

# Dimension Reduction in the Modeling of Large-Scale Neuronal Networks

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We introduce a fast population density method for simulating the activity of large networks of neurons with realistic (arbitrary) synaptic kinetics. This method is faster than conventional simulation and is accurate in test populations of neurons.

A small section of cortex, one cubic millimeter in volume, typically contains a network of thousands of neurons and millions of synapses. A great challenge is to try and understand the behavior of networks like this and larger. A realistic model of such a network is often simply too complicated to analyze.

Typically, in an effort to understand such networks, one will utilize Monte-Carlo simulations. Conventional methods of simulation tracking the state of each neuron and synapse require enormous amounts of computational resources. As well, it can be quite difficult to extract the dynamics of a large population of neurons from these simulations. One is forced to cut corners by over-simplifying the underlying neuron model or by reducing the number of neurons and synapses in the network for simulation. Such simplifications can result in a loss of the network dynamics that are observed in the physiology (e.g. post-inhibitory rebound or network oscillations). Ideally, one would like to enlarge these models in order to more closely approximate the networks in the brain.

Efforts to understand the dynamical behavior of large-scale populations of neurons have focused on treating the population firing rate as the sole dynamical variable that describes a population. These methods are generally based on considerations of the steady-state input-output relationship of a neuron. Much research in population dynamics has been based on the Wilson-Cowan equations for the population firing rate. However these methods can fail to capture many qualitative aspects of the population dynamics (e.g. rapid transients) and can miss behavior at low firing rates. As well, these methods ignore the intrinsic noise in a neuronal system.

Here we turn to an alternative method that is a valuable tool both for uncovering the dynamics of large-scale neuronal networks and for the efficient simulation of such networks, based on ideas introduced by Knight, Sirovich and colleagues (Knight *et al.*, 1996). In the population density framework, one tracks the evolution of a probability density function (PDF) that describes the distribution over the state space of the neurons in each population. In neural network applications, this probability density is used to determine the proportion

of neurons in the population occupying a certain volume of state space. In these networks, the neurons are coupled together by stochastic synapses. This technique allows for the simulation of networks which are, in effect, of unlimited size.

The first Nykamp and Tranchina (2000a) implementation of this method uses an integrate-and-fire point neuron model with instantaneous synapses. In this model, the state of a neuron is completely described by its membrane potential; hence, the PDF is one-dimensional. The population firing rate is given by the flux of probability across the threshold voltage for firing an action potential. The evolution equations are a set of coupled partial differential integral equations, and numerical methods were developed for efficiently solving these equations.

Here we extend the method to include non-instantaneous excitatory and inhibitory synaptic kinetics. There are both physiological and theoretical motivations for this extension. The excitatory conductances gated by the NMDA (N-methyl-D-aspartic acid) class of glutamate receptors have very slow kinetics. NMDA receptors are found throughout the central nervous system and are thought to play an important role in synaptic plasticity. The metabotropic class of glutamate receptors gate a cation conductance through a second messenger system with slow kinetics. There are theoretical reasons to believe that the details of synaptic kinetics in general determine the stability of asynchronous activity and the degree of population synchrony in coupled networks (Abbott *et al.*, 1993).

In this setting of non-instantaneous synaptic kinetics, the state of the neuron is not only described by its membrane potential but also by the state of its synaptic currents. Thus the state space may be high-dimensional. This increase in dimensionality leads to an exponential decrease in the computational efficiency of the population density method.

A one-dimensional model for this high-dimensional process is detailed in Haskell, Nykamp and Tranchina (2001). Although this method appears to work well, the authors also discussed its breakdowns. As this is purely a modelling approach, the question remains about how these breakdowns relate to the modelling versus the probability density method.

A dimension reduction technique for a network with slow inhibition and instantaneous excitation was explored by Nykamp and Tranchina (2000b). This technique was insufficient in the presence of slow excitation. We extend upon this method in order to find an exact evolution equation for the voltage-marginal density function in the presence of slow synaptic kinetics.

We find this approach to be a surprisingly accurate description of the neuron population. To demonstrate this accuracy, we compare the firing rate of the population to that of Monte-Carlo simulation of analogous populations of integrate-and-fire neurons.

The speed of the population density approach will facilitate the simulation of larger and more complex neural networks than is reasonable by direct Monte-Carlo simulation of individual neurons. In our test simulations we find the population density method to be about one hundred times faster than direct simulation. Hence, the population density method may be a valuable tool for the modeling of large-scale neural networks in the brain.

## References

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