proposed method is shown in Column 2 and Column 3 shows the segmentation of Hc using ITK-SNAP 2.4.0.

V. Conclusion

In this paper, we have proposed a system that extracts the hippocampus from the sagittal MRI of human brain. The proposed method uses morphological filtering techniques to get the refined boundary of hippocampus. The proposed method also overcomes many of the problems discussed above. It can also be extended to segment hippocampus from axial and coronal images also. The proposed scheme can also be used for developing 3D segmentation technique.

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