Quantification of Blood Flow in Great Vessels from Cardiac Magnetic Resonance Imaging

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Abstract

This paper presents a new tool developed to quantify and characterize blood flow in great vessels. The aim is to quantify the flow during the cardiac cycle from sequences of Magnetic Resonance images of the vessel cross-section. The proposed method tracks the vessel contour to automatically quantify the maximum velocity and flow through the cardiac cycle and finally obtains the instantaneous stroke volume. The techniques proposed are based on active contours coupled with a motion estimation method. Results in ten different sequences from patients and healthy subjects have been obtained, showing values similar to other flow measurement techniques. A repeatability study was done to assess the robustness of the proposed tool.

1. Introduction

Fast magnetic resonance (MR) imaging is a powerful non-invasive technique that is gaining increasing importance in the diagnosis of cardiovascular diseases. One of its possibilities is the use of Phase-Contrast cine imaging [1] that provides quantitative information of blood velocity: using the appropriate MR sequences, signal intensities provide a magnitude or anatomic image, while the phase information provides a velocity-encoded image. This is specially useful to study blood flow through heart valves and in great vessels like aorta and pulmonary arteries. Postprocessing of the velocity information, including the delineation of vessel edges to calculate their cross-sectional area, provides clinically useful parameters such as instantaneous flow, mean flow per cardiac cycle and cardiac output.

Although the main scanner manufacturers have postprocessing software packages to compute these parameters, these programs usually rely on a manual or semi-automatic delineation of the vessel edges [2]. The changes of position and shape of the great vessels make this edge detection very time-consuming and observer dependent.

The purpose of this work was to design a software tool to easily quantify blood flow in great vessels and derive specific parameters from Phase-Contrast MR sequences [3]. The proposed method processes the modulus image to obtain the vessel contour through the cardiac cycle. This contour is then exported to the phase image to obtain the velocity for every point within the vessel. Knowing the area of the cross-section, the mean flow and stroke volume through the vessel cross-section can be computed.

The cardiac output can be evaluated at different levels of the cardiac structure: aortic ring, mitral valve, pulmonary valve and tricuspid valve. The most reliable values are found in the aortic ring due to its circular shape and smallest deviation during systole. This has been our selected image plane.

During a cardiac cycle the position and shape of a vessel cross-section change due to the heart beating and pressure changes in the arteries and, in general, this change is relatively small in comparison to the movement of the cross-section [4]. This leads us to the idea of developing different algorithms so as to track movement and deformation of our contour.

2. Materials and Methods

The segmentation of the vessel cross-section during the cardiac cycle is based on active contour models [5] and includes an initial segmentation in the first image of the sequence, the propagation of this segmentation to the next image (motion detection) and a fine adjustment in this second image (shape detection). The procedure is repeated until the whole sequence is processed. Then flow parameters are computed.

2.1. Initialization.

The approximate central point of the vessel of interest is manually located by the user in a selected frame. An adaptive region growing algorithm allows to obtain a first contour initialization taking this central point as main seed. The criterion for including pixels in the final region uses the standard deviation of the pixel values included in a small region around the given central point.

The first contour determined with this method will then be exported to the next image and considered as the initial contour for the active contour algorithm. This active contour will be moved and deformed following

the maximum image gradient for every image in the sequence, in two different steps: motion detection and shape detection as described in the next paragraphs.

2.2. Motion detection.

This first step tracks the motion of the vessel cross-section without deforming the contour, performing an exhaustive search of the maximum gradient. We calculate several contours around the initial one and select the one with the maximum gradient. Studying in different sequences the maximum shift of the contour (due to the heart beating) between consecutive images, we have limited its movement to two pixels in any direction. We can apply this exhaustive search due to the small moving field of the contour; otherwise it would require a huge computational load. The graphical representation of this concept can be seen in Figure 1.

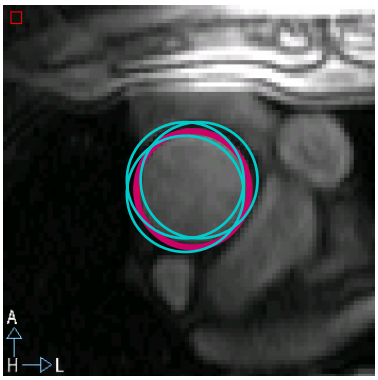

Figure 1. Motion detection step. Initial (*red*) and calculated contours following the image gradient (*blue*).

2.3. Shape detection.

Once we have obtained a contour that is close to the real edges of the vessel, the second step is to adjust it to the new vessel cross-section shape. Active contour models (or *snakes*) are proposed for this task [6]. Assuming that we have already reached a good approximation to the final contour, we just need a small deformation of the snake. Snake parameters have been carefully and experimentally adjusted [7].

By using the 'a priori' knowledge of the circular shape of our contours, we have introduced a slight modification in the iterative process, considering only the movements in the radial direction. This provides us with a constrained circular model that iterates in a quicker and easier way.

2.4. Parameter computation

Once the segmentation is completed through the whole sequence the software program is able to compute the most relevant parameters.

The segmentation procedure defines, for each modulus image in the sequence, the contour of the vessel, usually the aorta. The contour in every image is then exported to the phase sequence. These segmented contours allow to calculate the cross section area and the maximum velocity in every frame. The blood flow through the cross-section is computed by multiplying these two values. After the whole sequence is processed, the flow curve is obtained. The stroke volume is the integration through the cardiac cycle of instantaneous flow curve, being the cardiac output the stroke volume multiplied by the heart rate.

Figure 2 shows the user interface of the software developed. There are two different windows for the anatomic and phase contrast MR images and different options to initialize and start the segmentation procedure. Figure 3 shows a cross section of the aorta segmented and the flow curve obtained from one of the analyzed sequences.

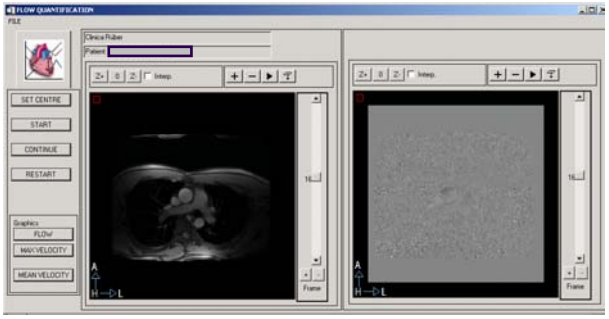

Figure 2. Application interface

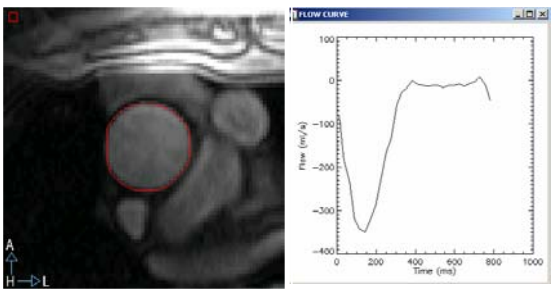

Figure 3. Segmentation of the aorta cross-section (*left)* and the flow curve through the cardiac cycle (*right*)

3. Results

The proposed method was tested in sequences of images of the aorta from 10 patients with different cardiac pathologies. Images were acquired with a GE 1.5 T Signa with a Fast Cine sequence (GE Medical Systems, Milwaukee, WI, USA). Both magnitude (anatomic) and phase contrast (velocity) images were acquired. Cardiac output, mean velocity and maximum velocity curves were computed and compared with the

results provided by a commercial software with manual segmentation. Results with both methods were very similar, with negligible differences.

The software developed here gives the user the possibility of visualizing the selected sequence, initialize the algorithm in any desired frame and perform the segmentation in a fully automatic way (after selecting an initial point inside the vessel). Figures 4 and 5 show different frames of an analyzed sequence, the corresponding curves obtained (maximum velocity, mean velocity and flow curve) and extracted parameters (stroke volume and cardiac output).

A repeatability study was also performed to verify the robustness and repeatability of the methodology. Two different observers quantified the 10 sequences twice. Interobserver and intraobserver variabilities in the computation of the stroke volume were smaller than 0.2 %.

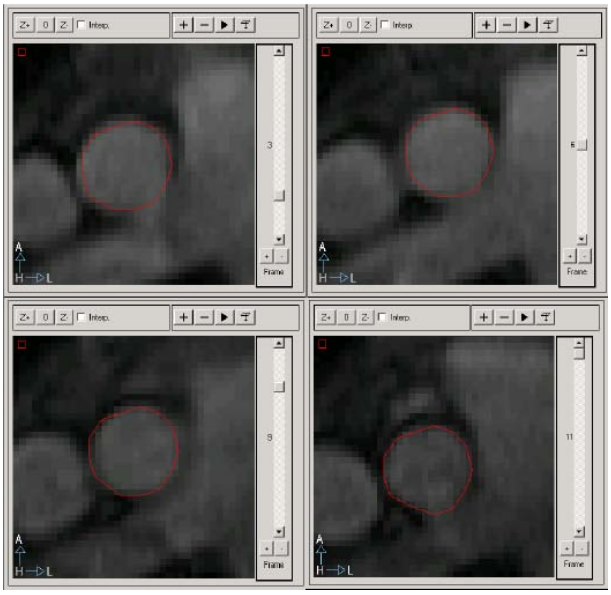

Figure 4. Four frames of a processed sequence.

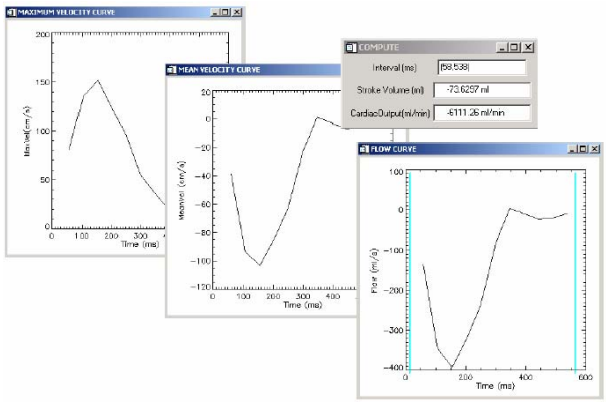

Figure 5. Graphics and results

4. Conclusions

The developed tool provides a solution to the problem of blood flow quantification in MR images. The software tool is automatic except for the initial location of the central point in the blood vessel section. It is easy to use and accurate enough for clinical practice. Therefore, it fulfills the initial requirements, covering the whole process from the automatic tracking of great vessels contours until the calculation of the relevant parameters strongly related to cardiac diagnosis, such as the stroke volume or the cardiac output.

5. Acknowledgments

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6. References

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