

Advances in Neuroinformatics VI

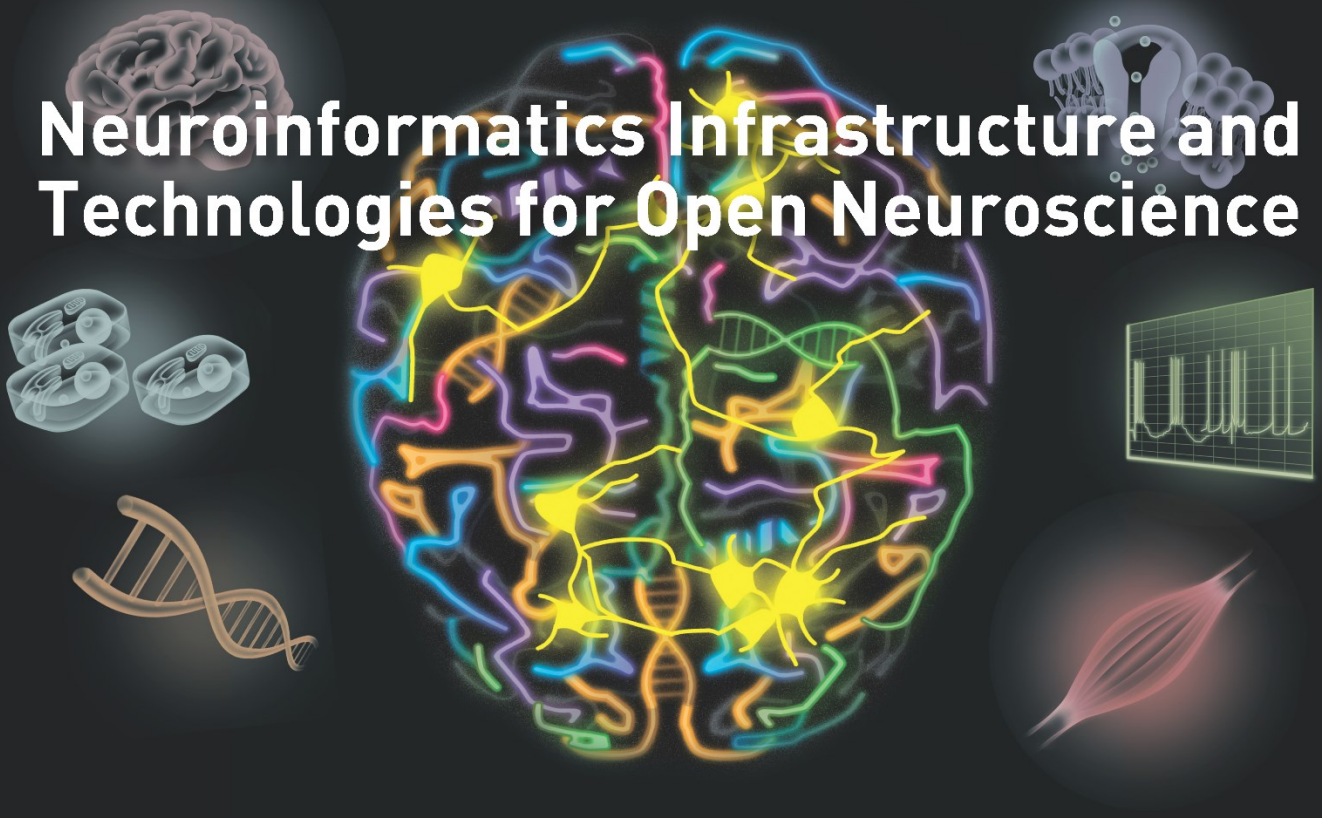
6th INCF Japan Node International Workshop

Advances in Neuroinformatics

AINI 2018

Abstracts

**Neuroinformatics Infrastructure and
Technologies for Open Neuroscience**



December 21-22, 2018

Okochi Hall, RIKEN
Wako, Saitama, Japan

Advances in Neuroinformatics VI

***6th INCF Japan Node International Workshop
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Abstracts***

6th INCF Japan Node International Workshop **Advances in Neuroinformatics 2018**

Date

December 21-22, 2018

Place

Okochi Hall, RIKEN, 2-1 Hirosawa, Wako, Saitama, Japan

Chair

Taishin NOMURA, Ph.D

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The Institute of Statistical Mathematics

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The Japan Neuroscience Society

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Neuroinformatics Unit, Integrative Computational Brain Science Collaboration Center, RIKEN
Center for Brain Science
2-1 Hirosawa, Wako, Saitama, Japan

* This Workshop is a part of the RIKEN Symposium Series

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Message from Workshop Chair

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It is my great pleasure to announce that INCF Japan Node International Workshop on Advances in Neuroinformatics 2018 (AINI2018) will be held in RIKEN as the 6th annual international workshop.

In the era of artificial intelligence and biological/biomedical big data, the role of neuroinformatics has become increasingly important. In particular, effective sharing and use/reuse of large scale data from individuals are the highest priority issue not only for industrial and clinical applications for advanced health and welfare in the super-aged society, but surely also for academic researches, which have been addressed by the international concerted effort in the last two decades to establish novel scientific methodologies, technology infrastructure, and sustainable mechanisms for data acquisition, maintenance and management. AINI2018 will try to provide an exciting opportunity for disseminating continuous contribution from Japan Node to the global concerted effort by INCF and for fostering the exchange of ideas and opinions among researchers in the related fields.

We really look forward to your active participation in the workshop.

Keynote Lecture

Finding relations among genes, brain and behavior in heterogeneous functional genomics data

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Disorders of the central nervous system pose many unique challenges for bioinformatics. Brain and behavioral disorders are difficult to classify and often have highly overlapping characteristics. Biological mechanisms of behavior are shared across multiple disorders. The relationship of behavioral disorders and human behavioral traits to model organism traits is also uncertain. These challenges may hinder progress in the diagnosis and treatment of brain and behavioral disorders. Using an integrative multi-omics strategy, it is possible to find relationships among disorders, evaluate evidence across diverse experiments, and identify conservation of disease related neurobiological mechanisms across species. As data heterogeneity increases, analyses become less quantitative and more generalizable to a greater range of experimental platforms and populations. Genomic and systems genetic studies are used to find molecular correlates of behavioral traits and neurobehavioral processes in humans and mice. Statistical and combinatorial approaches allow the discovery of common genetic and genomic mechanisms across diverse traits within and across species. These approaches are implemented in integrative data resources and modular analysis tool sets in the Mouse Phenome Database, GeneWeaver and other systems. Together they enable data driven discovery of the shared mechanisms of behavioral traits.

Acknowledgements

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KANPHOS (Kinase-Associated Neural PHospho-Signaling), a comprehensive database for specific substrates of kinases

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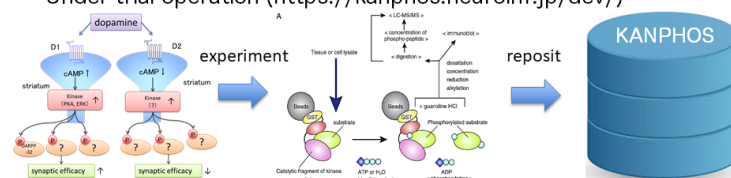
doi:10.14931/aini2018.kl.2

More than 500 protein kinases are encoded in the human genome. Although several kinases have been well-characterized and demonstrated to be physiologically important, the functions of a number of kinases remain to be elucidated. To identify the specific substrates for the specific kinases, we have recently developed an in vitro approach termed the kinase-interacting substrate screening (KISS) method (Amano et al. J Cell Biol 2015) and an in vivo approach termed kinase-oriented substrate screening (KIOSS) method (Nagai et al. Neuron 2016; Nagai et al. Trend Pharmacol Sci 2016). By using these methods, we identified the PKA substrates downstream of dopamine from mouse striatum, and found more than one hundred candidate substrates of PKA, including Rap1 GEF (Rasgrp2). We also found that PKA phosphorylation of Rasgrp2 activated its guanine nucleotide exchange activity on Rap1. Cocaine exposure activated Rap1 in nucleus accumbens in mice through dopamine. The expression of constitutively active PKA or Rap1 in accumbal D1R-expressing medium spiny neurons (D1R-MSNs) enhanced neuronal firing rates and behavioral responses to cocaine exposure through MAPK. These findings demonstrate a novel DA-PKA-Rap1-MAPK intracellular signaling mechanism in D1R-MSNs that increases neuronal excitability to enhance reward-related behaviors. We also constructed an on-line database system, named KANPHOS (Kinase-Associated Neural PHospho-Signaling), that provides the phosphorylation signals identified by our methods as well as those previously reported in the literature. We here discuss the phospho-proteomic approach and the database.

KANPHOS (Kinase-Associated Neural Phospho-Signaling)

Key features

- Providing a set of substrates phosphorylated by 15 kinases so far
- A lot of novel data identified by our methods using mass spectrometry
- Quality-controlled by specialists
- Including curated data from published papers
- Under trial operation (<https://kanphos.neuroinf.jp/dev/>)



(Nagai et al. Trend Pharmacol Sci 2016)) Supported by INCF

Figure1: KANPHOS (Kinase-Associated Neural Phospho-Signaling)

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Novel trends in research data utilisation based on open science

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Recently, the momentum behind open science has increased, particularly in Europe and Japan, and specific measures are being taken in several directions to realise open science, such as government measures and information platform development. Although open science is yet to be concretely or clearly defined, it broadly aims to make research more efficient and enable researchers to produce more innovative results by publishing and sharing knowledge and data with each other, via more open activities in a range of research fields that a variety of people can participate in over the Web. Open science began with open access to research papers, but recently the next step has been taken by opening research data. Also, the findable, accessible, interoperable and reusable (FAIR) principle has been widely accepted by the scientific community. However, this has not yet led to significant data publication and sharing.

In this presentation, we aim to encourage the development of open research data by discussing the development and operation of a new life-science database platform called the RIKEN MetaDatabase (<http://metadb.riken.jp>), based on the FAIR principle and its related tools. The RIKEN MetaDatabase allows RIKEN's biologists to create, integrate and publish their research result datasets together with suitable metadata. As of November 2018, it already includes 59 RIKEN databases and 72 external databases, including mammalian, plant, protein, bioresource and image datasets, described using 26 public ontologies. We will also review several standardised technologies, including the resource description framework (RDF) and ontologies used to describe metadata and discuss ways researchers can collaborate to organize data and create databases via INCF Japan Node Hackathon events (<https://www.neuroinf.jp/>). Thereafter, we demonstrate data search and inference using real and practical examples.

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Vector-based navigation using grid-like representations in artificial agents

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Deep neural networks have achieved impressive successes in fields ranging from object recognition to complex games such as Go. Navigation, however, remains a substantial challenge for artificial agents, with deep neural networks trained by reinforcement learning failing to rival the proficiency of mammalian spatial behaviour, which is underpinned by grid cells in the entorhinal cortex. Grid cells are thought to provide a multi-scale periodic representation that functions as a metric for coding space and is critical for integrating self-motion (path integration) and planning direct trajectories to goals (vector-based navigation). Here we set out to leverage the computational functions of grid cells to develop a deep reinforcement learning agent with mammal-like navigational abilities. We first trained a recurrent network to perform path integration, leading to the emergence of representations resembling grid cells, as well as other entorhinal cell types. We then showed that this representation provided an effective basis for an agent to locate goals in challenging, unfamiliar, and changeable environments—optimizing the primary objective of navigation through deep reinforcement learning. The performance of agents endowed with grid-like representations surpassed that of an expert human and comparison agents, with the metric quantities necessary for vector-based navigation derived from grid-like units within the network. Furthermore, grid-like representations enabled agents to conduct shortcut behaviours reminiscent of those performed by mammals. Our findings show that emergent grid-like representations furnish agents with a Euclidean spatial metric and associated vector operations, providing a foundation for proficient navigation. As such, our results support neuroscientific theories that see grid cells as critical for vector-based navigation, demonstrating that the latter can be combined with path-based strategies to support navigation

Citation: Banino A, Barry C, Uria B, Blundell C, Lillicrap T, Kumaran D (2018) Vector-based navigation using grid-like representations in artificial agents. *Advances in Neuroinformatics* 2018. doi:10.14931/aini2018.kl.4

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Organized Session I
Large Scale Mouse Brain Data

Endophenotype in the brain: A key concept for understanding the relationships between genes and behavior

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Genetic studies have revealed millions of polymorphisms in human genome, and these polymorphisms can have infinite possible combinations. However, the human personality can be represented by a small number of traits and that extreme forms of personalities can be categorized into a limited number of psychiatric disorders. An interesting question is: how, despite such huge genomic variability, are there distinct categories of individuals showing similar behavioral patterns? We have been investigating the relationships between genes and behaviors by using a comprehensive behavioral test battery in genetically engineered mice, which covers a broad range of behavioral domains, such as sensorimotor functions, emotionality, and cognition. So far, we have subjected approximately 200 different strains of mutant mice to this test battery. Among them, α calcium/calmodulin-dependent protein kinase II heterozygous-knockout mice show several strong behavioral phenotypes, such as hyper-locomotion, abnormalities in social behavior, and a working memory deficit. Detailed molecular and electrophysiological analyses revealed that almost all neurons in their dentate gyrus are in a pseudo-immature status; we named this phenotype “immature dentate gyrus.” Surprisingly, this phenotype is observed in several other strains of mutant mice showing behavioral phenotypes similar to that of the KO mice as well as in wild-type mice subjected to chronic anti-depressant treatment or having epileptic seizures. Moreover, studies on post-mortem brains suggest that the phenotype exists in certain populations of patients with psychiatric disorders. It might be an endophenotype onto which many unique genetic and non-genetic features converge and through which a similar pattern of behavioral traits emerges. I will discuss the impact of “endophenotype of the brain” concept on understanding the pathways linking genes to behavior and also the importance of large-scale database on such phenotypes.

Citation: Miyakawa T (2018) Endophenotype in the brain: A key concept for understanding the relationships between genes and behavior. *Advances in Neuroinformatics* 2018. doi:10.14931/aini2018.osi.1

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Brain Transcriptome Database (BrainTx)

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The Brain Transcriptome Database (BrainTx) (<http://www.cdtodb.neuroinf.jp>) is a neuroinformatics database that contains gene expression information related to various stages and states of the mammalian brain and aims to create an integrated platform for visualizing and analyzing the these gene information data. BrainTx is systematized by large amounts of spatio-temporal gene expression data obtained by developmental time-series microarray analyses, in situ hybridization brain images (brain regional and cellular expression patterns) and tissue distribution patterns microarray analyses, etc. BrainTx not only provides the easy-to-use interface to cross-search for expression data, but also includes brain image viewers, graph analysis tools, gene ontology search function, etc. All registered genes have hyperlinks to websites of many relevant bioinformatics regarding genome, proteins, pathways, neuroscience and literatures. Therefore, BrainTx also acts as a portal to these bioinformatics websites. We aim to systematize our original data and the publicly accessible big data on the brain transcriptome in different stages and states, including time and space, physiological conditions, environment, age, diseases, etc. We try to apply machine learning to brain transcriptome data and aim to discover new findings on gene expression and brain diseases. We are also developing on neural gene ontology about a large amount of neuroscience terms, trying cooperation with BrainTx systems, and aiming at a systematic understanding of gene expression and related neural matters. These neuroinformations help to understand the genetic mechanisms underlying complicated neural processes and circuits and on the brain and nervous systems. BrainTx has already been demonstrated to be valuable for neuroscience research (for example, identification of several brain genes important for neural circuit development).

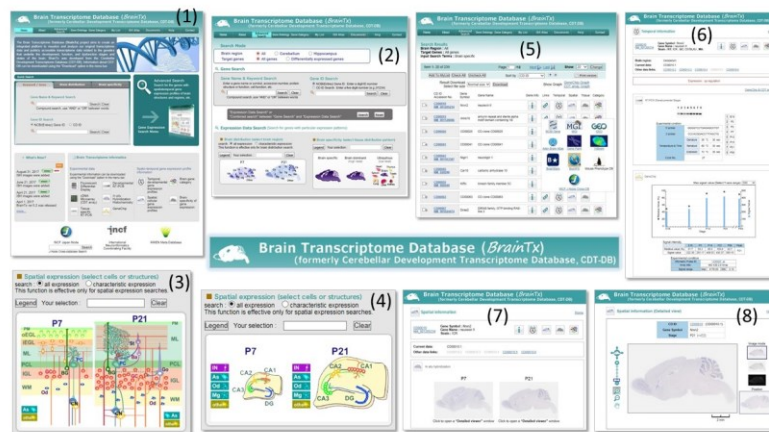


Figure1: Figure: BrainTx Top page (1), Search page (2), Search functions for cerebellum (3) and hippocampus (4), Search results page (5), Temporal (6) and Spatial (7) gene expression pages, and ISH brain image viewer page (8).

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Citation: Sato A, Furuichi T (2018) Brain Transcriptome Database (BrainTx). Advances in Neuroinformatics 2018. doi:10.14931/aini2018.osi.2

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RDF-based data integration of mouse phenotype

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In the life science, bio-resource is one of the most important fundamentals. Especially, bio-resources as experimental materials are crucial for scientific researches to secure reproducibility of the experimental results. Therefore, development of the data dissemination and sharing infrastructures for meta-information of bioresources is one of the significant issues for research resource centers. Phenotype data is crucial for researchers to choose appropriate experimental materials for their studies. Recently sharing of phenotype data of experimental animals are performed various databases using phenotype ontologies as standardized vocabularies. Using Resource Description Framework (RDF) related technologies, candidates of disease model can be shown through the disease-phenotype relationship between across human, rodents, fish, worms and flies. Therefore, dissemination of phenotype-related information, RDF technologies becomes one of the best solutions.

In this talk, I introduce our efforts for wider data dissemination of experimental animals produced in Japan using RDF-related technologies.

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Organized Session II
Neuroinformatics and Drug Discovery

Potential of KANPHOS Platform for drug discovery

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Protein phosphorylation is a major and essential post-translational modification in eukaryotic cells that plays a critical role in various cellular processes including neural plasticity and development. While recent advances in mass spectrometry based proteomics allowed us to identify approximately 200,000 phosphorylation sites [1], it is not fully understood which sites are phosphorylated by a specific kinase and which extracellular stimuli regulate the protein phosphorylation via intracellular signaling cascades. To uncover the basic issue, we developed a new methodology for comprehensive screening of the target phosphorylation sites of a given kinase (or extracellular signal) [2,3]. KANPHOS (Kinase-Associated Neural PHOspho-Signaling) Platform is an online database system designed to provide the phosphorylation signals identified by our methods as well as those previously reported in the literature. In the first half of this talk, we introduce basic functions of KANPHOS Platform with a case study [4]. Also, kinases are recognized as promising drug targets because dysfunction of kinases has been implicated in pathophysiology of human diseases. In fact, 37 kinase inhibitors have received FDA approval for treatment of malignancies such as breast and lung cancer [5]. In the last half, we briefly review the history of kinase inhibitor drug discovery and discuss how KANPHOS Platform could contribute to the discovery of novel drugs.

Acknowledgements

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Towards creating an engine of scientific discovery

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With the explosion of data in different dimensions of drug discovery, biomedicine, and healthcare, a key challenge is the ability to connect the disparate data sources, discover the right analytics tools, particularly machine learning and artificial intelligence (AI) techniques for a specific analysis and navigate through inter-operable analytics to provide executable insights.

Garuda is an open, community-driven, platform that provides a framework to discover, connect & navigate through different applications on devices as well as in the cloud. Garuda connects with various machine learning tools, algorithms through our Gandhara platform to provide insights and visualizations. In this talk, we provide an overview of the Garuda platform, the alliance eco-system and a brief demonstration of the platform in action together with its various components. Specifically, we focus on case studies of the application of Garuda platform in molecular biology and their connection to healthcare. We demonstrate a case study of how different sensors, wearables and monitoring devices are connected on Garuda to aggregate signals, analyze data-points and identify patterns to enable decision-making.

We summarize with a vision on re-imagining connectivity in the age of digital medicine, healthcare and beyond

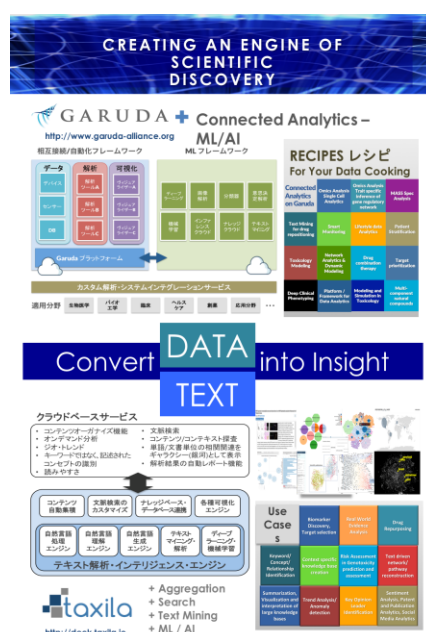


Figure1: From Tools to platforms

Acknowledgements

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Citation: Ghosh S (2018) Towards creating an engine of scientific discovery. *Advances in Neuroinformatics* 2018. doi:10.14931/aini2018.osii.2

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High Performance Computing Drug Discovery - Toward Targeting Protein-Protein Interactions

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Protein-protein interaction (PPI) plays a core role in cellular functions. In recent years, PPI prediction methods based on protein docking have been developed and have been applied for large-scale PPI network prediction based on tertiary structures. We have developed an ultra-high-throughput PPI prediction system based on rigid-body protein-protein docking and supercomputing, named MEGADOCK[1, 2] for PPI-targeted drug discovery. MEGADOCK can perform faster docking based on its improved scoring function[3] and implementation for heterogeneous supercomputers[2, 4-6]. MEGADOCK achieved an excellent scalability on supercomputing environments, such as K computer and TSUBAME, and realized genome-wide scale PPI network prediction. We applied MEGADOCK system to a number of interactome analyses; (a) bacterial chemotaxis[7], (b) human apoptosis[8], (c) human EGFR signaling, and (d) RNA decay at the early cellular reprogramming stage[9].

In addition, we have constructed an integrated database of PPI predictions named MEGADOCK-Web[10] to accelerate PPI researches. MEGADOCK-Web provides the four functions, 1) Searching PPI predictions from 28,331,628 prediction results, 2) displaying known PPI, 3) visualizing candidate of interaction with query protein on biochemical pathway, and 4) visualizing predicted complex structure by 3D molecular viewer. Our MEGADOCK-Web and high-performance-computing-based virtual screening techniques will accelerate drug R&D cost reduction and development of drugs for new targets.

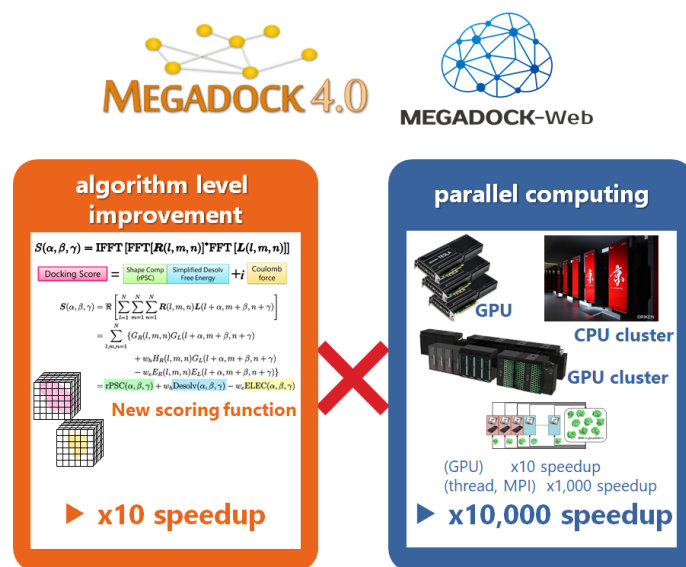


Figure1: MEGADOCK overview. We achieved "million pairs per day docking" calculation through two approaches, one is algorithm level improvement and the other is combination of parallel processing techniques.

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Organized Session III
Neuroinformatics in INCF Japan Node

Neuroinformatics and FAIR in INCF Japan Node

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International Neuroinformatics Coordinating Facility was launched in 2005 to promote neuroscience as collaboration across different domains and different countries by means of computer science and internet technologies. INCF Japan Node (J-Node) started in 2005 to develop neuroinformatics platforms as web databases and infrastructures by assigning Neuroinformatics Japan Center (NIJC) as J-Node secretariat at RIKEN Brain Science Institute [2], which has been inherited to Neuroinformatics Unit (NIU), RIKEN Center for Brain Science. In these decades, there were rapid development in technologies and also in the understanding the importance of sharing of scientific data on the internet. The guideline for digital data sharing becomes more and more important. The FAIR principle was published as a set of guiding principles to make data Findable, Accessible, Interoperable and Reusable[1].

In J-Node, we have now 13 neuroinformatics platforms which cover from gene, whole brain and psychology or from invertebrate to primate.

The interoperability of these multimodal data is a challenge in neuroinformatics for next stage of neuroscience.

In this line, J-Node promoted to develop infrastructures common among different fields. It includes Xoops/XoonIps, standards in data/metadata such as odML, RDF, ontology. These activities are at the starting point for future FAIR data. The challenge is not only in the technologies but also in communities or organizations. The summary of J-Node activities shall be devoted to discussion on the future perspective of neuroinformatics.

Acknowledgements

The author would like to acknowledge all J-Node community members and INCF members for their continuous collaborative efforts on neuroinformatics. She also thank Drs. Shun-ichi Amari, Shiro Usui, Keiji Tanaka for their guidance on J-Node activities.

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Citation: Yamaguchi Y (2018) Neuroinformatics and FAIR in INCF Japan Node. *Advances in Neuroinformatics* 2018. doi:10.14931/aini2018.osiii.1

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ViBrism DB: data and platforms

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We will introduce ViBrism DB for integrated analysis of comprehensive gene expression of the mouse brain in anatomical 2D/3D maps and in topological co-expression network graphs. The gene expression densities were measured with a microtomy-based-RNA-measurement method, Transcriptome Tomography. Now, 172,023 maps of overall gene expression in the four maturing stages after the birth are searchable by gene IDs. The expression maps are seen in the 3D MRI space compatible to the INCF mouse standard brain coordinate (WHS), along with selected 2D ISH images, which are transformed from BrainTx platform images. Results are shown with the BAH Viewer that was created through INCF Japan-node Brain Atlasing Hackathon (BAH) activities. Gene-by-gene correlation of co-expression are calculated using Pearson correlation coefficient as a similarity measure and then co-expression search results are browsed as network tables and graphs associated with the 2D expression maps in the Network Viewer. These anatomical and topological platforms were connected by one click operation. The frameworks enable to comprehensively assess expression patterns underlying brain structures and function. ViBrism DB is a unique database for anatomy/function association based on gene expression.

Acknowledgements

A part of the computational work was performed in Brain Atlas Ideathon/Hackathon and INCF Japan Node Hackathon organized by RIKEN BSI. WHS MR images were provided by INCF Waxholm Space Task Force of the Program. Measurement of transcripts by microarray is executed by RIKEN RRD.

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Citation: Okamura-Oho Y (2018) ViBrism DB: data and platforms. *Advances in Neuroinformatics* 2018. doi:10.14931/aini2018.osiii.2

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Open and sustainable repositories for sharing data and models in neuroscience are indispensable to deepening understanding dynamic information processing in the brain

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The vital importance of data/model sharing and reuse in modern sciences, including neuroscience, and development information-technology-infrastructure (e.g., neuroinformatics platforms) that can support the sharing has been recognized gradually but steadily by the communities of researchers. This can be seen from the fact that publications of first-order data (i.e., primary data prior to data processing to compress into summary statistical measures) as journal papers from major publishers (e.g. [1,2]). This is not only because of the social demand to ensure transparency and to increase reproducibility of each research outcome published, but also because of high expectations that systematic accumulation of appropriately annotated primary data, as observations of output from complex systems, and mathematical models (particularly dynamical system models) that can numerically simulate the corresponding systems would lead to a creation of novel knowledge of how the systems behaves and about the mechanisms that govern dynamics of the complex systems. For example, the data-assimilation with high performance computing resources has become a promising technology to deepen our understanding of the brain, if a good set of biological/physiological data and a good mathematical model for simulating the corresponding dynamics encounter through a navigation of the data/model sharing platforms. In this talk, we address issues associated with the data/model sharing, and consider a possible form of platforms (such as OpenNeuro Platform at INCF J-Node) that can facilitate the data/model sharing efficiently.

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Citation: Nomura T, Yamaguchi Y (2018) Open and sustainable repositories for sharing data and models in neuroscience are indispensable to deepening understanding dynamic information processing in the brain. *Advances in Neuroinformatics* 2018. doi:10.14931/aini2018.osiii.4

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Organized Session IV
Challenges in Data Analysis for Innovation in Neuroscience

Big data in neuroscience

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Data obtained in neuroscience is getting bigger and bigger and more and more complex. On the other hand, A.I. or supervised machine learning techniques are advancing extremely rapidly and getting more and more powerful, still, they are not yet effective enough to solve all problems in the real world automatically. In this organized session, Shinji Kakei, an experimental neuroscientist, Yoshinobu Kano, a specialist in natural language processing and Alexander Woodward, who have been creating large scale brain image data processing pipelines for connectomics and have been using A.I., come together and address how to optimize cooperation between neuroscience and data science. After short presentation of important research topics by each speaker, they are going to make a panel discussion on critical issues, including curation, quality assurance and quality control of data.

Citation: Kakei S, Kano Y, Woodward A (2018) Big data in neuroscience. *Advances in Neuroinformatics* 2018. doi:10.14931/aini2018.osiv.1

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Automated Connectomics Pipelines on HPCs using A.I and Computer Vision.

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The automation of data processing pipelines is critical for doing large-scale connectomics in neuroscience, where any manual procedure becomes a bottleneck. Here, the variability between individual specimens, the overall complexity of biological data, the heterogeneity in contrast mechanism across imaging systems, and the noise sources inherent in the imaging device are some of the main challenges faced in developing stable pipelines. I will talk about the use of artificial intelligence and computer vision techniques for overcoming many of these issues. A key idea is that annotated data from domain experts can be leveraged and input into artificial intelligence systems to come up with robust data processing.

As a use-case I will talk about the development of a high-throughput 3D brain reconstruction pipeline for tracer injection studies of the common marmoset in Japan's Brain/MINDS project [1]. The pipeline segments and normalizes neuroimaging data such as 2D histology or fluorescence images, and 3D MRI data into a common space with a 3D brain atlas [2]. Data is processed in parallel on an HPC and the assembled results are being used for mesoscale connectomics (the gross projection patterns of axons).

Despite the obvious successes of A.I. and computer vision it is important to consider how quality control and assurance protocols can be developed to reduce the noise and variability in acquired data and improve machine readability. By doing so we can develop pipelines that can ensure reliability and reproducibility of results without the need for advanced computational processing. I will touch on these points also.

Acknowledgements

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Natural Language Processing, Neuroscience, and "AI"

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I will introduce our NLP (Natural Language Processing) projects related to neuroscience to provide seeds of this discussion. Firstly, I introduce a project that aims to extract information from neuroscience papers. Secondly, I introduce a medical project that infers mental diseases from human conversations. While both projects perform NLP, there are underlying common issues such as machine learning techniques, feature selections, and data size and its preparation, which could be one of topics for the following discussion part.

Citation: Kano Y (2018) Natural Language Processing, Neuroscience, and "AI". *Advances in Neuroinformatics* 2018. doi:10.14931/aini2018.osiv.3

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Poster Session

Connectome informatics: Reverse engineering of whole brain networks

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The goal of connectome informatics is to establish the architecture of information processing in the brain by exploiting the structure of whole brain networks. A key strategy towards this goal is to reveal communities, which refer to sets of nodes of the network that are mutually connected at higher probability [1]. This strategy is based on the hypothesis that communities of whole brain networks are associated with functional modules of the whole brain architecture [2]. Here we demonstrate this approach applied to the mouse connectivity data of Allen Brain Atlas (<http://connectivity.brain-map.org/>) [3, 4], especially focussing upon the visual cortex [5]. We have successfully extracted ventral and dorsal streams as communities of the visual cortical network (Figure 1, left). Each connection of the visual cortical network can be classified as feedforward (top-down) or feedback (bottom-up) according to the laminar projection pattern ($P < 0.01$). With this classification, we have found that the ventral stream mostly comprises feedforward connections, thus constituting a one-way directed pathway (Figure 1, right, green box). Such an organization resembles the architecture of a class of artificial deep neural networks that are highly suitable for object recognition. The connection structure of the dorsal stream is somewhat more complicated. It comprises a higher ratio of feedback connections (Figure 1, right, yellow box), which implies that the dorsal stream is engaged in more modulatory roles.

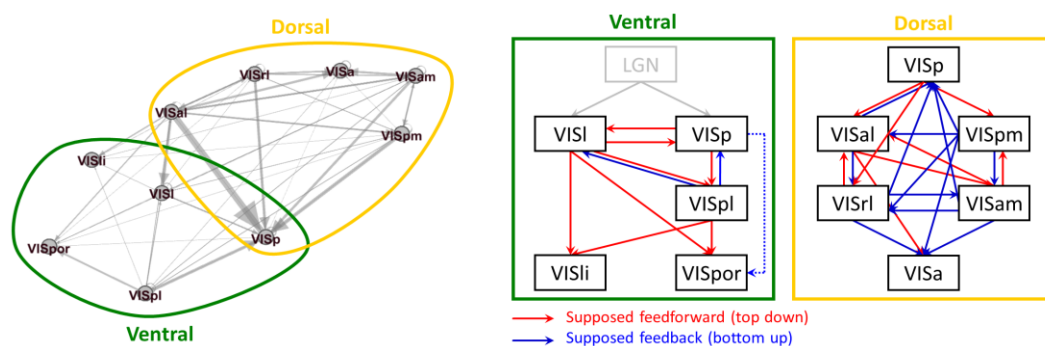


Figure1: Left, Ventral (circled green) and dorsal (circled yellow) streams extracted as communities of the visual cortical network. Right, Connection architectures of ventral (green box) and dorsal (yellow box) streams.

Acknowledgements

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Current activities of BrainTx platform - Brain transcriptome and Neural gene ontology projects

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The Brain Transcriptome Database (BrainTx) (<http://www.cdtodb.neuroinf.jp>) is a neuroinformatics database that contains large amounts of spatio-temporal gene expression data obtained by developmental time-series microarray analyses, in situ hybridization brain images (brain regional and cellular expression patterns) and tissue distribution patterns microarray analyses to investigate brain-specific expression patterns, etc. To aim to create an integrated platform for visualizing and analyzing gene expression information data related to various stages and states of the mammalian brain, we are going to systematize our original data and the publicly accessible big data on the brain transcriptome in different stages and states, including time and space, physiological conditions, environment, age, diseases, etc. and try to apply machine learning to these brain transcriptome data to discover new findings on, for example, gene expression and brain diseases (Brain transcriptome project). We are also developing on systematization about a large amount of neuroscience terms related to neural genes, brain anatomy, brain diseases, physiology and behavior, etc. (Neural gene ontology project). In the future, we aim to incorporate these project systems into BrainTx platform and to deepen systematic understanding and to innovate new findings on the genetic mechanisms underlying complicated neural processes and circuits on the brain and nervous systems.

Acknowledgements

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Development of simulation platform for multiple cortico-thalamic circuits using pyNEST

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Cortico-thalamic circuit consists of multiple subregions that perform different information processing with interacting with basal ganglia and cerebellum. To elucidate the mechanism of information processing in the brain, it is essential to understand how the major brain regions interact with each other. However, it remains challenging to examine the complicated interactions through huge numbers of connections among the entire brain regions.

Our group aims to investigate and understand the interaction by simulation of large-scale spiking neural networks on supercomputers. Here, we introduce a simulation platform for multiple cortico-thalamic circuits using the neural network simulator NEST.

On the platform, we developed models of cortices and thalamus based on physiological and spatial properties of mouse brain including neural density, layer thickness, connection probability function of a distance between neurons. We targeted modeling of somatosensory and motor cortex and corresponding thalamus. We modeled each cortical region as a layered sheet using the Topology module of the NEST.

Our platform may allow us to investigate the functional role of the interaction between cortices and thalamus. It will also work for developing extended model consisting of the cortex, basal ganglia, and cerebellum.

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Construction of the honeybee standard brain for primary auditory center

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Honeybees use “waggle dance” to inform the direction and distance of feeding site to their hive mates. During the waggle phase, the dancer keeps wingbeats which produce trains of vibration pulses which the dance follower could perceive. However, it has still unknown how they decode duration of the vibration pulses into the distance information. Recently, we identified several critical interneurons that have specific response patterns to the waggle dance-mimicked vibration stimuli (Ai et al., 2017). Ai et al. (2017) analyzed the response properties and neural morphology of each neuron in primary auditory center (PAC), however it was still unrevealed the synaptic connections among these. To reveal possible synaptic connections among neurons, honeybee standard brain (HSB) is useful for common platform for registration of neurons (Rybak, 2010). PAC consists of dorsal lobe (DL), dorsal subesophageal ganglion (dSEG) and posterior protocerebral lobe (PPL), but the present HSB does not have PAC as neuropiles. It makes registration of PAC neurons difficult into the HSB. So, we have been developing the standard brain specialized in the primary auditory center (pacHSB), which enables us to evaluate the arborization and connection of neurons in PAC region. We obtained the average brain shape by averaging serial LSM images of honeybee brains stained with Anti-Synapsin(n=5). Neuropil boundaries and tracts in these images were segmented and registered into it. We are estimating synaptic connections by registering neurons arborizing in PAC into the pacHSB.

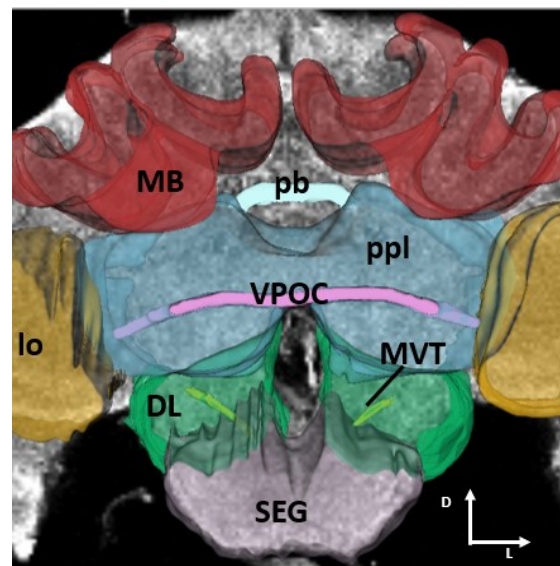


Figure1: The brain image focusing on midbrain area. The contours of DL, SEG, and PPL were acquired from GABA immunostained LSM mage. pb: protocerebrum bridge, MVT: median ventral tract, VPOC: ventral posterior optic commissure, MB: mushroom body, PL: protocerebrum lobe, AL: antennal lobe, DL: dorsal lobe

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Development of a unified environment for automated neuronal network reconstruction from EM images

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Recent years have seen a rapid expansion in the field of connectomics, which targets the large-scale anatomy of the brain. Especially, 3D reconstruction of neuronal networks from a stack of 2D electron microscopic (EM) images has attracted attention, because such micro-connectomics is expected to directly elucidate neuronal functions at the local circuit level. Thanks to deep neural networks (DNN) that enable automated neuronal segmentation, the spatial scale of the 3D reconstruction grows rapidly over 1 mm³. Advanced research teams have developed their own pipelines for the large-scale segmentation (Informatics 2017, 4:3, 29). Those pipelines are series of client-server software for alignment, segmentation, proofreading, etc., each of which requires specific PC environments. Because of such complexity, it is difficult even for computer experts to use them, and impossible for experimentalists. This makes a serious divide between the advanced and general experimental laboratories.

To bridge this divide, we are now trying to unify pieces of software for automated EM segmentation [1]. We first focused on proofreading software Dojo (IEEE Trans. Vis. Comput. Graph. 20, 2466–2475), because Dojo shares the same framework with Tensorflow for DNN-based segmentation, i.e., their backend web servers are based on Python, and their frontend clients work on a web browser. Those two pieces of software were unified, and an GUI and 3D viewer were developed to use them as single application software for EM segmentation, inspection, and proofreading (Figure 1). Multiple users can simultaneously use it through web browsers. This software works on Microsoft Windows, and the other operating systems in future. We believe that this is a small but important first step for developing informatics software for EM segmentation in this country.

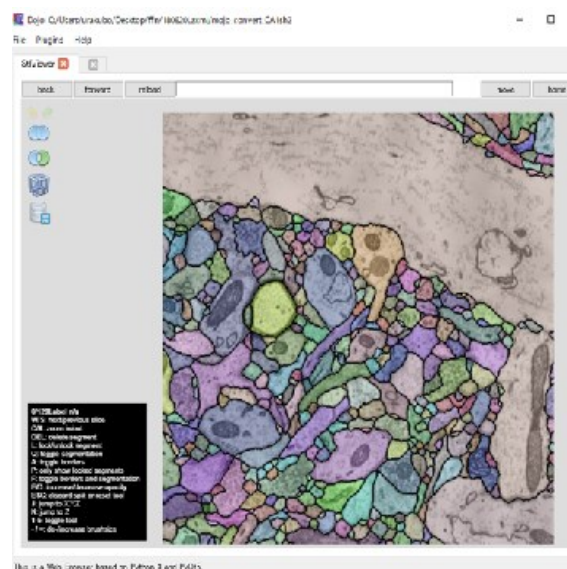


Figure1: Screenshot of the unified environment for EM connectomics

Acknowledgements

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Individuality of macro-scale connectome of common marmoset with global fiber reconstruction by diffusion MRI

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Common marmosets (*Callithrix jacchus*) are primates, which have a small brain size (~8g), grow up early and can be genetically manipulated. These features are suitable for understanding the complex structure and connectome of the primate's brain, when we compare the marmoset with the other primates. These complexities of the primate indicate that there are much differences of the structure and connectome between individuals. The RIKEN BSI team obtain the diffusion magnetic resonance imaging (dMRI) data of large numbers of the marmoset brain (~50) to reveal macro-scale connectome and their individuality of the marmoset brain. Here, we construct a pipeline for obtaining the macro-scale connectome of the RIKEN's marmoset data and analyze their individual differences of the structure and connectome. We analyze the RIKEN's data with our pipeline and obtain the individual and average connectivity matrix of the marmoset brain. The graph structure of the connectivity matrices of marmoset show the exponential decay rule (EDR), which is the strength of the two region is exponential decay against the distance between the regions. This rule is consistent with the graph structure of the connectivity matrix given by the microscopic studies about the other species (mouse and macaque monkey). We evaluate and visualize the individuality of the marmoset connectivity matrix using t-SNE, which is one of the low-dimensional manifold mapping method. We find that we can discriminate the all different individuals with each connectivity matrix, although the experimental setting of the dMRI, b-value, is different among the individuals.

Acknowledgements

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Issues in evaluation of movement disorders

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We are developing a new system for quantitative evaluation of movement disorders. The aim of the system is a reform of the remotest part of the medicine from data science: neurology.

Neurological diseases, such as stroke, Parkinson's disease or spinocerebellar degeneration are currently incurable and waiting for a revolution in the field of regenerative medicine. Unfortunately, evaluation of these movement disorders totally depend on subjective judgment by neurologists. This century-old system is poorly quantitative and poorly recordable. Judgments vary from physician to physician, depending on their experience or skill. Apparently, the classical system is not suitable for development of next generation treatments.

Therefore, we are motivated to develop a novel system for quantitative evaluation of movement disorders. The subjects perform simple visually-guided movements using a simple motion capture, e.g. Kinect v2. Our system dissociates and analyzes three components of pursuit movement: predictive control, feedback control and noise. The first and second components mainly represent condition of higher motor centers and the third component appears to reflect condition of lower motor centers.

To achieve our goal, we need resources to link the movement data with medical records, to develop a large-scale database and to use deep learning to find important data that need special attention from physicians. Unfortunately, none of these resources do not belong to our speciality. Therefore, we are asking vigorous support from data scientists.

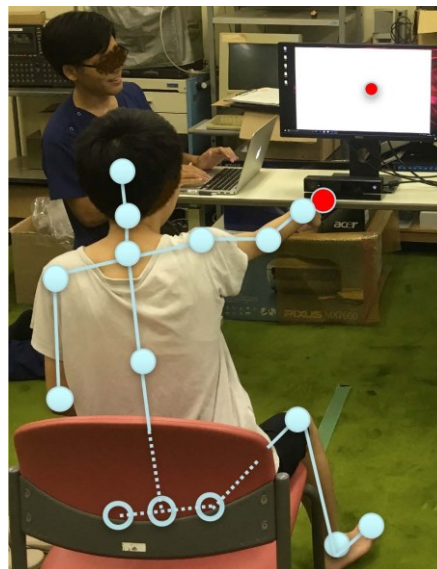


Figure1: Evaluation of movement disorders in a patient

Citation: Kakei S (2018) Issues in evaluation of movement disorders. *Advances in Neuroinformatics* 2018. doi:10.14931/aini2018.ps.7

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The Brain/MINDS Cortical Flat Map for Visualize Neuroimaging Data

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The Brain/MINDS (Brain Mapping by Integrated Neurotechnologies for Disease Studies) project aims to map the connectome of the common marmoset monkey (*Callithrix jacchus*) and use this knowledge to develop cures for human brain disease [1].

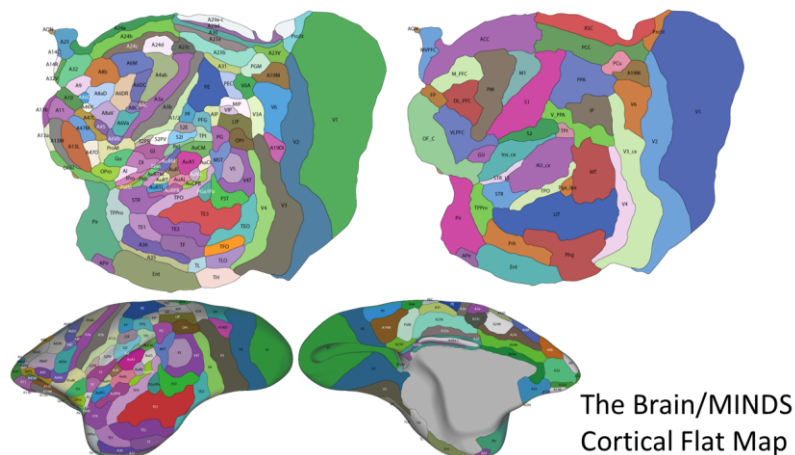
One approach for mapping between species is to examine the homologies between their cortical flat maps through surface registration [2]. Generally, a cortical flat map can be constructed as a projection of the mid-layer surface through the cortex from 3D to 2D. This 2D representation can be used for visual comparison of experimental data mapped onto it, such as fluorescent tracer, or functional MRI.

We present the Brain/MINDS cortical flat map for the common marmoset brain, compatible with the Brain/MINDS atlas [3] and the first downloadable marmoset flat map that can be loaded into popular software such as Connectome workbench for projection of data. The flat map contains two different region groupings: 116 regions corresponding to the Brain/MINDS atlas parcellation, and a coarser grained 41 region parcellation appropriate for MRI studies.

The Brain/MINDS flat map was constructed using the Caret software by first reconstructing the 3D mid-surface of the left hemisphere of the Brain/MINDS atlas mapped to a population T2 average MRI, removing the non-cortical regions, and then making cuts in the mid-surface so that it could be flattened out into 2D while minimizing distortions.

Within the Brain/MINDS project, the flat map is used to understand the project patterns and columnar structures appearing in segmented tracer injection study data. The 2D flat map provides an easy way to compare visual means of tracer data from several experiments, such as multiple injections targeting the same region.

The flat map for both hemispheres in GIFTI format will be released on the Brain/MINDS data portal [4].



Acknowledgements

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Citation: Gong R, Woodward A, Nakae K, Ichinohe N, Watakabe A, Yamamori T, Yamaguchi Y (2018) The Brain/MINDS Cortical Flat Map for Visualize Neuroimaging Data. *Advances in Neuroinformatics 2018*. doi:10.14931/aini2018.ps.8

Copyright: © (2018) Gong R, Woodward A, Nakae K, Ichinohe N, Watakabe A, Yamamori T, Yamaguchi Y

Analysis of Local Excitatory-Inhibitory Balance using Whole-Brain Model based on the Common Marmoset MRI Data

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The brain function depends on the activities of excitatory and inhibitory neurons, and the balance between these connections plays an important role in the brain dynamics. Recent studies in connectome based computational brain network modeling have shown that global coupling parameter plays an important role in brain dynamics of the resting state network [1,2] but how the excitatory-inhibitory balance affects the brain dynamics is not fully explored.

Here we constructed a whole brain network model based on the structural connectivity matrix of 104 anatomical regions estimated from diffusion-weighted MRI data of common marmosets and analyzed how the functional connectivity (FC) and functional connectivity dynamics (FCD) [3] are affected by the excitatory-inhibitory balance. Through comparison of the model behaviors and resting-state MRI data, we found that the correlation between simulated and empirical FC was improved by tuning the balanced of local excitatory-inhibitory connections and that high fittings were obtained with the similar parameter regions for both FC and FCD fitting. We conclude that the balance between local excitatory and inhibitory connections has similar effects on the mean spatial structure and the temporal structure of those spatial correlation in the resting state activity.

Acknowledgements

This work was supported by the program for Brain Mapping by Integrated Neurotechnologies for Disease Studies (Brain/MINDS) from Japan Agency for Medical Research and Development, AMED.

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Citation: Tsukada H, Hamada H, Gutierrez CE, Nakae K, Skibbe H, Ishii S, Woodward A, Hata J, Okano H, Doya K (2018) Analysis of Local Excitatory-Inhibitory Balance using Whole-Brain Model based on the Common Marmoset MRI Data. *Advances in Neuroinformatics* 2018. doi:10.14931/aini2018.ps.9

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MarmU-Net: Axon tracer signal detection using an artificial neural network

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Understanding the connectivity in the brain is an important prerequisite for understanding how the brain processes information. Recent connectivity studies on vertebrate brains used two-photon microscopy fluorescence images of axonal projections to collect the neuron connectivity from defined brain regions at the mesoscopic scale [1,2]. The processing of the images requires the detection and segmentation of the axonal tracer signal. In [1,2], the signal segmentation is based on manually defined features and parameters. This is difficult because there is a trade-off between the detection of as much tracer signal as possible while not misclassifying other background structures as signal. Imaging noise, a cluttered image background, distortions or varying image contrast make problems. We propose to solve this problem using state-of-the-art machine learning techniques. We use MarmU-Net, an artificial neural network based on the U-net architecture [3] to detect the tracer signal in two-photon microscopy fluorescence images of the marmoset brain, and we demonstrate its advantage over standard segmentation approaches.

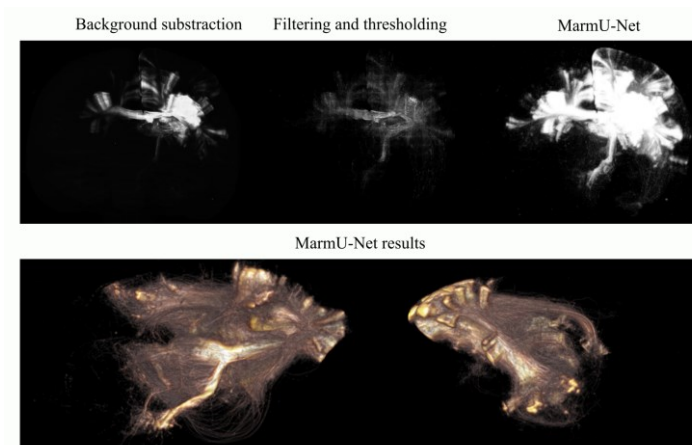


Figure1: MarmU-Net compared to background subtraction and axon filter based tracer detection

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Non-asymptotic analysis of Fisher information matrices of Multi-layer perceptron, ResNet, and Batch-normalization

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This study analyzes the Fisher information matrices of multi-layer perceptron, ResNet, and batch-normalization by applying functional analysis to the above neural networks with random weights.

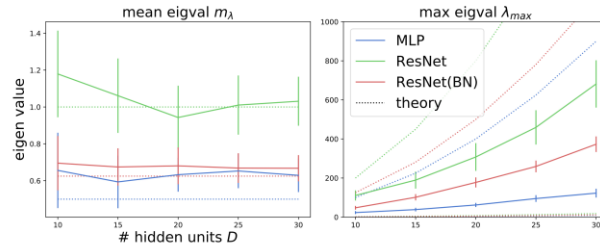
We theoretically find three interesting results which show how the architecture of the above neural networks affects the eigenvalues of the Fisher information matrix.

The first result is regarding the effect of the number of units in the hidden layer. Mean of the eigenvalues is independent of the number of the hidden units. However, the maximum eigenvalue grows with the square of it. This implies the loss landscape is locally flat in most dimensions but strongly steep in the other directions.

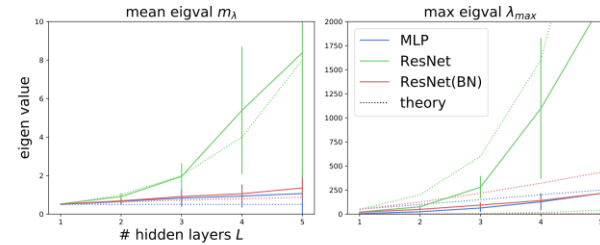
The second result is regarding the effect of skip-connection in ResNet. The eigenvalues of multi-layer perceptron are independent of its depth. On the contrary, the skip-connection in ResNet makes the eigenvalues grow exponentially with its depth. This implies training deep ResNet is difficult compared with multi-layer perceptron due to its steep loss landscape.

The last result is the effect of batch-normalization. Batch-normalization changes the exponential dependence of the depth of ResNet on the eigenvalues into at most the linear dependence. This implies batch-normalization makes training ResNet easy.

□ Eigenvalues of neural nets with different width D



□ Eigenvalues of neural nets with different depth L



* dot lines in right figures are upper bound and lower bound.

Figure1: Theoretical results (dot lines) and simulation results (bold lines) of the eigenvalues of the Fisher information matrices of multi-layer perceptron, ResNet, and ResNet with batch-normalization.

Acknowledgements

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Postural and beta-band electroencephalogram responses to floor-surface perturbations during human quiet standing

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Human posture control is one of the simplest motor functions performed by the central nervous system, providing foundations for a variety of motions. Traditionally, it has been considered that the upright stance is stabilized asymptotically by a rigidity of the anti-gravity muscles and tendon with a help of stretch reflexes, which can be modeled simply by a conventional proportional-derivative (PD) controller. However, Loram et al. (2004) observed novel muscle dynamics, which cannot be explained by the PD controller, in the calf muscles during quiet stance using an ultrasonic imaging, and they suggested an involvement of a sophisticated active neural control. In order to unravel such mechanisms for the postural control, mathematical models in recent years attempt to stabilize an inverted pendulum as a model of standing body, while exhibiting joint flexibility and postural sway patterns characterized by the power law scaling behavior (Asai et al. 2005). An alternative approach that we take in this study to understanding neural control during upright stance is to clarify neural activity of the brain during standing. We measured postural sway and electroencephalogram (EEG) simultaneously during quiet stance with floor-surface perturbations and computed event-related spectral perturbation (ERSP). We found that beta band power decreased immediately after the perturbation and then increased in one-two seconds. We hypothesized that the increase in the beta band power in the latest phase of the postural response reflects an active neural information processing to determine whether an active muscular force generation should be suppressed or not to maintain the postural stability. This hypothesis might be examined in our future work by the use of transcranial alternating-current stimulation (tcAC), according to Pogosyan et al. (2009) that showed a relationship between beta synchrony and movement suppression by a well-timed tcAC stimulation with the beta band.

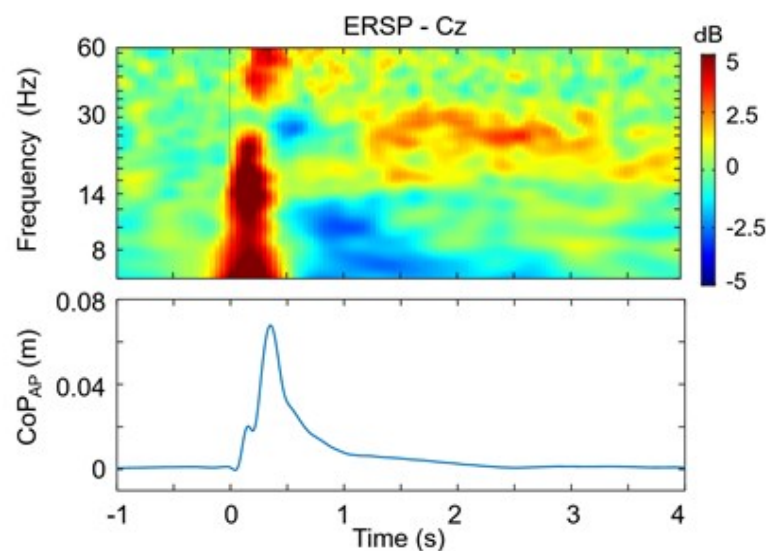


Figure1: ERSP and CoP. Perturbations were applied at 0 s. Power of beta band (13-30 Hz) decreased around 0-1s and then increased after that.

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Citation: Nakamura A, Suzuki Y, Nomura T (2018) Postural and beta-band electroencephalogram responses to floor-surface perturbations during human quiet standing. *Advances in Neuroinformatics 2018*. doi:10.14931/aini2018.ps.12

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New release of cerebellar platform

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Recently, we can easily get more information from big data on the world wide web system. However, it takes too long time to find precise information. Moreover, it is difficult to get information from all journal papers. We extended activities of the cerebellar platform (<https://cerebellum.neuroinf.jp>) providing simulations of theoretical models by using simulation platform, and database system including source code of theoretical models, images obtained from experiments, and references. The extended cerebellar platform (<https://pf.cerebellum.neuroinf.jp>) provides you with the newest information for the cerebellum easily and quickly by automatic collection of journal papers. Especially, developed mobile app service of the extended cerebellar platform, which you can download on the Apple Store and the Google Play, automatically inform you of the newest paper information in which you are interested. The extend cerebellar platform also helps users collaborate with each other by using comment system on a page of paper details. In future, it is possible to provide arranged experimental data and analyze them by using a cloud system on the cerebellar platform (e.g. a quantitative evaluation of motor functions of cerebellar patients).

Citation: Honda T, Nagao S, Yamazaki T, Hirata Y, Yamaguchi Y, Kakei S (2018) New release of cerebellar platform. *Advances in Neuroinformatics* 2018. doi:10.14931/aini2018.ps.13

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Brain/MINDS Database System Design for Large-Scale Dataset Registration, Sharing and Publication.

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The goal of the Brain/MINDS database is to integrate structural and functional data of the common marmoset brain obtained from the research groups participating in the Brain/MINDS project. We started development of a central server system to provide this database, "SAKI", in 2014 to realize smooth sharing, analysis and publication of big and heterogeneous datasets over the internet and between groups at the core institute (RIKEN) and also at external organizations. SAKI consists of a large-scale shared storage (1.2 Petabytes), a research portal for registering and sharing data in the database, servers providing analysis tools, a HPC cluster and an open access data portal. The HPC cluster can access the LSSS storage and provides computational resources for data analysis. The design of the Brain/MINDS database aims to follow the FAIR principles (Findable, Accessible, Interoperative, and Reusable). To promote this we recently developed command line tools for data registration, sharing and publication.

The Research Portal has a web user interface for registering, sharing and publishing data intuitively. However, this interface is not appropriate for processing multiple datasets at once. In order to lighten user workload we developed a command line tool for multiple data registration, sharing and publication. The architecture is shown in Figure 1.

This tool provides for large-scale data sharing amongst groups in just a few steps. Firstly, a user puts a number of datasets on the LSSS. Each dataset is in a separate directory with metadata described in a JSON file. Secondly, in a setting file, the user describes the list of directories that they want to share, and the target groups for each directory. Finally, the user runs a command line tool to share those datasets.

Thus, SAKI is ready for big data operation. This tool will be used for data publication of around 10^3 individual data items on the Data Portal in the near future.

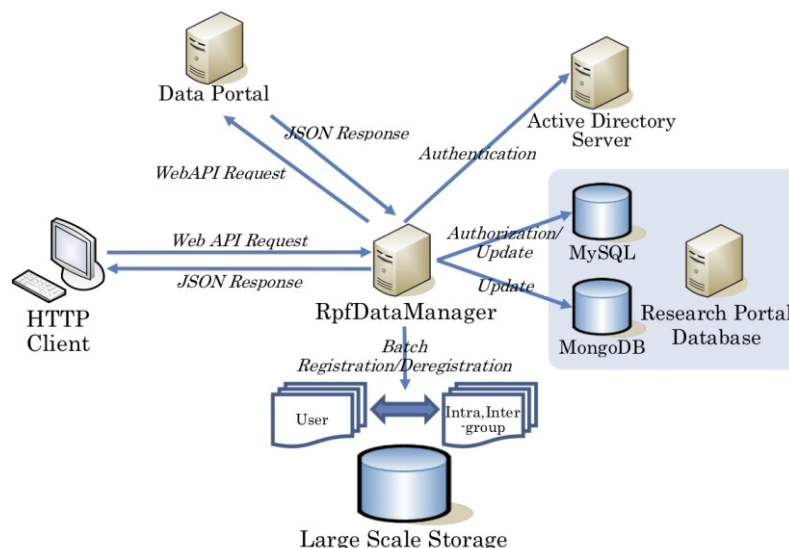


Figure1: architecture of the command line tool

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Spiking neural network model of the basal ganglia with realistic topological organization

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We previously built a biologically plausible spiking neural network model of the basal ganglia (BG) and reproduced resting state firing and action selection properties [Liénard et al., 2018 (SBDM/SfN)]. Here we introduced realistic topological organization of the BG circuit into the model using NEST [Gewaltig and Diesmann, 2007] and ran simulation using hybrid parallelization approach on K supercomputer [Miyazaki et al., 2012]. The topological model reproduced the basic firing rates and action selection properties. We further connect the BG model with topological models of the thalamus and the cortex to investigate of the closed loop dynamics of the BG-thalamo-cortical circuit. We are also testing their scaling properties on highly parallel computing nodes.

Citation: Gutierrez C, Liénard J, Girard B, Igarashi J, Doya K (2018) Spiking neural network model of the basal ganglia with realistic topological organization. *Advances in Neuroinformatics 2018*. doi:10.14931/aini2018.ps.15

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The Conductance-based model for neurons in the olfactory circuit of *Bombyx mori*

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Many computational models of neuronal activities have been suggested to understand the behaviors of neurons quantitatively. Among them, the conductance-based models consider neurons as equivalent electrical circuits with time-varying resistances and show high reproducibility for various neuronal phenomena [1]. However, their complexity makes model estimation from experimental data a challenging problem [1].

We constructed conductance-based models of neurons in the olfactory system of *Bombyx mori*. Detailed electrophysiological data [2] enabled us to obtain more realistic models for neurons. A neurons collective behavior is determined by channels in its cell membrane. From voltage clamp data [2], parameters which control channel kinetics have been computed. Based on these parameters, we estimated residual parameters such as the density for each channel type from current clamp data. The models constructed in this project will help us to understand biophysical properties of neurons in the olfactory system of *Bombyx mori* and enable large-scale simulations of a generic model insect brain.

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We are indepted to M. Tabuchi and K. Nakatani whose physiological data were used for fitting.

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Construction of functional hypothesis about brain local circuit by integrating neuroscientific knowledge as a framework

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Hypothesis on a computational function corresponding to structure of neural circuits are needed to use neuroscientific knowledge as reference of a human-level artificial intelligence. Potentially, there exist enough knowledge to narrow down the hypothesis of computational functions about some local circuits. Because of too rapid knowledge accumulation, efforts to build that kind of hypothesis tend to be postponed.

Under such circumstances, we aim to develop a method and an open platform to improve understanding of neural circuit function through integrating neuroscientific data of several modality. As a preliminary step toward that, in this poster, we build a framework of the entorhinal cortex(EC), the gateway of information flow of the hippocampus. This framework integrates the existing neuroanatomical knowledge of hippocampus and medial entorhinal cortex (MEC) and arrange the network structure of them.

Then, we also propose a computational hypothesis about the path integration (PI). PI is a computational mechanism which estimate current position in the metric space by integrating information of past position and that of movement of the animal. As a kind of grid cells, every layers of MEC contains spatial representations with metric, which is necessary for the PI calculation. Here, we identify the type of neuron which execute the PI calculation and the layer in which these cells exist.

By referring EC framework structure, we propose that stellate cells in MEC2 and pyramidal cells in MEC3 would be candidates to perform PI calculation. Then, considering the fact that place cells projected from grid cells in MEC2 exist in DG/CA3 in the hippocampus, stellate cells in MEC2 projecting to DG/CA3 would be more plausible to compute PI. Additionally, MEC2 receives the theta rhythm projection from the medial septum to adjust the timing of current position input from the postrhinal cortex. This also supports the idea that the stellate cells in MEC2 compute PI.

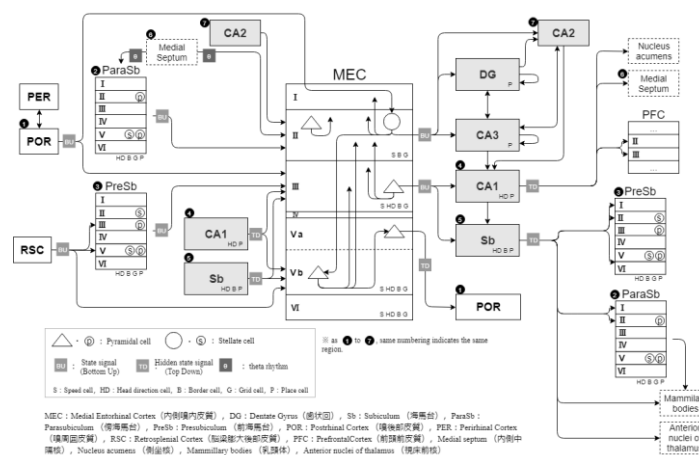


Figure1: Framework of the entorhinal cortex

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Creating real scale simulation model of optic lobe based on *Drosophila*'s neural information

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An optic lobe of *Drosophila* has been surveyed to know a neural mechanism of biological motion recognition. Today many mathematical models based on circuits of *Drosophila* optic lobe were suggested, and some electro-physiological characteristics of the cell of optic lobe were revealed. However, how *Drosophila* deal with multiple visual situation of the nature with at most thousands of ommatidium is still incompletely understood. Recently, research about creating large scale simulation model using neural information as it is has increased, with the progression of research about neural network and the ascertainment of the optic lobe connectome.

Then, we tried to uncover the mechanisms of *Drosophila*'s optical robustness with simulation approach. We devised real scale simulation model of *Drosophila*'s optic lobe with NEURON Simulator, modulated neural parameters so that the model reproduce the neural characteristics of the retinal receptor neuron, lamina monopolar neuron and T4 cells in lobula, and measured electrical response to motion stimuli with changing neural parameters of electro-physiologically unknown cells.

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Simulation for Simplified Neural Network Model of Structures Within an Olfactory Sensory Unit for Nestmate and Non-nestmate Discrimination in the Japanese Carpenter Ant

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Ants are known to use a colony-specific blend of cuticular hydrocarbons (CHCs) as a pheromone to discriminate between nestmates and non-nestmates. Recent experimental study showed that more than 100 unbranched dendritic processes of olfactory receptor neurons (ORNs) have characteristic beaded structure [1]. At beads, the cell membranes of the dendritic processes were closely adjacent in the interdigitated profiles, suggesting functional electrical interactions between dendritic processes via gap junctions in ORNs.

In this study, we perform numerical simulations based on the cable theory in order to investigate the role of gap junctions between cables. We consider a multi-compartment model consisting of multiple cables with mutual connections via gap junctions; each cable is assumed to consist of serially connected multiple compartments. When an input current is given to the most distal compartment of cable, the inward current passively propagate along the stimulated cables. The most proximal compartment can generate impulses, only when the inward current is larger than a threshold at the impulse generating site. By introducing various patterns of gap junctions between cables, we numerically investigate the effect of mutual electrical connections between dendritic processes on impulse generation.

By numerical simulations, we find that the number of impulses tends to increase when gap junctions are concentrated on the distal part. In contrast, the number of impulses tends to decrease when gap junctions are concentrated on the proximal part. Namely, we find that gap junctions between cables have a functional role in controlling the generation of impulses. Furthermore, these simulated results suggest that a neural network within an olfactory receptor unit contributes to the distinct discrimination of colony-specific blends of CHCs or other odor detection.

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Spatial property of excitation and inhibition in a spatial neural network of the rodent primary somatosensory cortex

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Spatial organization of connections in the neocortex is considered to work as an information processing device. However, it remains unknown how different types of connections with different spatial extent work for sensory processing in the primary somatosensory cortex (S1). We developed a spatial spiking neural network model of the S1 based on anatomical and electrophysiological data of rodents.

The S1 model comprised 7 layers (L1: 2 inhibitory neuron types; L2 and L3: 3 inhibitory and 1 excitatory neuron types; L4, L5A, L5B & L6: 2 inhibitory and 1 excitatory neuron types). We used the layer thicknesses and the cell densities of the mouse's S1 data. Leaky integrate-and-fire neuron model was used for all neuron types. We used the information of spatial extents, probabilities, and connectivity from the reports of laser-scanning photostimulation (LSPS) experiments and patch clamp recordings. We used Gaussian functions for the connection probability function of a horizontal distance between two neurons. We made a virtual slice of the S1 whose shape was a cube of 1400 x 400 x 1400 micron.

We first performed virtual LSPS experiments for excitatory and inhibitory connections to all neuron types. The responses of neurons to LSPS were qualitatively similar to those in the LSPS experiments.

Next, to investigate the relation between excitatory and inhibitory signals, we compared the excitatory and inhibitory conductance with changing distances between simulation site and positions of recorded neurons. The excitatory and inhibitory synaptic conductance of L2/3 and L5 excitatory neurons similarly decayed with increasing in the horizontal distance between stimulation sites and positions of recorded neurons, which is similar to real experimental results. These results suggest that spatial extents of different connections may cause spatially coupled excitation and inhibition in L2/3 and L5A, which may lead to cooperative information processing by excitation and inhibition.

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