BMC Neuroscience

BioMed Central

Oral presentation

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Fast and reliable methods for extracting functional connectivity in large populations

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from Eighteenth Annual Computational Neuroscience Meeting: CNS*2009
Berlin, Germany. 18–23 July 2009

Published: 13 July 2009

BMC Neuroscience 2009, **10**(Suppl 1):O9 doi:10.1186/1471-2202-10-S1-O9

This abstract is available from: http://www.biomedcentral.com/1471-2202/10/S1/O9

The simplest model for describing multi-neuron spike statistics is the pairwise Ising model [1,2]. To start, one divides the spike trains into small time bins, and to each neuron i and each time bin t assigns a binary variables $s_i(t)$ = -1 if neuron i has not emitted any spikes in that time bin and 1 if it has emitted one or more spikes. One then can construct an Ising model, $P(s) = Z^{-1}\exp\{h's+s'Js\}$ for the spike patterns with the same means and pair correlations as the data, using Boltzmann learning, which is in principle exact. The elements J_{ij}, of the matrix J can be considered to be functional couplings. However, Boltzmann learning is prohibitively time-consuming for large networks. Here, we compare the results from five fast approximate methods for finding the couplings with those from Boltzmann learning.

We used data from a simulated network of spiking neurons operating in a balanced state of asynchronous firing with a mean rate of ~10 Hz for excitatory neurons. Employing a bin size of 10 ms, we performed Boltzmann learning to fit Ising models for populations of size N up to 200 excitatory neurons chosen randomly from the 800 in the simulated network. We studied the following methods: A) a naive mean-field approximation, for which J is equal to the negative of the inverse covariance matrix, B) an independent-pair approximation, C) a low rate, small-population approximation (the low-rate limit of (B), which is valid generally in the limit of small Nrt, where r is the average rate (spikes/time bin) and t is the bin width [3], D) inversion of the TAP equations from spin-glass theory [4] and E) a weak-correlation approximation proposed recently by Sessak and Monasson [5]. We quantified the quality of these approximations, as functions of N, by computing the RMS error and R^2, treating the Boltzmann couplings as the true ones. We found, as shown in figure 1, that while all the approximations are good for small N, the TAP, Sessak-Monasson, and, in particular, their average outperform the others by a relatively large margin for N. Thus, these methods offer a useful tool for fast analysis of multineuron spike data.

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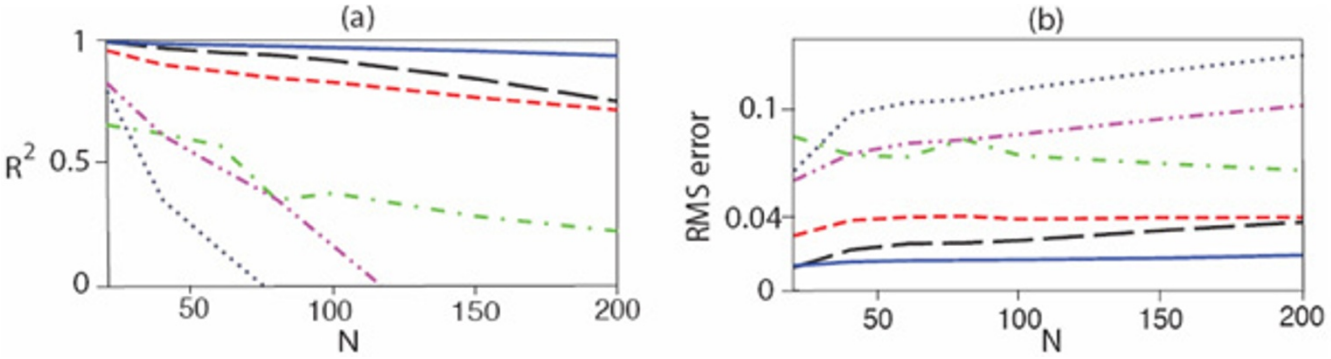

Figure 1
(a) R^2 and (b) RMS error for various approximate methods. Green (dashed dotted), naive mean-field; Purple (dashed double-dotted) low-rate, small *N*; Gray (dotted) independent-pair; Red (dashed), TAP; Black (dashed), Sessak-Monasson; Blue, average of TAP and Sessak-Monasson.