

Quantitative neuroanatomy for connectomics in *Drosophila*

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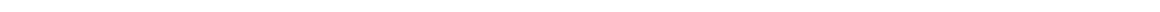
Abstract

Neuronal circuit mapping using electron microscopy demands laborious proofreading or reconciliation of multiple independent reconstructions. Here, we describe new methods to apply quantitative arbor and network context to iteratively proofread and reconstruct circuits and create anatomically enriched wiring diagrams. We measured the morphological underpinnings of connectivity in new and existing reconstructions of *Drosophila* sensorimotor (larva) and visual (adult) systems. Synaptic inputs were preferentially located on numerous small, microtubule-free 'twigs' which branch off a single microtubule-containing 'backbone'. Omission of individual twigs accounted for 96% of errors. However, the synapses of highly connected neurons were distributed across multiple twigs. Thus, the robustness of a strong connection to detailed twig anatomy was associated with robustness to reconstruction error. By comparing iterative reconstruction to the consensus of multiple reconstructions, we show that our method overcomes the need for redundant effort through the discovery and application of relationships between cellular neuroanatomy and synaptic connectivity.

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The nervous system contains cells called neurons, which connect to each other to form circuits that send and process information. Each neuron receives and transmits signals to other neurons via very small junctions called synapses. Neurons are shaped a bit like trees, and most input synapses are located in the tiniest branches. Understanding the architecture of a neuron's branches is important to understand the role that a particular neuron plays in processing information. Therefore,









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