Discrete dynamics of the oscillations in excitatory-inhibitory neural networks

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The primary goal of this work is to characterize the oscillatory behavior of excitatory-inhibitory networks. Biologically, oscillatory neural synchronization can be defined as the process by which two or more neurons oscillate in relative phase angles. In transiently synchronized neural oscillations, different subsets of neurons fire at different phases of oscillatory cycles. Networks displaying these types of behavior arise in many areas of the nervous system such as the olfactory bulb of mammals, antennal lobe of insects, thalamocortical system for sleep generation, and in the visual cortex [1-4]. Models representing the observed behaviors are highly nonlinear, they include a large number of parameters and they typically exhibit a complex structure of oscillatory behavior. Mathematical analyses of these systems have considered reduced models for individual cells and special network architectures and has led to important insights for when these networks may lead to synchronous or anti-phase behavior [5-7], it still remains poorly understood how these results generalize to more biologically realistic networks with more realistic neuron models.

The approach used in this work for studying a general class of networks is to first reduce the full system of differential equations to a discrete-time dynamical system using Poincaré map like approach. This is done in a systematic way so that every parameter in the full model corresponds to some parameter, or combination of parameters, in the discrete model. The full model is reduced to a discrete one by constructing a map, which keeps track of which cells fire during each episode. That is, if it is known which cells fire during one episode, then the discrete map determines which cells fire during the next one. However, it turns out that it is not enough to simply keep track of which cells fire during an episode. One must also know what the calcium levels of these cells are. In some sense, the calcium levels can be thought of as a slow variable, in the sense of geometric singular perturbation theory. So if one knows which cells fire during an episode and what the calcium levels of all the cells are, then the map determines which cells fire during the next episode and what the calcium levels of all the cells are during the next episode.

I begin in the work by considering small excitatory-inhibitory networks with special network architectures. By considering small networks, I am able to more easily demonstrate how the discrete is constructed; moreover, I perform a detailed mathematical of the types of solutions that these networks exhibit and how they depend on parameters. The analysis leads to concrete formulas for the number of spikes each cell exhibits during each episode and conditions for when there exists bi-stability of solutions. In particular, I obtained an explicit formula for the number of spikes per burst depending on initial calcium values and system parameters. Using this formula, I constructed an explicit map and analyzed existence and stability of its fixed points for various networks. Discrete map also leads to a clear understanding of the roles each component of the model, including the ionic currents on network architecture, plays in generating the network behavior. I also give the results of a detailed study in which I compared solutions of the full model to the solutions of the discrete system. This analysis clearly demonstrates that the discrete model faithfully reproduces the full model's dynamics.

References

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