

Analyzing whole brain activities of a worm using data-driven models

Author Name1: Chentao Wen

wen@nsc.nagoya-cu.ac.jp

Graduate School of Natural Science, Nagoya City University

Author Name2: Kotaro Kimura

kokimura@nsc.nagoya-cu.ac.jp

Graduate School of Natural Science, Nagoya City University

Abstract

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How our brains process environmental information to regulate behaviors is a critical question in neuroscience. Scientists have long been monitoring whole brain activities with relatively lower resolutions using EEG, MEG, fMRI, etc. while recent advances in imaging techniques have allowed us to monitor it at the cellular resolution in the small brains of "model" animals, such as zebrafish, fruit fly and worm. However, despite the accumulation of "brain big data", knowledge extraction from the brain activity data has been far from satisfactory. Previous analyses focused on visualizing whole brain activities by dimensionality reduction methods such as PCA (Kato et al. 2015), extracting connectivity between sub-regions by calculating correlations (Ahrens et al. 2013), or Granger causality scores (Seth et al. 2015), which do not accurately describe the relationships between neurons. Here we suggested exploring the mechanism of information processing by accurately modeling whole brain activities. Our methods are based on machine learning techniques and are superior to the previous methods in 3 aspects: (1) It can accurately predict the effect on an individual neuron from multiple other neurons using a non-linear and non-additive model; 2. Predictions of future activities are generated thus can be quantitatively tested; 3. We do not compress the data using dimensionality reduction techniques, thus avoid the loss of potentially critical information. We built models of whole brain activities of the worm *Caenorhabditis elegans*. We found the tree-based random forest model is more accurate than the linear model, a neural network model (LSTM) or support vector regression. Based on the best models, we extracted the potential causal links and the "activity flows" among neurons. In the future, we will apply our method to different datasets to extract general patterns in the worm's brain as well as human brain fMRI data, which consists of ~140 activity regions. The above results indicate that our method for studying mechanism of information processing in the brain is useful for the worms, and hopefully for other animals and humans.

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