Hidden Dynamical Structure in Stochastic Intracellular Calcium Dynamics

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Intracellular calcium dynamics offer a biologically vital example of a noisy nonlinear system exhibiting diverse behaviors, including simple oscillations, bursting, and chaos. While deterministic models predict distinct dynamical regimes, intrinsic fluctuations from finite molecular populations in real cells often obscure these signatures. This raises the question of whether the underlying deterministic organization survives under realistic biological noise.

To address this, we use a stochastic model based on the feedback between calcium release and degradation, generating eight distinct dynamical states via a chemical Langevin description. Under realistic noise, these states become visually and statistically indistinguishable. We deploy a large-kernel convolutional neural network (CNN) designed to capture long-range temporal correlations over multiple oscillation cycles. Trained entirely on synthetic trajectories, the network distinguishes the eight noisy states with 90% accuracy.

Furthermore, the CNN generalizes remarkably well to real experimental calcium trajectories from pancreatic beta cells, achieving 96.8% classification accuracy. These results demonstrate that intrinsic cellular noise blurs but does not destroy the parameter-dependent deterministic structure of calcium oscillations. More broadly, this study proves that complex temporal patterns can be successfully recovered from highly fluctuating biological data using tailored deep learning methods.

Reference: J. Choi, A. L. Chanu, and S. Awasthi, PLOS Computational Biology 22, e1014240 (2026). DOI: 10.1371/journal.pcbi.1014240.