

Inference of neuronal network topology: a sparse reconstruction approach

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Along the latests years the technological advancements have been fundamental to improve the recording capability from brain areas and neural populations [1]. For example, multi-site recordings can be achieved from thousands of channels (sites) with a good spatial and temporal resolution yielding a good description of the underlying network dynamics. Given that, the brain operates on a single trial basis such recordings are becoming important to understand the neural code [2]. As a first step, multi-site recordings allow to quantify the information flow in the network. The anatomical wiring (i.e. Structural Connectivity, SC) clearly plays a fundamental role to understand how cells communicate among them but it is often not well known neither it can by itself explain the overall network activity. Multi-site recordings can be used to infer statistical dependencies (i.e. Functional Connections, FC) among the recorded units and to track the information flow in the network [3]. On the other hand the Effective Connectivity (EC) denotes the directed causal relationship between the recorded sites. Experimentally, the EC is typically estimated by stimulating one cell and studying the effects on the connected elements. Alternatively the EC can also be studied by using a causal mathematical model between the recorded units data.

Importantly, multi-site recordings raise some limitations that need to be evaluated carefully before any further analysis. First, the experimental sessions are often severely limited in time. Second, the high dimensional data sets involve a set of numerical and mathematical problems that would be hard to face even with long enough recording sessions. These issues are common to different fields and have been coined as 'curse of dimensionality'. To overcome these issues, two approaches are typically foreseen. A first solution consists into a reductionist approach that projects the data on a lower dimensional space that can better elucidate the underlying processing. Another possibility consists into fitting the observed data to a low-dimensional model that captures the salient properties of the dynamics.

Recently, we introduce a model of effective connectivity that gets rid of the dimensionality problem by introducing a natural constrain of almost all biological networks: the sparseness among the connected units [4]. Other approaches, such as the multivariate autoregressive model, allow for the possibility of a fully connected network in which every node may influence all the other nodes. However this is somewhat unrealistic for biological networks (i.e. each neuron is directly influenced by only a small subset of neurons) and it also leads to practical challenges. Moreover, some of the major tools to understand the communication among neuronal populations are based on linear models although it is widely recognized that the interactions (i.e. synaptic currents) among neural cells are nonlinear. In order to capture nonlinear interactions between even short and noisy time series, we consider an event-based model. Then, we involve the physiological basis of the signal, which is likely to be mainly nonlinear.

Specifically, we suppose that we are able to observe the dynamical behaviors of individual components of a neuronal networks and that few of the components may be causally influencing each other. The variables could be time series from different parts of the brain. In order to introduce our method we have considered a simulated cerebellar granule cell network capturing nonlinear interactions between even short and noisy time series. Although the proposed EC algorithm cannot be applied straightforwardly to the experimental data, our preliminary results are quite promising from many point of views. First, despite the algorithm was applied only a short simulation (5 seconds) it achieved to filter out noisy from causal responses yielding a reliable estimate of the underlying connections in the network. Second, the approach is quite general and it could be further adapted to different types of electro-physiological signals. Third, the sparse reconstructions method is also quite robust respect to bidirectional connections in the network. This is of fundamental importance since it has been recognized in the latest years that bidirectional network motifs are quite abundant in the brain.

References

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