Analysis of Neuronal Morphology in X-ray Synchrotron Images of Drosophila Melanogaster Brains

Ching-Che Charng[1*], Ting-Yuan Wang[2], Nan-Yow Chen[3], Chao-Chun Chuang[3], Chun-Chung Chen[2,5], Chi-Tin Shih[4], Ting-Kuo Lee[6], Chung-Chuan Lo[1]

[1]*Institute of Systems Neuroscience, National Tsing Hua University, HsingChu, Taiwan*
[2]*Institute of Physics, Academia Sinica, Taipei, Taiwan*
[3]*National Center for High-Performance Computing, HsingChu, Taiwan*
[4]*Institute of Neuroscience, National Yang-Ming University, Taipei, Taiwan*
[5]*Department of Applied Physics, Tunghai University, Taichung, Taiwan*
[6]*Department of Physics, National Sun Yat-sen University, Kaohsiung, Taiwan*

Connectome, or the map of neural connections, provides crucial information for understanding operation principles of the brain. Although the fluorescent confocal microscopy and the electronic microscopy have been extensively used in large-scale projects on connectome mapping, we still lack a method that images neural circuits in a high-throughput fashion at the cellular resolution, and that generates samples from a large number of individuals efficiently. Without the availability of a large sample size, our understanding of the circuitry may become restricted. A novel imaging technique, Accelerated X-ray Observation of Neurons (AXON), was developed based on the synchrotron X-ray imaging and the Golgi stain. Using such a technique, we can acquire brain images rapidly with a fine resolution close to 0.5 μm. In the present study, we develop imaging analysis tools for AXON and apply them on the Drosophila brain images. We show that similarity between images of neurons can be assessed based on the spatial innervation, the morphology, and the orientation of a neuron. Next, to perform image registration, we develop an algorithm to identify the fiber bundles. We treat the bundles as the skeletons of a brain and align different brain images based on these skeletons. Finally, we compare the AXON images with the fluorescent-image-based FlyCircuit database and identify new fiber bundles and features that are not available in the FlyCircuit database.

Keywords: A Drosophila connectome, AXON, the Golgi stain, neuronal classification, neuronal bundles

Email:charngchingche@lolab-nthu.org