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A computational model-based approach for atlas construction of aortic Doppler velocity profiles for segmentation purposes

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ABSTRACT

Echocardiography is the leading imaging modality for cardiac disorders in clinical practice. During an echocardiographic exam, geometry and blood flow are quantified in order to assess cardiac function. In clinical practice, these image-based measurements are currently performed manually. An automated approach is needed if more advanced analysis is desired.

In this article, we propose a new hybrid framework for the construction of a disease-specific atlas to improve Doppler aortic outflow velocity profile segmentation. The proposed method is based on combining realistic computational simulations of the cardiovascular system for common cardiac conditions (using CircAdapt) with a validated image-based atlas construction method. The coupling is realized via model-based generation of echocardiographic images of virtual populations with a statistically approved parameter variation. We created virtual populations of 100 healthy individuals and 100 patients with aortic stenosis, synthesized their aortic Doppler velocity images and constructed the corresponding atlases. We validated atlases' performances by comparing their segmentation of real clinical images with the manually segmented ground truth. The experimental results show that the segmentation accuracy obtained using the proposed atlases is comparable to the accuracy obtained using classical clinical image-based atlases. Moreover, this framework eliminates the time-consuming acquisition of a sufficient number of representative images in clinical practice, offering a substantial time efficiency and flexibility in creating a disease specific atlas and ensuring an observer-independent automated segmentation. The proposed approach can easily be extended towards the creation of atlases for segmenting any Doppler trace in the cardiovascular circulation in a specific disease.

1. Introduction

Clinical imaging of cardiovascular structure and function often results in images that need further analysis for an accurate diagnosis. This analysis can depend on the underlying disease process. For example, in aortic stenosis, the orifice of the aortic valve is narrowed, causing partial obstruction of the blood flow from the heart into the aorta and onward to the rest of the body. If left untreated, it can lead to heart failure. Doppler echocardiography of the blood flow through the valve is the standard procedure for evaluating suspected valvular heart disease in a patient. Specifically, in continuous-wave (CW) Doppler mode, all velocity values along a scanline are detected simultaneously, forming a velocity spectrum in time. Since the fastest blood flow is expected within the valve, diagnostic information is encoded in the spectral envelope. Diagnosis is based on valuation of the maximum blood flow velocities (amplitude of the envelope) and the transaortic pressure gradient (area under the curve) [3]. Additional computational analysis of transaortic outflow profile attributes may infer latent, but discriminative information about the valvular condition and its influence on the left ventricular function [6]. The extraction of the spectral trace envelope for a detailed analysis represents an image segmentation problem.

While manual evaluation of the spectral amplitude is common in clinical practice, it is characterized by high inter- and intra-observer variability of both the velocity value [37] and the severity

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of heart valve disease [23]. A precise manual delineation would enable a more detailed analysis of the aortic outflow during specific phases of a cardiac cycle. However, it is time-consuming and thus only performed roughly in order to improve patient throughput in echocardiographic laboratories. Automated segmentation is a solution that can overcome these disadvantages – it is faster, accurate, consistent and reproducible, thus facilitating and supporting clinical image interpretation and immediate patient evaluation. Also, it allows for a computational analysis of the blood flow profile features, which is especially useful for resolving possible ambiguities in diagnosing conditions with similar clinical pictures.

Contemporary image segmentation approaches are often based on the use of representative atlases created from real-world images and their labellings [15]. However, for segmentation of images with disease-specific alterations captured at hand, their performance is highly dependent on the quantity and the representativeness of the acquired images and the preciseness of the performed labellings. In other words, it relies on availability and variability of patients and time costly manual delineation of all acquired images. To overcome this, we offer an alternative where the images can be computationally simulated for the condition of interest.

In this article, we describe the novel approach towards atlas construction for automated atlas-based segmentation of aortic outflow Doppler profiles, in order to support evidence-based diagnosis of cardiac diseases with high accuracy. Instead of working with acquired patient images, we propose to create the data set independently by using a computational model capturing the relevant pathophysiological changes. In this study we use the CircAdapt model [1,28], validated for different cardiovascular conditions, to simulate rich populations of healthy individuals and patients with (different degrees of) aortic stenosis. Inter-individual diversity is achieved by varying the model parameters over an expected range of values for each population. The model simulation results can be transformed into virtual echocardiographic images using a modality-specific imaging simulator [38], which further serve as input for anatomical atlas construction. The more specific an atlas is to the structure that is being segmented, the registration algorithm will converge faster to a more accurate solution. Even though a Doppler valve velocity profile appears to be a simple structure, for different valves, different valve conditions and different conditions severities, these profiles can have quite different shapes. This is the reason for introducing *disease-specific atlases* into the process of automatic image segmentation. This coupled computational modelling and velocity profile atlas construction is validated for atlas-based segmentation in a specific clinical population. The pipeline of the coupling is visualized in Fig. 1, together with all steps conducted in the experiment.

Since the proposed method unites different research areas, a brief overview of each of them is given below.

1.1. Atlas-based segmentation of medical images

In the past five decades, the automatic analysis of anatomical structures in medical images has become a valuable tool for clinical practice. Amongst a variety of existing approaches [31,39], atlas-based segmentation has proven to be an efficient method, with the benefit of introducing *a priori* knowledge into the process of segmentation. An anatomical atlas provides the “default” anatomical structure within the observed population, with a label for each of the structures. By propagating its segmentation and labels to a new image, the same structures in the new image can be identified.

The majority of atlases for segmentation have been derived from a set of representative clinical images. Simple techniques for atlas construction employ random selection within the image data set [45] or taking the average intensity (mean or median), usually coupled with the average-shape [12,32]. More complex methods utilize probabilistic calculus [13,22], or a multi-atlas approach merging several atlas propagations into the resulting image [46]. The use of imaging modality simulators has been proposed to create large sets of images that can capture the appearance of clinical images for a particular modality, given knowledge on the content shape variation [42,43]. In this paper, we extend this idea towards Doppler images and simulating both the content appearance in these images (using information on the imaging modality) as well as the content shape (using knowledge about physiological processes in cardiovascular system).

1.2. Segmentation of aortic Doppler velocity profiles

Even though quantification of blood flow velocity profiles is a frequent task in clinical practice, there has not been extensive research dealing with the problem of its automation. While the segmentation of velocity profiles reported by [4] is manual, they emphasize the need for automatic assessment for improved diagnosis or clinical research purposes. Automatic segmentations of similar Doppler traces in heart valves (other than aortic), based on a series of simple image processing operations, were described by [11,44]. Gaillard et al. [10] describe the aortic and mitral Doppler wave segmentation using a more advanced active contour method, initialized with a shape of the centers of divergence of the gradient vector flow field, reporting sensitivity of the method to the image contrast. Motivated by the clinicians’ need for not only fast and automatic delineation but also for automatic extraction of condition-descriptive mathematically-derived features from the aortic valve velocity profile shape, Kalinić et al. [16–18] applied and developed several methods for atlas-based segmentation of Doppler velocity images. Some of those are adapted and incorporated here as a part of our novel hybrid method.

1.3. Computational modelling of the cardiovascular system

The human cardiovascular system is a closed multiphysics system that can be described with mathematical equations. Several approaches have resulted in a large number of available lumped- and distributed-parameter computational models [36,40], and the two coupled [26]. Lumped-parameter or 0-D models simplify the anatomy by assuming a uniform distribution of fundamental variables within the compartments, but they also simplify the calculus and allow for larger (or even closed-loop) circulation systems to be modelled. Regardless of their simplification, these models are accurate enough to capture various properties of cardiovascular physiology. They have been used as an educational tool for understanding cardiovascular (patho)physiology and as a research tool in examining the effectiveness of therapy (pacemakers, valve replacements, pharmaceutical products, etc.) [8,5,9,19,35]. Coupling these models with clinical measurements represents the state-of-the-art in biomedical engineering, with a great perspective of integrating them into clinical practice.

Often, the parameters of the computational cardiac models (such as radiuses, lengths, walls thicknesses, etc.), are set for an average healthy individual or even deduced from in vitro experiments on different species. Since each person is characterized with their own set of parameter values (also depending on their health state), such generalization has inherent limitations and might not be representative for a population.

The model we used in our study is a MATLAB implementation [34] of CircAdapt, by T. Arts [1] and J. Lumens [28]. It is a lumped-parameter computer model that enables beat-to-beat simulation of the heart and circulatory dynamics. In most pathologies, a single physiological defect invokes a series of adaptive mechanisms in the rest of the system, in order to compensate for the reduced functionality of the defective part. In computer simulations, it means