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Abstract

It has now become possible to map the synaptic connectivity of neural circuitry at the cellular resolution using electron microscopy [1]. In this work, we present a new class of models for the analysis of connectomic data. Many theories of neural computation propose specific patterns of neural connectivity tied to the tuning properties of neurons. We propose an extension to traditional latent space models [2] to uncover continuous hidden structure in these connectomes, such as the neural tuning property of a neuron and the function that determines neural connectivity. Our scalable model provides the flexibility to recover structure in both directed and undirected graphs. We demonstrate our model on synthetic connectomes and on the recently published mouse retinal connectome.



We fit our non-convex models using stochastic gradient descent, using Theano for symbolic (exact) evaluation of the gradient. Adagrad is used when the stepsize could not otherwise be determined.



Asymmetric Block Model The asymmetric block model assumes the existence of discrete latent types and connection probabilities depending solely on those types. By using a triplet loss and 2d split space embedding, we can recover the clustered cell types.

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tion. By using a split 2D space with triplet loss, we can recover the ring structure and the underlying link connectivity.

Dense serial electron microscopy of a \$114um x 80 um area in the mouse retina [1] yielded a listing of places where neurons come into contact. There were over 1000 cells originally, and selected the 950 for which the location of the soma could be reconstructed . Ultimately this left a matrix between the total synapse-like contact area between all pairs of 950 cells. Area was thresholded at 0.1um, determined by hand, to yield a 950x950 entry matrix that served as input to our algorithm.

Latent Embeddeding of Retina

We fit a D =8 latent kernel single-space model to the mouse retina connectome with a symmetric rational quadratic kernel. The first two dimensions recover the intralaminar spatial organization of cells in the retina.

We can hold out connections from the training set and predict the missing connections and compute the area under the resulting precision-recall curve to assess model fit.

Early results are promising. Our next goal is to try a wider variety of kernels and space configurations on real connectomes. While the triplet embedding has shown promise, we need better was of assessing model fit.

Mouse Retina Connectome

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Assessing Model Fit

Next Steps

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