BMC Neuroscience



Poster presentation

Open Access

Development of standard brain for silkworm moth, Bombyx mori, linked with a neuron database

Hidetoshi Ikeno*¹, Tomoki Kazawa², Shigehiro Namiki^{2,3}, Stephan Shuichi Haupt², Akira Takashima², Ryota Fukushima^{2,3}, Ikuko Nishikawa⁴ and Ryohei Kanzaki²

Address: ¹School of Human Science and Environment, University of Hyogo, Himeji, Hyogo 670-0092, Japan, ²Research Center for Advanced Science and Technology, The University of Tokyo, Tokyo, 153-8904, Japan, ³Graduate School of Life and Environmental Sciences, University of Tsukuba, Tsukuba, Ibaraki, 405-8572, Japan and ⁴College of Information Science and Engineering, Ritsumeikan University, Kusatsu, Shiga, 525-8577, Japan

Email: Hidetoshi Ikeno* - ikeno@shse.u-hyogo.ac.jp

from Eighteenth Annual Computational Neuroscience Meeting: CNS*2009 Berlin, Germany. 18–23 July 2009

Published: 13 July 2009

BMC Neuroscience 2009, 10(Suppl 1):P53 doi:10.1186/1471-2202-10-S1-P53

This abstract is available from: http://www.biomedcentral.com/1471-2202/10/S1/P53

© 2009 Ikeno et al; licensee BioMed Central Ltd.

Understanding the mechanisms controlling behavior in natural environment is one of the principal aims in brain research. One approach directed towards this goal is to rebuild neural systems by simulation. However, the simulation of mechanisms in a whole brain has not yet been achieved because of factors such as complexity and individual variations in experimental data. Several brain functions resulting from interactions with the environment, such as adaptive information processing can conveniently be investigated by using a simple model system, which can be simulated as a whole from the sensory mechanisms to the generation of behavior. We aim to reconstruct and simulate neuronal circuits in the silkworm moth brain and to reveal the design principles of the brain by focusing on this simple model system.

We are examining to integrate their morphological profiles with a standard brain based on whole brain and single neuron data in our database. As a first step of our study we are constructing a detailed standard brain model, focusing on key regions, the lateral accessory lobe (LAL) and the ventral protocerebrum (VPC). These areas are thought to generate premotor signals for behavioral control.

Confocal images of whole brain are downloaded from the database. The brain profiles are extracted semi-automatically from these image data. In this analysis, the origin of the coordinate system in the map is set to the center of the oesophageal foramen. Anterior, posterior and dorsal sectional images are used for detecting sub-regions and representative points. The individual difference between brains is measured and compared based on the size and position of characteristic regions, such as the central body and the antennal lobe. To construct a standard brain shape, we applied transformation and deformation techniques to produce an average shape. The lengths and directions of lines between the origin and anchoring points also determine the contour of the standard brain.

At the same time, we have extracted morphological structures of LAL-VPC neurons. Extracted results are registered to the database and shared through a Virtual Private Network. They are classified into two groups, bilateral interneurons and local interneurons. We can provide a simulation environment of neurons and networks based on their morphologies and by assuming ionic channels properties. Strength of synaptic connections between neu-

^{*} Corresponding author

rons is estimated by measuring the overlap volume of the arborizations of neuritis.

Several research groups have integrated neuron morphology obtained from different animals into standard brains. We are following same approach, but we are going to estimate the sources of variability and errors by examination of the mapping of the same identified neurons from different brain samples. It is indispensible to evaluate the spatial resolution of such geometrical normalization process to determine the scale at which it can be used.

Publish with **Bio Med Central** and every scientist can read your work free of charge

"BioMed Central will be the most significant development for disseminating the results of biomedical research in our lifetime."

Sir Paul Nurse, Cancer Research UK

Your research papers will be:

- available free of charge to the entire biomedical community
- peer reviewed and published immediately upon acceptance
- cited in PubMed and archived on PubMed Central
- \bullet yours you keep the copyright

Submit your manuscript here: http://www.biomedcentral.com/info/publishing_adv.asp

