

EN.580.694: Statistical Connectomics

Final Project Report

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Understanding the Functional Organization of Neuronal Populations for Encoding Different Behavioral States

Opportunity

Information in the nervous system can be encoded at the level of neuronal ensemble [2]. These ensemble activities may directly represent perceptual objects in a distributed fashion and provide an organized substrate for downstream processing. Recent developments in electrophysiological recording with multielectrode array and two-photon calcium imaging have provided the possibility to obtain hundreds or even thousands single neuron activities with high temporal resolution in behaving animals [6]. These technologies have provided us great opportunities to explore the properties of neuronal ensembles in behaving animals and to test hypothesized neural algorithm with experimentally observed data [4, 5].

Challenge

In order to determine what information, such as behavioral states, is encoded in a population of neurons, a common approach is to use an ideal observer to decode behavioral states from recorded activities [3]. However, such analysis is usually unable to reveal the underlying organization and computational principle of the ensembles.

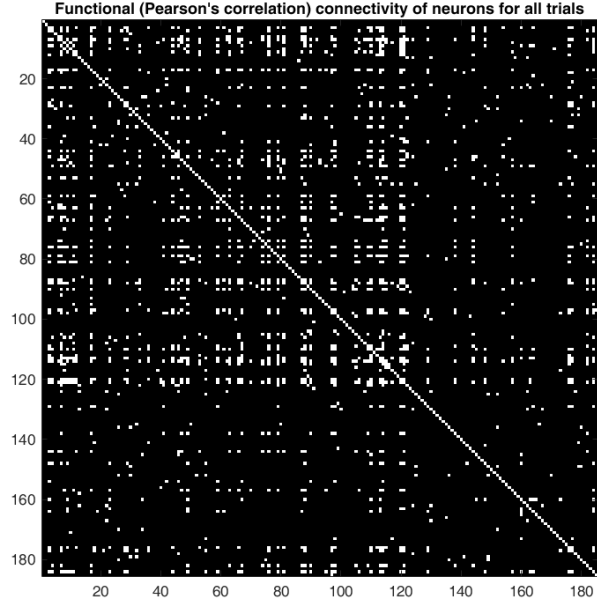
Data used in this project was obtained by two-photon calcium imaging of populations of layer 2/3 neurons in mice barrel cortex (part of primary sensory cortex where each barrel primarily receives input from one whisker) when animals were performing a whisker stimulation detection task with reward to the correct response. To represent different behavioral states including hit, miss, false alarm, and correct rejection with corresponding reward outcomes, does the observed neuronal population encode these states information collectively, or only a subset of neurons is encoding, or different subsets of neurons encode different states independently? To answer these questions, an analysis applicable to such high dimensional data while being able to preserve the intrinsic structure would be of great value.

Action

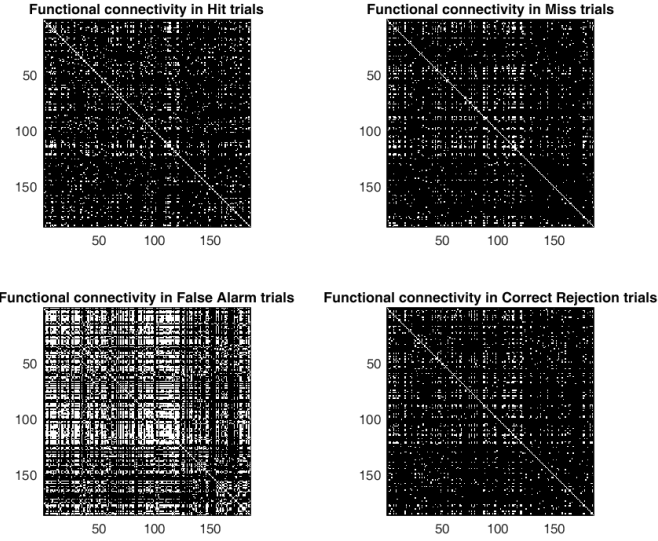
Statistical graph analyses have been applied on electrophysiology to reveal the temporal relationship of neural assemblies and their relevance to animal behaviors [1]. In this project,

Pearson's correlation matrices were computed from calcium signals ($\Delta F/F$) time series of 185 neurons. In order to convert the correlation matrices into adjacency matrices of functional connectivity graphs, any correlation value greater than 0.5 or less than -0.5 was set to 1 indicating

an edge, otherwise 0 meaning no connection. The same procedure was applied both to the whole session (i.e. all trials) (Fig.1A) and to each subset of trials with the same behavior states (Fig.1B).



A



B

Figure 1 Functional connectivity graphs of 185 neurons in the session (A) and in trails with four different behavioral states (B).

Stochastic Blocks Model ($SBM^k(\rho, \beta)$, $\rho \in \Delta_k$, $\beta \in (0, 1)^{k \times k}$) was used to reveal the intrinsic organization of neuronal subpopulations where the cluster numbers, k , represents the hypothesized number of subpopulations, ρ possesses subpopulation labels of each neuron, and β indicates probabilities of intra- and inter-subpopulational connections. The ρ was determined by performing K-means clustering on the adjacency matrix of the session, and the resulting class assignment was used for all following SBMs. Since we were trying to know the number of subpopulations, different k values (from 1 to 8) were chosen and β s were computed by fitting $SBM^k(\rho)$ to graphs of the four behavioral states, respectively (Fig.2).

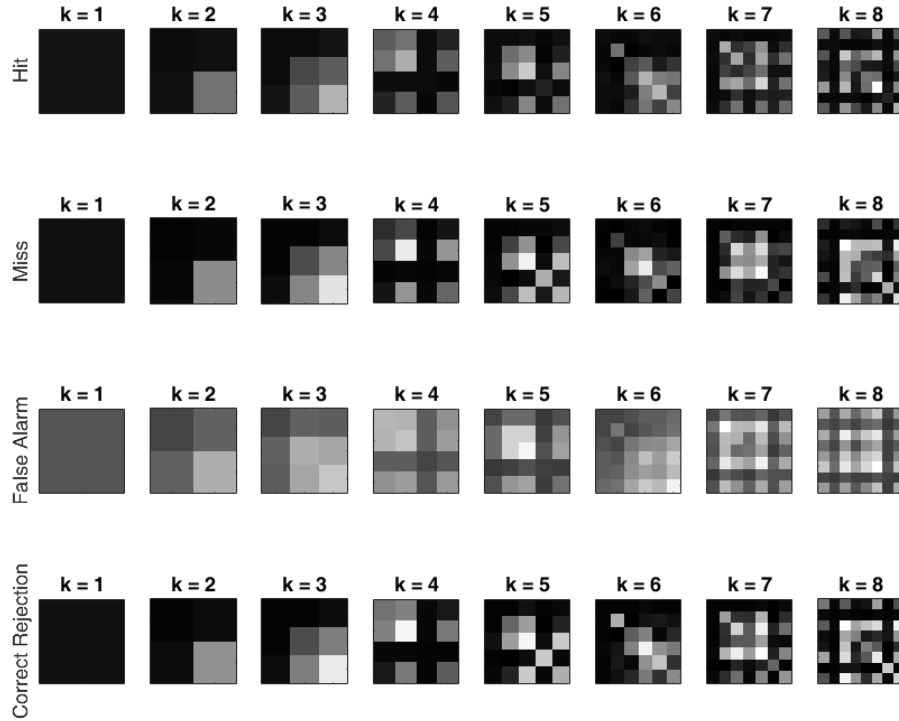


Figure 2 Fitting Stochastic Block Models with various cluster number, k , to data from four different behavioral states.

Optimization was performed to evaluate which model best explains different behavioral states. Specifically, the log-likelihoods that a graph sampled from the SBM of one behavioral state is drawn from another, $\sum_{s_i=1}^n \sum_{s_j=1}^n \text{Log}P(G_{s_i} | \rho_{s_j}, \beta_{s_j}), s_i \neq s_j$, was computed for each k (Fig.3). The model with least sum log-likelihood reflects the most necessary (may not sufficient) functional organization to hold and process information of different behavioral states.

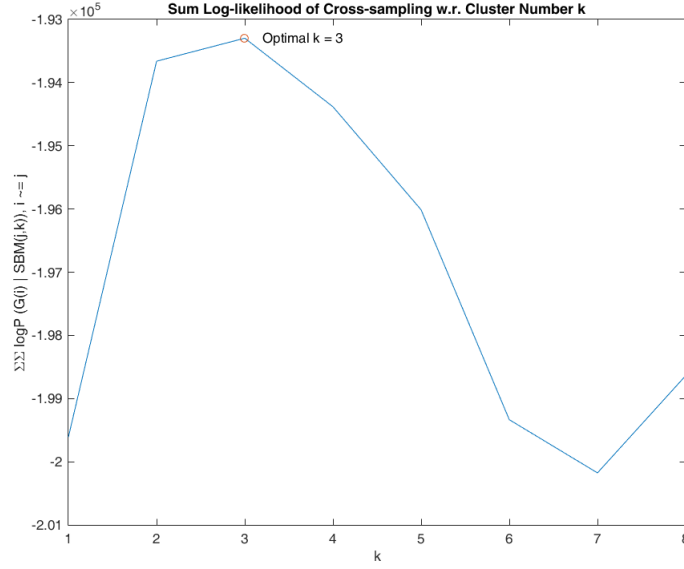


Figure 3 Optimization for the cluster number, k

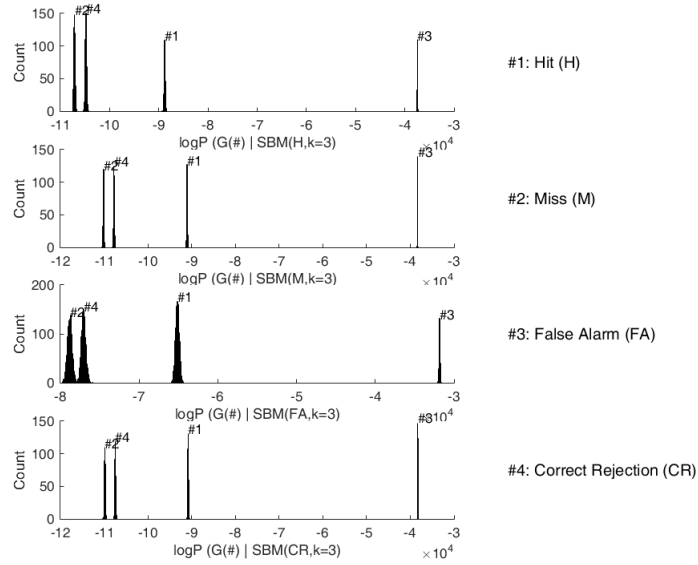


Figure 4 Parametric bootstrapping on the model (with the optimal cluster number) showing the degree of separation among different behavioral states.

Given this organization, it would be interesting to know to what degree was each behavioral state differentially encoded comparing to other states in primary sensory cortex. To this end, parametric bootstrap was performed to quantify the discriminability (Fig.4).

Resolution

Based on the Stochastic Block Model, the number of subpopulations with which different behavioral states were best distinguished is 2 (occasionally 3, due to the stochastic nature of K-means algorithm). In addition, knowing the subpopulation identities of each neurons allows us to track back their anatomical locations in the raw image (data not shown). Finally, parametric bootstrapping result (Fig.4) suggests that hit and false alarm states were represented very differently from other states. However, the miss and correct rejection states were much more similar which can be explained by the fact that both states were results of the same perception and action.

Future

The formation of a representation in neuronal ensemble may evolve through different stages. Being able to characterize this process is crucial for gaining insight about the dynamics of neural networks. Statistical graph models that incorporate temporal information will be very useful to reveal the progression of representations - from stimulus detection to choice value and eventually to action.

References

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