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Reduced order method for finite difference modeling of cardiac propagation

Abstract: Efficient numerical simulation of cardiac electrophysiology is crucial for studying the electrical properties of the heart tissue. The cardiac bidomain model is the most widely accepted representation of the electrical behaviour of the heart muscle. The bidomain model offers fast cardiac potential variation, which can lead to high computational cost due to the required large grid sizes and small time steps. In this paper, the complexity of the finite difference approximation of the bidomain equations is reduced with the model order reduction technique. Proper orthogonal decomposition, a projection-based algorithm, is used to efficiently approximate the original high fidelity cardiac bidomain model with a low-dimensional system of equations. The low-dimensional basis functions are computed first from the 'snapshots,' which contain the solutions of the full-order system for different temporal and spatial parameters. Galerkin projection of the original cardiac bidomain system onto the subspace of the reduced order basis functions reduces the size of the linear system. Numerical results confirm the efficiency of the proposed reduced order modeling technique, reducing the simulation time by a factor of 9.54, while maintaining an RMS error of 0.769 mV between the original full order solution and the reduced order POD solution.

Keywords: Bidomain model, Galerkin projection, model order reduction, proper orthogonal decomposition, semi-implicit method.

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1 Introduction

The study of electrical signal propagation in the heart has been performed with electrophysiology-based models, which is now playing an increasingly significant role in clinical applications. Due to the propagation of the electrical signal, an electric potential is generated between the interior and exterior spaces of a cardiac cell, which is termed transmembrane potential [1]. Different ions can flow through the cell membrane because of this potential. The bidomain model is one of the most popular mathematical representations of the heart, as it can replicate the dynamics of the cardiac electrophysiology efficiently [2]. It is a system of two degenerated parabolic reaction-diffusion partial differential equations governing the behaviour of the intracellular and extracellular regions, linked to an elliptic equation characterizing the ionic current through the cell membrane. With the assumption of inhomogeneous and anisotropic conductivities, the bidomain model yields a computationally intensive system.

In this work, the computational complexity of the cardiac bidomain model is reduced by using the model order reduction (MOR) method. MOR has been intensely explored for efficient modeling of large-scale, complex biological and engineering systems [3]. The proposed MOR method extracts the main characteristics of the dynamics of the original system and provides a low-dimensional approximation of the solution [4]. Generally, the MOR algorithm involves two main steps: the offline construction of reduced order basis functions, and projecting the full order system onto the basis functions' subspace to obtain the expected reduced order model in an online phase. Different MOR methods offer different mathematical formulations to compute the subspace and the reduced order model. In this paper, the Proper Orthogonal Decomposition (POD) technique has been used [5]. The state-of-the-art POD method is preferred because it contains only standard matrix computations, and it has been effectively applied in nonlinear model reduction [6]. In the first step, the 'snapshot' matrix is generated from a simulation of the original system sampled at particular discrete time instants. Next, the classical POD is used to find a low dimensional basis from the orthonormal eigenvectors associated with the largest eigenvalues of the snapshots. Finally, the Galerkin projection, in conjunction with the POD method, gives the lower dimensional approximation of the governing system [7].

The finite difference method is employed in the spatial

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discretization of the bidomain system. The snapshot matrix is computed from the original solution of the transmembrane and interstitial potentials. The RMS error (between the full order and reduced order models) of these potentials and the solution time has been investigated. The novelty of this work lies in the study of the POD-Galerkin projection-based reduced order modeling implemented on the finite difference solution of cardiac bidomain equations.

2 Bidomain model of cardiac electrophysiology

The bidomain model is one of the most completed representations of cardiac electrical activity. The unknowns in the model are transmembrane potential, V_m, and interstitial potential, φ_o. The corresponding bidomain equations are:

$$\beta C_m \frac{\partial V_m}{\partial t} = -\nabla \cdot (\bar{\bar{\sigma}}_o \nabla \varphi_o) - I_{so} - \beta \sum I_{ion} \quad (1)$$

$$-\nabla \cdot \bar{\bar{\sigma}}_i \nabla V_m - \nabla \cdot (\bar{\bar{\sigma}}_i + \bar{\bar{\sigma}}_o) \nabla \varphi_o = I_{si} + I_{so} \quad (2)$$

Equations (1) and (2) are defined in a spatial domain $\Omega \subset \mathbb{R}^3$ and a fixed time period $[0, T]$. C_m denotes the capacitance per unit area, and β is the ratio of membrane area to tissue volume. I_{si} and I_{so} represent the stimulation source currents. $\bar{\bar{\sigma}}_i$ and $\bar{\bar{\sigma}}_o$ are the intracellular and interstitial anisotropic conductivity tensors, which change continuously with the fiber orientation.

The ionic current, $\sum I_{ion}$, is modeled as the reaction term in the governing equations, which has a nonlinear dependence on the transmembrane potential and the gating variables. In this study, the Luo-Rudy phase 1 model is used to compute the ionic current $\sum I_{ion}$ [8].

2.1 Spatial and temporal discretization

The proper selection of the spatial and temporal discretizing methods is crucial, as it has a substantial impact on the stability, complexity, accuracy, and computational time of the bidomain solution. The spatial derivatives of the Laplacian term are estimated with the finite difference method. For temporal discretization, the semi-implicit technique is used to take advantage of the stability of the implicit method and the simplicity of the explicit approach [9]. Due to the steep variation of the electrical signal in the heart and complex nonlinear dynamics, large grid size and small time step size are required, which leads to a computationally demanding solution.

3 POD-Galerkin reduced order model

One objective of this paper is to derive a lower order bidomain model by projecting the original equations onto the subspace of orthonormal basis functions, as described below.

3.1 POD basis construction from snapshots

The POD basis is constructed from the snapshot matrix, which is obtained from the numerical simulations of the original system at selected time instances. Snapshots are full order solutions of the two unknown potentials, V_m and φ_o, for N states computed at each time step $t_1, \ldots, t_M \in [0, T]$:

$$\boldsymbol{X} = \begin{pmatrix} V_m(x_1, t_1) & V_m(x_1, t_2) & \cdots & V_m(x_1, t_M) \\ \vdots & \vdots & & \vdots \\ V_m(x_N, t_1) & V_m(x_N, t_2) & & V_m(x_N, t_M) \\ \varphi_o(x_1, t_1) & \varphi_o(x_1, t_2) & & \varphi_o(x_1, t_M) \\ \vdots & \vdots & \cdots & \vdots \\ \varphi_o(x_N, t_1) & \varphi_o(x_N, t_2) & & \varphi_o(x_N, t_M) \end{pmatrix} \in \mathbb{R}^{2N \times M} \quad (3)$$

Next, the eigen-decomposition of the covariance matrix $\boldsymbol{C}$ of the zero-mean snapshots is found. The POD basis functions are found from the linear combination of the snapshots and eigenvectors $\boldsymbol{v}$ of the covariance matrix $\boldsymbol{C}$:

$$\boldsymbol{\psi} = \frac{1}{\sqrt{\lambda}} \boldsymbol{X} \boldsymbol{v} \quad (4)$$

where λ represents the eigenvalues of the covariance $\boldsymbol{C}$ matrix**.** The size of the POD basis depends on the magnitudes of the eigenvalues corresponding to the eigenvectors of the covariance matrix. The l dominant eigenvalues associated with l eigenvectors give the dimension of the reduced order POD basis. The ratio of the sum of the energies of the selected l eigenvectors to the energies of all the eigenvectors is known as relative information content I.

3.2 Reduced order model from Galerkin projection

The final step of the reduced order modeling is the projection of the original bidomain formulation on the reduced order POD basis $\boldsymbol{\psi} \in \mathbb{R}^{\boldsymbol{N} \times \boldsymbol{l}}$. The full order state vectors $\bar{x} = (\overline{V_m}; \overline{\varphi_o}) \in \mathbb{R}^{2N}$ are assumed to be a linear combination of POD basis as $\bar{x} \approx \boldsymbol{\psi} \overline{x_r}$, where $\overline{x_r} \in \mathbb{R}^{\boldsymbol{l}}$ is the anticipated reduced order state vector [5]. As the dimension of the state vector has been reduced from $2N$ to l; consequently, the

number of equations and computational complexity will be reduced. When only spatial discretization is considered, the bidomain model consists of a system of nonlinear ODEs, which are represented as $d\bar{x}/dt = \bar{f}(\bar{x}; t)$. Next, the Galerkin orthogonality is applied, which states that the range of the reduced order basis function $\boldsymbol{\psi}$ and the residual of the original model are orthogonal to each other [7],

$$\boldsymbol{\psi}^T\left(\bar{f}(\bar{x}; t) - {}^{d\bar{x}}/_{dt}\right) = 0 \tag{5}$$

Finally, the reduced order problem is obtained in terms of the new state vector $\overline{x_r}$ as

$$\frac{d\overline{x_r}}{dt} = \boldsymbol{\psi}^T \bar{f}(\boldsymbol{\psi}\overline{x_r}; t) \tag{6}$$

Equation (6) is a system of nonlinear ODEs of lower dimension, and the same semi-implicit method is used for its temporal discretization. It is interesting to note that the discretization of the reduced order system in (6) demonstrates a dense coefficient matrix $[\boldsymbol{A}]_r = \boldsymbol{\psi}^T[\boldsymbol{A}]\boldsymbol{\psi} \in \mathbb{R}^{l\times l}$ on the left-hand side, which has a much smaller dimension.

4 Results and discussion

In this section, the numerical results are presented for the POD-Galerkin reduced order method for the cardiac bidomain model. The cardiac tissue considered is a rectangular volume with a length of 0.5 cm in the x direction and a length of 0.1667 cm in the y and z direction. The anisotropic tissue conductivities in the longitudinal (x) and transverse (y and z) directions are 0.174 and 0.0193 S/m, respectively [10]. The heart is stimulated with a point source current of constant magnitude ($I_{si} = -I_{so} = 500\beta$) lasting 1 ms at the bottom left corner of the tissue. The temporal derivative is discretized with the first order semi-implicit method ($\theta_1 = \theta_2 = 0.5$), and the second order central finite difference scheme ($p = 3$) is used to approximate the spatial Laplacian term. The finite difference grid has 72×72×72 nodes, with $\Delta x = 0.069$ mm and $\Delta y = \Delta z = 0.023$ mm, so there are 2×72^3 state variables or unknowns in the linear system.

The snapshot matrix comprises the full order solutions of both V_m and φ_o for all the finite difference nodes at different time instants. An equidistantly distributed snapshots $\{\bar{x}(t_i)\}_i^M$ with M = 1,200 in the interval [0, T = 12 ms] are constructed and used to obtain the POD basis. The default Krylov-Schur eigenvalue solver of the Scalable Library for Eigenvalue Problem Computations (SLEPc) is employed to compute the reduced order POD subspace of the snapshot matrix in an offline step [11]. The reduced order basis functions capture the most essential information of the state variables, V_m and φ_o, in the training dataset. The largest 18,562 eigenvalues of the snapshot matrix capture 99.9% of the relative information content or energy in the full order bidomain solution, i.e., the POD modes satisfy the condition:

$$\boldsymbol{\psi_l} = \arg\min_l \left(\frac{\sum_i^l \lambda_i}{\sum_i^{2N} \lambda_i} \geq 0.999\right) \tag{7}$$

Next, the 18,562 POD modes are used to obtain the reduced order solution using the Galerkin projection. The system of equations is solved with the iterative conjugate gradient method (for both the full and reduced order models). Since the number of unknowns or equations is reduced, the CPU time required is also reduced. The required simulation time for the full order and reduced order models are 10,285 s and 1,078 s, respectively, i.e., the CPU time is reduced by a factor of ~9.54. Though the number of unknowns is decreased by a factor of ~40, the CPU time is only reduced by a factor of ~10, because the POD basis functions lead to a dense system matrix instead of a sparse one.

Next, the accuracy of the reduced order modeling technique is evaluated in terms of the RMS error between the original and POD solutions. As shown in Figure 1, transmembrane potentials from the full order and POD solutions have close agreement with each other. Table 1 demonstrates the RMS errors of V_m and φ_o for the reduced order model, when compared with the full order model. The results indicate that the POD method approximates the transmembrane potential better than the interstitial potential.

Table 1: RMS error in mV and CPU time reduction factor of the POD-Galerkin reduced order method.

RMS error for V_m	RMS error for φ_o	CPU time reduction factor
0.769	1.093	9.54

5 Conclusion

Modeling complex biological systems is computationally challenging because of their inherently complicated structures and complex nonlinear dynamics. To address this problem, an MOR method has been explored to solve the cardiac bidomain system. The POD-Galerkin approach offers lower dimensional approximations of the high fidelity models. Numerical simulations show that such an approach

reduces both the order of system and simulation time, while

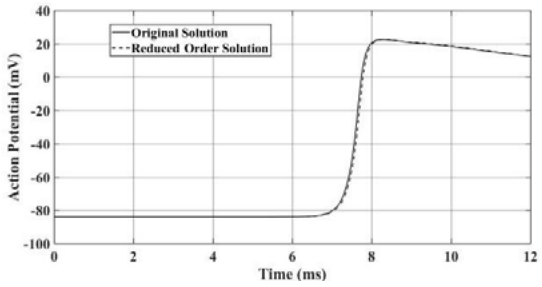

Figure 1: Transmembrane potential of the original full order and reduced order POD solution.

maintaining acceptable accuracy. More robust online projection algorithms and snapshot clustering can be investigated in the future.

Author Statement

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