# Hierarchical generalized linear models of dendritic integration and somatic membrane potential

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Accumulating evidence suggests that dendritic trees play a crucial role in single-neuron information processing. While dendritic integration is currently studied experimentally and using compartmental or cable-theoretic models, there exists no simple, analytically tractable, and canonical mathematical model for dendritic processing. Poirazi et al. (2003) suggested that the thin dendrites of pyramidal neurons may be viewed as a "two-layer neural network" in which a weighted sum of the synaptic inputs to each dendrite is passed through a dendrite-specific sigmoidal nonlinearity before being globally summed to yield the somatic membrane potential. However, their approach focused only on static inputs and output and a particular subclass of dendrites of a particular subclass of neurons.

We developed a data-driven model of dendritic integration by building hierarchies of generalized linear models (GLMs), which have previously been successfully applied to modeling the stimulus-dependent spiking behavior of sensory neurons (Pillow et al., 2008). Our hierarchical GLM model generalizes previous work by (1) representing the dependence of a cell's somatic membrane potential on arbitrary spatiotemporal inputs to its dendrites, rather than only static inputs, and (2) flexibly inferring the appropriate hierarchy of GLMs from experimental data, rather than assuming *a priori* the number of layers and particular identification of synapses with subunits. We demonstrate the success of a maximum likelihood fitting procedure on synthetic data from single-dendrite and two-layer networks.

In subsequent work, we validate our fitting procedure on synthetic data from GLM hierarchies of more than two layers. We also explore the success of our framework in modeling synthetic data from compartmental models and data from glutamate-uncaging experiments produced by the labs of Michael Häusser, Judit Makara, and Szabolcs Káli. In doing so, our method allows us to assess how "functional" morphology, that is the GLM hierarchy inferred from electrophysiological data, relates to anatomical morphology.

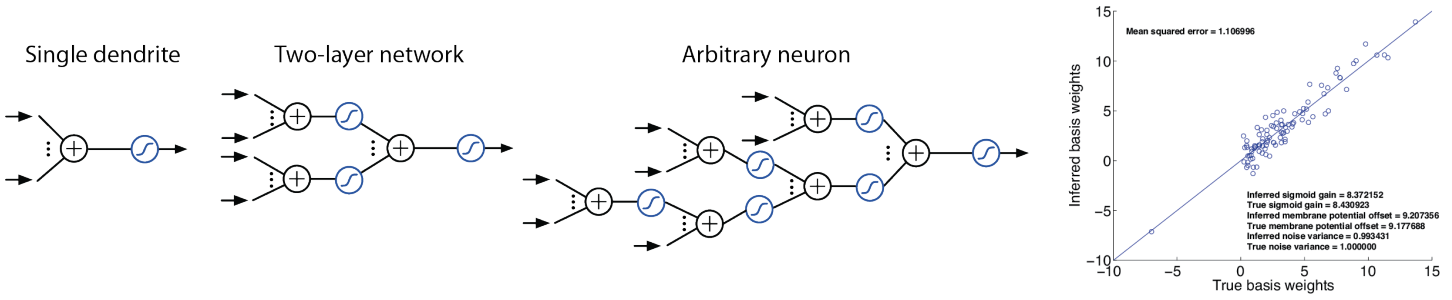


Figure 1: *Left: Schematic representation of a single dendrite, two-layer network, and arbitrary neuron using hierarchical GLMs. Right: Successful estimation of GLM parameters for a single-dendrite network.* Left: Black arrows represent synaptic inputs, black circles weighted summations, and blue circles nonlinearities. Synaptic inputs include both immediate and recent inputs, so that weighted summations are taken over both space and time and cells may exhibit a (nonlinear) dependence on spatial and temporal features of their inputs. Formally, we denote the relevant stimulus history at time $t$ for a single dendrite with $N$ synapses and memory length $\tau_{max}$ as the $N\tau_{max}$-length column vector $\mathbf{s}(t)$, where the first $N$ element represent the vector of synaptic inputs at time $t$, the second $N$ elements the inputs at time $t-1$, and so on. We assume that this spatiotemporal pattern of inputs is passed through a linear filter $\mathbf{k}$ followed by a global nonlinearity $g(\cdot)$, which we take to be sigmoidal, and that the noise $\eta(t)$ is additive, white, zero-mean, and Gaussian. In this case, the somatic membrane potential at time $t$ is given by $v(t) = g\left(\mathbf{k}^T\mathbf{s}(t)\right) + \eta(t)$. The two-layer network is formed by taking the weighted summation of several single-dendrite GLMs, while in general, neurons are modeled as arbitrarily deep hierarchies of GLMs. Right: Data was generated from a single-dendrite model akin to that described in this paragraph, except with the temporal dependence of the linear filters represented as a weighted summation over smoothly varying basis functions (Pillow et al., 2008). The scatterplot depicts the success of the maximum likelihood estimation of the basis function weights, while in-figure text summarizes the accurate estimation of other model parameters.