Dendritic subunits: the crucial role of input statistics and a lack of two-layer behavior

DJ Strouse*, Balázs Ujfalussy, Máté Lengyel

Computational & Biological Learning Lab, Dept. of Engineering, University of Cambridge

*present address: Dept. of Physics, Princeton University

Accumulating evidence suggests that dendritic trees play a crucial role in single-neuron information processing, yet there exists no simple, canonical formalization of dendritic computation. At one extreme, multi-compartmental models retain as much biophysical detail as possible, enabling them to exhibit the spatial and temporal dendritic nonlinearities observed in experiments, but sacrificing ease of fitting, mathematical tractability, and computational interpretability. At the opposite extreme, heuristic "two-layer network" models [Poirazi et al., Neuron 2003, Polsky et al., Nat. Neuro. 2004], which assume that the somatic membrane potential is produced by passing the instantaneous synaptic inputs through a two-layer linear-nonlinear cascade, are easy to analyze mathematically and interpret computationally but were designed to work only with static inputs and outputs, restricting their experimental application to artificial stimulus protocols involving brief, intense stimulation, rather than extended spike trains with realistic statistical properties. Moreover, because of this restriction, the associated metrics for judging nonlinear dendritic behavior were based only on either instantaneous firing rates or peaks/means of somatic membrane potentials, rather than predictiveness of dynamically changing firing rates or full membrane potential traces.

Here we propose a model class consisting of a hierarchical cascade of linear-nonlinear stages (hLN model) that retains the simplicity and interpretability of the two-layer network model class but generalizes it to handle dynamic inputs, model dendritic trees of arbitrary complexity, and be judged by its predictiveness of full somatic membrane potential traces. By fitting the hLN model to data generated from a biophysically realistic multi-compartmental model of a cortical pyramidal neuron, we demonstrate how the nonlinear dendritic properties discovered depend on the stimulation protocol and synapse locations. In particular, we find that, over a wide range of synaptic input statistics and in marked contrast to previous findings using static inputs and outputs, two-layer models offer little to no improvement over one-layer models in capturing the behavior of cortical pyramidal neurons.

Additional detail: A pictoral representation of the hLN model is presented in Figure 1. Two biophysical model experiments are shown in Figures 2 & 3. We used the cortical pyramidal neuron model with AMPA and NMDA synapses described in [Branco et al., Science 2010]. The first experiment sought to demonstrate a simple point – that the identification of dendritic nonlinearities would depend on both synapse location and correlations in the stimulus (i.e. input spike trains). To do so, we stimulated 10 synapses that were either clustered on a single basal dendrite or distributed across 10 different branches, using a stimulus protocol that was designed to allow parametric variation of correlations with fixed marginal statistics of $r = 20Hz$ stimulation to each synapse. Results are shown in Figure 2. The second experiment sought to elicit two-layer behavior by stimulating 20 synapses, 10 each on 2 different branches, using a similar but modified protocol. Results are shown in Figure 3.
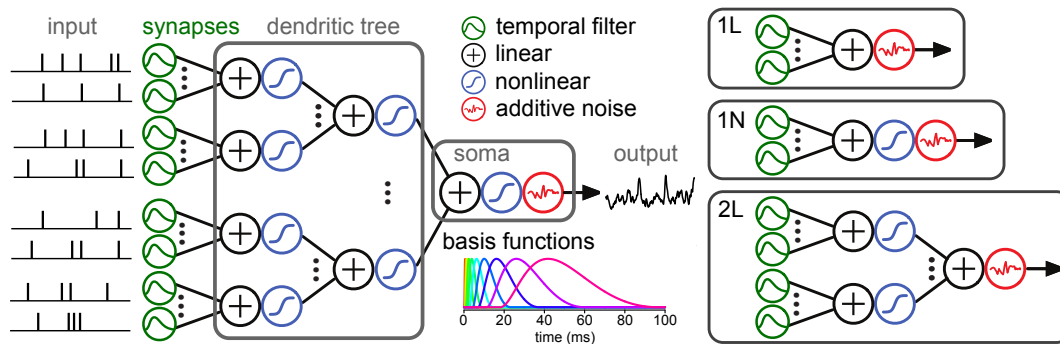

Figure 1: **Pictoral representation of the hLN model.** Spike train inputs are passed through temporal filters (representing synapses), followed by a hierarchy of LN cascades (representing dendrites), and a final linear or LN step (representing the soma), along with the addition of additive white Gaussian noise, to produce a somatic membrane potential. Example models at far right are a one-layer linear model (1L), one-layer nonlinear model (1N), and a two-layer linear model (2L); the larger example model at left is a three-layer nonlinear (3N) model.
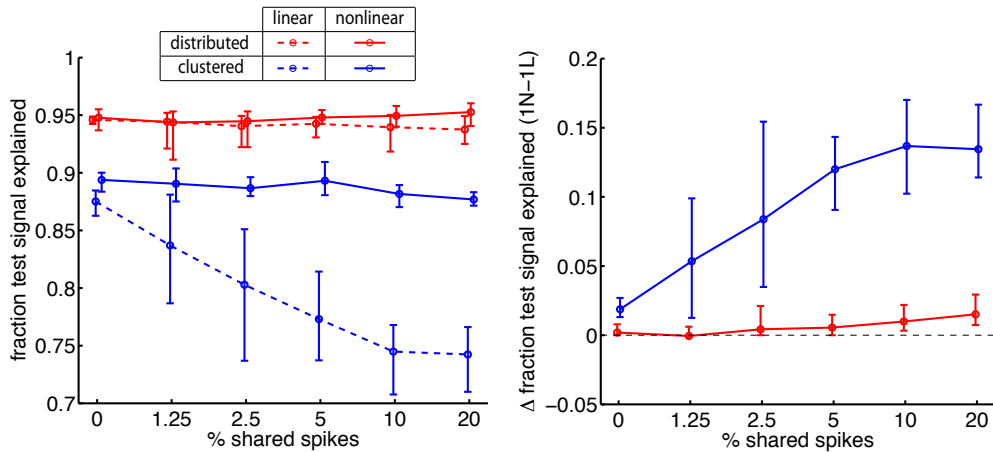
Figure 2: **Clustered vs. distributed synapses and independent vs. synchronized inputs.** The input spike train to each synapse consisted of two Poisson components: (1) an independent component with rate $(1 - \alpha) r$, where $0 \leq \alpha \leq 1$, and (2) a shared component with rate αr. While the independent component was private to each synapse (i.e. 10 different trains were generated), the shared component was common to all synapses (i.e. only one was generated). Thus, α denotes the fraction of shared (synchronous) spikes, $\alpha = 0$ corresponds to independent inputs, and $\alpha = 1$ corresponds to synchronous inputs only. The spike train to each synapse then consisted of the sum of the independent and shared spike trains. Each condition (i.e. clustered vs. distributed, value of α) was repeated for 10 trials, each with 16s of training data and 4s of test data. Model performance was measured by the fraction of the test signal explained, defined as $f \equiv 1 - \frac{\epsilon}{s}$ where ϵ is the root-mean-square (rms) test set prediction error and s is the s.d. of the test signal (i.e. the test set somatic membrane potential). The right plot shows the trial-by-trial difference between f for the 1L and 1N models (1N minus 1L). Circles and error bars indicate across-trial means and 95% confidence intervals. Note that nonlinear behavior is elicited only for correlated inputs to clustered synapses; distributed synapses or independent inputs both lead to linear behavior.
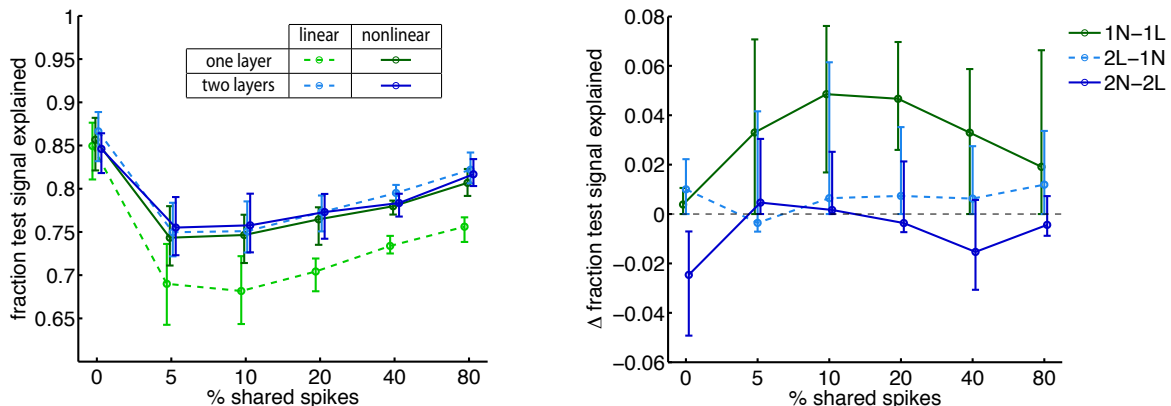

Figure 3: **Two branches with varying amounts of within- and across-branch synchronization.** The input spike trains again were the sum of an independent and shared component, here totalling $r = 2Hz$ for each synapse. Each shared spike event was this time shared across a random subset of the synapses (8 of 20), regardless of location. Thus, the shared events included ones in which one branch was stimulated much more strongly than the other (asymmetric), as well as events in which both branches were stimulated evenly (symmetric). For each α, we ran 12 trials, each with 32s of training data and 8s of test data. We expected that this stimulus protocol would elicit two-layer behavior because the asymmetric events would be above threshold for the local nonlinearities, while the symmetric events and independent Poisson inputs would be below threshold and elicit only linear integration, leading the 2L model to significantly outperform the 1L and 1N models. Note that despite creating conditions in which the two-layer models were expected to outperform one-layer models, the 1N model was as good as any two-layer model — thus showing no evidence for two-layer behaviour in active dendrites.

2