Using a Network Modeling Environment to Evaluate Statistical Methods of Identifying Network Structure

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Motivation

Validate and develop statistical methods in neuroscience.

- Recent advances in network modelling provide a framework for controlling the generation of spiking data.
- Statistical methods of evaluating network structure can thus be validated, and new methods developed.

Goals and Methods

Modify LIF to get at true firing rate. Create interesting network.

- Using NENGO, a large scale neural simulation package, networks with complex and interesting dynamics can be generated.
- NENGO allows access to and modification of input to the network through any node and connections between nodes.
- A modification of normal spiking LIF neurons, probabilistic LIF (p-LIF), is used to get accurate instantaneous firing rates (iFRs) of individual neurons.
- p-LIF neurons have probability of firing governed by their voltage as follows:

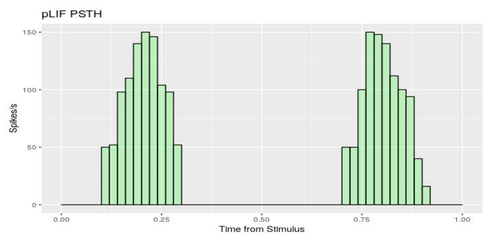
$$P(firing|v) = \frac{e^{k*v+b}}{1+e^{k*v+b}}$$

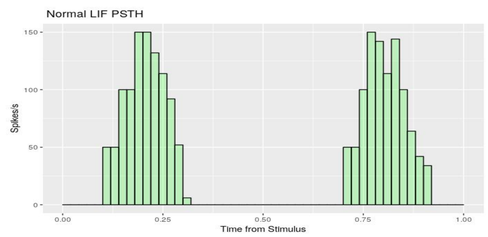
- The parameters of this distribution are adjusted to fit the behavior of normal LIF neurons.

p-LIF Results

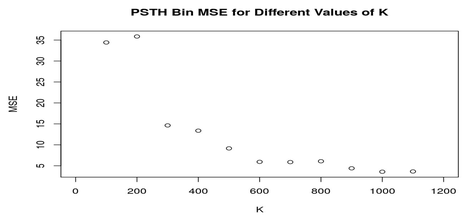
pLIF neurons fit the PSTH of LIF neurons well given stochastic input. ISI distributions are more difficult to match.

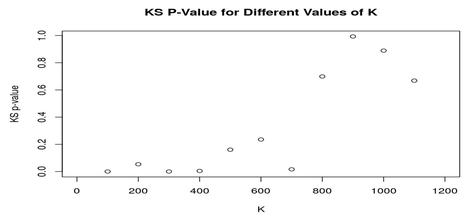
- p-LIF neurons matches LIF behavior well, as measured by MSE between PSTH bins and the KS-statistic between each neuron model distribution of inter-spike intervals, over 100 trials.
- Neurons are stimulated with spikes generated from an inhomogeneous Poisson process, itself modelling the input of various proportions of spiking excitatory and inhibitory neurons.
- Threshold of normal LIF neurons is defined as “1”. Inputs and the firing distribution of p-LIF neurons are scaled accordingly.



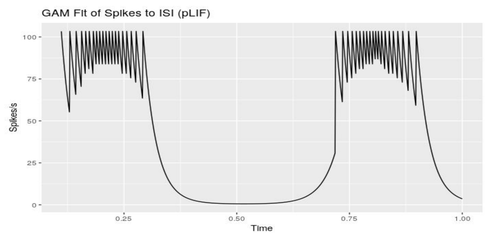


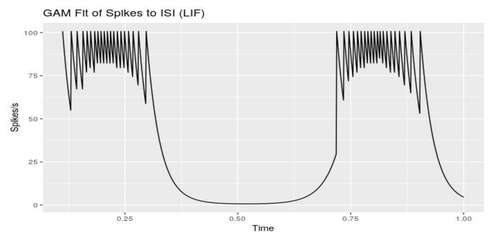
- The PSTH of a p-LIF neuron (with k= 100, b = 97.8) is visually very similar to that of the normal LIF.
- The binning of the PSTH, as well as the stochastic input, compensate for the probabilistic nature of the p-LIF.





- Bin MSE decreases largely uniformly as model becomes less stochastic.
- KS-test not significant until very high values of *k*, corresponding to a more deterministic p-LIF.





- A Poisson GAM with a log link is fit over just ISI data for a single trial. Both the p-LIF and LIF neuron models have fitted rates similar to the PSTH.

Current Steps

Fit iFR and compare to actual. Develop and test a full network.

- Fit iFR with a Poisson regression with spline basis elements on time and time since last spike.

$$\log\lambda(t, t-s_*(t)) = \log\lambda_1(t) + \log\lambda_2(t-s_*(t))$$

- Set connections between p-LIF neurons that produce interesting network dynamics.
- Evaluate statistical methods for the identification of network structure.

Conclusion

ISIs are potentially a problem. Must compare estimated iFR to true iFR.

- Though the p-LIF PSTH visually matches that of the normal LIF well for even low parameter values, the KS test is not significant.
- The p-LIF has a different distribution of ISIs from the LIF due to the probabilistic nature of spiking - it will spike *around* the same time the LIF will spike, but with some variation.
- This is the cause of the non-significant KS test for low values.
- The iFRs of each neuron model *appears* to be fit very well by a Poisson GAM model including only ISIs across one trial. Inspection of the actual iFR of the p-LIF model will confirm or refute this.

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