

Model Order Reduction of Cardiac Monodomain Model using Deep Autoencoder Based Neural Networks

Riasat Khan¹ and Kwong T. Ng²

¹Department of Electrical and Computer Engineering, North South University, Dhaka, Bangladesh
riasat.khan@northsouth.edu

²Department of Electrical and Computer Engineering, New Mexico State University, Las Cruces, NM 88003, USA
ngnsr@nmsu.edu

Abstract — The numerical study of electrocardiology involves prohibitive computational costs because of its complex and nonlinear dynamics. In this paper, a low-dimensional model of the cardiac monodomain formulation has been developed by using the deep learning method. The restricted Boltzmann machine and deep autoencoder machine learning techniques have been used to approximate the cardiac tissue's full order dynamics. The proposed reduced order modeling begins with the development of the low-dimensional representations of the original system by implementing the neural networks from the numerical simulations of the full order monodomain system. Consequently, the reduced order representations have been utilized to construct the lower-dimensional model, and finally, it has been reconstructed back to the original system. Numerical results show that, the proposed deep learning MOR framework gained computational efficiency by a factor of 85 with acceptable accuracy. This paper compares the accuracy of the deep learning based model order reduction method with the two different techniques of model reduction: proper orthogonal decomposition (POD) and dynamic mode decomposition (DMD). The model order reduction deploying the deep learning method outperforms the POD and DMD concerning the modeling accuracy.

Index Term — Autoencoder, Cardiac monodomain model, deep learning technique, dynamic mode decomposition, proper orthogonal decomposition, reduced order modeling, semi-implicit scheme.

I. INTRODUCTION

Cardiac electrophysiology is a bioelectromagnetic phenomenon, where the electrical activities of the heart tissue are studied. Electrocardiological numerical simulations seek reliable and efficient mathematical models for cellular membrane dynamics. The monodomain equation used to model the cardiac electrical activity requires the solution of a nonlinear

partial differential equation with appropriate boundary and initial conditions [1]. The monodomain equation leads to a complex dynamical system because of the involvement of the nonlinearity of different ionic currents and steep wavefront propagation. The solution of the monodomain equation can be obtained with various numerical techniques, e.g., finite volume method (FVM), finite difference method (FDM), and finite element method (FEM). The discretization of the monodomain equation with the finite difference method involves a large number of degrees of freedom [2]. In the literature, reduced order modeling has been studied to approximate the nonlinear dynamics of the complex systems. The most widely used order reduction method is the proper orthogonal decomposition (POD) technique, which captures the characteristic dynamics of the original discretized system [3]. POD is a projection-based model order reduction method, where a lower order basis is computed first from the original system. Finally, the reduced order model is obtained from the full order model's projection onto this small dimensional POD basis. The approximation of the obtained reduced order model requires considerably less computational complexity, with insignificant compromise on the accuracy. Different model order reduction approaches have been successfully applied in the field of cardiac electrophysiology, such as POD [4] and dynamic mode decomposition method (DMD) [5].

The neural network is a machine learning algorithm, loosely modeled from the human brain, which has been designed to detect a similar pattern in the data. Many machine learning algorithms have been successfully used in the field of dimensionality reduction to reduce overfitting, data preprocessing, and simpler data visualization [6]. Autoencoder, also known as auto-associative neural network, with three delicate layers, is an unsupervised learning algorithm. It is a neural network that learns the original system with multiple levels of representations and can predict the nonlinear dynamics of the data [7]. Autoencoder is primarily

composed of two networks, an encoder, and a decoder. The encoder is an analysis network which learns to detect all the most significant characteristics and hidden representations of the input high fidelity system. The encoder has a representation of latent-space, which contains the compressed essential properties of the input nodes [8]. The decoder is a synthesis network that recomposes the exact system from the hidden representations with minimum reconstruction error. Autoencoder with single perceptron and linear activation in the projection and reconstruction phases works almost similar to the state-of-the-art dimensionality reduction method principal component analysis (PCA).

In this work, the dimension or order of the transmembrane potential of the cardiac monodomain system has been effectively reduced with the implementation of a deep autoencoder based deep learning approach. As opposed to a traditional autoencoder, it consists of additional deep-belief layers and consequently learns more complex features. The restricted Boltzmann machine (RBM), which is the elementary element of the deep-belief networks, constructs the deep autoencoder architecture's complex layers. In the first step, the high dimensional spatiotemporal dynamics of the monodomain model has been minimized to lower order representations. Next, the lower order representations have been approximated to a reduced order dynamic model, which can replicate the dynamics of the original system. Finally, the approximated solution is reconstructed from the prediction of the lower order model. The computational efficiency and modeling accuracy of the proposed order reduction approach are examined and compared with the popular proper orthogonal decomposition and dynamic mode decomposition methods.

II. FULL ORDER CARDIAC MONODOMAIN GOVERNING EQUATION

This paper considers the nonlinear partial differential monodomain equation describing the dynamics of cardiac electric transmembrane potential $\bar{V} = V(\bar{x}, t)$, which can be formulated as:

$$\begin{cases} \frac{\delta \bar{V}}{\delta t} = \frac{1}{c_m} \left\{ \frac{1}{\beta} [\nabla \cdot (\bar{\sigma}_i \nabla \bar{V}) + I_{si}] - \sum I_{ion}(\bar{V}, w) \right\} \\ \frac{dw}{dt} + g(\bar{V}, w) = 0, \end{cases} \quad (1)$$

with Neumann boundary conditions and initial condition $V(\bar{x}, 0) = V_0(\bar{x})$ and $w(\bar{x}, 0) = w_0(\bar{x})$. The equation is considered in a spatial domain of $\Omega \in \mathbb{R}^3$, which is the considered section of the myocardium, and a temporal domain of $t \in [0, T]$. Here, C_m denotes the membrane capacitance per unit area, and β is the ratio of the membrane surface area to volume. $\bar{\sigma}_i$ is the intracellular anisotropic conductivity tensor, which changes continuously with the fiber angle rotation, and I_{si} represents the intracellular source current, which initiates

the stimulation.

The reaction element in the governing equation is the ionic current term, $\sum I_{ion}(\bar{V}, w)$, which has a nonlinear relation with the transmembrane potential and the gating parameters $w(\bar{x}, t)$. The Luo-Rudy model has been applied to obtain the ionic current, which yields the solution of eight coupled nonlinear ordinary differential equations. The finite difference method has been used to discretize the spatial derivatives of the Laplacian term of (1) [9]. The temporal discretization has been achieved by implementing the semi-implicit method [10], which leads to:

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

where $\theta = 0.5$ represents the Crank-Nicolson semi-implicit temporal parameter. The two major excessive computational components at each time step involve the solution of the matrix equation (2) and evaluation of the ionic current, which includes the calculation of the gating parameters and the solution of the ODEs.

III. REDUCED ORDER MODELLING WITH DEEP LEARNING APPROACH

Considering only spatial approximation, the governing nonlinear cardiac monodomain equation transforms into a system of ordinary differential equation in the time domain as:

$$\frac{d\bar{V}}{dt} = \bar{f}(\bar{V}, t) \quad (3)$$

where \bar{f} is a set of nonlinear functions. The snapshots of the original spatiotemporal dynamic system have been obtained from its numerical simulations using (2). The snapshots are obtained from the finite difference solution of the full order monodomain system at the N spatial locations x_1, \dots, x_N , and M temporal instances $t_1, \dots, t_M \in [0, T]$. The ultimate goal of this work is to derive a lower order solution V_r from the high fidelity snapshot matrix of the transmembrane potential solution $\{V(x_i, t)\}_{i=1, t=1}^{N, M}$.

First, a lower order representation V_1 can be derived from the nonlinear projection $f_1: \mathbb{R}^N \rightarrow \mathbb{R}^{N_r}$ as:

$$V_1 = f_1(V), \quad (4)$$

where N_r is the reduced dimension with $N_r \ll N$. Next, the reduced order dynamic modeling of the lower dimensional representations is completed. As the dimension has been reduced, the reduced order modeling involves fewer computational resources than the original full order model. After applying the lower dimensional dynamic modeling, the reduced order form of (3) will be $\frac{d\bar{V}_r}{dt} = \bar{f}_r(\bar{V}_1, t)$, where V_r is the predicted solution of the cardiac transmembrane potential. Finally, the reduced order solution is reconstructed back to the approximated

solution by implementation the nonlinear reconstruction function $f_2: \mathbb{R}^{N_r} \rightarrow \mathbb{R}^N$ as:

$$\tilde{V} = f_2(V_r). \quad (5)$$

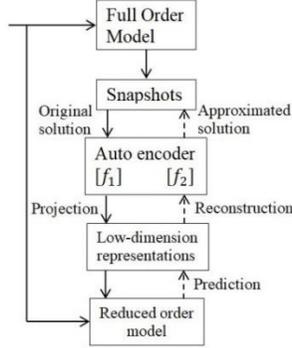


Fig. 1. Neural network based model order reduction architecture.

The modeling accuracy of the proposed order reduction method will be evaluated by minimizing the RMS error between the original solution V and approximated solution \tilde{V} of the cardiac transmembrane potential. During the training stages of the deep autoencoder architecture, the RMS error of the following cost function is minimized:

$$f(V, \tilde{V}) = \sqrt{\frac{\sum_1^M (V - \tilde{V})^2}{M}}. \quad (6)$$

Here M denotes the total number of the training dataset. The projection and reconstruction should be performed simultaneously for a good approximation of the original spatiotemporal dynamics.

Figure 1 shows the architecture of the proposed neural network based model order reduction method. In Fig. 1, the hidden layers of the autoencoder are composed of the projection layer f_1 , intermediate bottleneck layer for reduced order modeling, and the reconstruction layer f_2 . Nonlinear sigmoid activation functions have been used for the nodes of the projection and reconstruction layers, as:

$$\begin{aligned} f_1(V) &= \sigma_n(W_n(\sigma_1(W_1V + b_1) + \dots + b_n)) \\ f_2(V_r) &= \sigma_1(W'_1(\sigma_n(W'_nV_r + b_n) + \dots + b_1)), \end{aligned} \quad (7)$$

where σ_i is the sigmoid function of i^{th} layer, W_i and b_i denote the weights and bias between the layers i and $i + 1$.

III. RESULTS AND DISCUSSION

In this section, numerical performances of the proposed deep learning based order reduction approach on the cardiac monodomain equation will be presented. A three-dimensional myocardial tissue of $0.5 \text{ cm} \times 0.1667 \text{ cm} \times 0.1667 \text{ cm}$ has been considered as the computational domain. The longitudinal (x) and transverse (y and z) conductivities to the fiber have been assigned as: $\sigma_{il} = 0.174 \text{ S/m}$ and $\sigma_{it} = 0.0193 \text{ S/m}$ [9]. The tissue was stimulated by a point current source at one corner of I_{si}

$= 500\beta$ with a duration of 1 ms and $\beta = 2000 \text{ cm}^{-1}$. The first order semi-implicit method ($\theta = 0.50$) and the second order central finite difference technique have been utilized for the temporal and spatial discretizations, respectively.

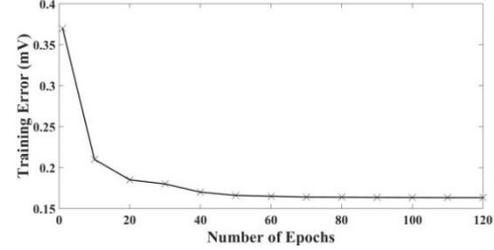


Fig. 2. RMS error (mV) vs the number of epochs during the backpropagation process.

The proposed model order reduction method initiates with the construction of the snapshots from the above-mentioned full order monodomain simulations with a time step size of $\Delta t = 0.01 \text{ ms}$ and for a time domain of $t \in [0, 20 \text{ ms}]$. The deep autoencoder architecture comprises two symmetrical deep-belief networks for encoding and decoding functions, with 8 RBM layers and 40 neurons in each of the hidden layers. 75% of the full order simulation data at time domain $t \in [0, 15 \text{ ms}]$ was used for training, and the remaining data ($t \in [15, 20 \text{ ms}]$) was utilized for the testing of the proposed algorithm, and the training of the model has been performed on the Google Collaboratory. The backpropagation training error in Fig. 2 confirms the convergence of the deep learning process. Next, the number of reduced order modes is varied to study the efficiency of the MOR method. The RMS error decreases by almost 50% with the increase of the reduced order modes from 100 to 180. Figure 3 demonstrates that the modeling accuracy does not improve significantly if the modes number is increased after that, and hence the reduced order modes number is set to 180.

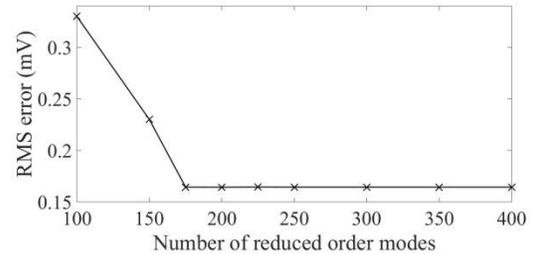


Fig. 3. RMS error (mV) for different number of reduced order modes.

Finally, the predicted solution is reconstructed back to the full order system to obtain the error between the original and reduced order solutions. The waveforms

of the original and approximated solutions of the transmembrane potential have been shown in Fig. 4 at a specific spatial point in the computational domain ($x = 0.25$ cm and $y = z = 0.083$ cm). The close agreement of the full order and reduced order solutions confirms the proposed method is capable of offering an accurate reconstruction of the transmembrane potential most of the time, and subsequently, the accuracy of the neural network based order reduction method. Next, the RMS error has been calculated the solutions, and it has been compared with the error obtained from the POD and DMD methods. According to Table 1, the proposed deep learning MOR technique offers approximately 4.65 and 2.41 times better modeling accuracy in terms of RMS error than the POD and DMD methods, respectively.

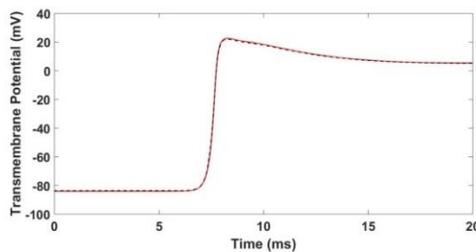


Fig. 4. Cardiac transmembrane potential waveforms of the original solution (V in red solid line) and approximated solution (\tilde{V} in black dashed line).

Table 1: RMS error of the transmembrane potential between the full order and reduced order solutions for different MOR methods

Order Reduction Techniques	RMS Error (mV)
DMD	0.762
POD	0.396
Proposed deep learning	0.164

Finally, the acquired CPU time reduction factor of the proposed deep learning based MOR method has been investigated. All the simulations have been performed on a 2.4-GHz Intel Xeon E5645 processor. The required CPU time to obtain the full order and reduced order solutions are 5,399 s and 65 s, respectively. The CPU time for the proposed neural network method has a reduction factor of almost 85. The CPU time includes the required time for the online modeling and decoding steps, i.e., the prediction stage and the reconstruction phase of the original solution. It is interesting to note that, the mentioned CPU time does not include the training time, as well as, the required time to obtain the reduced order basis as this step is performed only once.

V. CONCLUSION

In this paper, a neural network method has been used for the first time to reduce the order of the cardiac complex monodomain system. An unsupervised machine

learning approach, deep autoencoder, has been used for this purpose of dimensionality reduction. The autoencoder maps the full order system into a lower feature representation, as well as reconstructs the original solution from the compressed latent-space representations. Numerical results demonstrate that, the proposed MOR method achieved remarkable computational savings with a factor of almost 85. A significant contribution of this work is to compare the modeling accuracy of the proposed deep learning based technique with the conventional order reduction methods, POD, and DMD. The proposed MOR method has a better accuracy of dimension reduction than the POD and DMD. In the future, the proposed deep learning MOR strategy can be applied to the cardiac bidomain system.

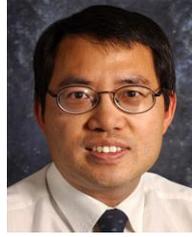
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Riasat Khan is an Assistant Professor of the Electrical and Computer Engineering Department at North South University, Bangladesh. He obtained his M.S. and Ph.D. degrees in Electrical Engineering from New Mexico State University, Las Cruces, NM. His 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.