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Poster presentation

Improving pattern retrieval in an auto-associative neural network of spiking neurons

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Introduction

Similarities between neural network models of associative memory and the mammalian hippocampus have been examined [1,2]. Here we compare and contrast the recall dynamics and quality of a biologically based spiking network [3] which is comprised of 1000 biologically realistic Pinsky-Rinzel two-compartment model CA3 pyramidal cells [4] with the previously published results for the ANN associative memories [1,2].

Methods

We study biologically plausible implementations of the Winners-Take-All approach to unit (neuron) thresholding during recall of previously stored patterns. The WTA approach simply chooses the required number of units with the highest dendritic sum to fire during pattern recall. Various mathematical transforms of the dendritic sum can compensate for partial network connectivity and noise due to pattern overlap [1]. We investigate whether biologically plausible implementations of these transforms can be found in order to improve the performance of pattern recall in the spiking network. This includes the use of structured inhibition to account for partial connectivity, and nonlinear amplification of EPSPs in pyramidal cells to help disambiguate overlapping patterns.

Results

Using these methods we found that the mean quality recall can be improved. The mean recall over all 200 stored patterns show a statistically significant improve-ment in both methods with a greater improvement measured when using the structured inhibition. An interesting result found in both methods was the increase in synchronous activity, where the number of iterations recorded over the simulation was increased. This could suggest that local inhibitory and cellular modification could play a role in further synchronization of cells during memory retrieval.

The network capacity is also tested by measuring the pattern stability during recall when an entire pattern is instantiated upon both an ANN model and the biological network. Applications of the similar WTA recall algorithms allows direct comparison of the network properties during recall. Preliminary results from a net consisting of 100 units and 1000 units suggest interesting network dynamics in the biological net. Over 1 iteration the artificial net performed better than the biological net containing 100 PCs. The biological network over literation containing 1000 PCs performed better than the artificial network. Over 5 iterations, both the 100 and 1000 PC configurations of the biological net showed distinctive improvements compared to the artificial nets. Suggesting the role of inhibition in the biological network plays a very important role in pattern retrieval.

Acknowledgements

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