

Biologically plausible solutions for spiking networks with efficient coding

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Understanding how the dynamics of neural networks is shaped by the computations they perform is a fundamental question in neuroscience. Recently, the framework of efficient coding proposed a theory of how spiking neural networks can compute low-dimensional stimulus signals with high efficiency. Efficient spiking networks are based on time-dependent minimization of a loss function related to information coding with spikes. To inform the understanding of the function and dynamics of biological networks in the brain, however, the mathematical models have to be informed by biology and obey the same constraints as biological networks. Currently, spiking network models of efficient coding have been extended to include some features of biological plausibility, such as architectures with excitatory and inhibitory neurons. However, biological realism of efficient coding theories is still limited to simple cases and does not include single neuron and network properties that are known to be key in biological circuits. Here, we revisit the theory of efficient coding with spikes to develop spiking neural networks that are closer to biological circuits. Namely, we find a biologically plausible spiking model realizing efficient coding in the case of a generalized leaky integrate-and-fire network with excitatory and inhibitory units, equipped with fast and slow synaptic currents, local homeostatic currents such as spike-triggered adaptation, hyperpolarization-activated rebound current, heterogeneous firing thresholds and resets, heterogeneous postsynaptic potentials, and structured, low-rank connectivity. We show how the complexity of E-E connectivity matrix shapes network responses.

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