Connectomics

The production and study of connectomes, known as connectomics, may range in scale from a detailed map of the full set of neurons and synapses within part or all of the nervous system of an organism to a macro scale description of the functional and structural connectivity between all cortical areas and subcortical structures. The term “connectome” is used primarily in scientific efforts to capture, map, and understand the organization of neural interactions within the brain.

Research has successfully constructed the full connectome of one animal: the roundworm C. elegans (White et al., 1986,[Varshney et al., 2011. Partial connectomes of a mouse retina and mouse primary visual cortex have also been successfully constructed. Bock et al.'s complete 12 TB data set is publicly available at Open Connectome Project.

The ultimate goal of connectomics is to map the human brain. This effort is pursued by the Human Connectome Project, sponsored by the National Institutes of Health, whose focus is to build a network map of the human brain in healthy, living adults.

Advances in brain connectomics set the need for detailed knowledge of functional properties of myelinated and non-myelinated (if present) axons in specific white matter pathways. The corpus callosum (CC), a major white matter structure interconnecting brain hemispheres, is extensively used for studying CNS axonal function. Unlike another widely used CNS white matter preparation, the optic nerve where all axons are myelinated, the CC contains also a large population of non-myelinated axons, making it particularly useful for studying both types of axons. Electrophysiological studies of optic nerve use suction electrodes on nerve ends to stimulate and record compound action potentials (CAPs) that adequately represent its axonal population, whereas CC studies use microelectrodes (MEs), recording from a limited area within the CC.

Li et al., introduce a novel robust isolated “whole” CC preparation comparable to optic nerve. Unlike ME recordings where the CC CAP peaks representing myelinated and non-myelinated axons vary broadly in size, “whole” CC CAPs show stable reproducible ratios of these two main peaks, and also reveal a third peak, suggesting a distinct group of smaller caliber non-myelinated axons. We provide detailed characterization of “whole” CC CAPs and conduction velocities of myelinated and non-myelinated axons along the rostro-caudal axis of CC body and show advantages of this preparation for comparing axonal function in wild type and dysmyelinated shiverer mice, studying the effects of temperature dependence, bath-applied drugs and ischemia modeled by oxygen-glucose deprivation. Due to the isolation from gray matter, our approach allows for studying CC axonal function without possible “contamination” by reverberating signals from gray matter. Our analysis of “whole” CC CAPs revealed higher complexity of myelinated and non-myelinated axonal populations, not noticed earlier. This preparation may have a broad range of applications as a robust model for studying myelinated and non-myelinated axons of the CNS in various experimental models [1)].

1)

Li L, Velumian AA, Samoilova M, Fehlings MG. A Novel Approach for Studying the Physiology and Pathophysiology of Myelinated and Non-Myelinated Axons in the CNS White Matter. PLoS One. 2016 Nov 9;11(11):e0165637. doi: 10.1371/journal.pone.0165637. PubMed PMID: 27829055.