REGULARIZED CELL COMPETITION ALGORITHM FOR BOUNDARY DELINEATION IN A SERIES OF 2D SONOGRAMS

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Abstract: A nearly automatic image segmentation algorithm is proposed for 2D series of breast sonogram. This algorithm is based on watershed transformation, cell competition mechanism, and the highly coherent relation between consecutive slices. Cell competition process is conducted to alleviate over-segmentation and is regularized by the object boundary derived from previous slice. The resulting boundary is propagated to next slice until all slices are processed. This algorithm was tested with six sets of 2D series of breast sonograms. The mean absolute distances (MAD) of these six series to the manually delineated boundaries are 2.99 ± 0.49, 3.60 ± 0.60, 2.18 ± 0.60, 2.37 ± 0.50, 2.97 ± 0.44 and 2.64 ± 0.32 pixels respectively.

Introduction

Segmentation task is an essential subject encountered in analyzing medical image. After getting the contour information of the target of interest, researchers can identify the textural properties, analyze static shape features, quantify the dynamic behavior of targets and even make clinical decisions. However, segmentation is a very hard task for ultrasound images. Owing to the complex inherence of sonography - speckle, artifact, shadowing, and tissue-related texture - the ture target boundary may be distorted and blurred. This deficiency may thwart traditional edge detection mechanism and cripple deformal models. Watershed transform is an effective approach to identifying bondaries of potential closed areas. Althougth it suffers oversegmentation constantly, watershed transform has the advantage of preserving significant but weak edges. Also, concurrently delineating multiple targets is easily achieved within the framework of watershed transform. Chen [2] provided a discrete version of dual-snake model, in which watershed transform paves the deforming path for the two snakes and narrows down the searching space of cost minimization.

There have been several studies on analysis of sequential sonograms. Sayan et al. [3] utilized some basic prior knowledge, such as shape and echo pattern, to help edge detection task in prostate ultrasound images. In [4], a deformable superellipse is devised for segmentation of prostate sonograms. For echocardiography, a Bayesian framework is applied in [5] to surface optimization problem. This framework is used to integrated prior knowledge of the shape of left ventricle and the low level image evidence. In [6], Bayesian framework is also adopted with random field model to cope with segmentation in 3D intravascular ultrasonic images. While shape has served as important prior knowledge in several sonographic applications, it is not easy to assume a shape model for breast lesion in general. For a series of breast sonograms, the shape and size of the target may vary substantially and one target may be even split into multiple parts in some slices. With these difficulties and the inherence of ultrasound image, boundary extraction in a freehand series of breast sonograms is a relatively formidable problem.

A nearly automatic boundaries delineation mechanism in a series of 2D sonograms is presented in this paper. This mechanism conducts a merge/spit activity based on cell in each slice. Further, the activity is regularized by the contour information from previous slice for the sake of coherence. The process iterates until every slice is processed.

Materials and Methods

The freehand series may be acquired by rotating, shifting or compressing the probe. The diversity of acquirement exacerbates the difficulty of modelling the segmenting procedure. Nevertheless, utilizing the mutual relation of consecutive slices suggests a possible solution. In this algorithm, boundaries information are cross-referenced and propagated throughout the series to detect the contour of each slice. Figure 1 sketches the processing diagram.

For each slice, de-noising is carried out by Gaussian filtering. Watershed transform, more specifically, the immersion method [1], tessellates the gradient map, which is generated from Sobel filter. Following that, weak edges are broken to produce the second tessellation such that all edges are more statistically significant. The connected component in the second tessellation and catchments basin in the first tessellation are denominated as cell and rudimentary cell respectively. The watershed lines between two adjacent cells are called edges, while those separate two abuttal

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rudimentary cells are called edge segments. Figure 2 shows the hierarchy between first and second tessellation. In the figure 2, the rudimentary cells are contoured with dotted lines and cells are encompassed with bold lines.

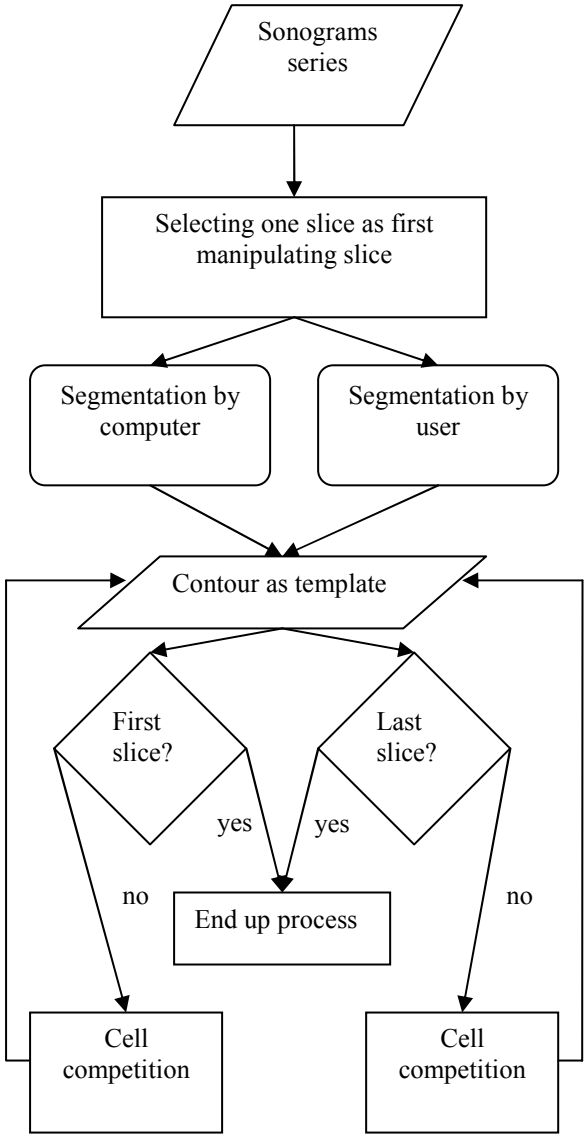

Figure 1: System flow chart

The contour information from previous slice, serving as a template, plays a crucial role in delineating the boundary of target. The template partitions the cells into two regions, inside target region (ITR) and outside target region (OTR). The segmentation task is fulfilled by launching the competition process between ITR and OTR. ITR and OTR compete for the bilateral cells of the edges set separating the two regions (Ω). The competition process is modelled as a cost minimization problem, which is characterized by P-cost and R-cost. P-cost stands for local measurement of the significance of edge. R-cost describes the degree of spatial deviation between template and edge. Via minimizing the cost of Ω ($\hbar$), a delineation of taget with pertinent saliency and coherence may be attained. Equation (1) defines the cost of Ω.

$$\begin{aligned} \hbar &= \Re + \lambda \aleph \\ &= \sum_{\forall i \in \Omega} \gamma_i + \lambda \sum_{\forall i \in \Omega} p_i \end{aligned} \tag{1}$$

where γ_i represents R-cost of one edge, p_i p-cost, and λ the weighting ratio of the two terms.

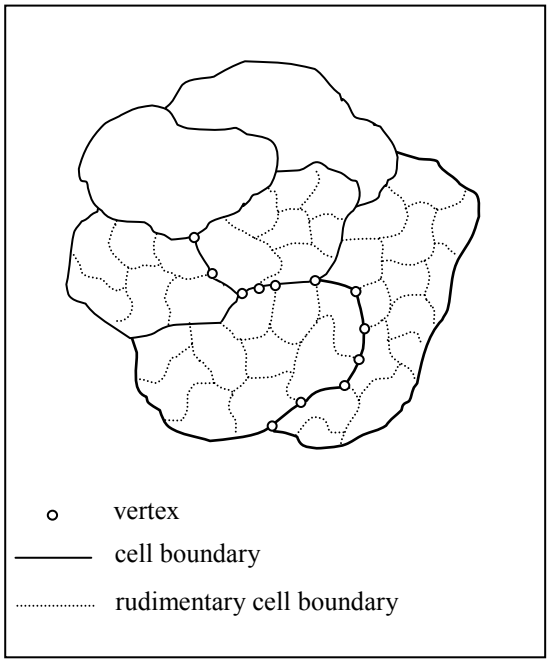

Figure 2: The hierarchy of cell and rudimentary cell. One edge is composed of several edge segments which are lined up between two vertices.

P-cost is the local measurement of edge significance. The more salient the edge is, the lower the P-cost will be. Instead of taking the gradient measure as P-cost, the measurement is taken from the statistical characteristic of intensity around the edge. Taking into account the potential texture difference between two cells, using statistical test to fathom the local similarity of intensity between the bilateral vicinity and profile of edge is a reasonable choice. Equation (2) formulates P-cost of one edge.

$$\begin{aligned} p_i &= H + \log \rho_i \ ; \\ H &= \max_{\forall j \in \Phi} \{-\log \rho_j\} \ , \\ &\forall i \in \Phi \end{aligned} \tag{2}$$

where ρ_i is the p-value of statistical test of this edge.

The sample size of bilateral vicinity is critical to determine the p-value. Insufficient sample size can not distinguish weak-but-significant and weak-insignificant edges well. On the other end, over-sampling tends to produce a very small p-value. There are two possible approaches to sample the intensity of bilateral vicinity.

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One way is to use the morphological dilation from edge profile. This approach suffers from determining the apposite size of dilation band. The other approach utilizes the hierarchy of cell and rudimentary cell. The inner of rudimentary cells from both side of edge are taken as samples of statistical test. In this study, the later approach is adopted.

R-cost is endowed by template. R-cost penalizes one edge according to the degree of deviation from template. The quantitative property of R-cost positively relates on the deviation. One simplest way is to take R-cost as linear function of shortest distance between edge and template.

Cost minimization is enforced by gradient descent method. In every iteration, a greatest descending way is searched by striking the balance between P-cost and R-cost. The search will iterate till achieving the minimum, which preserves the property of significance and coherence.

Results

A preliminary test is taken on six sets of series breast sonograms. The computer generating contours (CGC) are compared to manual delineation by one expert (EMD). For each slice, we define the difference between CGC and EMD by calculating the mean absolute distance (MAD) between two curves. Given that CGC and EMD are represented as $C=\{c_1,c_2,c_3,...,c_n\}$ and $E=\{e_1,e_2,e_3,...,e_m\}$ respectively, the MAD between CGC and EMD are described in Equation (3) and $d(.,.)$ is defined in equation (4).

$$MAD(C,E)=\frac{1}{2}\{\frac{1}{n}\sum_{i=1}^{n}d(c_i,E)+\frac{1}{m}\sum_{j=1}^{n}d(e_j,C)\} \quad (3)$$

$$d(c_i,E)=\min_j(e_j,c_i)$$
$$d(e_j,C)=\min_i(c_i,e_j) \quad (4)$$

Table 1: The basic measuring unit of the statistics of MAD is pixel.

Number of Slices	MAD mean	MAD std.
10	2.9918	0.4874
48	3.6047	0.6004
26	2.1786	0.6045
9	2.3657	0.4971
15	2.9698	0.4405
16	2.6447	0.3243

With these definitions, we calculate MAD of every slice and summarize the MAD statistics of each series in Table 1. Figure 3 demonstrates results of several slices in one series acquired from continual compression while Figure 4 illustrates result of one series of shifting probe.

Among these six series, one series was acquired via shifting the probe and the others were collected by compressing the breast. These sonograms are courtesy of Dr. Yi-Hong Chou, Department of Radiology, Taipei Veterans Hospital.

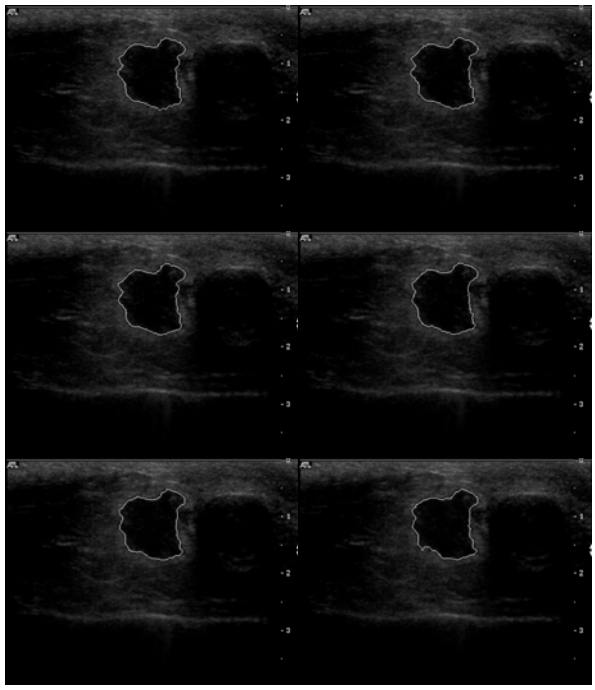

Figure 3: six consective slices of the third seires

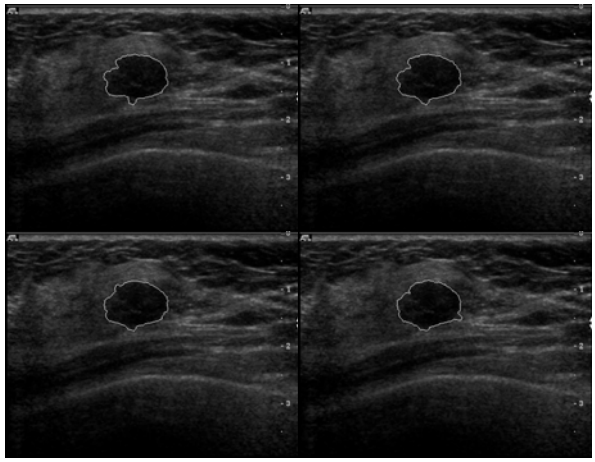

Figure 4: four consecutive slices of the fourth series

Discussion

In clinical diagnosis of breast cancer, it is more plausible to analyzing two or more slices than just merely one. Analyzing series of breast sonograms (possibly sagittal or transversal collection), radiologists can diagnose the lesion with static morphological and textural features. Recently, there are several studies, [7] [8], focusing on the elasticity of lesion. The dynamic

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behaviour of lesion under continual compression could possibly reveal useful information for clinical decision.

Certainly, in the field of CAD (Computer Assisted Diagnosis), it will discriminate between malignancy and benignancy more correctly with a set of slices from the same patient. The cornerstone of CAD with sequential sonograms is the contour information of target. Manual delineation is not feasible with formidable number of slices and the intraobserver variation in slices. Instead, computer generating contour can provide relatively stable depiction and quantize features efficiently if coherence and salience are considered simultaneously. Figure 4 compares the delineation from expert to computer generating result.

In this study, the weighting factor, λ, can be adjusted according to the gap bween consecutive slices. If the gap is large, a small λ can be considered for loose coherece. For dense series, a larger λ will be contemplated. The parameters of Gaussian filter are fixed under 13*13 mask size and standard deviation 4.0.

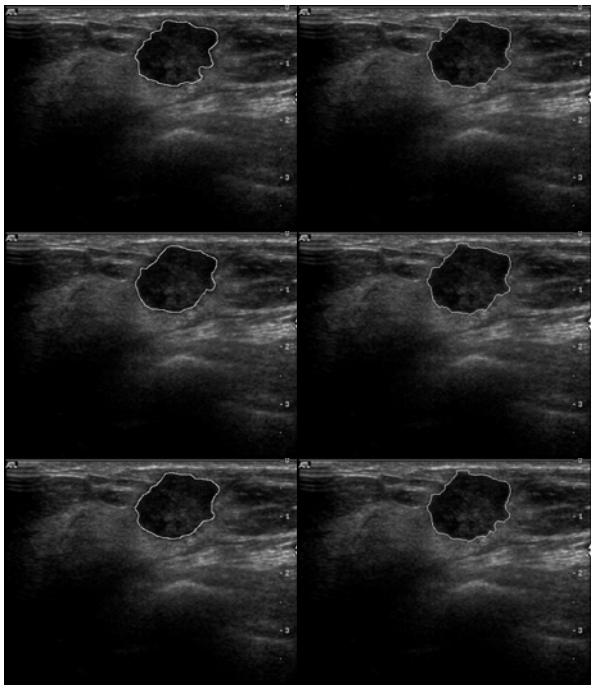

Figure 4: Images of left column are drawn by one expert and those of right column are generated by this algorithm. Contours drawn by one expert shows more variation.

Conclusions

Computer automatic delineation overwhelms manual demarcation for the following reasons:

- Circumventing formidable delineation efforts
- Less variation between consecutive slices (Because it is tedious for human to draw contour of one slice and reference previous slice at the same time.)
- Possibly less time consumption

With these reasons, developing computer automatic delineation can help radiologists saving time and effort to delineate the boundary of lesion. And with computer-generated contours, several characteristics could be excavated quantitatively and provide some more objective information.

One lesion could possible be divided into several parts in one slice. This situation is not considered in this study. Developing multiple targets detection and delineation in 2D series sonograms will be next step to make this algorithm more robust. This research is supported by National Science Council under the granted number NSC93-2622-E-002-004.

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