Local pairwise correlations and network states in cat primary visual cortex

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Introduction
Schneidman et al. (2006) showed that weak pairwise correlations are prevalent in retinal ganglion cell (RGC) networks in vitro, and that their influence on network behaviour is significant, yielding predictions of network state probabilities orders of magnitude better than if the cells were assumed to be independent. Furthermore, the influence of higher-order correlations was deemed insignificant. Shlens et al. (2006) additionally found that not only pairwise, but local pairwise correlations were sufficient to explain RGC activity. These results point to useful simplifications that reduce what could be a combinatorial explosion involving many higher-order neuronal correlations into a much more tractable (local) pairwise problem. This makes analysis considerably easier for the experimenter, and perhaps decoding easier for downstream areas in the brain.

We wondered: do these results generalize to in vivo cortical networks?

Methods
We recorded extracellularly from up to 150 multiple units in area 17 (V1) of anesthetized cat using silicon polytrodes (below) and a variety of natural and artificial visual stimuli. Spike trains were binned and digitized to create temporal binary codes (rows, lower panel). If a neuron spooled one or more times within a time bin, its activity was represented by a 1 in that bin. Otherwise, its activity was represented by a 0. Taking the binary codes of all the neurons together, the network state at any time bin could then be represented as a binary word of length N neurons (columns, lower panel).

We found $\rho \sim 0.01$–0.05, slightly higher than $\rho \sim 0.01$ in RGCs. $\rho$ distributions in V1 were generally independent of the visual stimulus. This suggests that much of the correlations observed here are not from visual input.

Results

Network state frequencies were scatter plotted (right), comparing actual frequencies to those predicted for a given model. For the independent model, network state probabilities are the product of the neuronal state probabilities ($P_i(1)\cdots P_j(1)\cdots$). The maximum entropy pairwise model additionally takes into account probabilities of cell pairs being simultaneously active, while maximizing total entropy to prevent introduction of any higher-order correlations. As in RGCs, the independent model ($\rho_1$) was orders of magnitude off in many of its network state frequency predictions, and the pairwise model (black) performed much better. For the pairwise model, the probability $P$ of a specific network state is given by

$$P(\sigma_1, \sigma_2, \ldots, \sigma_N) = \frac{1}{Z} \exp \left( \sum_{i=1}^{N} h_i \sigma_i + \frac{1}{2} \sum_{i,j} J_{ij} \sigma_i \sigma_j \right) ,$$

where $\sigma_i$ is the binary state of neuron $i$, $N$ is the number of neurons, $h_i$ is the activity weight, $J_{ij}$ is the interaction weight, and $Z$ is the normalizing partition function. The model was fit in Python (scipy.maxentropy, conjugate gradients).

Conclusions

• V1 has weak pairwise correlations, though they seem stronger than in retina
• A pairwise maximum entropy fitting model does a good job of explaining network state probabilities, but not as good as in retina
• Local pairwise correlations are stronger, and local pairs are more effective at predicting network states than distant pairs
• It’s likely that higher than second order correlations are at work in cortex

References

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