A BIOPHYSICALLY DETAILED COMPUTATIONAL MODEL OF THE FOUR CHAMBER HUMAN HEART ELECTROMECHANICS

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Introduction

Numerical simulations of the cardiac function are progressively becoming a powerful tool to better understand the heart function [1] and to support clinical decision-making [2]. Even though some area of heart modeling reached a certain level of maturity, whole heart models are emerging only in the last few years. Most of these works are focused on the ventricles almost neglecting the full atrial function. In this work we present a biophysically detailed fully coupled multiscale mathematical model of cardiac electromechanics (EM) of the whole human heart that accurately consider both atrial and ventricular contraction [3].

Models and Methods

Our whole heart model provides a 3D description of cardiac EM in all the four chambers and a 0D representation of the complete circulatory system. The 3D EM part includes: a novel anatomically-accurate rule-based method to properly represent the whole heart fiber architecture [4]; the cardiac electrophysiology, described by means of the monodomain equation with specific human ionic models; the mechanical activation, based on a sophisticated microscale active force generation model [5]; the myocardial tissue mechanic adopting an orthotropic active stress formulation with specific constitutive laws and model parameter for each cardiac region. The 3D EM is strongly coupled with a 0D closed-loop lamped parameters model of the entire cardiovascular network [6]. The coupling between the 0D-fluid and 3D-EM models is achieved by means of volume-consistency coupling conditions [6,7].

The numerical approximation of the whole heart model comprises: Finite Element (FE) Method and tetrahedral mesh, for the space discretization, and finite difference schemes, for the time discretization. The Segregated-Intergrid-Staggered numerical scheme is adopted: the models, contributing to both the cardiac EM and the blood circulation, are solved sequentially in a segregated manner using different resolutions in space and time [7]. Moreover, we employ recently developed stabilization terms, related to the circulation and the fibers-stretchrate feedback, that are crucial to obtain a stable formulation in a four-chamber scenario [8].

All the mathematical models and numerical methods have been developed within life^x, an in-house FE library focused on large-scale cardiac applications in a High Performance Computing framework [9].

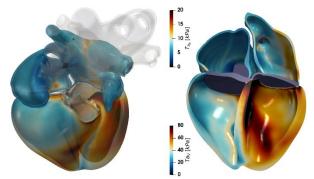


Figure 1: Deformed configuration of the heart during a cardiac cycle, colored with the active tension transients: external view (Left) and internal view (Right).

Results

The validity of the whole heart model was demonstrated through EM physiological simulations in an anatomically accurate geometry of the entire heart which includes the initial tracts of the cardiac arteries (see Figure 1). Relevant mechanical biomarkers, obtained by numerical simulations, are successfully compared with those provided by the data reported in the literature. We show that our results fall within the physiological reference ranges for all the four chambers. Furthermore, we highlight the importance of considering the atrial contraction and the fibers-stretchrate feedback terms, by comparing the results obtained with and without these features.

The proposed model provides an important contribution to the whole heart modeling and is a fundamental step towards the building block of physics based digital twin of the human heart.

References

- 1. A. Zingaro et al, arXiv.2301.02148, 2023.
- 2. M. Peirlinck et al, Biom. Model. Mech. 20:803-831, 2021.
- 3. M. Fedele et al, arXiv.2207.12460, 2022.
- 4. R. Piersanti et al, CMAME 373:113468, 2021.
- 5. F. Regazzoni et al, PLOS Comp. Bio. 16:e1008294, 2020.
- 6. F. Regazzoni et al, JCP 457:111083, 2022.
- 7. R. Piersanti et al, CMAME 391:114607, 2022.
- 8. F. Regazzoni et al, MOX report 17, 2022.
- 9. P.C. Africa, SoftX 20:101252, 2022.

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