Poster presentation

Computing a generative model for neural codes

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Introduction

Part of neuroscience is to understand the link between biophysical events that occur within a neuron and the information that is passed from one neuron to another. There are two theories for neural activities. The label line theory suggests that a neuron, or a group of neurons, signal a specific stimulus when active. The across-neuron-pattern theory argues that information about a stimulus is carried as a pattern from one neuron to another. Based on the across-neuron-pattern theory, we've created a Boolean Network (BN) to model the encoding process of four different taste stimuli to spike trains.

Background

The BN is a network of Boolean variables, or nodes, with values based on other nodes in the network. A BN can be computationally derived from given observed trajectories [1]. Inference starts by developing a transition table for each node, differing by the number and selection of parents assigned to a node. The inference process determines an optimal parent node combination for each node by multinomial hypothesis testing.

Data

Data consisted of taste-evoked spike trains recorded from the nucleus of the solitary tract (NTS; the first central relay in the taste pathway) of 18 male urethane-anesthetized-Sprague-Dawley rats [2]. All subjects were exposed to four stimuli: 0.1 M NaCl, 0.5 M Sucrose, 0.01 M Quinine HCl, and 0.01 M HCl in separate trials. Testing followed a strict order per stimulus: 10 sec baseline period with no stimulus present, 5 sec exposure to the stimulus, 5 sec waiting period, and a 20 sec distilled water rinse. Repeated stimulus trials continued for as long as the cell was well isolated. Data were recorded as spike trains with millisecond precisions.

Methods

Spike trains were discretized to binary sequences based on 10 msec intervals. Four input BN nodes were created to represent each stimulus. A stimulus node was assigned a value of 1 if the spike train under consideration was exposed to that stimulus. An output BN node was created for spike generation. Each trajectory was diversified by adding $\log_2 n$ internal nodes to the BN, n being the length of the longest trajectory. These additions constitute a hypothetical molecular interaction model occurring with a neuron. Afterwards, a BN was inferred from the diversified trajectories. Simulated trajectories were generated by the inferred BN, which were then compared with the diversified trajectories using the Hamming distance.

Results and conclusion

This is ongoing work with initial results expected by the end of February.

References

1. Song M, Lewis CK, Lance ER, Chesler EJ, Kirova R, Langston MA, Bergeson SE: **Inferring transcriptional regulation through logical networks from temporal mouse brain gene expression data.** Proceedings of 2nd Conference on Foundations of Systems Biology in Engineering (FOSBE), Stuttgart, Germany 2007:31-36.
2. Di Lorenzo PM, Victor JD: **Taste response variability and temporal coding in the nucleus of the solitary tract of the rat.** J Neurophysiol 2003, **90**:1418-1431.