

Automatic atlas-based contour extraction of anatomical structures in medical images

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Abstract. We present an extension of the live-wire approach to an automatic segmentation method. Similarities between anatomical structures in different patient data are exploited by transferring structure outlines from atlas to patient data. After preprocessing via affine registration methods, the automatic segmentation is done slice by slice. Atlas seed points are relocated in each patient slice and then connected by cost-trained live-wires. After the automatic contour extraction, an efficient graph search algorithm facilitates the interactive adjustment of the contours created. The evaluation with hip CT data showed that the tool simplifies the segmentation of anatomical hip structures because 51% of interaction time could be saved maintaining the segmentation quality compared to manually created segmentations. © 2005 CARS & Elsevier B.V. All rights reserved.

Keywords: Segmentation; Live-wire; Contour extraction; Graph search algorithm; Anatomical structures

1. Introduction

Medical image segmentation is a challenging problem and a necessary first step in many image analysis and quantification methods. The segmentation of anatomical objects presents a particular problem especially for surgery and radiotherapy planning. Our research was motivated by the need of detailed virtual 3D hip models during the computer-assisted 3D planning of orthopaedic interventions [1,2].

In the majority of cases, the segmentation work is done using manual or semiautomatic segmentation methods like region-/volume growing, thresholding, or snake methods. For many medical applications, the live-wire segmentation [3] has proved to be a robust and user-friendly semiautomatic method for the extraction of structure outlines. But for the

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segmentation of image volumes, the user has to create a contour in each slice. Hence, the method is very time-consuming and tedious.

The live-wire method has been extended to a semiautomatic segmentation of volume data in different approaches [4,5]. These methods use orthogonal slice segmentation or interpolation techniques, respectively, to segment the three-dimensional structures on the basis of some initial contours. User interaction is still necessary for creating adequate initial contours and for the interactive correction of the segmentation result.

In our approach, we use the organ outlines of an anatomical atlas, in order to automate the contour-based segmentation framework. Hence, we developed a method that exploits the similarities between anatomical structures in different patient data. The contour-based approach performs the segmentation by transferring the object contours slice by slice from atlas to patient data. Since in most clinical applications automatically created segmentation results have to be revised by experts and segmentation failures may still occur, we developed an intuitive adjustment interface that facilitates the correction and optimisation of automatically created contours.

Thus, the method combines the advantage of automation with the flexibility of a manual segmentation.

2. Methods

The goal of the method presented is to transfer the contours of the object of interest from a given segmented grey value volume (atlas) to the patient data.

2.1. Automatic contour creation

The object contour is generated automatically in four steps: registration, seed point transfer, contour creation and automatic correction. Afterwards, an interactive adjustment is possible to optimise the segmentation results.

In a first step, the data volumes are automatically matched by affine 3D registration methods [6] to ensure the correspondence of patient and atlas slices.

The following steps are done slice by slice.

Prominent atlas contour points are chosen to be transferred to the patient data. In our approach, these atlas seed points are automatically identified using the contour curvature [7]. The choice of the atlas seed points is crucial for the transfer to the corresponding patient slice and the automatic contour creation. Using atlas contour corners as seed points produces the best results during the transfer. Moreover, the abscission of structure parts is avoided using structure corners.

In the next step, the algorithm seeks patient seed points P_i that correspond to the given atlas seed points A_i . We define the points in a search area around an orthogonal projected point as candidates for the corresponding patient seed point P_i . The best candidate is identified using a similarity measure based on absolute grey value, gradient magnitude, gradient direction, and curvature distances, as well as the correlations of grey value areas for all candidates. The criteria are combined using rank sums. So a normalisation of the distances is not necessary.

The contour is created by connecting the transferred seed points P_i in the patient image. This connection is based on the calculation of cost optimal paths in a cost graph as seen in the live-wire segmentation method presented by Mortensen and Barret in 1996 [3]. The

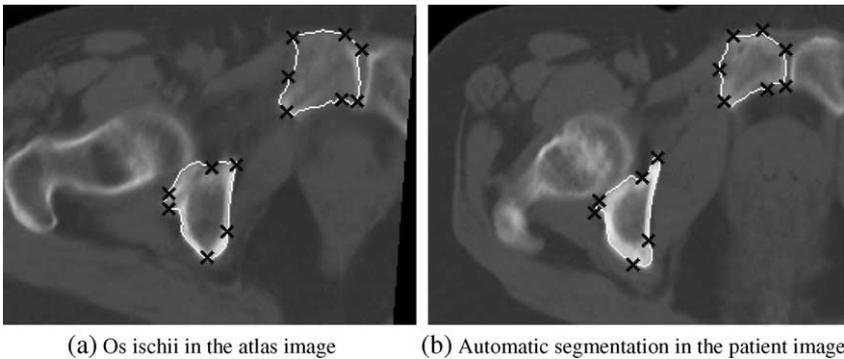


Fig. 1. Automatic segmentation of the os ischii by transferring the atlas contour.

vertices in this cost graph correspond to the pixels in the patient image. They are adjacent when the corresponding image pixels are neighbouring. The cost function is defined using gradient features. Graph edges that correspond to object contours obtain small costs and cost optimal paths align to the outline of the structure.

The patient seed points are connected by cost optimal paths forming a closed contour. We use Dijkstra's algorithm combined with Fibonacci heaps to compute the paths in an efficient way.

The cost training method [3] was adapted for using atlas information to afford an optimal positioning of the computed contour. For this purpose, the corresponding atlas contour segments are considered during the computation of the patient contour segments.

The cost function is modified so that edges with grey values, gradients, and curvature values similar to the values of the corresponding atlas contour segment obtain low costs.

Due to the differences between the image data sets incorrect seed point positions (outliers) and seed point sequence permutations occur. By comparing the features of corresponding contour sections, permutations can be corrected and outliers can be detected and removed. Fig. 1 shows the transfer of an atlas contour to the patient data in one slice.

2.2. Contour adjustment

After the automatic contour computation improperly positioned contour parts may be corrected interactively with few mouse clicks by the user. An intuitive user interface facilitates the insertion, removal and repositioning of patient seed points.

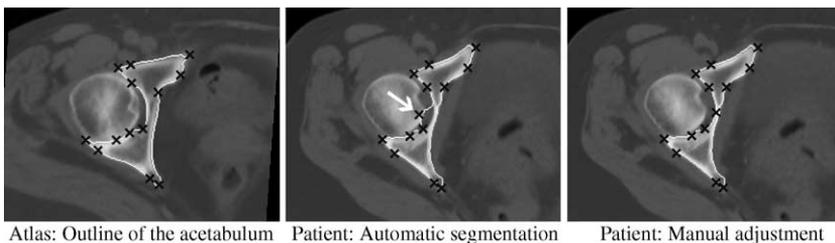


Fig. 2. Semiautomatic segmentation of the acetabulum. Moving one seed point corrects the contour.

Table 1
Time saving by automatic contour creation

Method	$t_{\text{interactive}}$ (s)				t_{Comp} (s)	t_{total} (s)
	B_1	B_2	B_3	mean		
Manual	2360	1920	859	1713	120	1950
Automatic	0	0	0	0	614	614
Automatic with adjustment	1107	840	576	841	614	1454

$t_{\text{interactive}}$: interaction time of three users and mean value. t_{Comp} : computation time for preprocessing and automatic contour creation.

Redundant seed points are automatically removed to avoid unnecessary interaction. Because of the efficient computation of new cost optimal paths the adjustment can be done in real time. Fig. 2 shows how an automatically created contour can be corrected by moving one seed point.

3. Results

The method presented has been evaluated using the segmentation of anatomical hip structures, which are needed during the 3D operation planning for bone tumour patients [1]. Three users with different segmentation experience applied the segmentation tool developed. The CT data sets consisted of 56 slices with a slice thickness of 4 mm and a pixel size of 0.71 mm×0.71 mm. We compared the manually created normal live-wire segmentations with the automatic created contours with and without interactive correction.

The manual segmentations were done in 1713 s mean interaction time. The verification and correction of the automatically created segmentations took a mean of 841 s interaction time which is 51% less than the manual segmentation time (Table 1).

The segmentation quality has been evaluated using the contour distances and the proportions R^+ and R^- (Table 2). The inter-observer variability of the manual segmentation averages a contour distance of 0.31 pixels. The distance between automatic and manual segmentations averages 0.71 pixels. The interactive adjustment lowered these values to 0.31 pixels contour distance. Hence, the differences between the manual and the interactively adjusted segmentation were in the range of the inter-observer variability. The maximum contour distances of up to 20 pixels were caused by remaining outliers and could easily be corrected manually. During the interactive adjustment, only 10% of the

Table 2
Segmentation error

Method	μ_{Dist}	R^+ (%)	R^- (%)
Inter-observer	0.31 px (0.22 mm)	98.3	99.9
Automatic to manual	0.73 px (0.52 mm)	95.9	99.9
Man. adjusted to manual	0.31 px (0.22 mm)	98.3	99.9

μ_{Dist} : Mean contour distance, R^+ : percentage of correct object-pixels to the total number of object-pixels, R^- : percentage of correct non-object-pixels analogously.

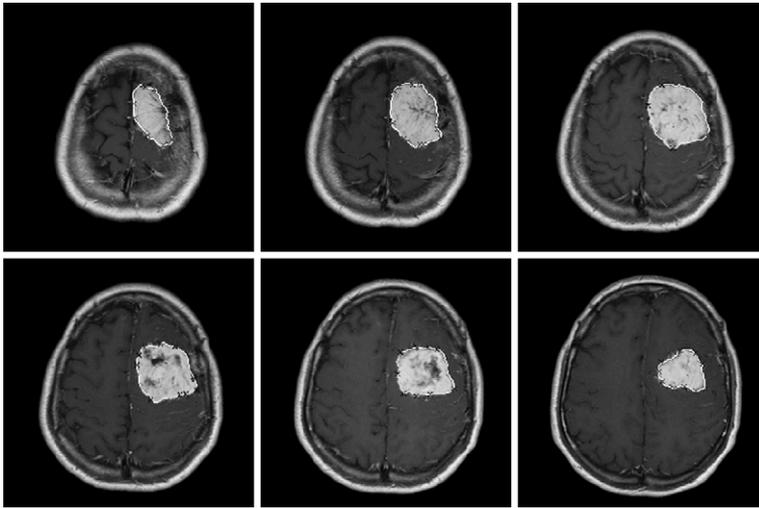


Fig. 3. Segmentation of a brain tumor. The manually created outline of the third slice has been transferred iteratively to the other slices.

automatic created seed points had to be corrected. The incorrect seed points were located in 26 of 56 slices.

4. Conclusion

We developed a robust and efficient method that transfers atlas contours to patient data sets.

The contours of anatomical structures are created automatically and the software provides an intuitive adjustment interface that facilitates the full flexibility of manual contouring methods.

The results showed that the tool simplifies the segmentation of anatomical hip structures because 51% of interaction time could be saved while the segmentation quality is similar to the quality of manually created segmentations.

Furthermore, the method can be applied to other medical problems, e.g., the contour transfer method has been adapted to the segmentation of pathological structures. In this adaptation, a manually created initial contour is transferred iteratively to the neighbored slices. This method shows a remarkable advantage in interaction time compared to manual methods during the segmentation of brain tumours in three-dimensional MR data sets (Fig. 3).

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