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POD-DEIM MODEL ORDER REDUCTION FOR THE MONODOMAIN REACTION-DIFFUSION EQUATION IN NEURO-MUSCULAR SYSTEM

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The neuro-muscular system is a complex multiscale coupled system, for which realistic simulations are computationally extremely demanding. The most challenging part of a chemo-electro-mechanical model of a skeletal muscle tissue is the monodomain reaction-diffusion equation. We study the feasibility of applying model order reduction techniques (MOR) to the monodomain equation. The equation comprises microscopic reactions existing at the cell membrane and diffusion of the action potentials along 1D muscle fibers,

$$\frac{\partial V_\mathrm{m}}{\partial t} = \frac{1}{A_\mathrm{m} C_\mathrm{m}} \left(\frac{\partial}{\partial x} \left(\sigma_\mathrm{eff} \frac{\partial V_\mathrm{m}}{\partial x} \right) - A_\mathrm{m} I_\mathrm{ion}\left(\boldsymbol{y}, V_\mathrm{m}, I_\mathrm{stim}\right) \right), \tag{1a}$$

$$\frac{\partial \boldsymbol{y}}{\partial t} = G_{\boldsymbol{y}}\left(\boldsymbol{y}, V_\mathrm{m}, I_\mathrm{stim}\right), \tag{1b}$$

where V_m is the action (transmembrane) potential, C_m is the capacity of the muscle fiber membrane (sarcolemma), A_m is the fiber's surface to volume ratio and σ_eff is the effective conductivity. x denotes the spatial coordinate along the fiber. I_ion is the ionic current flowing over the ion-channels and -pumps, which depends on V_m. Further state variables are summarized in $\boldsymbol{y}$, e. g. the states of different ion channels. I_stim is an externally applied stimulation current due to a stimulus from the nervous system. $G_{\boldsymbol{y}}$ summarizes the right-hand-side of all nonlinear ODEs associated with the state variables $\boldsymbol{y}$. Here, we consider the biophysically motivated model of Hodgkin and Huxely (1952) [1] which is the base model to describe the ionic mechanism in the cell membrane.

To study the feasibility of applying model order reduction to the above mentioned monodomain equation, we employ the proper orthogonal decomposition (POD). According to Figure 1, a sharp cut-off in the singular values of the snapshot matrix could be observed that shows the potential for model order reduction. The snapshot matrix consists of the action potentials on a grid of 200 nodes, which are gathered every 0.01 ms for 10 ms. To investigate more options for model order reduction, we employ the KerMor[1] matlab library, which provides "routines for model order reduction of dynamical systems using subspace projection and kernels methods".

[1] http://www.ians.uni-stuttgart.de/MoRePaS/software/kermor/

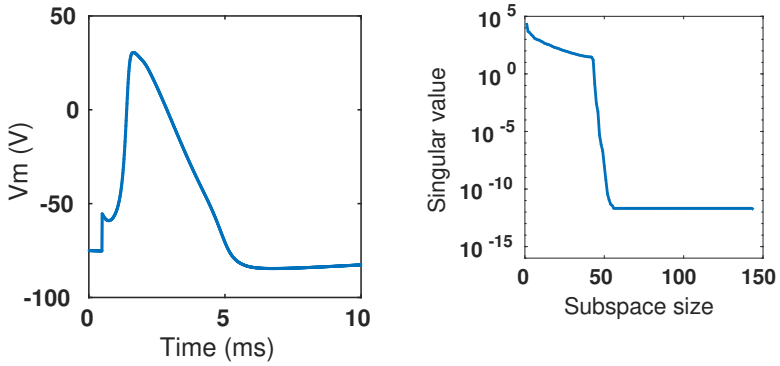

Figure 1: The action potential V_m (left) and singular value decomposition (right). POD snapshots have been taken from a grid of 200 nodes every 0.01 ms for 10 ms.

Table 1: Speed up and mean relative L2-norm error of the action potential and state variables of the ion channels applying the POD Galerkin method with respect to the full model. A grid of 80 elements is employed.

Modes	40	60	80	100	120	140	160	180
Error	0.0286	0.0045	4.8E-05	5.5E-06	3.8E-08	1.2E-08	1.3E-09	3.2E-10
Speed up	3.22	2.97	2.52	2.37	2.46	2.00	1.94	1.94

According to our simulations, a factor of 2 in the computation time could be saved using the POD-Galerkin approximation, which is shown in Table 1. A grid of 80 elements is employed and snapshots are considered from the solution of the action potential and three state variables (in total 324 modes) every 0.01 ms for 10 ms. The mean relative L2-norm error is computed with respect to the full order model and averaged over the whole computation time. Using finer meshes, a convergence is observed in the number of modes. It means that higher resolution systems could be reduced more efficiently and the speedups would be considerably higher.
In order to build the snapshot matrix, we consider two options. First, we consider snapshots of the action potential, which is present in both linear diffusion and nonlinear reaction terms. This strategy is employed in Figure 1. Second, we consider snapshots of the action potential and state variables of the reaction term as considered in Table 1. The first strategy results in a small-sized reduced system but the system matrix is not tridiagonal as in the full order model. Lower speedups are obtained in comparison to the ones reported in Table 1. The second reduction strategy results in a considerably large snapshot matrix as it contains all state variables as well. Comparing to this strategy, applying the discrete empirical interpolation method (DEIM) to the nonlinear term of the full order model results in smaller speedups. A combination of the POD (second strategy) with the DEIM method shows to be slower than each of both, separately. It could be due to the additional vector-matrix multiplication in the combination. Moreover, it seems that the modes present in the nonlinear reaction term are already captured by the POD (second strategy) without DEIM. According to our studies, we conclude that the potential for model order reduction lies mainly in reduction of the reaction term of the monodomain equation. This could be verified by considering more complicated microscopic models for chemical reactions such as the Shorten model [2], which contains much more state variables. However, combining the first reduction strategy above with the DEIM method, also using the Greedy-POD, is still an option to investigate in the next step.

REFERENCES

[1] Hodgkin, A. L. and Huxley, A. F. A quantitative description of membrane current and its application to conduction and excitation in nerve. *The Journal of physiology* (1952) **117**, No. 4, pp. 500–544.

[2] Shorten, P. R., O'Callaghan, P., Davidson, J. B. and Soboleva, T. K. A mathematical model of fatigue in skeletal muscle force contraction. *Journal of Muscle Research and Cell Motility* (2007) **28**, pp. 293–313.