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Numerical approximation of parametrized problems in cardiac electrophysiology by a local reduced basis method

Stefano Pagani*, Andrea Manzoni, Alfio Quarteroni

MOX, Dipartimento di Matematica, Politecnico di Milano, P.za Leonardo da Vinci 32, I-20133 Milano, Italy

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Abstract

The efficient solution of coupled PDEs/ODEs problems arising in cardiac electrophysiology is of key importance whenever interested to study the electrical behavior of the tissue for several instances of relevant physical and/or geometrical parameters. This poses significant challenges to reduced order modeling (ROM) techniques –such as the reduced basis method –traditionally employed when dealing with the repeated solution of parameter dependent differential equations. Indeed, the nonlinear nature of the problem, the presence of moving fronts in the solution, and the high sensitivity of this latter to parameter variations, make the application of standard ROM techniques very problematic. In this paper we propose a local ROM built through a k-means clustering in the state space of the snapshots for both the solution and the nonlinear term. Several comparisons among alternative local ROMs on a benchmark test case show the effectivity of the proposed approach. Finally, the application to a parametrized problem set on an idealized left-ventricle geometry shows the capability of the proposed ROM to face complex problems.

Keywords: Cardiac electrophysiology; Parametrized monodomain model; Local reduced order model; Reduced basis method; Proper orthogonal decomposition; Empirical interpolation method

1. Introduction

The propagation of the electrical signal through the heart cells is the main responsible of their contraction mechanism, finally resulting in atrial and ventricular contractions. At the macroscopic level, the propagation of electrical potentials is described by means of partial differential equations (PDEs) suitably coupled with ordinary differential equations (ODEs); the latter describe the ionic currents in the cells, depending on a set of gating variables [1]. For instance, coupling the so-called monodomain model for the transmembrane potential $u = u(\mathbf{x}, t)$ with a phenomenological model for the ionic currents – involving a single gating variable $w = w(\mathbf{x}, t)$ – in a domain Ω representing, e.g., a portion of the myocardium (or the whole left ventricle) results in the following time-dependent

* Corresponding author.
E-mail addresses: stefano.pagani@polimi.it (S. Pagani), andrea1.manzoni@polimi.it (A. Manzoni), alfio.quarteroni@polimi.it (A. Quarteroni).

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nonlinear differential system

$$\begin{aligned} \frac{\partial u}{\partial t} - \operatorname{div}(\mathbf{D}\nabla u) + I_{ion}(u, w) &= I_{app}(\mathbf{x}; t), && \mathbf{x} \in \Omega,\ t \in (0, T) \\ \frac{\partial w}{\partial t} + g(u, w) &= 0, && \mathbf{x} \in \Omega,\ t \in (0, T) \\ \frac{\partial u}{\partial \mathbf{n}} &= 0, && \mathbf{x} \in \partial\Omega,\ t \in (0, T) \\ u(\mathbf{x}, 0) = u_0, \quad w(\mathbf{x}, 0) &= w_0, && \mathbf{x} \in \Omega \end{aligned} \tag{1.1}$$

where u represents the transmembrane potential for cardiac cells, w the recovery variable, and t a rescaled time; $\mathbf{n}$ denotes the outward unit normal vector to the boundary $\partial\Omega$, whereas I_{app} is an applied current representing the initial activation of the tissue. $(1.1)_1$ is a nonlinear diffusion–reaction equation; the reaction term I_{ion} and the function g depend on both u and w, thus making the PDE and the ODE two-ways coupled. The most common choices for the two functions I_{ion} and g in order to efficiently reproduce the action-potential are, e.g., the FitzHugh–Nagumo [2,3], the Aliev–Panfilov [4,5] or the Mitchell and Schaeffer model [6]. The diffusivity tensor $\mathbf{D}$ usually depends on the fibers-sheet structure of the tissue, affecting conduction velocities and directions.

When a full-order model (FOM) such as, e.g., the FE method, is used, the accurate solution of such a coupled system is computationally demanding [7–10], because *(i)* strong constraints on the spatial mesh size have to be taken into account due to the propagation of very steep fronts, and *(ii)* very small time steps are required to capture the fast dynamics characterizing the propagation of the electrical signal. The same is true for the electrical potential of the atria [11]. The solution of the linear algebraic systems arising at each time step hinges upon the use of semi-implicit methods or operator splitting-based ones for the whole coupled PDEs/ODEs problem, requiring suitable preconditioning techniques [12–16].

1.1. The need of local reduced order models

Relying on full-order techniques is thus out of reach whenever a problem like (1.1) has to be solved many times, by varying parameter-dependent features affecting operators and/or data. These many-query problems can occur, for instance, when characterizing the evolution of the electrical potential for different tissue conductivity tensors $\mathbf{D}$, activation patterns I_{app}, physical coefficients in the expressions of I_{ion} and g or domains Ω possibly accounting for inter-subject variability. Long-term relevant goals include, among others, the solution of uncertainty quantification (UQ) problems [17–21] parameter estimation and inverse problems [22–25].

Reduced basis (RB) methods and, more generally, reduced order models (ROMs) have been deeply investigated in the last decade and applied to a broad range of parameter dependent PDEs [26]. A possible approach to tackle nonlinear, time-dependent PDEs relies on:

1. proper orthogonal decomposition (POD) to generate a (unique, global) lower dimensional subspace in which the solution of the ROM problem is sought; the reduced basis is then provided by the first right singular vectors of a matrix $\mathbf{S}_u$ collecting snapshots of the FOM obtained for different parameter values, at different time instants;
2. Galerkin or Petrov–Galerkin projection to generate the reduced-order arrays, whence the name of, e.g., *POD–Galerkin* ROM;
3. hyper-reduction techniques (such as the empirical interpolation (EIM) method, or its discrete counterpart (DEIM) [27–30]) to speed up the evaluation of nonlinear and nonaffine[1] arrays, avoiding to access the FOM arrays and ensuring the overall ROM efficiency.

Such a *global ROM* strategy, however, might yield inefficient ROM approximations because of the unaffordable large sets of global basis functions required to approximate both the solution and the nonlinear terms. This happens, e.g., when the solutions manifold (that is, the set of all solutions of the FOM for varying parameters) is characterized by large parameter variations, different physical regimes, or moving features such as fronts or discontinuities. This is indeed the case of the monodomain problem (1.1), for which the transmembrane potential u is characterized by a

[1] A vector $\mathbf{f}(\boldsymbol{\mu})$ and a matrix $\mathbf{A}(\boldsymbol{\mu})$ depend affinely on $\boldsymbol{\mu}$ if they are expressed as $\mathbf{f}(\boldsymbol{\mu}) = \sum_{q=j}^{Q_f} \Theta_j^f(\boldsymbol{\mu})\mathbf{f}_j$, $\mathbf{A}(\boldsymbol{\mu}) = \sum_{j=1}^{Q_a} \Theta_j^a(\boldsymbol{\mu})\mathbf{A}_j$, for given $\boldsymbol{\mu}$-dependent functions $\{\Theta_j^f\}_{j=1}^{Q_f}$, $\{\Theta_j^a\}_{j=1}^{Q_a}$, and $\boldsymbol{\mu}$-independent vectors $\{\mathbf{f}_q\}_{j=1}^{Q_f}$ or matrices $\{\mathbf{A}_j\}_{j=1}^{Q_a}$; Q_f and Q_a are given integers, indicating the *parametric complexity* of $\mathbf{f}$ and $\mathbf{A}$.