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Effective structure inference from multi-phase cortical neural activities

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Abstract— Effective structure of neuronal networks is inferred from firing data using Expectation-Maximization (EM) in conjunction with the inverse Ising model. We demonstrate that our algorithm infers the effective connectivity, neuronal cell-type and coupling strength using controllable synthetic and emulator data. Furthermore, we show that the neural activity predictions obtained using the inferred structures have a good fit with the original data.

1. Introduction

Structured in-vitro cortical brain tissues have attracted increasing attention in recent years as a promising tool for biological computation. For example, cortical brain organoids have been used as processing units for non-linear curve prediction [1] and cortical neural networks have been utilized for decision-making in a simulated gaming environment [2]. These applications are based on the assumption that plasticity and learning occur in cortical neural networks, in the form of topological changes and synaptic strength modifications, allowing the network to evolve into a structure capable of performing specific tasks with appropriate stimulation. It is essential to develop a tool that can reveal the emerging effective cortical network structure to understand the mechanism behind biological computing devices. Although there are some existing studies that offer principled methods for inferring the effective structure of cortical neural networks from their activities, they all have certain limitations.

Commonly used techniques for identifying effective connections, such as measuring transfer entropy [3], are strongly affected by the sparsity of firing rates and the need to set an appropriate threshold for identifying the existence of connections, both of which can be somewhat heuristic. Statistical physics-based techniques have been developed for inferring the underlying directional interaction strengths between neurons, including the mapping of neural activities onto the kinetic Ising model with inference using mean-field approximation [4]. However, these methods are based on unrealistic assumptions, such as that the network is fully connected and synaptic strengths are uniform and Gaussian distributed with a small variance. Moreover, a principled technique for identifying excitatory and inhibitory connections, the existence of links between neurons and taking structural considerations into account is still lacking.

In this work, we have developed an algorithm to infer the structure of biological neural networks from firing patterns using Bayesian techniques, machine learning methods and models from statistical physics.

2. Method

To infer the structure of neural networks, we use the kinetic Ising model of statistical physics to represent the underlying interaction between binary spike activities. This non-equilibrium probabilistic model is a discrete-time, where the N system neurons are denoted by discrete variables $S_i(t) = \pm 1$ when neuron i is spiking or silent at time step t, respectively, for $i = 1, \ldots, N$. The transition probability of neurons at time t is given by

$$P(\mathbf{S}(t)|\mathbf{S}(t-1)) = \prod_{i=1}^{N} \frac{\exp\left[\left(h_i + \sum_j J_{ij} S_j(t-1)\right) S_i(t)\right]}{2\cosh\left(h_i + \sum_j S_j(t-1)\right)}, \quad (1)$$

where the coupling strength J_{ij} represents the directional synaptic strength from neuron j to i. A negative (positive) value of J_{ij} suggests that j sends inhibitory (excitatory) signals to i when j spikes. Using the probabilistic model defined by the binary spiking activity data $\mathcal{D}$ and the imposed prior distribution $\mathcal{P}$, we can define the posterior probability $P(\mathbf{J}, \mathbf{H}|\mathcal{D}, \mathcal{P})$ and infer the magnitudes of $\mathbf{J}$ (cross-neuron interactions - directional synaptic links), and $\mathbf{H}$ (external field - firing properties of the individual neuron), directional connectivity and neuronal cell type by employing an Expectation-Maximization (EM) supported framework. Additionally, we can use Monte-Carlo simulations to predict neural activities by inserting the inferred variables back into Eq. 1.

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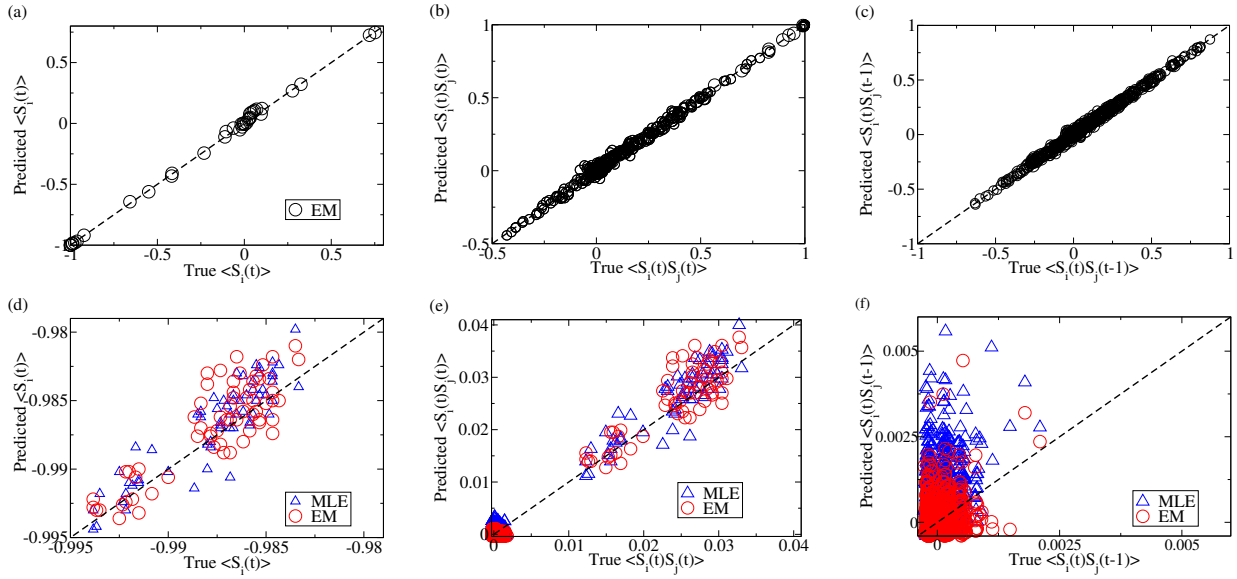

Figure 1: The panels (a), (b), and (c) illustrate the results by comparing the true and estimated values of the firing rate $\langle S_i(t)\rangle$, equal-time covariance $\langle S_i(t)S_j(t)\rangle$, and delayed-time covariance $\langle S_i(t)S_j(t-1)\rangle$, respectively, using the EM-inferred structure from data generated by a synthetic kinetic Ising model with a system size of $N = 20$ (angled brackets represent expectation values). On the other hand, the panels (d), (e), and (f) show the results of comparing the true and estimated values for the firing rate $\langle S_i(t)\rangle$, delayed-time covariance $\langle S_i(t)S_j(t-1)\rangle$, and equal-time covariance $\langle S_i(t)S_j(t)\rangle$, respectively, using the EM-inferred structure and Maximum Likelihood Estimation (MLE) from data generated by a dedicated neural activities emulator with $N = 20$ neurons.

3. Results

Our method has been tested on in-silico experiments using both synthetic data generated from the kinetic Ising model and neural activity emulator data that accurately simulates realistic scenarios. For the synthetic data, the system consists of 20 spins, and unlike conventional setups, we assume that the spins are sparsely connected and the coupling strength follows a mixture of 2 Gaussian distributions with positive and negative means (excitatory and inhibitory neurons, respectively). On the other hand, the emulator simulation consists of 20 neurons randomly distributed on a square panel, and the ratio between inhibitory and excitatory neurons is 2:8. The network connectivity and activities are first simulated based on [5]. Then, only binary spiking activities are used for the inference. As shown in Fig. 1, the predicted activities have a good similarity with both the synthetic and emulator data.

4. Discussion

By obtaining reliable effective connectivity of neural networks and predicting neuronal activities in silico, we can greatly reduce waiting times and improve the efficiency of in vitro experiments, leading to a better understanding of their physical properties. Furthermore, this approach can provide insights and a quantitative understanding of learning properties in cortical tissues in future studies.

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