

Automatic vessel tracking in abdominal ultrasound sequences

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Abstract

The observation of abdominal organs movement during respiration is important for diagnostic and high precision medical procedures. Analysis of this dynamic behavior are frequently performed by ultrasound, due its low risk to the patient and image generation in real time. We propose an automatic vessel tracking method in abdominal ultrasound sequences during normal respiration. The method is based on image processing techniques and data modeling to estimate the parameters of a periodic function describing the vessel motion. Sequences of the CLUST 2015 dataset of 2D+t real ultrasound images are employed for experimentation and validation.

1 Introduction

The internal motion of abdomen and thorax is an important parameter to diagnosis and medical procedures as puncture and radiotherapy. Magnetic resonance imaging and ultrasound have been employed to observe these movements in organs as liver and heart. However, a quantitative description of this dynamic behavior is still an open problem [1, 2, 3]. The boundaries identification of the anatomical structures is one of the main obstacles because these are blurred due motion.

We propose to estimate the parameters of a periodic function to fit it to the trajectory of a vessel in ultrasound sequences during normal respiration. This document is organized as follow: in section 2 the methodology is described, the preliminary results in the section 3, and finally the discussion in the section 4.

2 Methodology

Assuming that respiration motion has a periodic behavior and without disturbances, it can be expressed as a Fourier series, such that

$$F(t) = \frac{A_0}{2} + \sum_{n=1}^N A_n \sin(2\pi f n t + \phi_n) \quad (1)$$

where f is the respiratory frequency (Hz), t the time, A_n is the amplitude of the n harmonic, and A_0 and ϕ_n are translations in amplitude and

time of the signal, respectively. With this hypothesis, the estimate of the first harmonic of $F(t)$ is performed. This describes the position of the blood vessel P_v , which moves as a result of breathing in image sequences ultrasound abdomen, as illustrated in Figure 1. The $P_v(x, y)$ components,

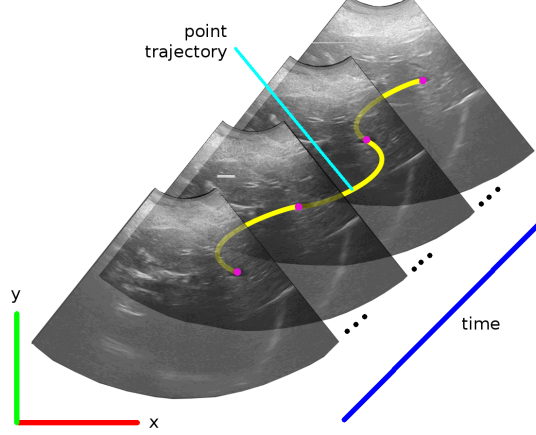


Figure 1: 2D abdominal ultrasound sequence. During the acquisition, the position of the probe is fixed and the patient breathing is normal. In this picture is depicted an approximation of the vessel motion vs time.

can be expressed as

$$\begin{aligned} x(k) &= a_0 + a_1 \sin(a_2 k + a_3) \\ y(k) &= b_0 + b_1 \sin(b_2 k + b_3), \end{aligned} \quad (2)$$

where k is the number of the image in the sequence. The parameters of $x(k)$ and $y(k)$ are estimated by means of an optimization process, where the input data are the position of the vessel obtained with image processing techniques, as illustrated in Figure 2. The first step consisted in

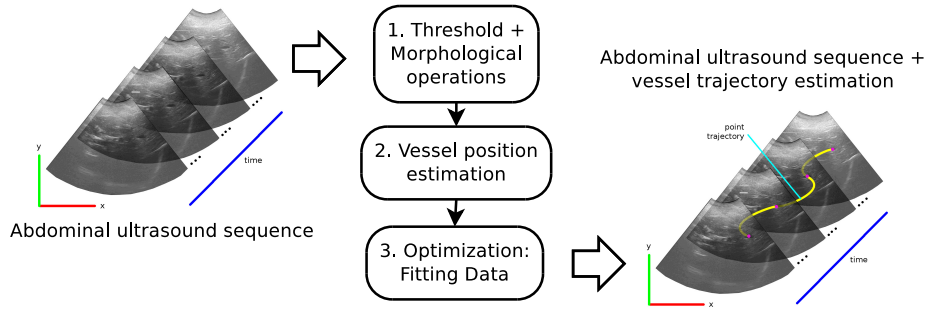


Figure 2: Diagram of the proposed method.

binarizing the images, to differentiate the inside from the outside of the vessel. This was done by applying thresholding on all images. The threshold was defined by an analysis of the first image histogram. Afterward, an opening morphological operation (first erosion, then dilation) was applied to remove noise and soften regions contours.

The second step estimates the central position of the vessel in the binary images, from a known point of the first image (annotation expert). This starting point is used as a seed to extract a region of pixels interconnected with the same intensity. The center of this region is the center of its bounding box of minimum area (oriented with the object). This center represents the position of the vessel. To find the center in the next image the process is repeated. In this case, the seed point is sought in the new image within the previous seed and center coordinates. If the seed point fails to find a vessel internal region, the center of that image is defined as the center of the previous image, until a new seed point will be found. An additional restriction is established. The center estimation is performed only when the size of the region is similar or less than the size of the region in the first image.

In the optimization process, the centers found in the previous stage are fitted to sinusoidal functions with a variable baseline, both for $x(k)$ and for $y(k)$. The process is performed by sectors due to the variation of the baseline of the signal. In each sector, the baseline is approximated a straight line using least squares [4]. This baseline is subtracted from the data to estimate the parameters of the sinusoidal signal by the Markov chain Monte Carlo (MCMC) [4]. Finally, the baseline is added to the sine signal, to find the estimate of the position of the vessel in the sequence.

3 Results

Preliminary experimentation was performed using the training sequence CIL-01 of the dataset built for the "Challenge on Liver Ultrasound Tracking - CLUST" MICCAI developed during 2014 and 2015 [5]. This image sequence has the following characteristics: image size = $480 \times 640 \text{ pixel}^2$, Image resolution = 0.3 mm/pixel , number of frames = 1342, Image rate = 22 Hz , number of annotations = 2, number of annotated frames = 144. Annotations of the first image in the sequence are presented in Figure 3. For the first stage, the threshold value was experimentally defined as the

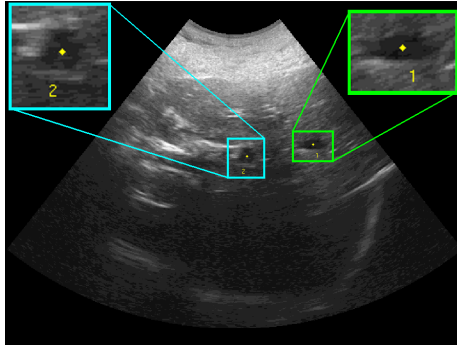


Figure 3: First images in the CIL-01 sequence. The position of the each two vessels were annotated by experts in several frames.

intensity value that separates the 70% of lower intensity pixels with 30% of the most intense. For the morphological opening operation, the structuring element was established as $3 \times 3 \text{ pixel}^2$. In the second stage, it was observed that the estimate of the centers has less noise if the region size

is less than or equal to 1.5 the size of the region extracted from the first image. Finally, for the optimization, the input data were evaluated every 15s (3 groups of 330 samples and one of 352). Results of the estimation of the Centers for vessels 1 and 2, before and after optimization, are presented in Figures 4 y 5, respectively. Quantitative measures of comparison between reference annotations with estimates of the method before and after optimization for the vessels 1 and 2, are presented in Tables 1 y 2, respectively.

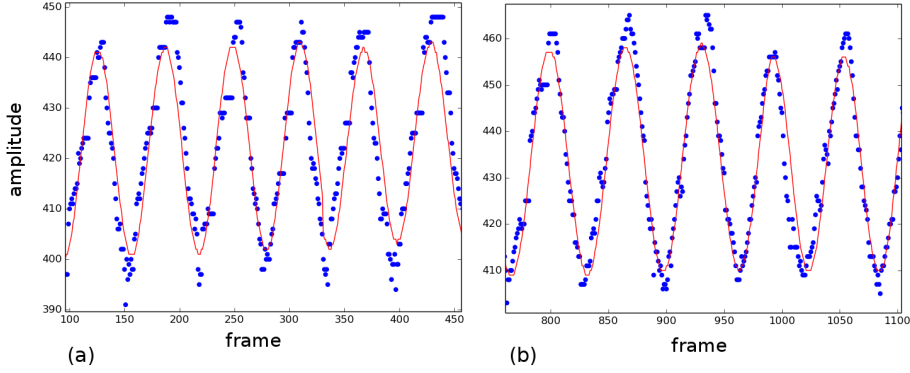


Figure 4: Tracking of $x(k)$ of vessel 1, before (blue) and after (red) the optimization process, where (a) first part of the sequence, and (b) last part of the sequence.

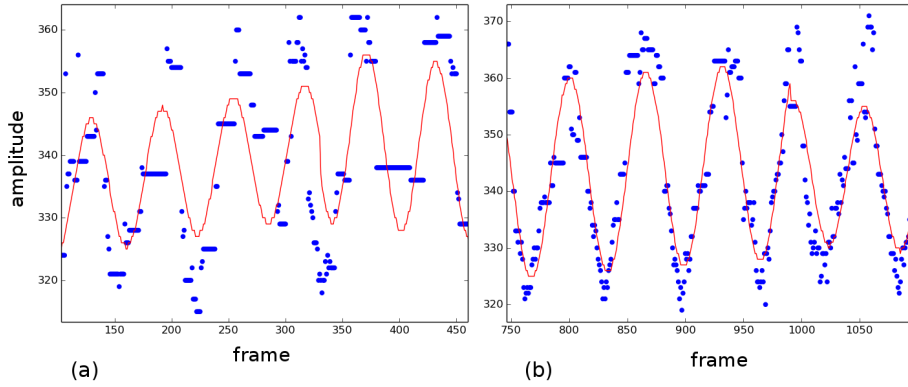


Figure 5: Tracking of $x(k)$ of vessel 2, before (blue) and after (red) the optimization process, where (a) first part of the sequence, and (b) last part of the sequence.

4 Discussion

The strategy proposal seeks a first approximation of the trajectory of a point due to respiration in abdominal ultrasound sequences. It is assumed that the movement is periodic and undisturbed. The proposed method

Table 1: Tracking results for vessel 1.

| Ground truth CIL-01_1.txt | Tracking error [mm] | | |
|------------------------------|---------------------|--------------------|-----------------|
| | mean | standard deviation | 95th percentile |
| Before optimization | 1.049 | 0.651 | 2.616 |
| After optimization | 1.579 | 0.994 | 3.185 |

Table 2: Tracking results for vessel 2.

| Ground truth CIL-01_2.txt | Tracking error [mm] | | |
|------------------------------|---------------------|--------------------|-----------------|
| | mean | standard deviation | 95th percentile |
| Before optimization | 1.956 | 1.731 | 5.778 |
| After optimization | 1.355 | 1.095 | 3.394 |

is automatic but it is not in real time. It does not require training data. The required parameters depend on the information of the first image. Therefore, it is important the good quality of this image.

Although the evaluation is done with a single sequence, this consists of two cases , one easy (vessel 1) and one hard (vessel 2). For the easy case, the optimization is not necessary. While for the difficult one, the optimization improves the results. The optimization gives stabilization to the system.

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