Estimating the Synaptic Efficacies of the Drosophila Optical Lobe Full Connectome with Predictive Coding

Rintaro Kai, Keisuke Toyoda, Naoya Nishiura, Masataka Watanabe
Department of System Innovation, The University of Tokyo
Bunkyo, Tokyo, Japan

Abstract

The neural circuitry of the drosophila brain is moderately complex and has long served as a model in neuroscience research; however, many existing models of the Drosophila brain rely on extreme simplifications or biologically implausible assumptions. Recently, Drosophila has gained further attention because the drosophila full connectome has been revealed. In this study, we constructed a biologically plausible autoencoder for visual processing using the complete connectome of the drosophila brain. By computing prediction errors between two anatomically closely related visual neurons, we implemented predictive coding. We also built an autoencoder with a randomly initialized connectivity matrix and found that it is harder to train than the model initialized with the real connectome. These findings suggest that the original connectome already has mechanisms akin to predictive coding. We hope that, in the future, initializing models with real connectome data will show biological characteristics that would not be shown in other initializations.

Keywords: Drosophila, Connectome, Autoencoder, Visual Processing, Predictive Coding

Introduction

Compared with simpler organisms such as *C. elegans*, the drosophila possesses a more complex brain and exhibits a wide range of behaviors. For this reason, it has been widely used as a model organism in neuroscience experiments, and many of its neural and behavioral characteristics are well understood. The connectome refers to the wiring diagram of the neural circuits in the brain. While the *C. elegans* connectome had been elucidated earlier (Cook et al., 2019), the fruit fly connectome has only recently been mapped in full (Dorkenwald et al., 2024).

Although some models have used parts of the connectome, they often simplified biological features or relied on assumptions that contradict known biology. For example, Lappalainen et al. (Lappalainen et al., 2024) demonstrated direction selectivity using a network derived from the connectome; however, their final output layer was an artificial construct, and they depended on supervised learning with specially annotated data—essentially a ”cheat”—which limits biological plausibility.

We constructed a neural network derived entirely from the complete drosophila connectome and developed an autoencoder trained with unsupervised learning. In doing so, we modeled the error-computation method after the predictive-coding mechanism (Rao & Ballard, 1999), which has been observed in biological systems.

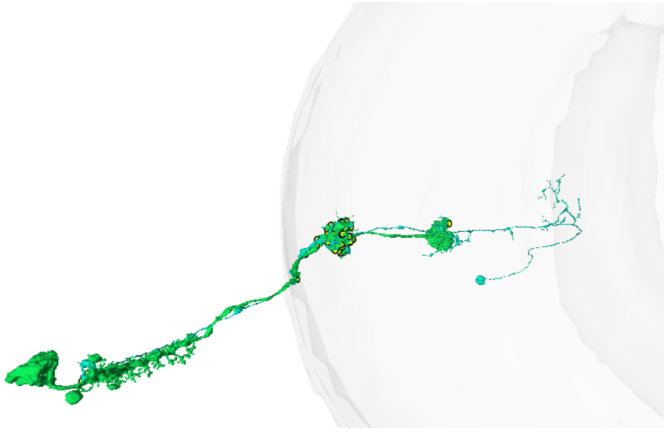

Figure 1: Example pair of L1(green) and C3(blue) neurons rendered on the FlyWire webUI

Methods

Architecture

From the FlyWire dataset (Dorkenwald et al., 2024), we extracted neural connectivity for the right visual lobe and built a single-layer recurrent neural network (RNN) based on approximately 2,700,000 synaptic connections. The output of each neuron was clipped, and synaptic weights were normalized relative to each postsynaptic neuron. Based on neurotransmitter information at each synapse, inhibitory connections were assigned negative values and excitatory ones positive values. Because directly using the raw normalized weights would cause neuron outputs to decay over time steps, we scaled the weight matrix so that its spectral radius equaled 1. The network was driven by directly updating the activities of photoreceptor neurons at each time step. These activity values were computed via simulation, taking into account the anatomical structure of the fly's eye. Because photoreceptor outputs are inhibitory, we initialized all neurons at time step 0 with small random values, then injected the input into the photoreceptors from time step 1 onward, allowing activity to propagate through the network.

Training and Evaluation

As the task, we implemented a simple autoencoder using predictive coding, computing the mean-squared error between the outputs of the anatomically adjacent L1 and C3 neurons.

We evaluated the trained model with other video input to verify that each neuron exhibited appropriate activity. We also compared the learning dynamics and outcomes with those of a model whose weights were randomly initialized.

Results and Discussion

In the model trained with the connectome-derived architecture, the task was successfully learned and the error converged to a very low value. Neurons not directly involved in the error calculation also exhibited appropriate activity, indicating that the network as a whole was functioning effectively. In contrast, with the model initialized with random weights—despite all other conditions being identical—training struggled to converge.

These results suggest that the connectome-derived architecture can learn in an unsupervised manner without artificial neurons or circuits, relying solely on error computations between biologically existing neurons. Moreover, the failure of the randomly initialized model to converge implies that the original L1 and C3 neurons may be intrinsically configured to exhibit similar activity, hinting at an innate predictive-coding mechanism.

Future work should evaluate whether the neural activity generated by the model is biologically plausible and whether the network's behavior and the functional roles of individual neurons are reproduced more robustly than with random initialization. This would further support the utility of constructing models directly from the connectome.

References

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