INTERACTIVE SEGMENTATION OF MULTI-DIMENSIONAL MEDICAL DATA WITH CONTOUR-BASED APPLICATION OF GENETIC ALGORITHMS

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ABSTRACT

In this paper we describe a method for contour-based segmentation of anatomical structures in tomographic images.

Our method requires three steps. First we manually trace one or more 2D contours of a structure of interest. Such contours are then used as training examples in designing a non-linear edge-detector using a genetic algorithm. Finally, by applying the edge detector to the whole dataset we perform a 3D segmentation and surface reconstruction.

Results obtained on magnetic resonance images of the brain are also reported.

1. INTRODUCTION

Segmentation is a central issue in most computer vision and imaging systems and a fundamental pre-processing step required from most visualization systems [1, 2, 3]. In medical practice, several tasks, from diagnosis to radiation treatment-planning, can benefit from tools that help speeding up and easing the segmentation process.

In fact, manual segmentation of a structure of interest is time-consuming and often infeasible in the clinical environment. On the other hand, totally automated procedures are still far from reliable, thus making some interaction inevitable between a user and the digital system.

We propose to leverage the visual, anatomic and clinical skills and experience of the end user by providing powerful tools that produce segmented boundaries based upon a small set of 2D seed contours.

In this paper we concentrate on the method we use to produce a full segmentation of a structure of interest from the information that can be extracted from a set of manually-traced contours.

In our approach, such contours are the input of a genetic algorithm (GA) that is used to design an edge detection/interpolation system that produce a segmented surface representation.

Our method can be split in three cascaded steps:

- interactive specification of "training" contours;
- GA design of an edge-detector;
- detection of edge points and extraction of the contours of the structure of interest.

In the following paragraphs we give a detailed description of the method and discuss some preliminary results we have obtained on magnetic resonance images of the brain.

2. BACKGROUND

2.1. Genetic algorithms

Genetic algorithms are optimization techniques inspired by natural evolution [4]. In GAs, solutions of an optimization problem are encoded as binary strings. After generating a first set of random solutions, these can be improved by iteratively applying operators, termed selection, crossover and mutation, that mimic the corresponding processes of natural evolution. In fact, selection lets only the fittest individuals (best solutions, according to some goodness criteria or 'fitness function') be present in the next generation (iteration of the algorithm); crossover lets them exchange tracts of their DNA (corresponding substrings) to generate offspring (new solutions), while mutation randomly introduces new genes (by flipping one or more bits of a solution).

Genetic algorithms can be successfully applied to problems characterized by a large and irregular search space. In those cases, they have been shown to compare favorably, in terms of applicability and efficiency, with other methods, such as simulated annealing [5]. Furthermore, GAs do not require that the search space be continuous, but can operate effectively in discrete and mixed discrete/continuous spaces.

In the field of signal processing, GAs have been used, among other applications, to design general-purpose digital filters [6, 7]. As regards biomedical signals, GAs have been used to design optimum QRS detectors [8],

0-8186-6950-0/94 $4.00

providing solutions characterized by an excellent trade-off between performance and computational load.

As in [8], we have used GAs both as a learning method for adaptive-filter design and to calculate a set of parameters that regulate the segmentation process.

2.2. Interactive contouring and segmentation

Many anatomical structures in both diseased and healthy tissue present formidable segmentation problems. Despite a lot of research has been done in the field [9, 10, 11, 12], automated segmentation systems are still far from yielding acceptable results for their practical use in a clinical environment.

The most accurate method that could be used to produce segmentations of 3D structures is still manual tracing of contours in each slice of the dataset. Obviously, due to its heavy requirements in terms of time on the part of the clinician, manual segmentation cannot be considered a viable approach to the problem.

Therefore, presently, adopting a semi-automated approach seems to be the only practical way to provide clinicians with effective tools to help them in such a task [13].

3. METHOD

In our approach, the parameters of a non-linear edge detector are first computed by a genetic algorithm in order to obtain optimum performances on reference (training) 2D slices in which the contours of a structure of interest have been manually delineated.

On such a detector we base our further processing. In fact, we adopt an iterative process in which the detector is applied to each slice, according to rules that depend on the position of the contour extracted on a previous one. The output of the detector (a set of edge points) is then interpolated to extract the contour of the structure of interest. Such a process is initially seeded by the training contours and is then iteratively propagated across the whole dataset.

3.1. Specification of contours

By manipulating arbitrary cutting planes through a 3D image set, the user simply draws two (or more) contours that specify the boundaries or seed outlines of the segmentation task to be performed. The first one will be used as input to the GA and the other(s) as reference outputs for the calculation of the fitness function.

The contours can be drawn on orthogonal sections or arbitrary oblique sections by means of a tool that was developed by A.B.Dobrzeniecki, based on a display-only sectioning system written at the Whitaker College Biomedical Imaging and Computation Laboratory [14].

3.2. Design of the edge detector

The detectors we use are 1D or 2D second-order polynomial filters applied on a scan region determined for each slice, k, as follows:

- For each point $P_{h,k-1}$ of the contour extracted on the $k-1$-th slice, calculate the (inward- or outward-oriented) normal.
- Along the direction of the normal, resample the input image on a $N_w \times N_h$ wide region centered around $P_{h,k-1}$.

Therefore, for $N_h = 1$ the scan region is actually a line on which a 1D filter can be applied. For $N_h > 1$ a 2D filter has to be designed. One of the main effects of this strategy is to limit the influence of edges, similar to the ones that characterize the structure to be segmented, that can be found outside the region of interest. In fact, for any slice, the filter is applied only in a neighborhood of the contour extracted on the previous one.

The detector has the following structure:

$$\begin{aligned} f(x(i,j)) \;=\; & c_0 + \sum_{k=1}^{N_p} c'_k \cdot x(i-d_{k,i}, j-d_{k,j}) + \\ & x(i-d_{k,i}, j-d_{k,j}) \cdot \\ & \sum_{l=k}^{N_p} c''_{k,l} \cdot x(i-d_{l,i}, j-d_{l,j}) \end{aligned}$$

where c_0, c'_k, $c''_{k,l}$ are the filter coefficients and $d_{t,i}$ and $d_{t,j}$ $(t = 1, \cdots, N_p)$ are the offsets along each coordinate axis, with respect to the actual sample, of the N_p samples that are involved in the calculation. All these parameters are optimized by the genetic algorithm.

The fitness function used in the GA returns a value that is proportional to the degree of similarity between the contour(s) produced by each genetically-evolved detector and the reference contour(s).

3.3. 3D segmentation

3.3.1. Detection of contour points

To perform the final segmentation of a slice, we apply the detector designed by the genetic algorithm on

a neighborhood of the contour extracted on the previous slice. For each scan region, the edge-detector described in the previous section provides a set of $N(h)$ edge points, h being the index of the scan region.

For some scan regions, $N(h)$ may be 0 or greater than 1 and the estimated position of the detected edge points may be altered by noise. This hampers the recovery of the contour to which such points belong. To overcome such problems, we have adopted a strategy, based upon the use of a certainty function that selects, for each scan region, the edge-point that is most likely to be the 'real' one, among the ones extracted by the detector. The edge points whose certainty value is below a preset threshold or the ones that would produce a sharp change of direction of the contour are rejected, even if they are the 'best choice' for the scan region under consideration.

3.3.2. Contour detection and final segmentation

For each edge point detected on the scan region h, we evaluate the following uncertainty measure:

$$\begin{aligned} C_k(h) \;=\; & W_{d1} * d(P_{h,k}, P_{h,k-1}) + \\ & W_{d2} * d(P_{h,k}, \hat{P}_{h-1,k}) + \\ & W_{conn} * CF(P_{h,k}, P_{h-1,k}) + \\ & W_c * \mid I(P_{h,k}) - \overline{I} \mid \end{aligned}$$

where

$$CF(P_a, P_b) = \begin{cases} 0 & \text{if a set of edge points exists, such} \\ & \text{that } P_a \text{ is connected to } P_b \\ 1 & \text{otherwise} \end{cases}$$

W_{d1}, W_{d2}, W_{conn} are weighting parameters; $d(a,b)$ is the euclidean distance; $P_{h,k-1}$ is the seed point for the h-th scan region and $\hat{P}_{h-1,k}$ is the best edge point detected in the $(h-1)$-th scan region of the same slice (i.e. the one with the highest certainty); $I(c)$ is the intensity of the edge located in c, and $\overline{I}$ is the average intensity of the best edges detected in the scan regions $1, \cdots h-1$.

After evaluating such a function, we add the edge point that minimizes it to our contour, requiring, however, that $C_k(h)$ be below a threshold C_{max} and that the variation of direction of the contour introduced with the choice of such edge point be below an angle α_{max}.

The edge detection/interpolation process is iterated starting from the training slice up to the end of the dataset, using the last-calculated contour as a seed for the next one. To limit error propagation, we use the central slice for training and then proceed with the segmentation in two different directions, towards opposite ends of the structure.

The extension of the scan region and the parameters of the certainty function (W_{d1}, W_{d2}, C_{max} and α_{thr}) are also optimized by the GA.

4. CURRENT RESULTS

Our method has been applied to sequences of slice-selected magnetic resonance images of the brain.

The datasets on which we have performed our tests present some of the typical problems that usually hamper automated-segmentation tasks. Among these, significant changes in shape across the sequence, the proximity, in the same slice, of edges similar to the ones that have to be detected, and the variability of edge features, even within the same slice.

In Fig.1, a sequence of magnetic resonance images of the brain are shown along with the contours that have been extracted with our method: the structure of interest that had to be segmented in this case was the brain ventricle.

As shown by the pictures, our method has proven to be relatively robust, with regard to the above-mentioned problems, thanks to the selectivity of the GA-designed detector and to the mild regularization of the contour that can be obtained with the above-described certainty function. In fact, while keeping the extracted contours smooth, our method was able to track even some sudden changes of shape between a slice and the following one.

5. FUTURE WORK

Although preliminary results are rather encouraging, there is still room for several further improvements. Actually, our method constitutes a framework within which many variants can be devised.

As regards the changes in contrast characteristics along the contour, a higher degree of adaptivity could be introduced in the detection scheme by identifying different segments of the contour, while manually generating the training image. In this case, for example, a different detector could be designed by the GA for each of such segments.

Also, as the tool used to generate the training image allows the user to trace contours on any plane in 3D space, adding some contours, traced on non-parallel planes, to the training ones could provide further constraints, resulting in a better segmentation.

As regards interpolation and contour-extraction, we are presently experimenting a differential elastic model

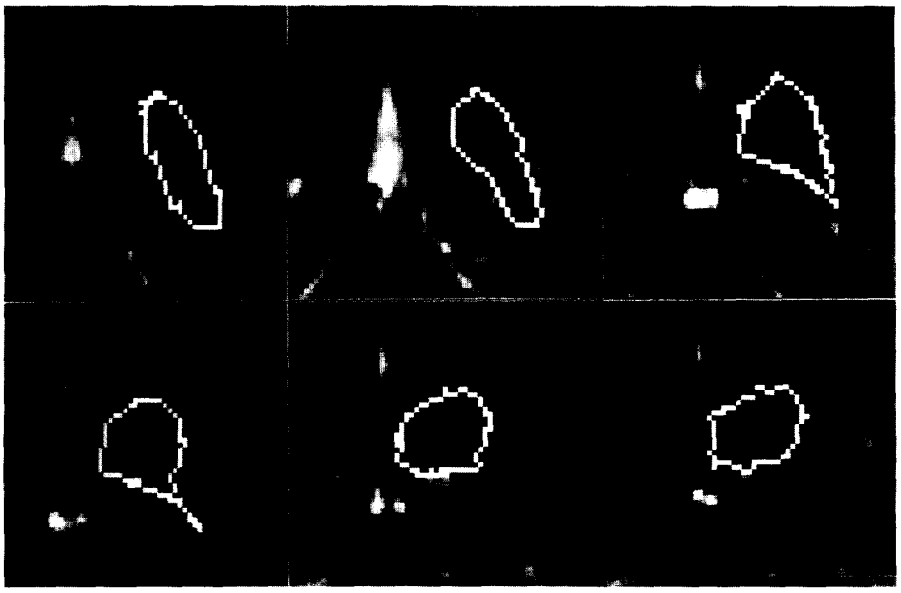

Figure 1: The extracted contours superimposed on the magnetic resonance images of the brain ventricles

for the contour that should improve the quality and smoothness of the resulting segmentation. By modelling the contour as an elastic line attached to the edge points by means of springs of different stiffness, proportional to the corresponding values of the certainty function, we believe that the extracted contour should become less sensitive to small displacements in the detected edges, caused, for example, by noise.

6. CONCLUSIONS

In this paper we have presented a new approach to semi-automated contouring and segmentation and some preliminary results.

The adaptivity and interactivity of our method offer the advantages of being tuned and optimal in some sense for a specific feature extraction task. By deriving filters and filter application techniques from data available along a few contours (drawn by a user or clinician), difficult segmentation tasks may be accurately completed in a semi-automated fashion.

By allowing the specifications of the contours to be done in 3D space along arbitrary cutting planes, and by producing segmented surfaces in near real-time, after the GA has been run, our method permits rapid exploration and analysis of a 3D data set.

With our method, the human interaction is limited to tracing the training contours and possibly some minor corrective intervention after the automatic segmentation has been performed. In fact, once the training phase is over, the detectors we use are very simple and demand little in terms of computation load. Thus, a possible manual refinement of the results that can easily be carried out by deleting wrong edge points would not prolong the whole procedure for more than a few minutes, despite requiring that most of the segmentation be performed once again.

7. ACKNOWLEDGEMENTS

This work was partially funded by CNR (Italian National Research Council).

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