

Ruxandra Barbulescu, L. Miguel Silveira

Advances in experimental neuroscience have generated substantial quantities of large-scale recordings of neural activity and detailed reconstructions of neuronal morphology and electrophysiology. Taking advantage of these complex neuronal collections poses several challenges. Chief among these are the development of accurate models as well as efficient algorithms for their simulation. While model generation is hindered by system complexity, a promising approach is to use as benchmarks simpler organisms, such as the nematode *C. Elegans* [1], for which behavioural and structural biology are well-known, and extend the methods and instruments thus developed to more complex systems. Even for relatively simple nervous system such as that of *C. Elegans*, the level of geometrical and biophysical detail can lead to models with thousands of degrees of freedom. To keep these models from becoming computationally intractable, model order reduction techniques have become an important tool neuroscience for extracting coherent features from large-scale networks that are not apparent at the neuron level [2].

We start from a detailed model of the *C. Elegans* nervous system (302 neurons, 6702 connections) including 3D geometrical descriptions and biophysical properties for each compartment [3]. Our goal is to generate a compressed model that accurately reproduces the input-output behaviour. We use a data-driven model reduction approach, based on Proper Orthogonal Decomposition (POD) and Discrete Empirical Interpolation Method (DEIM) [4]. Snapshots are generated in the NEURON simulator [5], representing the time response of the high-fidelity model for certain stimuli. POD modes are computed from Singular Values Decomposition (SVD) of the snapshots matrix (Figure 1A). The DEIM approximation reproduces the system's response with good accuracy even for order as low as 4 (model deviation around 10^{-2} , reaching 10^{-5} for order 10; the response of a randomly chosen neuron out of the 302 is shown in Figure 1B). The method allows a-posteriori error control, incrementally increasing order (adding POD basis functions) at no additional cost, since the SVD is already computed. POD modes and DEIM interpolation points hence generated are further used to approximate system response to different inputs, with good accuracy (Figure 1C). We suggest that the POD-DEIM method can generate low-order models that accurately predict the response of any neuronal network to a variety of different stimuli.

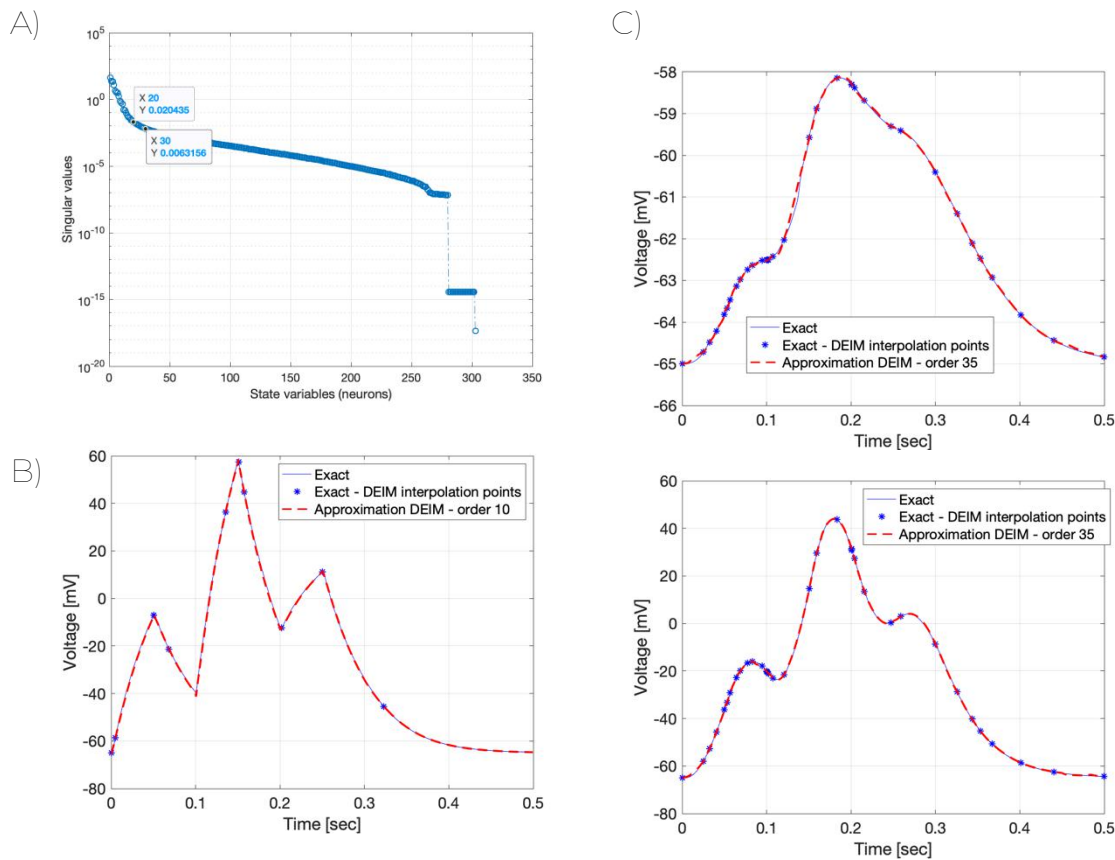


Figure 1. Model reduction with POD-DEIM. A) Singular values of the snapshots matrix. B) The response of one neuron (chosen randomly out of the 302 neurons) for the high-fidelity model and the POD-DEIM reduced model of order 10. C) The response of another neuron (chosen randomly out of the 302 neurons) for the high-fidelity model and the POD-DEIM reduced model of order 35, for different input.

References:

1. "WormBook, the online review of *C. elegans* biology," <https://www.wormbook.org/>, accessed: 2021-06-22.
2. B. Karasozen. Model Order Reduction in Neuroscience. arXiv preprint arXiv:2003.05133, 2020.
3. "OpenWorm," <http://openworm.org/index.html>, accessed: 2021-06-22.
4. S. Chaturantabut and D. C. Sorensen. "Nonlinear model reduction via discrete empirical interpolation." *SIAM Journal on Scientific Computing* 32.5 (2010): 2737-2764.
5. N. T. Carnevale and M. L. Hines, The NEURON book. Cambridge University Press, 2006.