DMD-Galerkin Model Order Reduction for Cardiac Propagation Modeling

Riasat Khan
Department of Electrical and Computer Engineering
New Mexico State University
Las Cruces, NM, USA
rkhan@nmsu.edu

Kwong T. Ng
Department of Electrical and Computer Engineering
New Mexico State University
Las Cruces, NM, USA
ngnsr@nmsu.edu

***Abstract*—Numerical simulation of cardiac propagation is a valuable tool for biomedical research. Due to the inhomogeneous, anisotropic conductive anatomy and complex nonlinear ionic current, numerical modeling of electrical activities in the heart is computationally demanding. Here, model order reduction is used to reduce the simulation time with a minimal effect on the accuracy. The semi-implicit finite difference method is used to discretize the governing equation of the monodomain (reaction-diffusion) model. The dynamic mode decomposition (DMD) is used in combination with the Galerkin projection to reduce the order of the original system. The reduced-order model is obtained by projecting the original system onto a subspace spanned by DMD basis vectors. Numerical results confirm the model order reduction decreases the simulation time by a factor of 5.96 while modifying the computed activation time, maximum time derivative and conduction velocity by 1.24%, 0.129%, and 0.639%, respectively.**

***Keywords*—Dynamic Mode Decomposition, Finite Difference Method, Galerkin Projection, Model Order Reduction, Monodomain, Transmembrane Potential.**

I. INTRODUCTION

Numerical modeling of cardiac electrical activities now plays a vital role in the search of effective treatments for arrhythmias. The action potential or transmembrane potential propagating in the heart generates an electric field that gives rise to the electrocardiogram recorded on the surface of a human body. This propagation is commonly simulated using the cardiac monodomain model that consists of a temporal derivative, a spatial Laplacian, and a nonlinear ionic current term [1]. A realistic three-dimensional cardiac tissue has a conductivity tensor (3×3 matrix) that varies continuously according to the fiber orientation in the tissue, so a numerical instead of an analytical solution is required. The numerical solution on appropriate spatial and temporal scales then requires finding multiple unknowns, including the transmembrane potential and ionic current components, at a large number of nodes that form a dense grid.

The transmembrane potentials at all the nodes form a high-dimensional or high-order state vector. As the computational complexity and solution time are proportional to the order of the state vector, researchers have developed order reduction techniques to improve computational efficiency through the definition of a new state vector with a lower order [2]. Among all such techniques, the dynamic mode decomposition (DMD) based approach has been chosen for its recent success in solving nonlinear problems in other scientific fields, e.g., fluid mechanics [3]. It involves only standard matrix computations and can capture frequency features of the dynamic systems [3–5]. DMD basis functions are constructed from the spatial distributions of the unknown of interest at specific time instants, known as the snapshots, which are obtained from an original full-order simulation. A truncated series of these basis functions encapsulate the characteristic dynamics of the original system. The reduced-order surrogate models are obtained by a Galerkin projection of the original system onto the vector space formed by DMD basis functions. DMD, in conjunction with the Galerkin projection, transforms the original full-order system, the discretized monodomain model in the present case, into a lower dimensional system, and subsequently reduces the computational cost. The root-mean-square (RMS) error of the transmembrane potential for the DMD-Galerkin order reduction will be examined together with its effect on solution time, activation time, maximum time derivative, and conduction velocity. To our knowledge, this is the first time computational performance results are presented for the application of model order reduction to finite difference modeling of cardiac propagation.

II. CARDIAC MONODOMAIN MODEL

The cardiac monodomain model derived from current continuity is described by a nonlinear reaction-diffusion partial differential equation,

$$\frac{\partial V_m}{\partial t} = \frac{1}{C_m}\left\{\frac{1}{\beta}\left[\nabla\cdot\left(\bar{\bar{\sigma}}\,\nabla V_m\right)+I_s\right]-\sum I_{ion}\right\}, \qquad (1)$$

where V_m is the transmembrane potential (the difference between the intracellular and interstitial potentials), C_m is the cell membrane capacitance per unit area, β is the membrane area per unit volume, and $\bar{\bar{\sigma}}$ denotes the inhomogeneous, anisotropic intracellular conductivity tensor. I_s is the source current that initiates the activation, and ΣI_{ion} represents the total ionic current through the membrane. The monodomain equation involves a temporal derivative and a Laplacian with spatial derivatives, $\nabla\cdot(\bar{\bar{\sigma}}\,\nabla V_m)$. The Laplacian is approximated with the second-order finite difference technique [6]. Temporal discretization is achieved with the semi-implicit or implicit-explicit scheme. Using an implicit method for the Laplacian and an explicit method for the ionic current, it avoids both the stability limit of the explicit technique and costly nonlinear

Submitted On: September 15, 2018
Accepted On: October 3, 2018

matrix inversion in a fully implicit method. The spatial and temporal discretization leads to a system of linear algebraic equations that can be put in a matrix form, $[A]\,\bar{x} = \bar{b}$, as:

$$\underbrace{\{[I] - \frac{\theta\Delta t}{C_m\beta}[D_o]\}}_{[A]}\underbrace{\bar{V}_m^{n+1}}_{\bar{x}} = \underbrace{\bar{V}_m^n + \frac{(1-\theta)\Delta t}{C_m\beta}[D_o]\bar{V}_m^n + \Delta t[\frac{1}{C_m\beta}\bar{I}_s^{n+1} - \frac{1}{C_m}\overline{\sum I}_{ion}^n]}_{\bar{b}}, \quad (2)$$

where $[I]$ is the identity matrix, $0 \le \theta \le 1$ is a temporal discretization constant, Δt is the time step size, and the bar denotes a vector containing the corresponding quantity's values at all the nodes. $[D_o]\bar{V}_m$ is the finite difference approximation of the Laplacian, and n is the time step index. To obtain the value of $\bar{V}_m$ at time step n+1 from that at previous step n, Equation (2) is solved using an iterative conjugate gradient technique with Jacobi preconditioner. The operator splitting has also been implemented in which the time derivative is considered as the sum of several components, and the update of the Laplacian and ionic current term are performed in alternate steps with different time step sizes Δt and $\Delta t_i = \Delta t/5$, respectively [7]. A smaller time step is used for the ionic current to capture its faster temporal variation. The primary objective of this work is to reduce the size of $\bar{V}_m$, by projecting it onto a low-dimensional subspace.

III. DYNAMIC MODE DECOMPOSITION

The reduced-order DMD basis functions are constructed from the training sets or snapshot matrix, which is obtained from a simulation using the original full model. Each column in this matrix is a snapshot consisting of the solution of the state vector $\overline{V}_m$ at a given time instant. The trajectories of the original model at discrete time instants are represented by the rows of the snapshot matrix. The snapshots together capture all the desired spatial and temporal variations for the reduced-order model. For the DMD analysis, a set of M equidistant snapshots (i.e., a snapshot matrix of dimension $\mathbb{R}^{N\times M}$) is considered, where N is the number of state variables. Two zero-mean data matrices are obtained from the snapshot matrix, $\bar{x}(t_i), i = 1, M$:

$$\boldsymbol{X} = [\bar{x}(t_1), \bar{x}(t_2), \dots\dots, \bar{x}(t_{M-1})];$$
$$\boldsymbol{Y} = [\bar{x}(t_2), \bar{x}(t_3), \dots\dots, \bar{x}(t_M)]. \quad (3)$$

Next, a matrix $\boldsymbol{A}$ is constructed from the singular value decomposition (SVD) of $\boldsymbol{X}$ as:

$$\boldsymbol{A} = \boldsymbol{u}^T\boldsymbol{Y}\boldsymbol{v}\boldsymbol{S}^{-1}, \quad (4)$$

where $\boldsymbol{u}$ and $\boldsymbol{v}$ are respectively the left and right singular vectors, and $\boldsymbol{S}$ is a diagonal matrix with the singular values of $\boldsymbol{X}$. The reduced-order DMD basis functions are finally obtained from the eigen-decomposition of $\boldsymbol{A}$,

$$\boldsymbol{\Psi} = \boldsymbol{u}\boldsymbol{W}, \quad (5)$$

where $\boldsymbol{\Psi}$ consists of the DMD basis functions and $\boldsymbol{W}$ is made up of the eigenvectors of $\boldsymbol{A}$. Despite the nonlinearity of the monodomain model, the magnitudes of the complex eigenvalues decrease fast. The truncated series of the normalized eigenvectors corresponding to eigenvalues with the largest magnitudes give the reduced-order basis functions. By including the eigenvectors with the largest eigenvalues, the reduced-order basis functions preserve the most important dynamics of the original system. The normalization of the DMD basis functions was found to provide a better approximation of the original system [8]. It is interesting to note that the generations of the snapshot matrix and reduced-order basis functions are implemented in an offline stage.

IV. REDUCED-ORDER MODEL FROM GALERKIN PROJECTION METHOD

The full-order monodomain model is projected onto the subspace of DMD basis functions by performing the Galerkin projection technique in two steps. The state vector $\overline{V}_m$, consisting of the transmembrane potential values at all the nodes, is first approximated as a linear combination of the reduced-order DMD modes,

$$\overline{V}_m \approx (\bar{q} = \boldsymbol{\Psi}\bar{z}), \quad (6)$$

where $\bar{z} \in \mathbb{R}^{d\times 1}$ represents the reduced-order state vector. Now, the number of unknowns or dimension is effectively reduced from N to d, with $d << N$, leading to a reduction in the number of equations.

With only spatial discretization, the monodomain equation, with $\overline{V}_m$ approximated by $\bar{q}$, turns into a system of nonlinear ordinary differential equations, $\frac{d\bar{q}}{dt} = \bar{f}(\bar{q}; t)$, where the unknown in each equation is the value of $\bar{q}$ at each node. In the second step, the Galerkin orthogonality condition is enforced such that the residual of the full-order model is orthogonal to the reduced-order DMD modal matrix $\boldsymbol{\Psi}$,

$$\boldsymbol{\Psi}^{\mathrm{T}}\left(\bar{f}\,(\bar{q}; t) - \frac{d\bar{q}}{dt}\right) = 0. \quad (7)$$

The above two steps lead to the following DMD-Galerkin reduced-order model equation for the state vector $\bar{z}$,

$$\frac{d\bar{z}}{dt} = \boldsymbol{\Psi}^{\mathrm{T}} f(\boldsymbol{\Psi}\bar{z}; t). \quad (8)$$

The semi-implicit method used for the original full-order model can also be used to perform the temporal discretization in (8).

V. RESULTS AND DISCUSSION

The three-dimensional cardiac tissue was 0.5 cm in x (horizontal) direction and 0.1667 cm in y and z (vertical) direction, as depicted in Fig. 1. Tissue fibers were assumed to lie in planes whose normal was at 20° to the z-axis, and the fiber angle with respect to the x-axis varied linearly in the normal direction with a rotation of 180° per centimeter. The conductivities longitudinal and transversal to the fiber are 0.174 S/m and 0.0193 S/m, respectively. The continuously inhomogeneous conductivity tensor (with respect to the x-y-z coordinate system) was assigned according to the fiber

orientation, and the derivatives of the conductivity tensor elements were evaluated analytically. The ionic current was computed as the sum of six different types of currents using the Luo-Rudy model. A 72×72×72 grid with 373,248 nodes (i.e., a dimension of 373,248) and a 1-ms point source with a constant magnitude and located at a vertex were used. A period of 12 ms was simulated with $\Delta t = 0.005$ ms. Equation (2) was implemented with $\theta = 0.5$. Results were obtained with and without operator splitting.

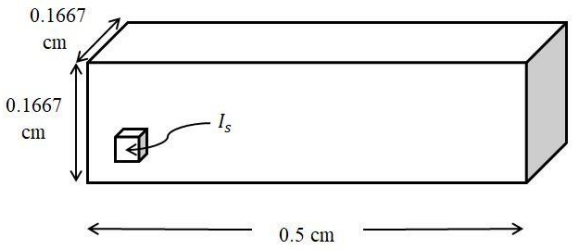

Fig. 1. Schematic representation of the three-dimensional cardiac tissue.

Equidistantly distributed snapshots in the interval $[0, T = 12$ ms] were constructed from a simulation of the original full-order monodomain solution. A specialized software library, Scalable Library for Eigenvalue Problem Computations [9], was utilized to generate the DMD basis functions in an offline stage. The default Krylov-Schur eigenvalue solver and thick-restart Lanczos SVD solver of SLEPc were used to obtain the DMD reduced-order subspace from the snapshot matrix. The largest 24,480 eigenvalues of the $\boldsymbol{A}$ matrix yielded 99.9% of the relative information content or energy, and the DMD subspace had a dimension of 24,480. The number of unknowns or state variables reduced by a factor of ~15 when the reduced-order model was used. Table I summarizes the RMS error (when compared the full-order and reduced-order solutions) and CPU time reduction for the DMD-Galerkin method. The order reduction decreases the CPU time by a factor of 5.96, while maintaining a small RMS error of 0.956 mV. For the operator split method, the RMS error improves to 0.762 mV, but the CPU time reduction factor decreases to 2.59. It is worth mentioning that the ionic current is updated in the operator split method with a smaller time step, which has an adverse effect on the solution time. Fig. 2 shows the close agreement between action potential waveforms obtained at node (36, 36, 36) with the full and reduced-order models using the operator split technique.

Table I. RMS error and CPU time reduction factor of the DMD-Galerkin reduced-order model with and without operator split.

Type of Solution	RMS Error (mV)	CPU Time Reduction Factor
Without operator split	0.956	5.96
Operator split	0.762	2.59

Activation time, maximum time derivative, and conduction velocity are parameters commonly used in electrophysiology studies. Table II gives their values computed using the full and reduced-order models. Specifically, maximum time derivative is the highest value of the time derivative of the transmembrane potential at node (36, 36, 36). Activation time is the specific time at which the maximum time derivative occurs. Conduction velocity is the distance between any two points divided by the difference between the activation times at these two points. The velocity was calculated for the propagation from node (36, 36, 36) to node (37, 37, 37). As shown in Table II, using model order reduction modifies the activation time, maximum time derivative, and conduction velocity by +1.24%, +0.129%, and –0.639%, respectively. With the use of the operator split, the corresponding modifications are +0.640%, +0.0887%, and –0.321%.

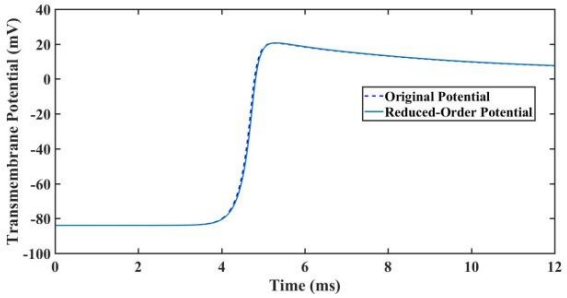

Fig. 2. Transmembrane potential for the full-order and reduced-order solutions with the operator split method.

Table II. Maximum time derivative, activation time, and conduction velocity of the full-order and DMD-Galerkin reduced-order models.

Parameters	Without Operator Split		Operator Split	
	Full-Order	Reduced-Order	Full-Order	Reduced-Order
Activation time (ms)	4.82	4.88	4.69	4.72
Maximum time derivative (V/s)	225.44	225.73	225.58	225.78
Conduction velocity (m/s)	0.313	0.311	0.312	0.311

VI. CONCLUSION

Model order reduction based on dynamic mode decomposition and Galerkin projection has been implemented for a finite difference monodomain model of cardiac tissue. Computational results demonstrate that the proposed approach improves computational efficiency. The dimension of the problem and required CPU time are reduced significantly while introducing less than 1 mV in RMS error and less than 1.3% error in the computed activation time, maximum time derivative, and conduction velocity. Operator splitting increases the accuracy but reduces the improvement in the required CPU time. Future studies may involve the implementation of more robust projection methods as well as techniques that capture the frequency features of cardiac propagation.

REFERENCES

[1] Z. Zhan and K. T. Ng, "Two-dimensional Chebyshev pseudospectral modelling of cardiac propagation," Medical and Biological Engineering and Computing, vol. 38, pp. 311-318, 2000.

[2] W. H. Schilders, v. d. Vorst, A. Henk, and J. Rommes, Model Order Reduction: Theory, Research Aspects, and Applications, 1st ed.,

Springer-Verlag, Heidelberg, Berlin, Germany, 2008.
[3] P. J. Schmid, "Dynamic mode decomposition of numerical and experimental data," Journal of Fluid Mechanics, vol. 656, pp. 5-28, 2010.
[4] P. J. Schmid, "Application of the dynamic mode decomposition to experimental data," Experiments in Fluids, vol. 50, pp. 1123-1130, 2011.
[5] B. W. Brunton, L. A. Johnson, J. G. Ojemann, and J. N. Kutz, "Extracting spatial-temporal coherent patterns in large-scale neural recordings using dynamic mode decomposition," Journal of Neuroscience Methods, vol. 258, pp. 1-15, 2016.
[6] R. Khan and K. T. Ng, "Higher order finite difference modeling of cardiac propagation," Proceedings of the IEEE International Conference on Bioinformatics and Biomedicine, pp. 1945-1951, 2017.
[7] S. Krishnamoorthi, M. Sarkar, and W. S. Klug, "Numerical quadrature and operator splitting in finite element methods for cardiac electrophysiology," International Journal for Numerical Methods in Biomedical Engineering, vol. 29, pp. 1243-1266, 2013.
[8] R. Khan and K. T. Ng, "Model order reduction for finite difference modeling of cardiac propagation using DMD modes," Proceedings of the International Applied Computational Electromagnetics Society Symposium, pp. 1-2, 2018.
[9] V. Hernandez, J. E. Roman, and V. Vidal, "SLEPc: A scalable and flexible toolkit for the solution of eigenvalue problems," ACM Transactions on Mathematical Software, vol. 31, pp. 351-362, 2005.

Riasat Khan is an Assistant Professor of the Electrical and Computer Engineering Department at North South University, Bangladesh. He obtained his M.S. and Ph.D. degrees in Electrical Engineering from New Mexico State University, Las Cruces, NM. His research interests include cardiac electrophysiology, bioelectromagnetics, computational electromagnetics, model order reduction, and power electronics.

Kwong T. Ng is a Professor of the Electrical and Computer Engineering Department at New Mexico State University, Las Cruces, NM. He received the M.S. and Ph.D. degrees from The Ohio State University, Columbus, in 1981 and 1985, respectively. His current research interests include bioelectromagnetics, computational electromagnetics, and biomedical instrumentation.