MODEL ORDER REDUCTION OF MULTISCALE MODELS IN NEUROSCIENCE

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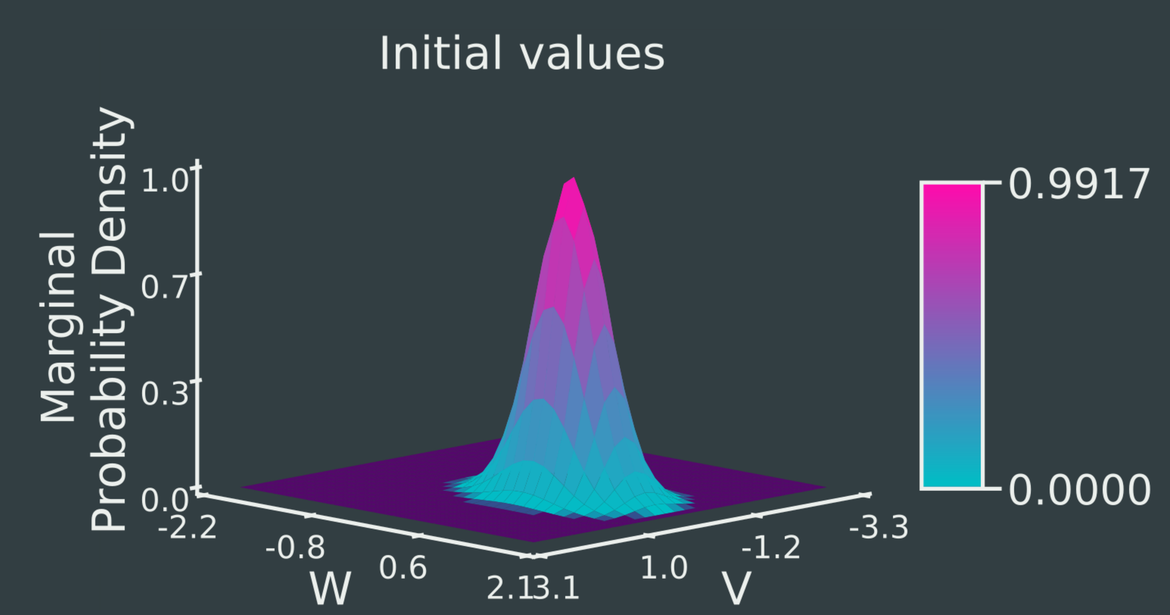
INTRODUCTION

The current trend in computational neuroscience is to incorporate multiple physical levels of the brain into mathematical models. Such comprehensive models with accurate system dynamics are necessary in order to increase understanding of different mechanisms in the brain. Mathematical analysis of these models is intractable, hence numerical methods are needed. However, their numerical simulation is very resource intensive.

We show that numerical simulation can be made significantly more efficient by employing mathematical Model Order Reduction (MOR). We use Proper Orthogonal Decomposition with Discrete Empirical Interpolation Method (POD-DEIM) [2]. Here we apply POD-DEIM to a mean-field model, in which cells are grouped together into populations based on their statistical similarities, in order to represent the dynamics of the system in terms of the mean ensemble behaviour. These populations can be described by a probability density function expressing the distribution of neuronal states at a given time. In this study we look at a McKean-Vlasov type equation that is derived from the FitzHugh-Nagumo (FN) neuronal network model as in [1]. This model uses the Fokker-Planck formalism, which results in a large system of coupled nonlinear partial differential equations (PDEs).



Initial marginal probability density calculated by integrating over synaptic conductance Y. V is membrane voltage and W is a recovery variable in the FN model.

DISCUSSION

As the need for multi-scale models of the brain is ever increasing, the ability to reduce the computational cost of these models is paramount. Mean-field models allow us to represent a population of neural cells in terms of their mean average, which in itself results in lower simulation times. Regardless, Fokker-Planck equations are computationally demanding to solve.

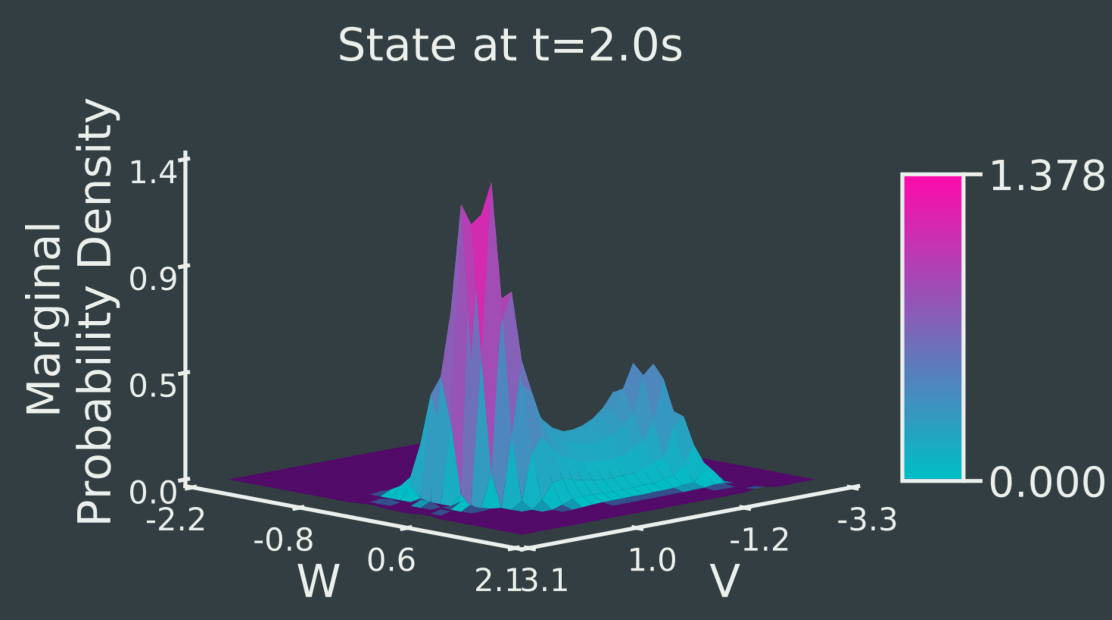
Nonlinearity of the model is a major challenge for solving *and* reducing models in neuroscience. As is evident from our results, the computation time of the present mean-field model can be further cut down by the implementation of the POD-DEIM method that is applicable to nonlinear systems.

We plan to implement the same approach to a number of different mean-field models in future projects to validate that these models are reliably reducible with mathematical MOR methods. Furthermore, employing reduced models in neural simulation software should be studied in order to encourage the adaptation of MOR for computational neuroscience.

RESULTS

The mean-field model is a McKean-Vlasov-Fokker-Planck equation [1] determined by the equation

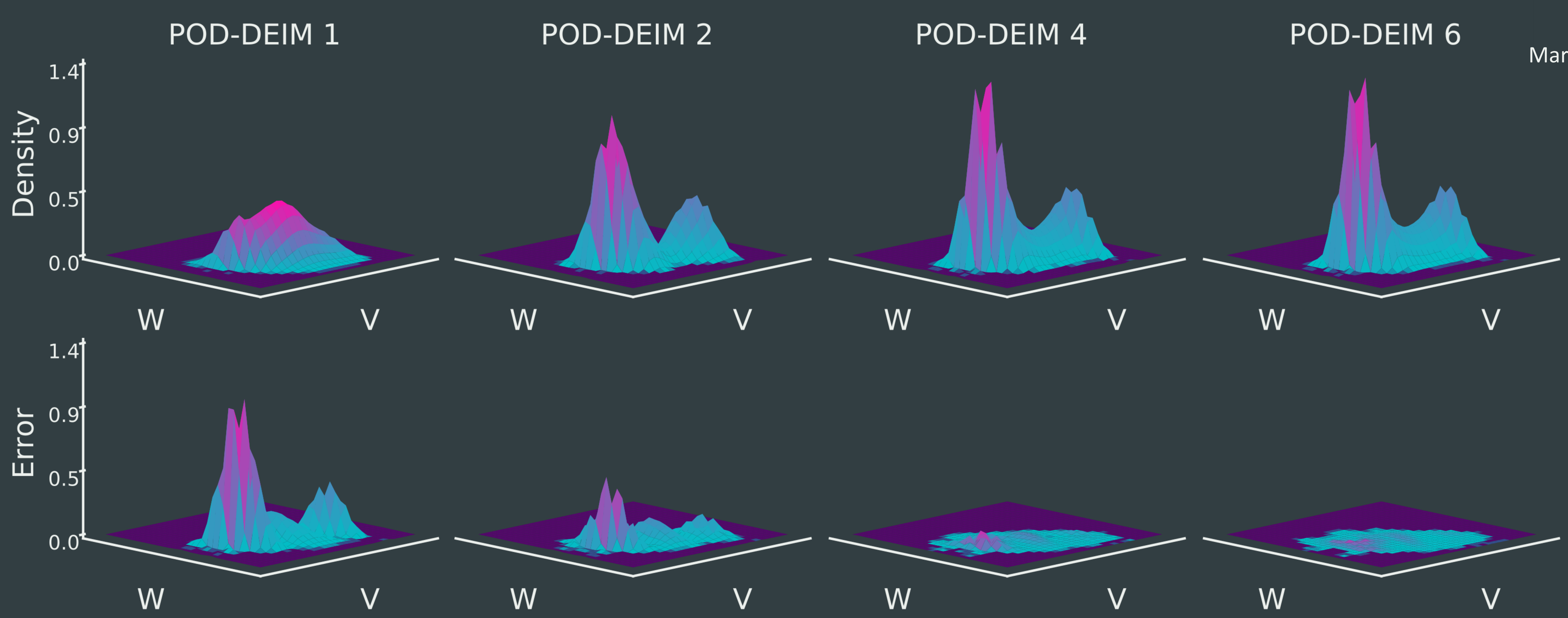
$$
\begin{aligned}
&\frac{\partial}{\partial t}p(t,V,W,Y) \\
&= \frac{1}{2}\sigma_J^2\overline{y}^2(t)\frac{\partial^2}{\partial V^2}[(V-V_{rev})^2 p(t,V,W,Y)] + \frac{1}{2}\sigma_{ext}^2\frac{\partial^2}{\partial V^2}[p(t,V,W,Y)] \\
&- \frac{\partial}{\partial V}\left[\left\{V-\frac{V^3}{3}-W+I-J(V-V_{rev})\overline{y}(t)\right\}p(t,V,W,Y)\right] + \frac{1}{2}\frac{\partial^2}{\partial Y^2}[\sigma_Y^2(V,Y)p(t,V,W,Y)] \\
&- \frac{\partial}{\partial Y}[\alpha_r S(V)(1-Y)-\alpha_d Y)p(t,V,W,Y)] - \frac{\partial}{\partial W}[a(V+b-cW)p(t,V,W,Y)], \\
&\overline{y}(t) = \iiint y p(t,V,W,Y)\, dv\, dw\, dy.
\end{aligned}
$$



Marginal Probability density after simulating for 2.0 seconds.

We discretize the model on a 30x30x30 grid using a fourth-order central difference scheme resulting in a system of 27 000 dimensions. Integrals are evaluated with Newton-Cotes method of order 6. The mean-field model is simulated for 2 seconds of biological time by a second order Runge-Kutta method with the initial states from the Gaussian distribution.

The reduced model recreates the original simulation correctly with very little error using less than 10 dimensions, while being over a thousand times faster to simulate. Reduction error increases rapidly as the dimension of the reduced model is lowered. A corresponding dimension-dependent gain in simulation speed is observed. These results show that mathematically reduced mean-field models are a highly potential approach towards modeling whole-brain dynamics.



State of reduced models at t=2.0s. Dimension increases to the right, which improves the approximation. Error is the absolute difference at each discretization point. POD dimension equals DEIM dimension in this illustration.

Read the QR-code and repeat the study!

METHODS

To reduce the dimensions of the model we applied the Proper Orthogonal Decomposition with Discrete Empirical Interpolation Method (POD-DEIM), a subspace projection method for reducing the dimensionality of general nonlinear systems [2]. We write the n-dimensional differential equation system in state space format

$$x' = Ax + f(x,t) + Bu(t)$$

POD and DEIM find matrices V_k, U_j, P_j, where $k, j \ll n$, that project the system to a small dimensional subspace. Here k is the POD dimension and j is the DEIM dimension. The reduced system is then

$$x'_k = V_k^* A V_k x_k + V_k^* U_j (P_j^T U_j)^{-1} P_j^T f(V_k, x_k, t) + V_k^* B u(t)$$

and with small dimensions simulating this system is computationally cheaper compared to the full system. At any time, the original variables can be restored with

$$x = V_k x_k$$

thus no variables are eliminated in the model reduction process.

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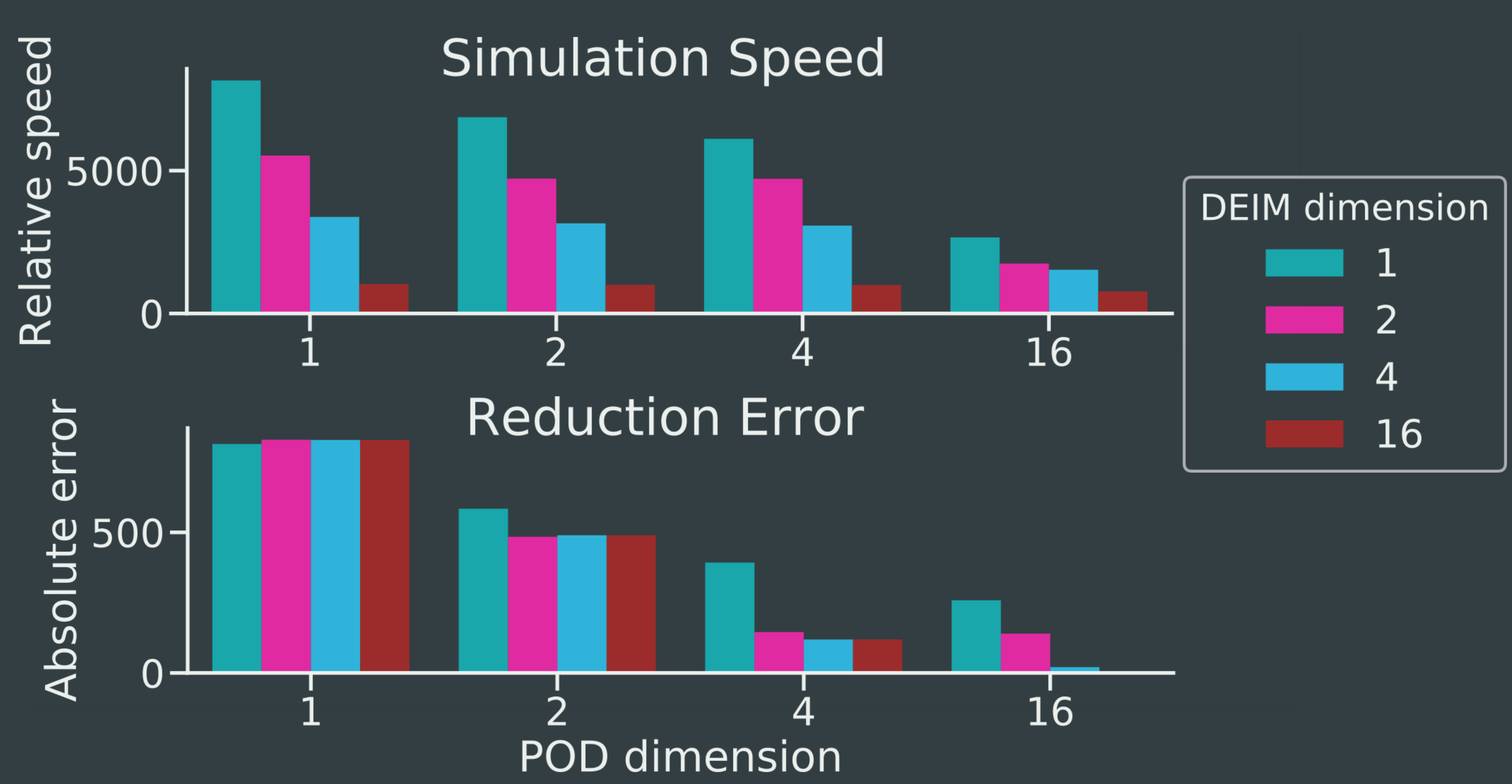

Gain in simulation speed as simulation time of the original model divided by the simulation time of the reduced model and reduction error as absolute difference at every discretization point summed. X-axis indicates POD dimension, while color shows DEIM dimension.

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[2] Chaturantabut, S. and Sorensen, D.C., Nonlinear model reduction via discrete empirical interpolation. SIAM Journal on Scientific Computing. 2010, 32(5), pp.2737-2764.