Automatic Needle Segmentation in 3D Ultrasound Data using a Hough Transform Approach

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Abstract. Segmentation in ultrasound data is a very challenging field of research in medical image processing. This article presents a method for automatic segmentation of biopsy needles and straight objects in noisy 3D image data. It uses a Hough-based segmentation approach, which has been exemplary adapted for the application on prostate biopsy data. An evaluation was performed on *in-vivo* 3D US data and shows promising results. Angular segmentation accuracy was evaluated with a mean of 2.1 degrees, which is comparable to human observers.

1 Introduction

Automatic segmentation of instruments in ultrasound (US) is a prerequisite for advancements in various diagnostic and therapeutic procedures. In this contribution, a novel method to segment needles in 3D US by means of Hough Transformation is presented. The algorithm detects straight objects in 3D images of bad quality; i.e. speckle noise bad contrast or blurry edges. Segmentation of surgical instruments on ultrasound images has to overcome certain difficulties, which are caused by ultrasound imaging itself. To those difficulties belong echo artifacts and the fact that one instrument may appear as a set of disconnected bright regions.

Exemplary, we adapted this method for the application of needle segmentation on prostate biopsy images. To test its feasibility it has been evaluated on in-vivo data sets of human prostate biopsies. The prostate biopsy is an intervention which could greatly benefit from automatic image processing. During the intervention a set of 12-16 tissue samples are taken from random positions. A major drawback is the lack of information about the exact origin. An estimation of this information based on 3D US images which are acquired during the intervention could lead to a remarkable improvement in the quality of diagnostic results. A precise determination of the tumour location could enable an accurate positioning of security margins during a resection planning and an improved conservation of surrounding healthy tissue.

Several methods have been invented to segment straight and bent needles in artificial and animal data in 2D and 3D ultrasound. Okazawa et al. [1] segmented curved needles in 2D based on a modified hough transformation technique. In 2003, Ding et al. [2] presented an early approach to 3D needle segmentation. For this purpose, binary projections of the region of interest (ROI) were made on orthogonal planes and the largest connected area was assumed as a projection of the needle. Barva et al. [3] extracted the line with the highest accumulated intensity (Parallel Integral Projection - PIP) by hierarchical mesh-grid search and classified it as the needle.

In contrast to previously presented work, we substituted iterative search methods for the generation of a global feature map with a subsequent analysis. This design concept has an increased robustness and delivers more reproducible results. Additionally, there is no risk of getting a local attractor as a result. A desirable side effect of this method is a predictable computation time. The accuracy of the analysis is flexibly scalable according to the demands of a specific task and available hardware. These key features motivate an evaluation on in-vivo data, which has -to our knowledge- not been done in previous work dealing with 3D US.

2 Methods

2.1 Automatic segmentation with Hough 3D

The basic idea of the algorithm is to find the brightest line in an image and to classify it as the needle axis. That key feature is equivalent to the highest integrated pixel value. Barva et al. [3] also used it in their PIP method and proved it to be a very robust feature. Such an approach implies that in a bent needle the longest straight part is detected and the rest neglected. However, to avoid difficulties of convergence a global approach was preferred to an iterative proceeding. Hence, the global maximum of the classification feature is robustly found and there is no risk of getting stuck at a local maximum.

In a first step, a thresholding is applied to reduce computation time. Whereas the overall brightness greatly differs among the images, a dynamic thresholding method has been used as a pre-filter. The threshold is chosen in a way that the darkest 90 % of the pixels are disregarded. This stage of preprocessing may be adjusted freely according to the actual field of application.

A second step is the generation of the so-called parameter space. To help understanding the structure of the parameter space, the mapping from source image to parameter space will be briefly introduced in the following paragraph. The aim is to find a parametrisation of lines, which is unambiguous and preserves angles. Subsequently, a bijective mapping from straight lines to the according parameters is derived. Finally, the set of coordinates which corresponds to a coordinate in the source picture is determined.

First, the set of lines running through a point in the source image has to be assigned to it. Basically, a line g in $\mathbb{R}^3$, which contains a point $\mathbf{p}$ in the source

image, can be described as follows:

$$g : \mathbf{a} = \mathbf{p} + t{\cdot}\mathbf{v};\ \mathbf{a}, \mathbf{p}, \mathbf{v} \in \mathbb{R}^{\mathbf{3}};\ t \in \mathbb{R} \tag{1}$$

The direction of the line is $\mathbf{v}$ and t is a free parameter. A suitable and unambiguous parametrisation for the direction $\mathbf{v}$ is shown in eq. 2. An angular parametrisation has been chosen, in order to facilitate an implementation which provides isotropic angular resolution:

$$\mathbf{v} = \mathbf{e}_r = \begin{pmatrix} \sin\Theta\cos\Phi \\ \sin\Theta\sin\Phi \\ \cos\Theta \end{pmatrix};\ \Theta \in [0, \pi];\ \Phi \in [0, \pi] \tag{2}$$

With the chosen ranges for Θ and Φ half of the sphere (S^2) is covered. Consequently, anti parallel lines are not distinguished from each other. As it can be seen in eq. 1 and eq. 2, a line is existing for each combination of point $\mathbf{p}$ and tuple (Θ, Φ). $\mathbf{p}$ is the remaining degree of freedom in eq. 1 to completely describe the line. Since we are looking for parameters, which are unambiguous, $\mathbf{p}$ is not suitable. By examination of two points $\mathbf{p}_1$ and $\mathbf{p}_2$, there is always a tuple (Θ_0, Φ_0) with:

$$\mathbf{p}_1 - \mathbf{p}_2 = t \cdot \mathbf{v}_0;\ \mathbf{v}_0 = \mathbf{e}_r(\Theta_0, \Phi_0) \tag{3}$$

For (Θ_0, Φ_0), the line containing $\mathbf{p}_1$ and $\mathbf{p}_2$ is identical. In other words, the line, which contains both points may be described by the two angles Θ_0 and Φ_0, and *one* point on the line. From now on, this point is chosen as the intersection with the orthogonal plane containing the origin. Orthonormal vectors build up the correspondent plane for the vector $\mathbf{e}_r$; we choose

$$\mathbf{e}_\Theta = \begin{pmatrix} \cos\Theta\cos\Phi \\ \cos\Theta\sin\Phi \\ -\sin\Theta \end{pmatrix};\ \mathbf{e}_\Phi = \begin{pmatrix} -\sin\Phi \\ \cos\Phi \\ 0 \end{pmatrix}; \tag{4}$$

The plane p

$$p : \mathbf{a} = s \cdot \mathbf{e}_\Theta + t \cdot \mathbf{e}_\Phi; s, t \in \mathbb{R} \tag{5}$$

describes a unique set of points for each tuple (Θ, Φ) in the given range. It does not contain any line g with the corresponding direction vector $\mathbf{e}_r$, because $\mathbf{e}_r$ is perpendicular on p. Thus, the interception of line g with plane p is suitable for an explicit description of this line. The interception may be identified by the two parameters s and t from eq. 5. Due to basic geometric considerations, the tuple (s, t) may be determined as:

$$s = \mathbf{p} \cdot \mathbf{e}_\Theta;\ t = \mathbf{p} \cdot \mathbf{e}_\Phi \tag{6}$$

Whereas $\mathbf{p}$ may be *any* point on the line. With the preceding considerations we get a mapping C, which fulfils all desired requirements.

$$C : \mathbb{R}^3 \rightarrow \mathcal{P}(S^2 \times \mathbb{R}^2) \tag{7}$$

Table 1. Angle between estimated needle by the algorithm (alg) and the human observers (o1-o3) gold standard in degrees.

ds #	o1	o2	o3	alg	ds #	o1	o2	o3	alg
1	0.64	1.07	0.99	1.88	8	0.24	0.13	0.75	0.52
2	1.09	1.35	2.14	0.95	9	2.04	0.55	2.09	2.89
3	2.65	2.73	1.90	1.41	10	1.81	0.13	3.90	0.55
4	2.90	1.76	3.05	6.80	11	0.90	0.67	2.61	1.58
5	0.14	0.87	0.54	2.38	12	1.25	0.89	3.96	1.86
6	2.22	1.43	1.47	2.35	13	4.05	1.28	1.26	3.54
7	1.67	1.64	1.84	0.50	14	0.98	0.94	1.54	55.4

with

$$\mathbf{x} \mapsto \{(\Theta, \Phi, \mathbf{x} \cdot \mathbf{e}_\Theta, \mathbf{x} \cdot \mathbf{e}_\Phi) : \Theta \in [0, \pi];\ \Phi \in [0, \pi]\} \tag{8}$$

If $v(\mathbf{x}) \in \mathbb{R}$ is the pixel value at coordinate $\mathbf{x}$, the integrated pixel value of one line which is described by the tuple $(\Theta_0, \Phi_0, l_0, s_0)$ is

$$I = \int_{\text{image}} v(\mathbf{x}) \delta(l_0 - \mathbf{x} \cdot \mathbf{e}_{\Theta 0}) \cdot \delta(s_0 - \mathbf{x} \cdot \mathbf{e}_{\Phi 0}) d^3x \tag{9}$$

Since I are the values in parameter space -which are being mapped on the according coordinates- the maximum of I is equivalent to the brightest line in the source image. The global maximum in the parameter space is determined and the respective parameters are transformed back into image coordinates.

The implementation of the algorithm has been done in C++ with two open source libraries; the Insight Segmentation and Registration Toolkit (ITK), and the Medical Imaging Interaction Toolkit (MITK).

2.2 Evaluation

The proposed method has been tested in fourteen in-vivo images, taken by a GE Voluson 730 US device. The size of the images is about 35 x 50 x 50 mm. The resolution is isotropic and about 4 pixels/mm. As gold standard for the evaluation, a manual segmentation of three experienced human observers has been applied. Evaluation parameter is the angle between the direction of one defined needle and the mean of the three manually segmented directions. It was calculated for each manual segmentation and compared with the automatically processed results. To reduce computation time and increase robustness, a ROI with size of 30 percent of the image volume was determined based on the known spatial relations of ultrasound transducer and biopsy needle.

3 Results

The results of the accuracy evaluation are shown in table 1. To quantify the deviation of the manual segmentation of all observers, the angle between the

determined needle direction of a single observer and the mean direction was calculated. Values vary from 0.53 to 4.05 degrees.

The same parameter was calculated for the results of the automatic detection. Apart from data set 4 and 14, the values for the detection precision are of the same magnitude as the results for human observers.

The computation time varies from 45 - 200 s on a 2,4 GHz Quad Core CPU with 4GB memory. During the segmentation, about 500 MB memory were allocated. Although the algorithm is basically suitable for multithreading, the actual implementation does not feature parallel computing.

4 Discussion

To face the ambitious challenge of the automatic segmentation task on noisy 3D US data, a generic algorithm for the segmentation of straight objects in images has been implemented and adjusted for the specific purpose of prostate biopsy images. The results show a robust needle detection with a tolerable error of 2.1 ° on 3D *in-vivo* ultrasound images. Thus, the presented method emerged to be comparably accurate to the evaluated interobserver variability.

In earlier work, Heimann et al. [4] present an automated approach to segment the prostate in 3D US data by means of a statistical shape model. Combined with this method, the presented algorithm can, for instance, be the basis of a powerful support in prostate cancer diagnosis. Since there are several approaches for the localisation of the tip -Barva et al. [3] provides a promising method to deal with that issue-, a fully automated reconstruction of the extraction spot in the prostate using a single 3D US data set is feasible.

The comparison between human observer and algorithm accuracy suggests this method to be a promising approach.

The usability of the presented algorithm is not limited to biopsies or even ultrasound as imaging modality. There might be various other beneficial fields of application, such as radio frequency ablations.

Future work will address improvements in robustness and the reduction of memory demands. For this purpose, it is planned to divide the image into disjunct regions.

References

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