Coupled Object Segmentation Using Entropy and Fuzzy Characteristics of Tissues

P. Bahman Bijari, A. Akhoundi Asl, H. Soltanian-Zadeh, *Senior Member, IEEE*

Abstract— **In this paper, we introduce a novel method based on level sets and fuzzy c-means clustering methods for the segmentation of medical images. Our new multi-structural method integrates the Herbulot's entropy minimization and fuzzy forces. We introduce a prior shape based on the tissue segmentation results of each image. This incorporates interactive knowledge-based evolution that increases the accuracy and aleviates the need for the prior statistical information about the shapes of the structures. We have applied the proposed method to segment ventricles, caudate, and putamen in magnetic resonance images (MRI) of the brain. Comparative results show the benefits of the proposed constraints. Accurate results and independency from the initialization are obtained when using the proposed method.**

I. Introduction

Medical image segmentation is a growing field of image processing. In this field, extracting structures and pathology features using magnetic resonance images (MRI) is a challenging problem. To this end, the evolving contour (snake) was first introduced by Kass and Terzopoulos in 1988 [1]. Based on their work, many other segmentation methods were proposed that mainly utilize image information to evolve the segmenting curve [2]-[4].

Using just boundary information [3],[4] or region information [5],[6] often does not lead to appropriate results. This is because of the low signal to noise ratio (SNR), field inhomogeneity, and low contrast between the soft tissues of the brain. Under such condition, the use of a prior shape model is necessary to restrict the deformation between the reference curve and the evolving contour. This segmentation method is limited to the parametric deformation between the reference shape and the evolving contour with restrictive deformation [7]. Other methods use a shape prior as a functional of the distance between the evolving contour and the reference curve [8]. Although using shape-prior segmentation increases the accuracy but always the need for the proper database makes the method dependent on the data used for calculation of the prior shape. In addition, there are prior anatomical knowledge that can further improve segmentation of specific structures, e.g., the tissue type of specific structures is useful.

Our method of estimating the probability density function (pdf) from all the structures made of the same tissue type, instead of each evolving contour itself, increases the accuracy by ensuring the segmented structures to have the same tissue type, e.g., gray matter for caudate and putamen or Cerebral Spinal Fluid (CSF) for the ventricles on both sides of the brain. Also, in all of the mentioned methods, it is assumed that the initial contour is placed in an appropriate position or there is a rich database for extracting the approximate prior shape of the desired structures. In this paper, using a criterion based on fuzzy c-means method, we propose a fuzzy prior-shape model for segmentation.

In our method, we segment double-sided structures (existing on both sides of the brain) accurately. We compare the results of using multi-structural pdf in the segmentation of caudate, putamen, and ventricles with non-interactive segmentation. In addition, we propose a fuzzy prior shape criterion to segment caudate and ventricles, while the initial contours are placed on both structures. The rest of this paper is organized as follows. In the next section, the level set and fuzzy c-means methods are described briefly. The proposed method is explained in Section III. Results and the conclusion are presented in Sections IV and V, respectively.

II. Level Set and Fuzzy C-means

A. Level Set Method

Level set method was first introduced by Osher and Sethian in 1988 [10]. Using an appropriate embedding function,

Payam. Bahman Bijari is with the Control and Intelligent Processing Center of Excellence, Electrical and Computer Engineering Department and , University of Tehran, Tehran, Iran, and School of Cognitive Sciences, Institute for Studies in Theoretical Physics and Mathematics (IPM), Tehran, Iran phone: +98-912-593-4674; (p.bijari@ ece.ut.ac.ir).

Alireza Akhoundi Asl is with the Control and Intelligent Processing Center of Excellence, Electrical and Computer Engineering Department, University of Tehran, Tehran, Iran, and School of Cognitive Sciences, Institute for Studies in Theoretical Physics and Mathematics (IPM), Tehran, Iran (a.akhundi@ece.ut.ac.ir).

Hamid Soltanian-Zadeh is with the Control and Intelligent Processing Center of Excellence, Electrical and Computer Engineering Department, University of Tehran, Tehran, Iran, School of Cognitive Sciences, Institute for Studies in Theoretical Physics and Mathematics (IPM), Tehran, Iran, and Image Analysis Laboratory, Radiology Department, Henry Ford Health System, Detroit, Michigan, USA (hszadeh@ut.ac.ir, hamids@rad.hfh.edu).

$\phi: I \times [0 \quad T] \to R$, it is possible to implicitly propagate boundaries $C(t)$ in the image plane such that $\Omega(t) = \{x \in I \mid \phi(x,t) = 0\}$ [11]. In order to solve the evolution equation, the level set theory is used in the proposed method. The active contour is equal to zero crossing of a higher dimensional signed distance function $\phi(x,t)$.

Suppose that the evolving contour is represented with $\Omega(t): [0,\infty] \to R^N$ and the initial contour is identified by $\Omega(0)$. $\phi(x,t=0): x \in R^N$ is then introduced so that $\phi(x,t=0) = \pm d$ is the distance between the point *x* and the initial contour $\Omega(t)$. Negative (positive) points are related to the points inside (outside) the contour [10]. $\phi(x,t)$ can be any function but, because of its properties, distance function is used in the literature. It is obvious that the active contour is associated with the zero level set of distance function $\Omega(t) = \{\phi(x,t) = 0\}$. Solving the Euler equation of ϕ and finding out pixels in which ϕ equals to zero generates the final boundary [10], [11]:

$$\frac{\partial \phi}{\partial t} = F|\nabla \phi| \tag{1}$$

ϕ is the level set function and *F* is called the evolving force which forces the contour into the desired boundaries. Using this method enables us to follow the topological changes of the contour. Also using narrow-band or fast marching approaches makes it possible to increase the evolving speed. In addition, the geometric parameters of boundary such as curvature $K = div(\frac{\nabla \phi}{|\nabla \phi|})$ or the normal vector $N = (\frac{\nabla \phi}{|\nabla \phi|})$ are accessible from the distance function ϕ. None of the above features can be observed in the classical active contours like the Snake method [1].

B. Fuzzy C–Means Clustering Method

One of the most commonly used types of the clustering schemes relies on the optimization of a cost function. Fuzzy c-means algorithm belongs to this type of clustering methods. In such family of clustering methods, each vector belongs simultaneously to more than one cluster [12].

Using a set of functions $u_j : X \to A, \; j = 1,..,m$ where $A = [0,1]$, in a fuzzy m-clustering method, vector X belongs to all clusters. There is a set of parameters which characterizes the shape of clusters. The following cost function is the most commonly used function in fuzzy clustering methods [12].

$$J_q(\theta,U) = \sum_{i=1}^{N}\sum_{j=1}^{m} u_{ij}^{q} d(x_i,\theta_j) \tag{2}$$

where $d(x_i,\theta_j)$ can be any distance measure as a dissimilarity function. Minimizing J with respect to θ and U subject to the constraints (3), the grade of membership of x_i to the $j-th$ cluster is defined.

$$\sum_{j=1}^{m} u_{ij} = 1, \qquad i = 1,.....,N \tag{3}$$

where

$$u_{ij} \in [0.1], \quad i = 1,...,N, \quad j = 1,.....,m,$$
$$0 < \sum_{i=1}^{N} u_{ij} < N, \qquad j = 1,2,...,m \tag{4}$$

In the fuzzy c-means clustering, which is used in our method, the distance measure function is as follows:

$$d(x_i,\theta_j) = (x_i - \theta_j)^T A (x_i - \theta_j) \tag{5}$$

where A is a symmetric, positive definite matrix. In the proposed method, we used (5) as the dissimilarity function.

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II. PROPOSED METHOD

Our proposed method is an appropriate method especially for the segmentation of structures which are of the same tissue type, e.g., gray matter, like putamen and caudate or lateral ventricles. Proposing a method which minimizes the entropy criterion of all the evolving contours simultaneously, the constraint that the related structures are composed of the same tissue type increases the accuracy and surly the method will become less dependent on the parameters and initial condition.

Almost all the current methods depend on the initial contour unless this dependency is reduced using the data set for approximating the location and the shapes of interest. This clearly increases the dependency of such methods to the selected data set and the registration process. In our method, each image is clustered in to 5 different classes as follows: 1. Background. 2. Skull. 3. Cerebrospinal Fluid. 4. Gray Matter. 5. White Matter. Using clustered data, we are proposing an energy term which makes the model to be located in its related tissue as much as possible.

Using the proposed criterion, the improper initial contours enter their related tissue. For instance, since ventricles and caudate are from different classes, this avoid any incorrect entering of caudate model to CSF or ventricle model to gray matter.

According to the anatomy texts [15], structures are composed of one tissue type only. Therefore, it is beneficial to minimize the entropy of the structures which are made of the same type of tissue.

A. Interactive Entropy Minimization

In our method, a functional based on the information theory is used. This is the first term in our energy minimization and is based on the work by Herbulot et al [9]. The function that represents the entropy of the image is [9]:

$$\varphi(q(I(x),\Omega)) = -q(I(x),\Omega)\ln(q(I(x),\Omega)) = E_{ent} \quad (6)$$

where $q(I(x),\Omega)$ is the probability density function of the image in the region Ω.

In the proposed method, in order to increase accuracy, entropy is estimated using all of the evolving contours of the structures with the same type of tissue simultaneously. To this end, Parzen window method is used as follows:

$$q(I(x),\Omega) = \frac{1}{|\Omega|}\int_{\Omega} K(I(x) - \hat{I}(x))d\hat{x} \quad (7)$$

where K represents the Gaussian kernels with mean of zero and standard deviation of σ. Using the shape gradient method and a dynamic scheme, the criterion can be modified as follows:

$$J(\Omega(\tau)) = \int_{\Omega(\tau)} (\varphi(q(I(x),\Omega(\tau)))dx \quad (8)$$

where the region Ω becomes continuously dependent on an evolution parameter τ and consists of all the models with the same tissue. For example, as shown in Figure 1, being composed of gray matter, probability density function $q(I(x),\Omega)$ is estimated using green and red contours simultaneously. Also, since ventricle system is made of CSF, Ω consists of both sides models estimating their related probability density function. Ventricle models are shown in blue.

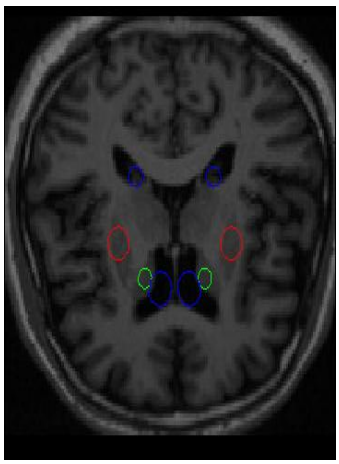


Fig 1. Putamen and caudate contours are shown in red and green respectively. Ventricle initial contour is in blue.

In order to define the curve evolution equation $J(\Omega(\tau))$ must be differentiated with respect to τ.

Based on [9],[12], the derivative is:

$$dJ_r(\Omega,V) = \int_{\Omega} \varphi_r'(q(I(x),\Omega),V)dx - \int_{\partial\Omega} \varphi\ (q(I(s),\Omega)(V.N)ds \quad (9)$$

where N is the unit inward normal of the contour and $\varphi_r'(q(I(x),\Omega),V)$ represents the derivative of φ in the direction of V.

Computing the domain derivative φ_r' [9],[13],[14], the following equation is obtained for the evolution of the contour:

$$F_{entropy} = \frac{\partial\Gamma}{\partial t} = [-q(I(\hat{x},\Omega))(\ln q(i(\hat{x},\Omega)) + 1) - \frac{1}{|\Omega|}(E(\Omega) - 1 + \int_{\Omega} K(I(x) - I(\hat{x}))\ln q(I(x),\Omega)dx]N \quad (10)$$

Therefore, the region-based criterion in our method is defined as [9]:

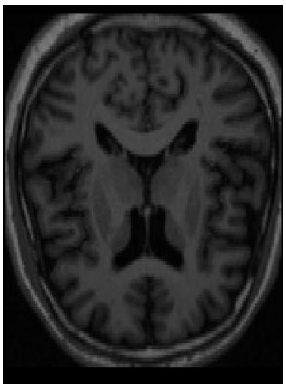
$$J(\Omega_{in},\Omega_{out}) = E_{entropy}^{\Omega_{in}} + E_{entropy}^{\Omega_{out}} \quad (11)$$

This is a competition between the background and the object region. In each iteration, the kernel uses all the related structures, this causes the estimation to be more accurate and also the segmented structures to be located in their related tissue.

B .Fuzzy Force

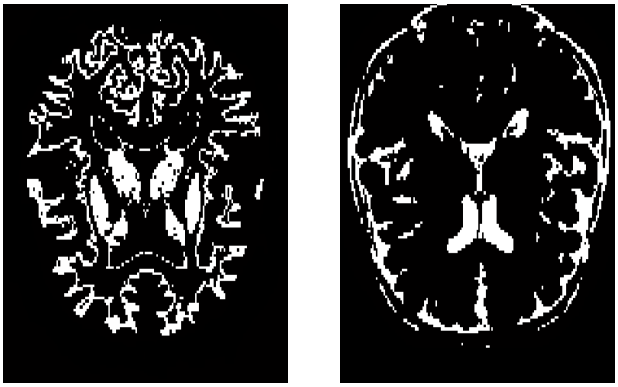
As discussed in Section II.B, using fuzzy c-means, each image is classified into 5 classes which are 1. Background. 2. Skull. 3. Cerebrospinal Fluid. 4. Gray Matter. 5. White Matter. In Figure 2, three main clusters which are white matter, gray matter, and CSF are shown.

In our work, ventricles, caudate and putamen are the structures of interests.



(a)

(b)



(c) (d)

Fig. 2. a. Main image. b. White matter. c. gray matter. d. CSF.

Clearly, their adjacency increases the difficulty especially when the initial contours cover both, such as that shown in Figure 3.

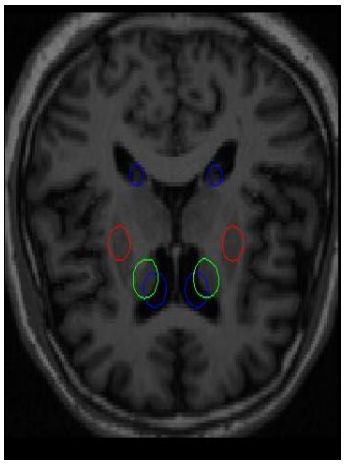


Fig. 3. An improper initialization. Green contours (caudate models) cover the ventricle and blue contours (ventricle models) cover the caudate.

Obviously, the green contours which were supposed to segment the caudate are evolving incorrectly towards the blue contours. Using the following fuzzy criterion, the contours gradually enter their related tissue (this is shown later in the Results Section).

As mentioned previously, proposed fuzzy criterion is added to the evolution equation as a second energy term. To this end, the fuzzy prior shape term is defined for the j^{th} structure as:

$$E_{fuzz_j} = \int_{\Omega_j} (H(\phi_j(x)) - fuzz_j(x))^2 dx \qquad (12)$$

In (12) ϕ_j is a signed distance function related to the j^{th} structure in each side of the brain and H represents the step function. The $fuzz_j$ is a function which uses the clustered image in order to identify the tissue related to the j^{th} structure, e.g., if the j^{th} structure is the left ventricle, since ventricle belongs to the cluster labeled CSF, $fuzz_j(x)$ is equal to zero if x belongs to CSF and is equal to one if it belongs to other clusters:

$$e.g.\ \ j: contour\ related\ to\ the\ left\ ventricle$$

$$fuzz_j(x) = \begin{cases} 0 & x \in CSF \\ 1 & x \notin CSF \end{cases} \qquad (13)$$

The Euler-Lagrange equation for updating ϕ_j is [9]:

$$F_{fuzz_j} = \frac{\partial \phi_j}{\partial t} = 2.\lambda(H(\phi_j) - fuzz_j)\delta(\phi_j) \qquad (14)$$

where $\delta(\phi_j)$ represents the Dirac delta function and $fuzz_j$ is the fixed function used for E_{fuzz_j} minimization.

Consequently, combining entropy force and fuzzy prior criterion, the following formula describes the total evolving force applied to the j^{th} model.

$$F_j = F_{entropy_j} + F_{fuzz_j} \qquad (15)$$

Note that in using F_{fuzz_j}, it is not necessary to provide the registered images. However, since our dataset is registered, the same initialization can be used for all of the images.

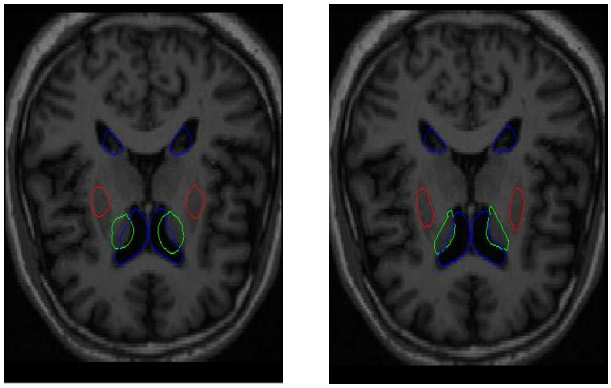
C. Registration and Dataset

Using the IBSR [16] dataset, we registered 18 volumes in our work. We used cardinality metric, in which caudate, ventricles, and putamen are labeled and the registration metric counts the number of corresponding pixels that have the same labels. Amoeba method is used in order to optimize the selected metric which does not require analytical derivatives. ITK [17] and SPM [18] are used for the registration of the labeled datasets and unsegmented volumes, respectively.

IV. RESULTS

Our experimental results show the advantages obtained using the proposed energy terms. In Figure 4.a, an improper initialization (Fig. 3) results in an incorrect evolution. The same initialization leads to the correct evolution when using the proposed F_{fuzz_j} (Fig 4.b).

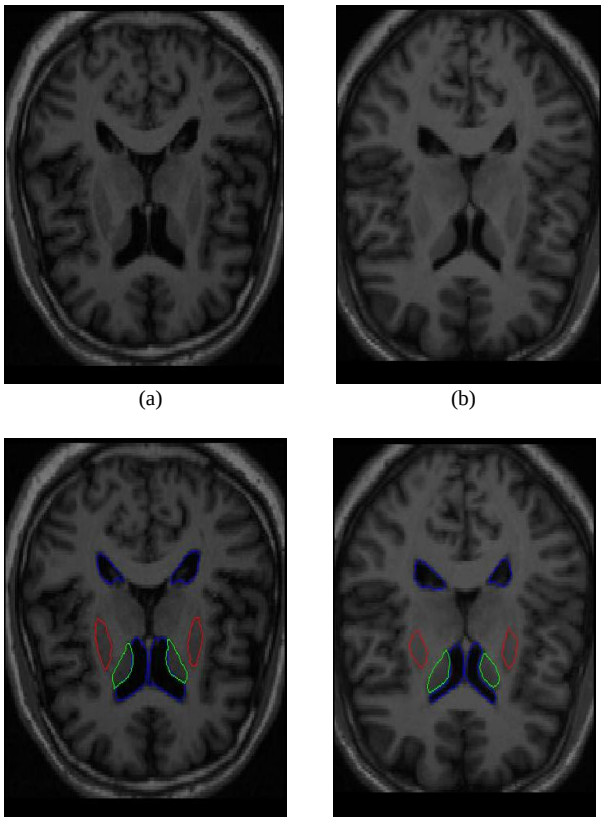
Using fuzzy characteristics of tissues, there is no need for prior knowledge about the location and shape of the model. The fuzzy criterion moves the model into its related tissue during the evolution.



(a) (b)

Fig. 4. a. Fuzzy information is not used and contours are evolving into each other. b. Using proposed fuzzy force avoids the contours entering incorrect tissues (an intermediate evolution stage).

In Figure 5, final results of the evolution are shown after reaching the steady state.



(a) (b)

(c) (d)

Fig. 5. a,b: representative images of two subjects. c,d: final extracted structures. Ventricle: blue. Caudate: green. Putamen: red.

The errors of the extracted structures are evaluated using Hausdorff distance between the segmented structures by the proposed method and by an expert radiologist. The results for putamen and caudate are shown in Fig. 6. The error is evaluated in pixels. The results for the ventricles are presented in Fig. 7.

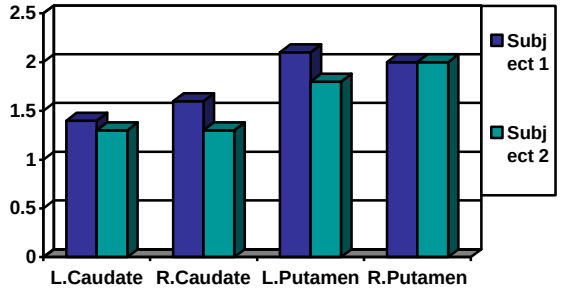


Fig. 6. The errors of the caudate and putamen structures using Hausdorff distance method. The unit of the vertical axis is pixel.

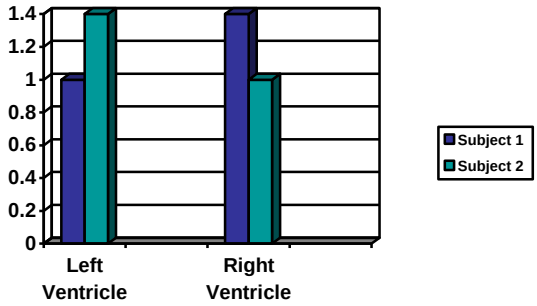


Fig. 7. The errors of the ventricle structures using Hausdorff distance method. The unit of the vertical axis is pixel.

V. Conclusion

In order to overcome two important problems in automatic segmentation of the brain structures, we proposed a novel method integrating level set and fuzzy methods. Our results show that using multi-structural entropy minimization results in more homogenous extracted structures in terms of their tissue type. In addition, using the tissue types in the image makes the method independent of the prior statistical information about the structures and the initial models used for the segmentation. Future work may add symmetry and linguistic shape information to the proposed model.

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