An Automated Enhanced FCM Based Hippocampus Segmentation

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Abstract
Fragmentation of image in digital image processing is a major issue in medical field. One of the unique characteristic of image is the interaction between adjacent pixels. To extract semantic relationship between the pixels segmentation is used. Lots of algorithms have been developed for segmentation. In recent years, human hippocampus has received the focus of research because of its close link with memory and neurological disorders. To identify and to diagnose neurological disorders, hippocampus is to be segmented. But its small size and complex structure make the segmentation process a very tedious task. In this paper an enhanced Fuzzy C-Means (FCM) method is present to extract hippocampus from human brain MRI. In this proposed method, segmentation of hippocampus is done in two stages: Stage1 involves validation and preprocessing whereas stage2 comprises of segmentation using FCM. To validate and confirm the performance of the presented method with previously available tool and for the comparison between proposed and manual segmented methods Jaccard (j) and dice (d) are calculated.
Key words: Dementia, Hippocampus, Image processing, Magnetic resonance imaging, Median filter, preprocessing, clustering, Segmentation,
.

1. Introduction

In medical field, identification of disease at the early stage is very important. Various medical imaging modalities like positron emission, magnetic resonance, electromagnetic radiation based X-radiation, computer tomography in which computer system is used with X-ray machine, single photon emission tomography here integration result of CT scan and radioactive tracer are used for identification of disease. These are used to create a detailed picture about inside of the body. MRI is one of the best methods in comparison to CT-SCAN and x-ray because it use magnet, radio waves, that are not harmful for the body .The brain is comprises of three major parts: cerebrum, cerebellum (little brain), brain stem. Brain play a vital role in the human being and is affected by many diseases among which some are very difficult to detect. Neurological disorders are common in this category. Dementia is a neuro disorder caused by damage to brain cells creates difficulties in daily activities, thinking and language. Alzheimer disorder (AD) is the another type of memory related disease dementia and Hippocampus (HC) is the first place affected by AD. HC is located near temporal lobe having the appearance like sea horse and interconnected by cornu ammonies and dentate gyrus. HC is located in both sides of the brain. To measure the HC volume and shape, MRI is used which gives HC in three planes: Axial, coronal and sagittal. Image septation is the procedure for the classification of image pixel into dissimilar groups based on color, texture or intensity. An unsupervised clustering technique is popular approaches for image sepration which can be classified into exclusive, overlapping, hierarchical and probabilistic clustering. Lots of works have been gone on in the scope of segmentation of image by using various automatic and semiautomatic segmentation techniques. In [1] a method for image segmentation is presented in which k-means and Normalized cut algorithm is used. For prospective division of images k-means is applied. Small approximation of k has given better result

compared to Greater approximation. For Greater approximation of k, parting becomes tangible and also numerous varieties into image spots at distinctive place. N-cuts algorithm gives better result for greater approximation of k. Segmentation of Medical Image is a difficult task due to the presence of partial volume effect (PVE). For PVE, FCM is the best algorithm but it also faces a great challenge in efficacy. For segmentation of partial volume effective medical image, a two phase's algorithm is presented in [2-4]: At first step, to deal with PVE effective medical image, improved FCM based on histogram HisFCM is utilized. HisFCM works in two stages: first Stage retrieves interval to compute cluster centroid. On second stage segmentation is done using improved FCM. At the end, comparison between fcm, fcm_s, EnFcm and HisFCM has been done by applying them on four images breast, head, tumor, and brain. HisFCM gives the best result in comparison to all others. Edge based image segmentation process is depend on the intensity in homogeneity of the picture at the edge, but they are unable to give accurate segmentation result. So, a new approach is presented by authors of boundary detection to fragment image without destroying image structure and boundary [5-7]. Before segmentation of hippocampus from human brain MRI morphological operations are applied to make the image free from noise and then k-means clustering is used to segment hippocampus. This method works on all the images which have weak edges. In [8-10, 11] segmentation of image is done by using hierarchical clustering method but takes large storage complexity for large data. Mean shift and hierarchical clustering (MSHC) are used to segment the images maintaining desirable discontinuity of image. This segmentation technique can be applied on color as well as medical images. To find out abnormality in human skin tissue, Haematoxylin and eosin (H&E) stained image, soft clustering FCM is used. This segmentation technique can find out the ROI from high resolution histological images [12-14]. Segmentation is most widely used in computer vision, pattern recognition, image processing. A Various technique have been developed in the area of segmentation of color image but not providing sufficient result. So, to get a desired result, for segmentation of color image enhanced watershed with region growing technique is implemented. N-cut eigenvectors are used to compare the original and converted image after which watershed algorithm is applied. Segmentation is based on seed selection region growing in which identification of segmented object is easy. The proposed method and the previous method are compared by evaluating the Liu's factor value. After comparison it is found that Liu's factor value of proposed method is lower than the existing work [15]. For segmentation of hippocampus from T2w sagittal image a prior shape-based model is used. To get location of hippocampus Union of manual segmented result is calculated and ROI of hippocampus is set which lies in the range $180 < p > 165$. Geometric mean filter is applied to make the strong edge of hippocampus and differentiate boundary of hippocampus from other objects by using $3*3$ structuring element. Image is converted into binary image because on binary image extraction of HC is easy by, using K means clustering which is taken for further segmentation. Connected components have been used to segment hippocampus from binary image. To identify and to diagnose brain abnormalities, 3D visualization of brain is utilized. MRI segmentation is the first and most important step in this procedure. Various Image segmentation techniques have been developed to segment the brain but found that unsupervised FCM and support vector machine give the accurate segmented result which helps the expert [16].

We have presented a novel method here to extract HC from human brain MRI. The remainder part of this research paper has been structured as mentioned here: part II describes methods and material used. Section III elaborates result and discussion. Finally, we have concluded with the section IV.

2. METHODS AND MATERIAL

2.1 Material

Data collected from Penn hippocampus atlas resource. PHA is medical resource that contains high resolution normalized segmented MRI and histology of human hippocampus. PHA was narrated by yushkevich [17].

Method

The proposed technique workflow is:-

- **Input Image**
  - ➢ **Validation**
    - ✓ **Construct HC maxima**
    - ✓ **Feature selection**
  - ➢ **Compare input image & HC maxima**
- **Enhancement**
- **Fuzzy C-Means**
- **Segmented Hippocampus**
- **Stop**

This process comprises of two phases namely validation and segmentation. During validation input slice is checked to determine whether HC is presented or not, which can be done only by comparing some image characteristic. Here we have taken mean, standard deviation and entropy by trial and error method as well as with the historical knowledge of manual segmented result priorly available which is done as follows manually segmented images are required for creating the mathematical model only once. But after the consumption of the model no manual intervention is required in the segmentation process and it can be applied to any data set with the same resolution. At the first stage, the manual segmented results available in PHA are analyzed and the structure of maximum hippocampus (HC maxima) is obtained, which is a common shape created by union between the manual segmented hippocampus from slices numbering penn002l_01070 to penn002l_01100 which is utilized for validation. $M_i(H)$ is a manual segmented HC in the ith slice, then HC maxima say M for the whole atlas is given by:-

$$M = \bigcup_{i=1}^{n} M_i(H) \qquad (1)$$

The HC maxima as created by equation (1) from penn002l_01070 to penn002l_01100 are shown in fig 2(a).
A sample input slice from penn002l_01070 to penn002l_01100 is given in in figure 2(b).
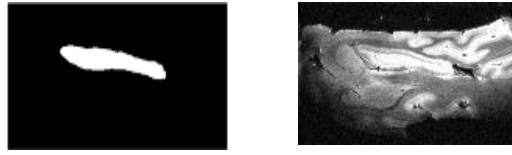
Figure 2. (a) HC maxima   (b) input slice

Computed features like mean, standard deviation, and entropy for HC in the manual segmented result and shown in Table1. which can be used for validation. To check if HC is present in the input image from any of the slice in the atlas, the respective HC maxima region is first cropped from the input slice. Compute mean, Standard deviation and entropy for the cropped HC maxima are compared with the priorly computed values of HC maxima. If the computed values lie within the expected range then the input slice comprises of HC and taken for further processing otherwise it is discarded.

The value of mean (Mmean) for the HC maxima is calculated

$$M_{mean} = \sum_{m=1}^{i} \sum_{n=1}^{j} p_{mn} \qquad (2)$$

Where p_{mn} denotes the intensity of the pixel and i,j denotes the dimension. Next feature is the Standard deviation ($S_{deviation}$) of the HC maxima which is calculated as:-

$$S_{deviation} = \sqrt{\frac{\sum_{m=1}^{i} \sum_{n=1}^{j} (p_{mn} - m_{mean})^2}{i*j}}$$

(3)

To measure the image texture feature, entropy which gives information about the spatial arrangement of intensity is calculated:

$$E_{entropy} = sum(h.*log2(h)) \qquad (4)$$

Where h denote histogram counts.

Table 1. Features of HC maxima

Feature	Min Value	Max Value
Mean	186.61	195.33
Standard deviation	50.059	56.581
Entropy	6.3999	6.8427

On the next step, the image is preprocessed to make the HC more clear. To reduce the noise from the image Gaussian low pass filter is applied can be expressed as the mathematical equation:

$$LoG(x,y) = -\frac{1}{\pi\sigma^2}\left[1 - \frac{x^2 + y^2}{2\sigma^2}\right]e^{-\frac{x^2+y^2}{2\sigma^2}} \qquad \textbf{(5)}$$

and to make HC more prominent by using median filter which is non linear filter that moves on image pixel by pixel to preserve the edge with the parameter 15 is applied[18-21]. The bottom hat operation is applied here to make the HC boundary more distinguishable

$$Bottom_{Hat}(B_H) = (F_I \cdot D_s) - F_I \quad (6)$$

Where F_I is median filtered image and D_S is the disk-shaped data structuring element.

On the next step to segment hippocampus from the preprocessed image a modified FCM is appled. The most efficient algorithm for classification of data is FCM given by J.C. DUNN in 1973 and later J.C.BEZDEK improved it[22-23]. This is used in pattern recognition, machine learning and image processing. According to FCM algorithm nature one part of data can belongs to more than one clusters. In modified FCM, first we fixed the number of the clusters i.e three clusters within the HC and outside the HC. To find the distance between the data and the cluster center in the place of Euclidean distance we used mahalanobis distance(m.d) which is suitable to find out the cluster for ellipsoid type shapes and given by P.C. mahalanobis and the equation for m.d

$$Distance_{mahalanobsis} = \left| (u_i - k_j)^{Transpose} cov^{-1}((u_i - k_j) \right|^2 \quad (7)$$

where T is the metrix transpose and C is the covariance matrix of μi and kj. Now the focus is on minimizing the objective function:

$$H_n = \sum_{i=1}^{N} \sum_{j=1}^{c} X_{ij} \left| (u_i - k_j)^{Transpose} cov^{-1}((u_i - k_j) \right|^2 \quad (8)$$

Where I≤n<∞ , N is real number which is usually more than 1, xij is membership degree of ui in group j, ui is the ith of d- dimensional measured data, kj is d-dimensional center of the group. This $|*|$ show the similarity between center and measure data. FCM can be carried out by using an iterative optimization process of the target function H_n, updation of x_{ij} and group center k_j

$$X_{ij} = \cfrac{1}{\sum_{k=1}^{c} \left[\cfrac{\left| (u_i - k_j)^{Transpose} - cov_1^{-1}(u_i - k_j) \right|}{\left| (u_i - k_j)^{Transpose} - cov_2^{-1}(u_i - k_j) \right|} \right]^{\frac{2}{q-1}}} \quad (9)$$

\Where $K_j = \frac{\sum_{i=1}^{N} x_{ij}{}^n . u_i}{\sum_{i=1}^{N} x_{ij}{}^n}$, Cov_1^{-1} and Cov_2^{-1} are inverse of covariance matrix of μi and ki and μi and kj.

This iteration break off when maximum $\{|x_{ij}^{(M+1)} - x_{ij}^{M}|\} < €$, where $€$ is a conclusion which will be decided between 0 and 1 where M is series of repetitive steps.

By historical analysis of data set we have determined that HC is enclosed within the window boundary with the following values of ROWmin=82, ROWmax=146, COLUMNmin=72, COLUMNmax =216 [16-19]. To get HC, we have to get rid of other objects within the cluster so discard all the objects which has pixel value outside the ROWmin=82, ROWmax=146, COLUMNmin=72, COLUMNmax =216 values and then rest of the object is HC.

3. Result and Discussion

A novel method using FCM has been proposed here to extract HC efficiently in MRI of human brain. The segmented results of some sample slices are presented in table 2. In data set total number of slice is 130 and HC Is available from slice number Penn002L_01_Seg_JP_2008002 to Penn002L_01_Seg_JP_2008117and the proposed method is suitable to extract HC from all the available slices in which HC is available.
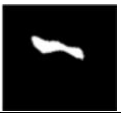
Slice No.	Manual segmentation	Proposed segmentation	ITK-SNAP-2.4.0
Penn002L_01078			
Penn002L_01084			
Penn002L_01096			
Penn002L_01099			
Penn002L_01100			

Table 2. Segmented results of sample slices

The performance analysis is given in the table 3, which shows that the proposed technique provides result closer to the gold standard as well as proved to be better than the existing method. This technique also reduces the time complexity and can assist the physician for diagnosing the AD.

Table 3. Performance Analysis

Slice	Jaccard	Dice	Sensitivity	Specificity	Predictive accuracy	FPR	FNR
Penn002L_01078	0.9986	0.9992	0.9990	0.7292	99.8614	0.0004	0.0010
Penn002L_01084	0.9991	0.9995	0.9994	0.928	99.9084	0.0003	0.0006
Penn002L_01096	0.9991	0.9995	0.9992	0.9014	99.91	0.0001	0.0008
Penn002L_01099	0.8029	0.8906	0.8481	0.9977	99.1762	0.0563	0.1519
Penn002L_01100	0.8892	0.9413	0.9102	0.9989	99.4845	0.0236	0.0898
AVERAGE **Proposed method**	**0.93778**	**0.96604**	**0.95118**	**0.91104**	**99.66811**	**0.01614**	
AVERAGE **ITK-SNAP**	**0.8679**	**0.9288**	**0.8988**	**0.9984**	99.4224	**0.0361**	

For quantitative analysis with the existing method we have computed the average values of performance metrics such as Jaccard coefficient(J), Sorensen-Dice or Dice similarity coefficient, sensitivity(S) which is used to correctly identified the specific disease , specificity(Sp) also known as selectivity, predictive accuracy (PA), between the hand segmented images, and the images segmented by the our presented method and software ITK-SNAP tool [26-27]. The calculated values of Jaccard, Sorensen Dice, Selectivity, Specificity, and predictive accuracy for our presented method and that of the ITK-SNAP against the gold standard given in Table 3.

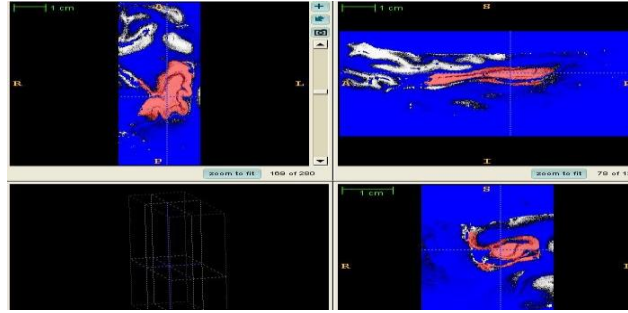The snapshots of this active contour evolution are shown in Figure 3

Figure 3: - ITK-SNAP snapshots for HC segmentation

For quantitative analysis we compute the jaccard, Dice, FPR (false positive rate), sensitivity, specificity and FNR (false negative rate) which are computed as follows: -

$$Jaccard(JD) = \frac{A \cap B}{A \cup B} \qquad Dice(D) = 2\frac{|A \cap B|}{|A| + |B|}$$

$$\boldsymbol{Sensitivity(SN)} = \frac{\boldsymbol{TP}}{\boldsymbol{TP+FN}} \quad \boldsymbol{Specificity(SP)} = \frac{\boldsymbol{TN}}{\boldsymbol{TN+FP}}$$

Any misclassification done by proposed method can be computed by using the quantitative function false positive rate (FPR) and false negative rate :

$$FPR = \frac{FP}{TP + FN} \qquad FNR = \frac{FN}{TP + FN}$$

The predictive accuracy is calculated as: -

$$Predictive\ Accuracy\ (PA) = 100 * \frac{TP + TN}{TP + FP + TN + FN}$$

The calculated average values of quantitative analysis Jaccard similarity (intersection over union) and Sorensen dice are 0.94 and 0.97 respectively which is near to 1 that shows the accuracy of our method.

CONCLUSION

Our proposed technique works well for the data set available in PHA. In future this method can be enhanced to provide 3-D HC.

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