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Neuronal couplings inferred by an efficient inverse Ising method

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Introduction

A structured, complex network of neurons in a vertebrate retina processes information collectively, as evidenced by correlated firing between pairs of cells [1]. Simultaneous spiking activity of tens of retinal ganglion cells, over periods of hours, has been recorded in multi-electrode experiments. Recently Schneidman et al. [2] and Shlens et al. [3] have used a maximal entropy principle to identify in the context of an Ising model the minimal model capable of reproducing both the average activity of the cells and the pairwise correlations between cells in an equal time window of size dt. Their analyses give access to the statistical pairwise interactions between cells.

Methods

In the present work, we propose a new and efficient algorithm to infer pairwise interactions from the Ising model. Our procedure exploits the fact that most cells are inactive in a time bin (if dt is small), and relies on an extension of large-field expansion from statistical mechanics. The computational effort required by our procedure is only polynomial in N. Our inference procedures provide us not only with the most likely interactions given the set of recorded spikes but also with the error bars on those interactions. As the data set is finite, the estimate of the average activity and pairwise correlations has a finite sampling error, and so are the inferred couplings and fields.

Results

As an example of potential application we have re-analyzed three previously published recordings of the activity of salamander ganglion cells. The first data set registers the activity of 40 cells when the retina is presented a natural movie [2]. The last two data set are recordings from 32 cells of the same salamander retina in dark and illuminated with randomly flickering bright squares [4].

Comparison of couplings on the same cells obtained in dark and flicker stimuli (M. Meister data)

The dependence of couplings upon stimulus has been studied for Dark and Flicker data sets registered from the same retina. We have compared for each pair of the 32 cells i, j, the values of the interactions J_{ij} inferred from Dark and Flicker. An interaction is said to be conserved if it has similar values in both sets. We find that reliable conserved interactions are mostly large and positive, but a few are negative or small. The converse is not true: some pairs of neurons with large interactions in Flicker have weak couplings in Dark.

Spatial Organization of the Network of Couplings

We used the inferred couplings to draw retinal maps in the receptive fields plane of the cells. For Dark, the largest coupling map define a planar graph with short range (almost nearest neighbor) connections. For flicker the strong non-conserved couplings pointed out in the previous section often are long-range interactions.

Discussion

The Ising model has several drawbacks. How do couplings change with the removal of cells from the recording? What temporal correlations are neglected in the Ising model (dependence on the bin size *dt*)? How do couplings inferred with a dynamical model (Integrate and Fire) compare with Ising couplings (see Abstract by Remi Monasson)?

References

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