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Scaling of spike-timing based neuron model for mammalian olfaction with network size

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We investigate extensions to the model put forward by Brody and Hopfield [1] for spike-timing based pattern recognition applied to mammalian olfaction. Their model implements a pattern recognition algorithm realized in the dynamics of a network of coupled IF neurons subject to a sine-wave rhythm. Subsets of these neurons can synchronize through the principle of one-to-one mode locking. Their network represents 3 layers of neural activity, the first two of which are inspired by the connectivity of glomeruli and mitral cells in mammalian olfactory circuits and the gamma-rhythm activity observed in the olfactory bulb. Specifically in this model a pattern of glomerular activity representing a given odor causes a particular subset of model mitral cells to synchronize and this synchronous activity can drive a “grandmother” model cortical cell through threshold triggering a recognition event. In this study we quantify the performance of their original model and compare it to our extensions of the model such as using a network-generated rhythm rather than a sine-wave, introducing inhibitive feedback and generalizing to p-q mode locking strategies. We compute the scaling with respect to the number of mitral neurons of a measure of the number of odor patterns the model can recognize. Quite remarkably we find this performance can increase very fast with increasing network size – consistent with exponential scaling.

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Reference

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