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ScienceDirect
Comput. Methods Appl. Mech. Engrg. 317 (2017) 248–273
Computer methods in applied mechanics and engineering
www.elsevier.com/locate/cma

Isogeometric approximation of cardiac electrophysiology models on surfaces: An accuracy study with application to the human left atrium

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Received 14 August 2015; received in revised form 12 December 2016; accepted 13 December 2016
Available online 21 December 2016

Abstract

We consider Isogeometric Analysis in the framework of the Galerkin method for the spatial approximation of cardiac electrophysiology models defined on NURBS surfaces; specifically, we perform a numerical comparison between basis functions of degree $p \geq 1$ and globally C^k-continuous, with $k = 0$ or $p - 1$, to find the most accurate approximation of a propagating front with the minimal number of degrees of freedom. We show that B-spline basis functions of degree $p \geq 1$, which are C^{p-1}-continuous capture accurately the front velocity of the transmembrane potential even with moderately refined meshes; similarly, we show that, for accurate tracking of curved fronts, high-order continuous B-spline basis functions should be used. Finally, we apply Isogeometric Analysis to an idealized human left atrial geometry described by NURBS with physiologically sound fiber directions and anisotropic conductivity tensor to demonstrate that the numerical scheme retains its favorable approximation properties also in a more realistic setting.

Keywords: Isogeometric analysis; Cardiac electrophysiology; Surface PDEs; High-order approximation

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http://dx.doi.org/10.1016/j.cma.2016.12.022

1. Introduction

The heart is a muscular organ that contracts due to a signal originating from the heart's natural pacemaker, the sinoatrial node, that enters the cardiac muscle through the His–Purkinje system. Once the electrical signal has entered the muscle, it travels on the cell membrane of the cardiac muscle cells (cardiomyocytes) and passes from cell to cell through the gap junctions. Under the so-called action potential the individual cells rapidly become depolarized as positively charged ions enter the cell, triggering the contraction of the cellular contractile units called sarcomeres. After a period of contraction the positively charged ions are pumped out of the cells and they repolarize to their resting potential, allowing the muscle to relax and wait for the next signal to contract again after a refractory period during which no excitation can take place. For insight on the physiological processes of cardiac activation, we refer to [1].

Mathematical modeling of electrophysiology has shown great promise in being a viable diagnosis and prediction tool that in the future may be used to guide clinical decision making [2–5]. The standard mathematical model for cardiac electrophysiology is the bidomain model, where the tissue is conceptually divided into the intracellular and extracellular spaces. A formal homogenization procedure is followed to reduce away the microstructure of the cells and leads to a system of two reaction–diffusion equations for the intracellular and extracellular potentials. A further assumption of equal anisotropic conductivities in the intra- and extracellular compartments leads to a simplified formulation in terms of the transmembrane potential that is defined as the difference of the two potentials, called the monodomain equation, requiring only the solution of a single reaction–diffusion equation. For details on the derivation of the equations and further bibliography on their mathematical approximation, see [2,6].

The bi-/monodomain equation(s) need to be completed by a model describing the ionic currents passing through voltage-sensitive protein structures called ion channels that give rise to the action potential. Since any single cell has hundreds of channels that regulate the passage of numerous different molecular species through the cell membrane, a large number of different membrane models of varying complexity have been developed in order to describe the cellular excitation process at increasing levels of complexity. The end result is a (typically very stiff) system of ordinary differential equations that needs to be coupled to the bi-/monodomain equation(s). The derivation and analysis of the membrane models we consider in this paper can be found in [7].

At the mesoscopic level, cardiac tissue has a highly anisotropic structure. The cardiomyocytes are organized into laminar sheetlets, where the muscle cells are tubular in shape and roughly oriented in the same direction locally, called the (mean) fiber direction. Embedding the muscle cells is a gelatinous interstitial foam supported by a fibrous extracellular matrix formed mainly of collagen proteins that is synthesized by cardiac fibroblast cells. In the two atria (antechambers of the heart) the walls are considerably thinner than in the ventricles, yet exhibit similar anisotropic structure that is less well documented and understood due to its more complex nature [8]. In many cases the atrial walls are assumed to be thin enough such that a typical simplification is to consider them as surfaces (two-dimensional manifolds) and to formulate the bi-/monodomain equation(s) as surface PDEs. This is the approach taken in this work. For a recent review on the challenges of computational modeling of the atria necessary to capture other physiological aspects that are not treated in this work, we refer to [9].

1.1. Challenges in numerical approximation of electrophysiology

While the numerical discretization of the bi-/monodomain equation(s) and the related membrane model is straightforward, several numerical difficulties are known to exist. The solutions of these equations exhibit traveling pulse solutions with sharp wavefronts, especially for the more realistic stiff membrane models found in literature. Unless sufficiently accurate resolution of the traveling front is performed, inaccurate propagation velocity and/or dynamics are obtained and as a result incorrect predictions about the cardiac activation pattern are made. Since the front propagation velocity depends on its curvature, in the surface PDE formulation it is especially important to use a sufficiently smooth function space for the spatial approximation that minimizes the effect of the numerical grid.

Numerical approximation of the bi-/monodomain equation(s) still relies heavily on low-order spatial approximations combined with highly refined uniform meshes in order to capture correctly the front propagation. In full-heart human electrophysiology simulations such "overkill" meshes lead to systems of hundreds of millions of degrees of freedom. Approaches to improving the front approximation without excessive global refinement that have been suggested in the literature include modifying the quadrature rule for the ionic currents [10], applying mesh adaptivity near the front [11–13], and more recently using high-order Spectral Element discretizations [14]. In this work, we investigate an approach similar to the latter, except that we replace orthogonal polynomials with B-splines or Non-Uniform Rational B-splines (NURBS) [15] in the context of Isogeometric Analysis (IGA) in the framework of the Galerkin method [16,17].