INTERACTIVE COUPLED OBJECT SEGMENTATION USING SYMMETRY AND DISTANCE CONSTRAINTS

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Abstract-**In this paper, we introduce a novel interactive method based on symmetry and distance constraints for the segmentation of medical images. Our new symmetry interaction and distance constraint are integrated with the Herbulot's entropy minimization and Chen's shape-prior segmentation methods. This incorporates knowledge-based constraints that increase the accuracy and reduce the initialization dependency. We applied our algorithm to segment ventricle and caudate in magnetic resonance images (MRI) of the brain. Comparative results show the effects of the proposed constraints. More accurate results and less dependency to initialization are obtained when using the proposed method.**

***Keywords* - Segmentation, Initial Contour, Entropy, Symmetry Interaction, Magnetic Resonance Imaging (MRI)**

I. INTRODUCTION

Medical image segmentation is one of the growing domains of image processing. In this field, extracting structures and pathology features, using magnetic resonance images (MRI), are challenging problems. 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-based information [5],[6], often does not lead to perfect 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 was 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 there are additional prior anatomical knowledge that can further improve segmentation of specific structures, e.g., symmetry of the structures on the two sides of a normal brain.

In all of the mentioned methods, it is assumed that the initial contour is placed in an appropriate position with respect to the structure of interest. For example, an initialization whose one half is in one structure and the other half in the other structure does not guarantee an appropriate segmentation. In this paper, using a criterion based on entropy [9], we propose a symmetric interacting prior-shape model for segmentation.

In this method, we segment double-sided structures accurately. We compare the results of using the symmetry interaction in the segmentation of caudate and ventricles with non-interactive segmentation. In addition, we propose a distance criterion to segment caudate and ventricles, while the initial contours are located exactly in both caudate and ventricle. The rest of this paper is organized as follows. In the next section, the level set method and entropy are discussed briefly. The proposed method is explained in Section III. Results and conclusion are presented afterwards.

II. LEVEL SET METHOD AND ENTROPY CRITERION

A. *Level set method*

Level set method was first introduced by Osher and Sethian in 1988 [10]. Using an appropriate embedding function $\phi : I \times \begin{bmatrix} 0 & T \end{bmatrix} \to R$, it is possible to implicitly, propagate boundaries $C(t)$ in the image plane. $\Omega(t) = \{ x \in I \mid \phi(x,t) = 0 \}$. In order to solve the equation of the evolution, the level set theory is used. The active contour is equal to zero crossing of a higher dimensional signed distance function $\phi(x,t)$.

ϕ Can be any function but because of its properties a distance function is used [11]. Solving the Euler equation for ϕ and finding pixels in which ϕ equals to zero yields the boundary [10], [11].

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

ϕ is the Level set function, F is the evolving force that forces the contour into the desired boundaries.

B. *Entropy Criterion*

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]:

$$\varphi(q(I(x),\Omega)) = -q(I(x),\Omega)\ln(q(I(x),\Omega)) = E_{ent} \tag{2}$$

where $q(I(x),\Omega)$ is the probability density function of the image in the region Ω. It is estimated using the Parzen window method.

$$q(I(x),\Omega) = \frac{1}{|\Omega|} \int_{\Omega} K(I(x) - \hat{I}(x)) d\hat{x} \tag{3}$$

where K represents the Gaussian kernels with 0-mean and σ-variance. Using the shape gradient method and a dynamic scheme, the criterion can be modified as follows:

$$J(\Omega(\tau)) = \int_{\Omega(\tau)} (\varphi(q(I(x),\Omega(\tau))))dx \qquad (4)$$

where the region Ω becomes continuously dependent on an evolution parameter τ. 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 :

$$dJ_r(\Omega,V) = \int_\Omega \varphi'_r(q(I(x),\Omega),V)dx \\ - \int_{\partial\Omega} \varphi\ (q(I(s),\Omega)(V.N)ds \qquad (5)$$

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],[12],[13], the following equation is obtained for the evolution of the contour:

$$F_{entropy} = \frac{\partial\Gamma}{\partial t} = [-q(I(\hat{x}),\Omega))(\ln q(i(\hat{x}),\Omega))+1) - \frac{1}{|\Omega|}(E(\Omega)-1 \qquad (6) \\ + \int_\Omega K(I(x)-I(\hat{x}))\ln q(I(x),\Omega)dx]N$$

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

$$J(\Omega_{in},\Omega_{out}) = E_A^{\Omega_{in}} + E_A^{\Omega_{out}} \qquad (7)$$

As mentioned in [9], this is a competition between the background and the object region, but since symmetry criterion is used in our method, the term $\int_\Gamma \lambda ds$, which minimizes the length of the contour, is omitted.

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III. PROPOSED METHOD

Our proposed method is an appropriate method especially for the segmentation of structures which are adjacent and also identical on both sides of the brain. Almost all the current methods depend on the initial contour and this dependency increases when segmentation of two adjacent structures is of interest. In such cases, the incorrect attraction of the contour to undesired structures is very probable while different structures are located around each other. For instance, ventricles and caudate are adjacent structures. Since they are different and separate structures, an initial contour, having intersections with both, should not lead to a mixed or overlapped segmentation. In order to avoid such problems, we propose a repelling force.

According to the anatomy texts [14], there exists shape symmetry on the two sides of the normal brain. Based on this, a symmetry force should improve the segmentation results. The benefit of using the symmetry interaction may be shown by improperly initializing the contour. Without using the symmetry interaction, the algorithm becomes much more parameter dependent in such a situation.

A. Distance Force

In our work, ventricles and caudate are the structures of interests. Clearly, their adjacency increases the difficulty especially when the initial contours cover both, such as that shown in Figure 1. Clearly, the green contours which were supposed to segment the caudate are evolving incorrectly towards the blue contours (see the first row of Figure 2). Using the following distance force, the contours gradually repel each other until each one is in its related tissue. Suppose that Ω_j^s is the jth evolving contour on the side S of the brain. Therefore ϕ_j^s is the corresponding signed distance function to be used for embedding the contour. Each curve Ω_j^s separates the image into two regions, $\Omega_{j_{in}}^s$ and $\Omega_{j_{out}}^s$. It is assumed that for all $(x,y) \in \Omega_{j_{in}}^s$, $\phi_j^s(x,y) < 0$ and for all $(x,y) \in \Omega_{j_{out}}^s$, $\phi_j^s(x,y) > 0$.

We introduce a thin band around the zero-level set of the Ω_j^s as the Repelling-Band:

$$\text{Re pelling\_Band} = \{(x,y): |\Omega_j^s(x,y)| < \delta\} \qquad (8)$$

Using the Repelling_Band, the distance force F_d is introduced as:

$$F_{d_j}^s = \begin{cases} \dfrac{\lambda}{1+\Omega_j^s(RB)} & \Omega_j^s(RB) < \delta \\ 0 & other \end{cases} \qquad (9)$$

where λ is a fixed constant in our method equal to -1. The effect of using the proposed distance constraint is shown in Figure 2 (second row). Note that the evolving contours do not intersect when the proposed force is used.

B. Symmetry Interaction and Prior Shape

We begin our interactive curve evolution with two separate contours for the two structures (ventricles and caudate). Then, the symmetry plane is detected based on Liu and Collins's work [15]. Next, the contours are reflected with respect to the symmetry plane to segment the structures on
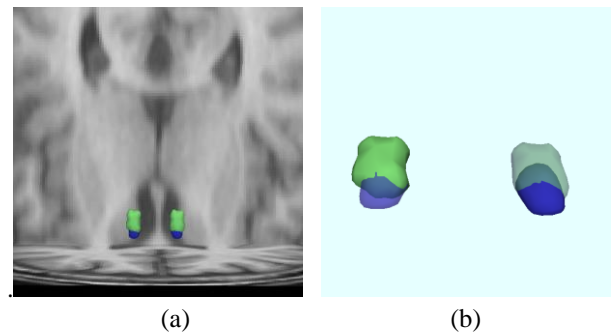

(a)   (b)

Fig. 1.a. Improperly initialized contours covering both structures b. contours are inside each other.

the other side of the brain. These steps are summarized below and explained in the rest of this section:

  1. Initialization on one side (e.g., right side)
  2. Symmetry plane detection
  3. Reflection and initialization on the other side

In each iteration:

  1. shape-prior evolution of the right side based on entropy minimization, distance force.
  2. Evolution of the left side, based on entropy minimization, distance force using the symmetry interaction.

B.1. Symmetry plane detection

There are several methods for the detection of the symmetry plane. Some methods maximize of the correlation between the image and its reflection with respect to the symmetry plane and some optimize other similarity measures [16]. We use Liu and Collins's method [14] to find the symmetry line (axis) in each slice. Using the symmetry axes of all slices, the plane of reflection is found for the entire volume. In this method, by rotating and cross-correlating the rotated image with its vertical reflection about the center, the offsets of the symmetry axis is found; see [14] for more details.

B.2. Symmetry interaction and prior shape

As mentioned previously, the symmetry criterion is added to the evolution the left side contour. To this end, the shape similarity term is defined for the jth structure as:

$$E_{sym_j} = \int_{\Omega_j^s} (H(\phi_j^L) - H(\phi_j^R))^2 dx \qquad (10)$$
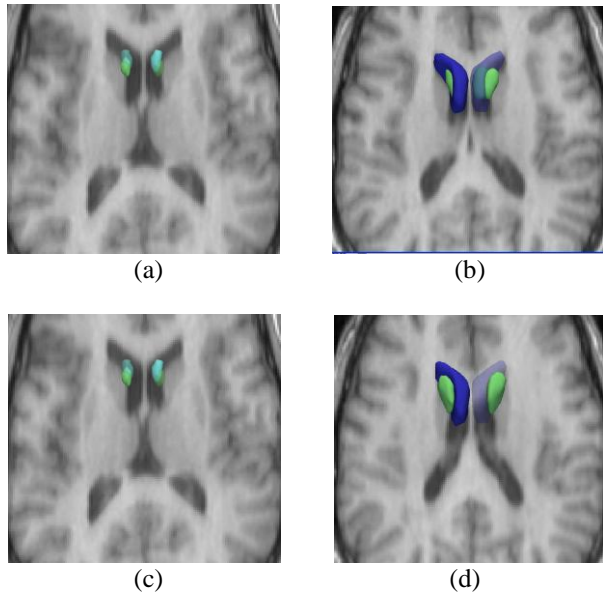

(a)   (b)

(c)   (d)

. Fig. 2. Improper initialization (a,c). Models are evolving into each other (b). Using distance constrain repels the models from each other (d).

In (10) ϕ_j^L and ϕ_j^R are signed distance functions related to the jth structure in the right and left sides of the brain,

respectively. The Euler-Lagrange equation for updating ϕ_j^L is [9]:

$$F_{sym_j}^L = \frac{\partial \phi_j^L}{\partial t} = 2.\lambda(H(\phi_j^L) - H(\phi_j^R))\delta(\phi_j^L) \qquad (11)$$

where $\delta(\phi_j^L)$ represents the Dirac delta function, ϕ_j^R is chosen to be fixed sign distance function for E_j^L minimization.

Consequently, combining symmetry force, distance force, and the entropy criterion, the following formula describes the total evolving force applied to the jth left side model.

$$F_j^L = F_{sym_j}^L + F_{d_j}^L + F_{entropy_j}^L \qquad (12)$$

Substituting ϕ_j^R with ϕ_{ref}, prior shape can be developed as:

$$F_{shape_j}^R = 2 \times \lambda \times (H(\phi_j^R) - H(\phi_{ref}))\delta(\phi_j^R) \qquad (13)$$

Using $F_{shape_j}^R$ the evolving force for the jth right side model will be:

$$F_j^R = F_{shape_j}^R + F_{d_j}^R + F_{entropy_j}^R \qquad (14)$$

Note that using the same comparison term for both of the reference shape and the symmetry interaction reduces the necessary calculation. As shown in Figure 3, symmetry interaction result1s in more accurate segmentation because of less sensitivity to the parameters.

C. registration and data set

Using the IBSR [17] data set we registered 18 volumes in our method. We used cardinality metric, in which caudate and ventricle 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 [18] and SPM [19] are used for the registration of the labeled data set and unsegmented volumes, respectively.
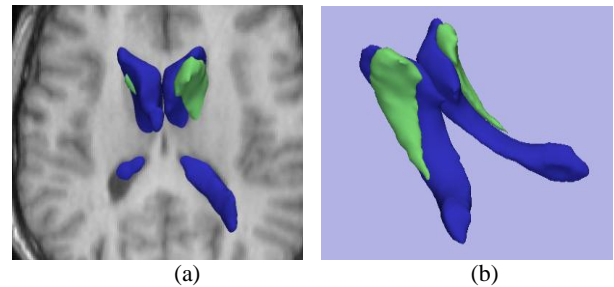

(a)   (b)

Fig. 3. (a) No symmetry interaction and incorrect result of the right side contour (the evolution is completed). (b) Using symmetry interaction generates correct evolution without any change of the parameters.

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IV. Results

In this work, the 3D-Slicer software [20] is used for showing the results. In Figure 4, the final caudate and ventricle models are shown. The errors of the extracted structures are evaluated using Hausdorff distance method for

the image matching and shown in Table 1. In Figure 4, our results are shown along with the neurologist segmented structures. The coupled segmented structures are shown in Figure 5.

TABLE I

The errors of the structures using Hausdorff distance method. The unit is Pixel.
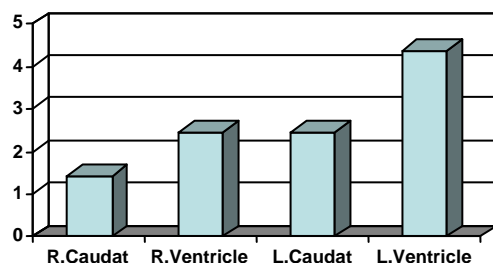
V. CONCLUSION

Our work has proposed novel methods to overcome two important problems in automatic segmentation of the brain structures: improper initialization and parameter sensitivity. Our results show that using symmetry interaction can guide incorrect models to follow the correct ones on the other side of the brain and thus there is no need to change the model parameters. In addition, the results generated using distance criterion with improper initialization, show the benefit of using this constraint.

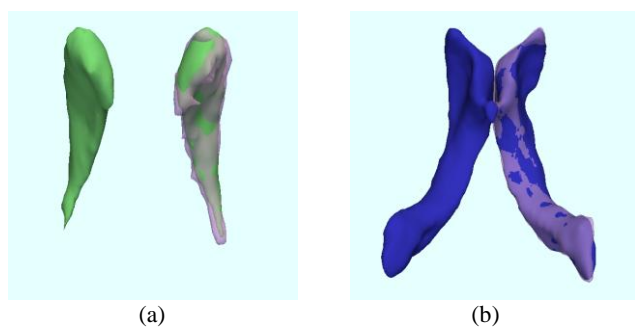(a)   (b)

Fig. 4. Final caudate and ventricle models are shown in green and blue in (a) and (b), respectively. The neurologist segmentation is shown in pepper.
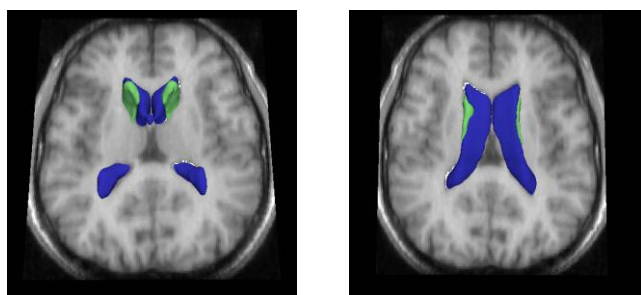

Fig. 5. Final segmentation of the caudate and ventricles superimposed on two of the original images.

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